Full wwPDB X-ray Structure Validation Report ⓘ

Mar 23, 2026 – 06:47 PM UTC

PDB ID	:	5DGV / pdb_00005dgv
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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

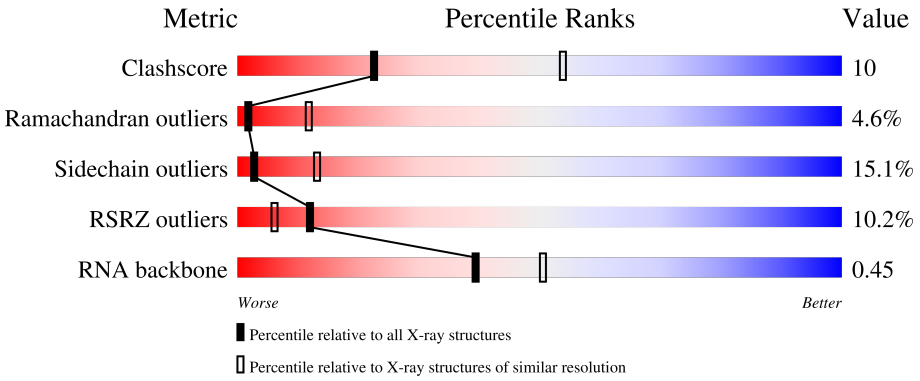
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal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

1 Overall quality at a glance (i)

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	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)
RNA backbone	3983	1022 (3.32-2.88)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	7% 48% 39% 12%
1	6	1800	5% 51% 37% 11%
2	S0	251	29% 45% 33% 18%
2	s0	251	14% 41% 35% 6% 18%

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Mol	Chain	Length	Quality of chain
3	S1	254	39% 35% 38% 9% 16%
3	s1	254	7% 44% 33% 7% 15%
4	S2	253	12% 48% 34% 14%
4	s2	253	9% 50% 27% 7% 14%
5	S3	239	13% 61% 27% 5% 7%
5	s3	239	20% 57% 28% 7% 7%
6	S4	260	12% 54% 37% 9%
6	s4	260	10% 59% 34% 6%
7	S5	224	32% 65% 22% 5% 8%
7	s5	224	30% 53% 31% 8% 8%
8	S6	236	32% 57% 34% 5%
8	s6	236	18% 56% 28% 8% 8%
9	S7	189	38% 55% 32% 10%
9	s7	189	22% 63% 30%
10	S8	200	10% 60% 26% 7% 6%
10	s8	200	15% 62% 28% 6%
11	S9	196	23% 56% 32% 5% 6%
11	s9	196	14% 54% 29% 11% 6%
12	C0	105	31% 53% 28% 10% 9%
12	c0	105	40% 40% 39% 10% 9%
13	C1	155	15% 71% 22% 6%
13	c1	155	14% 54% 31% 9% 6%
14	C2	142	35% 48% 32% 8% 13%
14	c2	142	49% 54% 25% 8% 13%
15	C3	150	15% 59% 33% 6%

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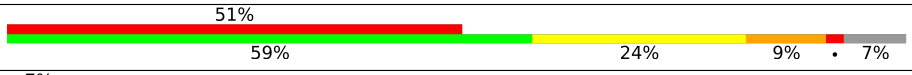
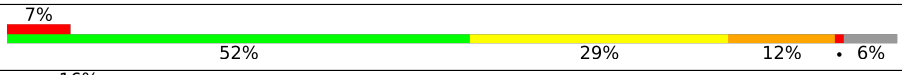
Mol	Chain	Length	Quality of chain
15	c3	150	
16	C4	136	
16	c4	136	
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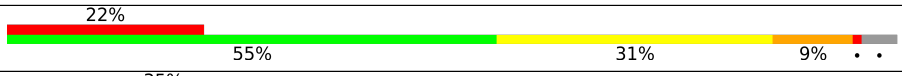
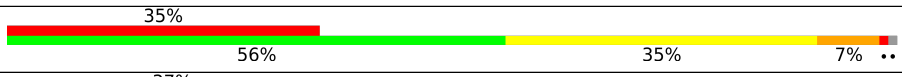
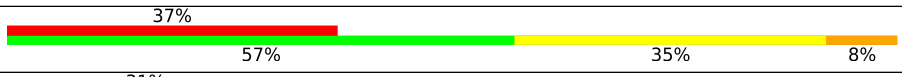
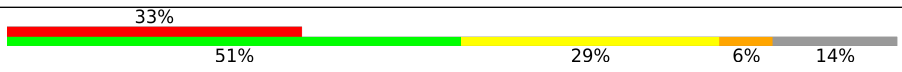
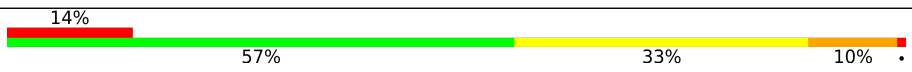
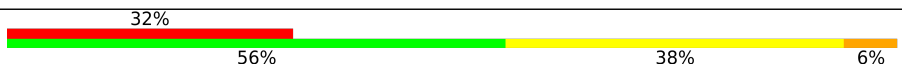
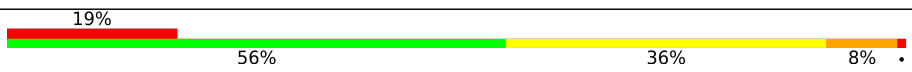
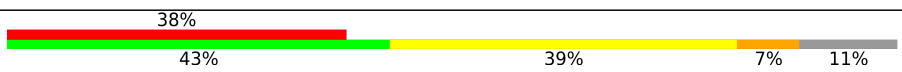
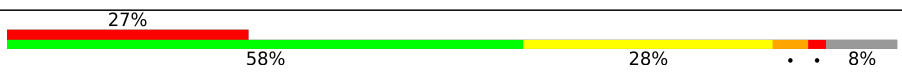
17	c5	141	
18	C6	142	
18	c6	142	
19	C7	136	
19	c7	136	
20	C8	145	
20	c8	145	
21	C9	143	
21	c9	143	
22	D0	120	
22	d0	120	
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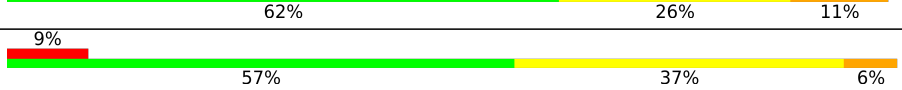
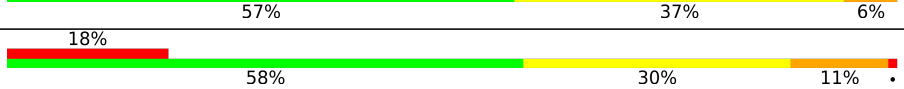
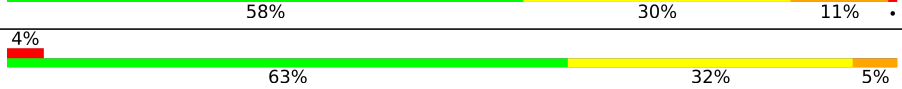
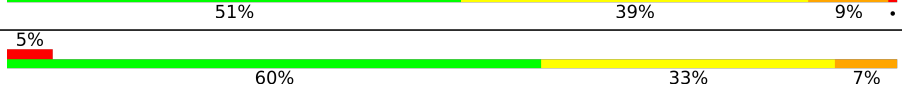
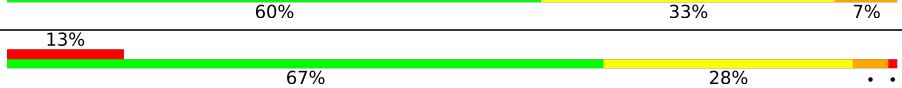
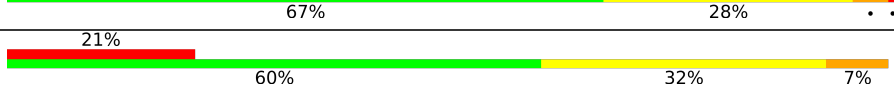
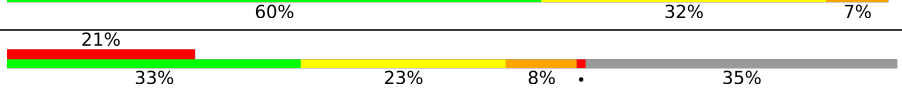
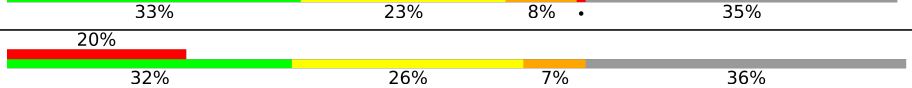
23	d1	87	
24	D2	129	
24	d2	129	
25	D3	144	
25	d3	144	
26	D4	134	
26	d4	134	
27	D5	107	
27	d5	107	

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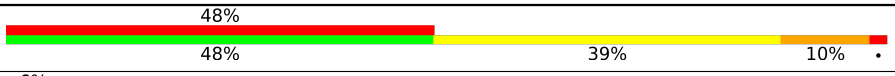
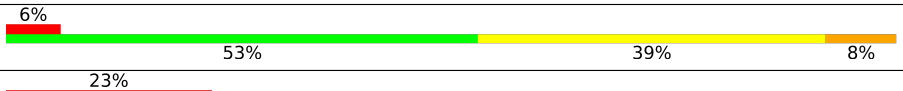
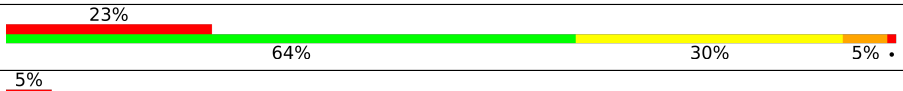
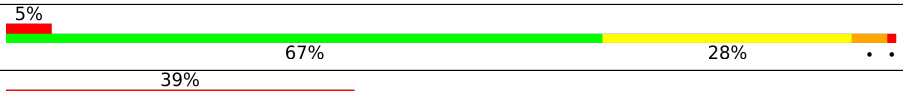
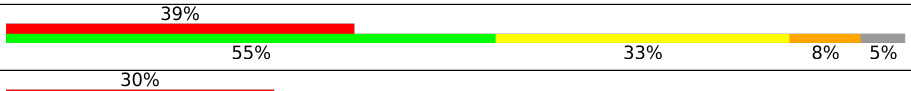
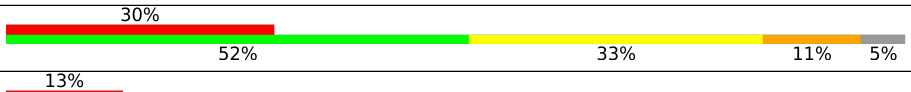
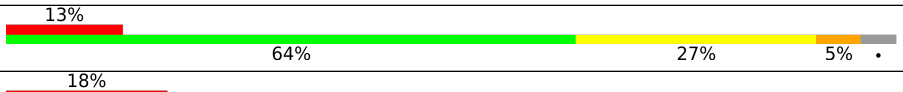
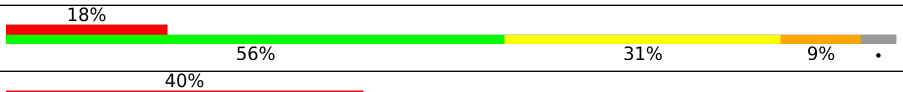
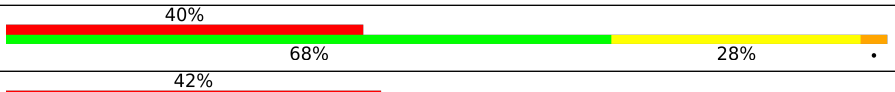
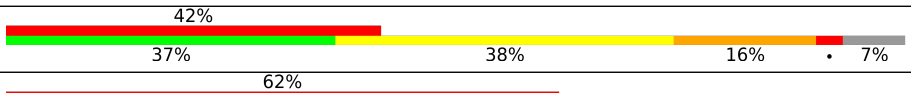
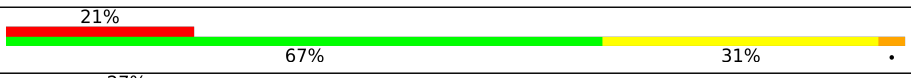
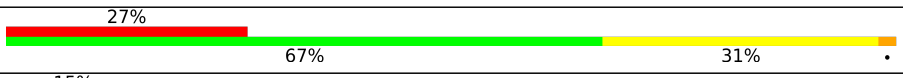
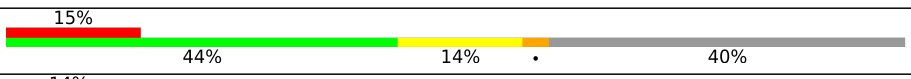
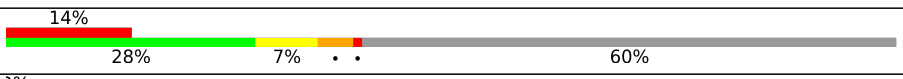
Mol	Chain	Length	Quality of chain
28	D6	97	
28	d6	97	
29	D7	81	
29	d7	81	
30	D8	66	
30	d8	66	
31	D9	55	
31	d9	55	
32	E0	60	
33	E1	76	
33	e1	76	
34	SR	318	
34	sR	318	
35	SM	263	
35	sM	263	
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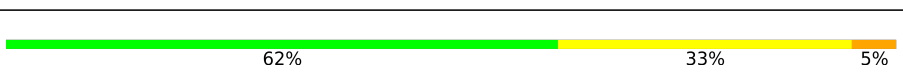
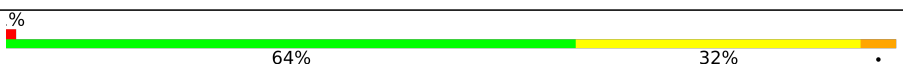
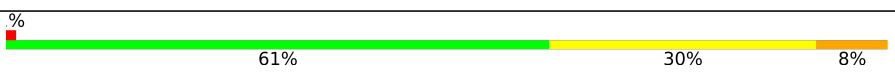
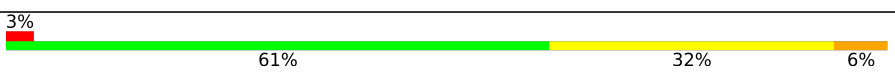
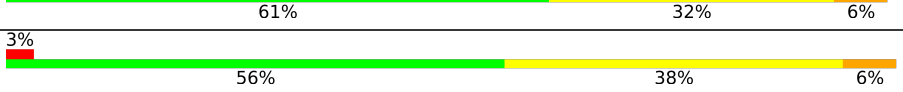
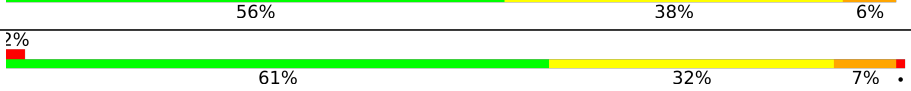
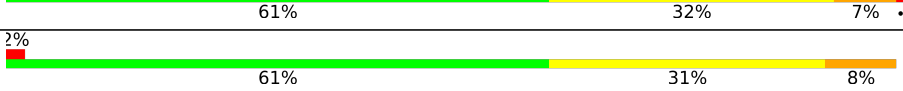
36	5	3396	
37	3	121	
37	7	121	
38	4	158	
38	8	158	
39	L2	253	
39	l2	253	
40	L3	386	
40	l3	386	

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Mol	Chain	Length	Quality of chain
41	L4	361	2% 60% 30% 10%
41	l4	361	% 61% 30% 7%
42	L5	296	6% 57% 35% 7%
42	l5	296	5% 59% 32% 7%
43	L6	175	2% 57% 26% 5% 11%
43	l6	175	5% 59% 22% 9% 10%
44	L7	243	2% 60% 21% 9% 9%
44	l7	243	62% 26% 8%
45	L8	255	8% 58% 26% 7% 9%
45	l8	255	12% 55% 29% 6% 9%
46	L9	191	3% 56% 34% 10%
46	l9	191	% 55% 35% 9%
47	M0	220	4% 51% 39% 5%
47	m0	220	5% 53% 35% 9%
48	M1	173	6% 51% 40% 6%
48	m1	173	% 61% 29% 6%
49	M3	198	4% 61% 29% 7%
49	m3	198	4% 61% 32%
50	M4	137	5% 59% 34%
50	m4	137	3% 61% 33% 5%
51	M5	203	2% 59% 36%
51	m5	203	3% 61% 34% 5%
52	M6	198	9% 69% 28%
52	m6	198	11% 61% 31% 7%
53	M7	183	9% 62% 32% 5%

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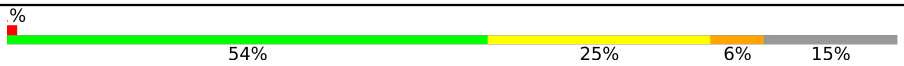
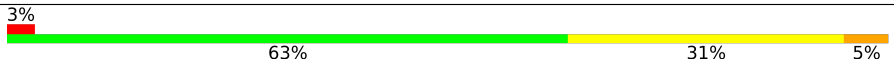
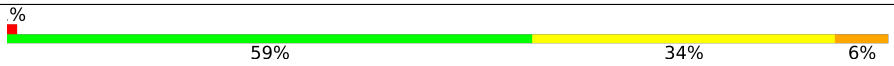
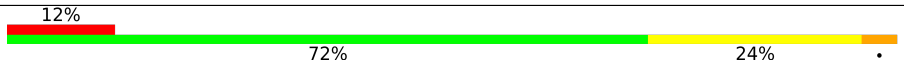
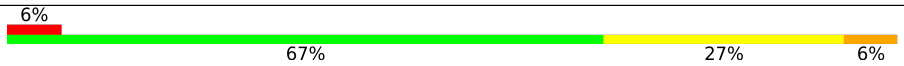
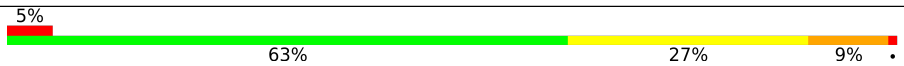
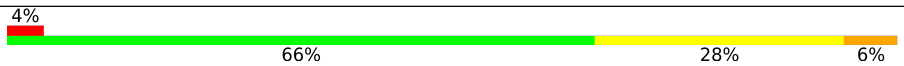
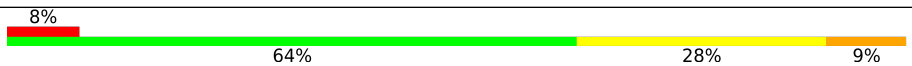
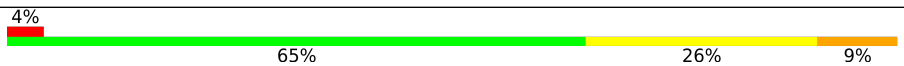
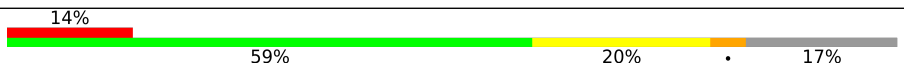
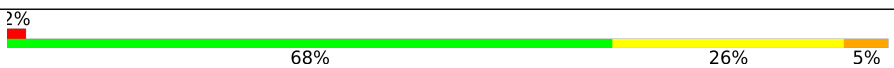
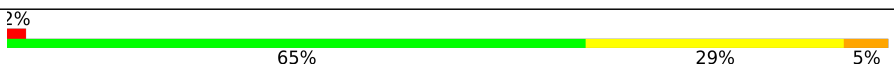
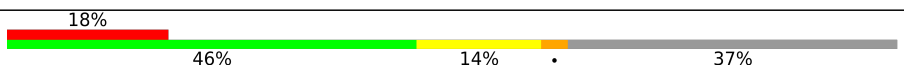
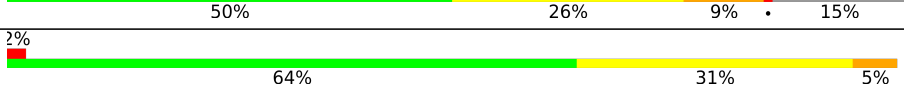
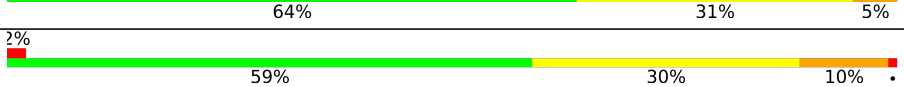
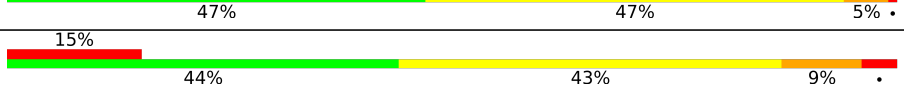
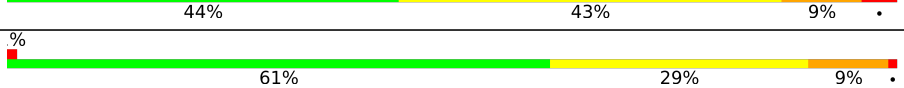
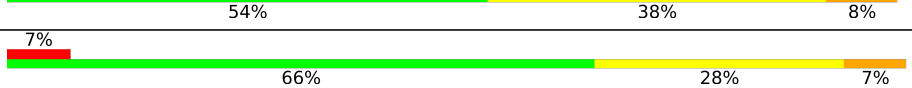
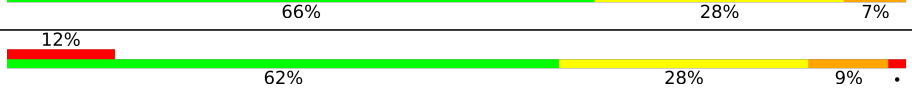
Mol	Chain	Length	Quality of chain
53	m7	183	
54	M8	185	
54	m8	185	
55	M9	188	
55	m9	188	
56	N0	172	
56	n0	172	
57	N1	159	
57	n1	159	
58	N2	120	
58	n2	120	
59	N3	136	
59	n3	136	
60	N4	155	
60	n4	155	
61	N5	141	
61	n5	141	
62	N6	126	
62	n6	126	
63	N7	135	
63	n7	135	
64	N8	148	
64	n8	148	
65	N9	58	
65	n9	58	

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Mol	Chain	Length	Quality of chain
66	O0	104	6% 56% 35% 7%
66	o0	104	7% 65% 26% 5%
67	O1	112	4% 64% 28%
67	o1	112	4% 57% 36%
68	O2	129	2% 60% 33% 5%
68	o2	129	4% 62% 29% 7%
69	O3	106	4% 62% 33% 5%
69	o3	106	2% 68% 27% 5%
70	O4	119	8% 57% 31% 5% 6%
70	o4	119	5% 58% 29% 6% 6%
71	O5	119	3% 65% 27% 8%
71	o5	119	12% 50% 38% 13%
72	O6	99	6% 56% 30% 14%
72	o6	99	2% 57% 34% 8%
73	O7	87	3% 61% 33% 6%
73	o7	87	6% 55% 36% 9%
74	O8	77	10% 48% 40% 12%
74	o8	77	10% 68% 27% 5%
75	O9	50	8% 56% 34% 10%
75	o9	50	2% 50% 38% 12%
76	Q0	52	4% 71% 23% 6%
76	q0	52	71% 25%
77	Q1	25	4% 56% 36% 8%
77	q1	25	56% 36% 8%
78	Q2	105	4% 51% 39% 10%

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Mol	Chain	Length	Quality of chain
78	q2	105	2% 65% 27% 8%
79	Q3	91	54% 41% 5%
79	q3	91	% 65% 29% 5%
80	e0	62	11% 48% 34% 16%
81	m2	160	89% 5% 6%
82	p0	311	17% 32% 12% 54%
83	p1	47	91% 9%
84	p2	46	96%
85	C	5	80% 20%
85	D	5	60% 40%

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
87	SPS	C	3401	-	X	-	-
87	SPS	D	3401	-	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	l2	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	l3	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	l4	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	l5	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	l6	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	l7	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	l8	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	l9	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	0	0	0
			796	516	131	149			
58	n2	98	Total	C	N	O	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	0	0	0
			993	625	192	176			

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

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

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

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

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

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

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

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

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

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

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

- 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	0	0	0
			612	391	115	106			
74	o8	77	Total	C	N	O	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 (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
86	D6	1	Total	Zn	0	0
			1	1		
86	D7	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	O7	1	Total	Zn	0	0
			1	1		
86	Q0	1	Total	Zn	0	0
			1	1		
86	Q2	1	Total	Zn	0	0
			1	1		
86	Q3	1	Total	Zn	0	0
			1	1		
86	d6	1	Total	Zn	0	0
			1	1		
86	d7	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	o7	1	Total	Zn	0	0
			1	1		
86	q0	1	Total	Zn	0	0
			1	1		
86	q2	1	Total	Zn	0	0
			1	1		

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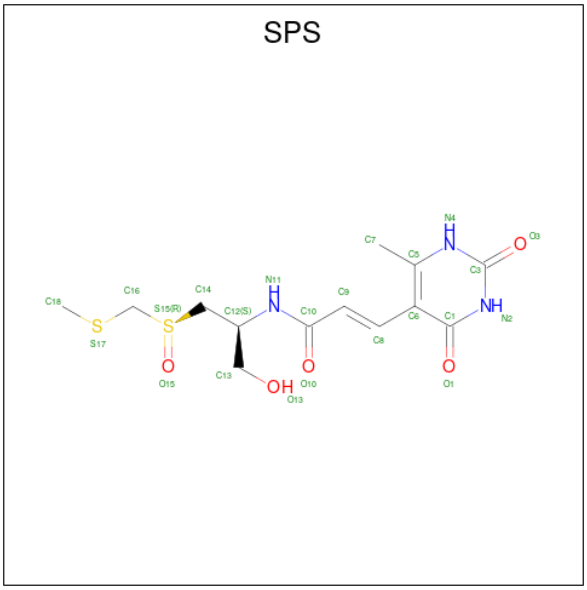
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
86	q3	1	Total Zn 1 1	0	0

- Molecule 87 is SPARSOMYCIN (CCD ID: SPS) (formula: $C_{13}H_{19}N_3O_5S_2$).



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

- Molecule 88 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

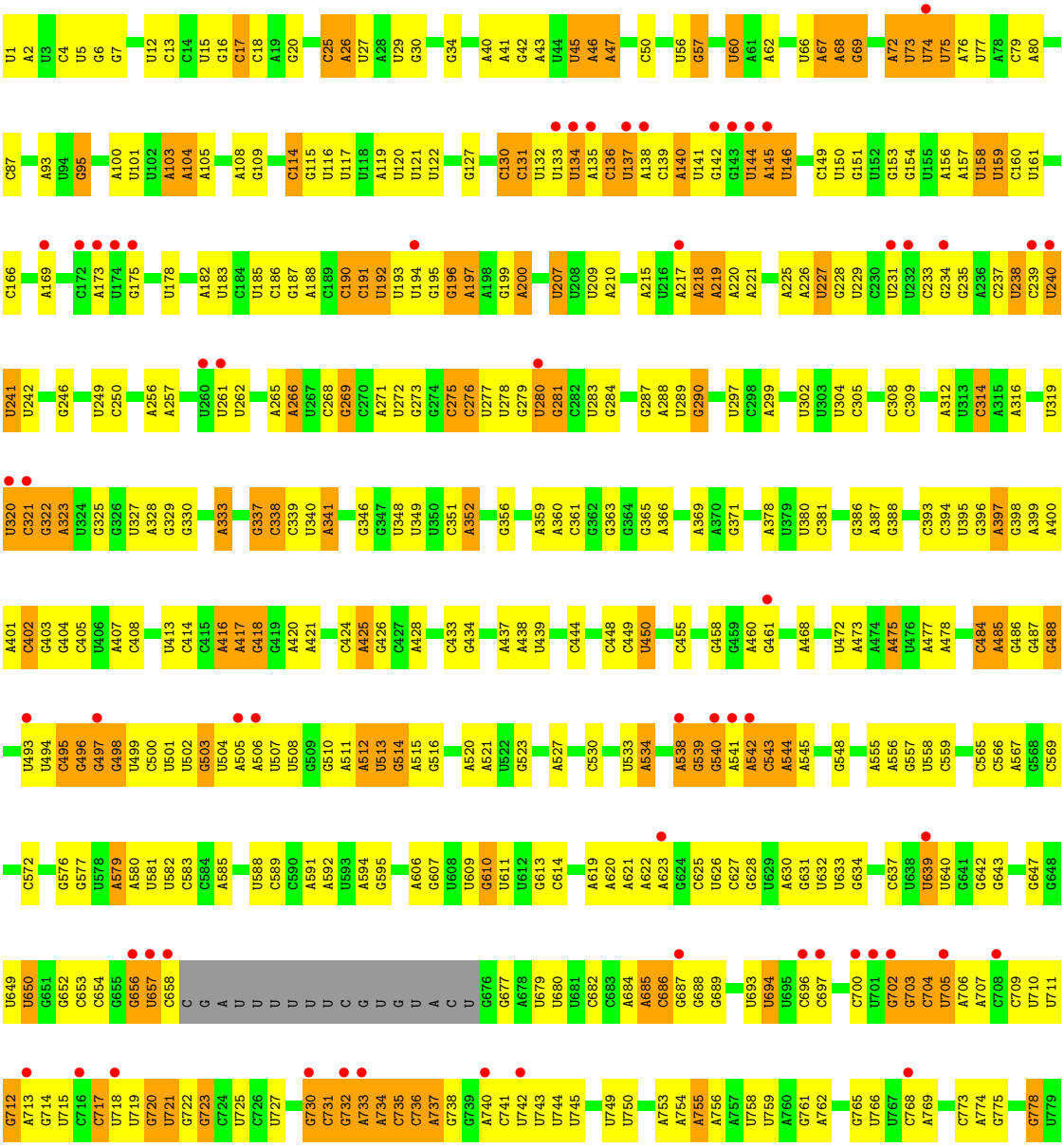
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
88	C	1	Total Mg 1 1	0	0
88	D	1	Total Mg 1 1	0	0

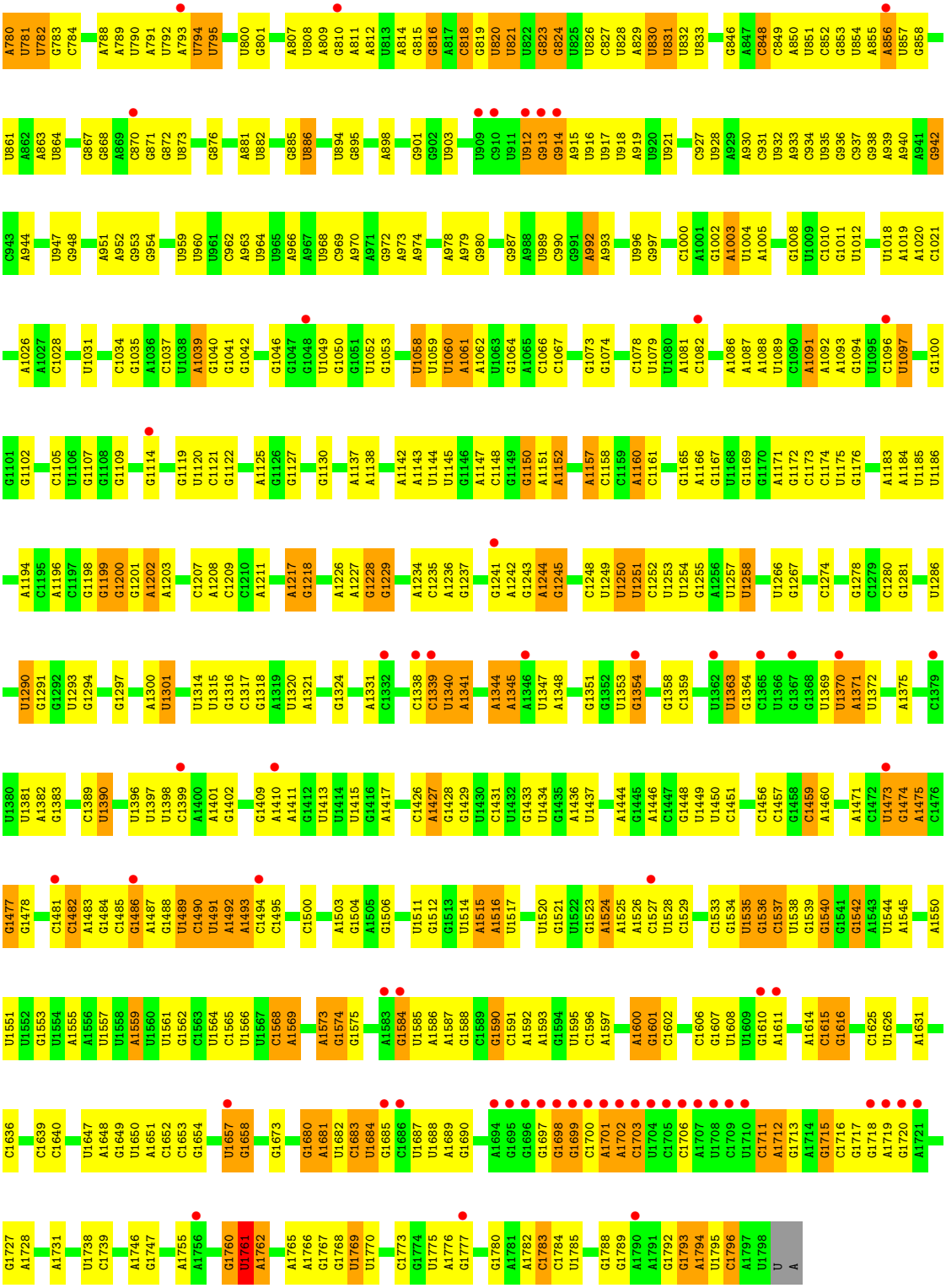
3 Residue-property plots (i)

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

• Molecule 1: Saccharomyces cerevisiae S288c RDN37-1 miscRNA

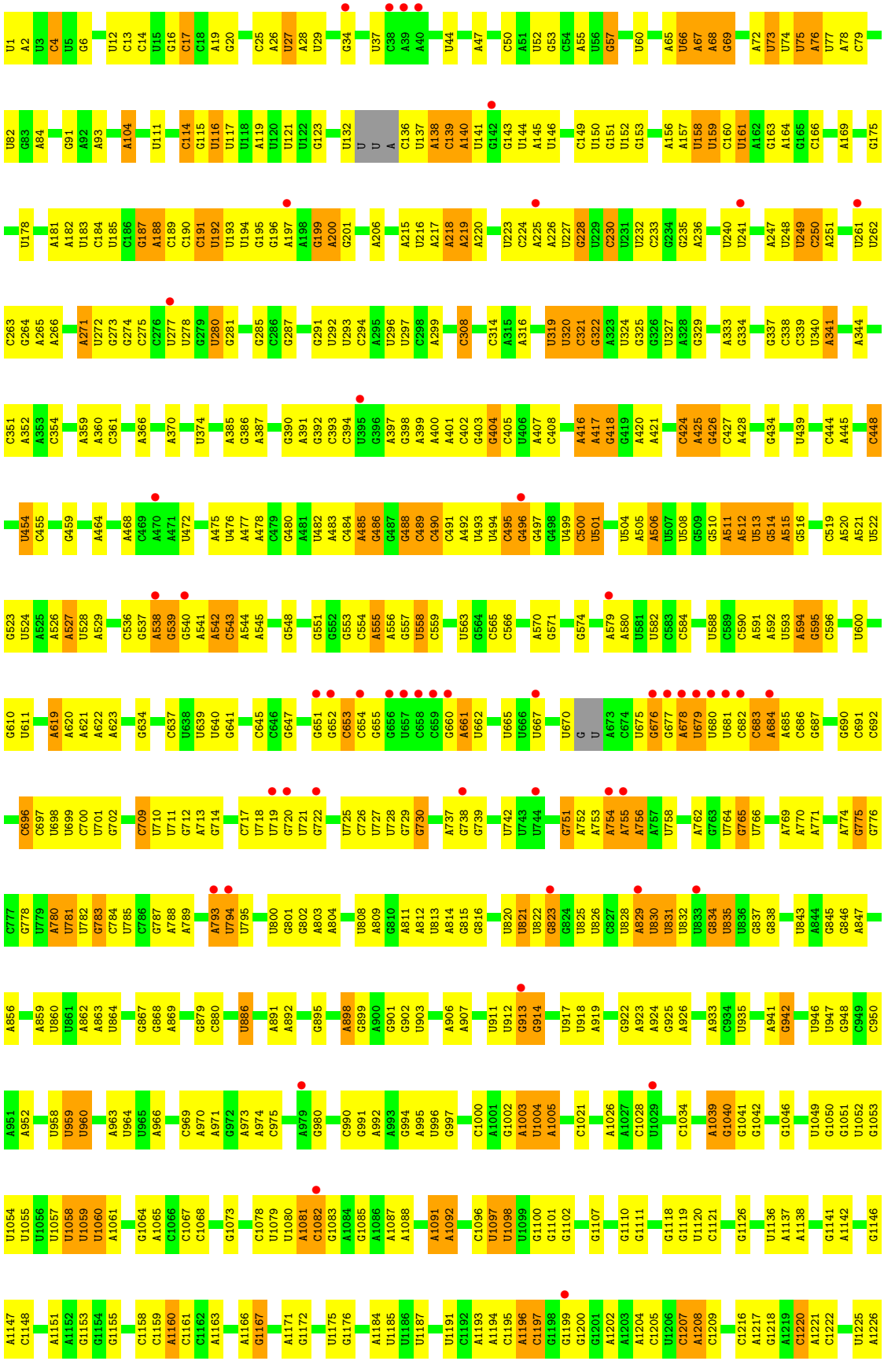
Chain 2:

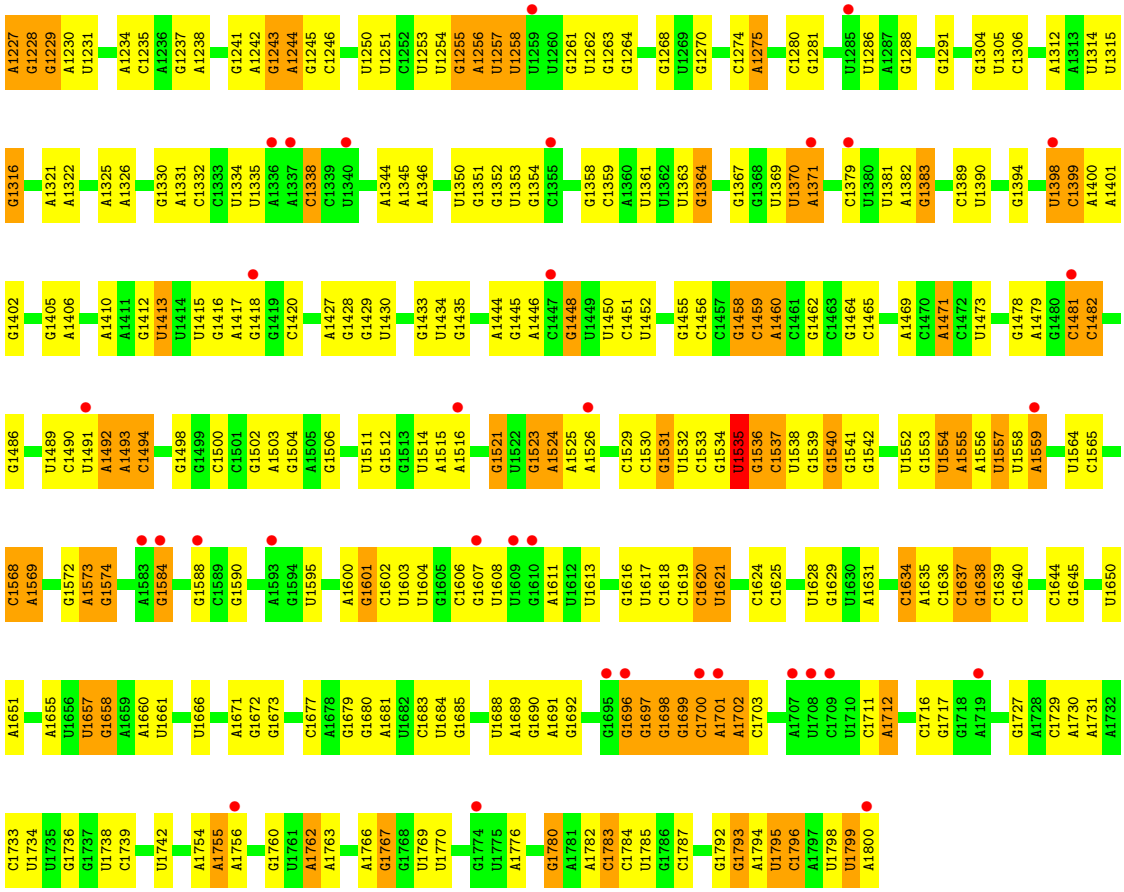




• Molecule 1: Saccharomyces cerevisiae S288c RDN37-1 miscRNA

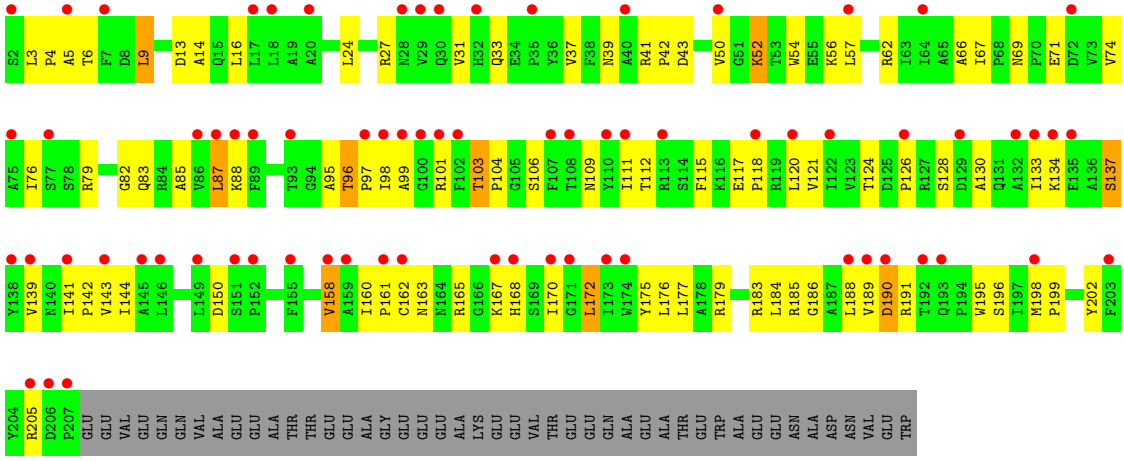
Chain 6:





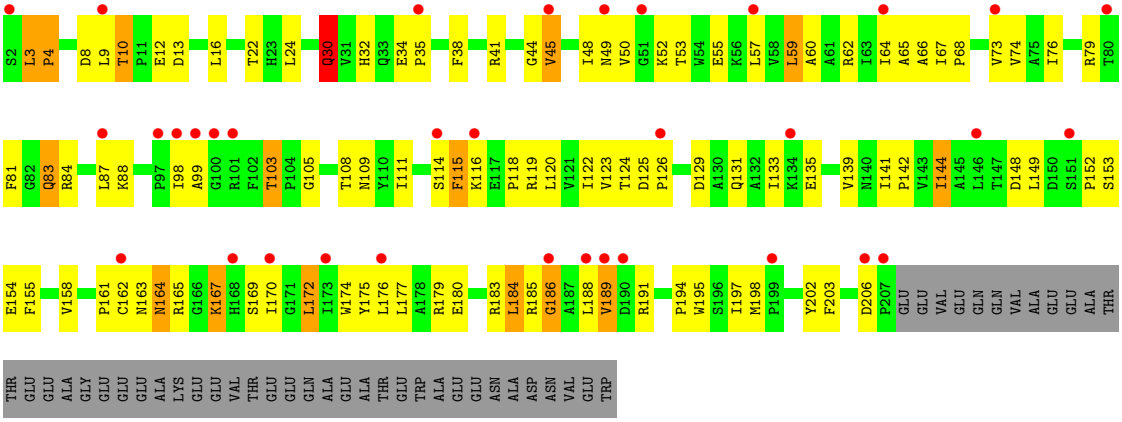
• Molecule 2: 40S ribosomal protein S0-A

Chain S0:



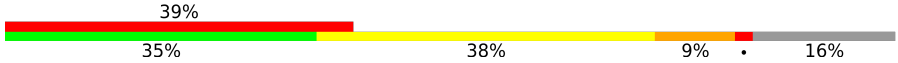
• Molecule 2: 40S ribosomal protein S0-A

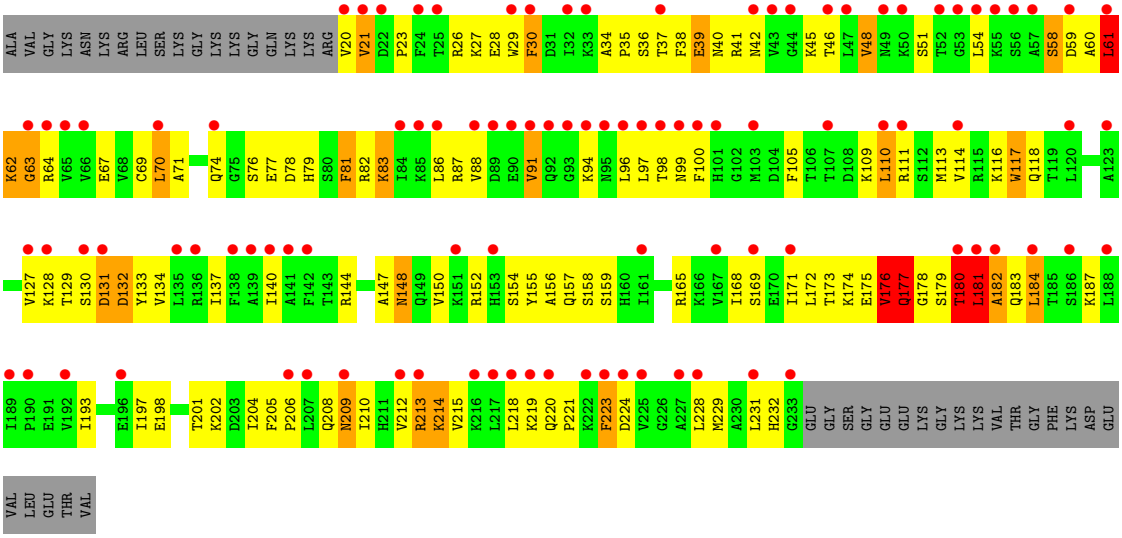
Chain s0:



• Molecule 3: 40S ribosomal protein S1-A

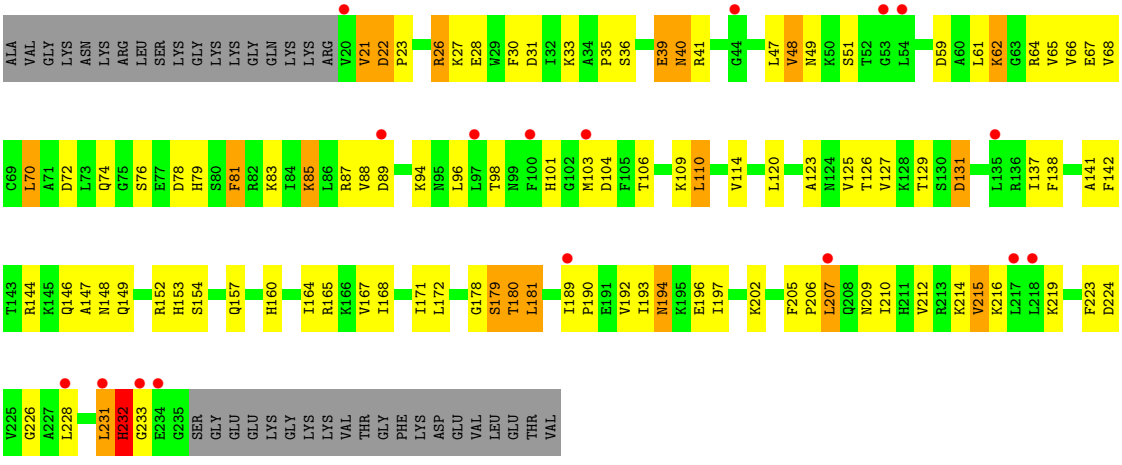
Chain S1:





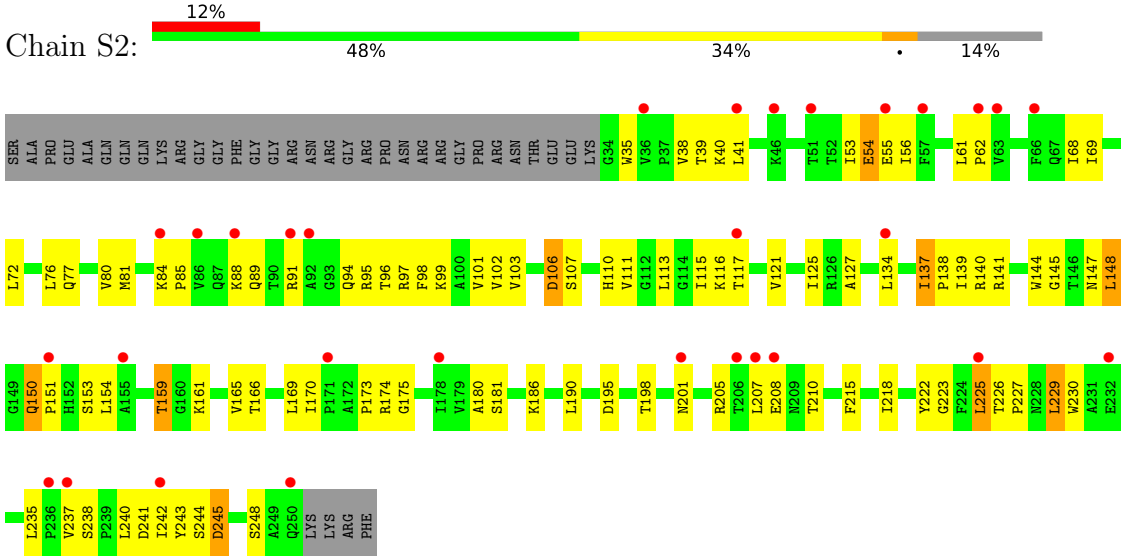
• Molecule 3: 40S ribosomal protein S1-A

Chain s1:



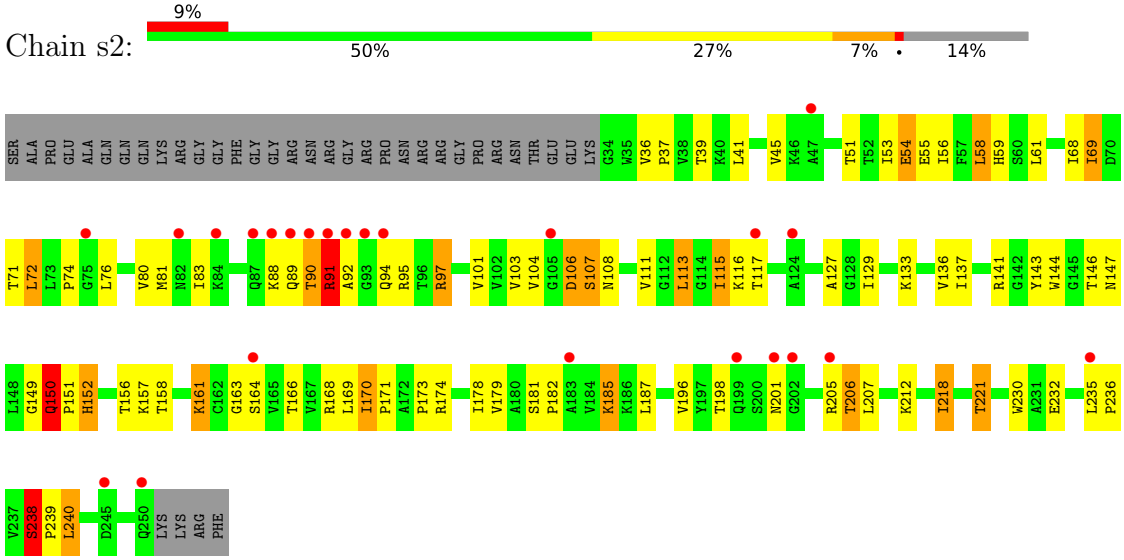
• Molecule 4: 40S ribosomal protein S2

Chain S2:



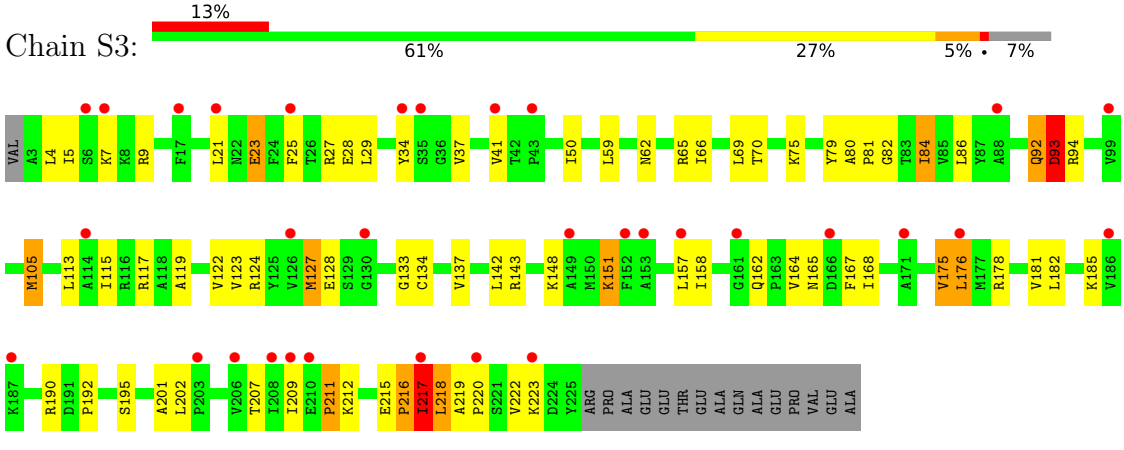
• Molecule 4: 40S ribosomal protein S2

Chain s2:



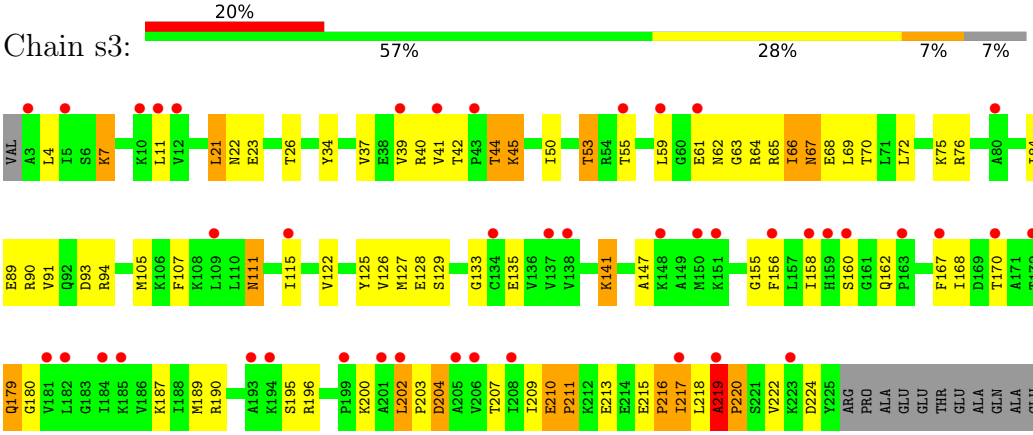
• Molecule 5: 40S ribosomal protein S3

Chain S3:



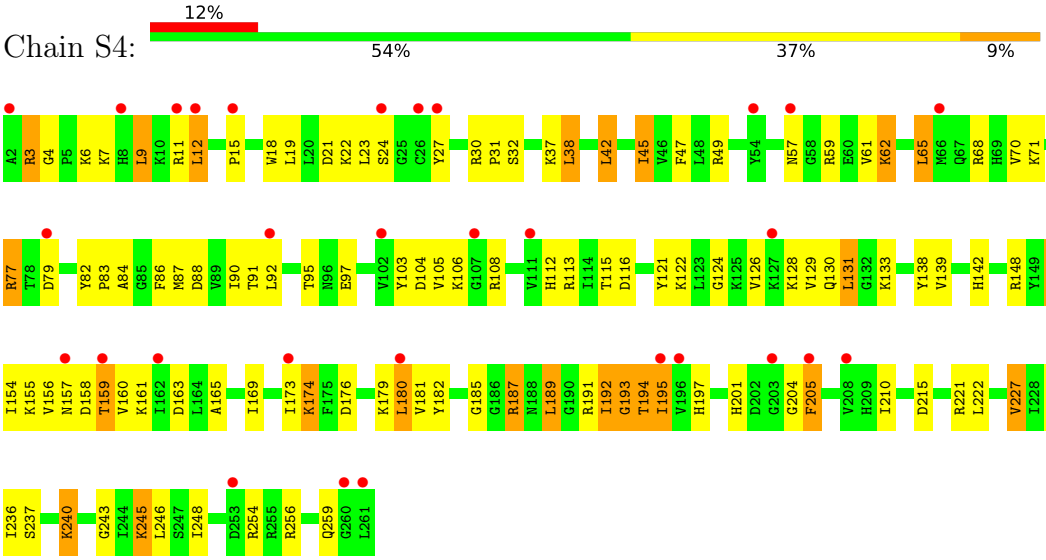
• Molecule 5: 40S ribosomal protein S3

Chain s3:



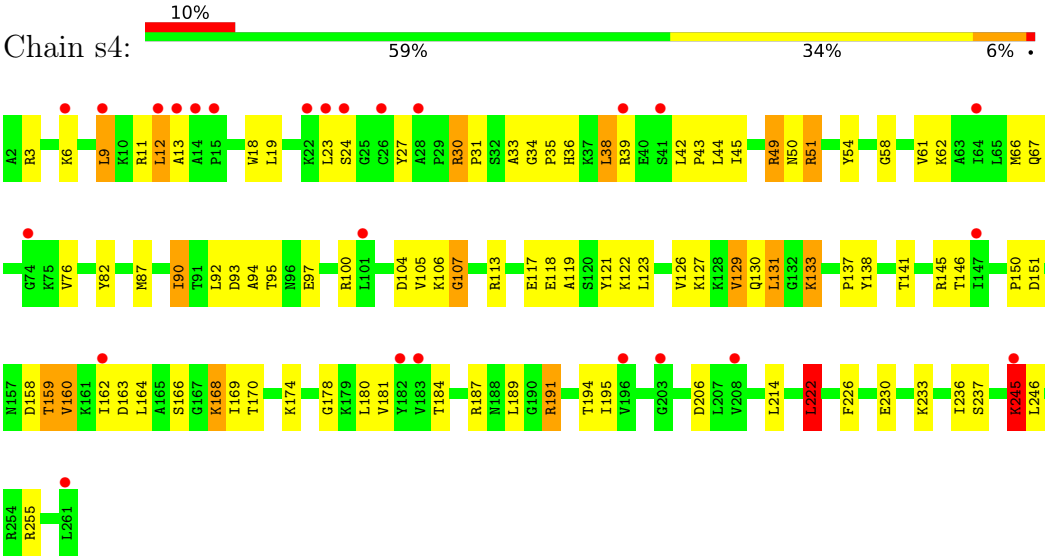
• Molecule 6: 40S ribosomal protein S4-A

Chain S4:



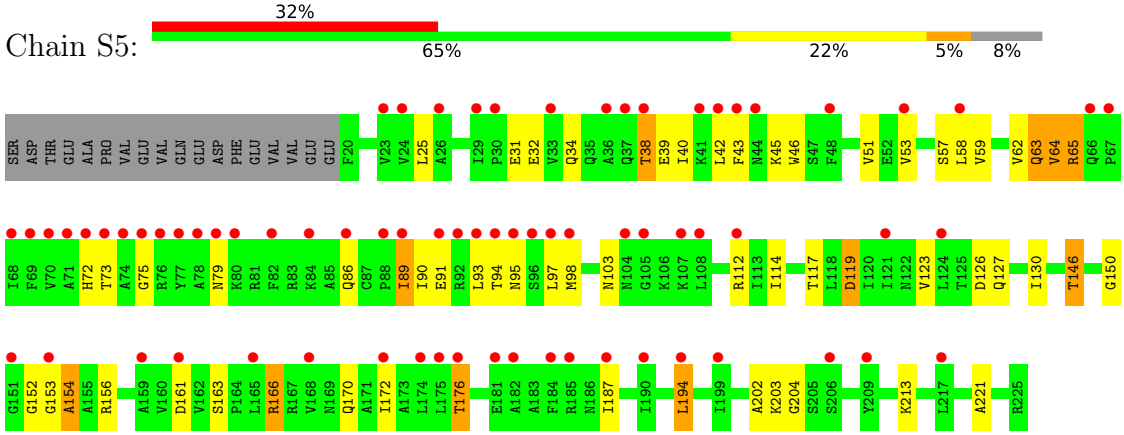
• Molecule 6: 40S ribosomal protein S4-A

Chain s4:



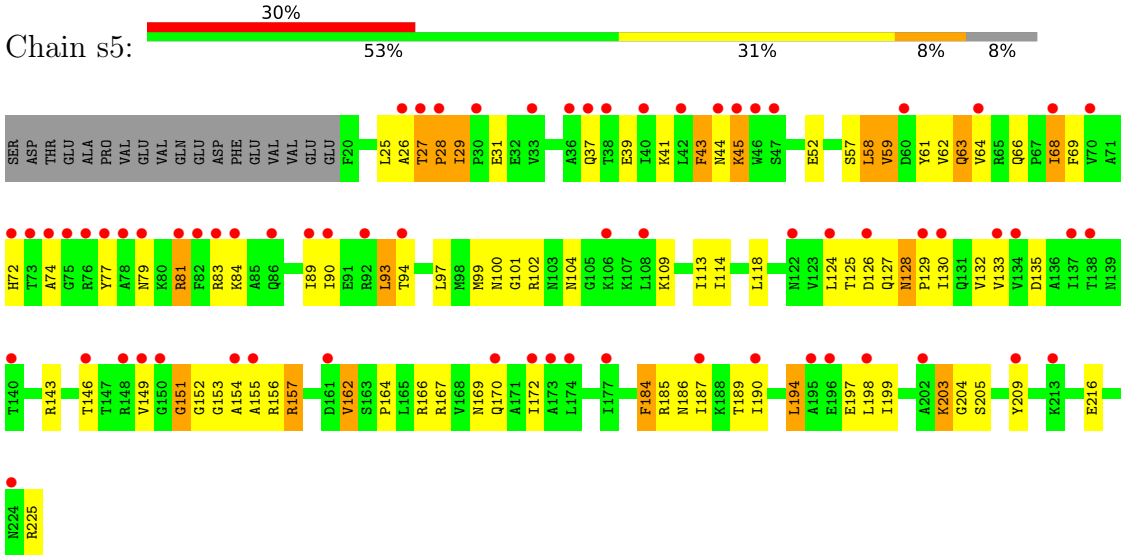
• Molecule 7: 40S ribosomal protein S5

Chain S5:



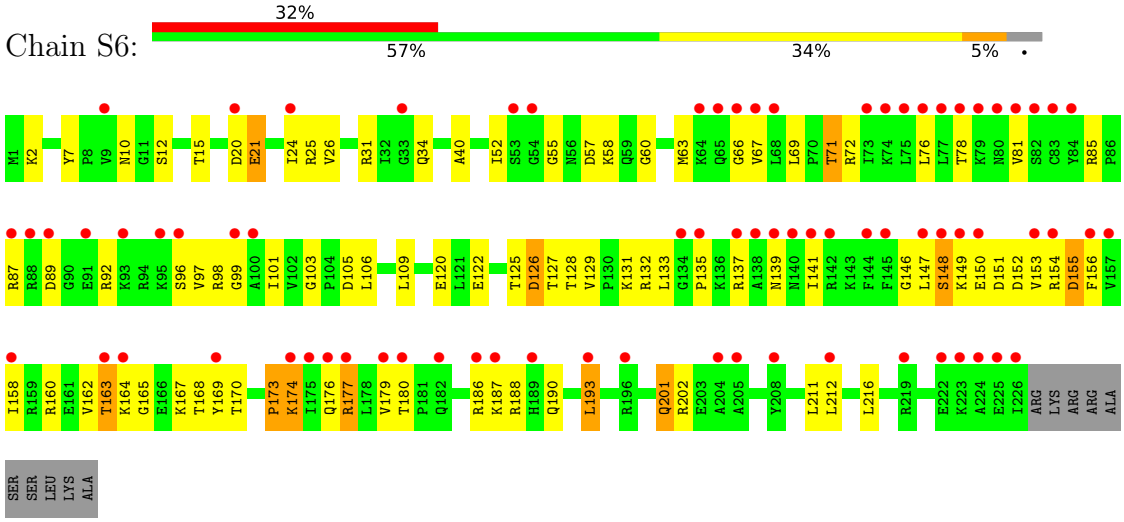
• Molecule 7: 40S ribosomal protein S5

Chain s5:



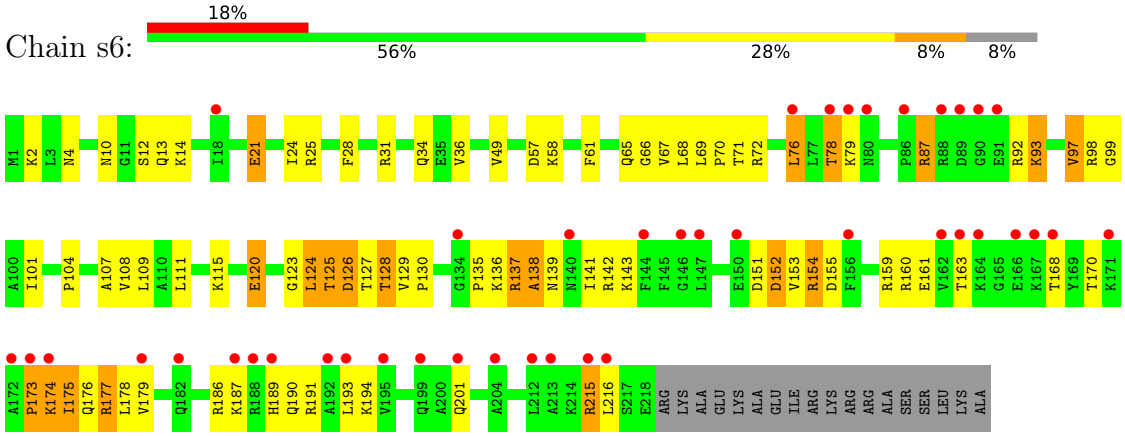
• Molecule 8: 40S ribosomal protein S6-A

Chain S6:



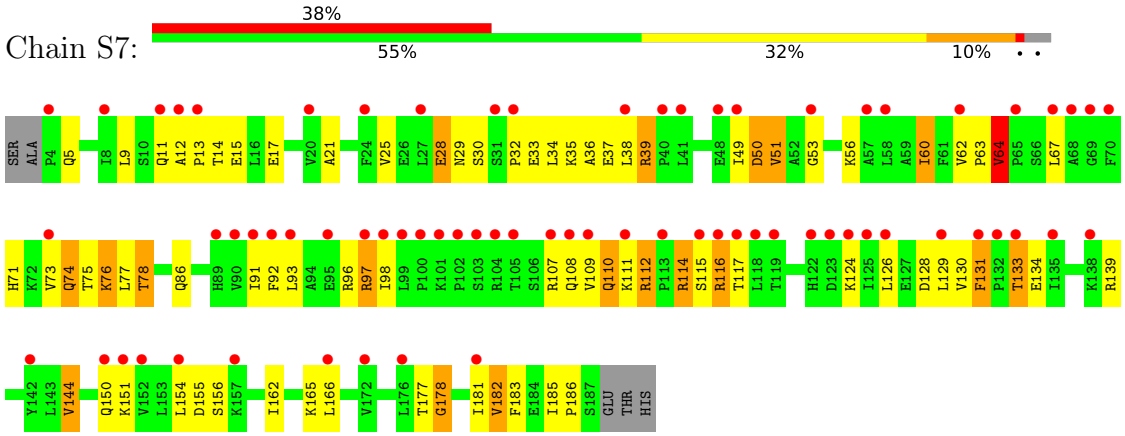
• Molecule 8: 40S ribosomal protein S6-A

Chain s6:



• Molecule 9: 40S ribosomal protein S7-A

Chain S7:



• Molecule 9: 40S ribosomal protein S7-A

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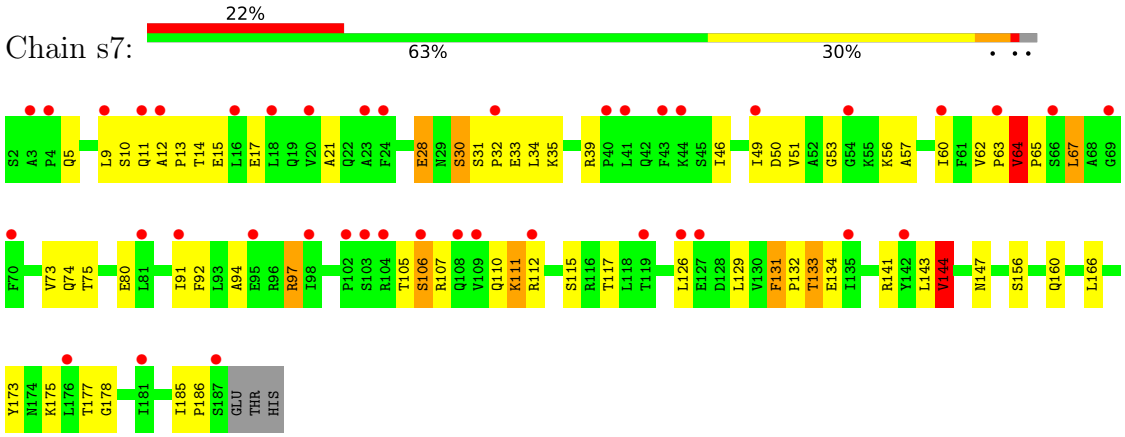
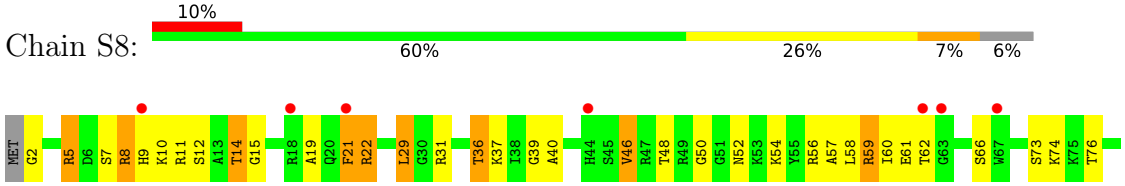
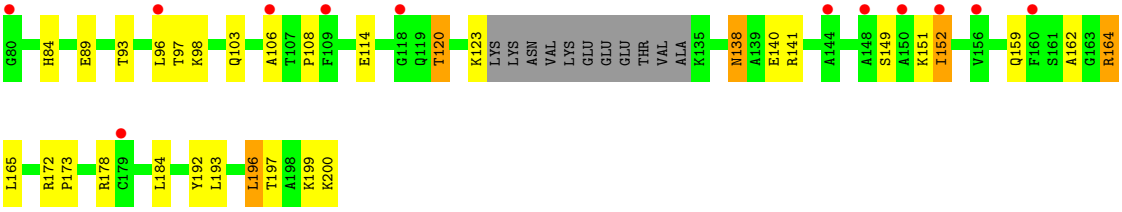


• Molecule 10: 40S ribosomal protein S8-A

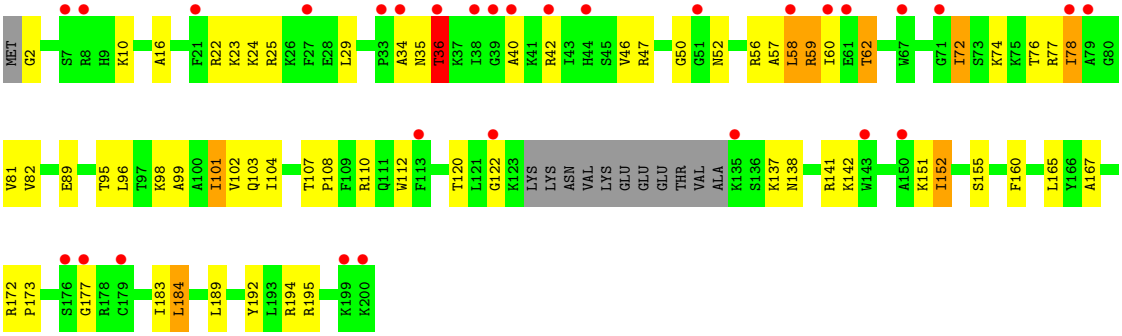
Chain S8:





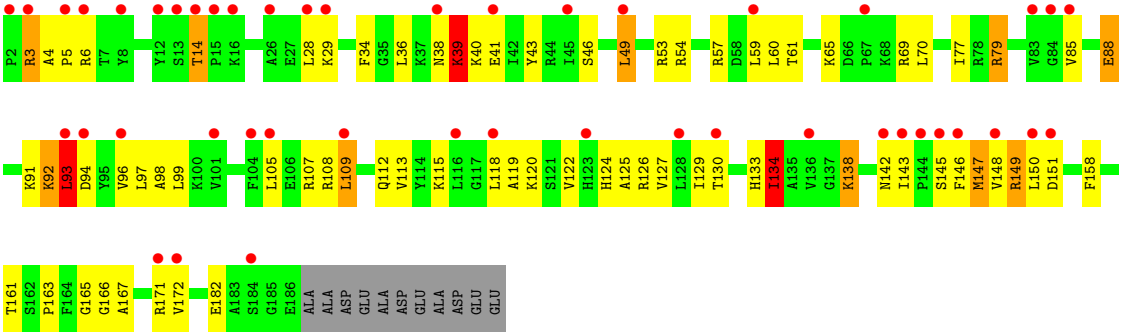
• Molecule 10: 40S ribosomal protein S8-A

Chain s8:



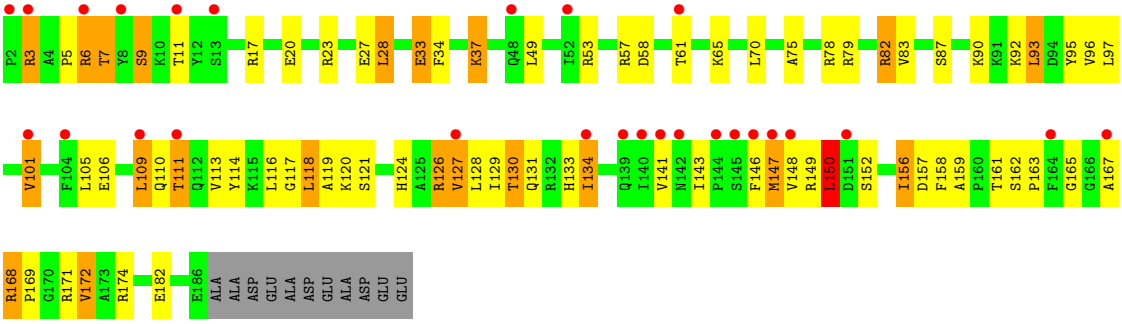
• Molecule 11: 40S ribosomal protein S9-A

Chain S9:



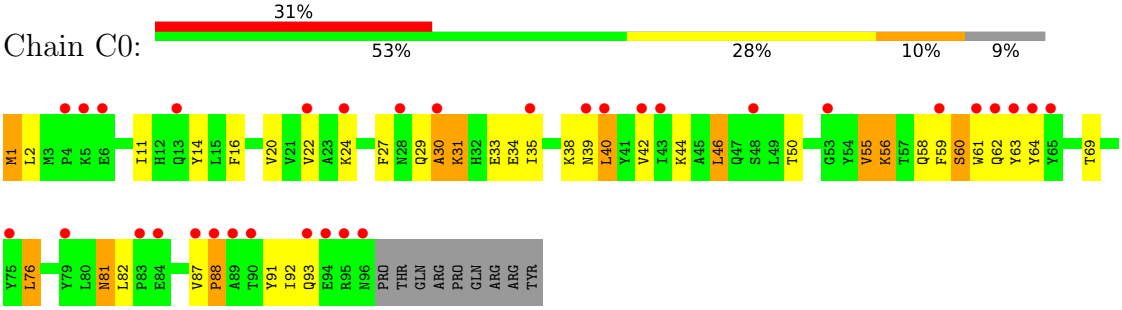
• Molecule 11: 40S ribosomal protein S9-A

Chain s9:



• Molecule 12: 40S ribosomal protein S10-A

Chain C0:



• Molecule 12: 40S ribosomal protein S10-A

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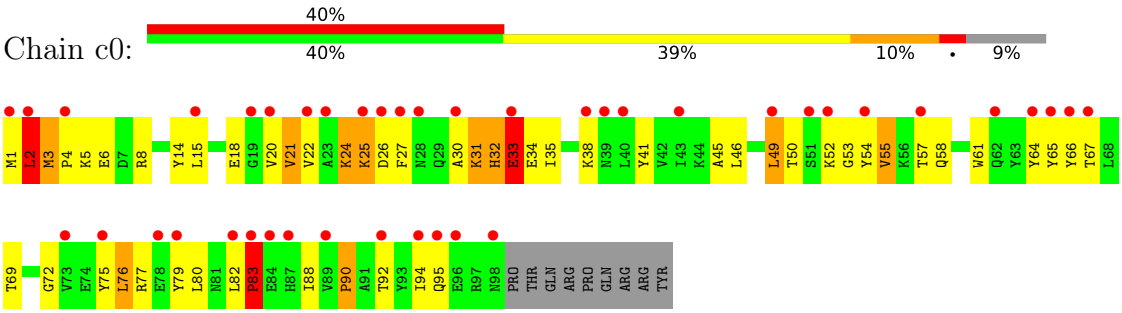
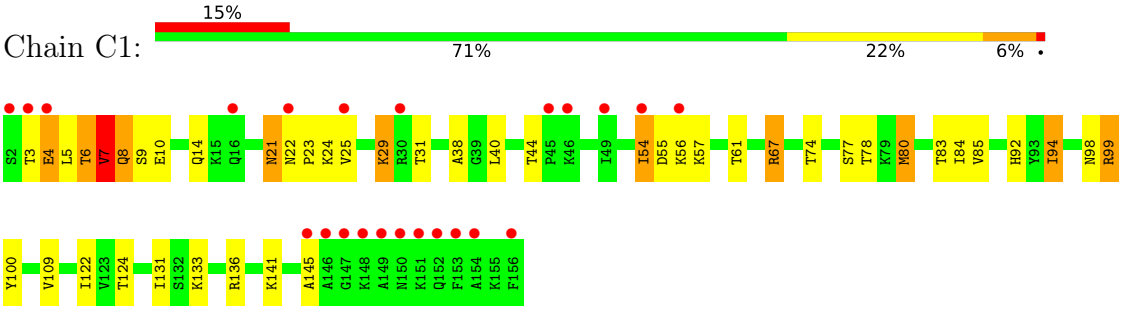


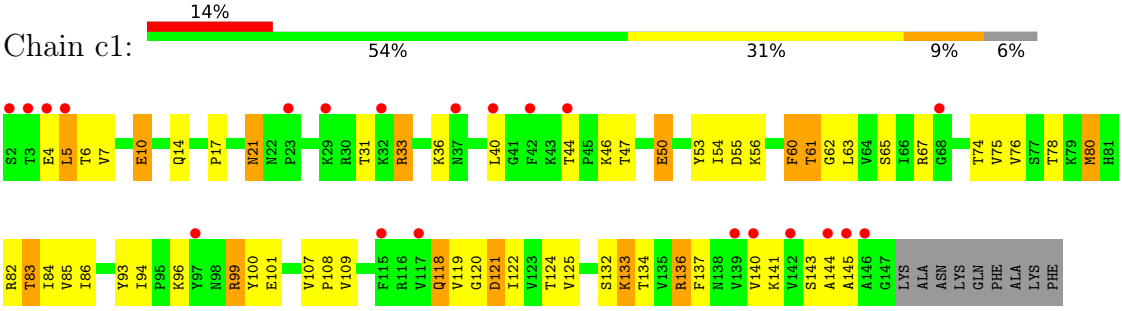
• Molecule 13: 40S ribosomal protein S11-A

Chain C1:



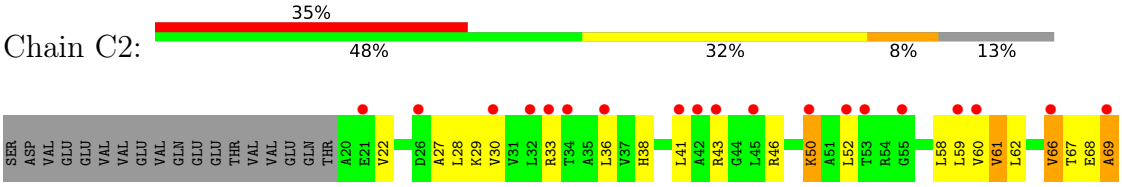
• Molecule 13: 40S ribosomal protein S11-A

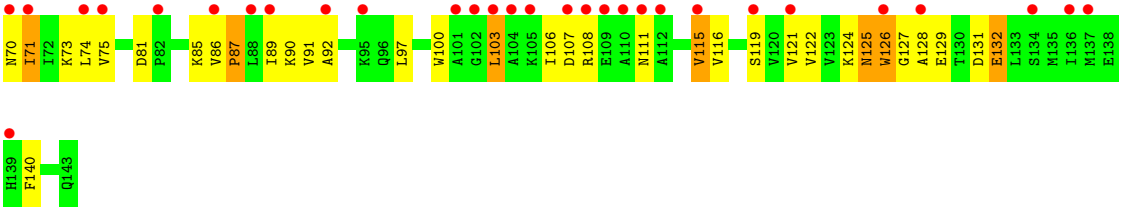
Chain c1:



• Molecule 14: 40S ribosomal protein S12

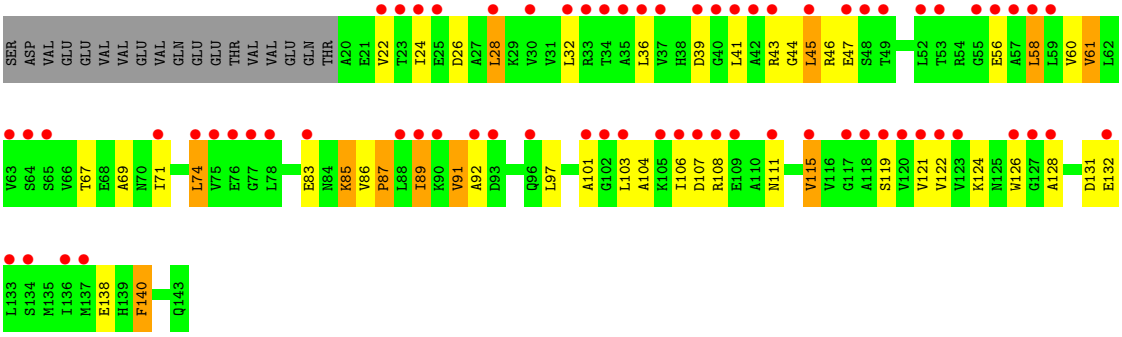
Chain C2:





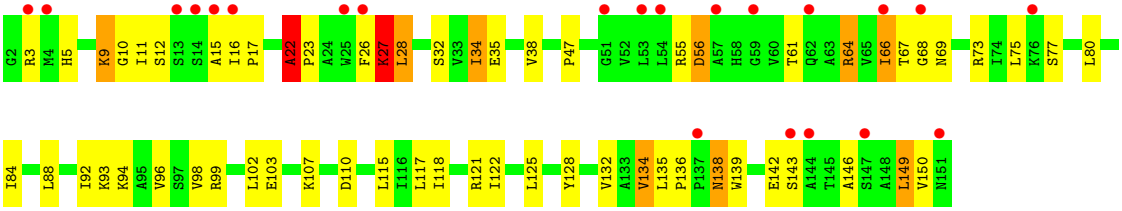
• Molecule 14: 40S ribosomal protein S12

Chain c2:



• Molecule 15: 40S ribosomal protein S13

Chain C3:



• Molecule 15: 40S ribosomal protein S13

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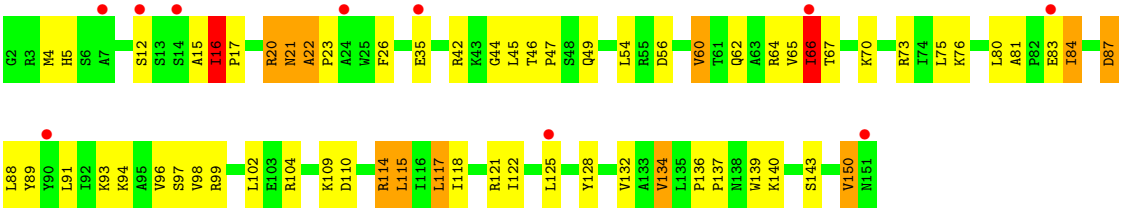
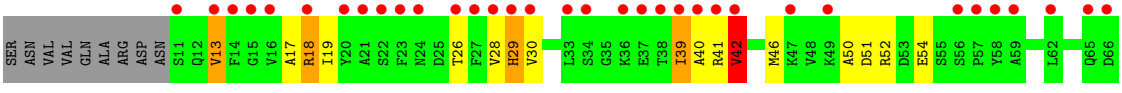
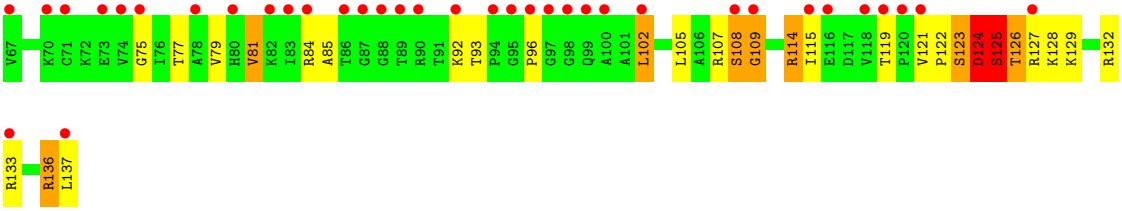


• Molecule 16: 40S ribosomal protein S14-A

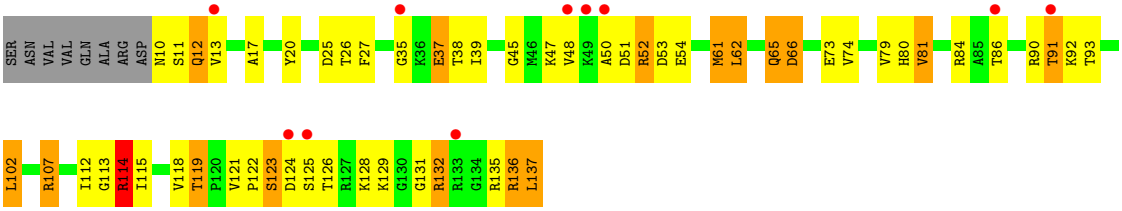
Chain C4:





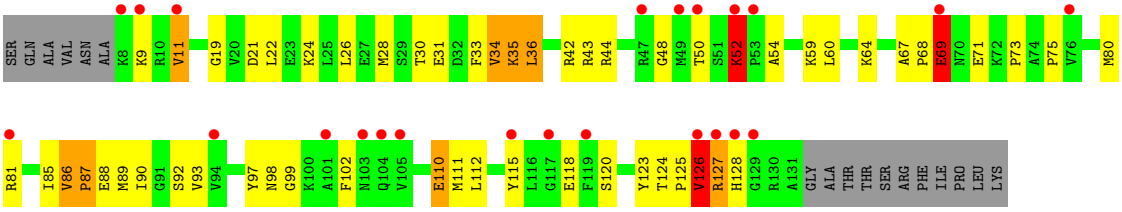
• Molecule 16: 40S ribosomal protein S14-A

Chain c4:



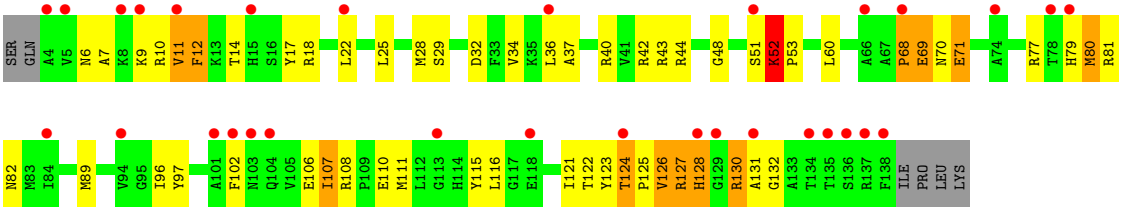
• Molecule 17: 40S ribosomal protein S15

Chain C5:



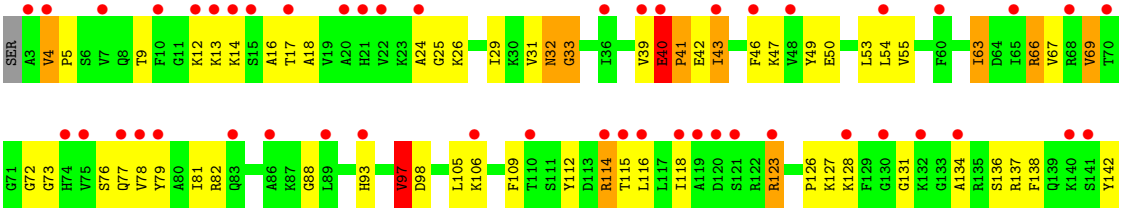
• Molecule 17: 40S ribosomal protein S15

Chain c5:



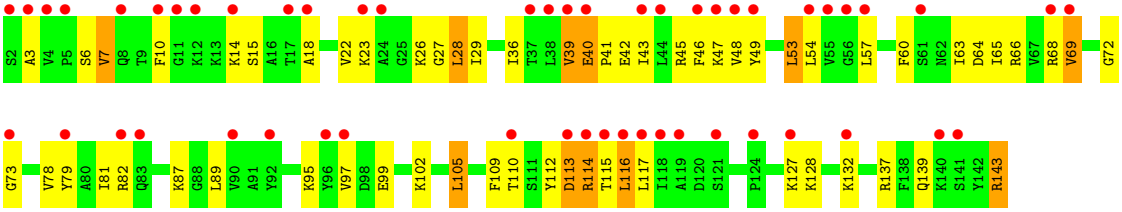
• Molecule 18: 40S ribosomal protein S16-A

Chain C6:



• Molecule 18: 40S ribosomal protein S16-A

Chain c6:



• Molecule 19: 40S ribosomal protein S17-A

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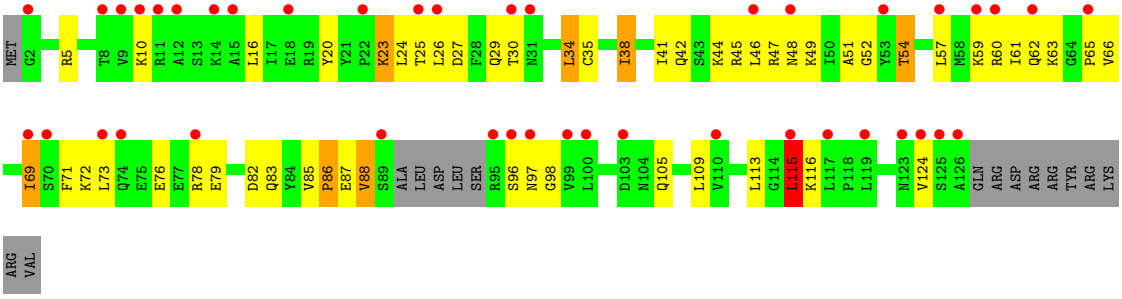
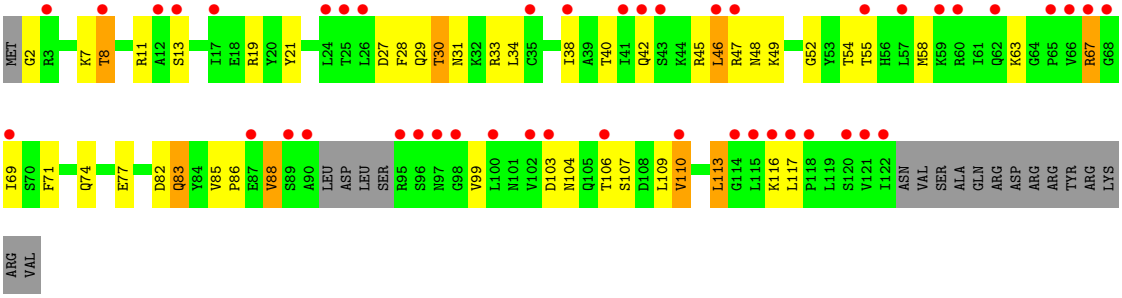


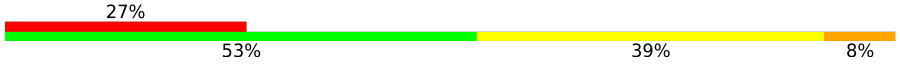
• Molecule 19: 40S ribosomal protein S17-A

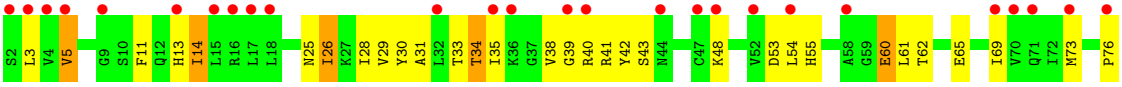
Chain c7:

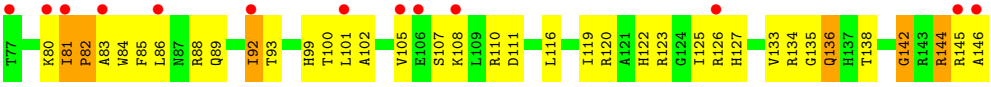


• Molecule 20: 40S ribosomal protein S18-A

Chain C8:

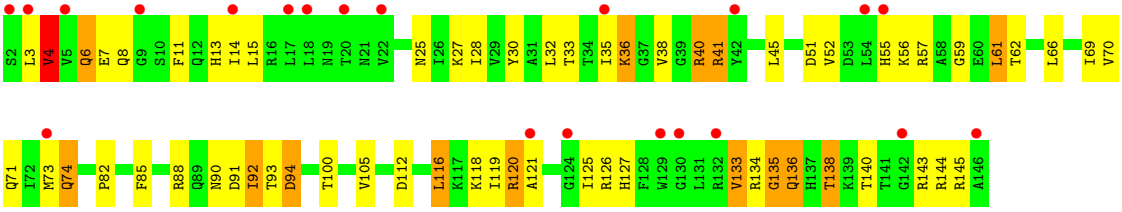






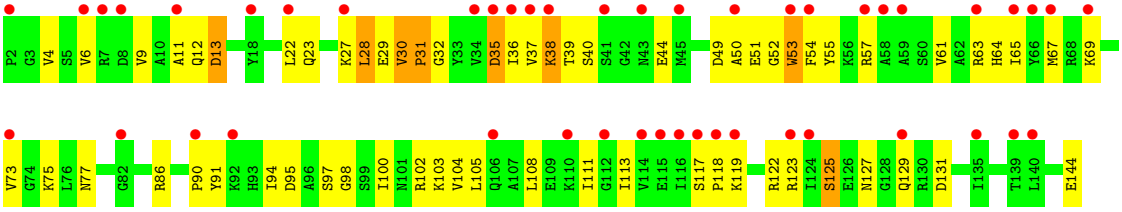
• Molecule 20: 40S ribosomal protein S18-A

Chain c8:



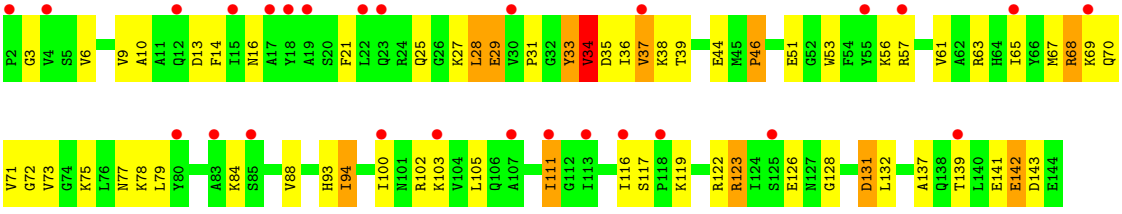
• Molecule 21: 40S ribosomal protein S19-A

Chain C9:



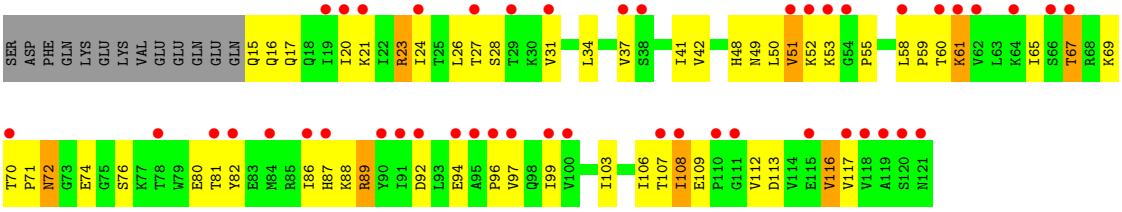
• Molecule 21: 40S ribosomal protein S19-A

Chain c9:



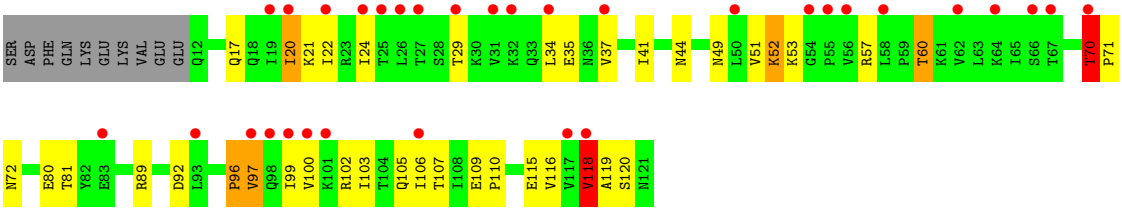
• Molecule 22: 40S ribosomal protein S20

Chain D0:



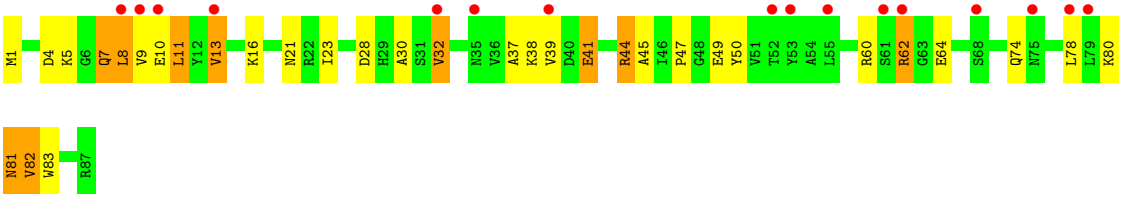
• Molecule 22: 40S ribosomal protein S20

Chain d0:



• Molecule 23: 40S ribosomal protein S21-A

Chain D1:

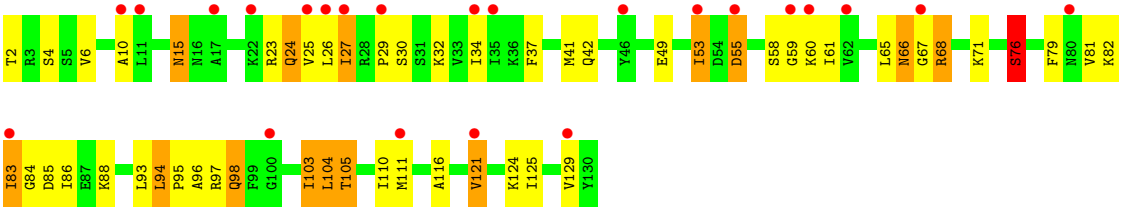


• Molecule 23: 40S ribosomal protein S21-A

Chain d1:

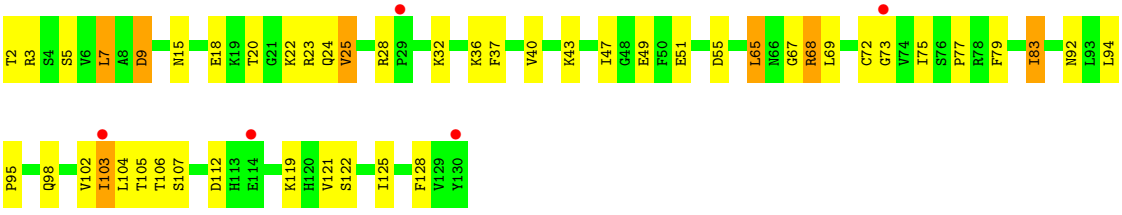
• Molecule 24: 40S ribosomal protein S22-A

Chain D2:



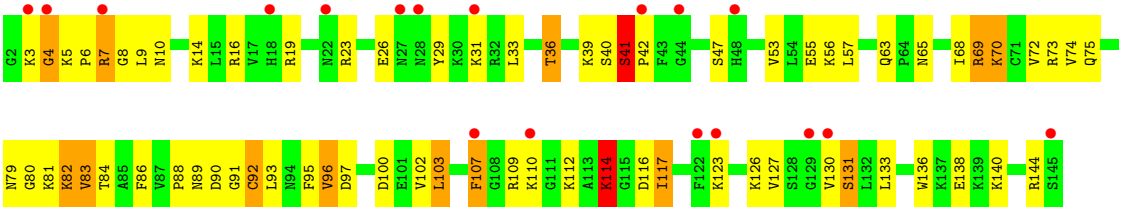
• Molecule 24: 40S ribosomal protein S22-A

Chain d2:



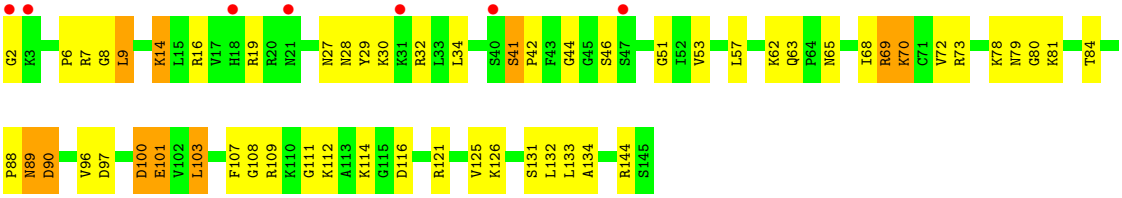
• Molecule 25: 40S ribosomal protein S23-A

Chain D3:



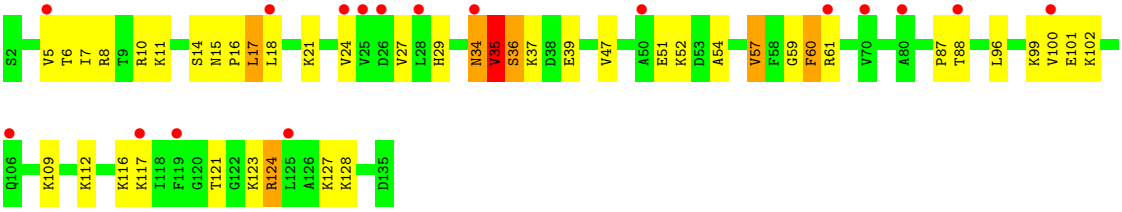
• Molecule 25: 40S ribosomal protein S23-A

Chain d3:



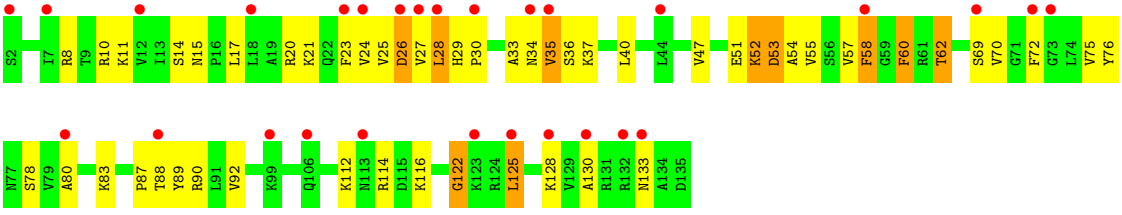
• Molecule 26: 40S ribosomal protein S24-A

Chain D4:



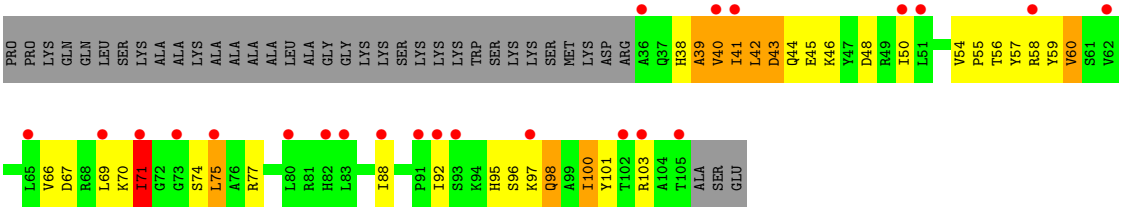
• Molecule 26: 40S ribosomal protein S24-A

Chain d4:



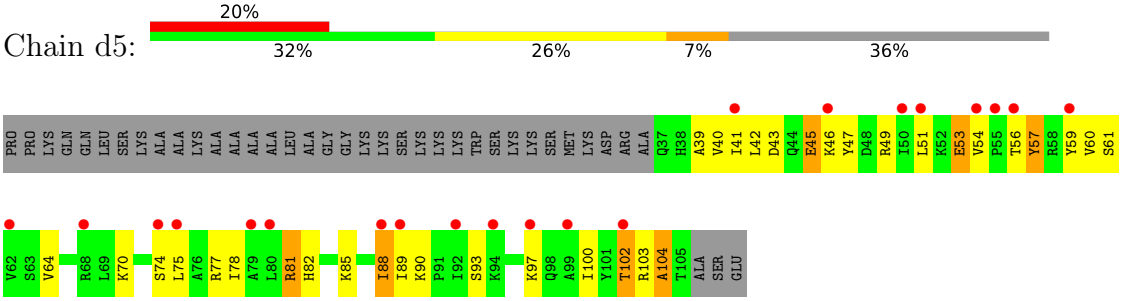
• Molecule 27: 40S ribosomal protein S25-A

Chain D5:



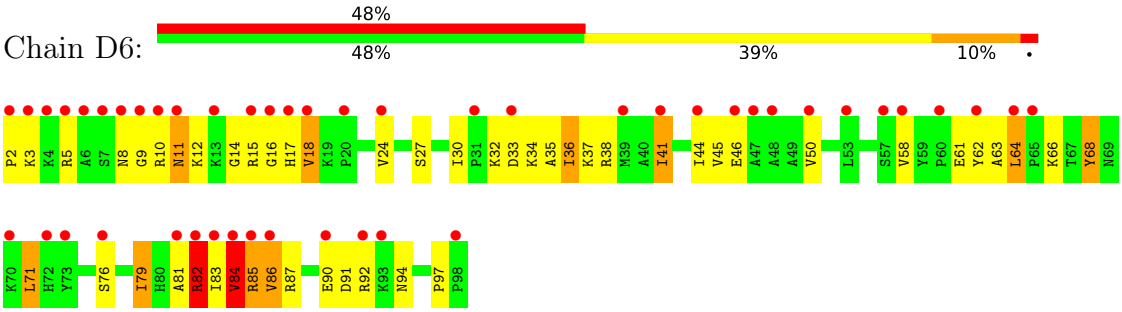
• Molecule 27: 40S ribosomal protein S25-A

Chain d5:



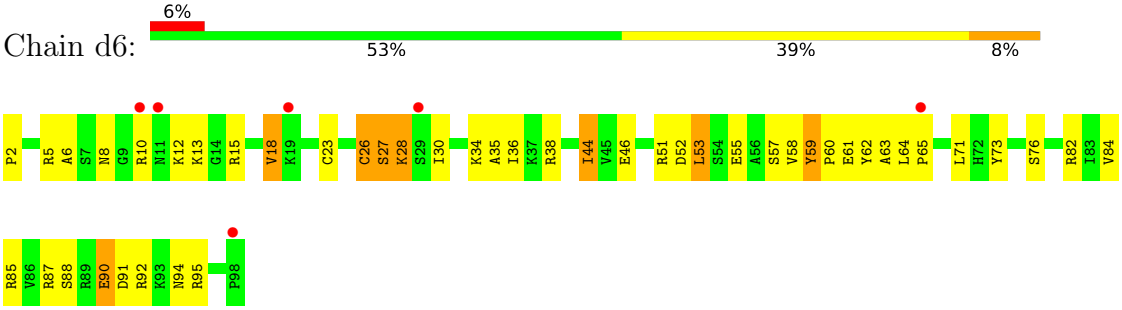
• Molecule 28: 40S ribosomal protein S26-B

Chain D6:



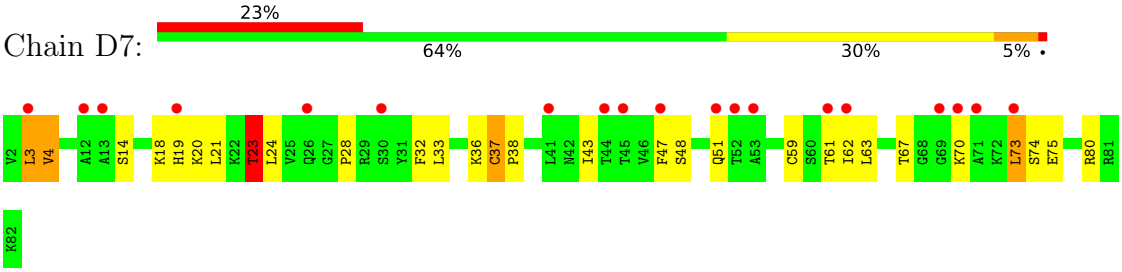
• Molecule 28: 40S ribosomal protein S26-B

Chain d6:



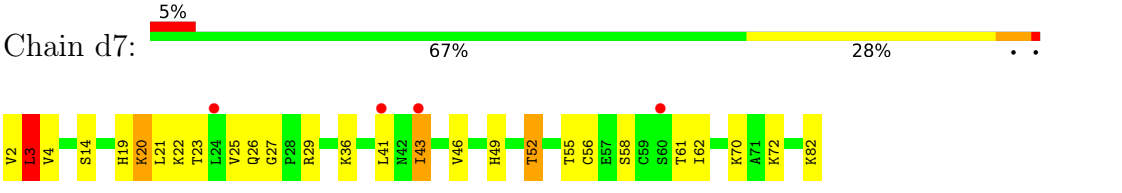
• Molecule 29: 40S ribosomal protein S27-A

Chain D7:



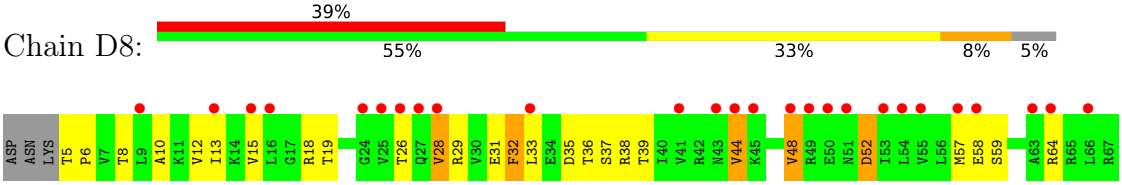
• Molecule 29: 40S ribosomal protein S27-A

Chain d7:



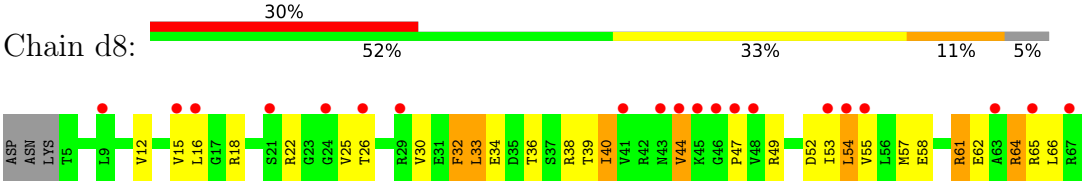
• Molecule 30: 40S ribosomal protein S28-A

Chain D8:



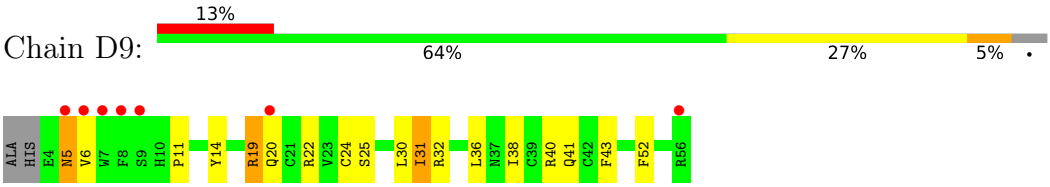
• Molecule 30: 40S ribosomal protein S28-A

Chain d8:



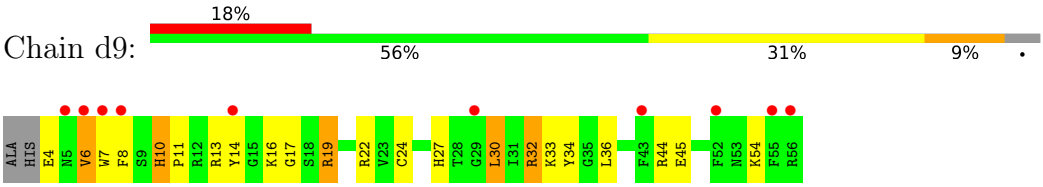
• Molecule 31: 40S ribosomal protein S29-A

Chain D9:



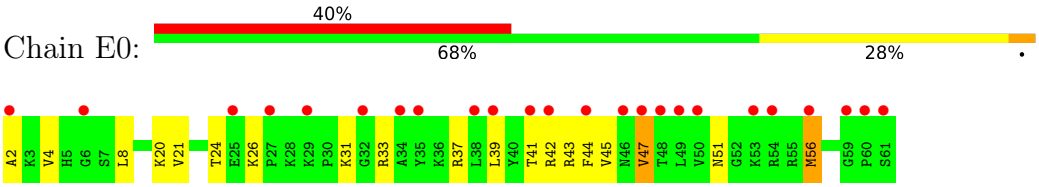
• Molecule 31: 40S ribosomal protein S29-A

Chain d9:



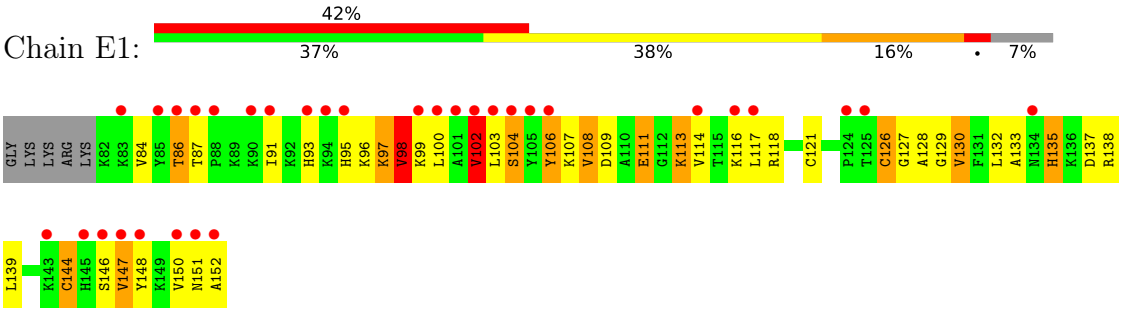
• Molecule 32: 40S ribosomal protein S30-A

Chain E0:



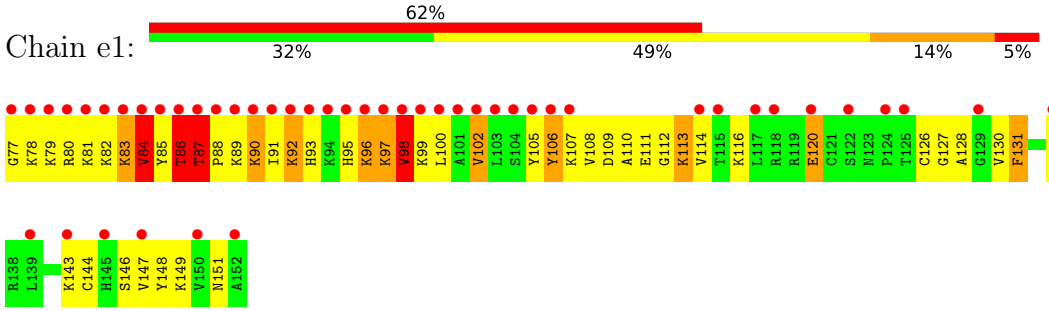
• Molecule 33: Ubiquitin-40S ribosomal protein S31

Chain E1:



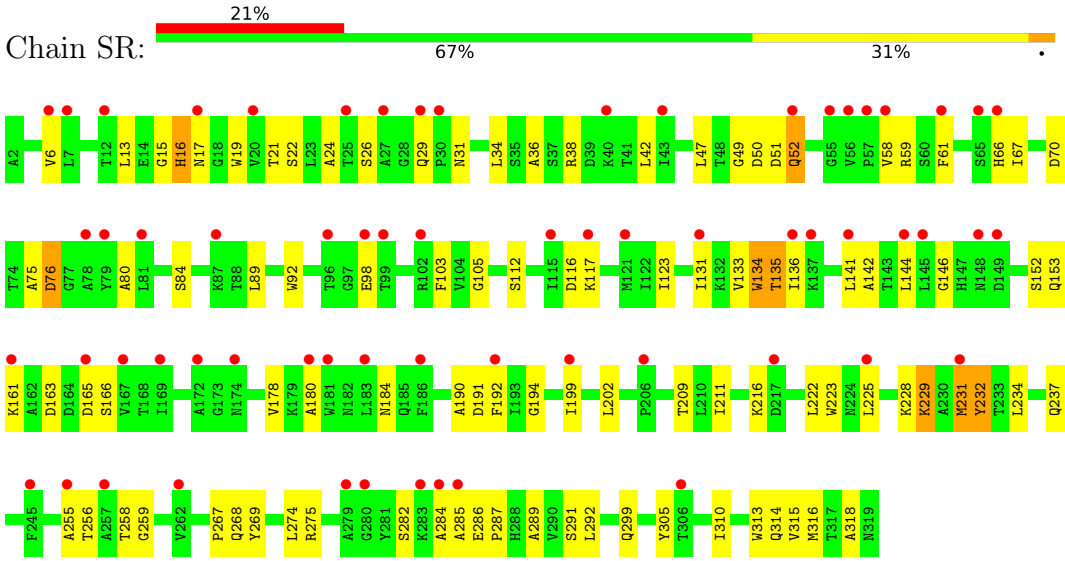
• Molecule 33: Ubiquitin-40S ribosomal protein S31

Chain e1:



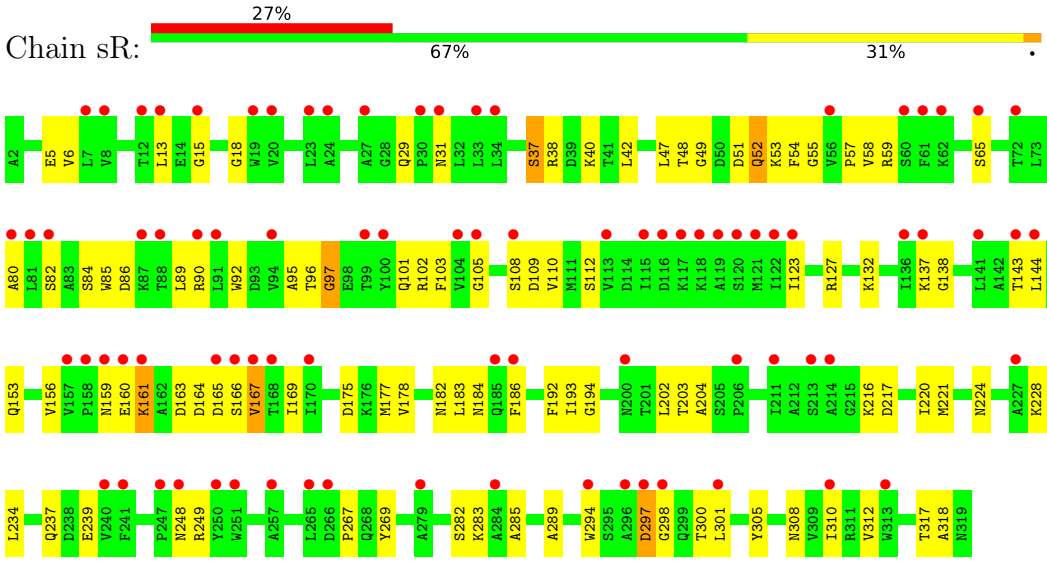
• Molecule 34: Guanine nucleotide-binding protein subunit beta-like protein

Chain SR:



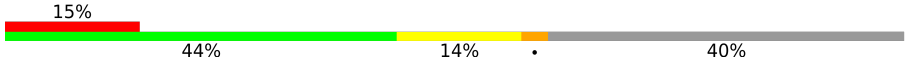
• Molecule 34: Guanine nucleotide-binding protein subunit beta-like protein

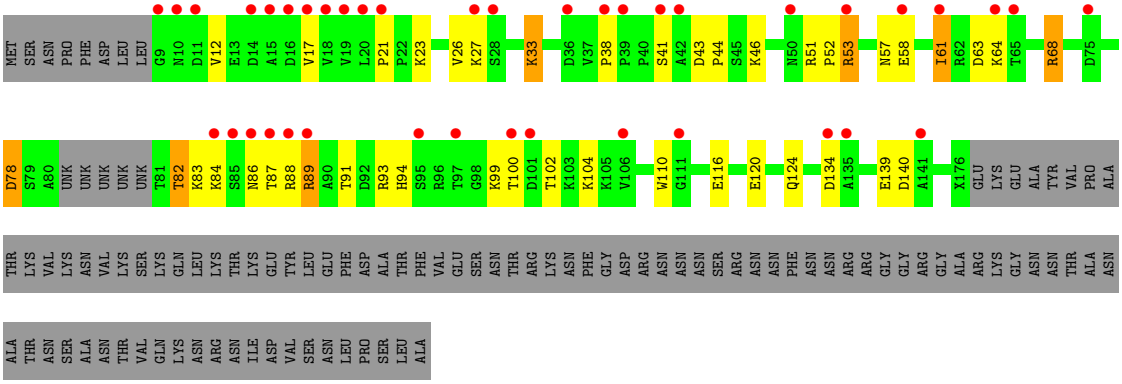
Chain sR:



• Molecule 35: Suppressor protein STM1

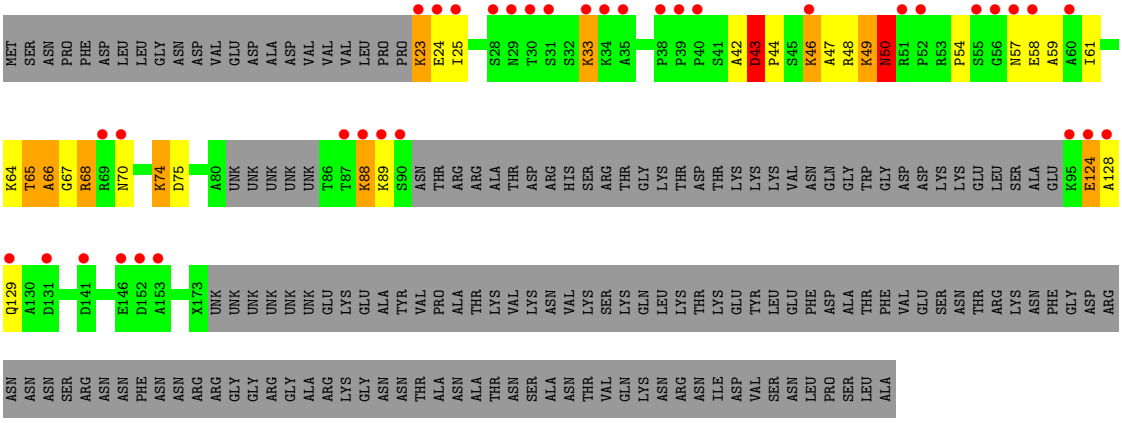
Chain SM:





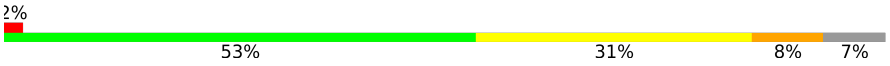
• Molecule 35: Suppressor protein STM1

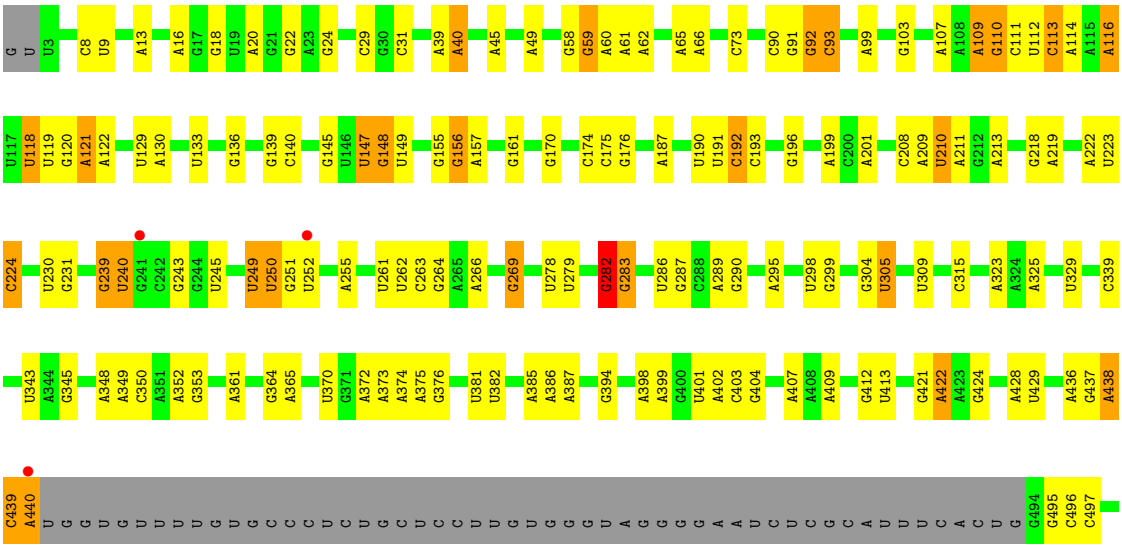
Chain sM:

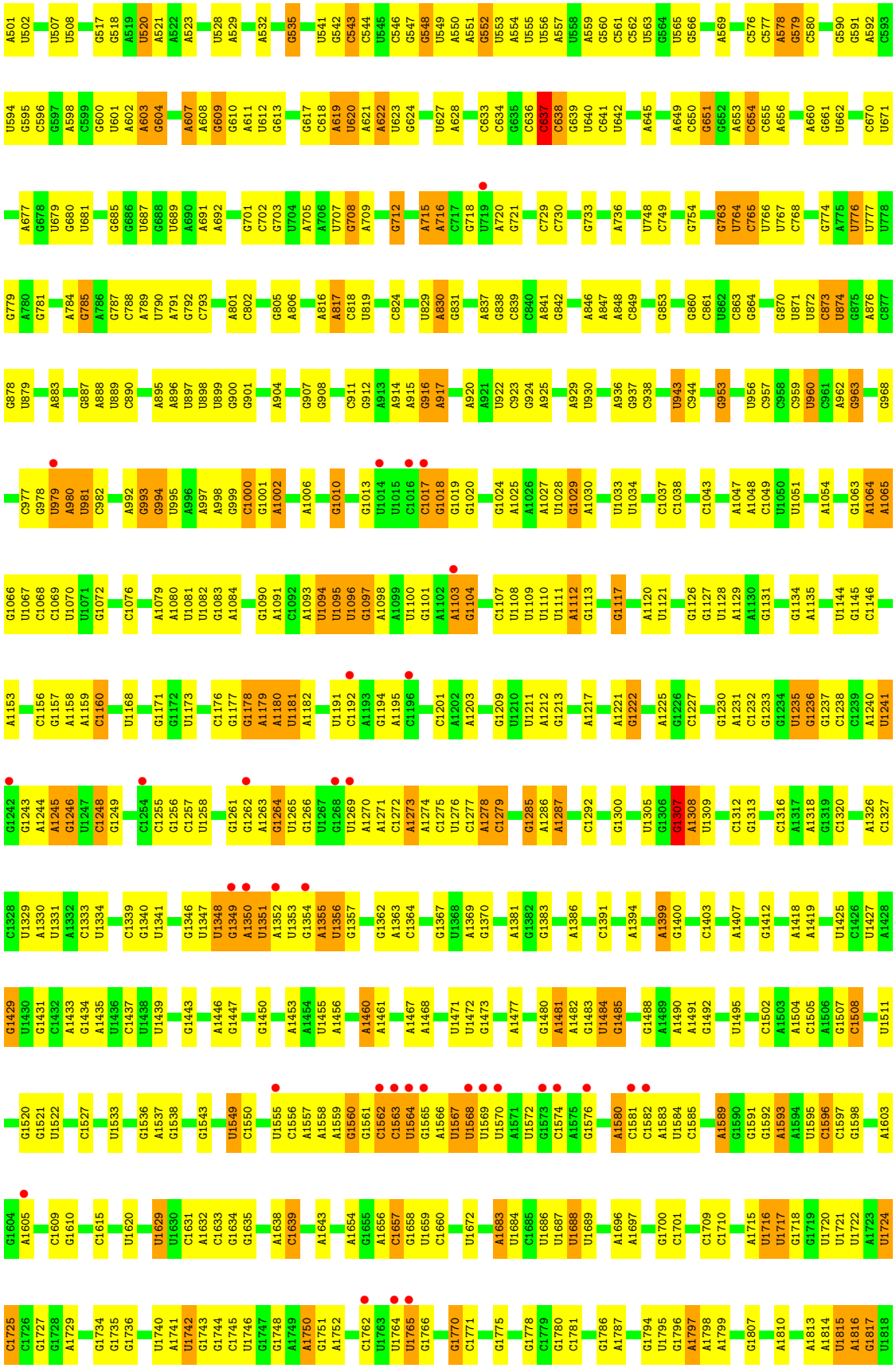


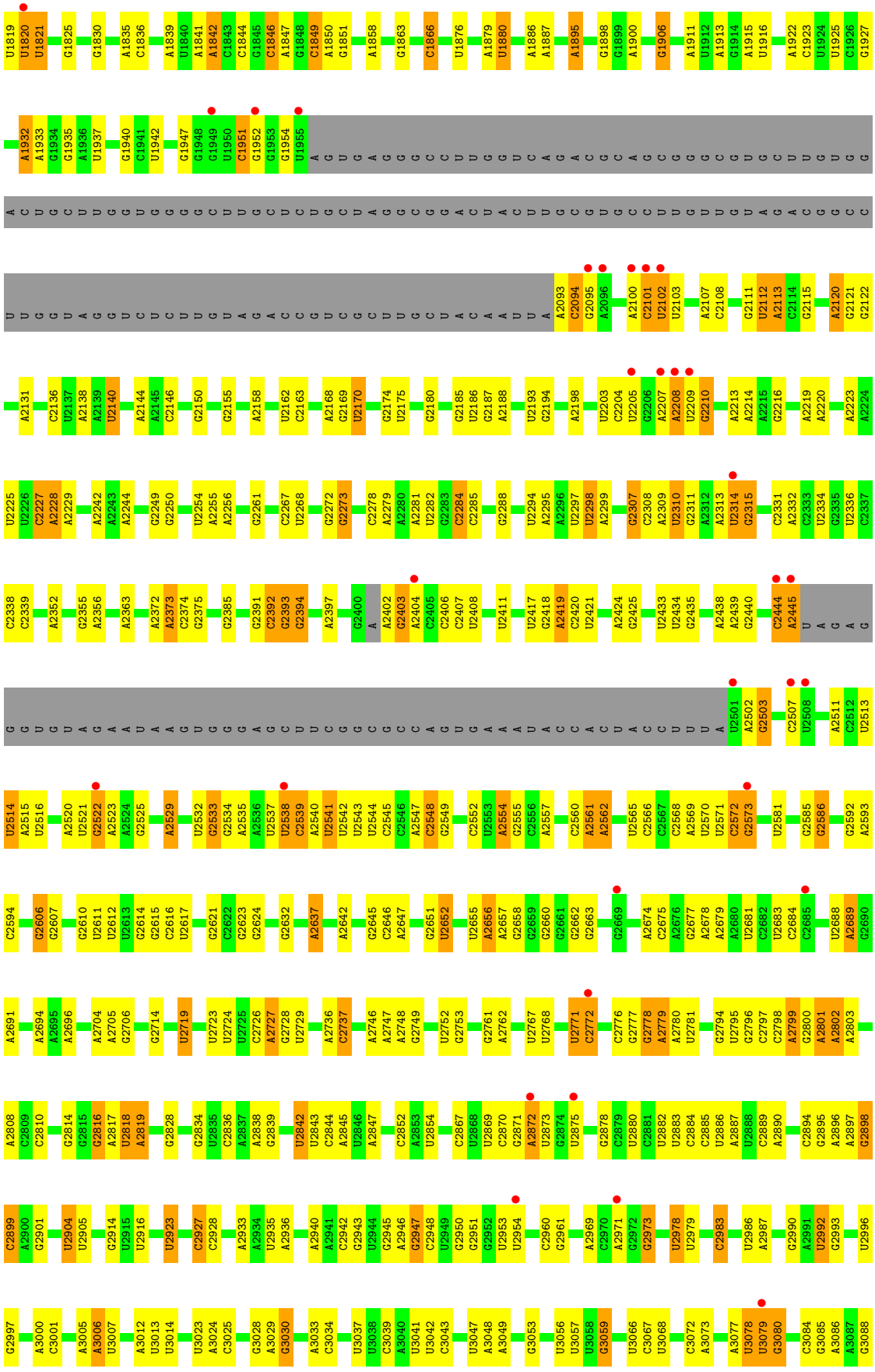
• Molecule 36: 25S ribosomal RNA

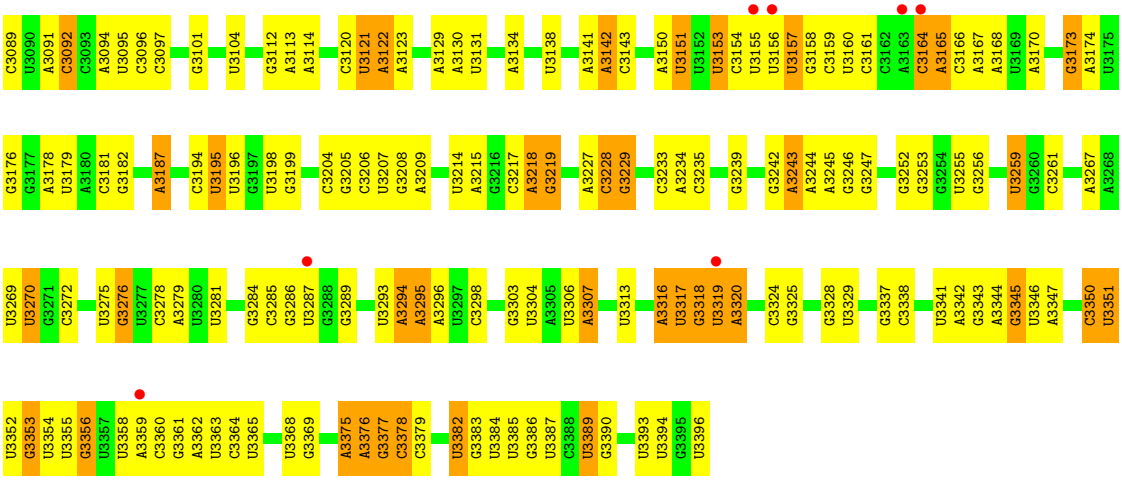
Chain 1:





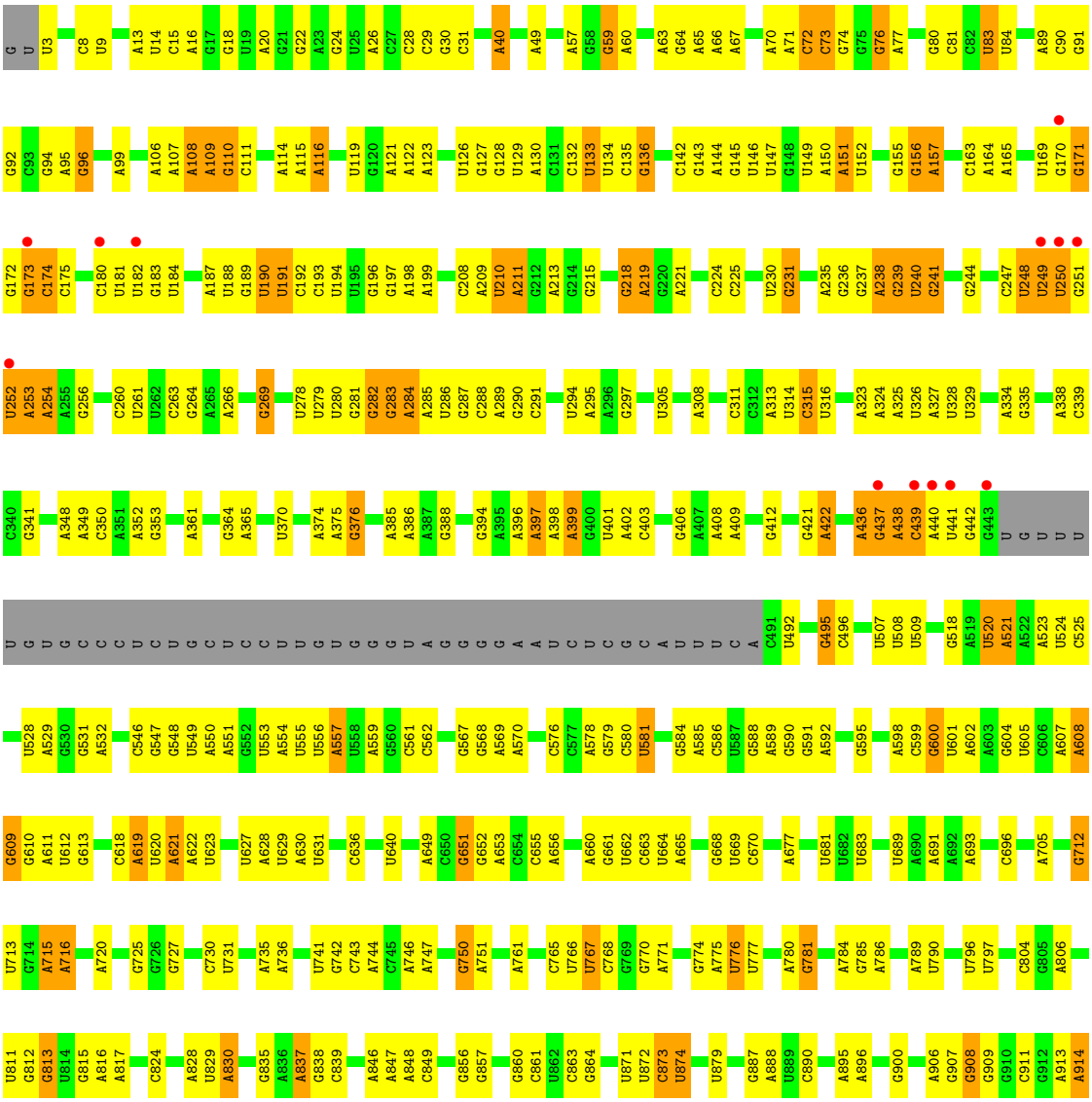


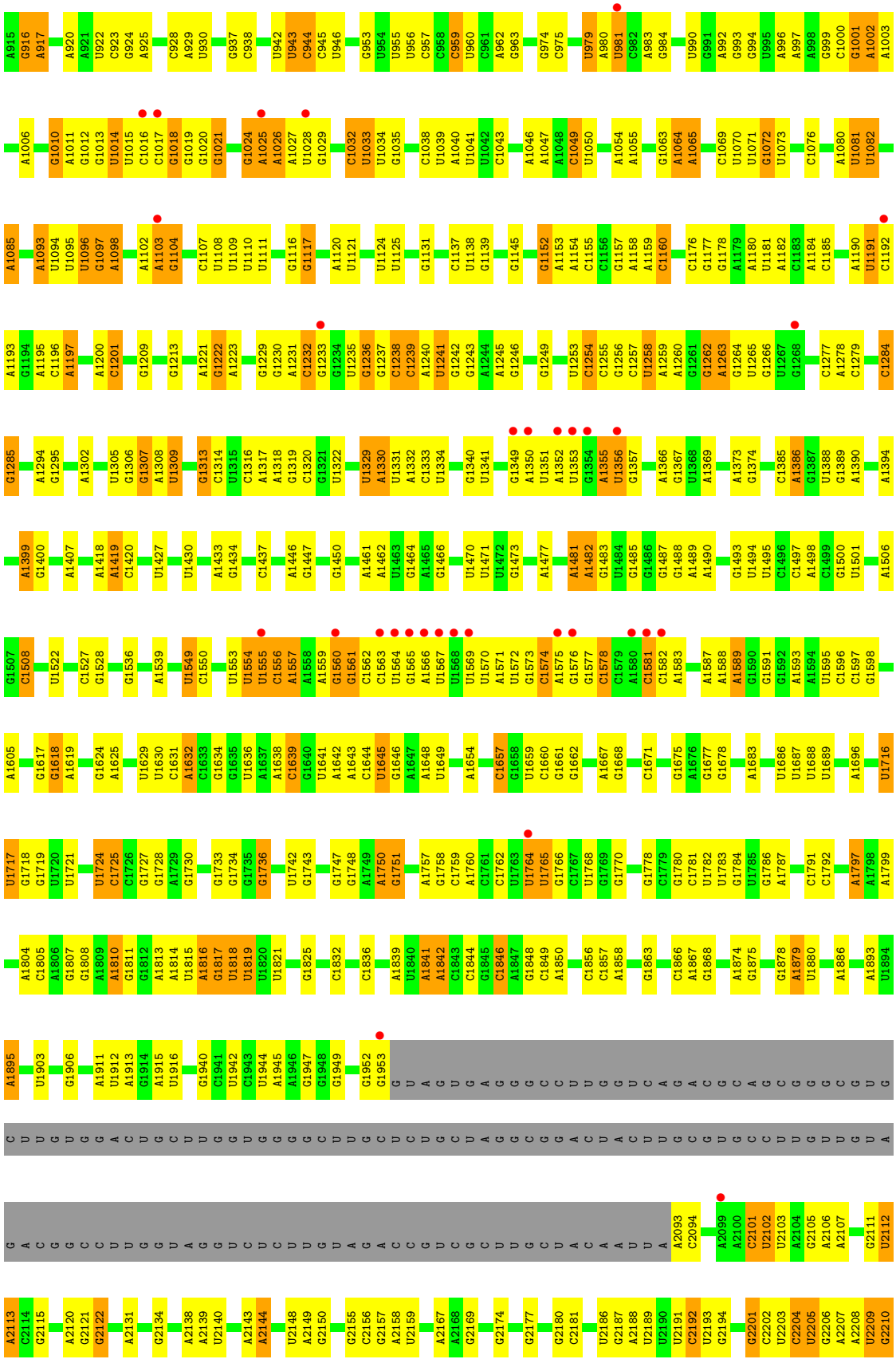

U1819 U1820 U1821 G1825 G1830 A1835 C1836 A1839 U1840 A1841 A1842 C1843 C1844 C1845 C1846 A1847 G1848 C1849 A1850 G1851 A1858 G1863 C1866 U1876 A1879 U1880 A1886 A1887 A1895 G1898 G1899 A1900 G1906 A1911 U1912 A1913 G1914 A1915 U1916 A1922 C1923 U1924 U1925 C1926 G1927
A1932 A1933 G1934 G1935 A1936 U1937 G1940 C1941 U1942 G1947 G1948 G1949 U1950 C1951 G1952 G1953 G1954 U1955
A2093 C2094 G2095 A2096 A2100 C2101 U2102 U2103 A2107 C2108 G2111 U2112 A2113 C2114 G2115 A2120 G2121 G2122
A2131 C2136 U2137 A2138 A2139 U2140 A2144 A2145 C2146 G2150 G2155 A2158 U2162 C2163 A2168 G2169 U2170 G2174 U2175 G2180 G2185 U2186 G2187 A2188 U2193 G2194 A2198 U2203 C2204 U2205 G2206 A2207 A2208 U2209 G2210 A2213 A2214 A2215 G2216 A2219 A2220 A2223 A2224
U2225 U2226 C2227 A2228 A2229 A2242 A2243 A2244 G2249 G2250 U2254 A2255 A2256 G2261 C2267 U2268 G2272 G2273 C2278 A2279 A2280 A2281 U2282 G2283 C2284 C2285 G2288 U2294 A2295 A2296 U2297 U2298 A2299 G2307 C2308 A2309 U2310 G2311 A2312 A2313 U2314 G2315 C2331 A2332 C2333 U2334 G2335 U2336 C2337
C2338 C2339 A2352 G2355 A2356 A2363 A2372 A2373 C2374 G2375 G2385 G2391 C2392 G2393 G2394 A2397 G2400 A A2402 G2403 A2404 C2405 C2406 C2407 U2408 U2411 U2417 G2418 A2419 C2420 U2421 A2424 G2425 U2433 U2434 G2435 A2438 A2439 G2440 C2444 A2445 U A G A G
G G U G U A G A A U A A G U G G G A G C U C G A A A C C C G U C C A C A C U U A U2501 A2502 G2503 C2507 U2508 A2511 C2512 U2513
U2514 A2515 U2516 A2520 U2521 G2522 A2523 A2524 G2525 A2529 U2532 G2533 G2534 A2535 A2536 U2537 U2538 C2539 A2540 U2541 U2542 U2543 U2544 C2545 C2546 A2547 C2548 G2549 C2552 U2553 A2554 G2555 C2556 A2557 C2560 A2561 A2562 U2565 C2566 C2567 C2568 A2569 U2570 U2571 C2572 G2573 U2581 G2585 G2586 G2592 A2593
C2594 G2606 G2607 G2610 U2611 U2612 U2613 G2614 G2615 C2616 U2617 G2621 C2622 G2623 G2624 G2632 A2637 A2642 G2645 C2646 A2647 G2651 U2652 U2655 A2656 A2657 G2658 G2659 G2660 C2661 G2662 G2663 G2669 A2674 C2675 A2676 G2677 A2678 A2679 A2680 U2681 C2682 U2683 C2684 C2685 U2688 A2689 G2690
A2691 A2694 A2695 A2696 A2704 A2705 G2706 G2714 U2719 U2723 U2724 U2725 C2726 A2727 G2728 U2729 A2736 C2737 A2746 A2747 A2748 G2749 U2752 G2753 G2761 A2762 U2767 U2768 U2771 C2772 C2776 G2777 G2778 A2779 A2780 U2781 G2794 U2795 G2796 C2797 C2798 A2799 G2800 A2801 A2802 A2803
A2808 C2809 C2810 G2814 G2815 G2816 A2817 U2818 A2819 G2828 G2834 U2835 C2836 A2837 A2838 G2839 U2842 U2843 C2844 A2845 U2846 A2847 C2852 A2853 U2854 C2867 U2868 U2869 C2870 G2871 A2872 U2873 G2874 U2875 G2878 C2879 U2880 C2881 U2882 U2883 C2884 C2885 U2886 A2887 U2888 C2889 A2890 C2894 G2895 A2896 A2897 G2898
C2899 A2900 G2901 U2904 U2905 G2914 U2915 U2916 U2923 C2927 C2928 A2933 A2934 U2935 A2936 A2940 A2941 C2942 G2943 U2944 G2945 A2946 G2947 C2948 U2949 G2950 G2951 G2952 U2953 U2954 C2960 G2961 A2969 C2970 A2971 G2972 G2973 U2978 U2979 C2983 U2986 A2987 G2990 A2991 U2992 G2993 U2996
G2997 A3000 C3001 A3005 A3006 U3007 A3012 U3013 U3014 U3023 A3024 C3025 G3028 A3029 G3030 A3033 C3034 U3037 U3038 C3039 A3040 U3041 U3042 C3043 U3047 A3048 A3049 G3053 U3056 U3057 U3058 G3059 U3066 C3067 U3068 C3072 A3073 A3077 U3078 U3079 G3080 C3084 G3085 A3086 A3087 G3088

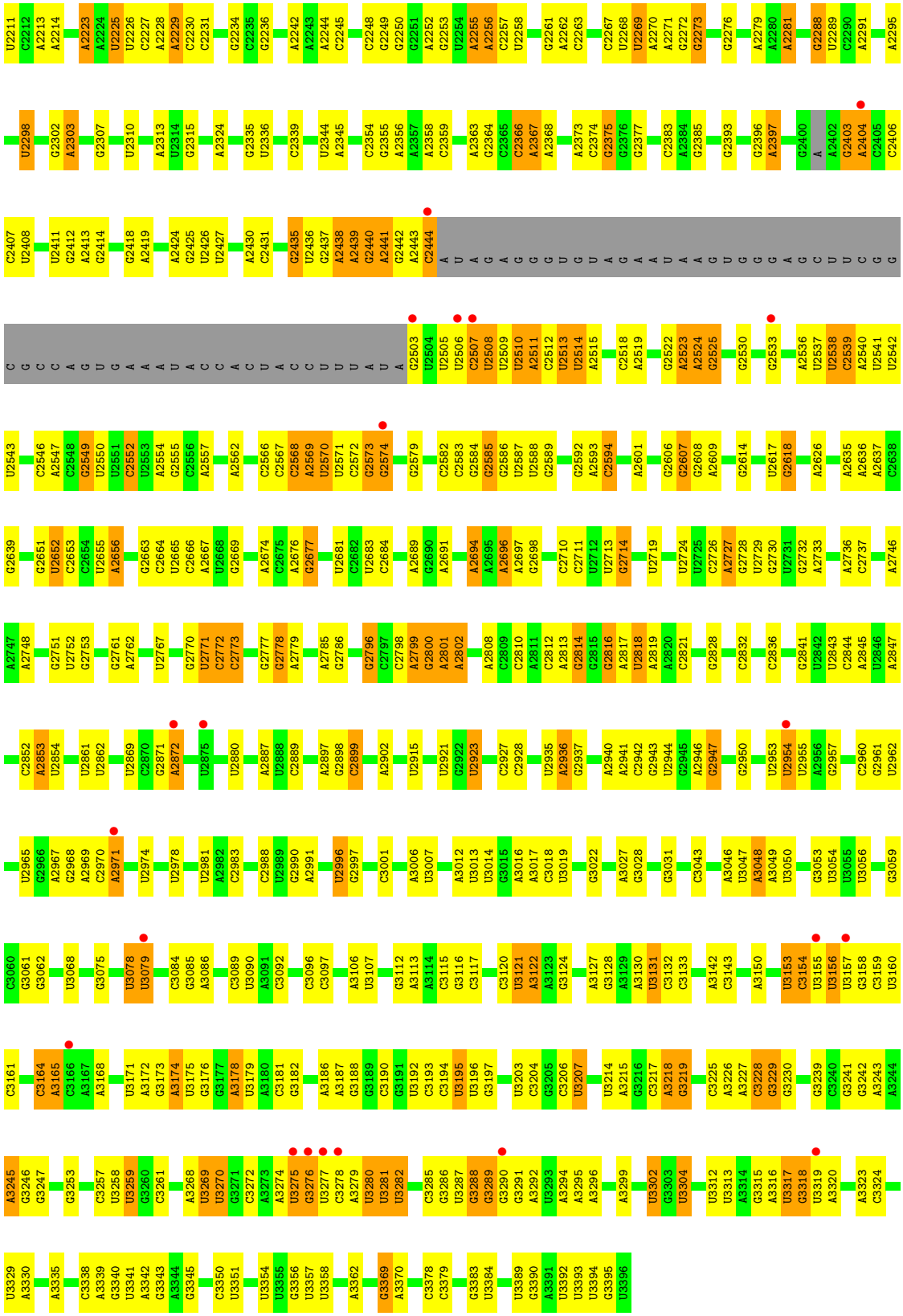


• Molecule 36: 25S ribosomal RNA

Chain 5:

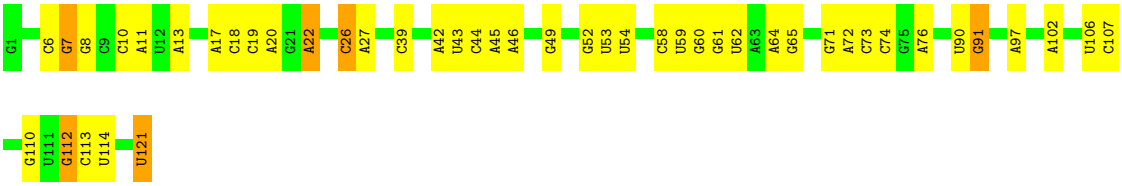






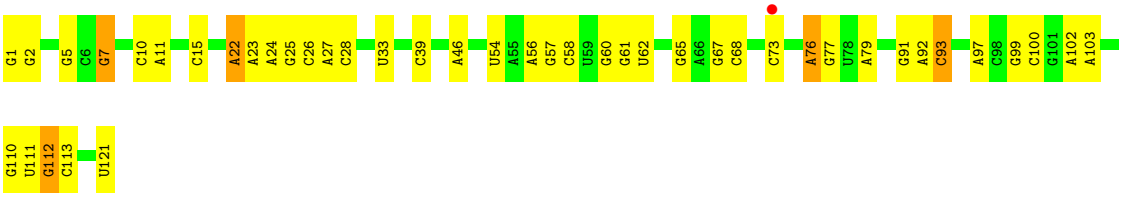
• Molecule 37: 5S ribosomal RNA

Chain 3:



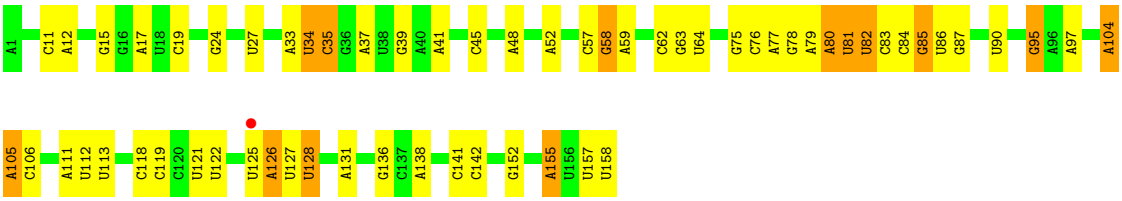
• Molecule 37: 5S ribosomal RNA

Chain 7:



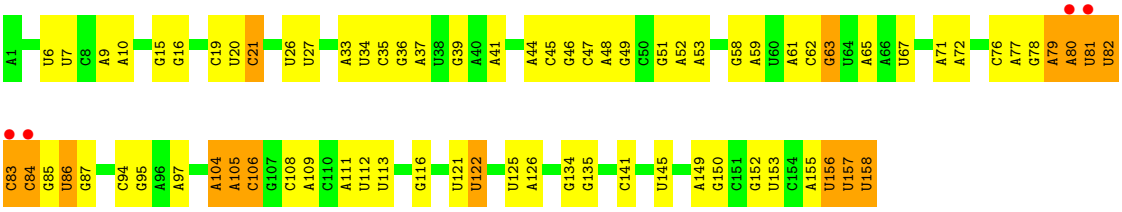
• Molecule 38: 5.8S ribosomal RNA

Chain 4:



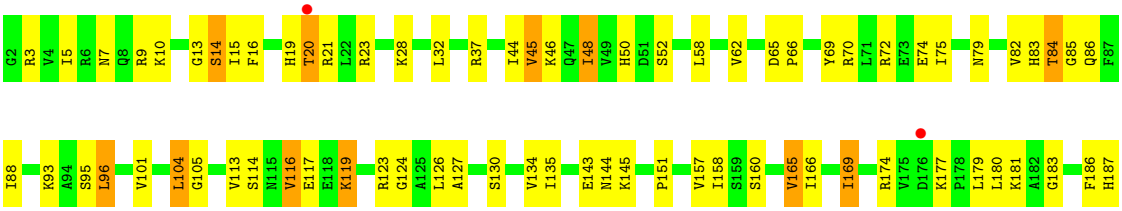
• Molecule 38: 5.8S ribosomal RNA

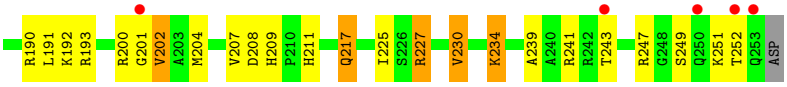
Chain 8:



• Molecule 39: 60S ribosomal protein L2-A

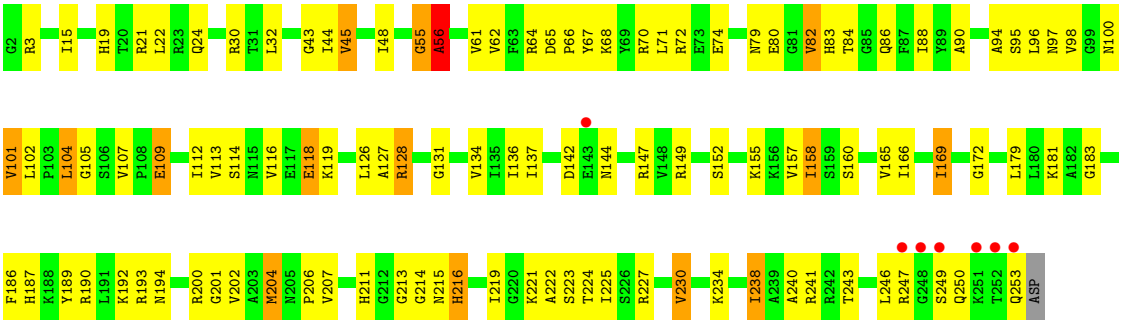
Chain L2:





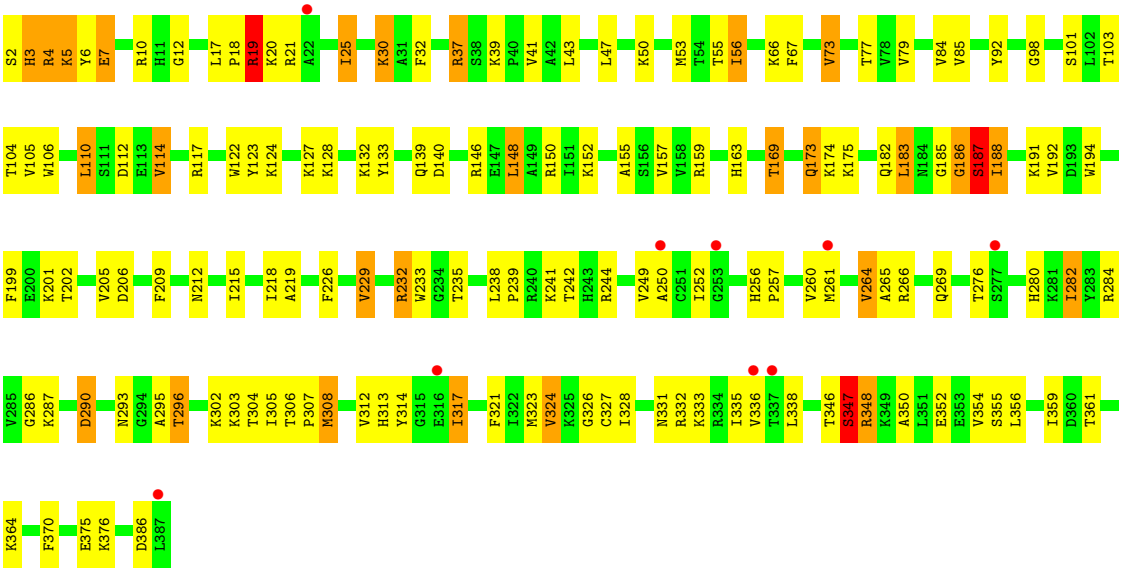
• Molecule 39: 60S ribosomal protein L2-A

Chain l2:



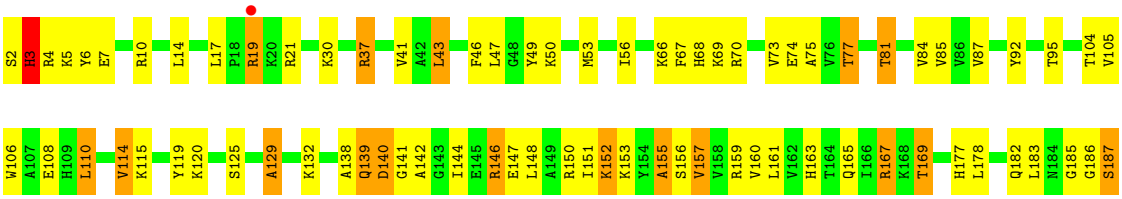
• Molecule 40: 60S ribosomal protein L3

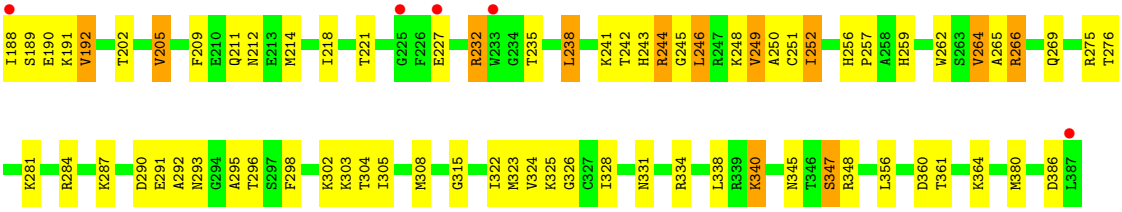
Chain L3:



• Molecule 40: 60S ribosomal protein L3

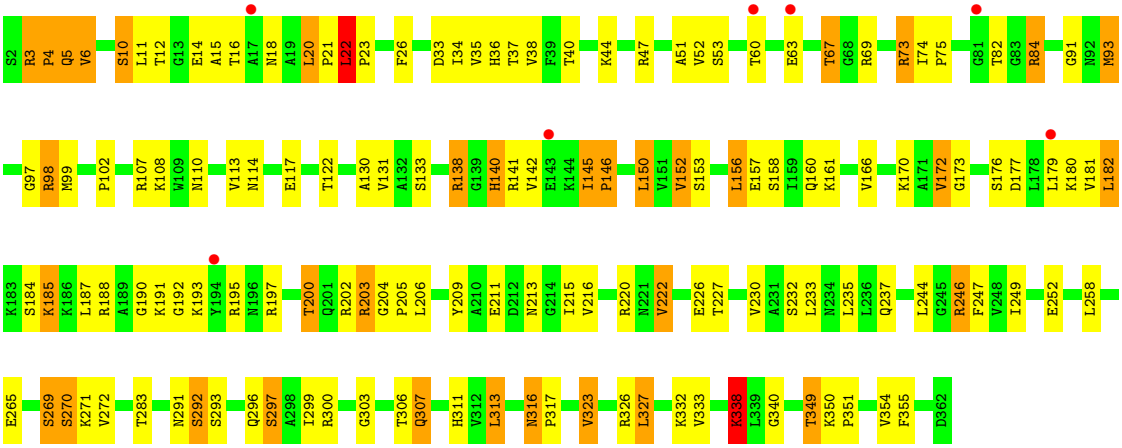
Chain l3:





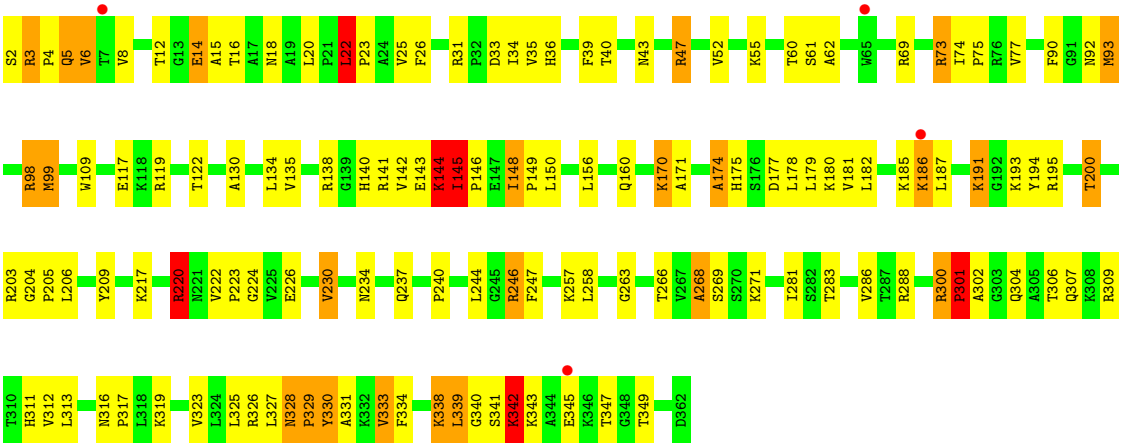
• Molecule 41: 60S ribosomal protein L4-A

Chain L4:



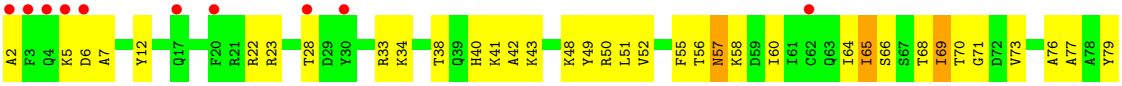
• Molecule 41: 60S ribosomal protein L4-A

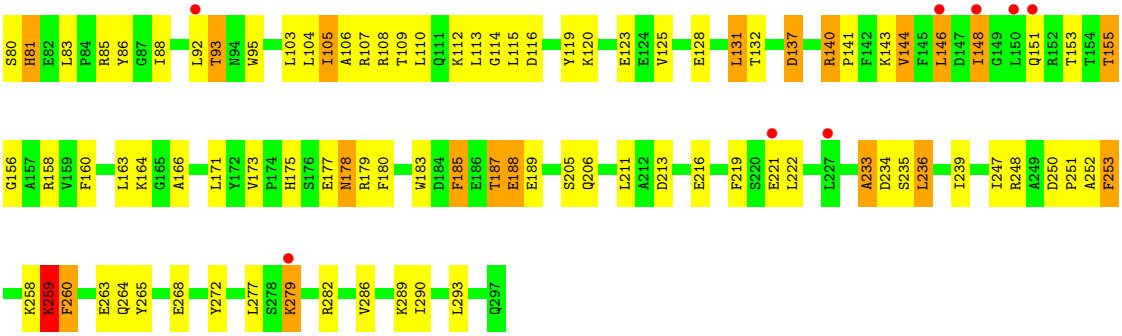
Chain l4:



• Molecule 42: 60S ribosomal protein L5

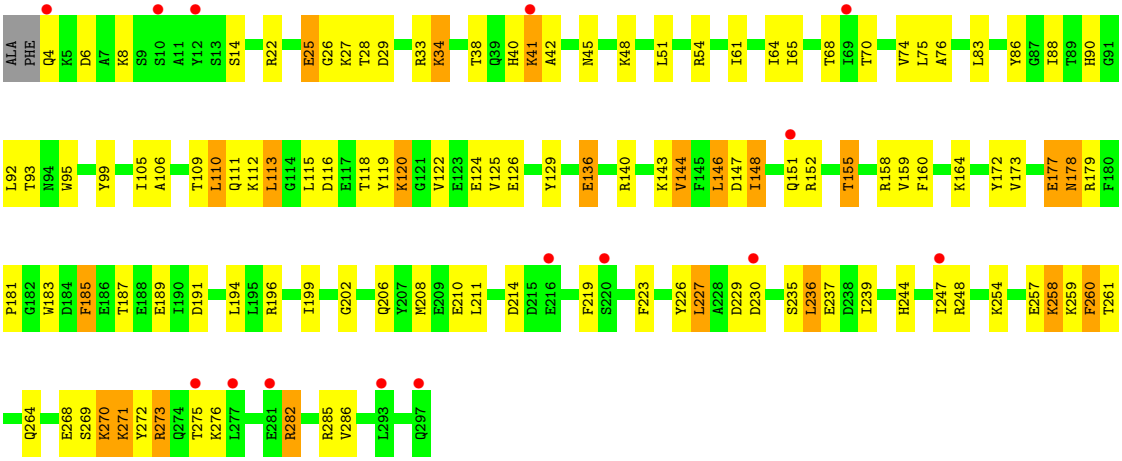
Chain L5:





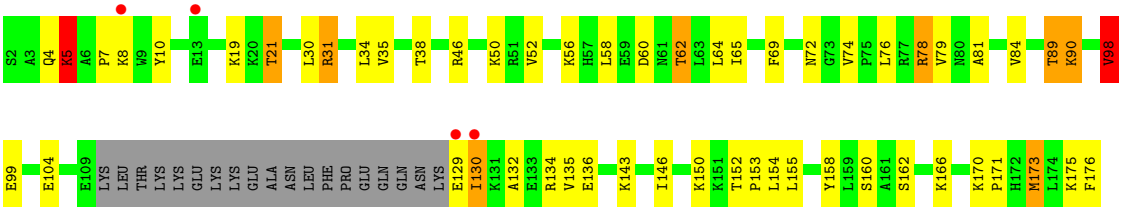
• Molecule 42: 60S ribosomal protein L5

Chain l5:



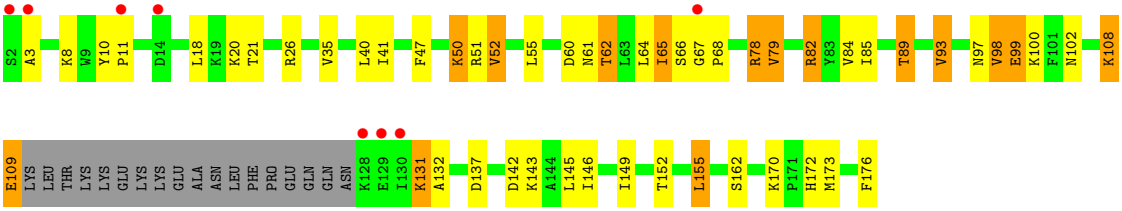
• Molecule 43: 60S ribosomal protein L6-A

Chain L6:



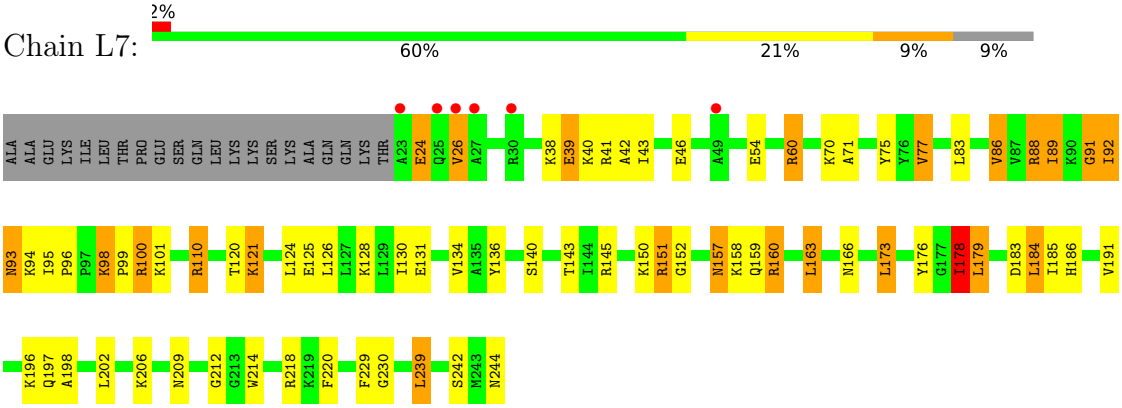
• Molecule 43: 60S ribosomal protein L6-A

Chain l6:



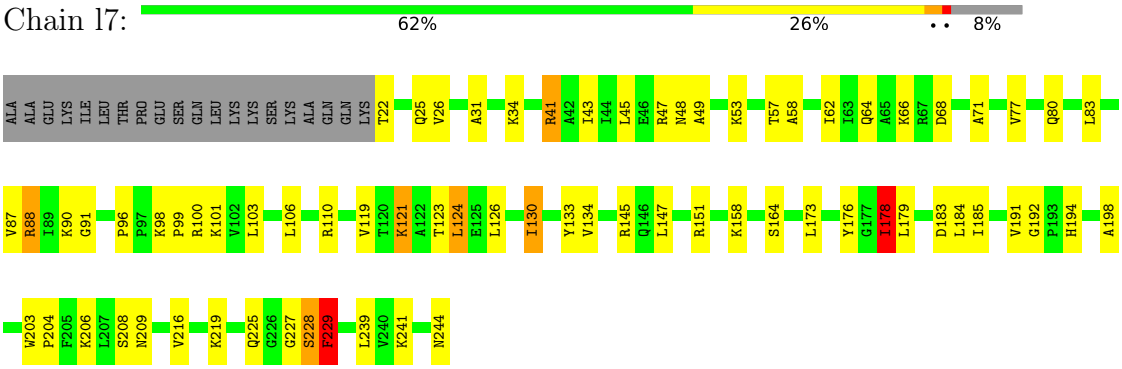
• Molecule 44: 60S ribosomal protein L7-A

Chain L7:



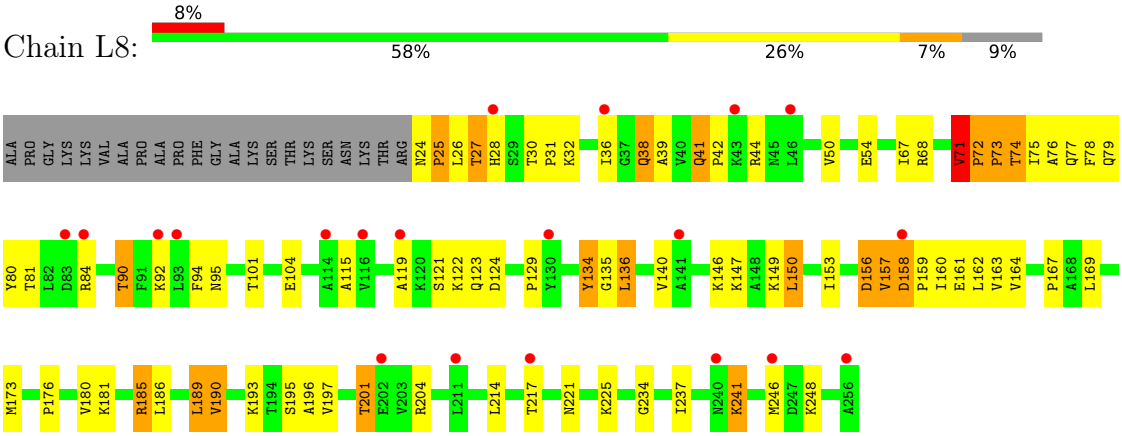
• Molecule 44: 60S ribosomal protein L7-A

Chain l7:



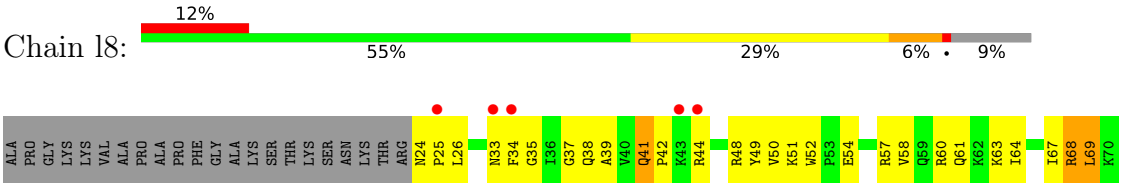
• Molecule 45: 60S ribosomal protein L8-A (eL8)

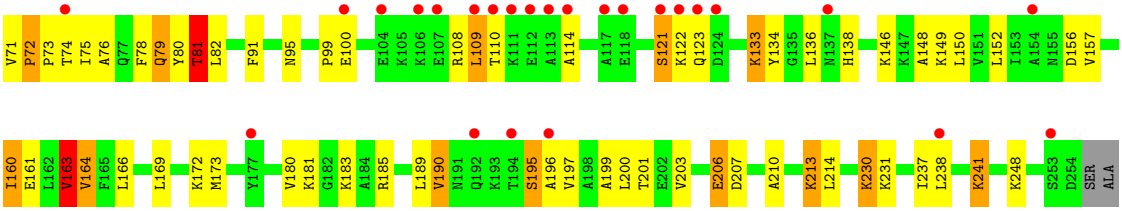
Chain L8:



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

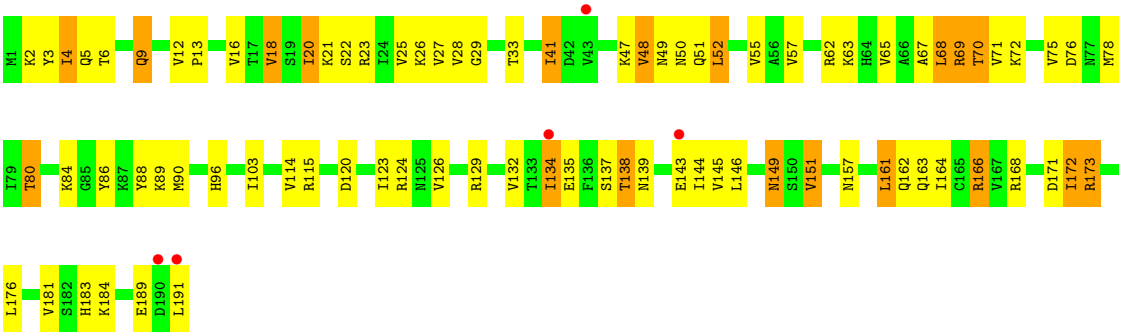
Chain l8:





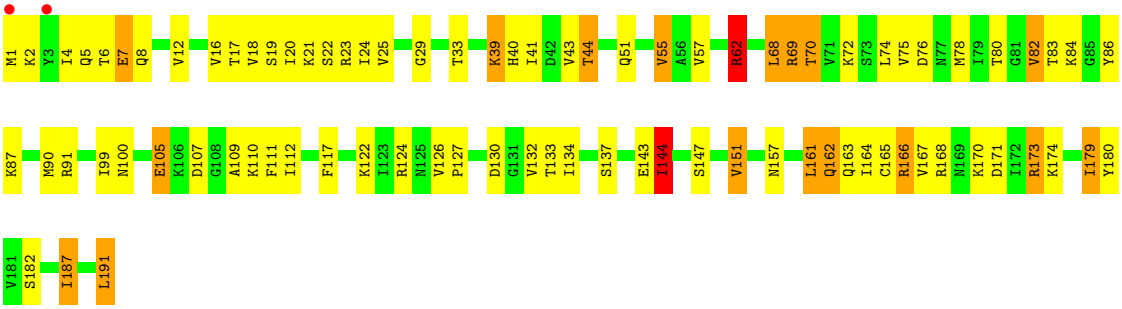
• Molecule 46: 60S ribosomal protein L9-A

Chain L9:



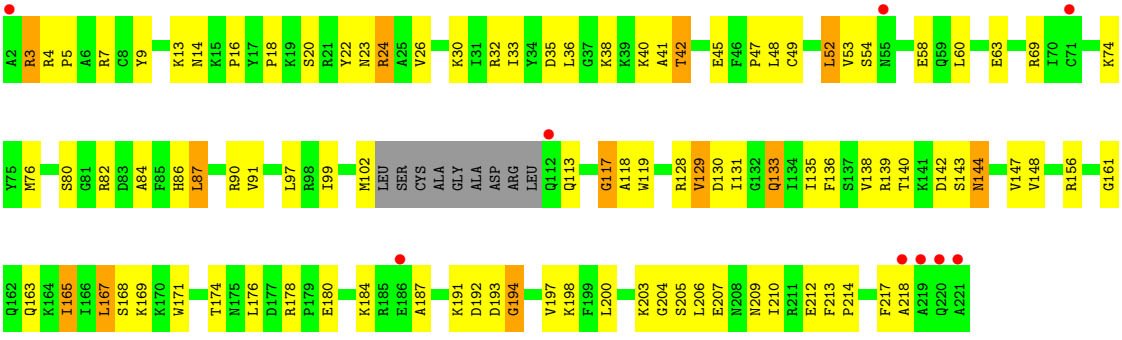
• Molecule 46: 60S ribosomal protein L9-A

Chain l9:



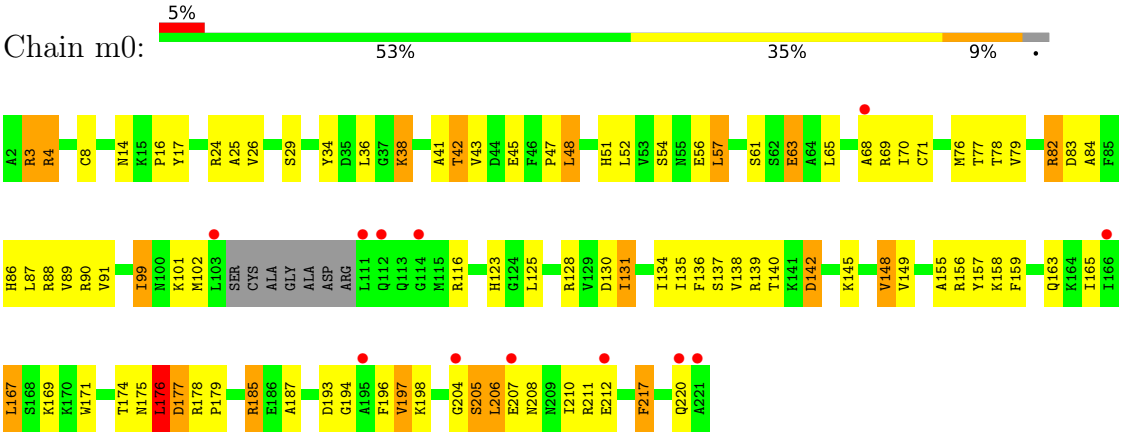
• Molecule 47: 60S ribosomal protein L10

Chain M0:



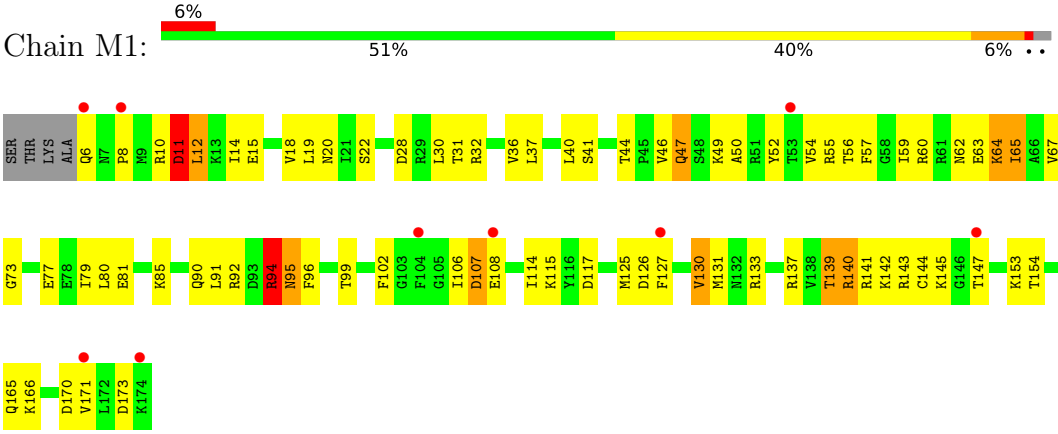
• Molecule 47: 60S ribosomal protein L10

Chain m0:



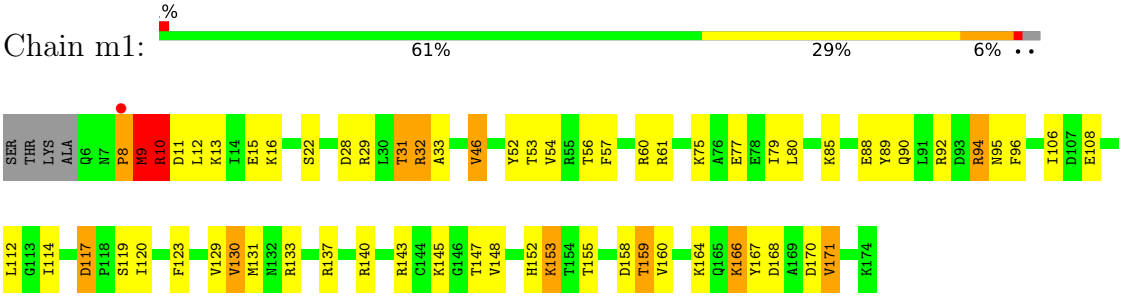
• Molecule 48: 60S ribosomal protein L11-B

Chain M1:



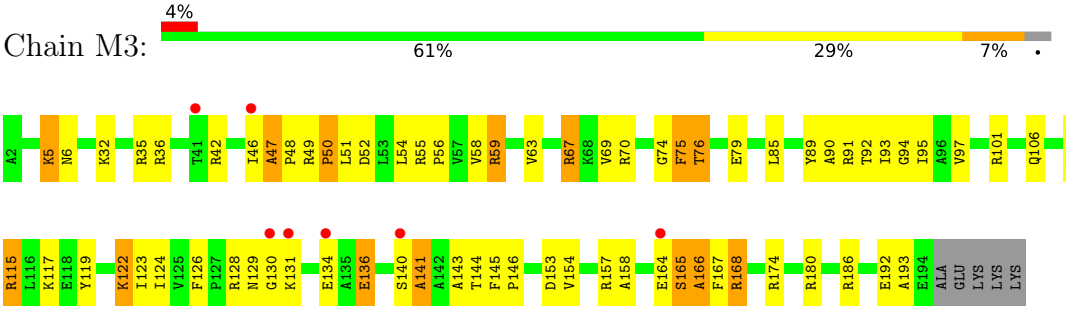
• Molecule 48: 60S ribosomal protein L11-B

Chain m1:



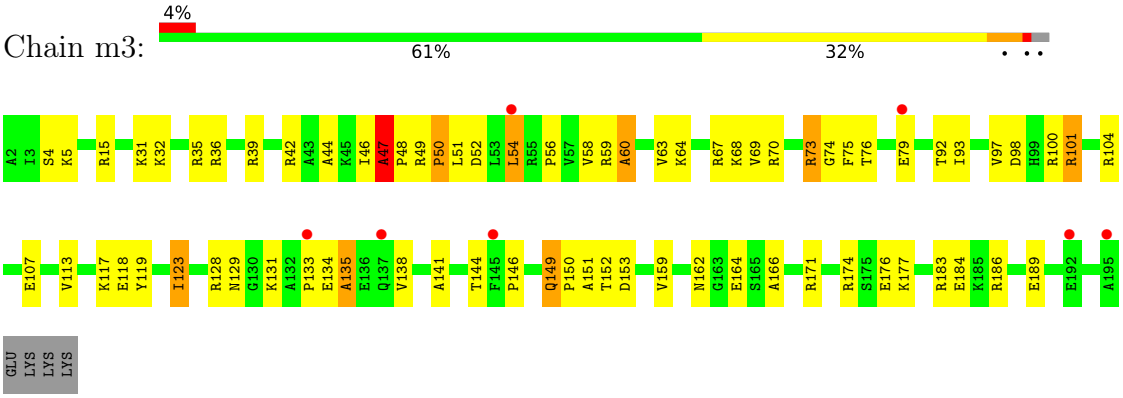
• Molecule 49: 60S ribosomal protein L13-A

Chain M3:



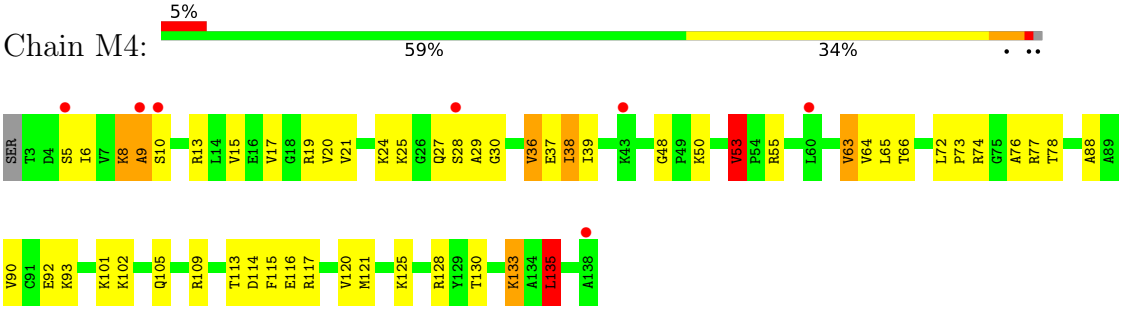
• Molecule 49: 60S ribosomal protein L13-A

Chain m3:



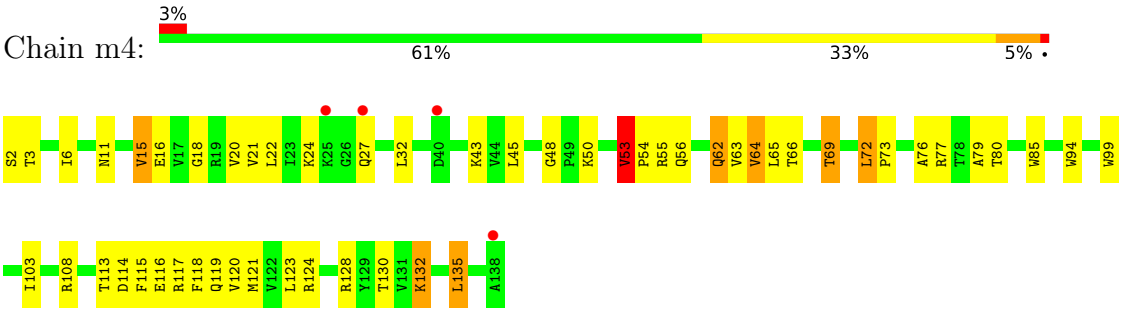
• Molecule 50: 60S ribosomal protein L14-A

Chain M4:



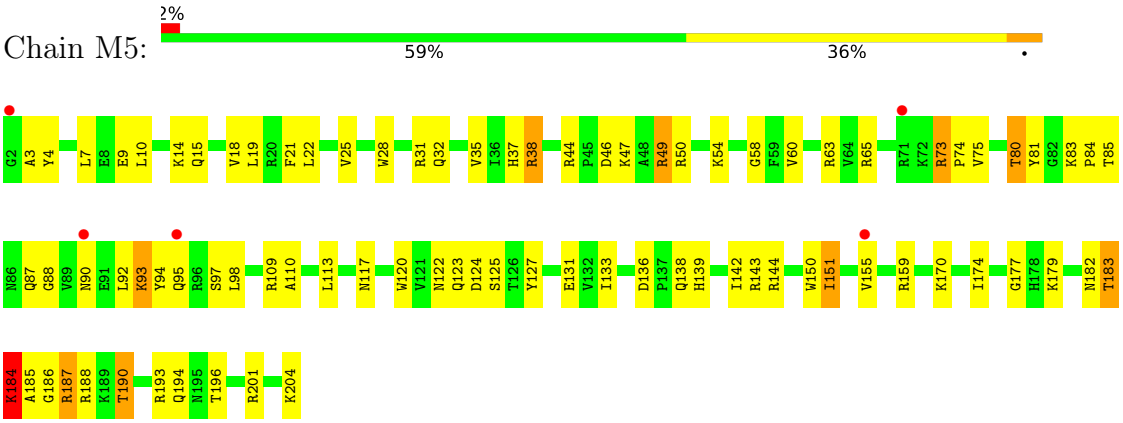
• Molecule 50: 60S ribosomal protein L14-A

Chain m4:



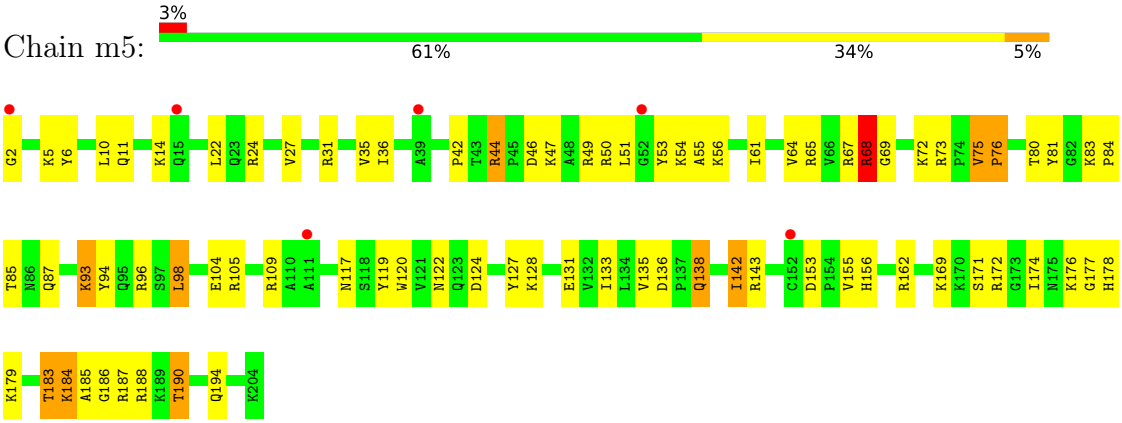
• Molecule 51: 60S ribosomal protein L15-A

Chain M5:



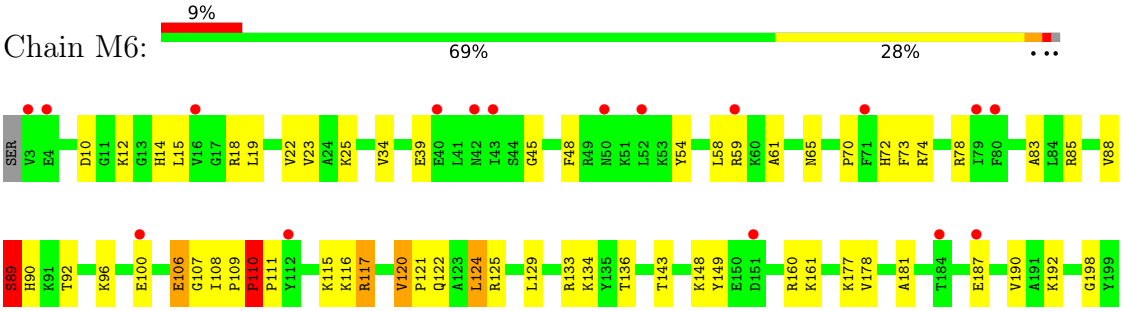
• Molecule 51: 60S ribosomal protein L15-A

Chain m5:



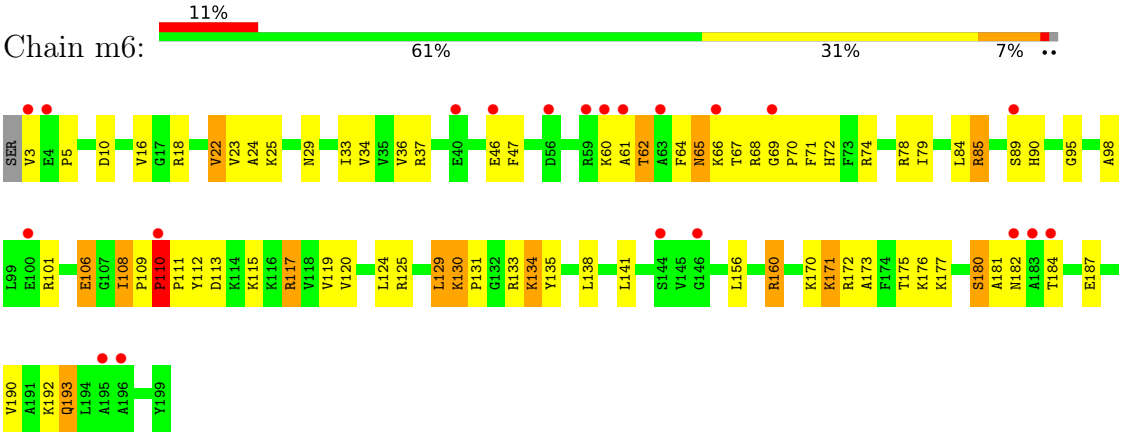
• Molecule 52: 60S ribosomal protein L16-A

Chain M6:



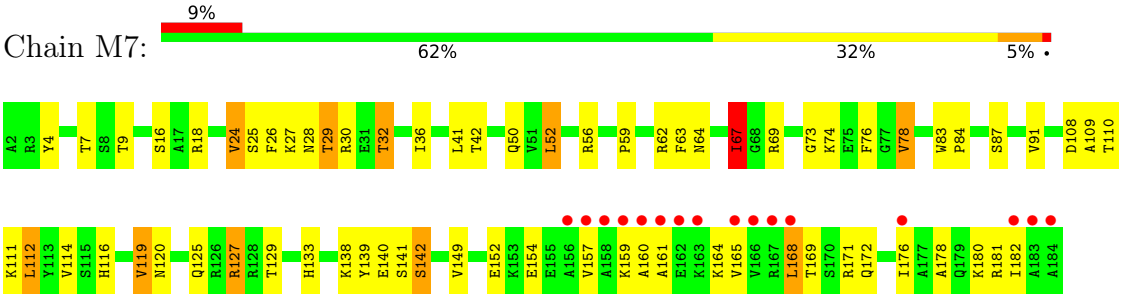
• Molecule 52: 60S ribosomal protein L16-A

Chain m6:



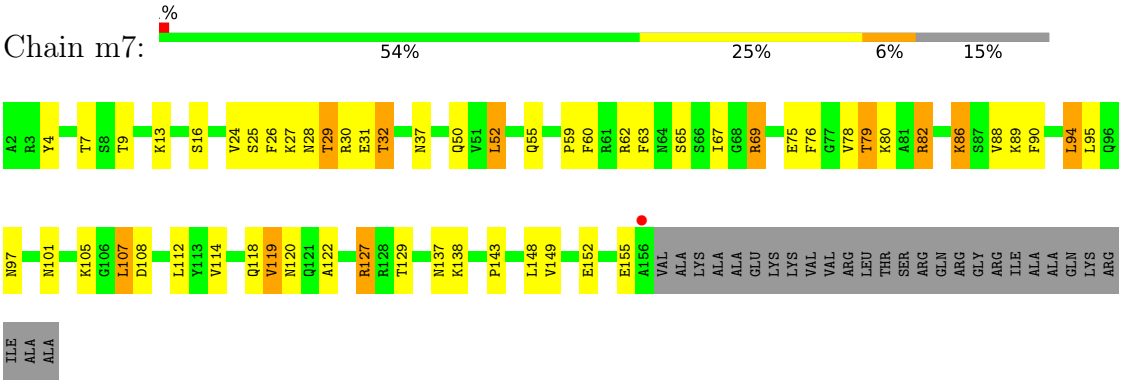
• Molecule 53: 60S ribosomal protein L17-A

Chain M7:



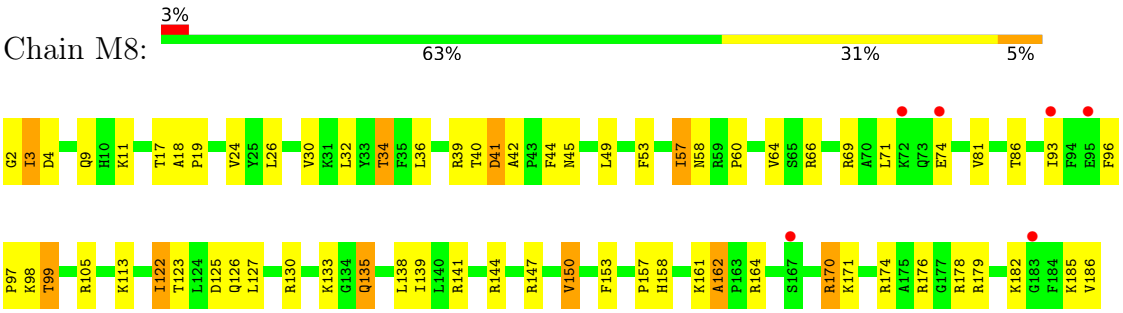
• Molecule 53: 60S ribosomal protein L17-A

Chain m7:



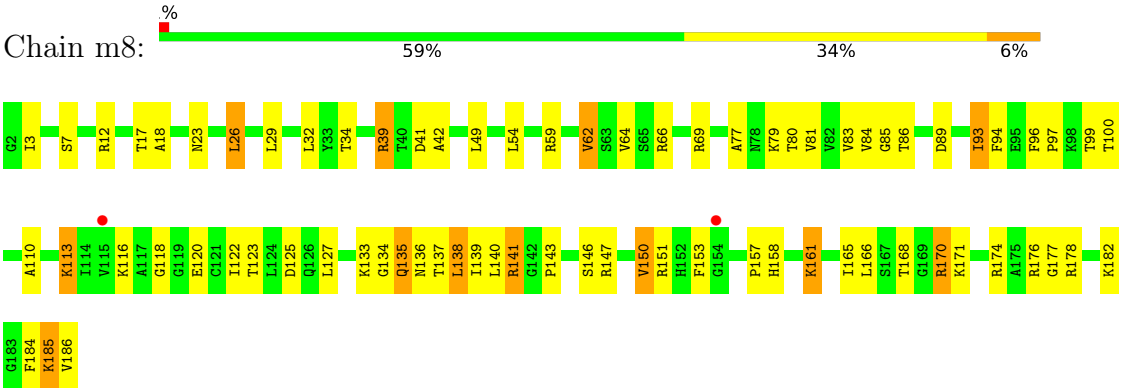
• Molecule 54: 60S ribosomal protein L18-A

Chain M8:



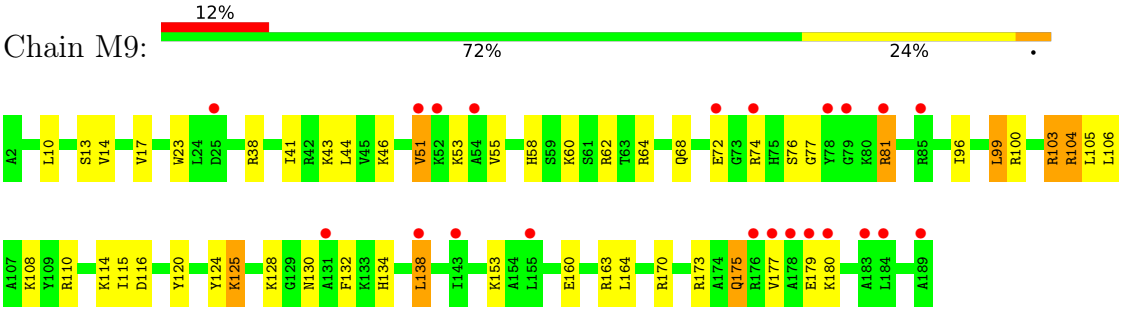
• Molecule 54: 60S ribosomal protein L18-A

Chain m8:



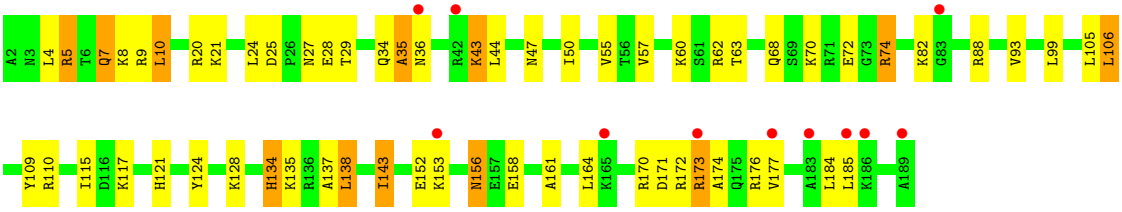
• Molecule 55: 60S ribosomal protein L19-A

Chain M9:



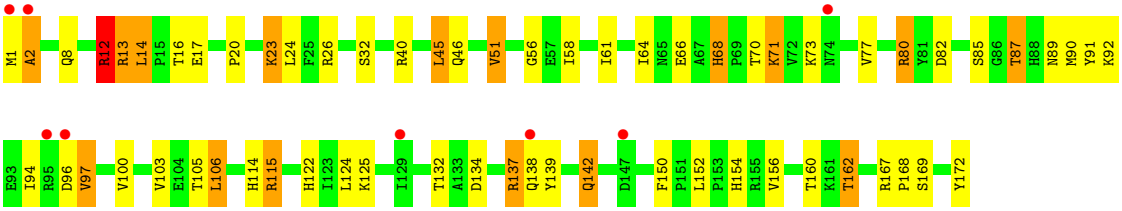
• Molecule 55: 60S ribosomal protein L19-A

Chain m9:



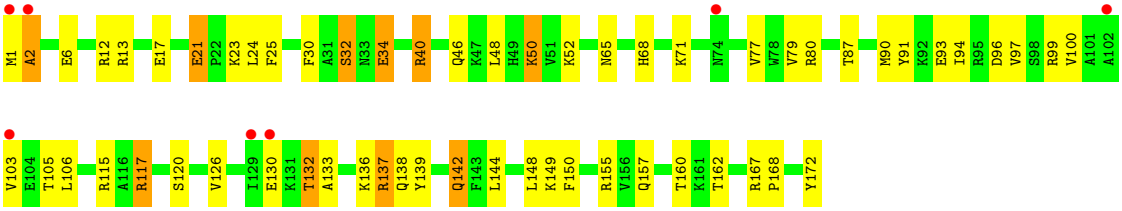
• Molecule 56: 60S ribosomal protein L20-A

Chain N0:



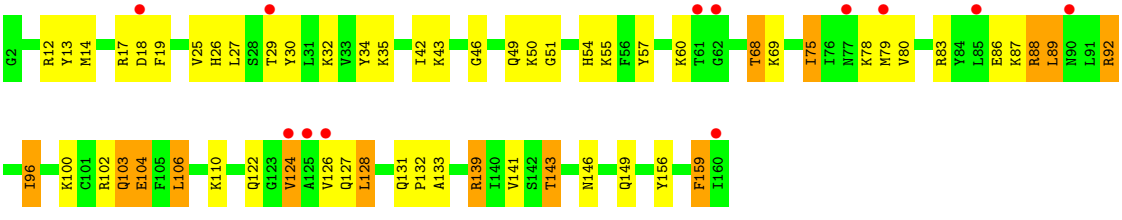
• Molecule 56: 60S ribosomal protein L20-A

Chain n0:



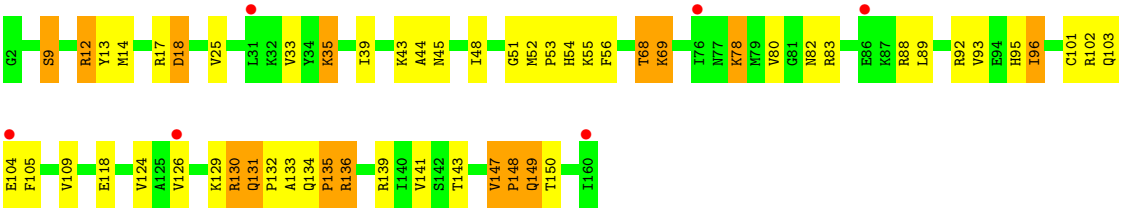
• Molecule 57: 60S ribosomal protein L21-A

Chain N1:



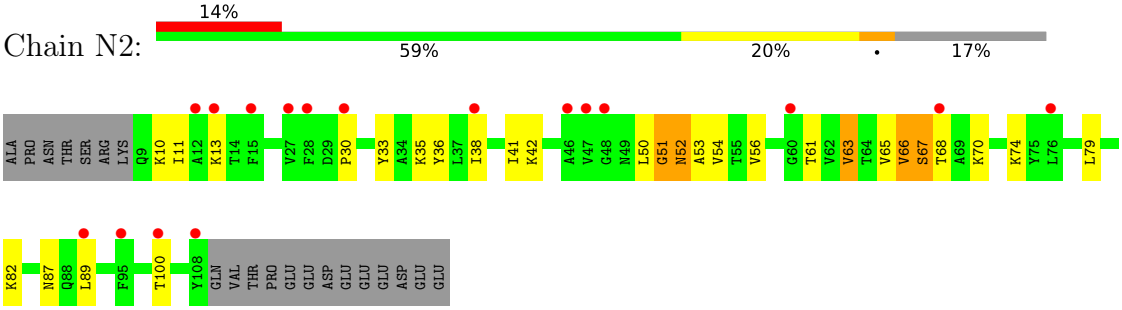
• Molecule 57: 60S ribosomal protein L21-A

Chain n1:



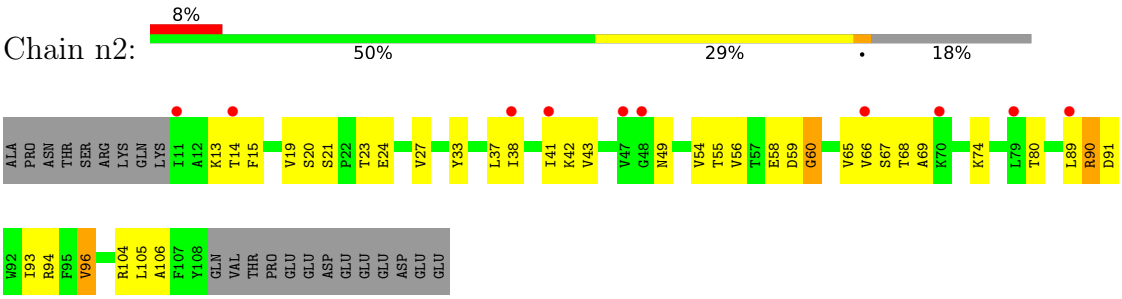
• Molecule 58: 60S ribosomal protein L22-A

Chain N2:



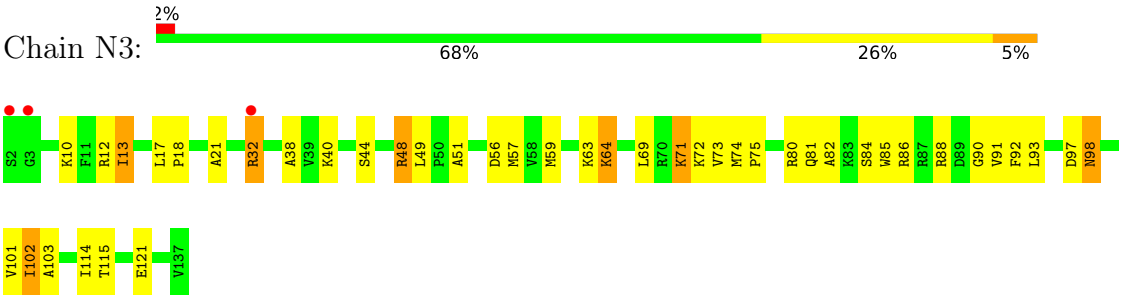
• Molecule 58: 60S ribosomal protein L22-A

Chain n2:



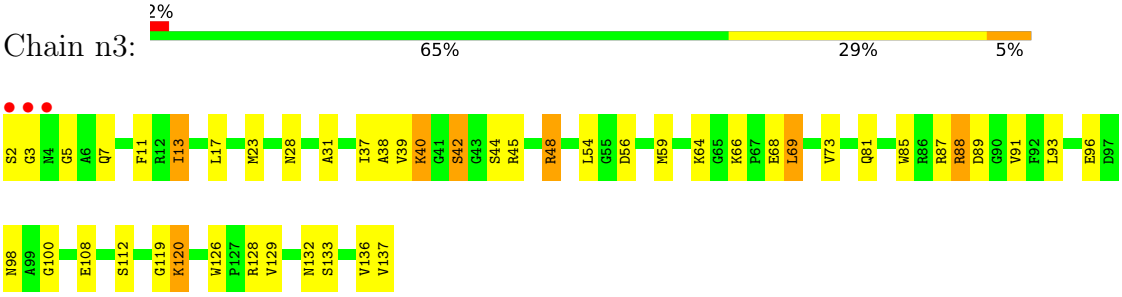
• Molecule 59: 60S ribosomal protein L23-A

Chain N3:



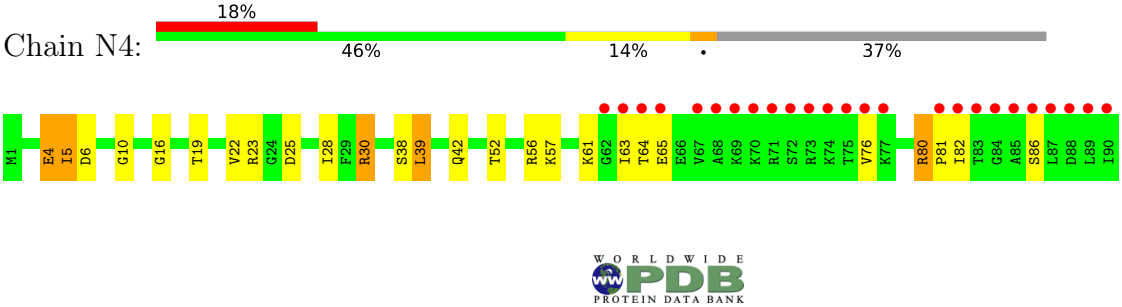
• Molecule 59: 60S ribosomal protein L23-A

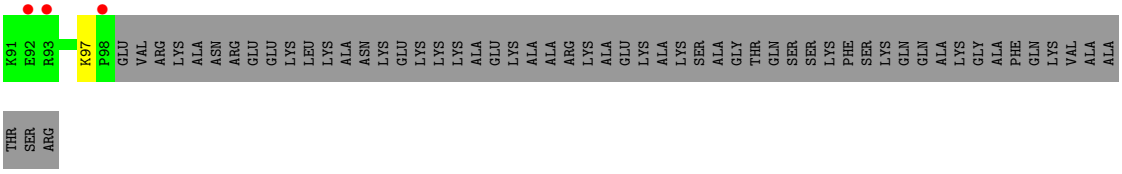
Chain n3:



• Molecule 60: 60S ribosomal protein L24-A

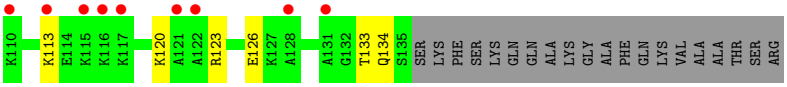
Chain N4:





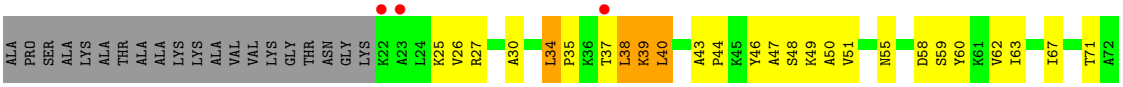
• Molecule 60: 60S ribosomal protein L24-A

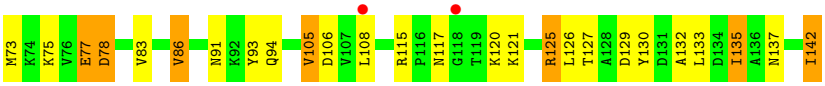
Chain n4:



• Molecule 61: 60S ribosomal protein L25

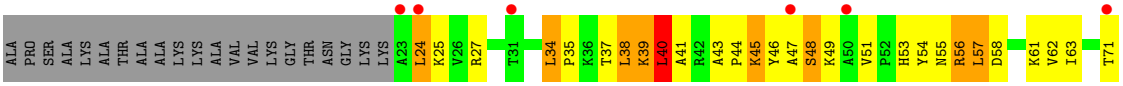
Chain N5:

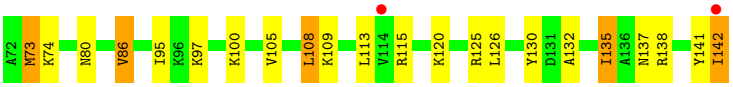




• Molecule 61: 60S ribosomal protein L25

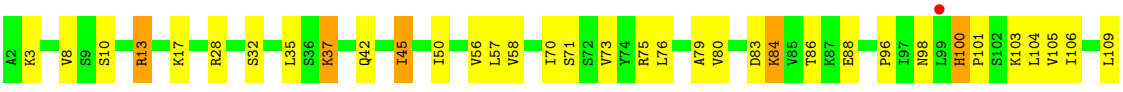
Chain n5:





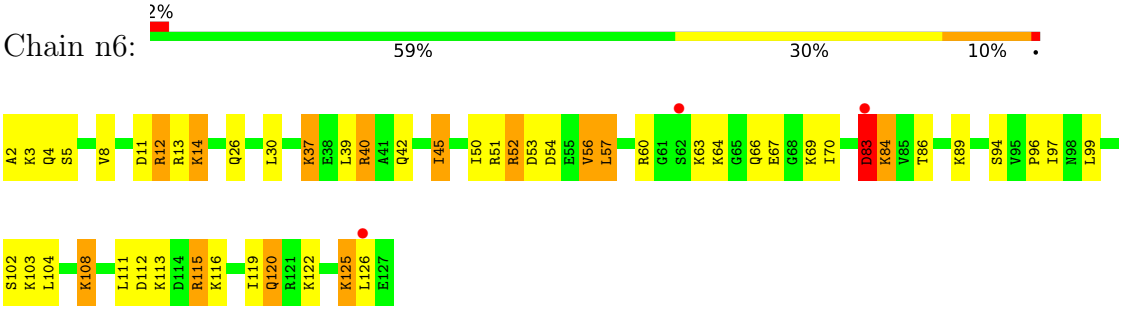
• Molecule 62: 60S ribosomal protein L26-A

Chain N6:



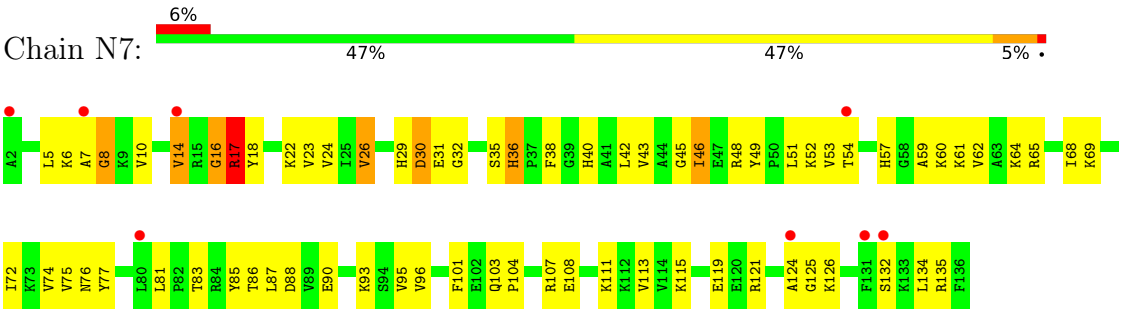
• Molecule 62: 60S ribosomal protein L26-A

Chain n6:



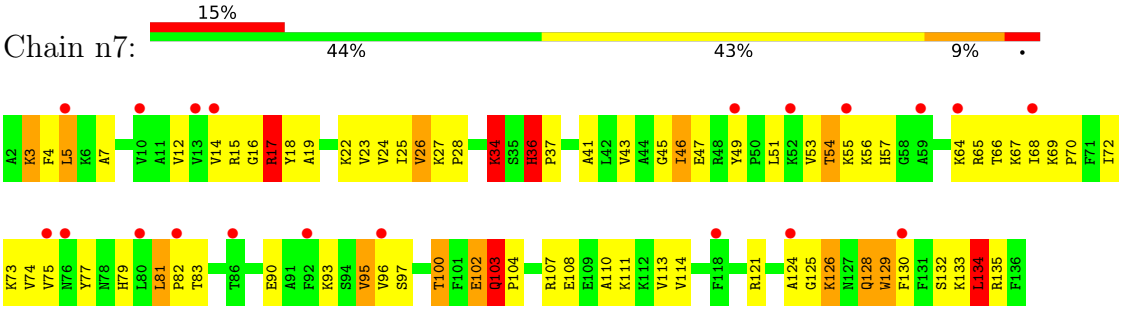
• Molecule 63: 60S ribosomal protein L27-A

Chain N7:



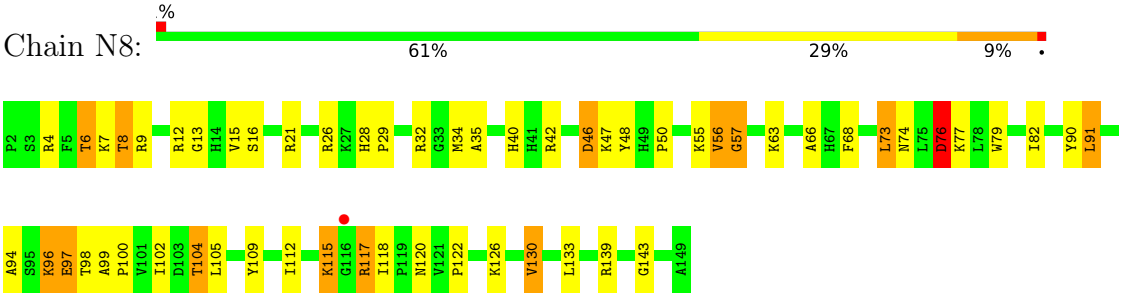
• Molecule 63: 60S ribosomal protein L27-A

Chain n7:



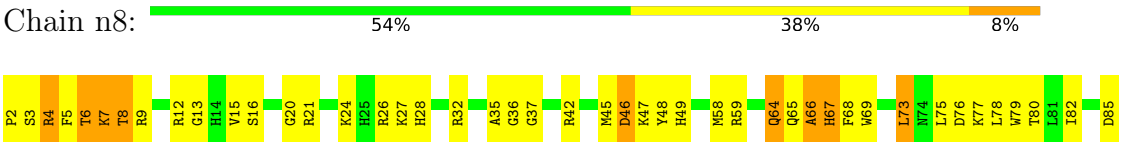
• Molecule 64: 60S ribosomal protein L28

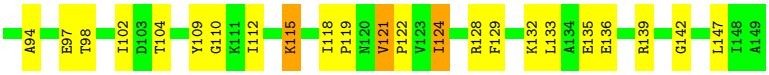
Chain N8:



• Molecule 64: 60S ribosomal protein L28

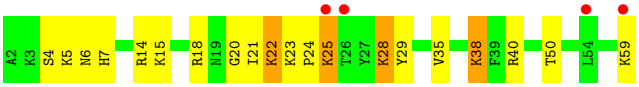
Chain n8:





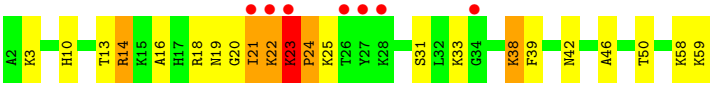
• Molecule 65: 60S ribosomal protein L29

Chain N9:



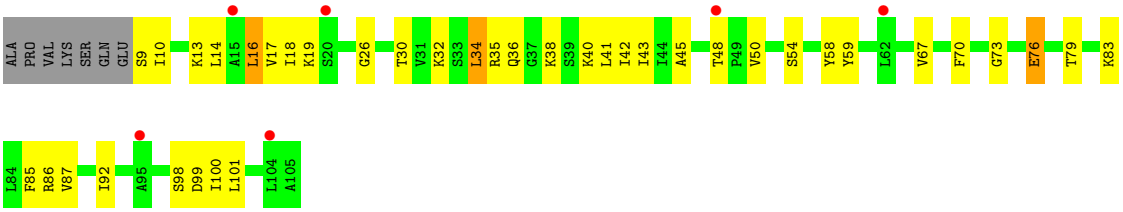
• Molecule 65: 60S ribosomal protein L29

Chain n9:



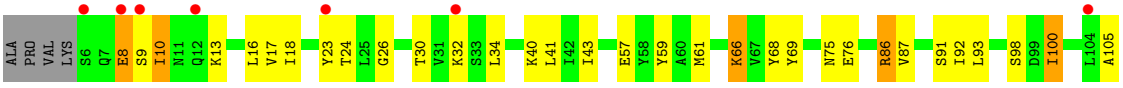
• Molecule 66: 60S ribosomal protein L30

Chain O0:



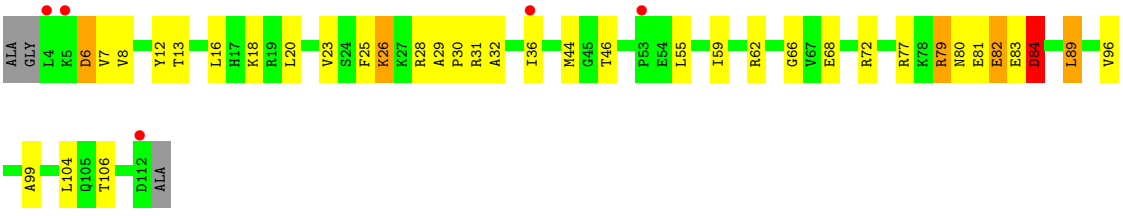
• Molecule 66: 60S ribosomal protein L30

Chain o0:



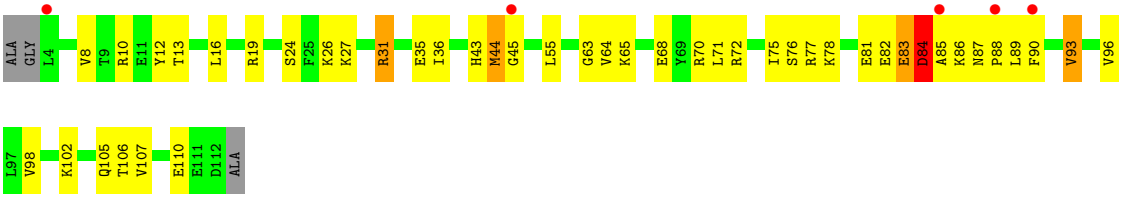
• Molecule 67: 60S ribosomal protein L31-A

Chain O1:



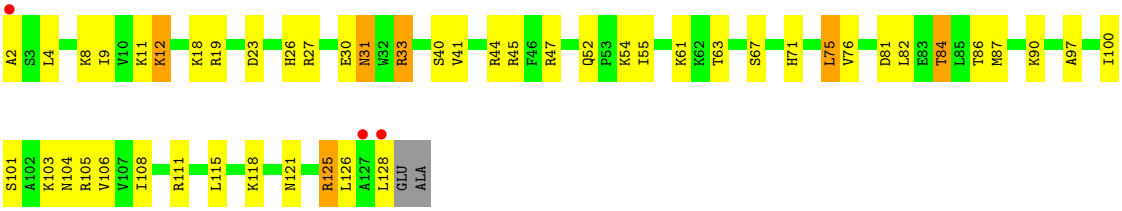
• Molecule 67: 60S ribosomal protein L31-A

Chain o1:



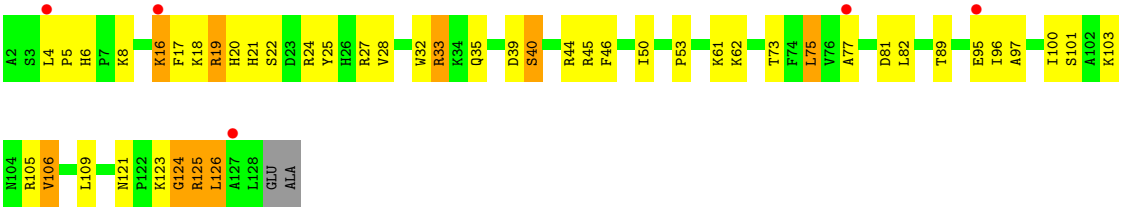
• Molecule 68: 60S ribosomal protein L32

Chain O2:



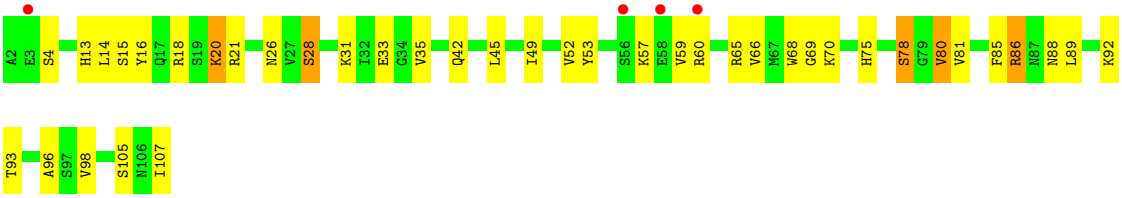
• Molecule 68: 60S ribosomal protein L32

Chain o2:



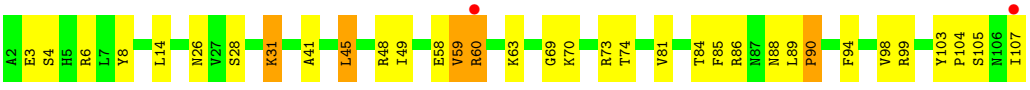
• Molecule 69: 60S ribosomal protein L33-A

Chain O3:



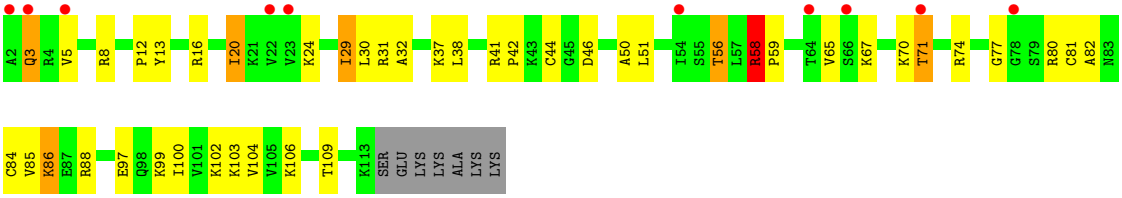
• Molecule 69: 60S ribosomal protein L33-A

Chain o3:



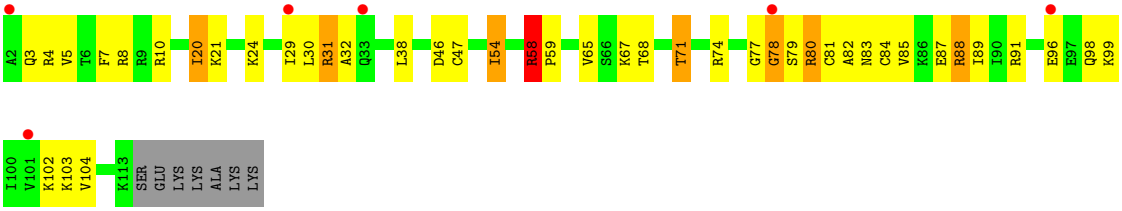
• Molecule 70: 60S ribosomal protein L34-A

Chain O4:



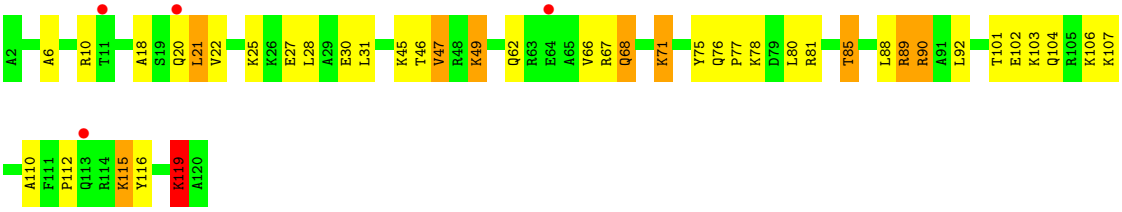
• Molecule 70: 60S ribosomal protein L34-A

Chain o4:



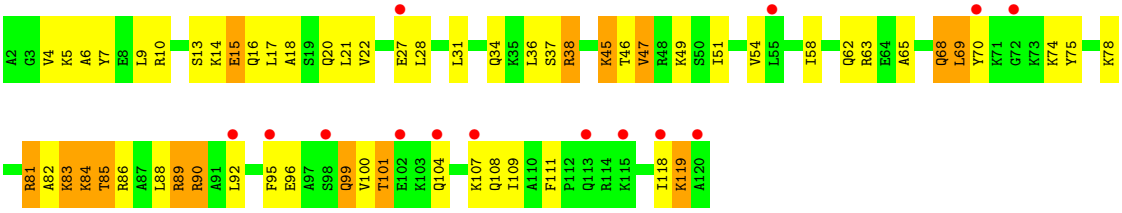
• Molecule 71: 60S ribosomal protein L35-A

Chain O5:



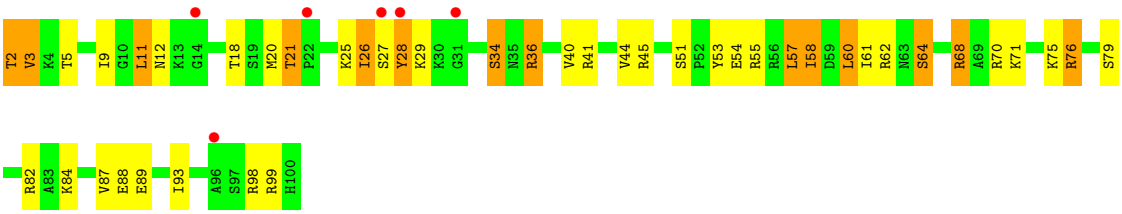
• Molecule 71: 60S ribosomal protein L35-A

Chain o5:



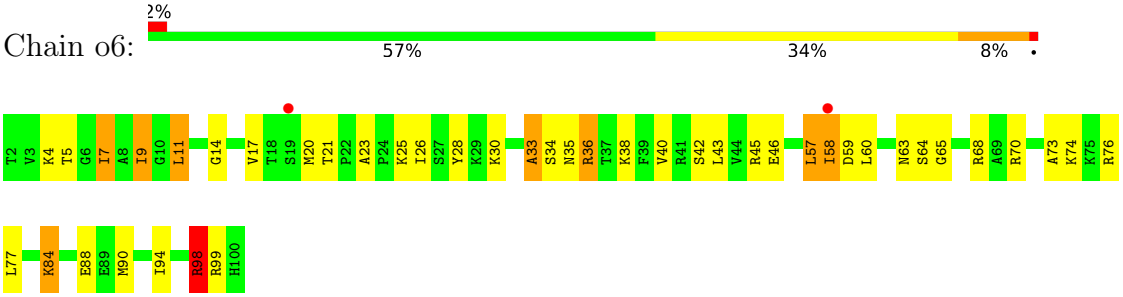
• Molecule 72: 60S ribosomal protein L36-A

Chain O6:



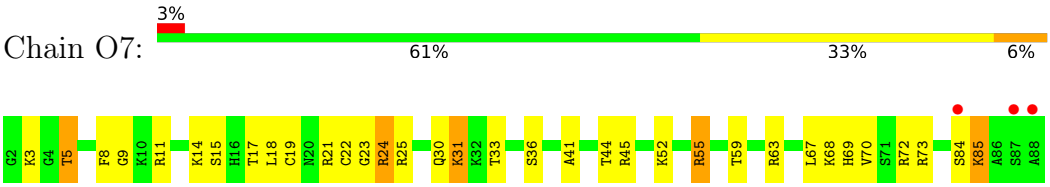
• Molecule 72: 60S ribosomal protein L36-A

Chain o6:



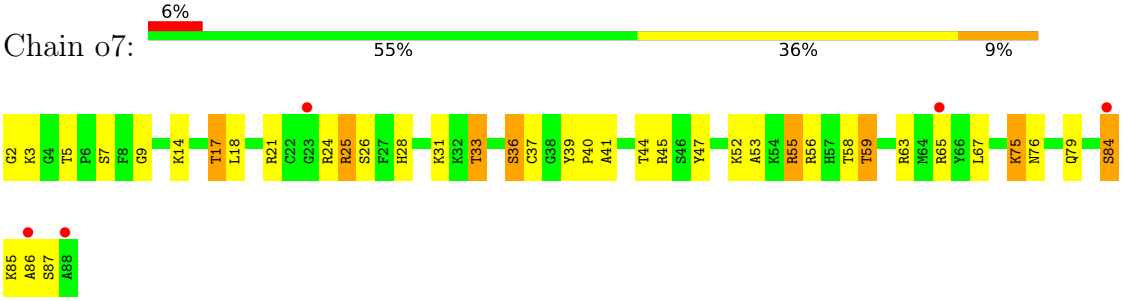
• Molecule 73: 60S ribosomal protein L37-A

Chain O7:



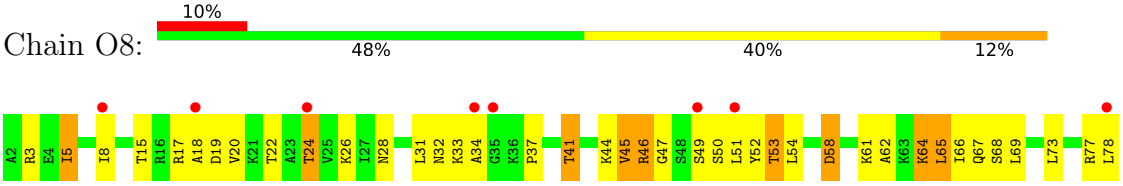
• Molecule 73: 60S ribosomal protein L37-A

Chain o7:



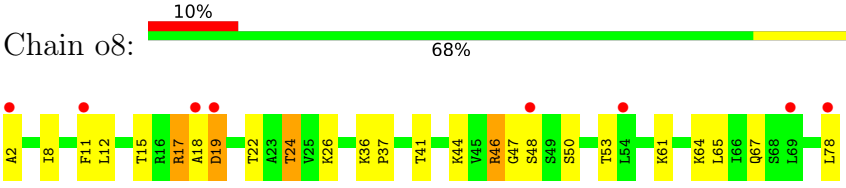
• Molecule 74: 60S ribosomal protein L38

Chain O8:



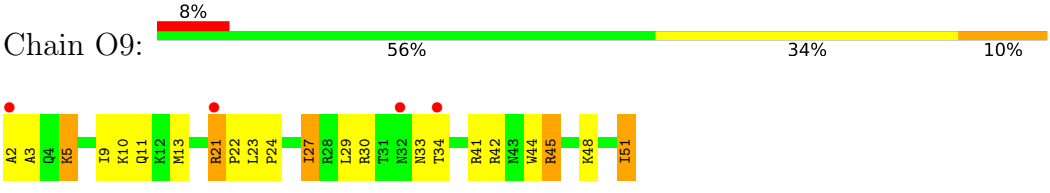
• Molecule 74: 60S ribosomal protein L38

Chain o8:



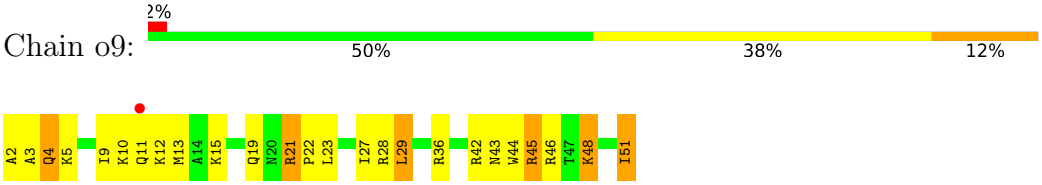
• Molecule 75: 60S ribosomal protein L39

Chain O9:



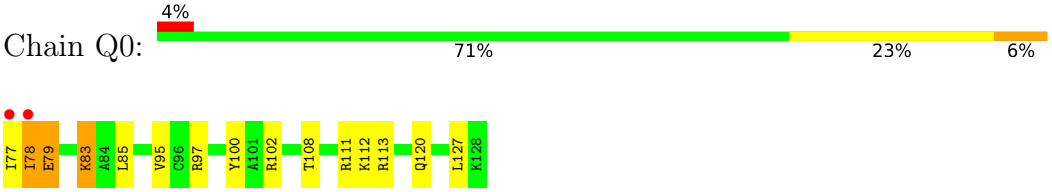
• Molecule 75: 60S ribosomal protein L39

Chain o9:



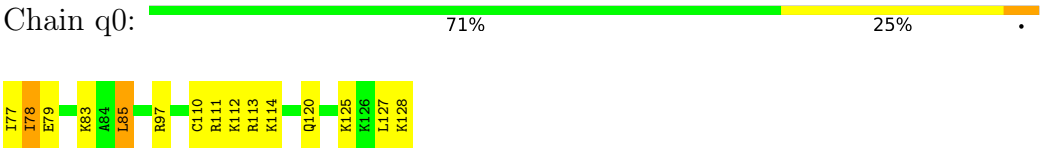
• Molecule 76: Ubiquitin-60S ribosomal protein L40

Chain Q0:



• Molecule 76: Ubiquitin-60S ribosomal protein L40

Chain q0:



• Molecule 77: 60S ribosomal protein L41-A

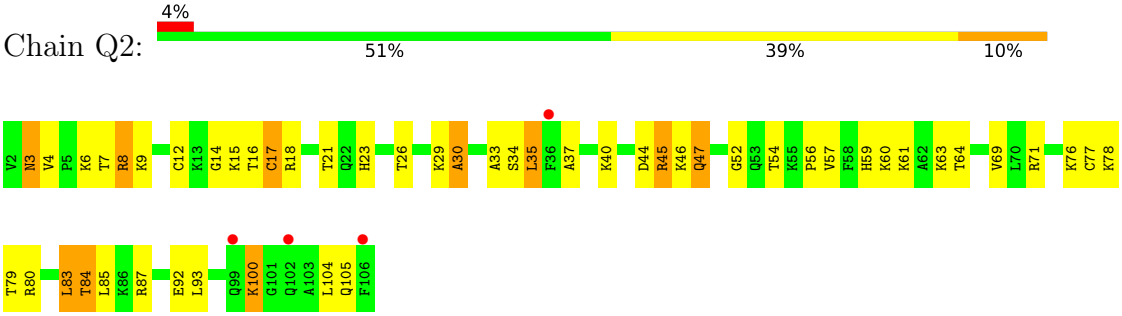
Chain Q1:

• Molecule 77: 60S ribosomal protein L41-A

Chain q1:

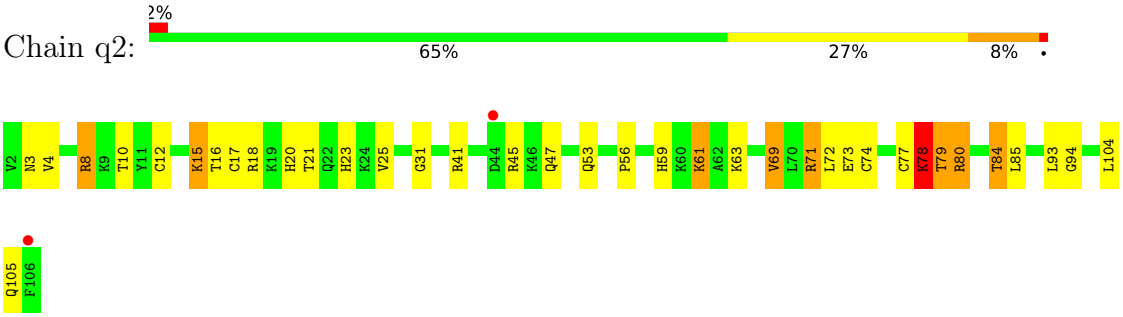
• Molecule 78: 60S ribosomal protein L42-A

Chain Q2:



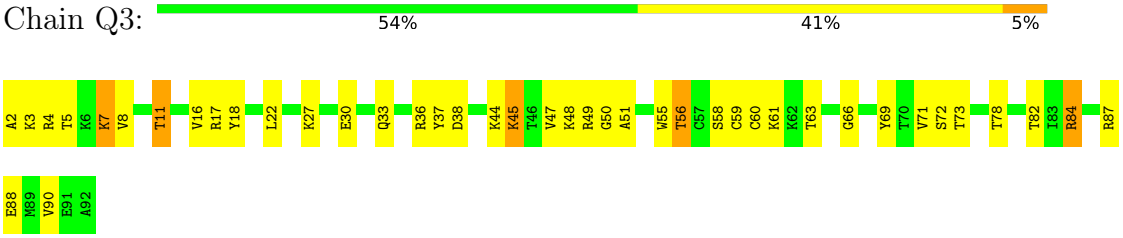
• Molecule 78: 60S ribosomal protein L42-A

Chain q2:



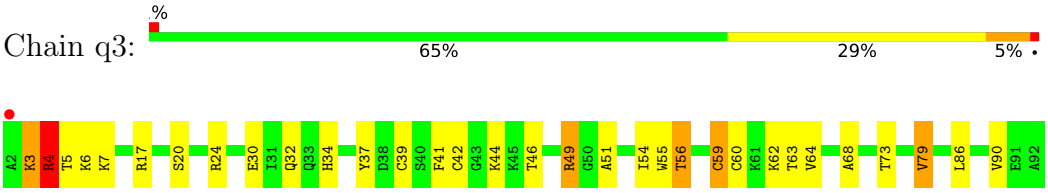
• Molecule 79: 60S ribosomal protein L43-A

Chain Q3:



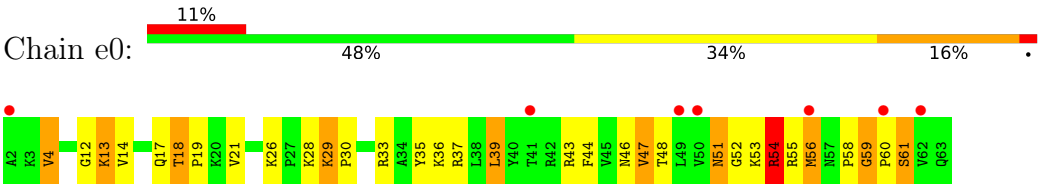
• Molecule 79: 60S ribosomal protein L43-A

Chain q3:



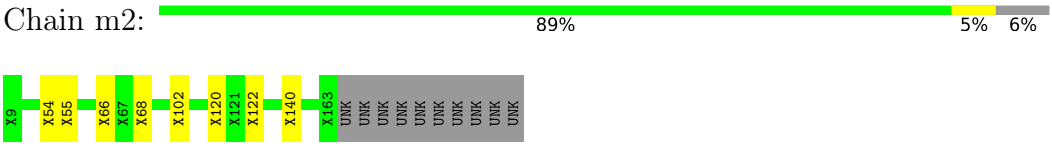
• Molecule 80: 40S ribosomal protein S30-A

Chain e0:



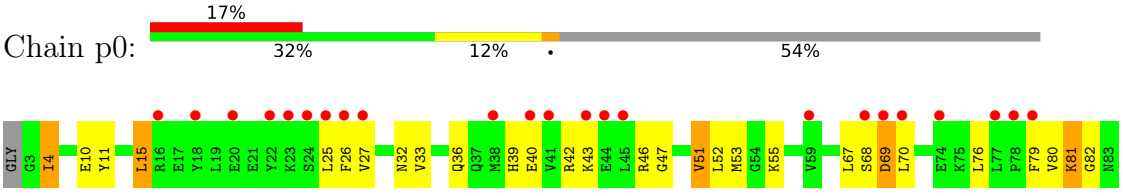
• Molecule 81: 60S ribosomal protein L12-A (uL11)

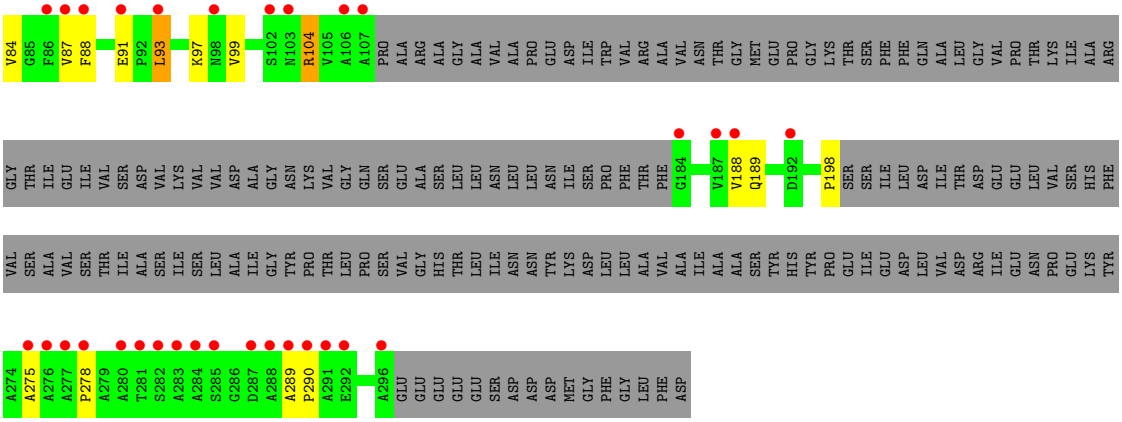
Chain m2:



• Molecule 82: 60S acidic ribosomal protein P0

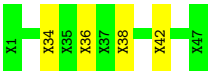
Chain p0:





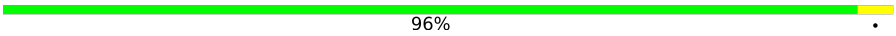
• Molecule 83: 60S ribosomal protein P1 alpha/P2 beta

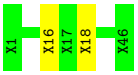
Chain p1:



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

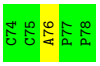
Chain p2:





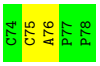
• Molecule 85: DNA (5'-R(*CP*CP*(8AN)*(Pro)*(Pro))-3')

Chain C:



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

Chain D:



4 Data and refinement statistics (i)

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 – 3.10 149.05 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (149.05-3.10) 99.9 (149.05-3.10)	Depositor EDS
R_{merge}	0.56	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.50 (at 3.07Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.238 , 0.284 0.244 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	73.7	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 72.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.31$	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.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: MG, SPS, ZN, 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	0.21	0/42467	0.40	1/66169 (0.0%)
1	6	0.23	0/42790	0.42	1/66673 (0.0%)
2	S0	0.36	0/1617	0.87	5/2215 (0.2%)
2	s0	0.39	0/1623	0.90	5/2222 (0.2%)
3	S1	0.33	0/1735	0.80	3/2335 (0.1%)
3	s1	0.38	0/1748	0.85	6/2352 (0.3%)
4	S2	0.38	0/1665	0.82	0/2263
4	s2	0.44	0/1665	0.92	6/2263 (0.3%)
5	S3	0.36	0/1759	0.80	4/2368 (0.2%)
5	s3	0.34	0/1759	0.78	4/2368 (0.2%)
6	S4	0.38	0/2109	0.86	5/2839 (0.2%)
6	s4	0.40	0/2109	0.83	3/2839 (0.1%)
7	S5	0.33	0/1629	0.81	1/2202 (0.0%)
7	s5	0.34	0/1629	0.83	5/2202 (0.2%)
8	S6	0.36	0/1823	0.77	4/2439 (0.2%)
8	s6	0.37	0/1779	0.83	2/2379 (0.1%)
9	S7	0.35	0/1506	0.87	4/2028 (0.2%)
9	s7	0.37	0/1516	0.83	5/2043 (0.2%)
10	S8	0.42	0/1514	0.81	0/2021
10	s8	0.44	0/1514	0.86	4/2021 (0.2%)
11	S9	0.34	0/1519	0.84	4/2035 (0.2%)
11	s9	0.39	0/1519	0.85	3/2035 (0.1%)
12	C0	0.36	0/790	0.83	1/1069 (0.1%)
12	c0	0.33	0/777	0.85	3/1049 (0.3%)
13	C1	0.41	0/1239	0.87	2/1673 (0.1%)
13	c1	0.46	0/1194	0.87	1/1610 (0.1%)
14	C2	0.35	0/900	0.76	0/1224
14	c2	0.32	0/900	0.72	0/1224
15	C3	0.39	0/1215	0.82	3/1638 (0.2%)
15	c3	0.45	0/1215	0.89	5/1638 (0.3%)
16	C4	0.37	0/901	0.87	3/1217 (0.2%)
16	c4	0.42	0/960	0.89	1/1290 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	C5	0.38	0/998	0.95	6/1341 (0.4%)
17	c5	0.40	0/1060	0.88	4/1426 (0.3%)
18	C6	0.36	0/1125	0.82	3/1510 (0.2%)
18	c6	0.38	0/1131	0.83	3/1518 (0.2%)
19	C7	0.39	0/935	0.87	0/1254
19	c7	0.35	0/914	0.79	0/1224
20	C8	0.35	0/1211	0.82	3/1628 (0.2%)
20	c8	0.35	0/1211	0.73	0/1628
21	C9	0.36	0/1130	0.81	2/1517 (0.1%)
21	c9	0.38	0/1130	0.85	1/1517 (0.1%)
22	D0	0.36	0/865	0.81	0/1169
22	d0	0.36	0/892	0.85	3/1205 (0.2%)
23	D1	0.35	0/693	0.79	3/935 (0.3%)
23	d1	0.39	0/693	0.80	0/935
24	D2	0.40	0/1038	0.94	5/1395 (0.4%)
24	d2	0.43	0/1038	0.84	1/1395 (0.1%)
25	D3	0.46	0/1139	0.91	3/1518 (0.2%)
25	d3	0.47	0/1139	0.87	4/1518 (0.3%)
26	D4	0.35	0/1087	0.78	0/1449
26	d4	0.38	0/1087	0.90	4/1449 (0.3%)
27	D5	0.38	0/571	0.89	0/768
27	d5	0.33	0/566	0.79	0/761
28	D6	0.41	0/782	0.90	1/1047 (0.1%)
28	d6	0.44	0/782	0.86	0/1047
29	D7	0.36	0/620	0.86	2/838 (0.2%)
29	d7	0.36	0/620	0.86	2/838 (0.2%)
30	D8	0.32	0/499	0.80	0/670
30	d8	0.35	0/499	0.81	0/670
31	D9	0.37	0/452	0.78	0/600
31	d9	0.38	0/452	0.89	2/600 (0.3%)
32	E0	0.37	0/483	0.84	0/643
33	E1	0.40	0/577	0.84	1/770 (0.1%)
33	e1	0.43	0/619	0.94	2/822 (0.2%)
34	SR	0.31	0/2490	0.74	2/3389 (0.1%)
34	sR	0.30	0/2495	0.72	2/3395 (0.1%)
35	SM	0.46	0/984	0.91	6/1323 (0.5%)
35	sM	0.45	0/585	0.80	0/788
36	1	0.30	0/75368	0.50	8/117502 (0.0%)
36	5	0.32	0/75388	0.50	0/117532
37	3	0.25	0/2883	0.41	0/4491
37	7	0.31	0/2883	0.49	0/4491
38	4	0.30	0/3746	0.47	0/5832
38	8	0.27	0/3746	0.45	0/5832

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
39	L2	0.52	0/1948	0.91	2/2617 (0.1%)
39	l2	0.54	0/1946	0.92	5/2614 (0.2%)
40	L3	0.49	0/3146	0.87	1/4228 (0.0%)
40	l3	0.55	0/3146	0.89	1/4228 (0.0%)
41	L4	0.53	0/2800	1.00	13/3790 (0.3%)
41	l4	0.52	0/2800	0.93	9/3790 (0.2%)
42	L5	0.40	0/2425	0.80	2/3271 (0.1%)
42	l5	0.48	0/2408	0.88	4/3248 (0.1%)
43	L6	0.48	0/1260	0.86	2/1694 (0.1%)
43	l6	0.50	0/1269	0.88	0/1705
44	L7	0.53	0/1821	0.88	2/2451 (0.1%)
44	l7	0.54	0/1828	0.94	3/2461 (0.1%)
45	L8	0.42	0/1836	0.92	9/2481 (0.4%)
45	l8	0.41	0/1796	0.86	5/2431 (0.2%)
46	L9	0.46	0/1539	0.83	1/2073 (0.0%)
46	l9	0.50	0/1539	0.88	1/2073 (0.0%)
47	M0	0.47	0/1741	0.84	1/2335 (0.0%)
47	m0	0.52	0/1758	0.88	2/2358 (0.1%)
48	M1	0.39	0/1374	0.83	2/1842 (0.1%)
48	m1	0.47	0/1374	0.87	0/1842
49	M3	0.51	0/1568	0.90	2/2106 (0.1%)
49	m3	0.49	0/1573	0.91	4/2113 (0.2%)
50	M4	0.47	0/1068	0.92	3/1438 (0.2%)
50	m4	0.52	0/1074	0.92	2/1446 (0.1%)
51	M5	0.51	0/1757	0.90	6/2354 (0.3%)
51	m5	0.46	0/1757	0.90	7/2354 (0.3%)
52	M6	0.37	0/1585	0.85	4/2128 (0.2%)
52	m6	0.41	0/1585	0.89	5/2128 (0.2%)
53	M7	0.54	0/1443	0.93	2/1944 (0.1%)
53	m7	0.57	0/1250	0.88	1/1683 (0.1%)
54	M8	0.51	0/1465	0.96	3/1965 (0.2%)
54	m8	0.51	0/1465	0.97	6/1965 (0.3%)
55	M9	0.42	0/1538	0.80	1/2050 (0.0%)
55	m9	0.45	0/1538	0.84	1/2050 (0.0%)
56	N0	0.50	0/1481	0.92	7/1990 (0.4%)
56	n0	0.51	0/1481	0.91	4/1990 (0.2%)
57	N1	0.48	0/1300	0.85	0/1743
57	n1	0.52	0/1300	0.89	4/1743 (0.2%)
58	N2	0.35	0/812	0.78	1/1099 (0.1%)
58	n2	0.35	0/794	0.87	2/1076 (0.2%)
59	N3	0.50	0/1018	0.86	0/1369
59	n3	0.60	0/1018	1.03	6/1369 (0.4%)
60	N4	0.41	0/712	0.95	2/958 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
60	n4	0.45	0/1052	0.89	1/1398 (0.1%)
61	N5	0.43	0/979	0.87	2/1321 (0.2%)
61	n5	0.44	0/974	0.88	2/1314 (0.2%)
62	N6	0.47	0/1004	0.93	2/1341 (0.1%)
62	n6	0.47	0/1004	0.84	0/1341
63	N7	0.38	0/1118	0.87	2/1497 (0.1%)
63	n7	0.38	0/1118	0.80	0/1497
64	N8	0.53	0/1204	0.90	1/1612 (0.1%)
64	n8	0.52	0/1204	0.92	4/1612 (0.2%)
65	N9	0.50	0/473	0.82	0/629
65	n9	0.56	0/473	1.24	2/629 (0.3%)
66	O0	0.37	0/751	0.82	0/1008
66	o0	0.38	0/775	0.73	0/1040
67	O1	0.44	0/890	0.82	0/1196
67	o1	0.50	0/897	0.85	0/1205
68	O2	0.53	0/1041	0.92	0/1394
68	o2	0.58	0/1041	0.88	1/1394 (0.1%)
69	O3	0.53	0/868	0.87	2/1168 (0.2%)
69	o3	0.57	0/868	0.97	2/1168 (0.2%)
70	O4	0.46	0/890	0.91	2/1189 (0.2%)
70	o4	0.46	0/890	0.93	2/1189 (0.2%)
71	O5	0.45	0/978	0.87	1/1301 (0.1%)
71	o5	0.40	0/974	0.83	0/1297
72	O6	0.46	0/778	0.87	1/1034 (0.1%)
72	o6	0.41	0/777	0.85	2/1033 (0.2%)
73	O7	0.54	0/696	0.91	2/923 (0.2%)
73	o7	0.53	0/696	0.89	2/923 (0.2%)
74	O8	0.39	0/618	0.80	0/826
74	o8	0.36	0/614	0.74	0/822
75	O9	0.52	0/443	0.85	0/588
75	o9	0.48	0/443	0.82	0/588
76	Q0	0.49	0/423	0.98	2/562 (0.4%)
76	q0	0.54	0/423	0.91	0/562
77	Q1	0.44	0/234	0.87	0/300
77	q1	0.50	0/234	0.89	0/300
78	Q2	0.54	0/860	0.87	0/1136
78	q2	0.52	0/860	0.88	0/1136
79	Q3	0.47	0/701	0.89	0/934
79	q3	0.52	0/701	0.89	0/934
80	e0	0.38	0/499	1.04	6/665 (0.9%)
82	p0	0.34	0/1091	0.84	3/1472 (0.2%)
85	C	0.49	0/54	0.72	0/76
85	D	0.34	0/57	0.57	0/80

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
All	All	0.36	0/430695	0.65	349/632350 (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

There are no bond length outliers.

All (349) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
60	N4	80	ARG	CA-C-N	11.09	133.71	119.84
60	N4	80	ARG	C-N-CA	11.09	133.71	119.84
65	n9	23	LYS	CA-C-N	-10.49	106.73	119.84
65	n9	23	LYS	C-N-CA	-10.49	106.73	119.84
69	o3	89	LEU	CA-C-N	9.15	131.28	119.84
69	o3	89	LEU	C-N-CA	9.15	131.28	119.84
41	L4	3	ARG	CA-C-N	9.14	131.26	119.84
41	L4	3	ARG	C-N-CA	9.14	131.26	119.84
21	C9	30	VAL	CA-C-N	8.93	131.01	119.84
21	C9	30	VAL	C-N-CA	8.93	131.01	119.84
49	m3	47	ALA	CA-C-N	-8.93	108.68	119.84
49	m3	47	ALA	C-N-CA	-8.93	108.68	119.84
7	s5	27	THR	CA-C-N	8.89	130.95	119.84
7	s5	27	THR	C-N-CA	8.89	130.95	119.84
2	s0	3	LEU	CA-C-N	8.88	130.94	119.84
2	s0	3	LEU	C-N-CA	8.88	130.94	119.84
52	m6	109	PRO	CA-C-N	8.52	129.15	120.38
52	m6	109	PRO	C-N-CA	8.52	129.15	120.38
11	S9	14	THR	CA-C-N	8.39	130.32	119.84
11	S9	14	THR	C-N-CA	8.39	130.32	119.84
44	l7	192	GLY	CA-C-N	8.32	130.24	119.84
44	l7	192	GLY	C-N-CA	8.32	130.24	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
72	O6	28	TYR	N-CA-C	-8.25	104.08	114.56
42	l5	271	LYS	N-CA-C	-8.18	102.86	112.92
3	S1	205	PHE	CA-C-N	8.13	130.00	119.84
3	S1	205	PHE	C-N-CA	8.13	130.00	119.84
17	C5	52	LYS	CA-C-N	-8.03	113.54	121.65
17	C5	52	LYS	C-N-CA	-8.03	113.54	121.65
54	m8	18	ALA	CA-C-N	-7.93	112.18	120.03
54	m8	18	ALA	C-N-CA	-7.93	112.18	120.03
17	C5	124	THR	CA-C-N	7.90	129.72	119.84
17	C5	124	THR	C-N-CA	7.90	129.72	119.84
61	n5	43	ALA	CA-C-N	7.90	129.72	119.84
61	n5	43	ALA	C-N-CA	7.90	129.72	119.84
52	M6	109	PRO	CA-C-N	7.77	128.38	120.38
52	M6	109	PRO	C-N-CA	7.77	128.38	120.38
45	l8	24	ASN	CA-C-N	7.75	129.53	119.84
45	l8	24	ASN	C-N-CA	7.75	129.53	119.84
54	M8	18	ALA	CA-C-N	-7.65	112.86	120.21
54	M8	18	ALA	C-N-CA	-7.65	112.86	120.21
2	S0	3	LEU	CA-C-N	7.64	129.39	119.84
2	S0	3	LEU	C-N-CA	7.64	129.39	119.84
5	s3	219	ALA	CA-C-N	7.55	129.28	119.84
5	s3	219	ALA	C-N-CA	7.55	129.28	119.84
35	SM	38	PRO	CA-C-N	7.34	127.94	120.38
35	SM	38	PRO	C-N-CA	7.34	127.94	120.38
12	C0	88	PRO	N-CA-CB	7.29	110.91	103.25
50	M4	53	VAL	CA-C-N	7.29	128.95	119.84
50	M4	53	VAL	C-N-CA	7.29	128.95	119.84
6	S4	105	VAL	N-CA-C	-7.19	106.88	113.71
80	e0	59	GLY	CA-C-N	7.18	128.81	119.84
80	e0	59	GLY	C-N-CA	7.18	128.81	119.84
56	n0	68	HIS	CA-C-N	7.16	126.79	119.56
56	n0	68	HIS	C-N-CA	7.16	126.79	119.56
24	D2	76	SER	CA-C-N	-7.03	111.58	120.23
24	D2	76	SER	C-N-CA	-7.03	111.58	120.23
12	c0	83	PRO	N-CA-CB	6.96	110.55	103.25
39	l2	55	GLY	N-CA-C	-6.95	103.17	112.14
62	N6	100	HIS	CA-C-N	6.88	127.45	119.47
62	N6	100	HIS	C-N-CA	6.88	127.45	119.47
82	p0	290	PRO	N-CA-CB	6.87	110.37	102.88
82	p0	278	PRO	N-CA-CB	6.86	110.45	103.25
53	M7	142	SER	CA-C-N	6.85	126.79	120.21
53	M7	142	SER	C-N-CA	6.85	126.79	120.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	S7	64	VAL	CA-C-N	-6.83	113.86	120.83
9	S7	64	VAL	C-N-CA	-6.83	113.86	120.83
17	C5	86	VAL	CA-C-N	6.81	128.35	119.84
17	C5	86	VAL	C-N-CA	6.81	128.35	119.84
41	l4	191	LYS	N-CA-C	-6.80	105.27	113.97
70	O4	58	ARG	CA-C-N	6.79	128.33	119.84
70	O4	58	ARG	C-N-CA	6.79	128.33	119.84
63	N7	32	GLY	N-CA-C	6.76	118.37	111.95
82	p0	76	LEU	N-CA-C	-6.75	105.67	114.04
35	SM	51	ARG	CA-C-N	6.74	128.27	119.84
35	SM	51	ARG	C-N-CA	6.74	128.27	119.84
73	O7	5	THR	CA-C-N	-6.74	112.76	119.56
73	O7	5	THR	C-N-CA	-6.74	112.76	119.56
17	c5	52	LYS	CA-C-N	-6.74	111.42	119.84
17	c5	52	LYS	C-N-CA	-6.74	111.42	119.84
20	C8	81	ILE	CA-C-N	6.68	128.19	119.84
20	C8	81	ILE	C-N-CA	6.68	128.19	119.84
17	c5	124	THR	CA-C-N	6.62	128.12	119.84
17	c5	124	THR	C-N-CA	6.62	128.12	119.84
18	c6	40	GLU	CA-C-N	-6.61	112.79	120.12
18	c6	40	GLU	C-N-CA	-6.61	112.79	120.12
12	c0	90	PRO	N-CA-CB	6.60	110.18	103.25
57	n1	147	VAL	CA-C-N	6.59	128.08	119.84
57	n1	147	VAL	C-N-CA	6.59	128.08	119.84
57	n1	134	GLN	CA-C-N	6.59	128.08	119.84
57	n1	134	GLN	C-N-CA	6.59	128.08	119.84
64	n8	67	HIS	N-CA-C	-6.58	104.51	112.54
76	Q0	79	GLU	CA-C-N	6.55	128.03	119.84
76	Q0	79	GLU	C-N-CA	6.55	128.03	119.84
28	D6	8	ASN	CB-CA-C	-6.54	109.02	116.54
41	l4	316	ASN	CA-C-N	6.52	127.98	119.84
41	l4	316	ASN	C-N-CA	6.52	127.98	119.84
52	m6	108	ILE	CA-C-N	6.50	124.34	119.66
52	m6	108	ILE	C-N-CA	6.50	124.34	119.66
9	S7	39	ARG	CA-C-N	-6.49	113.03	120.04
9	S7	39	ARG	C-N-CA	-6.49	113.03	120.04
25	d3	80	GLY	N-CA-C	-6.49	106.37	115.32
41	L4	222	VAL	CA-C-N	6.47	127.92	119.84
41	L4	222	VAL	C-N-CA	6.47	127.92	119.84
10	s8	172	ARG	CA-C-N	6.45	127.90	119.84
10	s8	172	ARG	C-N-CA	6.45	127.90	119.84
60	n4	84	GLY	N-CA-C	-6.44	106.19	115.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	d0	97	VAL	N-CA-C	6.41	116.89	110.23
3	s1	22	ASP	CA-C-N	6.39	126.52	119.87
3	s1	22	ASP	C-N-CA	6.39	126.52	119.87
45	L8	30	THR	CA-C-N	6.37	127.80	119.84
45	L8	30	THR	C-N-CA	6.37	127.80	119.84
22	d0	120	SER	CB-CA-C	-6.35	109.23	116.54
6	s4	34	GLY	CA-C-N	6.32	126.53	119.32
6	s4	34	GLY	C-N-CA	6.32	126.53	119.32
42	L5	65	ILE	N-CA-C	6.32	117.22	108.12
3	S1	180	THR	CB-CA-C	-6.32	108.27	115.79
51	M5	177	GLY	N-CA-C	6.32	118.48	112.04
25	d3	41	SER	CA-C-N	6.31	125.54	118.97
25	d3	41	SER	C-N-CA	6.31	125.54	118.97
3	s1	205	PHE	CA-C-N	6.30	127.71	119.84
3	s1	205	PHE	C-N-CA	6.30	127.71	119.84
11	s9	143	ILE	CA-C-N	6.29	126.77	119.47
11	s9	143	ILE	C-N-CA	6.29	126.77	119.47
15	c3	150	VAL	N-CA-C	-6.29	106.64	112.43
51	m5	75	VAL	CA-C-N	6.22	127.61	119.84
51	m5	75	VAL	C-N-CA	6.22	127.61	119.84
52	m6	109	PRO	O-C-N	6.21	124.07	121.15
49	m3	149	GLN	CA-C-N	6.20	127.59	119.84
49	m3	149	GLN	C-N-CA	6.20	127.59	119.84
24	D2	94	LEU	CA-C-N	6.20	125.88	119.56
24	D2	94	LEU	C-N-CA	6.20	125.88	119.56
18	C6	40	GLU	C-N-CD	-6.18	107.00	120.60
58	n2	21	SER	CA-C-N	-6.18	113.37	120.04
58	n2	21	SER	C-N-CA	-6.18	113.37	120.04
50	m4	53	VAL	CA-C-N	6.17	126.50	119.83
50	m4	53	VAL	C-N-CA	6.17	126.50	119.83
2	S0	167	LYS	CB-CA-C	-6.17	109.44	116.54
51	m5	67	ARG	N-CA-C	6.17	120.81	113.16
55	M9	177	VAL	N-CA-C	-6.17	106.98	112.90
5	S3	219	ALA	CA-C-N	6.15	127.53	119.84
5	S3	219	ALA	C-N-CA	6.15	127.53	119.84
4	s2	150	GLN	CA-C-N	6.15	127.53	119.84
4	s2	150	GLN	C-N-CA	6.15	127.53	119.84
7	S5	126	ASP	CB-CA-C	-6.14	109.51	116.63
34	sR	283	LYS	N-CA-C	-6.08	106.46	114.31
18	C6	40	GLU	CA-C-N	6.08	141.58	127.00
18	C6	40	GLU	C-N-CA	6.08	141.58	127.00
51	m5	177	GLY	N-CA-C	6.06	118.20	112.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	m9	57	VAL	N-CA-C	6.06	117.24	109.30
4	s2	181	SER	CA-C-N	6.05	127.40	119.84
4	s2	181	SER	C-N-CA	6.05	127.40	119.84
7	s5	29	ILE	CA-C-N	6.05	126.39	119.92
7	s5	29	ILE	C-N-CA	6.05	126.39	119.92
15	C3	22	ALA	CA-C-N	6.04	141.50	127.00
15	C3	22	ALA	C-N-CA	6.04	141.50	127.00
41	L4	269	SER	N-CA-C	6.04	119.96	112.59
2	S0	67	ILE	CA-C-N	6.03	127.38	119.84
2	S0	67	ILE	C-N-CA	6.03	127.38	119.84
31	d9	10	HIS	CA-C-N	6.01	127.35	119.84
31	d9	10	HIS	C-N-CA	6.01	127.35	119.84
56	N0	134	ASP	N-CA-C	-5.98	105.94	113.72
8	s6	61	PHE	CA-C-N	5.98	126.45	119.99
8	s6	61	PHE	C-N-CA	5.98	126.45	119.99
26	d4	122	GLY	N-CA-C	-5.98	106.80	113.79
13	C1	94	ILE	CA-C-N	5.97	125.35	118.85
13	C1	94	ILE	C-N-CA	5.97	125.35	118.85
42	l5	191	ASP	CA-C-N	5.97	125.65	119.56
42	l5	191	ASP	C-N-CA	5.97	125.65	119.56
40	L3	386	ASP	CB-CA-C	-5.92	108.74	115.79
59	n3	126	TRP	CA-C-N	5.91	125.39	119.24
59	n3	126	TRP	C-N-CA	5.91	125.39	119.24
11	S9	138	LYS	N-CA-C	-5.91	105.83	113.16
10	s8	107	THR	CA-C-N	-5.90	112.94	119.19
10	s8	107	THR	C-N-CA	-5.90	112.94	119.19
69	O3	92	LYS	N-CA-C	-5.88	105.59	112.89
61	N5	43	ALA	CA-C-N	5.88	127.19	119.84
61	N5	43	ALA	C-N-CA	5.88	127.19	119.84
41	L4	191	LYS	N-CA-C	-5.88	105.94	113.23
39	l2	214	GLY	N-CA-C	5.87	120.10	110.77
54	m8	42	ALA	CA-C-N	5.86	125.33	119.24
54	m8	42	ALA	C-N-CA	5.86	125.33	119.24
5	s3	210	GLU	CA-C-N	5.85	127.16	119.84
5	s3	210	GLU	C-N-CA	5.85	127.16	119.84
6	S4	4	GLY	CA-C-N	5.84	127.14	119.84
6	S4	4	GLY	C-N-CA	5.84	127.14	119.84
25	D3	41	SER	CA-C-N	5.84	125.31	119.24
25	D3	41	SER	C-N-CA	5.84	125.31	119.24
9	s7	131	PHE	CA-C-N	-5.82	113.97	119.85
9	s7	131	PHE	C-N-CA	-5.82	113.97	119.85
36	1	637	C	C4'-C3'-O3'	5.81	118.11	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
20	C8	102	ALA	CB-CA-C	-5.79	109.91	116.63
36	1	1307	G	P-O3'-C3'	5.79	128.88	120.20
6	s4	58	GLY	N-CA-C	-5.79	107.48	114.66
25	D3	80	GLY	N-CA-C	-5.78	106.80	114.95
46	L9	20	ILE	N-CA-C	5.76	115.12	106.42
2	s0	167	LYS	CB-CA-C	-5.74	109.94	116.54
51	M5	185	ALA	N-CA-C	-5.73	106.29	113.28
51	M5	73	ARG	CA-C-N	5.73	127.00	119.84
51	M5	73	ARG	C-N-CA	5.73	127.00	119.84
41	L4	20	LEU	CA-C-N	5.71	125.61	119.85
41	L4	20	LEU	C-N-CA	5.71	125.61	119.85
54	m8	59	ARG	CA-C-N	-5.70	114.51	120.38
54	m8	59	ARG	C-N-CA	-5.70	114.51	120.38
45	L8	72	PRO	CA-C-N	5.67	126.93	119.84
45	L8	72	PRO	C-N-CA	5.67	126.93	119.84
45	l8	75	ILE	N-CA-C	-5.65	107.31	112.96
8	S6	103	GLY	CA-C-N	5.65	126.90	119.84
8	S6	103	GLY	C-N-CA	5.65	126.90	119.84
69	O3	18	ARG	N-CA-C	5.64	116.72	108.14
15	C3	22	ALA	C-N-CD	-5.63	108.20	120.60
43	L6	170	LYS	CA-C-N	5.63	126.87	119.84
43	L6	170	LYS	C-N-CA	5.63	126.87	119.84
33	e1	87	THR	CA-C-N	-5.62	114.17	119.85
33	e1	87	THR	C-N-CA	-5.62	114.17	119.85
41	L4	22	LEU	CA-C-N	5.61	126.85	119.84
41	L4	22	LEU	C-N-CA	5.61	126.85	119.84
59	n3	17	LEU	CA-C-N	5.60	126.84	119.84
59	n3	17	LEU	C-N-CA	5.60	126.84	119.84
36	1	1307	G	C2'-C3'-O3'	5.60	117.90	109.50
80	e0	52	GLY	N-CA-C	-5.60	107.04	115.32
26	d4	60	PHE	N-CA-C	5.59	117.76	108.20
51	m5	185	ALA	N-CA-C	-5.58	106.24	113.16
26	d4	29	HIS	CA-C-N	5.58	126.81	119.84
26	d4	29	HIS	C-N-CA	5.58	126.81	119.84
52	M6	120	VAL	CA-C-N	5.57	125.03	119.24
52	M6	120	VAL	C-N-CA	5.57	125.03	119.24
56	N0	68	HIS	CA-C-N	5.57	125.93	119.47
56	N0	68	HIS	C-N-CA	5.57	125.93	119.47
23	D1	81	ASN	CB-CA-C	-5.56	110.18	116.63
36	1	1484	U	C2'-C3'-O3'	5.56	117.84	109.50
18	c6	14	LYS	CB-CA-C	-5.56	110.15	116.54
56	N0	12	ARG	N-CA-C	5.54	122.59	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
41	L4	316	ASN	CA-C-N	5.51	125.34	119.28
41	L4	316	ASN	C-N-CA	5.51	125.34	119.28
9	s7	64	VAL	CA-C-N	-5.50	114.01	120.12
9	s7	64	VAL	C-N-CA	-5.50	114.01	120.12
4	s2	238	SER	CA-C-N	5.49	126.71	119.84
4	s2	238	SER	C-N-CA	5.49	126.71	119.84
70	o4	58	ARG	CA-C-N	5.48	126.69	119.84
70	o4	58	ARG	C-N-CA	5.48	126.69	119.84
8	S6	85	ARG	CA-C-N	5.48	125.49	119.90
8	S6	85	ARG	C-N-CA	5.48	125.49	119.90
73	o7	5	THR	CA-C-N	-5.48	114.03	119.56
73	o7	5	THR	C-N-CA	-5.48	114.03	119.56
15	c3	16	ILE	CA-C-N	5.47	125.77	119.92
15	c3	16	ILE	C-N-CA	5.47	125.77	119.92
13	c1	120	GLY	N-CA-C	-5.47	100.22	113.18
22	d0	71	PRO	CA-C-O	-5.47	115.34	122.12
54	M8	60	PRO	O-C-N	5.46	123.82	121.31
21	c9	46	PRO	O-C-N	5.45	123.71	121.15
48	M1	73	GLY	CA-C-N	5.45	126.65	119.84
48	M1	73	GLY	C-N-CA	5.45	126.65	119.84
7	s5	44	ASN	N-CA-C	-5.45	105.24	111.07
39	l2	216	HIS	N-CA-C	-5.45	99.20	110.80
56	n0	21	GLU	CA-C-N	-5.44	114.64	120.03
56	n0	21	GLU	C-N-CA	-5.44	114.64	120.03
64	N8	15	VAL	N-CA-C	5.44	116.17	110.62
47	m0	17	TYR	CA-C-N	5.44	126.72	120.85
47	m0	17	TYR	C-N-CA	5.44	126.72	120.85
68	o2	40	SER	N-CA-C	5.44	118.45	110.30
6	S4	194	THR	N-CA-C	5.43	122.38	110.80
59	n3	5	GLY	N-CA-C	-5.43	107.82	115.32
39	l2	56	ALA	CA-C-N	5.42	125.62	120.31
39	l2	56	ALA	C-N-CA	5.42	125.62	120.31
41	l4	300	ARG	CA-C-N	5.40	126.59	119.84
41	l4	300	ARG	C-N-CA	5.40	126.59	119.84
49	M3	75	PHE	N-CA-C	5.39	119.55	112.92
29	d7	27	GLY	CA-C-N	5.39	125.30	119.85
29	d7	27	GLY	C-N-CA	5.39	125.30	119.85
51	M5	93	LYS	N-CA-C	5.39	120.54	112.94
63	N7	59	ALA	CB-CA-C	-5.38	109.91	117.23
46	l9	7	GLU	N-CA-C	5.37	116.43	108.86
1	2	1761	U	C2'-C3'-O3'	5.34	117.51	109.50
23	D1	13	VAL	CA-C-N	5.34	126.09	120.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	D1	13	VAL	C-N-CA	5.34	126.09	120.11
36	1	2872	A	C4'-C3'-O3'	5.34	117.41	109.40
72	o6	23	ALA	CA-C-N	5.33	125.25	119.76
72	o6	23	ALA	C-N-CA	5.33	125.25	119.76
34	SR	232	TYR	N-CA-C	5.33	115.28	108.24
36	1	2872	A	P-O3'-C3'	5.33	128.19	120.20
11	S9	39	LYS	N-CA-C	-5.32	106.64	113.23
42	l5	6	ASP	N-CA-C	-5.30	104.29	111.55
49	M3	50	PRO	CA-C-O	-5.29	117.40	121.31
56	N0	23	LYS	N-CA-C	5.28	117.95	111.82
24	D2	55	ASP	N-CA-C	-5.28	103.72	110.53
56	N0	152	LEU	CA-C-N	5.28	126.02	120.11
56	N0	152	LEU	C-N-CA	5.28	126.02	120.11
1	6	1535	U	C2'-C3'-O3'	5.28	117.42	109.50
34	SR	59	ARG	N-CA-C	5.28	117.10	108.55
35	SM	21	PRO	CA-C-N	5.28	125.22	119.78
35	SM	21	PRO	C-N-CA	5.28	125.22	119.78
9	s7	111	LYS	CB-CA-C	-5.26	109.53	115.79
33	E1	104	SER	N-CA-C	-5.26	106.70	113.23
51	M5	174	ILE	N-CA-C	5.26	111.84	106.21
45	L8	71	VAL	CA-C-N	5.26	125.80	120.38
45	L8	71	VAL	C-N-CA	5.26	125.80	120.38
5	S3	80	ALA	CA-C-N	5.25	126.41	119.84
5	S3	80	ALA	C-N-CA	5.25	126.41	119.84
50	M4	30	GLY	N-CA-C	-5.25	108.38	115.21
34	sR	37	SER	N-CA-C	5.25	115.22	108.34
15	c3	136	PRO	CA-C-N	5.25	126.41	119.84
15	c3	136	PRO	C-N-CA	5.25	126.41	119.84
45	l8	72	PRO	CA-C-N	5.25	125.56	119.47
45	l8	72	PRO	C-N-CA	5.25	125.56	119.47
2	s0	103	THR	CA-C-N	5.24	126.39	119.84
2	s0	103	THR	C-N-CA	5.24	126.39	119.84
39	L2	119	LYS	CA-C-N	-5.22	114.42	119.90
39	L2	119	LYS	C-N-CA	-5.22	114.42	119.90
71	O5	80	LEU	N-CA-C	-5.22	106.86	114.12
41	l4	22	LEU	CA-C-N	5.22	126.37	119.84
41	l4	22	LEU	C-N-CA	5.22	126.37	119.84
41	l4	340	GLY	N-CA-C	-5.22	100.81	113.18
16	c4	91	THR	N-CA-C	5.21	117.64	111.33
16	C4	93	THR	CA-C-N	5.21	126.35	119.84
16	C4	93	THR	C-N-CA	5.21	126.35	119.84
29	D7	37	CYS	CA-C-N	5.21	125.51	119.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
29	D7	37	CYS	C-N-CA	5.21	125.51	119.47
44	l7	229	PHE	CA-CB-CG	5.20	119.00	113.80
42	L5	123	GLU	N-CA-C	-5.19	107.33	113.97
41	l4	117	GLU	N-CA-C	-5.17	105.73	111.36
59	n3	44	SER	N-CA-C	5.16	117.48	108.76
44	L7	95	ILE	CA-C-N	5.15	125.69	120.38
44	L7	95	ILE	C-N-CA	5.15	125.69	120.38
80	e0	48	THR	CB-CA-C	-5.15	109.66	117.07
64	n8	121	VAL	CA-C-N	5.15	126.28	119.84
64	n8	121	VAL	C-N-CA	5.15	126.28	119.84
36	1	1484	U	P-O3'-C3'	5.15	127.92	120.20
47	M0	218	ALA	N-CA-C	-5.14	107.67	114.04
58	N2	67	SER	N-CA-C	5.13	117.48	109.52
3	s1	131	ASP	N-CA-C	-5.13	103.62	110.55
12	c0	33	GLU	N-CA-C	-5.13	107.08	113.55
40	l3	245	GLY	N-CA-C	5.13	118.04	112.29
36	1	282	G	C2'-C3'-O3'	5.12	121.39	113.70
45	L8	74	THR	N-CA-C	-5.12	107.20	113.50
45	L8	158	ASP	CA-C-N	-5.12	113.43	119.84
45	L8	158	ASP	C-N-CA	-5.12	113.43	119.84
25	d3	69	ARG	N-CA-C	5.12	118.55	112.72
64	n8	37	GLY	N-CA-C	-5.11	106.53	113.37
11	s9	101	VAL	N-CA-C	5.09	115.71	110.36
53	m7	82	ARG	N-CA-C	5.06	115.72	108.74
16	C4	123	SER	N-CA-C	-5.06	107.39	113.21
41	L4	84	ARG	N-CA-C	-5.06	106.28	112.90
6	S4	193	GLY	N-CA-C	5.05	125.16	113.18
24	d2	92	ASN	N-CA-C	5.04	116.86	111.36
80	e0	18	THR	CA-C-N	5.04	126.14	119.84
80	e0	18	THR	C-N-CA	5.04	126.14	119.84
51	m5	44	ARG	CA-C-N	5.04	124.53	119.19
51	m5	44	ARG	C-N-CA	5.04	124.53	119.19
3	s1	189	ILE	CB-CA-C	-5.01	108.94	113.70

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 (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	37970	0	19106	616	1
1	6	38260	0	19252	611	0
2	S0	1577	0	1567	50	0
2	s0	1583	0	1578	61	0
3	S1	1709	0	1784	83	0
3	s1	1722	0	1793	59	0
4	S2	1635	0	1723	52	0
4	s2	1635	0	1723	43	0
5	S3	1734	0	1817	50	0
5	s3	1734	0	1817	56	0
6	S4	2068	0	2154	69	0
6	s4	2068	0	2154	69	0
7	S5	1609	0	1675	30	0
7	s5	1609	0	1675	52	0
8	S6	1799	0	1879	54	0
8	s6	1755	0	1846	61	0
9	S7	1481	0	1572	49	0
9	s7	1491	0	1578	34	0
10	S8	1489	0	1525	51	0
10	s8	1489	0	1525	41	0
11	S9	1494	0	1573	48	0
11	s9	1494	0	1573	59	0
12	C0	773	0	729	24	0
12	c0	762	0	700	35	0
13	C1	1213	0	1257	30	0
13	c1	1168	0	1233	39	0
14	C2	892	0	891	32	0
14	c2	892	0	891	19	0
15	C3	1192	0	1255	41	0
15	c3	1192	0	1255	41	0
16	C4	891	0	883	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	c4	949	0	985	40	0
17	C5	977	0	1002	36	0
17	c5	1039	0	1050	36	0
18	C6	1105	0	1166	41	0
18	c6	1111	0	1171	38	0
19	C7	926	0	930	32	0
19	c7	906	0	909	31	0
20	C8	1192	0	1222	50	0
20	c8	1192	0	1222	46	0
21	C9	1112	0	1124	32	0
21	c9	1112	0	1124	44	0
22	D0	855	0	917	33	0
22	d0	882	0	939	18	0
23	D1	684	0	672	24	0
23	d1	684	0	672	23	0
24	D2	1021	0	1060	37	0
24	d2	1021	0	1060	35	0
25	D3	1121	0	1196	43	0
25	d3	1121	0	1196	36	0
26	D4	1073	0	1132	27	0
26	d4	1073	0	1132	37	0
27	D5	563	0	603	24	0
27	d5	558	0	598	21	0
28	D6	769	0	814	35	0
28	d6	769	0	814	36	0
29	D7	610	0	630	19	0
29	d7	610	0	631	21	0
30	D8	497	0	535	15	0
30	d8	497	0	535	19	0
31	D9	442	0	428	12	0
31	d9	442	0	428	13	0
32	E0	475	0	525	12	0
33	E1	566	0	602	25	0
33	e1	608	0	657	30	0
34	SR	2437	0	2386	50	0
34	sR	2442	0	2392	56	0
35	SM	1104	0	969	33	0
35	sM	681	0	591	22	0
36	1	67333	0	33838	848	0
36	5	67354	0	33851	852	1
37	3	2579	0	1304	34	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	58	0
39	L2	1914	0	1981	64	0
39	l2	1912	0	1976	69	0
40	L3	3075	0	3142	99	0
40	l3	3075	0	3142	90	0
41	L4	2748	0	2859	89	0
41	l4	2748	0	2859	86	0
42	L5	2375	0	2325	84	0
42	l5	2359	0	2311	85	0
43	L6	1239	0	1326	35	0
43	l6	1248	0	1339	32	0
44	L7	1784	0	1862	54	0
44	l7	1791	0	1869	44	0
45	L8	1804	0	1875	48	0
45	l8	1764	0	1821	52	0
46	L9	1518	0	1587	61	0
46	l9	1518	0	1587	54	0
47	M0	1705	0	1736	60	0
47	m0	1722	0	1755	62	0
48	M1	1353	0	1383	43	0
48	m1	1353	0	1383	40	0
49	M3	1543	0	1608	46	0
49	m3	1548	0	1613	40	0
50	M4	1053	0	1149	41	0
50	m4	1059	0	1154	34	0
51	M5	1720	0	1779	50	0
51	m5	1720	0	1779	53	0
52	M6	1555	0	1659	32	0
52	m6	1555	0	1659	54	0
53	M7	1420	0	1437	47	0
53	m7	1227	0	1236	36	0
54	M8	1441	0	1543	47	0
54	m8	1441	0	1543	43	0
55	M9	1521	0	1617	32	0
55	m9	1521	0	1617	37	0
56	N0	1445	0	1487	38	0
56	n0	1445	0	1487	29	0
57	N1	1276	0	1323	38	0
57	n1	1276	0	1323	38	0
58	N2	796	0	812	16	0
58	n2	778	0	791	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	N3	1003	0	1048	28	0
59	n3	1003	0	1048	30	0
60	N4	699	0	640	14	0
60	n4	1038	0	1071	15	0
61	N5	964	0	1025	31	0
61	n5	959	0	1023	29	0
62	N6	993	0	1081	21	0
62	n6	993	0	1081	34	0
63	N7	1092	0	1155	48	0
63	n7	1092	0	1155	43	0
64	N8	1173	0	1215	44	0
64	n8	1173	0	1215	44	0
65	N9	462	0	491	14	0
65	n9	462	0	491	14	0
66	O0	743	0	797	21	0
66	o0	767	0	816	17	0
67	O1	876	0	912	17	0
67	o1	883	0	918	19	0
68	O2	1020	0	1090	29	0
68	o2	1020	0	1090	32	0
69	O3	850	0	880	27	0
69	o3	850	0	880	16	0
70	O4	880	0	945	30	0
70	o4	880	0	945	31	0
71	O5	969	0	1078	29	0
71	o5	965	0	1067	46	0
72	O6	771	0	849	24	0
72	o6	770	0	846	22	0
73	O7	681	0	683	25	0
73	o7	681	0	683	30	0
74	O8	612	0	682	22	0
74	o8	608	0	671	10	0
75	O9	436	0	475	18	0
75	o9	436	0	475	22	0
76	Q0	417	0	455	5	0
76	q0	417	0	455	7	0
77	Q1	233	0	284	10	0
77	q1	233	0	284	6	0
78	Q2	847	0	914	24	0
78	q2	847	0	914	30	0
79	Q3	694	0	734	28	0
79	q3	694	0	734	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	e0	491	0	542	26	0
81	m2	750	0	180	6	0
82	p0	1076	0	1076	19	0
83	p1	235	0	53	2	0
84	p2	230	0	49	1	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	0	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	7258	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 (7258) 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	1.31	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
36:5:640:U:OP1	64:n8:21:ARG:NH2	2.01	0.94
40:l3:41:VAL:HA	40:l3:185:GLY:HA3	1.50	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	1.52	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	2.05	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
36:5:31:C:OP2	51:m5:188:ARG:NH2	2.06	0.89
36:1:2392:C:O2'	40:L3:266:ARG:NH2	2.06	0.88
47:m0:76:MET:HE2	47:m0:148:VAL:HG22	1.56	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	1.55	0.87
1:6:475:A:OP2	11:s9:126:ARG:NH1	2.08	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	1.40	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
75:o9:5:LYS:HD3	75:o9:13:MET:HE1	1.58	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
37:7:76:A:O2'	56:n0:50:LYS:NZ	2.10	0.85
36:5:3214:U:OP2	50:m4:128:ARG:NH2	2.09	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	1.58	0.84
7:s5:94:THR:HG22	7:s5:114:ILE:HG13	1.57	0.84
36:1:2940:A:N7	40:L3:2:SER:N	2.25	0.84
1:6:513:U:OP1	11:s9:133:HIS:NE2	2.10	0.84
1:6:1097:U:H4'	1:6:1098:U:H5'	1.59	0.84
23:d1:3:ASN:HD21	23:d1:7:GLN:HB2	1.42	0.84
63:n7:102:GLU:H	63:n7:107:ARG:HH21	1.25	0.84
2:S0:162:CYS:SG	2:S0:163:ASN:N	2.52	0.83
48:m1:94:ARG:O	48:m1:96:PHE:N	2.11	0.83
1:2:142:G:H22	1:2:173:A:H2	1.26	0.83
1:6:1588:G:H1	1:6:1608:U:H3	1.26	0.83
36:1:1639:C:OP2	70:O4:74:ARG:NH2	2.11	0.83
1:6:793:A:H3'	1:6:794:U:H5'	1.60	0.83
48:m1:15:GLU:HG2	48:m1:16:LYS:HG2	1.60	0.83
36:5:1471:U:OP1	55:m9:5:ARG:NH2	2.11	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:m0:38:LYS:HG2	47:m0:41:ALA:HB2	1.60	0.83
7:S5:94:THR:HG22	7:S5:114:ILE:HG13	1.60	0.82
41:l4:329:PRO:O	41:l4:331:ALA:N	2.12	0.82
36:5:2181:C:OP1	39:l2:193:ARG:NH2	2.11	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
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	2.13	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	2.55	0.81
69:O3:75:HIS:HB3	69:O3:80:VAL:HG12	1.62	0.80
1:6:647:G:H22	1:6:687:G:H1	1.27	0.80
47:M0:174:THR:HG23	47:M0:176:LEU:H	1.46	0.80
42:L5:22:ARG:NH2	42:L5:28:THR:OG1	2.14	0.80
46:L9:47:LYS:HZ2	50:M4:5:SER:HB2	1.45	0.80
51:M5:46:ASP:OD1	51:M5:50:ARG:NH2	2.15	0.80
28:d6:10:ARG:HH12	28:d6:36:ILE:HG13	1.43	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
5:S3:175:VAL:HG13	5:S3:182:LEU:HB2	1.64	0.80
37:3:45:A:OP1	42:L5:151:GLN:NE2	2.14	0.80
42:l5:120:LYS:O	42:l5:248:ARG:NH2	2.14	0.80
29:D7:36:LYS:HB3	29:D7:43:ILE:HG22	1.62	0.80
16:c4:20:TYR:HB3	16:c4:27:PHE:HB2	1.63	0.80
47:m0:207:GLU:HB3	47:m0:211:ARG:HH12	1.46	0.79
1:6:158:U:O2'	1:6:160:C:OP2	1.99	0.79
36:5:284:A:OP2	78:q2:41:ARG:NH1	2.16	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	1.48	0.79
36:1:3182:G:OP1	52:M6:160:ARG:NH2	2.12	0.79
1:6:1492:A:HO2'	1:6:1493:A:H8	1.31	0.79
40:l3:139:GLN:O	40:l3:141:GLY:N	2.13	0.79
9:S7:11:GLN:HG3	9:S7:13:PRO:HD2	1.63	0.79
36:5:1235:U:H4'	36:5:1236:G:H5'	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:s8:34:ALA:HB2	10:s8:56:ARG:HD3	1.64	0.78
1:2:1186:U:O4	1:2:1200:G:N2	2.15	0.78
36:5:992:A:H5"	57:n1:43:LYS:HD2	1.64	0.78
2:s0:66:ALA:HB2	23:d1:37:ALA:HB2	1.65	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	1.49	0.78
36:5:283:G:OP1	78:q2:45:ARG:NH2	2.17	0.78
1:2:283:U:H5"	8:S6:188:ARG:HD3	1.66	0.77
1:2:1542:G:N2	1:2:1569:A:OP2	2.18	0.77
40:L3:41:VAL:HA	40:L3:185:GLY:HA3	1.66	0.77
78:Q2:71:ARG:HE	78:Q2:80:ARG:HH11	1.32	0.77
36:5:2112:U:H4'	36:5:2113:A:H5'	1.66	0.77
36:5:3182:G:OP1	52:m6:160:ARG:NH2	2.16	0.77
41:l4:328:ASN:OD1	44:l7:48:ASN:ND2	2.17	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
1:6:1552:U:OP2	17:c5:43:ARG:NH2	2.17	0.77
17:C5:123:TYR:OH	20:C8:126:ARG:NH1	2.18	0.77
46:L9:9:GLN:HG3	46:L9:52:LEU:HD21	1.66	0.77
37:7:1:G:O2'	42:l5:270:LYS:HB3	1.84	0.77
18:C6:50:GLU:OE2	18:C6:82:ARG:NH2	2.18	0.76
37:3:17:A:OP1	42:L5:2:ALA:N	2.17	0.76
41:L4:16:THR:HG22	41:L4:18:ASN:H	1.49	0.76
53:M7:24:VAL:HB	53:M7:29:THR:HG21	1.65	0.76
16:c4:50:ALA:O	16:c4:52:ARG:N	2.18	0.76
36:5:155:G:H5"	36:5:156:G:C8	2.20	0.76
79:q3:6:LYS:HG2	79:q3:7:LYS:HG3	1.66	0.76
11:S9:109:LEU:HB2	11:S9:146:PHE:HB3	1.68	0.76
1:6:1370:U:H4'	1:6:1371:A:H4'	1.67	0.76
1:2:1046:G:OP1	3:S1:157:GLN:NE2	2.18	0.76
36:5:1874:A:OP2	55:m9:21:LYS:NZ	2.19	0.76
49:m3:46:ILE:HG22	49:m3:49:ARG:HB2	1.68	0.76
1:6:1369:U:OP1	21:c9:119:LYS:NZ	2.18	0.76
13:c1:4:GLU:OE1	13:c1:82:ARG:NH2	2.18	0.76
1:2:68:A:OP1	8:S6:160:ARG:NH2	2.17	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:O0:34:LEU:HD23	66:O0:59:TYR:HB3	1.68	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	1.68	0.76
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
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
20:c8:28:ILE:HD11	20:c8:56:LYS:HB2	1.69	0.75
36:5:838:G:O6	79:q3:4:ARG:NH2	2.19	0.75
4:s2:56:ILE:HG23	4:s2:61:LEU:HB2	1.68	0.75
51:m5:68:ARG:HA	51:m5:98:LEU:HD21	1.69	0.75
76:q0:77:ILE:HG23	76:q0:78:ILE:HG22	1.67	0.75
36:1:692:A:OP1	51:M5:201:ARG:NH2	2.19	0.75
47:M0:129:VAL:HG22	47:M0:133:GLN:HG2	1.68	0.75
21:c9:16:ASN:OD1	21:c9:56:LYS:NZ	2.18	0.75
36:5:1103:A:H3'	36:5:1104:G:H5'	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	1.68	0.75
80:e0:54:ARG:HE	80:e0:56:MET:HE1	1.49	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
36:5:2761:G:N7	78:q2:63:LYS:NZ	2.35	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
1:2:1459:C:OP1	20:C8:126:ARG:NH2	2.20	0.75
36:5:1493:G:O6	75:o9:2:ALA:N	2.19	0.75
36:5:3153:U:H4'	36:5:3154:C:H5'	1.68	0.75
44:l7:151:ARG:NH1	44:l7:244:ASN:O	2.20	0.75
59:n3:54:LEU:HD21	59:n3:119:GLY:HA3	1.67	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	1.51	0.75
2:S0:24:LEU:O	2:S0:163:ASN:ND2	2.20	0.74
36:1:3275:U:H5'	69:O3:68:TRP:HZ2	1.51	0.74
63:N7:52:LYS:O	63:N7:65:ARG:NH1	2.20	0.74
36:5:2201:G:H21	39:l2:224:THR:HG21	1.51	0.74
69:o3:6:ARG:NH1	69:o3:8:TYR:O	2.19	0.74
71:O5:78:LYS:HA	71:O5:81:ARG:HD2	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:e0:29:LYS:HG3	80:e0:30:PRO:HD2	1.68	0.74
40:l3:360:ASP:OD2	40:l3:364:LYS:NZ	2.19	0.74
13:c1:14:GLN:HB3	13:c1:54:ILE:HG13	1.68	0.74
36:5:3068:U:OP2	55:m9:62:ARG:NH2	2.20	0.74
1:2:237:C:H5"	1:2:238:U:H5'	1.69	0.74
5:s3:75:LYS:HB3	12:c0:22:VAL:HG22	1.67	0.74
21:c9:84:LYS:HD2	21:c9:94:ILE:HG13	1.67	0.74
68:o2:100:ILE:O	68:o2:105:ARG:NH1	2.21	0.74
10:S8:8:ARG:NH2	10:S8:19:ALA:O	2.21	0.74
79:Q3:30:GLU:HA	79:Q3:33:GLN:HG2	1.70	0.74
38:4:142:C:OP1	51:M5:38:ARG:NH1	2.20	0.74
1:6:93:A:H1'	6:s4:3:ARG:HB3	1.68	0.74
15:c3:65:VAL:HG23	15:c3:66:ILE:HG23	1.68	0.74
36:5:2569:A:H4'	36:5:2570:U:H5'	1.70	0.74
36:5:2814:G:OP1	41:l4:73:ARG:NH2	2.20	0.74
34:sR:178:VAL:HB	34:sR:192:PHE:HB2	1.69	0.74
71:o5:78:LYS:HA	71:o5:81:ARG:HD3	1.70	0.74
36:1:979:U:H1'	36:1:980:A:C8	2.23	0.73
46:L9:18:VAL:HB	46:L9:27:VAL:HG22	1.70	0.73
36:5:2444:C:H42	36:5:2503:G:H1	1.36	0.73
1:2:1102:G:OP1	24:D2:76:SER:OG	2.05	0.73
36:1:1786:G:H2'	36:1:1787:A:C8	2.23	0.73
36:5:13:A:H4'	61:n5:39:LYS:HG3	1.70	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	1.69	0.73
67:o1:19:ARG:HD3	67:o1:35:GLU:HG3	1.70	0.73
38:8:79:A:H3'	38:8:80:A:C8	2.24	0.73
1:6:79:C:H1'	8:s6:174:LYS:HG3	1.70	0.73
36:5:3274:A:H3'	36:5:3275:U:H5"	1.70	0.73
1:2:7:G:N7	4:S2:205:ARG:NH1	2.35	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
36:1:3375:A:O2'	36:1:3378:C:OP2	2.07	0.73
1:6:975:C:H5"	15:c3:109:LYS:HD2	1.68	0.73
1:2:169:A:H5"	8:S6:176:GLN:HG2	1.70	0.73
36:1:718:G:C2	36:1:721:G:H1'	2.24	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
47:M0:24:ARG:HH11	47:M0:24:ARG:HG3	1.54	0.73
11:s9:109:LEU:HB2	11:s9:146:PHE:HB3	1.68	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:l9:75:VAL:HA	46:l9:78:MET:HE3	1.69	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
41:l4:300:ARG:O	54:m8:39:ARG:NH1	2.22	0.73
70:o4:102:LYS:HB3	70:o4:103:LYS:HE3	1.70	0.73
41:L4:204:GLY:O	41:L4:246:ARG:NH1	2.22	0.73
41:l4:93:MET:H	41:l4:93:MET:HE2	1.54	0.73
44:l7:80:GLN:NE2	57:n1:135:PRO:O	2.21	0.73
47:m0:142:ASP:OD2	47:m0:178:ARG:NH2	2.22	0.73
6:s4:206:ASP:HB2	6:s4:222:LEU:HD12	1.71	0.72
36:1:2895:G:O2'	76:Q0:100:TYR:O	2.05	0.72
1:6:753:A:N7	6:s4:187:ARG:NH2	2.36	0.72
39:l2:149:ARG:HH22	39:l2:253:GLN:HA	1.53	0.72
54:m8:158:HIS:H	54:m8:186:VAL:HG12	1.54	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	2.22	0.72
8:s6:98:ARG:NH2	8:s6:101:ILE:O	2.20	0.72
49:m3:50:PRO:O	49:m3:52:ASP:N	2.22	0.72
2:S0:103:THR:O	2:S0:106:SER:OG	2.08	0.72
25:D3:102:VAL:HG12	25:D3:127:VAL:HG12	1.71	0.72
36:1:837:A:OP2	79:Q3:4:ARG:NH1	2.22	0.72
40:L3:173:GLN:O	40:L3:175:LYS:N	2.22	0.72
2:s0:142:PRO:HB3	23:d1:34:ILE:HD13	1.72	0.72
78:q2:15:LYS:HG3	78:q2:18:ARG:HH11	1.55	0.72
1:2:115:G:OP1	13:C1:67:ARG:NH1	2.22	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
1:6:151:G:N2	8:s6:13:GLN:OE1	2.22	0.72
18:c6:110:THR:HA	18:c6:113:ASP:HB2	1.71	0.72
1:2:1625:C:OP1	4:S2:91:ARG:NH2	2.23	0.72
36:1:595:G:H1	36:1:609:G:H5"	1.54	0.72
36:1:1942:U:HO2'	36:1:3345:G:HO2'	1.34	0.72
36:1:2216:G:OP1	72:O6:75:LYS:NZ	2.18	0.72
1:6:1460:A:OP2	20:c8:145:ARG:NH2	2.22	0.72
12:c0:21:VAL:HG12	12:c0:66:TYR:HB2	1.72	0.72
36:5:115:A:OP1	51:m5:49:ARG:NH2	2.21	0.72
61:N5:86:VAL:HG12	61:N5:120:LYS:HB3	1.71	0.72
56:n0:91:TYR:O	56:n0:137:ARG:NH1	2.22	0.72
78:q2:12:CYS:SG	78:q2:17:CYS:CB	2.76	0.72
7:S5:40:ILE:HG23	7:S5:42:LEU:HD22	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:S5:64:VAL:HG12	7:S5:65:ARG:HD3	1.71	0.72
36:1:670:C:OP1	54:M8:147:ARG:NH2	2.23	0.72
1:6:1534:G:OP2	20:c8:57:ARG:NH1	2.23	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	1.71	0.72
6:S4:19:LEU:HD11	6:S4:108:ARG:HD2	1.70	0.71
38:4:97:A:OP1	71:O5:67:ARG:NH2	2.23	0.71
78:q2:12:CYS:SG	78:q2:17:CYS:HB3	2.30	0.71
78:q2:73:GLU:OE1	78:q2:80:ARG:NH1	2.23	0.71
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
6:S4:192:ILE:HG13	6:S4:243:GLY:HA3	1.71	0.71
75:O9:10:LYS:HA	75:O9:13:MET:HE3	1.72	0.71
46:l9:20:ILE:HG12	46:l9:25:VAL:HG22	1.71	0.71
18:c6:7:VAL:HG12	18:c6:22:VAL:HB	1.71	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
80:e0:59:GLY:O	80:e0:61:SER:N	2.24	0.71
1:6:1251:U:H4'	33:e1:134:ASN:H	1.56	0.71
1:2:1585:U:H3	1:2:1611:A:H2	1.37	0.71
18:C6:40:GLU:HA	18:C6:42:GLU:N	2.06	0.71
36:1:58:G:H4'	51:M5:155:VAL:HG12	1.72	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
36:5:2156:C:OP2	39:l2:241:ARG:NH2	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
1:2:1544:U:OP1	20:C8:136:GLN:NE2	2.24	0.70
36:1:2572:C:O2'	36:1:2573:G:O4'	2.09	0.70
43:L6:31:ARG:NH2	43:L6:81:ALA:O	2.24	0.70
1:6:1034:C:HO2'	24:d2:2:THR:N	1.88	0.70
1:6:1462:G:N7	20:c8:143:ARG:NH2	2.39	0.70
3:s1:129:THR:OG1	3:s1:131:ASP:O	2.08	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	2.24	0.70
73:O7:21:ARG:NH2	73:O7:41:ALA:O	2.24	0.70
3:s1:72:ASP:OD1	16:c4:114:ARG:NH1	2.24	0.70
7:s5:90:ILE:HD11	7:s5:130:ILE:HG13	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:3190:C:OP1	52:m6:172:ARG:NH1	2.24	0.70
1:2:513:U:OP1	11:S9:133:HIS:NE2	2.21	0.70
1:2:1122:G:N2	1:2:1125:A:OP2	2.24	0.70
19:C7:47:ARG:NH1	19:C7:48:ASN:OD1	2.23	0.70
36:1:2688:U:OP1	42:L5:12:TYR:OH	2.09	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
14:c2:61:VAL:HG13	14:c2:121:VAL:HG23	1.71	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	1.56	0.70
1:2:280:U:O2'	1:2:281:G:OP2	2.08	0.70
1:2:788:A:H2'	6:S4:19:LEU:HD22	1.74	0.70
1:2:1382:A:H5"	22:D0:60:THR:HG22	1.73	0.70
13:C1:6:THR:O	13:C1:8:GLN:N	2.25	0.70
63:N7:46:ILE:HD13	63:N7:68:ILE:HG23	1.74	0.70
1:6:1000:C:N4	1:6:1003:A:OP2	2.24	0.70
21:c9:28:LEU:HA	21:c9:111:ILE:HD11	1.74	0.70
1:2:68:A:H5'	8:S6:160:ARG:HH12	1.56	0.70
1:2:104:A:OP2	1:2:308:C:N4	2.24	0.70
21:C9:52:GLY:O	21:C9:54:PHE:N	2.24	0.70
37:7:28:C:OP1	48:m1:137:ARG:NH1	2.23	0.70
14:C2:36:LEU:HG	14:C2:41:LEU:HD12	1.74	0.70
34:SR:133:VAL:HB	34:SR:142:ALA:HB3	1.72	0.70
36:5:437:G:H1	36:5:622:A:H61	1.40	0.70
65:n9:23:LYS:HB3	65:n9:24:PRO:CD	2.21	0.70
1:2:484:C:H42	1:2:503:G:H22	1.38	0.69
46:L9:149:ASN:N	46:L9:149:ASN:OD1	2.25	0.69
11:s9:106:GLU:O	11:s9:111:THR:OG1	2.10	0.69
25:d3:79:ASN:HB2	25:d3:81:LYS:H	1.57	0.69
62:n6:3:LYS:NZ	62:n6:5:SER:O	2.24	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
36:5:1238:C:O2'	36:5:1239:C:OP1	2.06	0.69
10:S8:76:THR:HG22	10:S8:108:PRO:HG2	1.73	0.69
12:C0:16:PHE:HD2	12:C0:76:LEU:HD23	1.58	0.69
36:5:20:A:OP2	71:o5:90:ARG:NH1	2.25	0.69
36:1:1603:A:OP1	55:M9:38:ARG:NH1	2.25	0.69
41:L4:203:ARG:NH1	41:L4:226:GLU:OE2	2.25	0.69
41:l4:144:LYS:HG2	41:l4:145:ILE:H	1.57	0.69
1:2:190:C:N4	1:2:196:G:O6	2.19	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:S9:129:ILE:HG22	11:S9:142:ASN:HA	1.73	0.69
1:6:144:U:H5	8:s6:137:ARG:HH12	1.38	0.69
1:6:1502:G:N7	21:c9:102:ARG:NH2	2.39	0.69
23:d1:74:GLN:HG2	23:d1:79:LEU:HB2	1.74	0.69
19:c7:47:ARG:NH1	19:c7:48:ASN:OD1	2.25	0.69
36:5:1639:C:OP2	70:o4:74:ARG:NH2	2.26	0.69
81:m2:120:UNK:O	81:m2:122:UNK:N	2.25	0.69
36:1:148:G:OP2	51:M5:4:TYR:OH	2.07	0.69
59:N3:40:LYS:HD3	59:N3:59:MET:HE2	1.73	0.69
1:6:1046:G:OP1	3:s1:157:GLN:NE2	2.25	0.69
1:6:1796:C:O2'	28:d6:95:ARG:NH1	2.23	0.69
17:c5:18:ARG:NH1	20:c8:90:ASN:O	2.26	0.69
38:8:63:G:O2'	71:o5:49:LYS:NZ	2.21	0.69
1:2:399:A:H4'	6:S4:3:ARG:HG2	1.73	0.69
3:S1:134:VAL:HB	3:S1:219:LYS:HB2	1.75	0.69
47:M0:14:ASN:O	47:M0:128:ARG:NH2	2.25	0.69
64:N8:96:LYS:O	64:N8:98:THR:N	2.26	0.69
6:s4:49:ARG:NH2	6:s4:50:ASN:OD1	2.21	0.69
17:c5:123:TYR:OH	20:c8:126:ARG:NH1	2.25	0.69
42:l5:76:ALA:HB3	42:l5:109:THR:HG22	1.74	0.69
36:1:1634:G:N7	63:N7:17:ARG:NH2	2.41	0.69
46:L9:22:SER:OG	46:L9:23:ARG:N	2.25	0.69
1:6:687:G:H5"	24:d2:119:LYS:HG2	1.75	0.69
1:6:800:U:H2'	1:6:801:G:H8	1.58	0.69
1:6:1330:G:N2	5:s3:204:ASP:OD1	2.24	0.69
1:6:1473:U:O2'	7:s5:102:ARG:NH1	2.26	0.69
17:c5:10:ARG:HA	48:m1:88:GLU:HB3	1.74	0.69
48:m1:9:MET:O	48:m1:11:ASP:N	2.25	0.69
62:n6:37:LYS:H	62:n6:37:LYS:HD3	1.58	0.69
67:o1:72:ARG:NH1	67:o1:105:GLN:O	2.24	0.69
71:o5:85:THR:HG22	71:o5:88:LEU:H	1.58	0.69
1:2:127:G:N7	8:S6:202:ARG:NH2	2.41	0.69
3:S1:127:VAL:HG11	3:S1:176:VAL:HG21	1.75	0.69
17:c5:126:VAL:HG13	17:c5:127:ARG:H	1.58	0.69
36:5:591:G:N2	36:5:612:U:OP1	2.26	0.69
59:n3:39:VAL:O	59:n3:42:SER:OG	2.10	0.69
1:2:140:A:OP2	8:S6:187:LYS:NZ	2.25	0.68
36:1:1076:C:O3'	65:N9:38:LYS:NZ	2.26	0.68
36:1:1748:G:OP1	74:O8:44:LYS:NZ	2.25	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	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:C4:85:ALA:H	16:C4:119:THR:HG22	1.57	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	1.74	0.68
36:5:1671:C:OP1	55:m9:60:LYS:NZ	2.23	0.68
39:l2:114:SER:HB2	39:l2:169:ILE:HD12	1.75	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
1:2:734:A:H5"	1:2:735:C:OP1	1.93	0.68
1:2:1584:G:N2	1:2:1611:A:OP2	2.18	0.68
4:S2:56:ILE:HG23	4:S2:61:LEU:HB2	1.74	0.68
11:s9:163:PRO:HB3	11:s9:169:PRO:HA	1.76	0.68
13:c1:33:ARG:NH1	13:c1:53:TYR:O	2.26	0.68
36:5:1320:C:O2	56:n0:115:ARG:NH2	2.27	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
22:D0:51:VAL:HG13	22:D0:94:GLU:HB2	1.75	0.68
36:1:3165:A:H61	36:1:3285:C:H42	1.39	0.68
62:N6:45:ILE:HD12	62:N6:119:ILE:HG23	1.74	0.68
1:6:754:A:N6	1:6:793:A:N7	2.35	0.68
36:5:2967:A:H5"	39:l2:213:GLY:HA3	1.75	0.68
39:l2:238:ILE:O	39:l2:240:ALA:N	2.26	0.68
51:m5:31:ARG:NH1	51:m5:124:ASP:OD1	2.27	0.68
63:n7:27:LYS:HD3	63:n7:93:LYS:HZ1	1.57	0.68
8:S6:57:ASP:HA	8:S6:106:LEU:HA	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	1.76	0.68
1:2:588:U:OP2	32:E0:26:LYS:NZ	2.27	0.68
1:2:1254:U:OP2	14:C2:46:ARG:NH1	2.27	0.68
1:2:1437:U:H5'	5:S3:176:LEU:HD23	1.76	0.68
36:1:1095:U:H4'	36:1:1096:U:H5'	1.75	0.68
40:L3:25:ILE:HD13	40:L3:25:ILE:H	1.59	0.68
57:N1:51:GLY:HA3	57:N1:92:ARG:HG3	1.75	0.68
68:O2:100:ILE:O	68:O2:105:ARG:NH1	2.27	0.68
49:m3:128:ARG:NH1	71:o5:109:ILE:O	2.26	0.68
9:S7:28:GLU:HG2	9:S7:35:LYS:HG3	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:c9:117:SER:HB2	21:c9:123:ARG:HB3	1.75	0.68
36:5:149:U:OP2	51:m5:49:ARG:NH1	2.26	0.68
63:n7:128:GLN:O	63:n7:130:PHE:N	2.27	0.68
1:2:284:G:N7	8:S6:188:ARG:NH1	2.42	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
1:6:79:C:OP1	8:s6:159:ARG:NH2	2.26	0.68
37:7:15:C:O3'	42:l5:8:LYS:NZ	2.25	0.68
36:1:551:A:O2'	36:1:552:G:O5'	2.10	0.68
1:6:152:U:O2	8:s6:4:ASN:ND2	2.25	0.68
1:6:274:G:OP2	60:n4:120:LYS:NZ	2.26	0.68
67:o1:78:LYS:HB2	67:o1:90:PHE:HB2	1.76	0.68
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
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
21:C9:37:VAL:HG11	21:C9:100:ILE:HD11	1.75	0.67
36:1:595:G:N1	36:1:609:G:H5"	2.08	0.67
41:L4:33:ASP:OD1	41:L4:34:ILE:N	2.26	0.67
1:6:140:A:OP2	8:s6:187:LYS:NZ	2.26	0.67
1:6:755:A:H2'	1:6:756:A:C8	2.29	0.67
45:l8:195:SER:O	45:l8:197:VAL:N	2.27	0.67
1:2:145:A:O2'	1:2:146:U:O5'	2.12	0.67
47:M0:76:MET:HE1	47:M0:138:VAL:HG11	1.76	0.67
36:5:341:G:N7	41:l4:195:ARG:NH2	2.42	0.67
36:5:2177:G:OP2	39:l2:128:ARG:NH1	2.26	0.67
42:L5:68:THR:HG22	42:L5:70:THR:H	1.58	0.67
42:L5:279:LYS:HE3	42:L5:282:ARG:HH12	1.57	0.67
57:n1:14:MET:HE1	57:n1:55:LYS:HB2	1.75	0.67
1:2:478:A:O2'	11:S9:124:HIS:ND1	2.26	0.67
4:S2:103:VAL:HG12	4:S2:190:LEU:HD12	1.76	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
37:3:10:C:OP2	57:N1:26:HIS:ND1	2.27	0.67
35:sM:23:LYS:HZ2	35:sM:24:GLU:H	1.42	0.67
8:S6:153:VAL:O	8:S6:155:ASP:N	2.28	0.67
2:s0:55:GLU:OE2	23:d1:80:LYS:N	2.28	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	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:SR:13:LEU:HB2	34:SR:310:ILE:HB	1.77	0.67
50:M4:88:ALA:O	50:M4:93:LYS:NZ	2.28	0.67
78:Q2:12:CYS:SG	78:Q2:17:CYS:CB	2.82	0.67
36:5:2852:C:N3	47:m0:158:LYS:NZ	2.42	0.67
1:2:781:U:HO2'	1:2:782:U:H6	1.41	0.67
1:2:1291:G:H22	1:2:1324:G:H22	1.42	0.67
44:L7:121:LYS:HB2	57:N1:133:ALA:HB3	1.77	0.67
47:M0:180:GLU:OE2	47:M0:184:LYS:NZ	2.27	0.67
1:6:206:A:OP1	6:s4:133:LYS:NZ	2.24	0.67
1:6:959:U:OP2	29:d7:20:LYS:NZ	2.22	0.67
13:c1:133:LYS:O	13:c1:136:ARG:NH1	2.28	0.67
36:5:2174:G:OP2	39:l2:193:ARG:NH1	2.28	0.67
53:m7:69:ARG:HG2	53:m7:79:THR:HG23	1.77	0.67
1:2:761:G:OP1	11:S9:54:ARG:NH1	2.27	0.67
75:O9:9:ILE:HG22	75:O9:13:MET:HE2	1.76	0.67
42:l5:148:ILE:HG23	42:l5:151:GLN:HB3	1.76	0.67
75:o9:10:LYS:HA	75:o9:13:MET:HE3	1.76	0.67
1:2:1537:C:O2'	1:2:1540:G:O6	2.12	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
48:M1:54:VAL:O	48:M1:56:THR:N	2.28	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
5:s3:63:GLY:O	5:s3:67:ASN:ND2	2.25	0.67
36:5:824:C:H5"	39:l2:21:ARG:HD3	1.77	0.67
36:5:1427:U:OP2	64:n8:4:ARG:NH2	2.28	0.67
36:5:1630:U:OP1	63:n7:67:LYS:NZ	2.24	0.67
44:l7:134:VAL:O	44:l7:229:PHE:HA	1.95	0.67
45:l8:134:TYR:CG	45:l8:190:VAL:HG11	2.30	0.67
3:S1:229:MET:SD	3:S1:232:HIS:ND1	2.61	0.67
34:SR:180:ALA:HB3	34:SR:190:ALA:HB3	1.77	0.67
42:L5:58:LYS:HD2	42:L5:93:THR:HG21	1.77	0.67
6:s4:178:GLY:H	6:s4:195:ILE:HB	1.59	0.67
14:c2:87:PRO:HA	14:c2:140:PHE:HE1	1.60	0.67
36:5:2156:C:P	39:l2:241:ARG:HH22	2.17	0.67
36:5:3241:G:H2'	36:5:3245:A:C8	2.30	0.67
17:C5:30:THR:HG23	17:C5:86:VAL:HG21	1.77	0.66
36:1:2645:G:OP2	47:M0:117:GLY:HA2	1.95	0.66
65:N9:14:ARG:CZ	65:N9:18:ARG:HD3	2.25	0.66
33:e1:91:ILE:HG12	33:e1:92:LYS:HG2	1.76	0.66
36:5:2356:A:OP1	53:m7:138:LYS:NZ	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
14:C2:61:VAL:HG13	14:C2:121:VAL:HG23	1.76	0.66
36:5:815:G:OP2	73:o7:31:LYS:NZ	2.25	0.66
36:5:1231:A:H5"	36:5:1232:C:H5'	1.77	0.66
42:l5:64:ILE:HG13	42:l5:109:THR:HG21	1.78	0.66
46:l9:126:VAL:HG21	46:l9:161:LEU:HA	1.77	0.66
47:m0:29:SER:HB2	47:m0:125:LEU:HD12	1.78	0.66
48:m1:15:GLU:HB3	48:m1:130:VAL:HG22	1.77	0.66
52:m6:65:ASN:HB3	52:m6:68:ARG:HD2	1.76	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
1:6:1080:U:H2'	1:6:1081:A:C8	2.29	0.66
5:s3:222:VAL:HG11	34:sR:229:LYS:HA	1.76	0.66
52:m6:61:ALA:HA	52:m6:70:PRO:HD2	1.76	0.66
1:2:93:A:H1'	6:S4:3:ARG:HB3	1.78	0.66
9:S7:50:ASP:HB3	9:S7:56:LYS:HG2	1.77	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
36:1:994:G:N2	36:1:995:U:O4	2.29	0.66
1:6:1420:C:O2'	5:s3:160:SER:O	2.11	0.66
36:5:607:A:OP1	43:l6:26:ARG:NH2	2.28	0.66
59:n3:28:ASN:HD21	59:n3:112:SER:H	1.43	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
36:1:2295:A:OP1	59:N3:63:LYS:NZ	2.29	0.66
49:M3:55:ARG:O	49:M3:115:ARG:NH2	2.29	0.66
36:5:1717:U:H2'	36:5:1718:G:C8	2.31	0.66
63:n7:25:ILE:HA	63:n7:43:VAL:HG12	1.76	0.66
3:S1:157:GLN:O	3:S1:159:SER:N	2.29	0.66
5:S3:127:MET:HE1	5:S3:133:GLY:HA2	1.77	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
36:1:2115: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	1.78	0.66
28:D6:87:ARG:NH2	28:D6:94:ASN:O	2.28	0.66
34:SR:258:THR:O	34:SR:275:ARG:NH1	2.29	0.66
36:1:1951:C:H42	36:1:2095:G:H1	1.43	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:523:G:OP2	26:D4:37:LYS:NZ	2.25	0.66
11:S9:93:LEU:HA	11:S9:96:VAL:HG13	1.78	0.66
36:1:2162:U:OP1	39:L2:234:LYS:NZ	2.28	0.66
45:L8:90:THR:HA	45:L8:214:LEU:HD21	1.77	0.66
63:N7:53:VAL:HG21	63:N7:62:VAL:HG13	1.78	0.66
36:5:63:A:OP1	51:m5:172:ARG:NH2	2.29	0.66
42:l5:211:LEU:HB3	42:l5:219:PHE:HB2	1.78	0.66
44:l7:88:ARG:NH1	44:l7:91:GLY:O	2.29	0.66
47:m0:99:ILE:HG13	47:m0:123:HIS:HB2	1.76	0.66
48:m1:148:VAL:HG12	48:m1:152:HIS:HB3	1.78	0.66
62:n6:11:ASP:HB3	62:n6:14:LYS:HG3	1.77	0.66
79:q3:39:CYS:HB3	79:q3:42:CYS:HB3	1.75	0.66
50:M4:55:ARG:NH2	50:M4:76:ALA:O	2.29	0.66
1:6:27:U:H2'	1:6:28:A:H8	1.61	0.66
36:5:2138:A:HO2'	73:o7:2:GLY:N	1.94	0.66
36:5:3280:U:O2'	36:5:3281:U:H5"	1.96	0.66
30:D8:10:ALA:HA	30:D8:32:PHE:HA	1.78	0.66
40:L3:56:ILE:HD11	40:L3:359:ILE:HG12	1.78	0.66
59:N3:10:LYS:HD2	59:N3:13:ILE:HD11	1.78	0.66
33:e1:126:CYS:HB3	33:e1:130:VAL:HG21	1.78	0.66
45:l8:81:THR:OG1	45:l8:82:LEU:N	2.26	0.66
1:2:581:U:OP2	5:S3:143:ARG:NH1	2.28	0.65
3:S1:183:GLN:HG2	3:S1:187:LYS:HE3	1.78	0.65
17:C5:111:MET:HG2	20:C8:119:ILE:HG23	1.77	0.65
36:1:1043:C:O3'	47:M0:90:ARG:NH1	2.28	0.65
61:N5:58:ASP:OD1	71:O5:25:LYS:NZ	2.26	0.65
1:6:399:A:H4'	6:s4:3:ARG:HG2	1.77	0.65
1:2:732:G:O2'	1:2:733:A:O4'	2.15	0.65
1:2:1794:A:H1'	28:D6:79:ILE:HD12	1.77	0.65
1:6:280:U:OP2	60:n4:113:LYS:NZ	2.25	0.65
1:6:1351:G:OP1	18:c6:66:ARG:NH1	2.29	0.65
42:l5:110:LEU:HA	42:l5:113:LEU:HB2	1.78	0.65
57:n1:39:ILE:HD12	57:n1:102:ARG:HE	1.60	0.65
36:1:1555:U:H5	36:1:1559:A:H61	1.44	0.65
1:6:764:U:OP2	11:s9:78:ARG:NH1	2.29	0.65
1:6:1569:A:OP2	1:6:1569:A:H8	1.78	0.65
11:s9:82:ARG:HH11	11:s9:149:ARG:HD3	1.60	0.65
17:c5:10:ARG:NH2	17:c5:70:ASN:OD1	2.29	0.65
36:5:979:U:H1'	36:5:980:A:C4	2.31	0.65
3:S1:173:THR:O	3:S1:177:GLN:NE2	2.29	0.65
22:D0:106:ILE:HG23	22:D0:107:THR:HG23	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
46:L9:171:ASP:OD2	46:L9:173:ARG:NH1	2.29	0.65
1:6:895:G:H1	1:6:917:U:H3	1.44	0.65
36:5:2818:U:H5'	36:5:2818:U:H6	1.62	0.65
51:m5:96:ARG:NH2	51:m5:104:GLU:OE2	2.29	0.65
72:o6:76:ARG:HA	72:o6:76:ARG:HE	1.60	0.65
3:S1:69:CYS:SG	16:C4:114:ARG:NH1	2.70	0.65
36:1:1307:G:H1'	36:1:1308:A:C8	2.31	0.65
36:1:2679:A:HO2'	48:M1:52:TYR:HH	1.39	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
1:6:228:G:H1	1:6:236:A:H61	1.45	0.65
1:2:514:G:H1	1:2:543:C:H5	1.45	0.65
23:D1:74:GLN:HE22	23:D1:83:TRP:H	1.42	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	1.78	0.65
36:5:1064:A:N6	36:5:1096:U:H3	1.93	0.65
40:l3:92:TYR:HB2	40:l3:157:VAL:HG13	1.77	0.65
3:S1:147:ALA:O	3:S1:148:ASN:ND2	2.22	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
11:s9:65:LYS:HA	11:s9:70:LEU:HD11	1.79	0.65
36:5:2157:G:N7	39:l2:152:SER:OG	2.25	0.65
37:7:2:G:O2'	37:7:23:A:N1	2.30	0.65
23:D1:41:GLU:O	23:D1:44:ARG:NH1	2.30	0.65
36:1:114:A:N1	36:1:266:A:O2'	2.28	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	1.77	0.65
8:s6:78:THR:HG23	8:s6:92:ARG:HG2	1.78	0.65
15:c3:56:ASP:OD2	29:d7:52:THR:OG1	2.15	0.65
37:7:28:C:H5"	48:m1:137:ARG:HG2	1.79	0.65
24:D2:30:SER:HA	24:D2:34:ILE:HD12	1.78	0.65
36:1:2150:G:H4'	79:Q3:22:LEU:HD21	1.78	0.65
36:1:2592:G:H4'	36:1:2594:C:C2	2.31	0.65
63:N7:29:HIS:O	63:N7:31:GLU:N	2.29	0.65
36:5:1750:A:H4'	36:5:1751:G:H5'	1.78	0.65
47:m0:177:ASP:OD2	47:m0:177:ASP:N	2.26	0.65
52:m6:190:VAL:HA	52:m6:193:GLN:HB2	1.78	0.65
79:q3:39:CYS:CB	79:q3:42:CYS:HB3	2.18	0.65
10:S8:138:ASN:OD1	10:S8:138:ASN:N	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:SR:282:SER:H	34:SR:285:ALA:HB3	1.62	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
4:s2:161:LYS:HG3	4:s2:166:THR:HG22	1.78	0.65
6:s4:45:ILE:HG13	6:s4:61:VAL:HG21	1.79	0.65
36:5:590:G:OP1	68:o2:62:LYS:NZ	2.28	0.65
22:D0:27:THR:HB	22:D0:88:LYS:HG3	1.79	0.64
36:1:1603:A:H61	61:N5:71:THR:HG21	1.61	0.64
36:1:3067:C:OP1	55:M9:58:HIS:NE2	2.25	0.64
40:L3:303:LYS:HD2	40:L3:361:THR:HG21	1.78	0.64
1:6:67:A:O2'	1:6:69:G:OP1	2.11	0.64
1:6:218:A:H2'	1:6:219:A:H5"	1.78	0.64
1:6:1600:A:H4'	1:6:1601:G:OP1	1.96	0.64
15:c3:22:ALA:HB1	15:c3:23:PRO:HA	1.79	0.64
36:5:1145:G:OP1	68:o2:44:ARG:NH1	2.30	0.64
42:l5:95:TRP:CH2	42:l5:181:PRO:HD3	2.32	0.64
44:l7:173:LEU:HD21	44:l7:198:ALA:HA	1.79	0.64
34:SR:216:LYS:HA	34:SR:239:GLU:HG3	1.78	0.64
41:L4:292:SER:OG	41:L4:293:SER:N	2.29	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	1.96	0.64
36:5:3115:C:OP1	46:l9:62:ARG:NH2	2.31	0.64
2:S0:120:LEU:HD11	2:S0:144:ILE:HG13	1.79	0.64
36:1:1722:U:OP1	55:M9:100:ARG:NH1	2.25	0.64
61:N5:105:VAL:HG11	61:N5:126:LEU:HD13	1.79	0.64
1:6:1465:C:OP1	18:c6:139:GLN:NE2	2.28	0.64
17:c5:44:ARG:NH2	17:c5:82:ASN:O	2.30	0.64
36:5:2180:G:H2'	36:5:2181:C:C6	2.32	0.64
3:S1:165:ARG:O	3:S1:169:SER:OG	2.15	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
36:5:2209:U:H1'	36:5:2210:G:H5"	1.79	0.64
1:2:814:A:H5"	55:M9:170:ARG:HH22	1.62	0.64
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
36:1:542:G:H1	36:1:549:U:H3	1.43	0.64
40:L3:53:MET:HE2	40:L3:77:THR:HG22	1.79	0.64
1:6:339:C:OP2	10:s8:10:LYS:NZ	2.26	0.64
1:6:1524:A:H2'	1:6:1525:A:C8	2.32	0.64
70:o4:8:ARG:HH21	70:o4:31:ARG:HD2	1.63	0.64
54:M8:71:LEU:HD13	54:M8:99:THR:HG21	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1220:C:H5'	12:c0:52:LYS:HE3	1.79	0.64
13:c1:17:PRO:HG3	13:c1:63:LEU:HD11	1.78	0.64
36:5:269:G:H5"	51:m5:14:LYS:HE2	1.79	0.64
37:7:5:G:OP1	48:m1:143:ARG:NH2	2.31	0.64
41:l4:26:PHE:HD1	41:l4:130:ALA:HB2	1.63	0.64
49:m3:113:VAL:HG12	49:m3:117:LYS:HE3	1.79	0.64
54:m8:100:THR:HG22	54:m8:120:GLU:HB3	1.80	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
6:S4:71:LYS:HG3	6:S4:91:THR:HB	1.80	0.64
25:D3:65:ASN:ND2	25:D3:116:ASP:OD1	2.31	0.64
36:1:1245:A:H3'	36:1:1246:G:H5"	1.78	0.64
36:1:1349:G:H5'	41:L4:291:ASN:OD1	1.98	0.64
36:1:2828:G:OP1	47:M0:7:ARG:NH1	2.31	0.64
59:N3:10:LYS:NZ	59:N3:56:ASP:OD1	2.25	0.64
34:sR:82:SER:OG	34:sR:92:TRP:NE1	2.26	0.64
42:l5:257:GLU:H	42:l5:257:GLU:CD	2.05	0.64
44:l7:103:LEU:HA	44:l7:130:ILE:HD11	1.78	0.64
1:2:741:C:O2	9:S7:107:ARG:NH2	2.30	0.64
1:2:1242:A:OP1	17:C5:59:LYS:NZ	2.30	0.64
47:M0:54:SER:HB3	47:M0:135:ILE:HD11	1.80	0.64
1:6:886:U:O2'	16:c4:121:VAL:O	2.14	0.64
34:sR:220:ILE:HB	34:sR:234:LEU:HB2	1.80	0.64
36:5:96:G:OP1	49:m3:15:ARG:NH2	2.31	0.64
40:l3:185:GLY:O	40:l3:191:LYS:NZ	2.20	0.64
40:l3:238:LEU:HB3	40:l3:242:THR:HG21	1.79	0.64
42:l5:54:ARG:NH2	42:l5:147:ASP:OD1	2.23	0.64
47:m0:175:ASN:OD1	47:m0:176:LEU:N	2.27	0.64
1:2:40:A:OP1	11:S9:3:ARG:NH1	2.29	0.64
1:2:380:U:O2	11:S9:3:ARG:NH2	2.31	0.64
10:S8:162:ALA:HA	36:1:3353:G:H5'	1.80	0.64
24:D2:82:LYS:O	24:D2:84:GLY:N	2.27	0.64
36:1:3151:U:H4'	36:1:3294:A:H1'	1.79	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
74:O8:31:LEU:HA	74:O8:37:PRO:HA	1.80	0.64
17:c5:37:ALA:O	17:c5:42:ARG:NH1	2.31	0.64
56:n0:77:VAL:HG13	56:n0:126:VAL:HG22	1.79	0.64
11:S9:108:ARG:HH21	11:S9:145:SER:HB2	1.63	0.64
36:1:1564:U:H2'	36:1:1565:G:H8	1.63	0.64
64:N8:6:THR:HG22	64:N8:9:ARG:HG2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:1447:G:H3'	53:m7:67:ILE:HD11	1.80	0.64
36:5:3122:A:N1	46:l9:70:THR:HG21	2.13	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
4:s2:69:ILE:HG12	4:s2:133:LYS:HB3	1.79	0.63
8:s6:12:SER:HB3	8:s6:124:LEU:HD12	1.80	0.63
23:d1:60:ARG:HA	23:d1:65:SER:HB2	1.80	0.63
63:n7:26:VAL:HG21	63:n7:96:VAL:HB	1.80	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
36:1:1631: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	2.15	0.63
64:n8:47:LYS:O	64:n8:49:HIS:N	2.28	0.63
64:n8:82:ILE:HD11	64:n8:102:ILE:HG12	1.80	0.63
47:M0:76:MET:HE3	47:M0:148:VAL:HA	1.79	0.63
25:d3:125:VAL:HG12	25:d3:126:LYS:HG3	1.80	0.63
28:d6:87:ARG:HB3	28:d6:91:ASP:HB2	1.80	0.63
36:5:2996:U:H4'	36:5:2996:U:OP1	1.97	0.63
64:n8:6:THR:HG22	64:n8:9:ARG:HG2	1.80	0.63
10:S8:39:GLY:HA2	10:S8:61:GLU:HB3	1.80	0.63
14:C2:103:LEU:HG	14:C2:116:VAL:HG22	1.81	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
40:L3:347:SER:HB3	40:L3:350:ALA:H	1.64	0.63
10:s8:110:ARG:HH22	10:s8:160:PHE:HB3	1.61	0.63
34:sR:216:LYS:HA	34:sR:239:GLU:HG3	1.80	0.63
42:l5:83:LEU:HB3	42:l5:88:ILE:HB	1.79	0.63
53:m7:67:ILE:HD12	53:m7:82:ARG:CZ	2.28	0.63
55:m9:173:ARG:HH21	55:m9:177:VAL:HG21	1.62	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
36:1:1362:G:H4'	44:L7:159:GLN:O	1.98	0.63
36:1:2736:A:OP1	57:N1:92:ARG:NH1	2.32	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	1.80	0.63
34:sR:89:LEU:HB2	34:sR:103:PHE:HB2	1.80	0.63
36:5:439:C:H4'	36:5:440:A:H5'	1.80	0.63
36:5:1949:G:OP2	55:m9:135:LYS:NZ	2.28	0.63
36:5:2588:U:OP1	45:l8:48:ARG:NH2	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:l7:22:THR:HA	44:l7:25:GLN:HG2	1.81	0.63
61:n5:48:SER:OG	61:n5:49:LYS:N	2.31	0.63
8:S6:10:ASN:ND2	8:S6:127:THR:O	2.32	0.63
36:1:1107:C:OP1	65:N9:25:LYS:NZ	2.30	0.63
36:1:2617:U:H5	36:1:2621:G:OP2	1.80	0.63
1:6:472:U:H5"	11:s9:11:THR:HG23	1.81	0.63
1:6:523:G:OP2	26:d4:37:LYS:NZ	2.29	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	2.31	0.63
36:5:1369:A:OP1	64:n8:21:ARG:NH1	2.32	0.63
40:l3:249:VAL:HG22	40:l3:252:ILE:HD12	1.79	0.63
65:n9:16:ALA:O	65:n9:20:GLY:HA3	1.97	0.63
72:o6:63:ASN:O	72:o6:65:GLY:N	2.31	0.63
1:2:1331:A:OP1	19:C7:45:ARG:NH2	2.31	0.63
1:2:1550:A:P	17:C5:42:ARG:HH22	2.20	0.63
36:1:1230:G:H1	36:1:1279:C:H42	1.46	0.63
41:L4:265:GLU:H	41:L4:265:GLU:CD	2.04	0.63
72:O6:2:THR:OG1	72:O6:3:VAL:N	2.12	0.63
1:6:1672:G:H2'	1:6:1673:G:C8	2.33	0.63
16:c4:128:LYS:NZ	28:d6:27:SER:OG	2.32	0.63
41:l4:217:LYS:HA	41:l4:220:ARG:HG2	1.79	0.63
70:o4:7:PHE:HD1	70:o4:20:ILE:HD12	1.63	0.63
25:D3:91:GLY:O	25:D3:93:LEU:N	2.27	0.63
36:1:1156:C:OP2	44:L7:94:LYS:NZ	2.32	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	1.81	0.63
36:5:2255:A:H5'	36:5:2261:G:H22	1.62	0.63
1:2:337:G:H3'	13:C1:133:LYS:HB2	1.81	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
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
37:7:91:G:H2'	37:7:92:A:C8	2.34	0.63
10:S8:103:GLN:HB3	10:S8:164:ARG:HG2	1.80	0.62
22:D0:58:LEU:HD12	22:D0:88:LYS:HD2	1.81	0.62
36:1:1027:A:H2'	36:1:1029:G:H5"	1.81	0.62
1:6:263:C:H4'	1:6:292:U:H5'	1.81	0.62
36:5:1781:C:H2'	36:5:1782:U:C6	2.34	0.62
36:5:2853:A:H5'	47:m0:63:GLU:HB2	1.81	0.62
72:o6:59:ASP:O	72:o6:63:ASN:ND2	2.28	0.62
36:1:59:G:H2'	38:4:33:A:O2'	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:2356:A:H61	36:1:2983:C:H5	1.46	0.62
68:O2:31:ASN:OD1	68:O2:31:ASN:N	2.26	0.62
36:5:598:A:OP1	44:l7:41:ARG:NH1	2.32	0.62
36:5:2102:U:H2'	36:5:2103:U:C6	2.35	0.62
46:l9:117:PHE:CE1	46:l9:165:CYS:HB3	2.34	0.62
1:2:706:A:N1	1:2:734:A:N6	2.47	0.62
22:D0:106:ILE:HG13	22:D0:107:THR:H	1.63	0.62
36:1:1069:C:H2'	36:1:1070:U:H6	1.63	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
1:6:1234:A:H4'	33:e1:146:SER:HB3	1.81	0.62
5:s3:40:ARG:HG2	22:d0:110:PRO:HB3	1.81	0.62
7:s5:63:GLN:HE22	7:s5:66:GLN:HB2	1.64	0.62
36:5:2514:U:H6	36:5:2514:U:OP1	1.82	0.62
52:m6:62:THR:H	52:m6:69:GLY:HA3	1.62	0.62
1:2:1401:A:OP1	19:C7:60:ARG:NH1	2.33	0.62
1:2:1769:U:O2	16:C4:136:ARG:NH1	2.32	0.62
1:2:539:G:N2	1:2:540:G:O6	2.32	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
45:L8:221:ASN:HA	45:L8:225:LYS:HE3	1.80	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
13:c1:78:THR:HA	13:c1:84:ILE:HG22	1.79	0.62
21:c9:37:VAL:HG11	21:c9:100:ILE:HD11	1.80	0.62
36:5:30:G:O5'	51:m5:172:ARG:HD2	1.99	0.62
44:l7:119:VAL:HG13	44:l7:124:LEU:HD23	1.80	0.62
34:SR:31:ASN:O	34:SR:47:LEU:N	2.29	0.62
52:M6:89:SER:O	52:M6:92:THR:OG1	2.17	0.62
1:6:448:C:OP2	6:s4:49:ARG:NH1	2.29	0.62
36:5:1747:G:H21	74:o8:2:ALA:HA	1.64	0.62
36:5:2584:G:H5'	36:5:2585:G:OP2	1.98	0.62
47:m0:42:THR:HG23	47:m0:45:GLU:HG3	1.82	0.62
49:m3:42:ARG:O	49:m3:46:ILE:HG12	2.00	0.62
64:n8:73:LEU:HB2	64:n8:109:TYR:CD2	2.35	0.62
1:2:68:A:O2'	1:2:69:G:OP2	2.17	0.62
1:2:790:U:OP1	6:S4:187:ARG:NH1	2.31	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
34:SR:76:ASP:OD1	34:SR:76:ASP:N	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:707:U:H2'	36:1:708:G:H5"	1.81	0.62
36:1:2960:C:H2'	36:1:2961:G:H8	1.65	0.62
1:6:1258:U:H4'	12:c0:2:LEU:HD22	1.82	0.62
6:s4:151:ASP:OD1	8:s6:215:ARG:NH1	2.31	0.62
13:c1:99:ARG:NH1	25:d3:7:ARG:O	2.33	0.62
15:c3:94:LYS:HG2	15:c3:118:ILE:HD13	1.81	0.62
36:5:744:A:OP1	54:m8:66:ARG:NH2	2.32	0.62
36:5:3050:U:O2'	60:n4:16:GLY:O	2.16	0.62
47:m0:68:ALA:HB1	47:m0:155:ALA:HB1	1.81	0.62
73:o7:21:ARG:HD2	73:o7:39:TYR:HB2	1.80	0.62
22:D0:27:THR:HG23	22:D0:113:ASP:HB3	1.82	0.62
36:1:2947:G:C2	40:L3:250:ALA:HB1	2.35	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
79:Q3:7:LYS:O	79:Q3:27:LYS:NZ	2.31	0.62
16:c4:80:HIS:ND1	16:c4:113:GLY:O	2.33	0.62
34:sR:149:ASP:HB2	34:sR:175:ASP:HB3	1.81	0.62
36:5:116:A:OP2	51:m5:2:GLY:N	2.33	0.62
36:5:768:C:OP1	49:m3:186:ARG:NH2	2.26	0.62
38:8:26:U:H2'	38:8:27:U:C6	2.34	0.62
49:m3:64:LYS:HG3	64:n8:69:TRP:CG	2.35	0.62
82:p0:40:GLU:OE2	82:p0:104:ARG:NE	2.32	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
2:S0:50:VAL:HG22	19:C7:109:LEU:HD21	1.82	0.62
9:S7:177:THR:OG1	9:S7:178:GLY:N	2.28	0.62
14:C2:124:LYS:O	14:C2:126:TRP:N	2.31	0.62
1:6:563:U:H4'	80:e0:17:GLN:NE2	2.15	0.62
5:s3:202:LEU:H	5:s3:202:LEU:HD22	1.65	0.62
6:s4:92:LEU:HD13	26:d4:17:LEU:HD11	1.82	0.62
12:c0:32:HIS:CD2	12:c0:33:GLU:H	2.17	0.62
34:sR:267:PRO:HD2	34:sR:269:TYR:HE1	1.65	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
36:1:3316:A:H2	36:1:3389:U:H5'	1.65	0.62
49:M3:76:THR:HG22	49:M3:101:ARG:HB3	1.81	0.62
78:Q2:12:CYS:SG	78:Q2:17:CYS:HB3	2.39	0.62
9:s7:49:ILE:HG13	9:s7:57:ALA:HB3	1.81	0.62
17:c5:25:LEU:HA	17:c5:28:MET:HE2	1.81	0.62
36:5:171:G:O6	36:5:247:C:N4	2.33	0.62
36:5:873:C:H5"	36:5:874:U:O5'	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:m0:78:THR:OG1	47:m0:79:VAL:N	2.31	0.62
53:m7:122:ALA:HB3	53:m7:143:PRO:HB2	1.81	0.62
1:2:762:A:OP1	11:S9:79:ARG:NH2	2.22	0.61
1:2:1145:U:O2'	4:S2:89:GLN:O	2.18	0.61
1:2:1591:C:H2'	1:2:1592:A:C8	2.35	0.61
3:S1:137:ILE:HD12	3:S1:172:LEU:HD22	1.82	0.61
23:D1:74:GLN:NE2	23:D1:81:ASN:O	2.32	0.61
36:1:1277:C:HO2'	36:1:1278:A:H8	1.48	0.61
36:1:1334:U:H5"	44:L7:206:LYS:HB3	1.82	0.61
36:1:1346:G:H1'	41:L4:307:GLN:HE22	1.65	0.61
40:L3:105:VAL:HG21	40:L3:148:LEU:HD13	1.83	0.61
1:6:800:U:H2'	1:6:801:G:C8	2.35	0.61
2:s0:83:GLN:HG2	2:s0:99:ALA:HB1	1.82	0.61
5:s3:72:LEU:HD22	12:c0:65:TYR:HD1	1.64	0.61
36:1:2683:U:H2'	36:1:2684:C:C6	2.35	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
48:M1:49:LYS:HB3	48:M1:62:ASN:HA	1.81	0.61
38:8:135:G:OP2	61:n5:56:ARG:NH2	2.34	0.61
43:l6:40:LEU:HD13	43:l6:84:VAL:HG11	1.82	0.61
1:2:1291:G:H22	1:2:1324:G:N2	1.98	0.61
1:2:1553:G:HO2'	31:D9:14:TYR:HH	1.42	0.61
1:2:1591:C:H2'	1:2:1592:A:H8	1.64	0.61
36:1:249:U:O2	36:1:250:U:N3	2.33	0.61
41:L4:36:HIS:O	41:L4:40:THR:HG23	2.00	0.61
1:6:57:G:OP1	26:d4:112:LYS:NZ	2.33	0.61
1:6:513:U:H2'	1:6:514:G:C8	2.35	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	2.33	0.61
45:l8:163:VAL:HG22	45:l8:166:LEU:HD12	1.82	0.61
58:n2:59:ASP:OD1	58:n2:60:GLY:N	2.31	0.61
8:S6:98:ARG:NH2	8:S6:101:ILE:O	2.26	0.61
17:C5:126:VAL:HG13	17:C5:127:ARG:H	1.64	0.61
27:D5:70:LYS:HG3	27:D5:71:ILE:H	1.66	0.61
36:1:409:A:H61	38:4:15:G:H1'	1.65	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
42:L5:40:HIS:HD2	42:L5:42:ALA:H	1.47	0.61
1:6:1568:C:OP2	20:c8:36:LYS:NZ	2.29	0.61
1:6:1799:U:O2'	3:s1:152:ARG:NH1	2.23	0.61
19:c7:27:ASP:O	19:c7:31:ASN:ND2	2.20	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:d2:25:VAL:HG22	24:d2:65:LEU:HD21	1.80	0.61
58:n2:19:VAL:HG12	58:n2:105:LEU:HD22	1.81	0.61
1:2:656:G:O2'	1:2:657:U:O4'	2.19	0.61
1:2:1657:U:H4'	1:2:1658:G:O5'	1.99	0.61
9:S7:74:GLN:O	9:S7:78:THR:OG1	2.18	0.61
11:S9:92:LYS:O	11:S9:94:ASP:N	2.33	0.61
36:1:1492:G:N7	75:O9:2:ALA:HB1	2.15	0.61
40:L3:53:MET:HE1	40:L3:327:CYS:HB3	1.83	0.61
68:O2:11:LYS:O	68:O2:12:LYS:HB2	2.00	0.61
16:c4:47:LYS:HB3	16:c4:62:LEU:HD23	1.82	0.61
59:n3:2:SER:N	59:n3:56:ASP:OD1	2.34	0.61
66:o0:75:ASN:HA	66:o0:86:ARG:HB2	1.83	0.61
16:C4:108:SER:OG	16:C4:109:GLY:N	2.33	0.61
20:C8:123:ARG:HG3	20:C8:133:VAL:HG21	1.83	0.61
36:1:2946:A:H5"	36:1:2947:G:H5'	1.81	0.61
71:O5:76:GLN:O	71:O5:81:ARG:NH1	2.34	0.61
1:6:75:U:O2'	1:6:76:A:O4'	2.19	0.61
17:c5:108:ARG:HH21	20:c8:119:ILE:HD12	1.65	0.61
36:5:114:A:N1	36:5:266:A:O2'	2.27	0.61
48:m1:53:THR:HG23	48:m1:60:ARG:HA	1.82	0.61
1:2:458:G:OP1	26:D4:109:LYS:NZ	2.32	0.61
20:C8:125:ILE:HD11	35:SM:57:ASN:HB3	1.80	0.61
1:6:1208:A:N1	1:6:1455:G:N2	2.48	0.61
36:5:297:G:OP2	36:5:297:G:N2	2.28	0.61
36:5:837:A:OP2	79:q3:4:ARG:NH1	2.27	0.61
53:m7:25:SER:O	53:m7:29:THR:OG1	2.19	0.61
73:o7:28:HIS:HB3	73:o7:31:LYS:HB2	1.83	0.61
22:D0:53:LYS:HB2	22:D0:92:ASP:HB2	1.81	0.61
36:1:2836:C:H5	36:1:2852:C:H42	1.48	0.61
48:M1:107:ASP:OD1	48:M1:107:ASP:N	2.33	0.61
1:6:558:U:OP2	80:e0:55:ARG:NH2	2.32	0.61
4:s2:101:VAL:HG22	4:s2:115:ILE:HG23	1.83	0.61
15:c3:91:LEU:HD12	15:c3:125:LEU:HD12	1.81	0.61
36:5:2102:U:H2'	36:5:2103:U:H6	1.66	0.61
36:5:2366:C:H5'	40:l3:259:HIS:CE1	2.36	0.61
1:2:487:G:H3'	1:2:488:G:H5"	1.83	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:L3:37:ARG:HG2	40:L3:187:SER:H	1.66	0.61
13:c1:109:VAL:HG12	13:c1:137:PHE:HB2	1.83	0.61
20:c8:40:ARG:NH2	21:c9:44:GLU:OE2	2.34	0.61
36:5:2562:A:N6	36:5:2579:G:O2'	2.32	0.61
36:5:2746:A:H2	42:l5:146:LEU:HB3	1.66	0.61
63:n7:47:GLU:OE2	63:n7:69:LYS:NZ	2.24	0.61
66:o0:34:LEU:HD23	66:o0:59:TYR:HB3	1.83	0.61
68:o2:40:SER:O	68:o2:44:ARG:HG3	2.01	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
5:S3:164:VAL:HG13	5:S3:168:ILE:HD11	1.83	0.61
24:D2:105:THR:HG23	24:D2:110:ILE:HG12	1.81	0.61
36:1:3294:A:OP1	40:L3:128:LYS:NZ	2.30	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
5:s3:210:GLU:OE2	19:c7:19:ARG:NH1	2.33	0.61
28:d6:26:CYS:HB3	28:d6:28:LYS:H	1.66	0.61
36:5:2921:U:H2'	36:5:2923:U:OP2	2.01	0.61
42:l5:40:HIS:CE1	42:l5:42:ALA:HB3	2.35	0.61
67:o1:83:GLU:O	67:o1:85:ALA:N	2.34	0.61
1:2:1511:U:H2'	1:2:1512:G:H8	1.66	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
36:1:3092:C:O2'	36:1:3094:A:OP2	2.16	0.60
70:O4:3:GLN:HB3	70:O4:30:LEU:HD12	1.82	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
36:5:1912:U:N3	36:5:2122:G:OP2	2.33	0.60
38:8:149:A:H2'	38:8:150:G:C8	2.35	0.60
3:S1:171:ILE:HD12	3:S1:197:ILE:HD13	1.82	0.60
12:C0:14:TYR:OH	12:C0:34:GLU:OE1	2.09	0.60
37:3:97:A:OP1	56:N0:40:ARG:NH1	2.34	0.60
40:L3:92:TYR:HB2	40:L3:157:VAL:HG22	1.83	0.60
53:M7:28:ASN:O	53:M7:32:THR:HG22	2.01	0.60
63:N7:38:PHE:O	63:N7:40:HIS:ND1	2.27	0.60
1:6:489:C:O2'	1:6:490:C:O4'	2.18	0.60
2:s0:13:ASP:OD1	2:s0:179:ARG:NH2	2.23	0.60
8:s6:138:ALA:HB1	8:s6:142:ARG:HH12	1.67	0.60
27:d5:56:THR:O	27:d5:103:ARG:NH2	2.34	0.60
36:5:629:U:H2'	36:5:630:A:C8	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:l3:303:LYS:HD2	40:l3:361:THR:HG21	1.84	0.60
49:m3:174:ARG:HG3	72:o6:9:ILE:HD11	1.83	0.60
64:n8:6:THR:HG23	64:n8:8:THR:HG23	1.84	0.60
67:o1:84:ASP:N	67:o1:84:ASP:OD1	2.34	0.60
83:p1:34:UNK:O	83:p1:36:UNK:N	2.34	0.60
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
1:6:1003:A:H4'	1:6:1004:U:O5'	2.00	0.60
1:6:1521:G:O6	21:c9:68:ARG:NH1	2.35	0.60
8:s6:98:ARG:HD3	8:s6:99:GLY:N	2.16	0.60
16:c4:50:ALA:HB3	16:c4:53:ASP:HB2	1.84	0.60
18:c6:39:VAL:HG12	18:c6:41:PRO:HD2	1.83	0.60
36:5:396:A:O2'	36:5:399:A:OP1	2.15	0.60
36:5:715:A:H8	64:n8:115:LYS:HG3	1.66	0.60
36:5:1080:A:OP2	42:l5:140:ARG:NH2	2.34	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
17:C5:123:TYR:OH	20:C8:122:HIS:NE2	2.34	0.60
36:1:1238:C:N4	36:1:1245:A:OP2	2.35	0.60
36:1:1354:G:H4'	43:L6:8:LYS:HE2	1.84	0.60
36:1:1724:U:H4'	36:1:1725:C:OP1	2.00	0.60
39:L2:204:MET:HE2	39:L2:209:HIS:HB2	1.84	0.60
41:L4:146:PRO:HG2	41:L4:150:LEU:HD21	1.83	0.60
62:N6:111:LEU:HD23	62:N6:116:LYS:HE2	1.83	0.60
36:5:1098:A:OP2	57:n1:130:ARG:NH1	2.30	0.60
51:m5:47:LYS:HE3	51:m5:51:LEU:HD11	1.83	0.60
61:n5:73:MET:HE1	61:n5:141:TYR:HE1	1.65	0.60
7:S5:57:SER:O	7:S5:59:VAL:N	2.30	0.60
25:D3:90:ASP:O	25:D3:136:TRP:NE1	2.31	0.60
36:1:883:A:H5'	53:M7:133:HIS:HA	1.83	0.60
71:O5:101:THR:HG22	71:O5:103:LYS:H	1.67	0.60
1:6:149:C:H2'	1:6:150:U:H6	1.66	0.60
36:5:2771:U:O2'	36:5:2772:C:O4'	2.15	0.60
36:5:3230:G:H4'	50:m4:132:LYS:HD3	1.84	0.60
81:m2:102:UNK:HA	81:m2:140:UNK:HA	1.84	0.60
55:m9:68:GLN:NE2	55:m9:72:GLU:OE2	2.34	0.60
28:D6:87:ARG:HB3	28:D6:91:ASP:HB2	1.83	0.60
44:L7:178:ILE:HA	44:L7:183:ASP:HB3	1.82	0.60
1:6:123:G:H21	6:s4:146:THR:HG21	1.66	0.60
8:s6:2:LYS:HB3	8:s6:108:VAL:HG12	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:s6:58:LYS:NZ	8:s6:104:PRO:O	2.35	0.60
10:s8:42:ARG:HB3	10:s8:59:ARG:HB2	1.84	0.60
10:s8:138:ASN:HA	10:s8:141:ARG:HD3	1.83	0.60
11:s9:113:VAL:HG12	11:s9:119:ALA:HB2	1.83	0.60
20:c8:92:ILE:HG23	20:c8:93:THR:HG23	1.82	0.60
36:5:2207:A:H2'	36:5:2208:A:O4'	2.02	0.60
1:2:818:C:N4	1:2:819:G:O6	2.35	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
36:1:1145:G:OP1	68:O2:44:ARG:NH1	2.33	0.60
41:L4:99:MET:SD	41:L4:102:PRO:HA	2.41	0.60
1:6:913:G:H3'	1:6:914:G:H5'	1.84	0.60
1:6:1087:A:H2'	1:6:1088:A:C8	2.37	0.60
1:6:1316:G:HO2'	1:6:1401:A:HO2'	1.50	0.60
7:s5:197:GLU:OE1	7:s5:209:TYR:N	2.35	0.60
9:s7:51:VAL:HG23	9:s7:53:GLY:H	1.65	0.60
11:s9:168:ARG:HD2	11:s9:174:ARG:NH2	2.17	0.60
40:l3:3:HIS:ND1	40:l3:3:HIS:O	2.35	0.60
1:2:304:U:H2'	1:2:305:C:H6	1.67	0.60
17:C5:87:PRO:HA	17:C5:90:ILE:HG13	1.83	0.60
20:C8:125:ILE:HG12	35:SM:61:ILE:HG23	1.84	0.60
42:L5:211:LEU:HB3	42:L5:219:PHE:HB2	1.83	0.60
1:6:1785:U:OP1	16:c4:136:ARG:NH1	2.35	0.60
3:s1:35:PRO:HB3	3:s1:231:LEU:HD11	1.82	0.60
36:5:18:G:OP1	71:o5:81:ARG:NH2	2.29	0.60
36:5:1095:U:H4'	36:5:1096:U:H5"	1.83	0.60
38:8:65:A:O3'	71:o5:10:ARG:NH2	2.35	0.60
63:n7:36:HIS:CD2	63:n7:74:VAL:HG11	2.37	0.60
72:o6:33:ALA:HB1	72:o6:38:LYS:HE3	1.84	0.60
2:S0:66:ALA:HB2	23:D1:37:ALA:HB2	1.84	0.60
46:L9:137:SER:HB3	46:L9:143:GLU:HB3	1.83	0.60
1:6:1471:A:OP1	7:s5:185:ARG:NH1	2.35	0.60
15:c3:76:LYS:HA	15:c3:81:ALA:HB2	1.84	0.60
36:5:2568:C:N4	36:5:2574:G:O6	2.35	0.60
45:l8:148:ALA:HA	45:l8:201:THR:HG22	1.83	0.60
1:2:1034:C:HO2'	24:D2:2:THR:N	1.99	0.60
1:2:1234:A:H4'	33:E1:146:SER:HB3	1.83	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:S9:107:ARG:NH1	11:S9:112:GLN:OE1	2.35	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
36:1:2514:U:H5'	45:L8:68:ARG:HG3	1.84	0.60
39:L2:20:THR:O	39:L2:23:ARG:HG3	2.01	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	2.31	0.60
4:S2:137:ILE:HG12	4:S2:138:PRO:HD2	1.84	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
1:6:1698:G:N2	1:6:1699:G:N7	2.50	0.59
3:s1:190:PRO:HG2	3:s1:192:VAL:HG23	1.84	0.59
61:n5:57:LEU:HA	61:n5:61:LYS:HG2	1.84	0.59
71:o5:54:VAL:HG12	71:o5:58:ILE:HD11	1.84	0.59
36:1:29:C:H4'	36:1:62:A:H4'	1.83	0.59
74:O8:46:ARG:HH21	74:O8:51:LEU:HB2	1.67	0.59
1:6:1:U:O2'	1:6:370:A:H5'	2.01	0.59
1:6:1681:A:H1'	8:s6:66:GLY:HA3	1.84	0.59
29:d7:55:THR:HG22	29:d7:62:ILE:HD12	1.83	0.59
36:5:156:G:OP2	72:o6:25:LYS:HB3	2.02	0.59
49:m3:74:GLY:O	49:m3:101:ARG:NH1	2.34	0.59
49:m3:166:ALA:HB1	64:n8:147:LEU:HD21	1.83	0.59
1:2:694:U:H6	9:S7:97:ARG:HH21	1.50	0.59
1:2:1449:U:H2'	1:2:1450:U:C6	2.36	0.59
7:S5:90:ILE:HD11	7:S5:130:ILE:HG13	1.83	0.59
7:S5:146:THR:HG23	7:S5:221:ALA:HA	1.85	0.59
17:C5:81:ARG:NH1	17:C5:97:TYR:O	2.34	0.59
36:1:707:U:C2'	36:1:708:G:H5"	2.33	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
49:M3:6:ASN:O	54:M8:164:ARG:NH1	2.32	0.59
1:6:1628:U:H2'	1:6:1629:G:C8	2.37	0.59
4:s2:178:ILE:HB	4:s2:185:LYS:HD3	1.84	0.59
36:5:3272:C:OP2	43:l6:78:ARG:NH1	2.34	0.59
38:8:21:C:OP1	41:l4:193:LYS:NZ	2.32	0.59
49:m3:177:LYS:HA	72:o6:11:LEU:HD22	1.84	0.59
34:SR:256:THR:OG1	34:SR:259:GLY:O	2.17	0.59
36:1:980:A:H2'	36:1:981:U:N1	2.18	0.59
40:L3:185:GLY:H	40:L3:191:LYS:HZ3	1.51	0.59
41:L4:98:ARG:HD2	41:L4:99:MET:O	2.03	0.59
1:6:947:U:H2'	1:6:948:G:C8	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:s5:68:ILE:HD13	7:s5:69:PHE:H	1.68	0.59
36:5:743:C:N3	54:m8:141:ARG:NH1	2.50	0.59
36:5:1284:C:O2'	36:5:1285:G:OP1	2.18	0.59
41:l4:330:TYR:HA	41:l4:333:VAL:HG13	1.84	0.59
59:n3:28:ASN:OD1	59:n3:28:ASN:N	2.33	0.59
1:2:329:G:H5"	10:S8:98:LYS:HB3	1.84	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
1:6:366:A:OP1	1:6:758:U:O2'	2.20	0.59
1:6:820:U:O2'	1:6:821:U:H5"	2.03	0.59
1:6:1699:G:H2'	1:6:1700:C:H5'	1.84	0.59
6:s4:13:ALA:O	6:s4:39:ARG:NH2	2.36	0.59
12:c0:14:TYR:OH	12:c0:34:GLU:OE1	2.20	0.59
18:c6:23:LYS:HG2	18:c6:64:ASP:HB2	1.84	0.59
36:5:94:G:H2'	36:5:95:A:C8	2.37	0.59
38:8:53:A:OP1	75:o9:19:GLN:NE2	2.35	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
36:1:289:A:O2'	51:M5:93:LYS:O	2.21	0.59
36:1:1129:A:OP1	47:M0:13:LYS:NZ	2.29	0.59
36:1:1609:C:H5"	61:N5:125:ARG:HH11	1.68	0.59
36:1:1724:U:H1'	36:1:1725:C:C6	2.37	0.59
38:4:126:A:O2'	38:4:128:U:OP1	2.21	0.59
36:5:422:A:C2	36:5:2363:A:H4'	2.37	0.59
36:5:2440:G:O2'	36:5:2441:A:OP1	2.20	0.59
71:o5:34:GLN:OE1	71:o5:38:ARG:NH1	2.35	0.59
82:p0:81:LYS:HD3	82:p0:82:GLY:H	1.67	0.59
11:S9:53:ARG:NH2	11:S9:97:LEU:O	2.36	0.59
67:O1:84:ASP:N	67:O1:84:ASP:OD1	2.35	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	2.36	0.59
24:d2:5:SER:O	24:d2:7:LEU:N	2.31	0.59
36:5:247:C:C2	36:5:248:U:H1'	2.38	0.59
50:m4:11:ASN:O	50:m4:11:ASN:ND2	2.35	0.59
57:n1:9:SER:O	57:n1:55:LYS:NZ	2.28	0.59
57:n1:51:GLY:HA3	57:n1:92:ARG:HG3	1.84	0.59
1:2:523:G:H5"	26:D4:59:GLY:O	2.02	0.59
4:S2:147:ASN:HB3	23:D1:4:ASP:HA	1.85	0.59
8:S6:98:ARG:HD3	8:S6:99:GLY:N	2.18	0.59
18:C6:47:LYS:NZ	18:C6:114:ARG:HG2	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1765:U:H5"	55:M9:43:LYS:HE2	1.83	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
1:6:755:A:O2'	1:6:756:A:O5'	2.21	0.59
1:6:1330:G:H21	19:c7:8:THR:HG21	1.67	0.59
4:s2:218:ILE:O	4:s2:221:THR:OG1	2.21	0.59
33:e1:98:VAL:HG12	33:e1:99:LYS:H	1.66	0.59
36:5:361:A:OP1	73:o7:24:ARG:NH1	2.35	0.59
38:8:83:C:H4'	38:8:85:G:N3	2.18	0.59
63:n7:16:GLY:O	63:n7:18:TYR:N	2.36	0.59
1:2:161:U:OP2	8:S6:87:ARG:NH2	2.36	0.59
1:2:637:C:O2	9:S7:114:ARG:NH2	2.36	0.59
3:S1:109:LYS:HG3	3:S1:113:MET:HE3	1.85	0.59
33:E1:139:LEU:HD12	33:E1:152:ALA:H	1.67	0.59
36:1:1278:A:O2'	36:1:1279:C:O5'	2.21	0.59
63:N7:14:VAL:HG13	70:O4:86:LYS:HG2	1.83	0.59
9:s7:73:VAL:O	9:s7:75:THR:N	2.35	0.59
11:s9:92:LYS:HB2	11:s9:95:TYR:HD2	1.67	0.59
36:5:132:C:H2'	36:5:133:U:H5"	1.83	0.59
43:l6:82:ARG:NH1	69:o3:105:SER:O	2.35	0.59
52:m6:79:ILE:HG21	52:m6:138:LEU:HD11	1.84	0.59
1:2:158:U:O2'	1:2:160:C:OP2	2.18	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
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
1:2:66:U:C5	8:S6:173:PRO:HG3	2.38	0.58
9:S7:51:VAL:HG23	9:S7:53:GLY:H	1.67	0.58
13:C1:77:SER:HB3	13:C1:85:VAL:HB	1.84	0.58
36:1:541:U:H2'	36:1:542:G:C8	2.38	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
1:6:1398:U:O2'	19:c7:67:ARG:NH2	2.36	0.58
36:5:942:U:N3	64:n8:16:SER:HA	2.18	0.58
36:5:2968:G:N7	39:l2:215:ASN:HB2	2.18	0.58
40:l3:323:MET:HE1	40:l3:356:LEU:HD11	1.83	0.58
43:l6:3:ALA:HB1	68:o2:75:LEU:HD13	1.84	0.58
61:n5:137:ASN:HB3	61:n5:142:ILE:HG13	1.84	0.58
19:C7:82:ASP:O	19:C7:83:GLN:NE2	2.36	0.58
29:D7:67:THR:OG1	29:D7:70:LYS:O	2.20	0.58
36:1:3042:U:OP2	36:1:3092:C:N4	2.29	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L4:33:ASP:O	41:L4:37:THR:HG23	2.03	0.58
41:L4:291:ASN:HA	41:L4:296:GLN:HE21	1.68	0.58
46:L9:69:ARG:HD3	46:L9:72:LYS:HD3	1.85	0.58
1:6:1041:G:H2'	1:6:1042:G:C8	2.38	0.58
28:d6:58:VAL:HG22	28:d6:59:TYR:H	1.68	0.58
36:5:662:U:H2'	36:5:663:C:C6	2.38	0.58
36:5:1110:U:H2'	36:5:1111:U:C6	2.38	0.58
43:l6:149:ILE:HG23	43:l6:155:LEU:HD13	1.84	0.58
51:m5:65:ARG:HG2	51:m5:127:TYR:CD1	2.38	0.58
70:o4:74:ARG:HD2	70:o4:85:VAL:HG21	1.85	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
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
19:C7:71:PHE:HE1	19:C7:73:LEU:HD22	1.68	0.58
20:C8:144:ARG:O	35:SM:68:ARG:NH2	2.35	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
49:M3:153:ASP:OD1	49:M3:157:ARG:NH2	2.36	0.58
53:M7:50:GLN:OE1	53:M7:56:ARG:NH2	2.36	0.58
60:N4:56:ARG:HB3	60:N4:61:LYS:HB2	1.86	0.58
70:O4:58:ARG:HG3	70:O4:59:PRO:HD2	1.84	0.58
1:6:324:U:OP1	13:c1:133:LYS:NZ	2.27	0.58
45:l8:99:PRO:HG2	45:l8:190:VAL:HG13	1.86	0.58
53:m7:27:LYS:HD3	53:m7:63:PHE:HB3	1.86	0.58
1:2:780:A:C8	26:D4:8:ARG:HB3	2.37	0.58
18:C6:49:TYR:HB3	18:C6:53:LEU:HD11	1.86	0.58
28:D6:24:VAL:HG21	28:D6:71:LEU:HD12	1.84	0.58
36:1:353:G:N7	73:O7:55:ARG:HD3	2.18	0.58
36:1:792:G:H2'	36:1:793:C:C6	2.38	0.58
36:1:994:G:H3'	57:N1:13:TYR:CD2	2.38	0.58
36:1:3166:C:H42	36:1:3284:G:H1	1.49	0.58
46:L9:48:VAL:HG13	46:L9:52:LEU:HB3	1.85	0.58
79:Q3:8:VAL:HB	79:Q3:11:THR:HG22	1.86	0.58
1:6:163:G:H8	1:6:163:G:O5'	1.86	0.58
7:s5:225:ARG:NH1	30:d8:58:GLU:OE1	2.36	0.58
36:5:1073:U:H1'	65:n9:50:THR:HG22	1.85	0.58
36:5:1659:U:H2'	36:5:1660:C:C6	2.37	0.58
42:l5:25:GLU:O	42:l5:27:LYS:N	2.35	0.58
44:l7:229:PHE:C	44:l7:229:PHE:HD1	2.11	0.58
1:2:405:C:O2'	8:S6:92:ARG:O	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:C8:69:ILE:HG22	20:C8:73:MET:HE2	1.85	0.58
39:L2:117:GLU:HG2	39:L2:124:GLY:H	1.68	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
42:l5:196:ARG:NH2	42:l5:237:GLU:OE1	2.35	0.58
73:o7:25:ARG:HB3	73:o7:25:ARG:HH11	1.69	0.58
1:2:1535:U:O2'	1:2:1536:G:N3	2.35	0.58
5:S3:209:ILE:HG22	19:C7:38:ILE:HG12	1.86	0.58
12:C0:11:ILE:HD13	12:C0:35:ILE:HG21	1.84	0.58
36:1:352:A:H61	36:1:365:A:H5"	1.68	0.58
37:3:110:G:OP2	42:L5:279:LYS:NZ	2.25	0.58
46:L9:57:VAL:HG23	46:L9:68:LEU:HG	1.84	0.58
74:O8:69:LEU:HD12	74:O8:73:LEU:HD23	1.85	0.58
3:s1:154:SER:O	3:s1:154:SER:OG	2.19	0.58
18:c6:18:ALA:HB2	18:c6:69:VAL:HG13	1.86	0.58
23:d1:71:ARG:HG3	23:d1:83:TRP:CZ2	2.39	0.58
36:5:920:A:OP1	36:5:922:U:H5	1.86	0.58
36:5:1001:G:N3	36:5:1041:U:H5'	2.18	0.58
51:m5:178:HIS:CD2	51:m5:179:LYS:HG3	2.39	0.58
71:o5:14:LYS:NZ	71:o5:62:GLN:OE1	2.35	0.58
1:2:1600:A:H4'	1:2:1601:G:OP1	2.03	0.58
15:C3:22:ALA:HB1	15:C3:23:PRO:HA	1.86	0.58
40:L3:284:ARG:NH2	40:L3:295:ALA:O	2.32	0.58
63:N7:88:ASP:HB3	63:N7:121:ARG:HH12	1.67	0.58
69:O3:16:TYR:OH	69:O3:89:LEU:O	2.20	0.58
71:O5:102:GLU:OE1	71:O5:106:LYS:HE3	2.03	0.58
1:6:1067:C:H2'	1:6:1068:C:H6	1.68	0.58
6:s4:166:SER:O	6:s4:168:LYS:HG2	2.04	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
36:5:3043:C:OP2	59:n3:48:ARG:NH2	2.31	0.58
44:l7:80:GLN:HG3	57:n1:136:ARG:HB2	1.86	0.58
46:l9:166:ARG:HD2	46:l9:168:ARG:HH11	1.67	0.58
50:m4:22:LEU:HB3	50:m4:64:VAL:HG13	1.86	0.58
52:m6:112:TYR:HA	52:m6:115:LYS:HB2	1.85	0.58
82:p0:43:LYS:HA	82:p0:46:ARG:HG2	1.86	0.58
1:2:1473:U:O2'	7:S5:103:ASN:ND2	2.36	0.58
7:S5:187:ILE:HG12	27:D5:66:VAL:HG11	1.86	0.58
15:C3:139:TRP:HZ2	15:C3:149:LEU:HD11	1.69	0.58
23:D1:39:VAL:HA	23:D1:45:ALA:HA	1.85	0.58
36:1:437:G:H2'	36:1:438:A:C8	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:824:C:H5”	39:L2:21:ARG:HD3	1.85	0.58
36:1:900:G:H1’	36:1:1589:A:N6	2.18	0.58
36:1:1010:G:N2	47:M0:193:ASP:OD2	2.37	0.58
36:1:1721:U:OP2	55:M9:124:TYR:OH	2.18	0.58
46:L9:172:ILE:HD13	46:L9:172:ILE:H	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
1:6:1332:C:OP2	19:c7:45:ARG:NH2	2.36	0.58
9:s7:105:THR:O	9:s7:107:ARG:N	2.37	0.58
36:5:750:G:H2’	36:5:751:A:H8	1.69	0.58
21:C9:117:SER:OG	21:C9:118:PRO:O	2.18	0.58
34:SR:166:SER:HA	34:SR:184:ASN:HD21	1.69	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
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
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
1:6:1065:A:N3	3:s1:146:GLN:NE2	2.49	0.58
10:s8:57:ALA:HB2	10:s8:177:GLY:HA2	1.86	0.58
34:sR:76:ASP:N	34:sR:76:ASP:OD1	2.36	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
47:m0:82:ARG:NH2	47:m0:83:ASP:OD1	2.37	0.58
1:2:895:G:H1	1:2:917:U:H3	1.50	0.58
1:2:1280:C:H2’	1:2:1281:G:H8	1.69	0.58
1:2:1682:U:O4	1:2:1720:G:N2	2.36	0.58
1:2:1684:U:O2	1:2:1718:G:N2	2.37	0.58
18:C6:5:PRO:HG2	18:C6:24:ALA:HB2	1.86	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
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
1:6:778:G:N7	26:d4:10:ARG:NH1	2.52	0.58
1:6:1163:A:N3	1:6:1613:U:O2’	2.32	0.58
8:s6:130:PRO:HB3	60:n4:81:PRO:HG2	1.83	0.58
64:n8:2:PRO:HG2	64:n8:5:PHE:CD2	2.39	0.58
68:o2:124:GLY:O	68:o2:126:LEU:N	2.36	0.58
1:2:159:U:O2’	8:S6:87:ARG:NH1	2.37	0.57

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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
7:S5:91:GLU:O	7:S5:95:ASN:ND2	2.37	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
72:O6:79:SER:HB2	72:O6:82:ARG:HG3	1.86	0.57
2:s0:115:PHE:HE1	4:s2:39:THR:HG22	1.69	0.57
36:5:1313:G:H2'	36:5:1314:C:H6	1.69	0.57
36:5:2093:A:P	55:m9:143:ILE:HG13	2.44	0.57
36:5:2507:C:O2'	36:5:2508:U:OP1	2.21	0.57
62:n6:99:LEU:HD13	62:n6:104:LEU:HD21	1.86	0.57
1:2:322:G:O2'	10:S8:10:LYS:NZ	2.33	0.57
36:1:92:G:OP2	36:1:93:C:H5"	2.04	0.57
36:1:283:G:O6	36:1:304:G:H1'	2.04	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	2.27	0.57
46:l9:163:GLN:O	46:l9:166:ARG:HG3	2.04	0.57
60:n4:85:ALA:HA	60:n4:89:LEU:HD13	1.85	0.57
1:2:1358:G:H2'	1:2:1359:C:C6	2.39	0.57
21:C9:30:VAL:O	21:C9:32:GLY:N	2.37	0.57
36:1:598:A:OP1	44:L7:41:ARG:NH1	2.36	0.57
36:1:1347:U:OP2	41:L4:300:ARG:NH2	2.36	0.57
47:M0:49:CYS:HB3	47:M0:168:SER:HB3	1.87	0.57
66:O0:40:LYS:HB3	66:O0:101:LEU:HD11	1.87	0.57
1:6:691:C:OP1	1:6:696:C:N4	2.29	0.57
3:s1:141:ALA:HB1	3:s1:207:LEU:HD22	1.86	0.57
11:s9:117:GLY:O	11:s9:119:ALA:N	2.36	0.57
40:l3:152:LYS:HD3	40:l3:189:SER:HA	1.85	0.57
52:m6:110:PRO:O	52:m6:113:ASP:N	2.31	0.57
78:q2:74:CYS:HB3	78:q2:77:CYS:SG	2.44	0.57
2:S0:83:GLN:HG2	2:S0:99:ALA:HB1	1.84	0.57
16:C4:29:HIS:HB3	16:C4:41:ARG:HG3	1.86	0.57
36:1:1069:C:H2'	36:1:1070:U:C6	2.40	0.57
36:1:3329:U:H5"	40:L3:308:MET:HE3	1.87	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
48:M1:94:ARG:C	48:M1:96:PHE:H	2.12	0.57
1:6:813:U:H5'	15:c3:76:LYS:HE2	1.86	0.57
18:c6:95:LYS:O	34:sR:59:ARG:NH2	2.37	0.57
1:2:207:U:O2	10:S8:178:ARG:NH1	2.36	0.57
4:S2:230:TRP:CE2	24:D2:68:ARG:HD3	2.39	0.57
23:D1:21:ASN:OD1	24:D2:23:ARG:NH2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:13:A:H4'	61:N5:39:LYS:HG3	1.87	0.57
36:1:1286:A:O2'	36:1:1287:A:OP2	2.20	0.57
36:1:3047:U:O2'	36:1:3048:A:H5'	2.05	0.57
1:6:27:U:H2'	1:6:28:A:C8	2.40	0.57
13:c1:21:ASN:OD1	13:c1:21:ASN:N	2.37	0.57
34:sR:37:SER:OG	34:sR:38:ARG:N	2.32	0.57
36:5:770:G:OP1	49:m3:171:ARG:HD3	2.05	0.57
58:n2:67:SER:OG	58:n2:69:ALA:O	2.23	0.57
1:2:614:C:OP2	25:D3:5:LYS:NZ	2.31	0.57
36:1:1054:A:H5"	36:1:2637:A:H61	1.69	0.57
36:1:2737:C:O5'	57:N1:68:THR:OG1	2.23	0.57
36:1:3215:A:O5'	50:M4:121:MET:HE1	2.05	0.57
44:L7:131:GLU:HG2	44:L7:230:GLY:HA2	1.86	0.57
45:L8:50:VAL:HG12	61:N5:30:ALA:HA	1.86	0.57
1:6:895:G:H21	16:c4:38:THR:HG21	1.69	0.57
3:s1:33:LYS:HE2	3:s1:41:ARG:HH12	1.68	0.57
4:s2:144:TRP:CE2	4:s2:173:PRO:HG3	2.40	0.57
6:s4:137:PRO:HG2	6:s4:150:PRO:HD2	1.86	0.57
25:d3:132:LEU:C	25:d3:134:ALA:H	2.13	0.57
36:5:2364:G:H22	36:5:2396:G:H1'	1.69	0.57
36:5:3001:C:OP1	40:l3:120:LYS:NZ	2.37	0.57
36:5:3241:G:H2'	36:5:3245:A:H8	1.67	0.57
37:7:22:A:H1'	42:l5:272:TYR:CZ	2.38	0.57
41:l4:237:GLN:O	41:l4:246:ARG:HG3	2.04	0.57
65:n9:20:GLY:O	65:n9:21:ILE:HB	2.04	0.57
82:p0:4:ILE:HD13	82:p0:4:ILE:H	1.68	0.57
1:2:460:A:H3'	1:2:461:G:H8	1.69	0.57
3:S1:168:ILE:HG12	3:S1:197:ILE:HD12	1.87	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
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
1:6:161:U:OP2	8:s6:87:ARG:NH2	2.37	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
36:5:3112:G:O2'	46:l9:70:THR:HB	2.04	0.57
42:l5:105:ILE:O	42:l5:109:THR:HG23	2.04	0.57
60:n4:120:LYS:HA	60:n4:123:ARG:HD2	1.87	0.57
1:2:159:U:H5'	26:D4:117:LYS:HD3	1.85	0.57
1:2:1426:C:H5"	35:SM:93:ARG:HH12	1.70	0.57
5:S3:162:GLN:OE1	5:S3:165:ASN:ND2	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:269:G:H5'	51:M5:120:TRP:CE3	2.39	0.57
36:1:562:C:OP2	50:M4:77:ARG:NH1	2.35	0.57
42:L5:85:ARG:NH2	42:L5:250:ASP:OD1	2.32	0.57
42:L5:233:ALA:O	42:L5:235:SER:N	2.38	0.57
48:M1:37:LEU:O	48:M1:41:SER:OG	2.10	0.57
74:O8:58:ASP:OD2	74:O8:61:LYS:N	2.25	0.57
1:6:16:G:H2'	1:6:17:C:C6	2.40	0.57
1:6:397:A:O3'	10:s8:50:GLY:HA2	2.05	0.57
1:6:1511:U:H2'	1:6:1512:G:C8	2.40	0.57
31:d9:6:VAL:O	31:d9:8:PHE:N	2.32	0.57
36:5:2696:A:H2'	36:5:2697:A:C8	2.39	0.57
44:l7:229:PHE:C	44:l7:229:PHE:CD1	2.82	0.57
79:q3:56:THR:HB	79:q3:63:THR:OG1	2.05	0.57
3:S1:131:ASP:O	3:S1:133:TYR:N	2.38	0.57
20:C8:62:THR:N	20:C8:65:GLU:OE1	2.36	0.57
54:M8:178:ARG:HE	64:N8:50:PRO:HG2	1.68	0.57
55:M9:160:GLU:HA	55:M9:163:ARG:HB2	1.87	0.57
2:s0:50:VAL:HG23	19:c7:109:LEU:HD21	1.87	0.57
29:d7:2:VAL:O	29:d7:3:LEU:HB2	2.05	0.57
36:5:561:C:H2'	36:5:562:C:C6	2.40	0.57
37:7:1:G:N3	42:l5:269:SER:OG	2.37	0.57
37:7:97:A:OP1	56:n0:40:ARG:NH1	2.38	0.57
40:l3:81:THR:HG21	40:l3:322:ILE:HD13	1.87	0.57
61:n5:132:ALA:HA	61:n5:135:ILE:HG22	1.86	0.57
1:2:338:C:H1'	10:S8:5:ARG:HB3	1.86	0.57
2:S0:33:GLN:NE2	23:D1:64:GLU:OE2	2.32	0.57
19:C7:26:LEU:HD22	19:C7:59:LYS:HA	1.87	0.57
36:1:2535:A:H61	36:1:2544:U:H3	1.51	0.57
36:1:3005:A:H5"	40:L3:98:GLY:HA3	1.86	0.57
42:L5:60:ILE:HB	42:L5:80:SER:HB3	1.86	0.57
52:M6:72:HIS:O	52:M6:74:ARG:NH1	2.35	0.57
62:N6:73:VAL:HA	62:N6:80:VAL:HG23	1.86	0.57
75:O9:5:LYS:HE3	75:O9:13:MET:HE1	1.86	0.57
1:6:321:C:H42	1:6:1666:U:H5"	1.70	0.57
1:6:1552:U:O4	17:c5:40:ARG:NH2	2.38	0.57
2:s0:183:ARG:NH2	2:s0:191:ARG:O	2.38	0.57
5:s3:170:THR:HG21	5:s3:187:LYS:HE2	1.84	0.57
11:s9:34:PHE:HD1	11:s9:111:THR:HG21	1.70	0.57
11:s9:146:PHE:O	11:s9:147:MET:HB2	2.04	0.57
17:c5:53:PRO:HB3	17:c5:80:MET:HE1	1.86	0.57
26:d4:51:GLU:O	26:d4:53:ASP:N	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:l5:270:LYS:HG3	42:l5:273:ARG:HB3	1.85	0.57
52:m6:36:VAL:HB	52:m6:108:ILE:HG22	1.87	0.57
58:n2:33:TYR:HE1	58:n2:80:THR:HG23	1.69	0.57
1:2:1456:C:H5"	1:2:1457:C:H5"	1.85	0.56
24:D2:6:VAL:HG12	24:D2:34:ILE:HD11	1.87	0.56
40:L3:219:ALA:HB2	40:L3:336:VAL:HG13	1.87	0.56
49:M3:164:GLU:O	49:M3:166:ALA:N	2.38	0.56
53:M7:172:GLN:OE1	69:O3:60:ARG:NH1	2.38	0.56
1:6:57:G:P	26:d4:116:LYS:HZ3	2.26	0.56
1:6:753:A:H62	6:s4:187:ARG:NH2	2.03	0.56
2:s0:126:PRO:HB2	2:s0:152:PRO:HG2	1.85	0.56
24:d2:24:GLN:HE22	29:d7:4:VAL:HA	1.70	0.56
36:5:1940:G:H21	36:5:3362:A:H8	1.52	0.56
46:l9:174:LYS:HB2	76:q0:127:LEU:HD11	1.87	0.56
4:S2:81:MET:HE1	4:S2:186:LYS:HB3	1.86	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
36:1:2193:U:H5'	36:1:2194:G:H5'	1.86	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
63:N7:115:LYS:NZ	63:N7:119:GLU:OE2	2.38	0.56
71:O5:68:GLN:HA	71:O5:71:LYS:HB2	1.88	0.56
1:6:65:A:H2	1:6:84:A:H62	1.52	0.56
1:6:69:G:H1	1:6:82:U:H3	1.53	0.56
1:6:864:U:H3'	24:d2:28:ARG:HH22	1.70	0.56
1:6:973:A:H2'	1:6:974:A:H8	1.69	0.56
1:6:1081:A:O2'	1:6:1082:C:O5'	2.23	0.56
24:d2:103:ILE:HA	24:d2:112:ASP:HA	1.87	0.56
25:d3:68:ILE:O	25:d3:70:LYS:NZ	2.38	0.56
28:d6:87:ARG:NH2	28:d6:94:ASN:O	2.34	0.56
40:l3:41:VAL:CA	40:l3:185:GLY:HA3	2.31	0.56
59:n3:129:VAL:O	59:n3:133:SER:OG	2.18	0.56
66:o0:24:THR:HG22	66:o0:91:SER:HB3	1.87	0.56
1:2:138:A:N6	1:2:266:A:H61	2.02	0.56
1:2:1160:A:H2'	1:2:1161:C:C6	2.40	0.56
2:S0:9:LEU:HD23	2:S0:54:TRP:CG	2.40	0.56
2:S0:31:VAL:HG12	2:S0:33:GLN:H	1.71	0.56
4:S2:161:LYS:HG3	4:S2:166:THR:HG22	1.87	0.56
8:S6:135:PRO:HB2	8:S6:141:ILE:HG12	1.87	0.56
8:S6:148:SER:O	8:S6:150:GLU:N	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:S8:114:GLU:HG2	10:S8:120:THR:HA	1.87	0.56
15:C3:67:THR:O	15:C3:69:ASN:N	2.37	0.56
16:C4:122:PRO:C	16:C4:124:ASP:H	2.14	0.56
33:E1:113:LYS:H	33:E1:113:LYS:HD2	1.71	0.56
36:1:1940:G:H21	36:1:3362:A:H8	1.53	0.56
36:1:2557:A:H2	45:L8:38:GLN:HA	1.70	0.56
36:1:3072:C:H2'	36:1:3073:A:O4'	2.05	0.56
43:L6:60:ASP:OD1	43:L6:62:THR:OG1	2.23	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
1:6:918:U:H2'	1:6:919:A:H8	1.69	0.56
2:s0:122:ILE:HG23	2:s0:144:ILE:HB	1.87	0.56
10:s8:194:ARG:HD2	10:s8:195:ARG:HH12	1.70	0.56
26:d4:52:LYS:O	26:d4:54:ALA:N	2.38	0.56
36:5:916:G:H5'	36:5:917:A:OP1	2.04	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
39:l2:234:LYS:HG2	39:l2:238:ILE:HD12	1.86	0.56
52:m6:46:GLU:HB3	52:m6:134:LYS:HB3	1.86	0.56
6:S4:176:ASP:HB2	6:S4:179:LYS:HZ3	1.71	0.56
6:S4:180:LEU:HA	6:S4:194:THR:HA	1.88	0.56
33:E1:102:VAL:O	33:E1:104:SER:N	2.38	0.56
36:1:839:C:O2'	36:1:1724:U:OP1	2.21	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
58:N2:30:PRO:HA	58:N2:33:TYR:HB3	1.88	0.56
1:6:1049:U:H5"	29:d7:70:LYS:HG3	1.87	0.56
20:c8:36:LYS:HB3	20:c8:105:VAL:HG21	1.88	0.56
29:d7:49:HIS:CE1	29:d7:70:LYS:HG2	2.40	0.56
34:sR:80:ALA:O	34:sR:92:TRP:N	2.36	0.56
36:5:1340:G:H2'	36:5:1341:U:H6	1.71	0.56
36:5:1638:A:N1	36:5:1736:G:O2'	2.34	0.56
36:5:2150:G:O2'	36:5:2189:U:OP1	2.20	0.56
45:l8:133:LYS:HB2	45:l8:199:ALA:O	2.05	0.56
47:m0:38:LYS:NZ	47:m0:45:GLU:OE1	2.38	0.56
47:m0:210:ILE:HA	47:m0:217:PHE:CE2	2.40	0.56
6:S4:9:LEU:HB2	6:S4:30:ARG:HB2	1.86	0.56
27:D5:42:LEU:HD12	27:D5:43:ASP:H	1.70	0.56
36:1:1412:G:OP1	68:O2:105:ARG:NH2	2.39	0.56
40:L3:18:PRO:O	40:L3:20:LYS:N	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:M6:187:GLU:HA	52:M6:192:LYS:HD3	1.87	0.56
14:c2:56:GLU:OE1	14:c2:124:LYS:NZ	2.39	0.56
36:5:1407:A:O3'	68:o2:33:ARG:NH2	2.38	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
40:l3:243:HIS:C	40:l3:244:ARG:HG3	2.31	0.56
44:l7:53:LYS:O	44:l7:57:THR:HG23	2.06	0.56
1:2:1500:C:OP1	21:C9:122:ARG:NH2	2.32	0.56
9:S7:150:GLN:HB3	9:S7:181:ILE:HD12	1.87	0.56
34:SR:24:ALA:HB3	34:SR:34:LEU:HB3	1.87	0.56
35:SM:53:ARG:HA	35:SM:53:ARG:HE	1.70	0.56
36:1:1176:C:H2'	36:1:1177:G:N2	2.21	0.56
63:N7:95:VAL:HG21	63:N7:113:VAL:HG11	1.87	0.56
78:Q2:14:GLY:O	78:Q2:16:THR:N	2.30	0.56
1:6:1280:C:O2'	22:d0:70:THR:HG23	2.05	0.56
1:6:1556:A:OP1	17:c5:115:TYR:OH	2.22	0.56
2:s0:118:PRO:HG2	2:s0:141:ILE:HD13	1.88	0.56
6:s4:117:GLU:HG2	6:s4:118:GLU:H	1.69	0.56
6:s4:191:ARG:HD3	6:s4:245:LYS:HB3	1.88	0.56
35:sM:64:LYS:O	35:sM:66:ALA:N	2.37	0.56
36:5:315:C:OP2	72:o6:28:TYR:OH	2.18	0.56
36:5:612:U:H2'	36:5:613:G:H8	1.71	0.56
36:5:2211:U:H5	36:5:2234:G:O6	1.89	0.56
36:5:3295:A:H2'	36:5:3296:A:C8	2.41	0.56
38:8:85:G:N1	62:n6:112:ASP:OD2	2.37	0.56
47:m0:51:HIS:HB3	47:m0:134:ILE:HG23	1.87	0.56
51:m5:11:GLN:HG2	51:m5:44:ARG:HH21	1.71	0.56
51:m5:119:TYR:OH	51:m5:131:GLU:OE1	2.18	0.56
59:n3:89:ASP:OD1	59:n3:91:VAL:HG12	2.05	0.56
68:o2:16:LYS:HD2	68:o2:18:LYS:HE3	1.87	0.56
1:2:1002:G:N2	1:2:1760:G:O3'	2.38	0.56
1:2:1067:C:H5"	3:S1:150:VAL:HG23	1.86	0.56
36:1:1720:U:OP2	55:M9:120:TYR:OH	2.17	0.56
39:L2:20:THR:HA	39:L2:23:ARG:HD2	1.86	0.56
1:6:1435:G:O6	12:c0:64:TYR:OH	2.15	0.56
6:s4:127:LYS:HA	6:s4:127:LYS:HE2	1.88	0.56
6:s4:230:GLU:HB2	6:s4:233:LYS:HE3	1.88	0.56
16:c4:107:ARG:HH21	16:c4:107:ARG:HB2	1.71	0.56
36:5:173:G:H1'	36:5:174:C:H5'	1.86	0.56
36:5:1506:A:H1'	36:5:1848:G:O6	2.06	0.56
36:5:2403:G:H5'	36:5:2872:A:C2	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:l2:45:VAL:HG22	39:l2:84:THR:HA	1.88	0.56
41:l4:33:ASP:OD1	41:l4:34:ILE:N	2.38	0.56
1:2:1520:U:OP2	21:C9:75:LYS:NZ	2.39	0.56
6:S4:97:GLU:OE1	6:S4:113:ARG:NH2	2.34	0.56
13:C1:21:ASN:HD22	13:C1:31:THR:HA	1.71	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
1:6:143:G:N7	8:s6:177:ARG:NH2	2.54	0.56
1:6:1435:G:N7	12:c0:25:LYS:NZ	2.37	0.56
17:c5:79:HIS:O	17:c5:81:ARG:N	2.38	0.56
18:c6:115:THR:O	18:c6:117:LEU:N	2.38	0.56
24:d2:67:GLY:O	24:d2:69:LEU:N	2.38	0.56
33:e1:78:LYS:O	33:e1:80:ARG:N	2.33	0.56
36:5:269:G:P	51:m5:44:ARG:HH22	2.29	0.56
36:5:2786:G:N2	64:n8:58:MET:SD	2.78	0.56
39:l2:131:GLY:H	39:l2:169:ILE:HG22	1.71	0.56
40:l3:19:ARG:HB3	40:l3:232:ARG:NH1	2.19	0.56
49:m3:56:PRO:HG3	49:m3:74:GLY:O	2.06	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
14:C2:50:LYS:NZ	33:E1:129:GLY:O	2.29	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
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
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
1:6:14:C:OP2	4:s2:206:THR:HG21	2.06	0.56
1:6:1689:A:H2'	1:6:1690:G:H8	1.71	0.56
6:s4:11:ARG:HB2	6:s4:27:TYR:C	2.31	0.56
33:e1:106:TYR:HE2	33:e1:116:LYS:HG2	1.71	0.56
36:5:2801:A:O2'	36:5:2802:A:H2'	2.05	0.56
40:l3:147:GLU:OE1	40:l3:150:ARG:NH2	2.38	0.56
45:l8:73:PRO:HA	45:l8:76:ALA:HB3	1.87	0.56
71:o5:101:THR:HG22	71:o5:104:GLN:HB2	1.87	0.56
1:2:1266:U:H2'	1:2:1267:G:C8	2.41	0.56
6:S4:151:ASP:HB3	6:S4:154:ILE:HG13	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:S5:72:HIS:ND1	18:C6:79:TYR:OH	2.28	0.56
16:C4:13:VAL:HG13	16:C4:77:THR:H	1.70	0.56
36:1:147:U:H5'	45:L8:136:LEU:HB2	1.88	0.56
36:1:1103:A:C8	44:L7:158:LYS:HD3	2.40	0.56
39:L2:130:SER:HA	39:L2:169:ILE:HG22	1.87	0.56
49:M3:180:ARG:HD2	72:O6:11:LEU:HD21	1.88	0.56
1:6:738:G:H2'	1:6:739:G:H8	1.70	0.56
1:6:886:U:OP2	3:s1:216:LYS:NZ	2.37	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
13:c1:93:TYR:HB2	13:c1:100:TYR:CE1	2.41	0.56
17:c5:81:ARG:NH1	17:c5:97:TYR:O	2.37	0.56
36:5:361:A:O3'	73:o7:45:ARG:NH2	2.39	0.56
36:5:1334:U:OP1	44:l7:206:LYS:HE2	2.05	0.56
36:5:3269:U:H4'	36:5:3270:U:O5'	2.06	0.56
61:n5:38:LEU:HD13	61:n5:40:LEU:HD22	1.87	0.56
63:n7:22:LYS:HE3	63:n7:134:LEU:HB2	1.88	0.56
70:o4:7:PHE:CD1	70:o4:20:ILE:HD12	2.41	0.56
1:2:340:U:H2'	1:2:341:A:C8	2.41	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
12:C0:46:LEU:O	12:C0:50:THR:HG23	2.06	0.55
19:C7:23:LYS:HB3	19:C7:34:LEU:HD11	1.87	0.55
22:D0:42:VAL:HG13	22:D0:52:LYS:HZ1	1.70	0.55
36:1:1688:U:H2'	36:1:1689:U:C6	2.40	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
1:6:196:G:N3	1:6:197:A:H1'	2.21	0.55
1:6:755:A:H2'	1:6:756:A:H8	1.68	0.55
9:s7:28:GLU:HG2	9:s7:35:LYS:HA	1.88	0.55
14:c2:28:LEU:HD22	14:c2:32:LEU:HG	1.88	0.55
20:c8:45:LEU:HD11	21:c9:36:ILE:HG22	1.88	0.55
36:5:1025:A:H3'	36:5:1026:A:H4'	1.87	0.55
36:5:2836:C:H4'	47:m0:157:TYR:CD1	2.41	0.55
36:5:3016:A:H2'	36:5:3017:A:H8	1.71	0.55
42:l5:259:LYS:HB2	42:l5:260:PHE:CD2	2.41	0.55
43:l6:100:LYS:NZ	43:l6:137:ASP:OD2	2.32	0.55
46:l9:29:GLY:HA3	46:l9:82:VAL:HG13	1.86	0.55
79:q3:30:GLU:HG2	79:q3:34:HIS:CE1	2.41	0.55
1:2:75:U:H2'	1:2:76:A:O4'	2.06	0.55
1:2:108:A:H2'	1:2:109:G:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1280:C:H2'	1:2:1281:G:C8	2.41	0.55
1:2:1369:U:OP1	21:C9:119:LYS:NZ	2.40	0.55
6:S4:160:VAL:HG13	6:S4:169:ILE:HG23	1.88	0.55
14:C2:60:VAL:HG23	14:C2:87:PRO:HG2	1.87	0.55
36:1:787:G:H2'	36:1:788:C:C6	2.42	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
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
58:N2:50:LEU:O	58:N2:52:ASN:N	2.39	0.55
1:6:486:G:O6	1:6:488:G:N2	2.38	0.55
27:d5:43:ASP:HB2	27:d5:46:LYS:HE3	1.88	0.55
36:5:2550:U:C6	45:l8:37:GLY:HA3	2.41	0.55
38:8:52:A:H62	75:o9:27:ILE:HD13	1.71	0.55
48:m1:155:THR:O	48:m1:159:THR:HG23	2.06	0.55
60:n4:63:ILE:O	60:n4:65:GLU:N	2.39	0.55
62:n6:63:LYS:HE3	62:n6:97:ILE:HD13	1.88	0.55
69:o3:45:LEU:HD11	69:o3:73:ARG:HA	1.88	0.55
1:2:591:A:H2'	1:2:592:A:H8	1.72	0.55
27:D5:43:ASP:O	27:D5:46:LYS:N	2.30	0.55
36:1:2438:A:H2'	36:1:2439:A:H8	1.71	0.55
1:6:292:U:H2'	1:6:293:U:C6	2.41	0.55
1:6:392:G:OP1	10:s8:24:LYS:NZ	2.37	0.55
1:6:686:C:H2'	1:6:687:G:C8	2.41	0.55
1:6:1091:A:H4'	1:6:1092:A:O5'	2.06	0.55
34:sR:249:ARG:NH1	34:sR:298:GLY:O	2.39	0.55
70:o4:38:LEU:H	70:o4:38:LEU:HD12	1.71	0.55
36:1:385:A:H2'	36:1:386:A:C8	2.42	0.55
36:1:662:U:OP1	64:N8:8:THR:HG21	2.05	0.55
36:1:1064:A:H4'	36:1:1065:A:O5'	2.06	0.55
36:1:1798:A:H2'	36:1:1799:A:C8	2.41	0.55
49:M3:50:PRO:O	49:M3:52:ASP:N	2.34	0.55
50:M4:17:VAL:HG11	50:M4:74:ARG:HA	1.89	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	2.39	0.55
28:d6:36:ILE:HG12	28:d6:84:VAL:HG11	1.89	0.55
36:5:1688:U:H2'	36:5:1689:U:C6	2.42	0.55
36:5:2155:G:O2'	39:l2:227:ARG:NH2	2.39	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:l2:70:ARG:NH1	39:l2:72:ARG:HH21	2.05	0.55
39:l2:172:GLY:HA3	79:q3:68:ALA:H	1.72	0.55
51:m5:190:THR:O	51:m5:194:GLN:HG2	2.07	0.55
1:2:686:C:H2'	1:2:687:G:H8	1.71	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
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
36:1:1740:U:H1'	36:1:1741:A:H2	1.72	0.55
36:1:3049:A:H5"	40:L3:53:MET:HB2	1.88	0.55
37:3:71:G:H2'	37:3:72:A:C8	2.40	0.55
42:L5:251:PRO:O	42:L5:253:PHE:N	2.40	0.55
1:6:511:A:H5"	11:s9:172:VAL:HG22	1.88	0.55
1:6:919:A:H5'	16:c4:35:GLY:HA3	1.87	0.55
7:s5:166:ARG:HA	7:s5:169:ASN:HB2	1.89	0.55
34:sR:156:VAL:HA	34:sR:169:ILE:HG22	1.87	0.55
36:5:215:G:H5"	62:n6:12:ARG:HD3	1.89	0.55
39:l2:66:PRO:HB2	39:l2:67:TYR:CE2	2.41	0.55
59:n3:11:PHE:CD1	59:n3:88:ARG:HD2	2.42	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
1:2:1606:C:H2'	1:2:1607:G:C8	2.41	0.55
18:C6:47:LYS:HZ2	18:C6:114:ARG:HG2	1.71	0.55
44:L7:157:ASN:O	44:L7:159:GLN:HG2	2.07	0.55
46:L9:126:VAL:HG21	46:L9:161:LEU:HA	1.88	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
1:6:1126:G:OP1	77:q1:15:ARG:NH1	2.37	0.55
15:c3:5:HIS:HB3	15:c3:117:LEU:HD13	1.88	0.55
15:c3:99:ARG:HE	15:c3:115:LEU:HD11	1.70	0.55
15:c3:99:ARG:NH1	15:c3:143:SER:OG	2.40	0.55
24:d2:22:LYS:HD2	29:d7:3:LEU:HD23	1.88	0.55
36:5:1807:G:H5'	63:n7:135:ARG:HH11	1.71	0.55
36:5:2954:U:O4	87:D:3401:SPS:H141	2.06	0.55
46:l9:86:TYR:CD1	46:l9:151:VAL:HG13	2.42	0.55
52:m6:85:ARG:HD3	52:m6:90:HIS:CE1	2.41	0.55
1:2:1097:U:O2'	4:S2:159:THR:OG1	2.22	0.55
1:2:1765:A:H5'	1:2:1767:G:N7	2.21	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
36:1:1468:A:N1	36:1:1880:U:O2'	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
51:M5:65:ARG:HG2	51:M5:127:TYR:CD1	2.41	0.55
79:Q3:49:ARG:HD2	79:Q3:50:GLY:N	2.21	0.55
4:s2:59:HIS:NE2	4:s2:236:PRO:HB2	2.22	0.55
36:5:1667:A:H2'	36:5:1668:G:C8	2.42	0.55
40:l3:242:THR:OG1	40:l3:246:LEU:HB3	2.06	0.55
46:l9:57:VAL:HG23	46:l9:68:LEU:HG	1.87	0.55
49:m3:159:VAL:HA	64:n8:124:ILE:HD11	1.89	0.55
67:o1:44:MET:HB3	67:o1:77:ARG:NH1	2.22	0.55
3:S1:212:VAL:O	3:S1:214:LYS:N	2.35	0.55
4:S2:229:LEU:O	23:D1:16:LYS:NZ	2.39	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
25:D3:68:ILE:O	25:D3:70:LYS:NZ	2.39	0.55
36:1:263:C:H2'	36:1:264:G:O4'	2.07	0.55
36:1:1320:C:O2	56:N0:115:ARG:NH2	2.40	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
36:1:2897:A:H2'	36:1:2899:C:H5"	1.89	0.55
41:L4:91:GLY:HA3	41:L4:93:MET:HE2	1.89	0.55
63:N7:101:PHE:HA	63:N7:107:ARG:HE	1.72	0.55
1:6:654:C:H2'	1:6:655:G:C8	2.42	0.55
1:6:1699:G:H22	1:6:1702:A:H5"	1.71	0.55
3:s1:178:GLY:O	3:s1:179:SER:HB2	2.06	0.55
6:s4:251:GLU:O	6:s4:255:ARG:HG2	2.06	0.55
36:5:3186:A:N3	46:l9:44:THR:HG22	2.22	0.55
43:l6:97:ASN:ND2	43:l6:99:GLU:OE1	2.40	0.55
46:l9:12:VAL:N	46:l9:51:GLN:O	2.33	0.55
51:m5:98:LEU:HD23	51:m5:128:LYS:HD2	1.87	0.55
52:m6:64:PHE:HE1	52:m6:68:ARG:HH11	1.55	0.55
54:m8:138:LEU:HD13	54:m8:140:LEU:HD21	1.89	0.55
1:2:1516:A:OP1	22:D0:88:LYS:NZ	2.31	0.55
2:S0:179:ARG:HD3	2:S0:183:ARG:HH11	1.71	0.55
36:1:873:C:H5"	36:1:874:U:O5'	2.07	0.55
36:1:2294:U:OP2	59:N3:71:LYS:HE2	2.07	0.55
36:1:2561:A:N1	45:L8:32:LYS:HB2	2.22	0.55
39:L2:45:VAL:HG22	39:L2:84:THR:HA	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:c7:13:SER:HA	19:c7:54:THR:HG22	1.89	0.55
22:d0:102:ARG:HE	22:d0:106:ILE:HD12	1.71	0.55
36:5:608:A:H5"	36:5:609:G:OP2	2.07	0.55
36:5:1678:G:O6	58:n2:74:LYS:NZ	2.40	0.55
36:5:3215:A:O5'	50:m4:121:MET:HE1	2.07	0.55
36:5:3302:U:H3	36:5:3312:U:H3	1.55	0.55
42:l5:136:GLU:H	42:l5:136:GLU:CD	2.15	0.55
1:2:848:C:H2'	1:2:849:C:H6	1.72	0.55
30:D8:36:THR:OG1	30:D8:37:SER:N	2.28	0.55
36:1:817:A:C2	73:O7:11:ARG:HB3	2.42	0.55
36:1:2213:A:H2'	36:1:2214:A:C8	2.42	0.55
36:1:2307:G:O2'	36:1:2310:U:OP2	2.17	0.55
58:N2:51:GLY:O	58:N2:52:ASN:ND2	2.40	0.55
1:6:1767:G:OP1	1:6:1770:U:H4'	2.07	0.55
11:s9:23:ARG:NH1	11:s9:27:GLU:OE2	2.34	0.55
36:5:1080:A:OP1	42:l5:140:ARG:HD3	2.07	0.55
36:5:1765:U:H4'	36:5:1765:U:OP1	2.06	0.55
36:5:1832:C:OP1	61:n5:120:LYS:NZ	2.30	0.55
36:5:2510:U:O2'	36:5:2511:A:H5"	2.06	0.55
37:7:112:G:H2'	37:7:113:C:C6	2.41	0.55
38:8:152:G:O2'	45:l8:63:LYS:NZ	2.30	0.55
42:l5:144:VAL:HG12	42:l5:173:VAL:HG22	1.89	0.55
70:o4:20:ILE:HD13	70:o4:32:ALA:HB1	1.87	0.55
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
11:S9:38:ASN:HB3	11:S9:40:LYS:H	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
34:SR:80:ALA:HB3	34:SR:92:TRP:HB2	1.89	0.54
36:1:149:U:OP2	51:M5:49:ARG:NH2	2.35	0.54
36:1:1180:A:OP1	69:O3:78:SER:OG	2.25	0.54
36:1:2138:A:C4	73:O7:3:LYS:HB3	2.42	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
38:4:104:A:C8	38:4:105:A:C8	2.95	0.54
1:6:151:G:H21	8:s6:13:GLN:CD	2.14	0.54
2:s0:155:PHE:O	23:d1:60:ARG:NH2	2.39	0.54
8:s6:67:VAL:HG23	8:s6:68:LEU:O	2.06	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
43:l6:40:LEU:HD12	43:l6:65:ILE:HD11	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:n2:14:THR:HG23	58:n2:66:VAL:HG22	1.89	0.54
65:n9:14:ARG:NH2	65:n9:18:ARG:HH11	2.04	0.54
13:C1:5:LEU:O	13:C1:7:VAL:N	2.31	0.54
13:C1:21:ASN:OD1	13:C1:21:ASN:N	2.40	0.54
38:4:35:C:H5"	73:O7:70:VAL:HG11	1.89	0.54
58:N2:50:LEU:HB3	58:N2:54:VAL:HG23	1.89	0.54
1:6:660:G:H2'	1:6:661:A:H4'	1.88	0.54
8:s6:57:ASP:HB3	8:s6:98:ARG:HG3	1.89	0.54
24:d2:83:ILE:HG13	24:d2:122:SER:HB2	1.89	0.54
26:d4:10:ARG:HB2	26:d4:24:VAL:HB	1.90	0.54
36:5:2663:G:H2'	36:5:2664:C:O4'	2.07	0.54
46:l9:166:ARG:HD2	46:l9:168:ARG:NH1	2.22	0.54
48:m1:16:LYS:HG3	48:m1:130:VAL:HG13	1.90	0.54
51:m5:36:ILE:HG12	51:m5:64:VAL:HG23	1.89	0.54
56:n0:93:GLU:OE1	56:n0:137:ARG:HB2	2.08	0.54
62:n6:5:SER:HB3	62:n6:8:VAL:HG22	1.89	0.54
63:n7:16:GLY:O	63:n7:19:ALA:N	2.39	0.54
1:2:823:G:H2'	1:2:824:G:C8	2.41	0.54
6:S4:153:ASN:O	6:S4:174:LYS:NZ	2.34	0.54
31:D9:5:ASN:OD1	31:D9:5:ASN:N	2.40	0.54
36:1:1103:A:H4'	36:1:1103:A:OP2	2.07	0.54
36:1:1367:G:OP1	68:O2:45:ARG:NH2	2.40	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
46:L9:28:VAL:HG13	46:L9:33:THR:HB	1.88	0.54
77:Q1:7:LYS:HE2	77:Q1:11:ARG:NH1	2.22	0.54
1:6:538:A:H8	1:6:543:C:H41	1.47	0.54
1:6:1187:U:H4'	33:e1:78:LYS:HE2	1.89	0.54
2:s0:195:TRP:CE2	2:s0:197:ILE:HD13	2.42	0.54
16:c4:84:ARG:HB3	16:c4:118:VAL:HG23	1.89	0.54
20:c8:134:ARG:O	20:c8:136:GLN:N	2.39	0.54
26:d4:52:LYS:C	26:d4:54:ALA:H	2.14	0.54
36:5:767:U:H1'	36:5:768:C:C6	2.42	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
36:5:2785:A:O2'	78:q2:41:ARG:NH2	2.40	0.54
52:m6:18:ARG:O	52:m6:22:VAL:HG12	2.06	0.54
59:n3:128:ARG:HB3	59:n3:128:ARG:HH21	1.72	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1401:A:O3'	19:C7:10:LYS:NZ	2.39	0.54
1:2:1525:A:H2'	1:2:1526:A:C8	2.43	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
9:S7:155:ASP:OD2	9:S7:156:SER:N	2.31	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
36:1:603:A:H2'	36:1:604:G:O4'	2.07	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
51:M5:143:ARG:HH21	71:O5:92:LEU:HD23	1.71	0.54
69:O3:14:LEU:HD11	69:O3:31:LYS:HB2	1.88	0.54
1:6:73:U:H2'	1:6:74:U:C6	2.42	0.54
1:6:1677:C:OP1	10:s8:42:ARG:NH1	2.41	0.54
6:s4:100:ARG:HH21	6:s4:122:LYS:HA	1.72	0.54
22:d0:118:VAL:HG13	22:d0:119:ALA:H	1.72	0.54
36:5:2186:U:OP2	39:l2:200:ARG:HD2	2.08	0.54
36:5:2651:G:H4'	36:5:2652:U:OP2	2.08	0.54
36:5:3243:A:C8	52:m6:156:LEU:HD13	2.42	0.54
39:l2:118:GLU:HG3	39:l2:126:LEU:HD21	1.89	0.54
62:n6:26:GLN:O	62:n6:30:LEU:HG	2.07	0.54
63:n7:54:THR:OG1	63:n7:55:LYS:N	2.40	0.54
10:S8:197:THR:HA	10:S8:200:LYS:HD2	1.89	0.54
21:C9:57:ARG:HG2	21:C9:104:VAL:HG21	1.90	0.54
36:1:911:C:N4	39:L2:3:ARG:HD3	2.22	0.54
42:L5:76:ALA:HB3	42:L5:109:THR:HG22	1.90	0.54
1:6:1481:C:O2'	1:6:1482:C:O5'	2.26	0.54
1:6:1558:U:H3	17:c5:122:THR:HG22	1.71	0.54
3:s1:61:LEU:HA	3:s1:64:ARG:HE	1.73	0.54
4:s2:90:THR:OG1	4:s2:91:ARG:N	2.39	0.54
7:s5:59:VAL:C	7:s5:61:TYR:H	2.14	0.54
10:s8:76:THR:HG22	10:s8:108:PRO:HG2	1.89	0.54
16:c4:112:ILE:H	28:d6:57:SER:HA	1.73	0.54
33:e1:90:LYS:HB2	33:e1:93:HIS:CE1	2.42	0.54
36:5:2748:A:O3'	42:l5:48:LYS:NZ	2.41	0.54
40:l3:3:HIS:C	40:l3:3:HIS:HD1	2.15	0.54
42:l5:244:HIS:O	42:l5:248:ARG:HG3	2.08	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)
1:2:649:U:O2'	1:2:650:U:O5'	2.24	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
5:S3:211:PRO:HG3	19:C7:20:TYR:CZ	2.43	0.54
25:D3:31:LYS:HD2	25:D3:36:THR:HG21	1.90	0.54
37:3:45:A:H2'	37:3:46:A:C8	2.41	0.54
52:M6:88:VAL:O	52:M6:90:HIS:N	2.40	0.54
57:N1:68:THR:OG1	57:N1:69:LYS:N	2.40	0.54
60:N4:23:ARG:NH2	60:N4:25:ASP:OD2	2.41	0.54
74:O8:17:ARG:O	74:O8:19:ASP:N	2.40	0.54
1:6:391:A:OP2	10:s8:23:LYS:NZ	2.38	0.54
1:6:1738:U:H2'	1:6:1739:C:H6	1.72	0.54
5:s3:203:PRO:HA	19:c7:42:GLN:HB2	1.90	0.54
6:s4:141:THR:OG1	6:s4:145:ARG:HB2	2.07	0.54
80:e0:51:ASN:HB3	80:e0:53:LYS:HG2	1.89	0.54
36:5:59:G:H2'	38:8:33:A:O2'	2.08	0.54
36:5:1160:C:O2	68:o2:45:ARG:NH1	2.41	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
39:l2:113:VAL:HG12	39:l2:166:ILE:HA	1.90	0.54
41:l4:317:PRO:HA	41:l4:323:VAL:HG13	1.90	0.54
41:l4:339:LEU:HA	41:l4:342:LYS:HB3	1.88	0.54
43:l6:176:PHE:HA	50:m4:114:ASP:HB2	1.90	0.54
48:m1:166:LYS:C	48:m1:168:ASP:H	2.16	0.54
49:m3:54:LEU:HD23	49:m3:141:ALA:HB1	1.90	0.54
70:o4:99:LYS:O	70:o4:103:LYS:HG2	2.07	0.54
1:2:715:U:H3	1:2:723:G:H1	1.56	0.54
1:2:1229:G:O2'	1:2:1255:G:N2	2.40	0.54
14:C2:67:THR:HG22	14:C2:68:GLU:HG3	1.88	0.54
36:1:2557:A:H5'	63:N7:135:ARG:HH11	1.72	0.54
37:3:6:C:O2'	42:L5:50:ARG:NH2	2.35	0.54
41:L4:6:VAL:N	41:L4:20:LEU:O	2.26	0.54
42:L5:83:LEU:HB3	42:L5:88:ILE:HB	1.90	0.54
46:L9:4:ILE:HG22	56:N0:142:GLN:OE1	2.08	0.54
52:M6:12:LYS:O	56:N0:167:ARG:NH2	2.30	0.54
1:6:867:G:N2	15:c3:87:ASP:OD1	2.38	0.54
21:c9:105:LEU:HD13	21:c9:122:ARG:HD3	1.88	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:2549:G:C2	45:l8:33:ASN:HA	2.43	0.54
39:l2:104:LEU:HD23	39:l2:158:ILE:HD11	1.89	0.54
1:2:116:U:H2'	1:2:117:U:C6	2.43	0.54
1:2:1169:G:N1	1:2:1575:G:OP2	2.39	0.54
1:2:1534:G:OP2	27:D5:74:SER:OG	2.20	0.54
6:S4:130:GLN:HB2	6:S4:138:TYR:CZ	2.42	0.54
36:1:361:A:O3'	73:O7:45:ARG:NH2	2.41	0.54
36:1:1033:U:H2'	36:1:1034:U:C6	2.43	0.54
70:O4:20:ILE:HD12	70:O4:32:ALA:HB1	1.89	0.54
1:6:1650:U:H2'	1:6:1651:A:C8	2.43	0.54
5:s3:23:GLU:OE2	12:c0:61:TRP:NE1	2.39	0.54
15:c3:84:ILE:HD11	15:c3:89:TYR:HD2	1.72	0.54
25:d3:69:ARG:NH1	25:d3:116:ASP:OD2	2.41	0.54
26:d4:14:SER:HA	26:d4:21:LYS:HG3	1.89	0.54
36:5:2256:A:H2'	36:5:2256:A:OP2	2.08	0.54
49:m3:166:ALA:N	64:n8:135:GLU:OE1	2.35	0.54
50:m4:123:LEU:HD22	52:m6:190:VAL:HG13	1.89	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
1:2:1649:G:H2'	1:2:1650:U:C6	2.43	0.54
3:S1:180:THR:HG22	3:S1:181:LEU:H	1.72	0.54
11:S9:107:ARG:NH2	11:S9:148:VAL:O	2.40	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
39:L2:227:ARG:HG2	39:L2:239:ALA:HB2	1.90	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:OD1	64:N8:46:ASP:N	2.40	0.54
1:6:712:G:H2'	1:6:713:A:C8	2.43	0.54
4:s2:157:LYS:HG2	4:s2:170:ILE:HG23	1.89	0.54
6:s4:95:THR:HG23	6:s4:97:GLU:HG3	1.89	0.54
20:c8:11:PHE:CZ	20:c8:59:GLY:HA3	2.43	0.54
36:5:911:C:N4	39:l2:3:ARG:HD3	2.23	0.54
51:m5:46:ASP:OD1	51:m5:50:ARG:NH2	2.41	0.54
76:q0:97:ARG:HG3	76:q0:120:GLN:O	2.07	0.54
6:S4:61:VAL:HG12	6:S4:65:LEU:HD12	1.88	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
36:1:1108:U:H2'	36:1:1109:U:H6	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1846:C:OP1	36:1:1849:C:N4	2.33	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
53:M7:29:THR:O	53:M7:119:VAL:HG11	2.08	0.54
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
36:5:1554:U:H1'	36:5:1555:U:H5"	1.90	0.54
52:m6:112:TYR:O	52:m6:117:ARG:NH1	2.40	0.54
1:2:122:U:O3'	6:S4:77:ARG:NH2	2.41	0.53
4:S2:227:PRO:HA	4:S2:230:TRP:CE2	2.42	0.53
31:D9:31:ILE:HB	31:D9:38:ILE:O	2.08	0.53
36:1:2207:A:H2'	36:1:2208:A:H5'	1.89	0.53
43:L6:56:LYS:HD2	43:L6:98:VAL:HG13	1.89	0.53
53:M7:29:THR:HG22	53:M7:87:SER:OG	2.08	0.53
53:M7:64:ASN:HA	53:M7:67:ILE:HD13	1.90	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
1:6:1498:G:H5"	21:c9:72:GLY:HA3	1.90	0.53
3:s1:30:PHE:HB3	3:s1:96:LEU:HD22	1.90	0.53
34:sR:52:GLN:HG2	34:sR:53:LYS:H	1.73	0.53
36:5:2617:U:O3'	47:m0:116:ARG:NH2	2.37	0.53
40:l3:5:LYS:HG2	40:l3:6:TYR:CE1	2.43	0.53
59:n3:45:ARG:HB3	59:n3:48:ARG:HG3	1.89	0.53
1:2:420:A:OP1	8:S6:96:SER:OG	2.13	0.53
7:S5:42:LEU:HB2	7:S5:46:TRP:O	2.08	0.53
14:C2:27:ALA:HB1	14:C2:132:GLU:HB3	1.90	0.53
28:D6:10:ARG:HB2	28:D6:34:LYS:HG3	1.90	0.53
36:1:289:A:H2	51:M5:93:LYS:HD2	1.71	0.53
36:1:1334:U:O2'	44:L7:151:ARG:NH2	2.41	0.53
36:1:2168:A:C6	36:1:2170:U:H1'	2.43	0.53
36:1:2538:U:O2'	36:1:2541:U:O4	2.21	0.53
40:L3:159:ARG:HG2	40:L3:182:GLN:HA	1.89	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
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
74:O8:44:LYS:HG2	74:O8:53:THR:HB	1.90	0.53
1:6:647:G:N2	1:6:687:G:H22	2.06	0.53
1:6:788:A:OP1	6:s4:106:LYS:NZ	2.40	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1171:A:H2'	1:6:1172:G:C8	2.43	0.53
6:s4:107:GLY:HA2	6:s4:189:LEU:HG	1.89	0.53
9:s7:12:ALA:HB3	9:s7:13:PRO:HD3	1.90	0.53
25:d3:103:LEU:HD12	25:d3:126:LYS:HD3	1.90	0.53
26:d4:57:VAL:HB	26:d4:60:PHE:HE2	1.73	0.53
36:5:1464:G:N2	36:5:1466:G:H3'	2.22	0.53
36:5:2586:G:N7	45:l8:241:LYS:HB2	2.22	0.53
38:8:63:G:HO2'	71:o5:49:LYS:HZ1	1.48	0.53
41:l4:174:ALA:O	41:l4:178:LEU:HG	2.08	0.53
54:m8:158:HIS:H	54:m8:186:VAL:CG1	2.20	0.53
1:2:939:A:H2'	1:2:940:A:C8	2.43	0.53
1:2:1427:A:OP2	35:SM:93:ARG:NH1	2.41	0.53
3:S1:110:LEU:HD11	3:S1:213:ARG:HD2	1.90	0.53
36:1:532:A:H2	36:1:560:G:H22	1.56	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
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
6:s4:160:VAL:HG13	6:s4:169:ILE:HG23	1.90	0.53
7:s5:133:VAL:HA	7:s5:198:LEU:HD22	1.90	0.53
34:sR:248:ASN:OD1	34:sR:249:ARG:N	2.41	0.53
36:5:1043:C:O3'	47:m0:90:ARG:NH1	2.41	0.53
36:5:2407:C:H2'	36:5:2408:U:C6	2.44	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
1:2:1228:G:H22	14:C2:67:THR:HB	1.74	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
10:S8:89:GLU:O	10:S8:93:THR:OG1	2.18	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
36:1:3227:A:O3'	50:M4:133:LYS:NZ	2.42	0.53
37:3:60:G:H2'	37:3:61:G:H8	1.73	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
64:N8:28:HIS:CD2	64:N8:32:ARG:HG2	2.43	0.53
1:6:393:C:OP2	10:s8:2:GLY:N	2.41	0.53
1:6:1312:A:OP1	19:c7:2:GLY:N	2.42	0.53
36:5:2404:A:N7	36:5:2872:A:N6	2.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:m9:43:LYS:O	55:m9:47:ASN:N	2.25	0.53
70:o4:81:CYS:O	70:o4:83:ASN:N	2.41	0.53
72:o6:57:LEU:HD11	72:o6:73:ALA:HB2	1.91	0.53
1:2:488:G:H4'	1:2:488:G:OP1	2.09	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
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
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
36:1:3178:A:C2	52:M6:115:LYS:HG2	2.44	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
8:s6:135:PRO:HB2	8:s6:141:ILE:HG12	1.89	0.53
10:s8:35:ASN:O	10:s8:95:THR:HG23	2.09	0.53
36:5:715:A:C8	64:n8:115:LYS:HG3	2.44	0.53
36:5:2812:C:H2'	36:5:2813:A:H8	1.74	0.53
39:l2:189:TYR:HA	39:l2:192:LYS:HG3	1.89	0.53
79:q3:3:LYS:HD2	79:q3:3:LYS:O	2.09	0.53
1:2:144:U:H5	8:S6:137:ARG:NH1	2.07	0.53
1:2:780:A:H8	26:D4:8:ARG:HB3	1.73	0.53
1:2:1370:U:H4'	1:2:1371:A:O5'	2.08	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
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
36:1:1038:C:H4'	42:L5:5:LYS:HE3	1.91	0.53
36:1:2433:U:H1'	51:M5:125:SER:HB3	1.91	0.53
36:1:3228:C:H4'	36:1:3229:G:O5'	2.07	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
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
1:6:1263:G:H2'	1:6:1264:G:O4'	2.09	0.53
3:s1:48:VAL:HG21	3:s1:61:LEU:HD22	1.90	0.53
9:s7:39:ARG:HH22	55:m9:185:LEU:HD22	1.72	0.53
11:s9:20:GLU:HB2	11:s9:23:ARG:HB3	1.91	0.53
36:5:2821:C:C2	87:D:3401:SPS:H182	2.44	0.53
1:2:473:A:H5'	1:2:769:A:H1'	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
25:D3:55:GLU:HG2	25:D3:73:ARG:HB2	1.90	0.53
36:1:129:U:H2'	36:1:130:A:C8	2.44	0.53
36:1:1307:G:OP2	52:M6:59:ARG:NH1	2.42	0.53
37:3:71:G:H2'	37:3:72:A:H8	1.74	0.53
50:M4:135:LEU:HD11	52:M6:178:VAL:HG22	1.90	0.53
1:6:427:C:O2'	1:6:459:G:N3	2.36	0.53
23:d1:9:VAL:HG22	23:d1:10:GLU:H	1.73	0.53
25:d3:100:ASP:O	25:d3:101:GLU:HB2	2.08	0.53
36:5:8:C:H2'	36:5:9:U:O4'	2.09	0.53
36:5:1758:G:OP1	58:n2:104:ARG:NH1	2.41	0.53
36:5:2618:G:OP1	47:m0:116:ARG:NE	2.42	0.53
36:5:3115:C:O2'	36:5:3117:C:N4	2.37	0.53
39:l2:201:GLY:HA2	39:l2:204:MET:SD	2.49	0.53
40:l3:3:HIS:ND1	40:l3:3:HIS:C	2.67	0.53
53:m7:97:ASN:O	53:m7:101:ASN:ND2	2.42	0.53
58:n2:104:ARG:HH11	58:n2:106:ALA:HB2	1.74	0.53
5:S3:176:LEU:HA	5:S3:181:VAL:HG12	1.91	0.53
8:S6:71:THR:OG1	8:S6:72:ARG:N	2.42	0.53
8:S6:153:VAL:O	8:S6:156:PHE:N	2.40	0.53
25:D3:56:LYS:NZ	25:D3:97:ASP:H	2.06	0.53
34:SR:26:SER:OG	34:SR:75:ALA:O	2.26	0.53
36:1:1844:C:O2	73:O7:9:GLY:HA2	2.09	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
1:6:1526:A:N1	1:6:1608:U:O2'	2.36	0.53
9:s7:156:SER:HB2	9:s7:186:PRO:HG2	1.91	0.53
11:s9:129:ILE:HA	11:s9:134:ILE:HG12	1.89	0.53
23:d1:36:VAL:O	23:d1:51:VAL:N	2.35	0.53
36:5:953:G:O2'	36:5:1116:G:H5'	2.09	0.53
40:l3:291:GLU:OE1	40:l3:302:LYS:NZ	2.35	0.53
47:m0:99:ILE:HD13	47:m0:101:LYS:HB2	1.91	0.53
55:m9:9:ARG:HH21	55:m9:10:LEU:HD13	1.74	0.53
1:2:330:G:OP2	10:S8:172:ARG:NH1	2.39	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:L7:125:GLU:HA	44:L7:128:LYS:HG3	1.91	0.53
44:L7:159:GLN:O	44:L7:160:ARG:C	2.51	0.53
48:M1:94:ARG:O	48:M1:96:PHE:N	2.41	0.53
53:M7:172:GLN:NE2	69:O3:60:ARG:O	2.42	0.53
73:O7:17:THR:HG22	73:O7:18:LEU:H	1.73	0.53
1:6:765:G:O6	11:s9:149:ARG:HD2	2.09	0.53
1:6:1606:C:H2'	1:6:1607:G:C8	2.44	0.53
2:s0:22:THR:HG22	2:s0:169:SER:HA	1.90	0.53
25:d3:46:SER:OG	25:d3:78:LYS:NZ	2.40	0.53
26:d4:25:VAL:HG12	26:d4:27:VAL:HG23	1.91	0.53
36:5:524:U:OP1	50:m4:77:ARG:NH2	2.29	0.53
36:5:2927:C:H2'	36:5:2928:C:C6	2.44	0.53
41:l4:148:ILE:HA	41:l4:149:PRO:C	2.34	0.53
42:l5:40:HIS:CE1	57:n1:69:LYS:HA	2.44	0.53
52:m6:10:ASP:CG	52:m6:37:ARG:HH21	2.16	0.53
66:o0:16:LEU:HB2	66:o0:98:SER:HB2	1.91	0.53
79:q3:3:LYS:O	79:q3:5:THR:N	2.42	0.53
1:2:46:A:N6	1:2:433:C:H4'	2.24	0.53
1:2:304:U:H2'	1:2:305:C:C6	2.44	0.53
36:1:440:A:H8	36:1:440:A:OP2	1.92	0.53
36:1:860:G:C6	39:L2:181:LYS:HB2	2.44	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
57:N1:103:GLN:HE21	57:N1:104:GLU:N	2.07	0.53
1:6:859:A:C5	15:c3:73:ARG:HD3	2.43	0.53
1:6:1535:U:H1'	1:6:1536:G:C2	2.44	0.53
5:s3:34:TYR:HE2	5:s3:37:VAL:HG13	1.73	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
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
50:m4:21:VAL:HG12	50:m4:65:LEU:HA	1.91	0.53
56:n0:13:ARG:NH2	56:n0:50:LYS:O	2.42	0.53
56:n0:137:ARG:HG2	56:n0:139:TYR:CE1	2.44	0.53
66:o0:43:ILE:HG23	66:o0:68:TYR:HD2	1.74	0.53
10:S8:48:THR:HG21	10:S8:54:LYS:HE3	1.90	0.52
34:SR:52:GLN:H	34:SR:52:GLN:CD	2.17	0.52
51:M5:28:TRP:O	51:M5:32:GLN:HG2	2.09	0.52
54:M8:158:HIS:H	54:M8:186:VAL:CG1	2.16	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:6:1620:C:H2'	1:6:1621:U:C6	2.43	0.52
39:l2:70:ARG:HH11	39:l2:72:ARG:HH21	1.56	0.52
40:l3:114:VAL:HG22	40:l3:163:HIS:CE1	2.44	0.52
48:m1:33:ALA:HB2	48:m1:123:PHE:CE1	2.44	0.52
1:2:74:U:O2'	1:2:75:U:OP2	2.26	0.52
9:S7:9:LEU:HD21	9:S7:17:GLU:HB3	1.92	0.52
18:C6:16:ALA:HB2	18:C6:72:GLY:HA3	1.91	0.52
30:D8:13:ILE:HD12	30:D8:29:ARG:HG2	1.91	0.52
36:1:2242:A:H5'	39:L2:243:THR:HG23	1.91	0.52
37:3:11:A:H4'	37:3:13:A:C8	2.45	0.52
39:L2:14:SER:OG	39:L2:15:ILE:N	2.42	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
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
1:6:1102:G:N7	25:d3:2:GLY:N	2.57	0.52
1:6:1120:U:H2'	1:6:1121:C:C6	2.44	0.52
1:6:1553:G:O2'	31:d9:14:TYR:OH	2.27	0.52
18:c6:79:TYR:HA	18:c6:82:ARG:HG2	1.91	0.52
36:5:364:G:OP1	41:l4:60:THR:HG23	2.09	0.52
36:5:1564:U:H2'	36:5:1565:G:C8	2.45	0.52
36:5:2396:G:OP1	36:5:2397:A:H4'	2.09	0.52
40:l3:105:VAL:HG11	40:l3:144:ILE:HG23	1.92	0.52
40:l3:252:ILE:HG13	40:l3:264:VAL:HG21	1.89	0.52
1:2:577:G:H2'	35:SM:99:LYS:NZ	2.24	0.52
1:2:870:C:H2'	1:2:871:G:C8	2.45	0.52
1:2:1066:C:O2'	3:S1:148:ASN:ND2	2.42	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
36:1:1126:G:H5"	47:M0:119:TRP:HZ3	1.73	0.52
40:L3:280:HIS:HB3	40:L3:324:VAL:CG2	2.39	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
54:M8:170:ARG:O	54:M8:171:LYS:HB2	2.08	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:N8:77:LYS:O	64:N8:79:TRP:N	2.43	0.52
4:s2:115:ILE:HD11	4:s2:212:LYS:HD2	1.91	0.52
36:5:1096:U:H4'	36:5:1097:G:O5'	2.10	0.52
36:5:2245:C:H4'	39:l2:221:LYS:O	2.10	0.52
41:l4:93:MET:H	41:l4:93:MET:CE	2.22	0.52
63:n7:46:ILE:HG12	63:n7:49:TYR:CE1	2.43	0.52
1:2:393:C:H4'	1:2:1673:G:O2'	2.10	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
2:S0:179:ARG:HD3	2:S0:183:ARG:HD2	1.91	0.52
9:S7:73:VAL:O	9:S7:75:THR:N	2.43	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
36:1:1103:A:H1'	36:1:1104:G:OP1	2.09	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
1:6:1338:C:H1'	1:6:1410:A:C4	2.44	0.52
4:s2:230:TRP:CE2	24:d2:68:ARG:HD2	2.44	0.52
35:sM:48:ARG:NH2	35:sM:50:ASN:HD22	2.07	0.52
36:5:109:A:H4'	36:5:110:G:OP1	2.09	0.52
36:5:835:G:O2'	36:5:857:G:N2	2.32	0.52
36:5:1157:G:H2'	36:5:1158:A:O4'	2.10	0.52
44:l7:88:ARG:HD2	44:l7:90:LYS:O	2.10	0.52
46:l9:90:MET:HE2	46:l9:179:ILE:HG22	1.92	0.52
47:m0:140:THR:HG21	47:m0:148:VAL:HG21	1.92	0.52
1:2:29:U:H2'	1:2:30:G:H8	1.73	0.52
1:2:901:G:N2	16:C4:54:GLU:OE1	2.40	0.52
1:2:1300:A:OP1	4:S2:99:LYS:NZ	2.42	0.52
1:2:1338:C:H1'	1:2:1410:A:C4	2.45	0.52
25:D3:107:PHE:CD2	25:D3:114:LYS:HB2	2.44	0.52
36:1:73:C:O2	49:M3:59:ARG:HD3	2.09	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
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
52:M6:22:VAL:HG21	52:M6:120:VAL:HG11	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:M7:59:PRO:HG3	53:M7:76:PHE:CD1	2.45	0.52
74:O8:17:ARG:NH2	74:O8:19:ASP:OD1	2.38	0.52
1:6:249:U:H3'	1:6:250:C:C5'	2.39	0.52
1:6:952:A:H5'	15:c3:98:VAL:HG22	1.91	0.52
1:6:1241:G:H2'	1:6:1242:A:O4'	2.10	0.52
3:s1:129:THR:OG1	3:s1:131:ASP:OD1	2.27	0.52
33:e1:86:THR:O	33:e1:87:THR:OG1	2.23	0.52
33:e1:144:CYS:HB3	33:e1:147:VAL:HG12	1.91	0.52
36:5:914:A:C2	39:l2:204:MET:HG2	2.45	0.52
36:5:2512:C:N4	36:5:2513:U:O4	2.42	0.52
38:8:77:A:H2'	38:8:78:G:O4'	2.09	0.52
67:o1:27:LYS:O	67:o1:31:ARG:HB2	2.10	0.52
69:o3:14:LEU:HD11	69:o3:31:LYS:HB2	1.90	0.52
72:o6:58:ILE:HG22	72:o6:90:MET:HG3	1.92	0.52
1:2:720:G:H1'	1:2:721:U:H5"	1.92	0.52
1:2:858:G:OP1	9:S7:116:ARG:NH2	2.42	0.52
1:2:918:U:O3'	16:C4:18:ARG:NH1	2.43	0.52
1:2:1542:G:H22	1:2:1568:C:H1'	1.74	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
10:S8:8:ARG:CZ	10:S8:21:PHE:HB3	2.40	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
36:1:2174:G:H8	36:1:2174:G:OP1	1.92	0.52
36:1:3325:G:H5'	67:O1:104:LEU:O	2.10	0.52
48:M1:164:LYS:HE3	48:M1:171:VAL:HB	1.92	0.52
49:M3:74:GLY:O	49:M3:101:ARG:NH1	2.42	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
76:Q0:83:LYS:HZ2	76:Q0:83:LYS:HB3	1.74	0.52
1:6:249:U:H3'	1:6:250:C:H5'	1.91	0.52
18:c6:99:GLU:HG2	34:sR:57:PRO:HB2	1.91	0.52
34:sR:80:ALA:HB3	34:sR:92:TRP:HB2	1.90	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
41:l4:138:ARG:HB3	41:l4:138:ARG:HH11	1.75	0.52
52:m6:110:PRO:O	52:m6:112:TYR:N	2.43	0.52
71:o5:5:LYS:O	71:o5:9:LEU:HG	2.10	0.52
1:2:226:A:C2'	1:2:227:U:H5'	2.40	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:C8:53:ASP:OD2	20:C8:55:HIS:ND1	2.39	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
40:L3:18:PRO:HG2	40:L3:20:LYS:HD2	1.90	0.52
41:L4:52:VAL:HG11	41:L4:99:MET:HE3	1.90	0.52
43:L6:158:TYR:OH	50:M4:114:ASP:OD2	2.17	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
1:6:1160:A:H2'	1:6:1161:C:C6	2.44	0.52
1:6:1500:C:OP1	21:c9:122:ARG:NH2	2.42	0.52
3:s1:197:ILE:HG22	3:s1:210:ILE:HD13	1.92	0.52
36:5:230:U:H2'	36:5:231:G:O4'	2.09	0.52
36:5:1313:G:H2'	36:5:1314:C:C6	2.45	0.52
36:5:2880:U:H1'	40:l3:250:ALA:HB3	1.92	0.52
36:5:2897:A:H2'	36:5:2899:C:H5'	1.90	0.52
38:8:86:U:H2'	71:o5:7:TYR:CE2	2.43	0.52
49:m3:133:PRO:O	49:m3:135:ALA:N	2.43	0.52
54:m8:170:ARG:O	54:m8:171:LYS:HB2	2.09	0.52
1:2:788:A:C5	6:S4:19:LEU:HD13	2.44	0.52
1:2:996:U:H3	1:2:1008:G:H1	1.58	0.52
1:2:1102:G:P	24:D2:76:SER:HG	2.33	0.52
1:2:1460:A:C8	17:C5:128:HIS:HB3	2.44	0.52
36:1:1194:G:H2'	36:1:1195:A:C8	2.45	0.52
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
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
47:M0:191:LYS:HE2	47:M0:212:GLU:HB3	1.92	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
79:Q3:36:ARG:HG2	79:Q3:48:LYS:HG3	1.92	0.52
1:6:647:G:N2	1:6:687:G:H1	2.02	0.52
1:6:1064:G:H2'	1:6:1065:A:C8	2.45	0.52
1:6:1793:G:H22	28:d6:76:SER:HG	1.57	0.52
21:c9:128:GLY:HA2	21:c9:131:ASP:HB2	1.91	0.52
41:l4:283:THR:HG21	41:l4:288:ARG:NH2	2.25	0.52
42:l5:196:ARG:HA	42:l5:199:ILE:HD12	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:l9:91:ARG:HG2	46:l9:182:SER:HB3	1.92	0.52
53:m7:26:PHE:HE1	53:m7:120:ASN:HA	1.74	0.52
63:n7:97:SER:O	63:n7:100:THR:OG1	2.24	0.52
1:2:346:G:O2'	13:C1:80:MET:HE3	2.10	0.52
1:2:1682:U:O2'	1:2:1683:C:H5'	2.10	0.52
11:S9:49:LEU:HD22	11:S9:53:ARG:HG3	1.92	0.52
17:C5:98:ASN:HB3	17:C5:120:SER:OG	2.10	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
45:L8:101:THR:HG23	45:L8:104:GLU:H	1.73	0.52
66:O0:43:ILE:HG22	66:O0:70:PHE:HB2	1.92	0.52
1:6:151:G:H1	1:6:163:G:H1	1.58	0.52
36:5:136:G:H5'	71:o5:95:PHE:CD2	2.44	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
42:l5:183:TRP:CZ3	42:l5:185:PHE:HA	2.45	0.52
44:l7:121:LYS:HB2	57:n1:133:ALA:HB3	1.92	0.52
51:m5:73:ARG:HG2	51:m5:75:VAL:HG13	1.92	0.52
72:o6:4:LYS:HD2	72:o6:14:GLY:HA3	1.92	0.52
1:2:1738:U:H2'	1:2:1739:C:C6	2.45	0.52
3:S1:91:VAL:HG23	3:S1:96:LEU:HB3	1.91	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
54:M8:170:ARG:HH11	64:N8:56:VAL:HG23	1.74	0.52
56:N0:137:ARG:HG2	56:N0:139:TYR:CZ	2.45	0.52
60:N4:63:ILE:O	60:N4:65:GLU:N	2.43	0.52
72:O6:55:ARG:O	72:O6:58:ILE:HD13	2.10	0.52
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
1:6:1382:A:H5"	22:d0:60:THR:HG22	1.92	0.52
26:d4:55:VAL:HG12	26:d4:75:VAL:HG22	1.92	0.52
36:5:1757:A:OP1	58:n2:94:ARG:NH2	2.42	0.52
38:8:67:U:H5"	73:o7:85:LYS:HB2	1.91	0.52
1:2:25:C:OP2	1:2:26:A:H2'	2.09	0.51
1:2:937:C:N4	28:D6:14:GLY:O	2.41	0.51
7:S5:152:GLY:O	7:S5:154:ALA:N	2.43	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
36:1:2953:U:H2'	36:1:2954:U:C6	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:M0:35:ASP:OD1	47:M0:86:HIS:NE2	2.42	0.51
73:O7:14:LYS:NZ	75:O9:51:ILE:HD11	2.25	0.51
1:6:1429:G:H2'	1:6:1430:U:C6	2.45	0.51
7:s5:166:ARG:NH1	7:s5:170:GLN:OE1	2.43	0.51
11:s9:126:ARG:HG3	80:e0:33:ARG:HD3	1.92	0.51
34:sR:90:ARG:HH21	34:sR:102:ARG:HE	1.56	0.51
36:5:353:G:N7	73:o7:55:ARG:HD3	2.24	0.51
36:5:385:A:H2'	36:5:386:A:C8	2.44	0.51
36:5:1522:U:H3'	61:n5:113:LEU:HD22	1.92	0.51
36:5:2356:A:H5'	53:m7:138:LYS:HZ2	1.75	0.51
37:7:92:A:C5	37:7:93:C:H1'	2.45	0.51
38:8:97:A:P	71:o5:63:ARG:HH21	2.33	0.51
42:l5:22:ARG:HA	42:l5:25:GLU:HG3	1.91	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
3:S1:171:ILE:O	3:S1:175:GLU:HG2	2.10	0.51
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
36:1:407:A:C2	38:4:17:A:H1'	2.46	0.51
36:1:645:A:N6	36:1:2869:U:OP1	2.39	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
38:4:121:U:H2'	38:4:122:U:C6	2.45	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
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
78:Q2:69:VAL:HG22	78:Q2:84:THR:HB	1.92	0.51
4:s2:116:LYS:HG2	4:s2:127:ALA:HB3	1.92	0.51
6:s4:184:THR:C	6:s4:189:LEU:HD13	2.35	0.51
8:s6:58:LYS:HA	8:s6:107:ALA:HB2	1.92	0.51
11:s9:114:TYR:HA	11:s9:119:ALA:HB3	1.92	0.51
16:c4:122:PRO:C	16:c4:124:ASP:H	2.18	0.51
24:d2:36:LYS:O	24:d2:40:VAL:HG23	2.09	0.51
36:5:507:U:H2'	36:5:508:U:C6	2.45	0.51
36:5:1636:U:H5"	63:n7:73:LYS:NZ	2.25	0.51
36:5:2442:G:H22	36:5:2506:U:H3	1.58	0.51
41:l4:138:ARG:HB3	41:l4:138:ARG:NH1	2.25	0.51
41:l4:191:LYS:HG3	41:l4:194:TYR:CZ	2.45	0.51
43:l6:170:LYS:HD2	43:l6:173:MET:HE2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:l8:81:THR:OG1	45:l8:181:LYS:HB2	2.09	0.51
73:o7:31:LYS:O	73:o7:33:THR:HG22	2.10	0.51
1:2:16:G:H2'	1:2:17:C:C6	2.46	0.51
1:2:1114:G:O2'	1:2:1130:G:O6	2.25	0.51
16:C4:128:LYS:NZ	28:D6:27:SER:OG	2.25	0.51
29:D7:61:THR:OG1	29:D7:62:ILE:N	2.41	0.51
36:1:261:U:H2'	36:1:262:U:C6	2.44	0.51
36:1:953:G:C8	36:1:1117:G:C8	2.98	0.51
37:3:39:C:N3	48:M1:70:THR:HG23	2.25	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
63:N7:46:ILE:HD11	63:N7:48:ARG:C	2.35	0.51
66:O0:13:LYS:NZ	66:O0:99:ASP:OD2	2.44	0.51
1:6:771:A:O2'	11:s9:6:ARG:NE	2.41	0.51
13:c1:46:LYS:HG3	13:c1:50:GLU:CD	2.35	0.51
14:c2:24:ILE:O	14:c2:26:ASP:N	2.41	0.51
36:5:437:G:H8	36:5:437:G:OP2	1.92	0.51
36:5:576:C:OP1	44:l7:241:LYS:NZ	2.43	0.51
36:5:1239:C:N4	36:5:1249:G:H1	2.01	0.51
50:m4:113:THR:O	50:m4:117:ARG:HG3	2.11	0.51
68:o2:16:LYS:O	68:o2:17:PHE:HB2	2.11	0.51
1:2:1683:C:O2'	1:2:1684:U:O5'	2.27	0.51
18:C6:25:GLY:H	18:C6:63:ILE:HA	1.75	0.51
20:C8:30:TYR:O	20:C8:33:THR:OG1	2.25	0.51
20:C8:108:LYS:NZ	20:C8:111:ASP:OD2	2.43	0.51
22:D0:28:SER:HB2	22:D0:112:VAL:HA	1.92	0.51
36:1:601:U:H2'	36:1:602:A:O4'	2.11	0.51
36:1:2565:U:H2'	36:1:2566:C:C6	2.46	0.51
36:1:2767:U:O2'	78:Q2:30:ALA:O	2.27	0.51
36:1:2818:U:H5'	36:1:2818:U:C6	2.37	0.51
40:L3:56:ILE:O	40:L3:73:VAL:HA	2.11	0.51
40:L3:293:ASN:HB2	40:L3:304:THR:HA	1.92	0.51
41:L4:265:GLU:OE1	41:L4:265:GLU:N	2.43	0.51
46:L9:129:ARG:O	46:L9:132:VAL:HG22	2.10	0.51
53:M7:26:PHE:HE1	53:M7:120:ASN:HA	1.76	0.51
1:6:794:U:H4'	1:6:795:U:OP2	2.09	0.51
2:s0:98:ILE:HD11	2:s0:116:LYS:HG3	1.92	0.51
15:c3:54:LEU:HB3	15:c3:60:VAL:HG13	1.92	0.51
19:c7:28:PHE:HA	19:c7:55:THR:HG21	1.92	0.51
24:d2:73:GLY:HA3	24:d2:128:PHE:CZ	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:d5:39:ALA:N	27:d5:70:LYS:O	2.43	0.51
36:5:408:A:H61	38:8:15:G:H1'	1.75	0.51
36:5:1419:A:H5"	41:l4:193:LYS:HZ3	1.75	0.51
41:l4:36:HIS:O	41:l4:40:THR:HG23	2.10	0.51
43:l6:131:LYS:HD3	43:l6:132:ALA:H	1.74	0.51
44:l7:145:ARG:HA	44:l7:185:ILE:HD13	1.92	0.51
46:l9:69:ARG:HD2	46:l9:69:ARG:O	2.10	0.51
47:m0:43:VAL:O	47:m0:171:TRP:NE1	2.38	0.51
52:m6:108:ILE:HD11	52:m6:160:ARG:CZ	2.40	0.51
53:m7:30:ARG:HA	53:m7:119:VAL:HG11	1.93	0.51
63:n7:5:LEU:HD22	63:n7:77:TYR:CZ	2.45	0.51
65:n9:14:ARG:CZ	65:n9:18:ARG:HD3	2.41	0.51
71:o5:45:LYS:O	71:o5:49:LYS:HG2	2.10	0.51
73:o7:52:LYS:HA	73:o7:55:ARG:HD2	1.93	0.51
78:q2:12:CYS:SG	78:q2:74:CYS:SG	3.09	0.51
1:2:325:G:H4'	13:C1:83:THR:HG21	1.91	0.51
9:S7:50:ASP:HA	9:S7:56:LYS:HA	1.92	0.51
9:S7:62:VAL:HG12	9:S7:64:VAL:H	1.75	0.51
14:C2:73:LYS:NZ	33:E1:108:VAL:HG13	2.25	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
36:1:2767:U:H2'	36:1:2768:U:C6	2.45	0.51
36:1:2947:G:OP2	36:1:2947:G:H4'	2.10	0.51
36:1:3187:A:H5"	50:M4:8:LYS:HE2	1.92	0.51
54:M8:58:ASN:HB3	54:M8:144:ARG:NH2	2.25	0.51
63:N7:54:THR:HG22	63:N7:57:HIS:CE1	2.45	0.51
67:O1:46:THR:OG1	67:O1:89:LEU:O	2.26	0.51
1:6:1405:G:H2'	1:6:1406:A:C8	2.45	0.51
1:6:1413:U:O2'	1:6:1416:G:OP1	2.24	0.51
15:c3:62:GLN:HG3	15:c3:65:VAL:HG22	1.91	0.51
36:5:1334:U:H1'	44:l7:208:SER:HB2	1.93	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
59:n3:31:ALA:HB2	59:n3:69:LEU:HD23	1.92	0.51
60:n4:79:GLN:HG3	60:n4:80:ARG:H	1.74	0.51
1:2:87:C:O2'	1:2:169:A:N1	2.41	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
30:D8:8:THR:OG1	30:D8:59:SER:OG	2.25	0.51
36:1:847:A:H2'	36:1:848:A:C8	2.45	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
48:M1:12:LEU:HD12	48:M1:131:MET:HE3	1.93	0.51
48:M1:143:ARG:HG2	48:M1:144:CYS:SG	2.51	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
1:6:1533:C:H4'	1:6:1539:G:N1	2.25	0.51
8:s6:10:ASN:HB3	8:s6:128:THR:HB	1.92	0.51
12:c0:55:VAL:HA	12:c0:69:THR:HG23	1.91	0.51
20:c8:33:THR:HA	20:c8:38:VAL:HG23	1.91	0.51
36:5:1389:G:H5"	68:o2:101:SER:HB3	1.93	0.51
36:5:3392:U:O2'	53:m7:75:GLU:OE2	2.24	0.51
49:m3:144:THR:C	49:m3:146:PRO:HD3	2.36	0.51
50:m4:114:ASP:HA	50:m4:117:ARG:NH1	2.26	0.51
78:q2:16:THR:OG1	78:q2:17:CYS:N	2.37	0.51
1:2:130:C:O2'	1:2:131:C:OP1	2.27	0.51
1:2:1171:A:H2'	1:2:1172:G:C8	2.45	0.51
1:2:1527:C:H2'	1:2:1528:U:C6	2.45	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
15:C3:146:ALA:HA	15:C3:149:LEU:HB2	1.93	0.51
36:1:1063:G:N7	36:1:1097:G:H2'	2.26	0.51
36:1:3173:G:C2	69:O3:96:ALA:HB2	2.46	0.51
40:L3:350:ALA:C	40:L3:352:GLU:H	2.19	0.51
58:N2:33:TYR:HE2	58:N2:63:VAL:HG21	1.75	0.51
1:6:1533:C:H4'	1:6:1539:G:C6	2.46	0.51
6:s4:43:PRO:HA	6:s4:82:TYR:O	2.10	0.51
16:c4:84:ARG:HA	16:c4:119:THR:HG22	1.93	0.51
26:d4:37:LYS:HD2	26:d4:57:VAL:HG23	1.91	0.51
36:5:2139:A:C4	73:o7:3:LYS:HE3	2.45	0.51
36:5:3242:G:N2	36:5:3245:A:H5"	2.26	0.51
36:5:3304:U:O2'	40:l3:334:ARG:NH2	2.43	0.51
47:m0:36:LEU:HD21	47:m0:69:ARG:HD3	1.93	0.51
48:m1:90:GLN:HG2	48:m1:170:ASP:HB2	1.93	0.51
64:n8:77:LYS:O	64:n8:79:TRP:N	2.44	0.51
1:2:396:G:N2	1:2:398:G:H3'	2.26	0.51
1:2:1278:G:OP1	5:S3:185:LYS:HE2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1616:G:O2'	30:D8:18:ARG:NH1	2.44	0.51
6:S4:180:LEU:N	6:S4:229:GLY:O	2.42	0.51
11:S9:85:VAL:HG12	11:S9:99:LEU:HD11	1.93	0.51
17:C5:24:LYS:O	17:C5:28:MET:HB2	2.10	0.51
36:1:805:G:H2'	36:1:936:A:H61	1.75	0.51
36:1:839:C:H4'	36:1:1724:U:H3'	1.92	0.51
36:1:1558:A:OP2	45:L8:54:GLU:HG3	2.11	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
38:4:81:U:H1'	38:4:82:U:H5'	1.92	0.51
40:L3:350:ALA:O	40:L3:352:GLU:N	2.35	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
76:Q0:97:ARG:HB2	76:Q0:120:GLN:O	2.11	0.51
1:6:6:G:N7	4:s2:205:ARG:NH1	2.58	0.51
1:6:374:U:OP1	13:c1:96:LYS:NZ	2.26	0.51
1:6:1227:A:O2'	14:c2:44:GLY:HA3	2.11	0.51
1:6:1254:U:OP1	33:e1:143:LYS:HD3	2.11	0.51
1:6:1729:C:O2'	10:s8:2:GLY:HA2	2.11	0.51
6:s4:93:ASP:C	6:s4:95:THR:H	2.18	0.51
7:s5:146:THR:HG23	7:s5:157:ARG:HB3	1.92	0.51
12:c0:54:TYR:HD2	12:c0:72:GLY:HA2	1.76	0.51
25:d3:53:VAL:HG13	25:d3:72:VAL:HB	1.93	0.51
36:5:670:C:OP1	54:m8:147:ARG:NH2	2.44	0.51
36:5:1120:A:H2'	36:5:1121:U:C6	2.46	0.51
40:l3:4:ARG:HG3	40:l3:6:TYR:O	2.11	0.51
51:m5:54:LYS:O	51:m5:56:LYS:N	2.44	0.51
58:n2:89:LEU:HB3	58:n2:93:ILE:HD12	1.93	0.51
59:n3:128:ARG:HB3	59:n3:128:ARG:NH2	2.26	0.51
61:n5:38:LEU:O	61:n5:39:LYS:HB2	2.10	0.51
70:o4:71:THR:HG22	70:o4:77:GLY:HA3	1.91	0.51
71:o5:86:ARG:HG3	71:o5:90:ARG:NH2	2.26	0.51
9:S7:154:LEU:HD21	9:S7:183:PHE:HD1	1.76	0.51
11:S9:65:LYS:HD3	11:S9:70:LEU:HD11	1.92	0.51
24:D2:104:LEU:HB2	24:D2:125:ILE:HA	1.93	0.51
37:3:7:G:O3'	42:L5:33:ARG:NH2	2.44	0.51
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:417:A:H4'	1:6:418:G:O5'	2.11	0.51
1:6:1316:G:OP1	19:c7:7:LYS:N	2.38	0.51
1:6:1451:C:H2'	1:6:1452:U:C6	2.46	0.51
1:6:1616:G:O2'	30:d8:18:ARG:NE	2.44	0.51
8:s6:163:THR:HA	8:s6:168:THR:HG22	1.92	0.51
9:s7:49:ILE:HG22	9:s7:175:LYS:HD3	1.92	0.51
12:c0:54:TYR:CE2	12:c0:75:TYR:HB2	2.45	0.51
20:c8:120:ARG:HD3	35:sM:61:ILE:HG21	1.91	0.51
24:d2:55:ASP:HB3	29:d7:25:VAL:HG22	1.93	0.51
31:d9:19:ARG:HD2	31:d9:32:ARG:HD2	1.91	0.51
36:5:1102:A:H4'	36:5:1103:A:C5	2.45	0.51
38:8:6:U:H2'	38:8:7:U:C6	2.46	0.51
43:l6:102:ASN:OD1	43:l6:102:ASN:N	2.41	0.51
59:n3:3:GLY:HA2	59:n3:40:LYS:HB3	1.92	0.51
71:o5:6:ALA:O	71:o5:10:ARG:HG3	2.11	0.51
1:2:854:U:O4	1:2:855:A:N6	2.44	0.51
1:2:1490:C:H4'	1:2:1491:U:OP1	2.10	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
36:1:269:G:H5"	51:M5:14:LYS:HE2	1.92	0.51
36:1:764:U:H3'	36:1:765:C:H5"	1.93	0.51
36:1:977:C:P	54:M8:141:ARG:HH22	2.34	0.51
36:1:1562:C:H2'	36:1:1563:C:C6	2.46	0.51
40:L3:37:ARG:HA	40:L3:186:GLY:H	1.76	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:H	74:O8:8:ILE:HD12	1.76	0.51
1:6:66:U:O5'	8:s6:173:PRO:HA	2.11	0.51
1:6:1166:A:H2'	1:6:1167:G:O4'	2.10	0.51
6:s4:159:THR:OG1	6:s4:160:VAL:N	2.44	0.51
36:5:2898:G:O6	76:q0:125:LYS:NZ	2.44	0.51
36:5:2988:C:OP1	52:m6:65:ASN:ND2	2.29	0.51
36:5:3324:C:OP1	67:o1:19:ARG:NH1	2.41	0.51
38:8:86:U:H2'	71:o5:7:TYR:HE2	1.76	0.51
44:l7:57:THR:OG1	44:l7:58:ALA:N	2.44	0.51
75:o9:28:ARG:NH1	75:o9:36:ARG:HH11	2.09	0.51
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
3:S1:67:GLU:OE2	3:S1:83:LYS:NZ	2.37	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:O	20:C8:34:THR:OG1	2.27	0.50
23:D1:1:MET:HE2	23:D1:13:VAL:HG22	1.93	0.50
34:SR:38:ARG:HG2	34:SR:67:ILE:HG23	1.93	0.50
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
36:1:768:C:OP1	49:M3:186:ARG:NH2	2.44	0.50
36:1:3218:A:H4'	36:1:3219:G:O5'	2.11	0.50
53:M7:16:SER:HB3	53:M7:149:VAL:HG22	1.93	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
1:6:340:U:H2'	1:6:341:A:H8	1.72	0.50
1:6:1078:C:H2'	1:6:1079:U:H6	1.76	0.50
1:6:1521:G:O2'	1:6:1523:G:OP2	2.28	0.50
1:6:1532:U:OP2	27:d5:77:ARG:HD2	2.11	0.50
1:6:1534:G:OP2	27:d5:74:SER:OG	2.18	0.50
20:c8:35:ILE:HB	20:c8:38:VAL:HG22	1.93	0.50
36:5:252:U:H4'	36:5:253:A:C5'	2.41	0.50
36:5:408:A:N6	38:8:15:G:H1'	2.26	0.50
36:5:2941:A:O5'	36:5:2943:G:H4'	2.11	0.50
39:l2:109:GLU:HA	39:l2:136:ILE:HG22	1.92	0.50
59:n3:13:ILE:HD11	59:n3:81:GLN:OE1	2.12	0.50
61:n5:46:TYR:HB3	71:o5:75:TYR:HB3	1.92	0.50
82:p0:51:VAL:HB	82:p0:87:VAL:HG22	1.92	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
6:S4:191:ARG:HH11	6:S4:245:LYS:HB3	1.76	0.50
9:S7:13:PRO:HB3	9:S7:14:THR:HB	1.93	0.50
10:S8:39:GLY:O	10:S8:59:ARG:HB3	2.11	0.50
15:C3:73:ARG:O	15:C3:77:SER:OG	2.19	0.50
16:C4:84:ARG:HG3	16:C4:119:THR:HA	1.93	0.50
36:1:352:A:N6	36:1:365:A:H5"	2.26	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
37:3:112:G:H2'	37:3:113:C:C6	2.45	0.50
41:L4:237:GLN:O	41:L4:246:ARG:HG3	2.12	0.50
55:M9:23:TRP:HB3	55:M9:51:VAL:HG22	1.92	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
6:s4:68:ARG:HB3	6:s4:76:VAL:HG11	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:c4:62:LEU:HA	16:c4:65:GLN:HG3	1.92	0.50
28:d6:87:ARG:NH2	28:d6:91:ASP:O	2.44	0.50
31:d9:30:LEU:HD13	31:d9:32:ARG:HD3	1.92	0.50
34:sR:13:LEU:HB2	34:sR:310:ILE:HB	1.93	0.50
37:7:22:A:H1'	42:l5:272:TYR:CE1	2.47	0.50
41:l4:52:VAL:HB	41:l4:99:MET:HE3	1.93	0.50
45:l8:134:TYR:CD1	45:l8:190:VAL:HG11	2.46	0.50
58:n2:13:LYS:HD2	58:n2:15:PHE:CZ	2.46	0.50
59:n3:96:GLU:OE1	60:n4:24:GLY:N	2.41	0.50
68:o2:21:HIS:CE1	68:o2:24:ARG:HD2	2.46	0.50
1:2:811:A:C2	1:2:858:G:H1'	2.47	0.50
36:1:120:G:N1	45:L8:124:ASP:OD2	2.43	0.50
36:1:1362:G:O2'	44:L7:158:LYS:HE3	2.12	0.50
41:L4:141:ARG:CZ	41:L4:180:LYS:HD3	2.41	0.50
49:M3:140:SER:HG	49:M3:143:ALA:H	1.55	0.50
49:M3:174:ARG:HB2	72:O6:9:ILE:HD12	1.94	0.50
1:6:590:C:H5"	80:e0:43:ARG:HH12	1.75	0.50
1:6:898:A:N1	1:6:911:U:O2'	2.28	0.50
1:6:1558:U:H3	17:c5:122:THR:CG2	2.24	0.50
7:s5:151:GLY:HA3	7:s5:155:ALA:HA	1.93	0.50
9:s7:9:LEU:HD11	9:s7:17:GLU:HB3	1.92	0.50
11:s9:3:ARG:H	11:s9:3:ARG:NE	2.09	0.50
11:s9:87:SER:HB3	11:s9:90:LYS:HB2	1.94	0.50
16:c4:47:LYS:HE2	16:c4:62:LEU:HB3	1.93	0.50
17:c5:29:SER:OG	17:c5:32:ASP:OD2	2.24	0.50
25:d3:57:LEU:HD22	80:e0:4:VAL:HG13	1.92	0.50
36:5:64:G:O2'	36:5:77:A:N3	2.43	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
49:m3:104:ARG:HA	72:o6:20:MET:O	2.10	0.50
57:n1:54:HIS:CE1	57:n1:55:LYS:HG2	2.46	0.50
61:n5:105:VAL:HG11	61:n5:126:LEU:HD13	1.92	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
15:C3:93:LYS:HA	15:C3:150:VAL:HG21	1.92	0.50
36:1:612:U:H2'	36:1:613:G:H8	1.77	0.50
36:1:3350:C:H2'	36:1:3351:U:H3'	1.93	0.50
38:4:131:A:H5"	61:N5:93:TYR:CE2	2.47	0.50
42:L5:155:THR:HA	42:L5:179:ARG:HA	1.94	0.50
51:M5:31:ARG:NH1	51:M5:124:ASP:OD1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:N6:112:ASP:HB2	62:N6:115:ARG:H	1.76	0.50
20:c8:41:ARG:NH2	21:c9:36:ILE:O	2.23	0.50
25:d3:90:ASP:OD2	80:e0:12:GLY:HA2	2.10	0.50
27:d5:102:THR:HG22	27:d5:103:ARG:H	1.76	0.50
36:5:743:C:O2	54:m8:141:ARG:HD3	2.11	0.50
36:5:1758:G:H5'	58:n2:104:ARG:NH2	2.26	0.50
36:5:2697:A:H2'	36:5:2698:G:C8	2.46	0.50
49:m3:123:ILE:HG22	71:o5:118:ILE:HG12	1.92	0.50
57:n1:18:ASP:OD2	57:n1:18:ASP:N	2.43	0.50
72:o6:70:ARG:HD3	72:o6:84:LYS:HG2	1.93	0.50
1:2:62:A:HO2'	1:2:268:C:HO2'	1.60	0.50
1:2:240:U:H4'	1:2:241:U:OP2	2.12	0.50
1:2:810:G:C6	9:S7:111:LYS:HE3	2.47	0.50
18:C6:18:ALA:HB2	18:C6:69:VAL:HG13	1.93	0.50
29:D7:23:THR:OG1	29:D7:24:LEU:N	2.40	0.50
36:1:520:U:O4	41:L4:349:THR:HG23	2.12	0.50
36:1:1456:A:N7	67:O1:26:LYS:HE2	2.27	0.50
36:1:1898:G:O2'	59:N3:21:ALA:HB2	2.11	0.50
36:1:2747:A:H5'	42:L5:175:HIS:HA	1.94	0.50
36:1:3047:U:O2'	40:L3:53:MET:HE1	2.12	0.50
55:M9:76:SER:O	55:M9:81:ARG:NH1	2.44	0.50
71:O5:89:ARG:HG2	71:O5:89:ARG:HH11	1.75	0.50
1:6:417:A:H5'	1:6:418:G:C5	2.46	0.50
1:6:771:A:OP1	11:s9:9:SER:OG	2.27	0.50
1:6:1780:G:N3	36:5:2262:A:O2'	2.45	0.50
2:s0:148:ASP:OD1	2:s0:149:LEU:N	2.44	0.50
9:s7:46:ILE:HG12	9:s7:60:ILE:HA	1.93	0.50
14:c2:104:ALA:HB2	14:c2:115:VAL:HG22	1.93	0.50
15:c3:84:ILE:H	15:c3:84:ILE:HD13	1.77	0.50
36:5:290:G:H4'	51:m5:69:GLY:O	2.10	0.50
36:5:3188:G:OP1	46:l9:22:SER:OG	2.24	0.50
38:8:76:C:H2'	38:8:77:A:O4'	2.12	0.50
41:l4:60:THR:HG22	41:l4:62:ALA:H	1.76	0.50
42:l5:282:ARG:O	42:l5:286:VAL:HG23	2.11	0.50
47:m0:84:ALA:O	47:m0:140:THR:HG22	2.12	0.50
52:m6:10:ASP:HB2	52:m6:117:ARG:HB2	1.94	0.50
52:m6:47:PHE:HE2	52:m6:141:LEU:HA	1.77	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
3:S1:88:VAL:HG11	3:S1:96:LEU:HD12	1.94	0.50
5:S3:27:ARG:HD2	12:C0:60:SER:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:S6:7:TYR:HE1	8:S6:125:THR:HG23	1.77	0.50
9:S7:50:ASP:OD1	9:S7:50:ASP:N	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
33:E1:106:TYR:HE2	33:E1:116:LYS:HG2	1.77	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
40:L3:206:ASP:OD1	40:L3:206:ASP:N	2.45	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
69:O3:26:ASN:HA	69:O3:88:ASN:OD1	2.11	0.50
1:6:199:G:HO2'	1:6:200:A:H8	1.58	0.50
1:6:846:G:H21	13:c1:46:LYS:HE2	1.76	0.50
1:6:1350:U:H2'	1:6:1351:G:C8	2.46	0.50
31:d9:33:LYS:HE2	31:d9:34:TYR:CZ	2.47	0.50
36:5:126:U:H2'	36:5:127:G:O4'	2.10	0.50
36:5:662:U:OP1	64:n8:8:THR:HG21	2.11	0.50
36:5:943:U:H3'	64:n8:13:GLY:HA2	1.93	0.50
36:5:1190:A:C8	36:5:1193:A:H1'	2.47	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
36:5:2522:G:O6	39:l2:70:ARG:NH1	2.44	0.50
36:5:2802:A:C8	78:q2:56:PRO:HA	2.46	0.50
36:5:2915:U:C5	40:l3:7:GLU:HG2	2.47	0.50
39:l2:206:PRO:HG3	39:l2:213:GLY:HA2	1.93	0.50
42:l5:64:ILE:HD12	42:l5:144:VAL:HG21	1.93	0.50
42:l5:210:GLU:O	42:l5:214:ASP:HB2	2.11	0.50
1:2:136:C:H4'	1:2:137:U:OP1	2.12	0.50
1:2:639:U:OP1	9:S7:117:THR:OG1	2.23	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
10:S8:39:GLY:H	10:S8:60:ILE:C	2.19	0.50
19:C7:76:GLU:HA	19:C7:79:GLU:HB2	1.93	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
40:L3:123:TYR:CE2	40:L3:124:LYS:HG3	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:L4:140:HIS:HA	41:L4:177:ASP:OD1	2.12	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:M7:4: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
1:6:1564:U:H2'	1:6:1565:C:C6	2.47	0.50
2:s0:52:LYS:HG2	23:d1:82:VAL:HG22	1.92	0.50
16:c4:66:ASP:N	16:c4:66:ASP:OD1	2.44	0.50
19:c7:71:PHE:CZ	19:c7:74:GLN:HB2	2.47	0.50
21:c9:61:VAL:O	21:c9:65:ILE:HG13	2.11	0.50
36:5:847:A:H2'	36:5:848:A:C8	2.46	0.50
36:5:2676:A:H4'	36:5:2677:G:O5'	2.10	0.50
40:l3:37:ARG:HG2	40:l3:187:SER:H	1.75	0.50
40:l3:167:ARG:C	40:l3:169:THR:H	2.20	0.50
41:l4:26:PHE:CD1	41:l4:130:ALA:HB2	2.43	0.50
53:m7:13:LYS:HB3	53:m7:152:GLU:HB2	1.94	0.50
75:o9:44:TRP:CZ3	75:o9:45:ARG:HG3	2.47	0.50
1:2:1175:U:H2'	1:2:1176:G:C8	2.46	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:S6:131:LYS:O	60:N4:82:ILE:HA	2.12	0.50
36:1:343:U:O2	36:1:1439:U:H1'	2.12	0.50
36:1:841:A:H5'	55:M9:125:LYS:O	2.12	0.50
36:1:943:U:H3'	64:N8:13:GLY:HA2	1.93	0.50
36:1:1591:G:O2'	36:1:1799:A:N1	2.35	0.50
72:O6:26:ILE:C	72:O6:28:TYR:H	2.18	0.50
1:6:1153:G:OP1	28:d6:85:ARG:NH1	2.45	0.50
1:6:1227:A:H4'	1:6:1228:G:H5'	1.92	0.50
1:6:1459:C:H2'	20:c8:138:THR:HB	1.94	0.50
4:s2:88:LYS:HG2	4:s2:89:GLN:H	1.76	0.50
8:s6:14:LYS:HD2	8:s6:123:GLY:HA3	1.93	0.50
24:d2:3:ARG:NH1	24:d2:9:ASP:OD2	2.43	0.50
24:d2:106:THR:HG21	24:d2:121:VAL:HG23	1.94	0.50
36:5:1727:G:OP1	79:q3:44:LYS:NZ	2.33	0.50
36:5:2406:C:H2'	36:5:2407:C:C6	2.47	0.50
37:7:46:A:OP1	42:l5:158:ARG:HD3	2.12	0.50
37:7:62:U:O3'	42:l5:285:ARG:NH1	2.45	0.50
41:l4:334:PHE:HA	41:l4:339:LEU:HD11	1.93	0.50
50:m4:123:LEU:HD13	52:m6:193:GLN:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:n8:132:LYS:O	64:n8:136:GLU:HG3	2.12	0.50
70:o4:46:ASP:OD2	70:o4:80:ARG:HD2	2.12	0.50
71:o5:13:SER:OG	71:o5:16:GLN:HB2	2.12	0.50
84:p2:16:UNK:O	84:p2:18:UNK:N	2.44	0.50
1:2:197:A:H61	10:S8:138:ASN:HD22	1.60	0.50
1:2:197:A:H61	10:S8:138:ASN:ND2	2.09	0.50
1:2:1078:C:H2'	1:2:1079:U:H6	1.77	0.50
5:S3:115:ILE:HG21	35:SM:110:TRP:HA	1.93	0.50
7:S5:172:ILE:O	7:S5:176:THR:OG1	2.24	0.50
20:C8:146:ALA:H	35:SM:68:ARG:HH21	1.59	0.50
36:1:409:A:N6	38:4:15:G:H1'	2.27	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
38:4:155:A:OP1	45:L8:185:ARG:NH2	2.44	0.50
41:L4:38:VAL:HG13	41:L4:113:VAL:HG11	1.94	0.50
46:L9:75:VAL:HA	46:L9:78:MET:HE3	1.94	0.50
46:L9:86:TYR:CE2	46:L9:151:VAL:HG22	2.47	0.50
46:L9:114:VAL:HB	46:L9:124:ARG:HB2	1.94	0.50
63:N7:10:VAL:O	63:N7:83:THR:HG22	2.12	0.50
75:O9:30:ARG:HB2	75:O9:33:ASN:HB2	1.94	0.50
75:O9:44:TRP:CZ3	75:O9:45:ARG:HG3	2.46	0.50
78:Q2:15:LYS:HA	78:Q2:18:ARG:HD2	1.93	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
4:s2:143:TYR:CD2	4:s2:147:ASN:HA	2.47	0.50
13:c1:124:THR:HB	13:c1:141:LYS:HB3	1.94	0.50
14:c2:60:VAL:HG23	14:c2:87:PRO:HG2	1.94	0.50
21:c9:21:PHE:O	21:c9:25:GLN:HB2	2.11	0.50
36:5:911:C:H42	39:l2:3:ARG:HD3	1.77	0.50
36:5:1145:G:H5'	68:o2:46:PHE:CE1	2.47	0.50
36:5:1555:U:H5'	36:5:1556:C:OP2	2.12	0.50
36:5:2818:U:H5'	36:5:2818:U:C6	2.44	0.50
41:l4:144:LYS:H	41:l4:144:LYS:HD2	1.77	0.50
41:l4:234:ASN:HB3	41:l4:237:GLN:HB2	1.94	0.50
41:l4:301:PRO:O	54:m8:39:ARG:NH1	2.40	0.50
41:l4:325:LEU:O	44:l7:41:ARG:NH2	2.41	0.50
54:m8:170:ARG:HA	54:m8:174:ARG:HD2	1.94	0.50
65:n9:46:ALA:O	65:n9:50:THR:HG23	2.12	0.50
68:o2:123:LYS:HA	68:o2:126:LEU:HD12	1.94	0.50
78:q2:12:CYS:SG	78:q2:17:CYS:HB2	2.50	0.50
1:2:320:U:H3'	1:2:321:C:C5'	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1037:C:O2	1:2:1094:G:N2	2.34	0.49
1:2:1258:U:H4'	12:C0:2:LEU:HD13	1.94	0.49
1:2:1344:A:H2'	1:2:1345:A:C8	2.47	0.49
2:S0:121:VAL:HG23	2:S0:141:ILE:HG21	1.94	0.49
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
13:C1:22:ASN:ND2	13:C1:25:VAL:HG23	2.27	0.49
36:1:145:G:OP2	45:L8:193:LYS:NZ	2.39	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
36:1:2522:G:H4'	36:1:2523:A:OP2	2.11	0.49
54:M8:96:PHE:CD2	54:M8:97:PRO:HD2	2.47	0.49
1:6:151:G:N2	1:6:163:G:N2	2.60	0.49
1:6:354:C:H5"	10:s8:16:ALA:HB2	1.94	0.49
1:6:846:G:N2	13:c1:46:LYS:HE2	2.26	0.49
20:c8:71:GLN:HA	20:c8:74:GLN:HE21	1.77	0.49
21:c9:14:PHE:CZ	21:c9:132:LEU:HD12	2.47	0.49
28:d6:90:GLU:H	28:d6:90:GLU:CD	2.19	0.49
34:sR:248:ASN:HD21	34:sR:298:GLY:HA3	1.77	0.49
36:5:238:A:O2'	36:5:239:G:OP1	2.27	0.49
36:5:1108:U:H2'	36:5:1109:U:C6	2.47	0.49
36:5:2523:A:C5	45:l8:51:LYS:HG3	2.46	0.49
39:l2:43:GLY:O	39:l2:88:ILE:N	2.40	0.49
42:l5:257:GLU:C	42:l5:258:LYS:HG2	2.36	0.49
47:m0:89:VAL:HG13	47:m0:136:PHE:CE1	2.47	0.49
55:m9:106:LEU:HD13	55:m9:138:LEU:HD11	1.93	0.49
70:o4:8:ARG:NH2	70:o4:31:ARG:HD2	2.25	0.49
74:o8:24:THR:HG23	74:o8:44:LYS:HB2	1.94	0.49
1:2:95:G:HO2'	1:2:460:A:HO2'	1.60	0.49
1:2:196:G:O6	10:S8:141:ARG:NH2	2.45	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
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
25:D3:79:ASN:HB2	25:D3:81:LYS:H	1.77	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
36:1:1135:A:H5'	65:N9:7:HIS:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
36:1:2557:A:OP1	39:L2:69:TYR:OH	2.28	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
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
54:M8:182:LYS:HE2	64:N8:55:LYS:O	2.11	0.49
70:O4:67:LYS:HA	70:O4:70:LYS:HE3	1.93	0.49
1:6:235:G:H2'	1:6:236:A:C8	2.46	0.49
1:6:879:G:H2'	1:6:880:C:C6	2.47	0.49
2:s0:66:ALA:HB1	23:d1:50:TYR:CE1	2.46	0.49
10:s8:152:ILE:H	10:s8:152:ILE:HD13	1.76	0.49
13:c1:109:VAL:HG11	13:c1:125:VAL:HG11	1.93	0.49
34:sR:84:SER:OG	34:sR:85:TRP:N	2.44	0.49
36:5:209:A:H4'	36:5:211:A:C8	2.47	0.49
36:5:1879:A:H2'	36:5:1879:A:N3	2.26	0.49
36:5:2554:A:H62	79:q3:62:LYS:HZ2	1.60	0.49
39:l2:105:GLY:HA3	39:l2:160:SER:HB3	1.92	0.49
39:l2:112:ILE:HD11	79:q3:79:VAL:HG11	1.94	0.49
47:m0:47:PRO:HB3	47:m0:171:TRP:CZ2	2.46	0.49
2:S0:150:ASP:OD1	2:S0:165:ARG:NH2	2.46	0.49
3:S1:154:SER:O	3:S1:154:SER:OG	2.21	0.49
16:C4:50:ALA:O	16:C4:52:ARG:N	2.41	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
39:L2:204:MET:CE	39:L2:209:HIS:HB2	2.41	0.49
42:L5:107:ARG:HH21	42:L5:110:LEU:HD23	1.76	0.49
43:L6:50:LYS:HE3	43:L6:72:ASN:HB2	1.93	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
1:6:1175:U:O4	20:c8:140:THR:OG1	2.30	0.49
1:6:1175:U:H2'	1:6:1176:G:C8	2.47	0.49
1:6:1394:G:OP1	34:sR:282:SER:OG	2.21	0.49
1:6:1434:U:H4'	31:d9:24:CYS:HB2	1.94	0.49
6:s4:62:LYS:HE3	6:s4:66:MET:HE3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:c0:46:LEU:HA	12:c0:49:LEU:HB2	1.94	0.49
16:c4:25:ASP:OD1	16:c4:26:THR:N	2.39	0.49
22:d0:109:GLU:HG3	22:d0:110:PRO:HD2	1.94	0.49
25:d3:97:ASP:O	25:d3:100:ASP:HB2	2.12	0.49
30:d8:25:VAL:HG21	30:d8:66:LEU:HD22	1.94	0.49
34:sR:42:LEU:HD21	34:sR:82:SER:HB3	1.93	0.49
36:5:196:G:C2	36:5:199:A:C8	3.00	0.49
36:5:595:G:H1	36:5:609:G:H5"	1.77	0.49
36:5:1080:A:P	42:l5:140:ARG:HH21	2.35	0.49
36:5:1317:A:O2'	36:5:1318:A:H3'	2.12	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
36:5:3379:C:H4'	40:l3:315:GLY:HA2	1.94	0.49
38:8:134:G:OP1	61:n5:56:ARG:HG2	2.12	0.49
41:l4:330:TYR:CZ	44:l7:49:ALA:HA	2.47	0.49
45:l8:54:GLU:HG2	45:l8:57:ARG:HH12	1.76	0.49
52:m6:90:HIS:HA	52:m6:95:GLY:HA3	1.93	0.49
1:2:855:A:C2	1:2:857:U:H1'	2.47	0.49
1:2:1252:C:O4'	33:E1:133:ALA:HB2	2.13	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
1:2:1783:C:OP2	77:Q1:1:MET:HB2	2.13	0.49
9:S7:96:ARG:HH22	9:S7:128:ASP:CG	2.21	0.49
9:S7:131:PHE:O	9:S7:133:THR:N	2.45	0.49
14:C2:29:LYS:HE2	14:C2:100:TRP:NE1	2.27	0.49
21:C9:11:ALA:HB2	21:C9:63:ARG:NH2	2.27	0.49
36:1:1560:G:N1	36:1:1580:A:N1	2.59	0.49
37:3:27:A:OP2	42:L5:57:ASN:HB2	2.12	0.49
40:L3:53:MET:HE2	40:L3:77:THR:CG2	2.41	0.49
45:L8:134:TYR:CG	45:L8:190:VAL:HG21	2.47	0.49
72:O6:89:GLU:O	72:O6:93:ILE:HG12	2.11	0.49
1:6:1229:G:O6	14:c2:47:GLU:HG2	2.11	0.49
1:6:1529:C:H2'	1:6:1530:C:C6	2.47	0.49
3:s1:27:LYS:NZ	3:s1:49:ASN:OD1	2.46	0.49
14:c2:67:THR:C	14:c2:69:ALA:H	2.19	0.49
15:c3:87:ASP:HB3	15:c3:125:LEU:HD11	1.94	0.49
25:d3:51:GLY:O	25:d3:101:GLU:HA	2.12	0.49
80:e0:46:ASN:OD1	80:e0:47:VAL:N	2.45	0.49
36:5:2550:U:H6	45:l8:37:GLY:HA3	1.76	0.49
42:l5:34:LYS:HE3	42:l5:38:THR:OG1	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:l5:177:GLU:H	42:l5:177:GLU:CD	2.19	0.49
50:m4:21:VAL:HB	50:m4:63:VAL:HG22	1.94	0.49
53:m7:59:PRO:HG3	53:m7:76:PHE:CD1	2.47	0.49
56:n0:167:ARG:HG3	56:n0:168:PRO:HD2	1.93	0.49
57:n1:56:PHE:CE1	57:n1:78:LYS:HD3	2.48	0.49
62:n6:120:GLN:NE2	62:n6:126:LEU:HA	2.27	0.49
75:o9:43:ASN:HB3	75:o9:46:ARG:HG3	1.94	0.49
77:q1:4:LYS:HG2	77:q1:5:TRP:CE3	2.46	0.49
1:2:1533:C:H4'	1:2:1539:G:N1	2.27	0.49
20:C8:33:THR:C	20:C8:35:ILE:H	2.20	0.49
36:1:791:A:OP1	41:L4:108:LYS:NZ	2.46	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
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
1:6:1118:G:P	77:q1:21:ARG:HH22	2.35	0.49
1:6:1389:C:O2'	19:c7:52:GLY:HA3	2.12	0.49
1:6:1482:C:OP2	1:6:1521:G:N2	2.45	0.49
5:s3:22:ASN:O	5:s3:26:THR:OG1	2.23	0.49
20:c8:145:ARG:NH2	35:sM:68:ARG:HD3	2.27	0.49
33:e1:108:VAL:HG12	33:e1:114:VAL:HG13	1.94	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
36:5:2940:A:N7	40:l3:2:SER:N	2.60	0.49
45:l8:161:GLU:HA	45:l8:164:VAL:HG22	1.95	0.49
1:2:545:A:H2'	32:E0:31:LYS:HD2	1.94	0.49
1:2:773:C:H5"	6:S4:21:ASP:HB2	1.94	0.49
3:S1:129:THR:HA	3:S1:177:GLN:HA	1.92	0.49
13:C1:98:ASN:O	13:C1:98:ASN:ND2	2.46	0.49
36:1:290:G:H1'	51:M5:93:LYS:HD3	1.94	0.49
36:1:424:G:O2'	68:O2:23:ASP:OD2	2.29	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
36:1:3096:C:H2'	36:1:3097:C:C6	2.47	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
63:N7:6:LYS:O	63:N7:8:GLY:N	2.45	0.49
1:6:1572:G:H1'	7:s5:185:ARG:HH12	1.77	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
3:s1:48:VAL:HG13	3:s1:64:ARG:HH21	1.78	0.49
20:c8:52:VAL:HG21	20:c8:69:ILE:HD11	1.94	0.49
20:c8:88:ARG:NH1	20:c8:112:ASP:OD2	2.40	0.49
36:5:1076:C:O3'	65:n9:38:LYS:HE2	2.12	0.49
36:5:2554:A:H62	79:q3:62:LYS:NZ	2.10	0.49
36:5:2736:A:OP1	57:n1:92:ARG:NH1	2.45	0.49
46:l9:166:ARG:NH2	46:l9:168:ARG:HH12	2.11	0.49
52:m6:98:ALA:HA	52:m6:101:ARG:HH11	1.78	0.49
55:m9:35:ALA:O	55:m9:36:ASN:ND2	2.45	0.49
73:o7:76:ASN:O	73:o7:79:GLN:HG3	2.13	0.49
1:2:72:A:O2'	1:2:73:U:H5"	2.12	0.49
1:2:512:A:H5"	11:S9:163:PRO:HG3	1.95	0.49
1:2:702:G:O2'	1:2:703:G:H8	1.95	0.49
5:S3:59:LEU:HA	5:S3:66:ILE:HG12	1.95	0.49
16:C4:102:LEU:HD22	16:C4:105:LEU:HD11	1.94	0.49
17:C5:19:GLY:N	20:C8:93:THR:O	2.46	0.49
17:C5:86:VAL:O	17:C5:89:MET:HG2	2.13	0.49
20:C8:38:VAL:HG12	20:C8:42:TYR:CD2	2.47	0.49
20:C8:110:ARG:HB3	20:C8:110:ARG:NH1	2.28	0.49
30:D8:52:ASP:N	30:D8:52:ASP:OD1	2.46	0.49
36:1:381:U:H2'	36:1:382:U:C6	2.48	0.49
36:1:1117:G:OP1	65:N9:4:SER:HB2	2.12	0.49
36:1:2284:C:H3'	36:1:2285:C:C6	2.48	0.49
36:1:2723:U:OP1	57:N1:87:LYS:HD3	2.12	0.49
40:L3:260:VAL:HG11	40:L3:266:ARG:NH1	2.27	0.49
1:6:1644:C:O2'	36:5:2255:A:N1	2.33	0.49
5:s3:42:THR:OG1	5:s3:45:LYS:O	2.31	0.49
9:s7:63:PRO:O	9:s7:64:VAL:HB	2.13	0.49
9:s7:132:PRO:O	9:s7:133:THR:OG1	2.30	0.49
11:s9:109:LEU:HD22	11:s9:113:VAL:HG23	1.94	0.49
11:s9:157:ASP:OD1	11:s9:158:PHE:N	2.38	0.49
29:d7:19:HIS:HB3	29:d7:22:LYS:HD2	1.94	0.49
36:5:997:A:O2'	37:7:79:A:N3	2.41	0.49
36:5:2375:G:O2'	36:5:2377:G:OP2	2.26	0.49
39:l2:95:SER:O	39:l2:97:ASN:N	2.45	0.49
47:m0:210:ILE:HG12	47:m0:217:PHE:CE2	2.47	0.49
51:m5:186:GLY:O	51:m5:190:THR:HG23	2.12	0.49
58:n2:94:ARG:HG2	58:n2:96:VAL:HG22	1.95	0.49
60:n4:20:LEU:HD21	60:n4:28:ILE:HG23	1.94	0.49
61:n5:58:ASP:O	61:n5:62:VAL:HG23	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:n6:86:THR:HG22	62:n6:96:PRO:HA	1.95	0.49
66:o0:26:GLY:O	66:o0:30:THR:HG23	2.12	0.49
69:o3:69:GLY:HA3	69:o3:85:PHE:HA	1.94	0.49
71:o5:45:LYS:HD2	71:o5:49:LYS:HD3	1.93	0.49
1:2:352:A:H8	1:2:352:A:OP2	1.96	0.49
24:D2:29:PRO:HB2	24:D2:58:SER:HB2	1.93	0.49
24:D2:111:MET:HE3	24:D2:116:ALA:HA	1.94	0.49
33:E1:107:LYS:HB2	33:E1:117:LEU:HD11	1.93	0.49
34:SR:228:LYS:O	34:SR:229:LYS:NZ	2.29	0.49
34:SR:299:GLN:NE2	34:SR:315:VAL:O	2.46	0.49
36:1:209:A:OP1	41:L4:161:LYS:NZ	2.46	0.49
36:1:818:C:H2'	36:1:819:U:O4'	2.13	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
38:4:64:U:OP1	71:O5:49:LYS:NZ	2.46	0.49
40:L3:215:ILE:HD12	40:L3:338:LEU:HB3	1.94	0.49
41:L4:44:LYS:HB3	41:L4:47:ARG:NH1	2.26	0.49
41:L4:269:SER:C	41:L4:271:LYS:H	2.19	0.49
42:L5:40:HIS:CD2	42:L5:42:ALA:HB3	2.48	0.49
42:L5:107:ARG:NH2	42:L5:110:LEU:HD23	2.27	0.49
44:L7:54:GLU:OE2	44:L7:186:HIS:NE2	2.36	0.49
56:N0:45:LEU:HD12	56:N0:51:VAL:HG21	1.95	0.49
61:N5:105:VAL:HG13	61:N5:130:TYR:CD2	2.48	0.49
1:6:751:G:H2'	1:6:752:A:C8	2.48	0.49
2:s0:48:ILE:HD13	2:s0:161:PRO:HB2	1.94	0.49
2:s0:76:ILE:HG12	2:s0:98:ILE:HB	1.93	0.49
28:d6:44:ILE:HD13	28:d6:65:PRO:HG2	1.94	0.49
36:5:2437:G:H2'	36:5:2438:A:O4'	2.13	0.49
38:8:84:C:H1'	62:n6:113:LYS:HB2	1.95	0.49
40:l3:290:ASP:OD2	40:l3:292:ALA:N	2.34	0.49
45:l8:41:GLN:HG3	45:l8:44:ARG:HH22	1.77	0.49
54:m8:62:VAL:HG11	54:m8:83:VAL:HG21	1.95	0.49
59:n3:87:ARG:HH22	59:n3:137:VAL:HG22	1.77	0.49
85:D:75:C:P	87:D:3401:SPS:HN4	2.36	0.49
1:2:686:C:H2'	1:2:687:G:C8	2.48	0.49
1:2:1290:U:OP1	4:S2:95:ARG:NH1	2.45	0.49
1:2:1345:A:H2'	1:2:1348:A:N6	2.27	0.49
34:SR:231:MET:HE2	34:SR:232:TYR:CE2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:655:C:H2'	36:1:656:A:H8	1.78	0.49
36:1:1245:A:N6	36:1:1272:C:O2'	2.46	0.49
55:M9:60:LYS:HE3	55:M9:64:ARG:NH2	2.28	0.49
70:O4:99:LYS:O	70:O4:103:LYS:HG2	2.13	0.49
2:s0:52:LYS:HE2	23:d1:82:VAL:HA	1.94	0.49
5:s3:64:ARG:NH1	5:s3:68:GLU:OE2	2.46	0.49
5:s3:179:GLN:OE1	5:s3:180:GLY:N	2.46	0.49
5:s3:209:ILE:HG22	19:c7:38:ILE:O	2.13	0.49
15:c3:15:ALA:HB2	29:d7:20:LYS:HG3	1.94	0.49
36:5:1232:C:O2'	82:p0:36:GLN:OE1	2.22	0.49
36:5:1240:A:N6	36:5:1241:U:O4	2.46	0.49
36:5:1483:G:C8	36:5:1485:G:C8	3.01	0.49
36:5:1841:A:N3	75:o9:45:ARG:NH2	2.61	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
24:D2:85:ASP:HA	24:D2:88:LYS:HG3	1.94	0.49
36:1:364:G:OP1	41:L4:60:THR:HG23	2.13	0.49
36:1:412:G:H1'	53:M7:120:ASN:HB3	1.94	0.49
36:1:805:G:H1'	41:L4:73:ARG:NH1	2.27	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
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
79:Q3:59:CYS:O	79:Q3:61:LYS:N	2.39	0.49
1:6:385:A:H2'	1:6:386:G:C8	2.48	0.49
1:6:758:U:OP1	11:s9:7:THR:HG21	2.12	0.49
1:6:1102:G:OP2	25:d3:7:ARG:HD2	2.13	0.49
1:6:1241:G:H5'	17:c5:102:PHE:CZ	2.48	0.49
4:s2:152:HIS:CD2	4:s2:152:HIS:H	2.31	0.49
4:s2:179:VAL:O	4:s2:198:THR:OG1	2.21	0.49
6:s4:252:ARG:NH2	6:s4:252:ARG:HB3	2.28	0.49
7:s5:93:LEU:HD23	7:s5:172:ILE:HG23	1.94	0.49
28:d6:88:SER:O	28:d6:92:ARG:HG3	2.12	0.49
36:5:73:C:C2	49:m3:59:ARG:HD3	2.47	0.49
36:5:129:U:H2'	36:5:130:A:C8	2.48	0.49
36:5:874:U:P	40:l3:241:LYS:HE3	2.53	0.49
36:5:1654:A:O2'	70:o4:59:PRO:HD3	2.12	0.49
36:5:2339:C:OP2	59:n3:48:ARG:HG2	2.13	0.49
36:5:2812:C:H2'	36:5:2813:A:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:o1:44:MET:HB3	67:o1:77:ARG:CZ	2.43	0.49
1:2:56:U:H4'	1:2:57:G:H5'	1.95	0.48
1:2:114:C:H5'	1:2:114:C:H6	1.78	0.48
3:S1:61:LEU:O	3:S1:63:GLY:N	2.46	0.48
5:S3:92:GLN:CD	5:S3:92:GLN:H	2.20	0.48
5:S3:215:GLU:N	5:S3:215:GLU:OE2	2.46	0.48
7:S5:161:ASP:O	30:D8:44:VAL:HA	2.13	0.48
36:1:543:C:H42	36:1:548:G:H1	1.61	0.48
36:1:784:A:C6	54:M8:93:ILE:HG22	2.48	0.48
36:1:2108:C:H1'	36:1:3344:A:C8	2.48	0.48
43:L6:50:LYS:HG2	43:L6:74:VAL:HG21	1.95	0.48
45:L8:27:THR:O	45:L8:28:HIS:ND1	2.45	0.48
66:O0:98:SER:OG	66:O0:99:ASP:N	2.46	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
1:6:1681:A:H8	8:s6:65:GLN:HG3	1.77	0.48
2:s0:84:ARG:HD3	2:s0:203:PHE:O	2.12	0.48
3:s1:146:GLN:O	3:s1:148:ASN:N	2.45	0.48
4:s2:169:LEU:HD23	4:s2:198:THR:HG22	1.94	0.48
26:d4:122:GLY:HA2	26:d4:125:LEU:HB2	1.94	0.48
40:l3:46:PHE:CD2	40:l3:205:VAL:HG13	2.47	0.48
43:l6:60:ASP:O	43:l6:61:ASN:HB2	2.13	0.48
45:l8:54:GLU:O	45:l8:58:VAL:HG23	2.13	0.48
46:l9:43:VAL:HG11	46:l9:55:VAL:HG12	1.95	0.48
46:l9:83:THR:OG1	46:l9:84:LYS:N	2.45	0.48
53:m7:108:ASP:N	53:m7:152:GLU:OE2	2.41	0.48
58:n2:33:TYR:CE1	58:n2:80:THR:HG23	2.47	0.48
62:n6:120:GLN:OE1	62:n6:126:LEU:HG	2.13	0.48
1:2:936:G:N7	28:D6:15:ARG:NH1	2.61	0.48
5:S3:137:VAL:HG22	5:S3:151:LYS:HG3	1.96	0.48
33:E1:144:CYS:HB3	33:E1:147:VAL:HG13	1.94	0.48
34:SR:289:ALA:HA	34:SR:305:TYR:HA	1.95	0.48
36:1:92:G:H5'	36:1:93:C:O5'	2.14	0.48
36:1:385:A:H2'	36:1:386:A:H8	1.77	0.48
36:1:1610:G:P	61:N5:125:ARG:HH12	2.36	0.48
39:L2:5:ILE:HG22	39:L2:208:ASP:O	2.13	0.48
39:L2:13:GLY:O	39:L2:16:PHE:N	2.37	0.48
39:L2:114:SER:HB2	39:L2:169:ILE:HD12	1.95	0.48
48:M1:139:THR:HG22	48:M1:147:THR:HA	1.96	0.48
64:N8:94:ALA:HB1	64:N8:122:PRO:HD2	1.94	0.48
1:6:4:C:O2'	11:s9:17:ARG:NH1	2.46	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
1:6:1207:C:H42	1:6:1456:C:H5	1.60	0.48
1:6:1553:G:O6	17:c5:43:ARG:NH1	2.46	0.48
4:s2:106:ASP:OD1	4:s2:108:ASN:N	2.38	0.48
7:s5:41:LYS:HD2	18:c6:54:LEU:HD21	1.93	0.48
7:s5:118:LEU:HD22	7:s5:129:PRO:HB2	1.95	0.48
11:s9:53:ARG:O	11:s9:57:ARG:HB2	2.13	0.48
11:s9:118:LEU:HD23	11:s9:158:PHE:CE1	2.48	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
36:5:438:A:H4'	36:5:439:C:OP2	2.14	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
36:5:2344: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
39:l2:114:SER:CB	39:l2:169:ILE:HD12	2.42	0.48
41:l4:60:THR:HG21	41:l4:77:VAL:HG22	1.94	0.48
42:l5:88:ILE:HD13	42:l5:239:ILE:HG22	1.95	0.48
46:l9:8:GLN:HG2	46:l9:68:LEU:HD13	1.95	0.48
59:n3:11:PHE:CG	59:n3:88:ARG:HD2	2.48	0.48
1:2:1073:G:H4'	15:C3:10:GLY:HA2	1.94	0.48
1:2:1566:U:H5"	20:C8:39:GLY:H	1.78	0.48
1:2:1788:G:P	16:C4:127:ARG:HH12	2.35	0.48
1:2:1793:G:N2	28:D6:76:SER:OG	2.42	0.48
2:S0:189:VAL:HG22	2:S0:190:ASP:H	1.77	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
33:E1:121:CYS:HB2	33:E1:132:LEU:HD21	1.95	0.48
36:1:428:A:H2'	36:1:429:U:C6	2.48	0.48
36:1:718:G:OP1	64:N8:117:ARG:NH2	2.45	0.48
36:1:1658:G:H2'	36:1:1659:U:C6	2.49	0.48
36:1:2646:C:H5"	47:M0:119:TRP:CG	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
54:M8:40:THR:C	54:M8:42:ALA:H	2.21	0.48
73:O7:5:THR:HA	73:O7:8:PHE:CD2	2.48	0.48
1:6:250:C:H2'	1:6:251:A:H8	1.77	0.48
1:6:856:A:N6	9:s7:115:SER:O	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s0:139:VAL:HG13	2:s0:141:ILE:HG13	1.94	0.48
2:s0:163:ASN:O	2:s0:165:ARG:N	2.46	0.48
3:s1:48:VAL:HG22	3:s1:61:LEU:HD13	1.94	0.48
3:s1:103:MET:HE2	3:s1:215:VAL:HG12	1.95	0.48
12:c0:24:LYS:O	12:c0:26:ASP:N	2.47	0.48
24:d2:18:GLU:HG2	24:d2:65:LEU:HG	1.94	0.48
26:d4:27:VAL:HG21	26:d4:40:LEU:HD21	1.95	0.48
80:e0:13:LYS:HE3	80:e0:17:GLN:HE22	1.78	0.48
36:5:252:U:H4'	36:5:253:A:H5"	1.93	0.48
36:5:1098:A:O2'	57:n1:130:ARG:O	2.22	0.48
36:5:1258:U:O2	36:5:1260:A:H8	1.96	0.48
36:5:1488:G:O2'	70:o4:10:ARG:O	2.30	0.48
36:5:2440:G:H2'	36:5:2441:A:C8	2.49	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
37:7:68:C:OP1	42:l5:14:SER:OG	2.32	0.48
39:l2:219:ILE:HD13	39:l2:223:SER:HB3	1.95	0.48
40:l3:151:ILE:O	40:l3:155:ALA:HB3	2.13	0.48
46:l9:171:ASP:OD2	46:l9:173:ARG:NH1	2.46	0.48
49:m3:60:ALA:HB2	49:m3:70:ARG:HE	1.79	0.48
57:n1:48:ILE:HB	57:n1:95:HIS:CE1	2.49	0.48
62:n6:103:LYS:HD3	62:n6:103:LYS:HA	1.62	0.48
63:n7:102:GLU:H	63:n7:107:ARG:NH2	2.03	0.48
8:S6:186:ARG:O	8:S6:190:GLN:HG2	2.13	0.48
9:S7:139:ARG:HD3	24:D2:53:ILE:HA	1.95	0.48
19:C7:96:SER:HA	19:C7:97:ASN:HA	1.60	0.48
25:D3:92:CYS:HG	25:D3:136:TRP:CD1	2.31	0.48
34:SR:255:ALA:HB2	34:SR:292:LEU:HD22	1.95	0.48
36:1:898:U:H2'	36:1:899:U:O4'	2.13	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
36:1:1821:U:C4	70:O4:67:LYS:HD2	2.49	0.48
36:1:3194:C:H2'	36:1:3195:U:H2'	1.95	0.48
39:L2:192:LYS:HB3	39:L2:193:ARG:CZ	2.44	0.48
43:L6:72:ASN:HB3	43:L6:160:SER:HA	1.96	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
66:O0:13:LYS:HB3	66:O0:100:ILE:HG23	1.95	0.48
74:O8:45:VAL:HG23	74:O8:52:TYR:HB2	1.96	0.48
1:6:37:U:O2'	1:6:770:A:N1	2.36	0.48
1:6:701:U:H2'	1:6:702:G:H8	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:s1:180:THR:OG1	3:s1:181:LEU:N	2.44	0.48
8:s6:120:GLU:HG3	8:s6:125:THR:HB	1.96	0.48
9:s7:67:LEU:HG	9:s7:94:ALA:HB2	1.95	0.48
11:s9:150:LEU:C	11:s9:152:SER:H	2.21	0.48
17:c5:107:ILE:HA	17:c5:111:MET:SD	2.53	0.48
18:c6:6:SER:HA	18:c6:23:LYS:HA	1.96	0.48
36:5:116:A:OP1	72:o6:36:ARG:NH1	2.47	0.48
36:5:887:G:H2'	36:5:888:A:C8	2.48	0.48
39:l2:83:HIS:CE1	39:l2:86:GLN:HB2	2.48	0.48
46:l9:112:ILE:HB	46:l9:126:VAL:HB	1.96	0.48
57:n1:135:PRO:O	57:n1:136:ARG:HB2	2.14	0.48
1:2:778:G:H22	26:D4:10:ARG:HH12	1.62	0.48
1:2:1201:G:N2	1:2:1600:A:H5"	2.28	0.48
2:S0:117:GLU:O	4:S2:40:LYS:NZ	2.45	0.48
9:S7:12:ALA:HB3	9:S7:13:PRO:HD3	1.95	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
36:1:40:A:H5"	64:N8:35:ALA:HB1	1.94	0.48
36:1:838:G:O6	79:Q3:4:ARG:NH2	2.47	0.48
36:1:1348:U:H4'	36:1:1348:U:OP1	2.13	0.48
36:1:3353:G:O2'	36:1:3356:G:OP2	2.29	0.48
39:L2:225:ILE:HG21	39:L2:234:LYS:HA	1.94	0.48
1:6:138:A:H62	1:6:266:A:H61	1.61	0.48
1:6:891:A:H2'	1:6:892:A:C8	2.49	0.48
1:6:1559:A:H5"	20:c8:135:GLY:HA3	1.94	0.48
7:s5:157:ARG:HE	7:s5:157:ARG:N	2.11	0.48
9:s7:62:VAL:HG12	9:s7:64:VAL:H	1.78	0.48
16:c4:107:ARG:NH2	28:d6:52:ASP:OD1	2.34	0.48
25:d3:103:LEU:HB2	25:d3:126:LYS:HB2	1.95	0.48
36:5:3192:U:H2'	36:5:3193:C:C6	2.48	0.48
38:8:84:C:N3	62:n6:116:LYS:NZ	2.52	0.48
40:l3:209:PHE:HE1	40:l3:340:LYS:HB3	1.79	0.48
41:l4:138:ARG:HH21	41:l4:240:PRO:HB2	1.79	0.48
41:l4:170:LYS:HE3	41:l4:175:HIS:ND1	2.28	0.48
50:m4:72:LEU:HD23	50:m4:73:PRO:HD2	1.94	0.48
51:m5:143:ARG:HH21	71:o5:92:LEU:HA	1.79	0.48
53:m7:25:SER:HB3	53:m7:28:ASN:HB2	1.94	0.48
61:n5:105:VAL:HG13	61:n5:130:TYR:CD2	2.47	0.48
68:o2:97:ALA:HB3	68:o2:100:ILE:HG12	1.95	0.48
1:2:12:U:H2'	1:2:13:C:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:340:U:H2'	1:2:341:A:H8	1.78	0.48
1:2:932:U:OP2	3:S1:155:TYR:OH	2.27	0.48
1:2:1000:C:N4	1:2:1003:A:OP2	2.46	0.48
5:S3:70:THR:HG22	5:S3:86:LEU:HB2	1.96	0.48
33:E1:135:HIS:HB2	33:E1:138:ARG:HB2	1.94	0.48
36:1:437:G:H22	36:1:622:A:H61	1.61	0.48
36:1:654:C:OP1	68:O2:27:ARG:NH2	2.46	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
37:3:19:C:H2'	37:3:20:A:H8	1.78	0.48
40:L3:77:THR:HG23	40:L3:326:GLY:O	2.13	0.48
40:L3:188:ILE:O	40:L3:192:VAL:HG12	2.14	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
61:N5:25:LYS:H	61:N5:25:LYS:HD2	1.79	0.48
70:O4:41:ARG:HA	70:O4:56:THR:HB	1.96	0.48
74:O8:26:LYS:O	74:O8:41:THR:HA	2.14	0.48
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
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
3:s1:23:PRO:HB3	3:s1:26:ARG:NH1	2.28	0.48
4:s2:69:ILE:HD13	4:s2:136:VAL:HG21	1.95	0.48
5:s3:64:ARG:O	5:s3:66:ILE:N	2.46	0.48
13:c1:122:ILE:HB	13:c1:143:SER:HB2	1.94	0.48
36:5:107:A:O2'	36:5:324:A:N3	2.38	0.48
36:5:929:A:H5"	41:l4:61:SER:HB3	1.95	0.48
36:5:1277:C:H2'	36:5:1278:A:C8	2.48	0.48
36:5:2383:C:H5'	52:m6:71:PHE:CE2	2.47	0.48
45:l8:206:GLU:HG2	45:l8:207:ASP:N	2.26	0.48
52:m6:22:VAL:HG11	52:m6:120:VAL:HG11	1.95	0.48
52:m6:24:ALA:HB2	52:m6:84:LEU:HG	1.95	0.48
59:n3:87:ARG:HH12	59:n3:137:VAL:HG11	1.79	0.48
64:n8:28:HIS:ND1	64:n8:32:ARG:HG2	2.29	0.48
66:o0:57:GLU:OE1	66:o0:69:TYR:OH	2.19	0.48
70:o4:81:CYS:SG	70:o4:84:CYS:SG	3.11	0.48
71:o5:47:VAL:O	71:o5:51:ILE:HG13	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:q3:49:ARG:HB2	79:q3:55:TRP:CZ3	2.49	0.48
1:2:576:G:OP1	35:SM:104:LYS:NZ	2.47	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
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
6:S4:42:LEU:N	6:S4:84:ALA:O	2.38	0.48
11:S9:59:LEU:HD22	11:S9:69:ARG:HA	1.95	0.48
14:C2:29:LYS:HE2	14:C2:100:TRP:CD1	2.48	0.48
34:SR:222:LEU:O	34:SR:231:MET:HB2	2.14	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
36:1:912:G:OP2	39:L2:9:ARG:NH1	2.46	0.48
36:1:2993:G:H2'	36:1:3142:A:N6	2.28	0.48
49:M3:89:TYR:O	49:M3:92:THR:OG1	2.29	0.48
54:M8:93:ILE:HG13	54:M8:113:LYS:HE2	1.95	0.48
59:N3:17:LEU:HD21	59:N3:98:ASN:ND2	2.29	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	1.94	0.48
7:s5:81:ARG:NH2	30:d8:47:PRO:HB3	2.27	0.48
7:s5:203:LYS:O	7:s5:205:SER:N	2.46	0.48
9:s7:9:LEU:HG	9:s7:10:SER:H	1.78	0.48
17:c5:127:ARG:O	17:c5:130:ARG:NH1	2.46	0.48
18:c6:127:LYS:HE2	18:c6:132:LYS:O	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
36:5:1294:A:O2'	36:5:1295:G:H5"	2.14	0.48
41:l4:283:THR:HG21	41:l4:288:ARG:HH22	1.78	0.48
51:m5:143:ARG:NH2	71:o5:92:LEU:HD23	2.27	0.48
51:m5:183:THR:HB	51:m5:187:ARG:HB2	1.95	0.48
57:n1:17:ARG:HH12	57:n1:45:ASN:ND2	2.11	0.48
57:n1:17:ARG:HH12	57:n1:45:ASN:CG	2.21	0.48
66:o0:23:TYR:HA	66:o0:93:LEU:HD12	1.95	0.48
1:2:17:C:O2'	1:2:1137:A:N1	2.40	0.48
2:S0:118:PRO:HG2	2:S0:141:ILE:HD13	1.95	0.48
6:S4:163:ASP:O	6:S4:165:ALA:N	2.45	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
35:SM:26:VAL:HG11	48:M1:49:LYS:HE3	1.96	0.48
36:1:608:A:O3'	41:L4:326:ARG:NH1	2.47	0.48
36:1:1246:G:H8	36:1:1246:G:OP1	1.97	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
43:L6:38:THR:HA	43:L6:90:LYS:HG3	1.95	0.48
55:M9:104:ARG:HH21	55:M9:108:LYS:NZ	2.12	0.48
1:6:399:A:C4'	6:s4:3:ARG:HG2	2.43	0.48
1:6:775:G:N7	26:d4:11:LYS:NZ	2.55	0.48
1:6:856:A:N7	9:s7:97:ARG:HB2	2.29	0.48
1:6:907:A:N3	1:6:997:G:O2'	2.40	0.48
1:6:1067:C:H2'	1:6:1068:C:C6	2.47	0.48
8:s6:189:HIS:HE1	8:s6:193:LEU:HD12	1.79	0.48
10:s8:184:LEU:HB3	10:s8:189:LEU:HB2	1.94	0.48
17:c5:10:ARG:HD3	48:m1:88:GLU:OE1	2.13	0.48
20:c8:41:ARG:CZ	21:c9:46:PRO:HG3	2.44	0.48
20:c8:121:ALA:O	20:c8:125:ILE:HG13	2.14	0.48
36:5:386:A:H8	36:5:386:A:O5'	1.97	0.48
36:5:1721:U:OP2	55:m9:124:TYR:OH	2.27	0.48
36:5:2947:G:C2	40:l3:250:ALA:HB1	2.49	0.48
46:l9:87:LYS:HZ2	46:l9:191:LEU:HD11	1.78	0.48
51:m5:94:TYR:CE2	51:m5:96:ARG:HB2	2.49	0.48
63:n7:51:LEU:HB2	63:n7:65:ARG:HD2	1.96	0.48
1:2:642:G:H2'	1:2:643:G:H8	1.79	0.48
11:S9:149:ARG:O	11:S9:151:ASP:N	2.46	0.48
27:D5:50:ILE:O	27:D5:54:VAL:HG23	2.12	0.48
28:D6:37:LYS:C	28:D6:38:ARG:HD2	2.38	0.48
28:D6:84:VAL:HG13	28:D6:85:ARG:H	1.78	0.48
34:SR:211:ILE:HD11	34:SR:225:LEU:HD13	1.95	0.48
36:1:612:U:OP1	43:L6:21:THR:HB	2.13	0.48
40:L3:19:ARG:HB3	40:L3:232:ARG:NH1	2.28	0.48
41:L4:63:GLU:C	41:L4:75:PRO:HA	2.39	0.48
42:L5:110:LEU:HD13	42:L5:171:LEU:HD23	1.96	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
78:Q2:57:VAL:HG12	78:Q2:59:HIS:CE1	2.49	0.48
1:6:476:U:O4	11:s9:37:LYS:HE3	2.13	0.48
1:6:584:C:H1'	80:e0:18:THR:HG21	1.95	0.48
1:6:964:U:H5"	15:c3:128:TYR:CE1	2.47	0.48
1:6:1237:G:H2'	1:6:1238:A:C8	2.48	0.48
80:e0:29:LYS:HG2	80:e0:35:TYR:HE2	1.79	0.48
36:5:528:U:H2'	36:5:529:A:C8	2.49	0.48
36:5:618:C:O2'	36:5:621:A:N3	2.37	0.48
36:5:655:C:OP1	68:o2:27:ARG:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:689:U:O4	41:l4:209:TYR:OH	2.27	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
40:l3:106:TRP:CH2	40:l3:161:LEU:HD13	2.48	0.48
41:l4:205:PRO:HB3	41:l4:247:PHE:CD2	2.49	0.48
57:n1:12:ARG:HD3	57:n1:13:TYR:CZ	2.49	0.48
66:o0:66:LYS:H	66:o0:66:LYS:HD2	1.76	0.48
73:o7:17:THR:HG22	73:o7:18:LEU:H	1.79	0.48
1:2:1049:U:H2'	1:2:1050:G:C8	2.49	0.48
11:S9:143:ILE:HG22	11:S9:145:SER:H	1.79	0.48
20:C8:84:TRP:HA	20:C8:89:GLN:NE2	2.28	0.48
36:1:993:G:N3	36:1:2637:A:H2'	2.29	0.48
36:1:1460:A:H2'	36:1:1461:A:H8	1.79	0.48
36:1:2548:C:OP2	39:L2:93:LYS:NZ	2.47	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
38:4:155:A:H5'	45:L8:185:ARG:CZ	2.44	0.48
39:L2:28:LYS:HB3	39:L2:123:ARG:HB3	1.96	0.48
44:L7:239:LEU:O	44:L7:242:SER:OG	2.27	0.48
53:M7:29:THR:HA	53:M7:32:THR:CG2	2.44	0.48
54:M8:64:VAL:HG22	54:M8:96:PHE:CE2	2.49	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
1:6:1382:A:O2'	1:6:1383:G:H5"	2.14	0.48
6:s4:71:LYS:O	6:s4:90:ILE:HA	2.14	0.48
6:s4:93:ASP:O	6:s4:95:THR:N	2.47	0.48
8:s6:186:ARG:O	8:s6:190:GLN:HG2	2.14	0.48
10:s8:110:ARG:NH2	10:s8:160:PHE:HB3	2.28	0.48
17:c5:51:SER:C	17:c5:53:PRO:HD2	2.39	0.48
19:c7:104:ASN:C	19:c7:106:THR:H	2.22	0.48
24:d2:77:PRO:HD2	24:d2:79:PHE:CE2	2.49	0.48
34:sR:167:VAL:HG23	34:sR:183:LEU:HB2	1.95	0.48
36:5:289:A:C2	51:m5:93:LYS:HG3	2.48	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
42:l5:129:TYR:CG	42:l5:177:GLU:HG3	2.49	0.48
43:l6:108:LYS:HE2	43:l6:108:LYS:HB3	1.74	0.48
48:m1:92:ARG:NH2	48:m1:94:ARG:HH11	2.11	0.48
54:m8:176:ARG:NH1	64:n8:46:ASP:OD2	2.47	0.48
57:n1:131:GLN:HG3	57:n1:132:PRO:HD2	1.96	0.48
62:n6:54:ASP:HB2	62:n6:70:ILE:HD13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:q2:71:ARG:HH21	78:q2:80:ARG:CZ	2.26	0.48
78:q2:77:CYS:O	78:q2:78:LYS:HD3	2.14	0.48
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
1:2:1681:A:H1'	8:S6:66:GLY:HA2	1.96	0.47
5:S3:105:MET:HG2	5:S3:122:VAL:HG21	1.95	0.47
34:SR:67:ILE:C	34:SR:84:SER:HG	2.20	0.47
36:1:709:A:P	54:M8:179:ARG:HH22	2.37	0.47
36:1:2407:C:H2'	36:1:2408:U:C6	2.49	0.47
36:1:3039:C:OP1	59:N3:88:ARG:NH2	2.47	0.47
36:1:3121:U:H1'	36:1:3122:A:H5"	1.95	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
40:L3:257:PRO:HG2	40:L3:261:MET:CE	2.43	0.47
41:L4:23:PRO:HD2	41:L4:26:PHE:HD2	1.78	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
68:O2:40:SER:O	68:O2:44:ARG:HG3	2.14	0.47
69:O3:52:VAL:HG22	69:O3:66:VAL:HG22	1.95	0.47
78:Q2:52:GLY:O	78:Q2:54:THR:HG23	2.14	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	2.42	0.47
36:5:627:U:H4'	36:5:1399:A:O2'	2.13	0.47
36:5:999:G:C6	36:5:1000:C:N4	2.82	0.47
36:5:1329:U:O2'	36:5:1330:A:H5"	2.14	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
41:l4:144:LYS:H	41:l4:144:LYS:CD	2.27	0.47
41:l4:304:GLN:O	41:l4:306:THR:N	2.47	0.47
70:o4:96:GLU:O	70:o4:99:LYS:HB2	2.14	0.47
1:2:730:G:H21	1:2:731:C:H5"	1.79	0.47
1:2:868:G:OP1	15:C3:121:ARG:NH1	2.47	0.47
3:S1:76:SER:OG	3:S1:78:ASP:OD1	2.28	0.47
4:S2:245:ASP:OD1	4:S2:245:ASP:N	2.46	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
36:1:175:C:H2'	36:1:176:G:O4'	2.14	0.47
38:4:58:G:O6	73:O7:63:ARG:NH2	2.42	0.47
40:L3:106:TRP:HB2	40:L3:133:TYR:CE2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:L3:114:VAL:HG22	40:L3:163:HIS:CE1	2.49	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
45:L8:140:VAL:HG21	51:M5:3:ALA:HB2	1.96	0.47
50:M4:36:VAL:HG11	50:M4:55:ARG:NH2	2.28	0.47
1:6:1060:U:H4'	1:6:1061:A:H5"	1.95	0.47
4:s2:106:ASP:OD1	4:s2:107:SER:N	2.47	0.47
10:s8:40:ALA:O	10:s8:59:ARG:HB3	2.14	0.47
11:s9:124:HIS:CE1	11:s9:128:LEU:HD11	2.50	0.47
18:c6:15:SER:O	18:c6:72:GLY:N	2.47	0.47
26:d4:80:ALA:HA	26:d4:83:LYS:HB2	1.95	0.47
36:5:1011:A:H2'	36:5:1012:G:C8	2.49	0.47
36:5:1419:A:H5"	41:l4:193:LYS:NZ	2.29	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
38:8:104:A:C8	38:8:105:A:C8	3.02	0.47
39:l2:97:ASN:HB2	39:l2:100:ASN:ND2	2.29	0.47
52:m6:177:LYS:O	52:m6:181:ALA:N	2.47	0.47
1:2:912:U:H4'	1:2:913:G:H2'	1.95	0.47
20:C8:29:VAL:O	20:C8:43:SER:OG	2.31	0.47
22:D0:72:ASN:N	22:D0:72:ASN:OD1	2.48	0.47
34:SR:211:ILE:HG13	34:SR:225:LEU:HB2	1.96	0.47
36:1:929:A:H2'	36:1:930:U:C6	2.49	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
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
47:M0:169:LYS:HZ2	57:N1:159:PHE:H	1.61	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
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
1:6:593:U:O4	80:e0:36:LYS:NZ	2.47	0.47
1:6:1142:A:H5"	28:d6:2:PRO:HB3	1.95	0.47
1:6:1196:A:H1'	1:6:1602:C:O2'	2.14	0.47
3:s1:194:ASN:OD1	3:s1:194:ASN:N	2.47	0.47
27:d5:54:VAL:HA	27:d5:57:TYR:CE1	2.49	0.47
34:sR:203:THR:OG1	34:sR:204:ALA:N	2.47	0.47
35:sM:50:ASN:OD1	35:sM:50:ASN:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:sM:57:ASN:O	35:sM:61:ILE:HG22	2.15	0.47
36:5:2106:A:H2'	36:5:2107:A:H8	1.79	0.47
36:5:2828:G:O2'	47:m0:4:ARG:NH1	2.42	0.47
48:m1:117:ASP:OD2	48:m1:119:SER:HB3	2.15	0.47
52:m6:187:GLU:HG2	52:m6:192:LYS:HE3	1.97	0.47
61:n5:86:VAL:HG21	61:n5:95:ILE:HG12	1.96	0.47
68:o2:105:ARG:O	68:o2:109:LEU:HB2	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
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
24:D2:111:MET:HE1	24:D2:121:VAL:HG23	1.95	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
36:1:309:U:OP1	72:O6:84:LYS:NZ	2.42	0.47
36:1:1472:U:H2'	36:1:1473:G:H8	1.80	0.47
36:1:1795:U:H2'	39:L2:50:HIS:ND1	2.29	0.47
36:1:3028:G:H2'	36:1:3029:A:O4'	2.14	0.47
39:L2:83:HIS:NE2	39:L2:86:GLN:HB2	2.30	0.47
41:L4:293:SER:O	41:L4:297:SER:OG	2.24	0.47
41:L4:338:LYS:C	41:L4:340:GLY:H	2.23	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
59:N3:38:ALA:HB3	59:N3:59:MET:HB2	1.96	0.47
61:N5:58:ASP:O	61:N5:62:VAL:HG23	2.14	0.47
67:O1:79:ARG:H	67:O1:79:ARG:NE	2.12	0.47
74:O8:62:ALA:O	74:O8:66:ILE:HG13	2.14	0.47
1:6:524:U:O2'	1:6:526:A:N7	2.43	0.47
1:6:753:A:H62	6:s4:187:ARG:HH22	1.61	0.47
1:6:1383:G:O2'	22:d0:35:GLU:OE2	2.27	0.47
1:6:1619:C:H2'	1:6:1620:C:H6	1.79	0.47
6:s4:44:LEU:HG	6:s4:82:TYR:HB3	1.97	0.47
18:c6:36:ILE:HD11	18:c6:48:VAL:HG22	1.95	0.47
18:c6:45:ARG:O	18:c6:48:VAL:HG12	2.14	0.47
36:5:316:U:O4	72:o6:28:TYR:HA	2.15	0.47
36:5:668:G:H2'	36:5:669:U:O4'	2.15	0.47
36:5:1816:A:O2'	36:5:1817:G:OP1	2.26	0.47
46:l9:99:ILE:HG21	46:l9:179:ILE:HD11	1.97	0.47
59:n3:28:ASN:ND2	59:n3:112:SER:H	2.09	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:n7:95:VAL:HG21	63:n7:113:VAL:HG11	1.95	0.47
63:n7:110:ALA:O	63:n7:114:VAL:HG23	2.15	0.47
73:o7:24:ARG:O	73:o7:26:SER:N	2.48	0.47
74:o8:8:ILE:HD12	74:o8:8:ILE:H	1.78	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
1:2:1789:G:OP2	16:C4:132:ARG:NH2	2.47	0.47
3:S1:40:ASN:ND2	3:S1:42:ASN:O	2.46	0.47
5:S3:124:ARG:HD3	35:SM:124:GLN:HA	1.96	0.47
17:C5:30:THR:O	17:C5:34:VAL:HG13	2.15	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
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:M1:96:PHE:CD1	48:M1:102:PHE:HB3	2.50	0.47
56:N0:90:MET:HE1	56:N0:114:HIS:CD2	2.49	0.47
67:O1:80:ASN:OD1	67:O1:81:GLU:N	2.48	0.47
1:6:699:U:H3	1:6:739:G:H1	1.62	0.47
1:6:958:U:H5'	29:d7:49:HIS:CD2	2.49	0.47
1:6:958:U:P	29:d7:20:LYS:HZ1	2.37	0.47
1:6:1325:A:OP2	19:c7:11:ARG:NH2	2.43	0.47
3:s1:70:LEU:HB3	3:s1:79:HIS:HB3	1.97	0.47
4:s2:45:VAL:HG21	4:s2:68:ILE:HG23	1.96	0.47
6:s4:117:GLU:O	6:s4:119:ALA:N	2.37	0.47
6:s4:117:GLU:C	6:s4:119:ALA:H	2.22	0.47
11:s9:159:ALA:O	11:s9:165:GLY:HA3	2.15	0.47
31:d9:17:GLY:HA2	31:d9:27:HIS:CE1	2.49	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
48:m1:85:LYS:HA	48:m1:89:TYR:CE2	2.49	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
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
6:S4:139:VAL:HG13	6:S4:150:PRO:HG3	1.96	0.47
15:C3:5:HIS:CE1	15:C3:121:ARG:HG3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:C6:40:GLU:HA	18:C6:42:GLU:H	1.78	0.47
20:C8:26:ILE:HD11	20:C8:31:ALA:HA	1.95	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
23:D1:7:GLN:O	23:D1:9:VAL:N	2.47	0.47
26:D4:14:SER:HA	26:D4:21:LYS:HG3	1.96	0.47
36:1:590:G:C2	36:1:610:G:H2'	2.50	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
37:3:45:A:H2'	37:3:46:A:H8	1.78	0.47
42:L5:58:LYS:CD	42:L5:93:THR:HG21	2.43	0.47
47:M0:9:TYR:CG	47:M0:97:LEU:HD13	2.49	0.47
47:M0:36:LEU:HD13	47:M0:87:LEU:HD13	1.97	0.47
49:M3:47:ALA:HB3	49:M3:49:ARG:HG3	1.95	0.47
50:M4:48:GLY:HA3	50:M4:53:VAL:HG13	1.95	0.47
59:N3:72:LYS:HB2	59:N3:72:LYS:HE3	1.77	0.47
1:6:28:A:H2'	1:6:29:U:C6	2.49	0.47
1:6:1433:G:N1	31:d9:45:GLU:OE2	2.46	0.47
1:6:1554:U:OP1	31:d9:13:ARG:NH2	2.41	0.47
1:6:1698:G:H1'	1:6:1699:G:OP1	2.14	0.47
3:s1:168:ILE:O	3:s1:172:LEU:HG	2.14	0.47
6:s4:126:VAL:HG21	6:s4:155:LYS:O	2.15	0.47
13:c1:132:SER:O	13:c1:132:SER:OG	2.31	0.47
14:c2:83:GLU:C	14:c2:85:LYS:H	2.22	0.47
27:d5:103:ARG:HG2	27:d5:104:ALA:H	1.80	0.47
36:5:314:U:H2'	36:5:315:C:C6	2.50	0.47
36:5:2557:A:H5'	63:n7:135:ARG:HH22	1.79	0.47
36:5:3335:A:N7	36:5:3370:A:O2'	2.43	0.47
40:l3:292:ALA:HB1	40:l3:295:ALA:HB3	1.96	0.47
46:l9:112:ILE:N	46:l9:126:VAL:O	2.36	0.47
47:m0:86:HIS:HB3	47:m0:139:ARG:CG	2.43	0.47
54:m8:94:PHE:CZ	64:n8:119:PRO:HD3	2.50	0.47
64:n8:21:ARG:O	64:n8:24:LYS:HE3	2.14	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
1:2:1746:A:H2'	1:2:1747:G:O4'	2.15	0.47
1:2:1755:A:C8	25:D3:63:GLN:HG3	2.49	0.47
2:S0:185:ARG:HB2	23:D1:45:ALA:H	1.80	0.47
3:S1:59:ASP:HA	3:S1:62:LYS:NZ	2.30	0.47
3:S1:109:LYS:HE3	3:S1:113:MET:HE3	1.95	0.47
3:S1:117:TRP:HE1	3:S1:152:ARG:CZ	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:S5:187:ILE:H	7:S5:187:ILE:HD12	1.80	0.47
8:S6:163:THR:HG22	8:S6:168:THR:HG22	1.97	0.47
11:S9:57:ARG:HG3	11:S9:97:LEU:HD21	1.95	0.47
13:C1:22:ASN:HD21	13:C1:24:LYS:HB2	1.79	0.47
13:C1:78:THR:HG22	13:C1:84:ILE:HG22	1.97	0.47
14:C2:97:LEU:HD11	14:C2:121:VAL:HG22	1.97	0.47
14:C2:103:LEU:HD23	14:C2:115:VAL:HA	1.96	0.47
18:C6:78:VAL:O	18:C6:81:ILE:HG12	2.14	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
36:1:1168:U:H1'	44:L7:209:ASN:ND2	2.29	0.47
36:1:2646:C:H4'	47:M0:119:TRP:CE2	2.50	0.47
36:1:3078:U:H4'	36:1:3079:U:O5'	2.14	0.47
36:1:3306:U:H5"	40:L3:21:ARG:NH1	2.30	0.47
39:L2:177:LYS:HD3	79:Q3:69:TYR:CZ	2.49	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
46:L9:47:LYS:NZ	50:M4:5:SER:HB2	2.22	0.47
48:M1:54:VAL:HG23	48:M1:59:ILE:HD11	1.97	0.47
53:M7:27:LYS:HG2	53:M7:63:PHE:CG	2.50	0.47
64:N8:82:ILE:HD11	64:N8:102:ILE:HD11	1.96	0.47
70:O4:99:LYS:HG2	70:O4:103:LYS:HE3	1.95	0.47
1:6:159:U:O2'	8:s6:87:ARG:NH1	2.47	0.47
1:6:224:C:H2'	1:6:225:A:C8	2.48	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
1:6:845:G:H2'	1:6:846:G:C8	2.46	0.47
1:6:950:C:H4'	15:c3:104:ARG:HH22	1.80	0.47
1:6:1216:C:O2'	1:6:1444:A:N1	2.36	0.47
1:6:1358:G:H2'	1:6:1359:C:C6	2.50	0.47
2:s0:64:ILE:HG23	2:s0:73:VAL:HG11	1.97	0.47
2:s0:172:LEU:HD22	2:s0:176:LEU:HG	1.95	0.47
2:s0:184:LEU:O	2:s0:186:GLY:N	2.41	0.47
3:s1:67:GLU:CD	3:s1:83:LYS:HE2	2.40	0.47
9:s7:14:THR:OG1	9:s7:15:GLU:N	2.45	0.47
9:s7:141:ARG:HG2	24:d2:51:GLU:CD	2.40	0.47
10:s8:36:THR:OG1	10:s8:96:LEU:HB2	2.15	0.47
10:s8:62:THR:HA	10:s8:76:THR:O	2.14	0.47
11:s9:28:LEU:HB3	80:e0:44:PHE:HZ	1.80	0.47
13:c1:46:LYS:HD2	13:c1:46:LYS:HA	1.62	0.47
13:c1:108:PRO:HG3	13:c1:134:THR:HB	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:c8:52:VAL:HG13	20:c8:61:LEU:HD21	1.95	0.47
21:c9:57:ARG:O	21:c9:61:VAL:HG23	2.14	0.47
27:d5:42:LEU:HD22	27:d5:47:TYR:HB2	1.95	0.47
28:d6:10:ARG:HD3	28:d6:34:LYS:HG3	1.95	0.47
29:d7:61:THR:OG1	29:d7:62:ILE:N	2.41	0.47
36:5:412:G:OP1	53:m7:62:ARG:NH1	2.48	0.47
36:5:1190:A:H5'	36:5:1191:U:OP1	2.15	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
39:l2:183:GLY:O	39:l2:186:PHE:HB3	2.15	0.47
45:l8:91:PHE:HE2	45:l8:185:ARG:HB3	1.79	0.47
46:l9:86:TYR:CE2	46:l9:151:VAL:HG22	2.49	0.47
53:m7:26:PHE:CE1	53:m7:120:ASN:HA	2.50	0.47
54:m8:157:PRO:HD3	64:n8:47:LYS:HB2	1.96	0.47
55:m9:105:LEU:HD23	55:m9:138:LEU:HD12	1.96	0.47
57:n1:44:ALA:HB2	57:n1:53:PRO:HG2	1.97	0.47
60:n4:79:GLN:HG3	60:n4:80:ARG:N	2.30	0.47
60:n4:103:ALA:O	60:n4:107:GLU:HB2	2.15	0.47
61:n5:45:LYS:HG2	71:o5:75:TYR:HD2	1.79	0.47
61:n5:86:VAL:HG11	61:n5:95:ILE:HD11	1.96	0.47
64:n8:64:GLN:HB3	64:n8:67:HIS:CD2	2.50	0.47
1:2:478:A:OP1	32:E0:37:ARG:NH1	2.45	0.47
1:2:1433:G:C8	31:D9:41:GLN:HG2	2.50	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
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
48:M1:139:THR:O	48:M1:139:THR:OG1	2.25	0.47
55:M9:104:ARG:HB3	55:M9:104:ARG:HH11	1.80	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
1:6:68:A:OP1	8:s6:160:ARG:NH2	2.40	0.47
1:6:522:U:O4'	26:d4:34:ASN:ND2	2.48	0.47
1:6:830:U:C2'	1:6:831:U:H5'	2.45	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:s1:120:LEU:HG	3:s1:142:PHE:CE1	2.49	0.47
5:s3:69:LEU:HD12	5:s3:72:LEU:HD12	1.97	0.47
7:s5:99:MET:HA	7:s5:104:ASN:ND2	2.30	0.47
7:s5:143:ARG:HB2	30:d8:57:MET:HE2	1.97	0.47
13:c1:5:LEU:HD13	13:c1:5:LEU:H	1.79	0.47
19:c7:104:ASN:O	19:c7:106:THR:N	2.43	0.47
34:sR:95:ALA:C	34:sR:97:GLY:H	2.22	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
40:l3:77:THR:HG23	40:l3:326:GLY:O	2.15	0.47
42:l5:99:TYR:CG	42:l5:199:ILE:HG23	2.50	0.47
46:l9:124:ARG:HB3	46:l9:164:ILE:HD13	1.96	0.47
58:n2:90:ARG:O	58:n2:91:ASP:HB2	2.14	0.47
68:o2:19:ARG:HH11	68:o2:28:VAL:HG13	1.80	0.47
79:q3:86:LEU:O	79:q3:90:VAL:HG13	2.14	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
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
2:S0:121:VAL:HB	2:S0:143:VAL:HG22	1.97	0.47
6:S4:59:ARG:HH12	26:D4:87:PRO:HG3	1.80	0.47
6:S4:124:GLY:HA2	6:S4:142:HIS:CE1	2.49	0.47
7:S5:73:THR:HG22	7:S5:75:GLY:N	2.29	0.47
9:S7:109:VAL:O	9:S7:111:LYS:N	2.48	0.47
10:S8:36:THR:HG21	10:S8:173:PRO:HB2	1.97	0.47
10:S8:46:VAL:HG13	10:S8:54:LYS:HB3	1.96	0.47
20:C8:110:ARG:HB3	20:C8:110:ARG:HH11	1.80	0.47
36:1:595:G:C8	36:1:609:G:C6	3.03	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
36:1:2586:G:N7	45:L8:241:LYS:HB2	2.30	0.47
36:1:3151:U:H4'	36:1:3294:A:C1'	2.43	0.47
42:L5:34:LYS:O	42:L5:38:THR:HG23	2.15	0.47
42:L5:114:GLY:C	42:L5:116:ASP:H	2.23	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
69:O3:13:HIS:NE2	69:O3:28:SER:OG	2.38	0.47
73:O7:31:LYS:O	73:O7:33:THR:HG22	2.15	0.47
1:6:491:C:H42	1:6:497:G:H21	1.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1039:A:O2'	1:6:1040:G:O5'	2.32	0.47
1:6:1098:U:OP2	4:s2:168:ARG:NE	2.47	0.47
1:6:1619:C:H2'	1:6:1620:C:C6	2.50	0.47
2:s0:41:ARG:N	2:s0:45:VAL:O	2.45	0.47
7:s5:43:PHE:CZ	7:s5:90:ILE:HG21	2.50	0.47
7:s5:58:LEU:HD11	7:s5:167:ARG:NH1	2.29	0.47
8:s6:137:ARG:O	8:s6:141:ILE:HG13	2.15	0.47
13:c1:50:GLU:H	13:c1:50:GLU:HG2	1.50	0.47
26:d4:58:PHE:CE2	26:d4:72:PHE:HB3	2.49	0.47
34:sR:132:LYS:NZ	34:sR:143:THR:OG1	2.40	0.47
34:sR:159:ASN:O	34:sR:161:LYS:N	2.38	0.47
36:5:57:A:H1'	51:m5:162:ARG:HH11	1.79	0.47
36:5:776:U:H5	36:5:2719:U:O2	1.97	0.47
36:5:955:U:H2'	36:5:956:U:C6	2.50	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
36:5:2115:G:O2'	55:m9:82:LYS:HE3	2.15	0.47
36:5:2206:G:O2'	36:5:2207:A:H5'	2.14	0.47
36:5:3178:A:C2	52:m6:115:LYS:HG2	2.50	0.47
41:l4:269:SER:C	41:l4:271:LYS:H	2.22	0.47
45:l8:68:ARG:O	45:l8:69:LEU:HB2	2.15	0.47
56:n0:12:ARG:HB3	56:n0:24:LEU:HD23	1.97	0.47
62:n6:120:GLN:HE22	62:n6:126:LEU:HA	1.79	0.47
67:o1:63:GLY:O	67:o1:65:LYS:N	2.48	0.47
78:q2:21:THR:O	78:q2:23:HIS:ND1	2.48	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
1:2:1218:G:N2	1:2:1444:A:OP2	2.34	0.47
1:2:1244:A:H3'	1:2:1244:A:N3	2.30	0.47
1:2:1339:C:O2'	1:2:1340:U:OP1	2.33	0.47
1:2:1477:G:H2'	1:2:1478:G:C8	2.50	0.47
1:2:1647:U:O2	32:E0:2:ALA:HA	2.15	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
24:D2:27:ILE:HD11	24:D2:61:ILE:HD12	1.96	0.47
33:E1:133:ALA:O	33:E1:139:LEU:HA	2.15	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
36:1:2878:G:H5"	40:L3:5:LYS:HE2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:3318:G:OP2	36:1:3318:G:H2'	2.15	0.47
39:L2:114:SER:HB2	39:L2:169:ILE:CD1	2.45	0.47
44:L7:152:GLY:O	44:L7:163:LEU:HG	2.14	0.47
45:L8:75:ILE:C	45:L8:77:GLN:H	2.23	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:HA	63:N7:64:LYS:HD3	1.69	0.47
1:6:926:A:H2	16:c4:125:SER:HB2	1.80	0.47
1:6:1255:G:O2'	1:6:1256:A:O5'	2.31	0.47
3:s1:62:LYS:O	3:s1:88:VAL:HB	2.15	0.47
4:s2:95:ARG:HD3	4:s2:97:ARG:HD2	1.96	0.47
30:d8:32:PHE:CE2	30:d8:40:ILE:HD13	2.50	0.47
36:5:750:G:H2'	36:5:751:A:C8	2.48	0.47
36:5:3203:U:H2'	36:5:3204:C:C6	2.49	0.47
36:5:3329:U:H5"	40:l3:308:MET:HE3	1.97	0.47
42:l5:148:ILE:HG13	42:l5:159:VAL:HG21	1.96	0.47
42:l5:271:LYS:HD3	42:l5:271:LYS:HA	1.55	0.47
44:l7:216:VAL:HG11	44:l7:227:GLY:HA2	1.97	0.47
58:n2:19:VAL:O	58:n2:23:THR:OG1	2.24	0.47
64:n8:75:LEU:HB3	64:n8:118:ILE:HG23	1.97	0.47
67:o1:19:ARG:HB3	67:o1:35:GLU:HG2	1.97	0.47
1:2:820:U:H2'	1:2:821:U:H4'	1.95	0.46
1:2:1144:U:H2'	1:2:1145:U:C6	2.49	0.46
3:S1:99:ASN:OD1	3:S1:100:PHE:N	2.46	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
36:1:1103:A:H2'	36:1:1103:A:N3	2.30	0.46
41:L4:338:LYS:HD2	41:L4:338:LYS:HA	1.47	0.46
42:L5:289:LYS:HD3	47:M0:206:LEU:HD23	1.97	0.46
47:M0:38:LYS:HG2	47:M0:41:ALA:HB2	1.97	0.46
53:M7:138:LYS:HD2	53:M7:140:GLU:CD	2.40	0.46
78:Q2:33:ALA:O	78:Q2:34:SER:HB3	2.14	0.46
1:6:1082:C:H41	1:6:1091:A:N6	2.13	0.46
2:s0:123:VAL:HG11	2:s0:133:ILE:HD11	1.96	0.46
3:s1:28:GLU:OE2	3:s1:94:LYS:NZ	2.38	0.46
3:s1:81:PHE:HB3	3:s1:109:LYS:HG2	1.97	0.46
10:s8:57:ALA:HB1	10:s8:60:ILE:HD11	1.95	0.46
25:d3:44:GLY:H	25:d3:78:LYS:NZ	2.13	0.46
36:5:256:G:H4'	71:o5:111:PHE:HZ	1.80	0.46
36:5:1040:A:O2'	47:m0:198:LYS:HE2	2.15	0.46
36:5:2180:G:H2'	36:5:2181:C:H6	1.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:7:27:A:H2'	37:7:28:C:C6	2.49	0.46
41:l4:230:VAL:HG21	41:l4:257:LYS:HD3	1.97	0.46
43:l6:68:PRO:HB2	43:l6:142:ASP:CG	2.39	0.46
44:l7:178:ILE:HA	44:l7:183:ASP:HB3	1.96	0.46
45:l8:133:LYS:HD2	45:l8:138:HIS:HE1	1.80	0.46
47:m0:149:VAL:HG13	47:m0:165:ILE:HG21	1.96	0.46
48:m1:94:ARG:C	48:m1:96:PHE:H	2.14	0.46
56:n0:2:ALA:HB3	56:n0:32:SER:HB3	1.96	0.46
66:o0:9:SER:OG	66:o0:10:ILE:N	2.48	0.46
67:o1:85:ALA:O	67:o1:87:ASN:N	2.48	0.46
68:o2:32:TRP:CZ2	68:o2:53:PRO:HD2	2.50	0.46
1:2:109:G:H1	1:2:305:C:H42	1.63	0.46
1:2:1785:U:OP2	16:C4:133:ARG:NH2	2.48	0.46
3:S1:181:LEU:O	3:S1:182:ALA:C	2.58	0.46
14:C2:62:LEU:HD22	14:C2:75:VAL:HG11	1.98	0.46
17:C5:75:PRO:HG3	17:C5:93:VAL:HG11	1.98	0.46
17:C5:85:ILE:HG22	17:C5:112:LEU:HD23	1.98	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
36:1:208:C:H2'	36:1:209:A:O4'	2.16	0.46
36:1:594:U:H2'	36:1:609:G:O6	2.15	0.46
36:1:2894:C:H2'	36:1:2895:G:H8	1.80	0.46
38:4:127:U:H2'	38:4:128:U:H5'	1.98	0.46
43:L6:130:ILE:HG21	43:L6:135:VAL:HG23	1.96	0.46
48:M1:91:LEU:HD22	48:M1:95:ASN:HD22	1.79	0.46
57:N1:106:LEU:HD13	57:N1:106:LEU:HA	1.78	0.46
63:N7:5:LEU:HD11	66:O0:35:ARG:HD2	1.97	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
5:s3:66:ILE:O	5:s3:70:THR:HG23	2.16	0.46
5:s3:211:PRO:HG2	19:c7:19:ARG:HB2	1.98	0.46
6:s4:151:ASP:HB3	6:s4:154:ILE:HG13	1.96	0.46
7:s5:162:VAL:HG22	7:s5:167:ARG:HG2	1.96	0.46
11:s9:126:ARG:O	11:s9:130:THR:HG23	2.15	0.46
14:c2:91:VAL:HG11	14:c2:97:LEU:HD23	1.97	0.46
33:e1:97:LYS:HA	33:e1:97:LYS:HD2	1.84	0.46
35:sM:23:LYS:HZ2	35:sM:24:GLU:N	2.10	0.46
36:5:278:U:H2'	36:5:279:U:C6	2.50	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:2407:C:H2'	36:5:2408:U:H6	1.80	0.46
36:5:2713:U:O2'	78:q2:8:ARG:HD2	2.15	0.46
36:5:3275:U:C4	69:o3:60:ARG:HD2	2.50	0.46
39:l2:158:ILE:H	39:l2:158:ILE:HD13	1.80	0.46
41:l4:74:ILE:HD12	41:l4:75:PRO:HD2	1.97	0.46
45:l8:146:LYS:HD3	45:l8:173:MET:O	2.15	0.46
48:m1:52:TYR:HA	48:m1:61:ARG:HG3	1.97	0.46
51:m5:35:VAL:HG13	51:m5:65:ARG:HB3	1.97	0.46
51:m5:136:ASP:OD2	51:m5:138:GLN:HG2	2.15	0.46
67:o1:88:PRO:C	67:o1:89:LEU:HD12	2.40	0.46
71:o5:90:ARG:H	71:o5:90:ARG:HG2	1.60	0.46
76:q0:110:CYS:SG	76:q0:111:ARG:N	2.87	0.46
1:2:886:U:O2'	16:C4:121:VAL:O	2.23	0.46
4:S2:215:PHE:O	4:S2:218:ILE:HG13	2.15	0.46
13:C1:14:GLN:HB3	13:C1:54:ILE:HG12	1.98	0.46
15:C3:15:ALA:H	29:D7:20:LYS:HZ1	1.63	0.46
18:C6:41:PRO:O	18:C6:42:GLU:HB3	2.15	0.46
19:C7:63:LYS:HE2	34:SR:284:ALA:HB2	1.96	0.46
24:D2:82:LYS:C	24:D2:84:GLY:H	2.20	0.46
28:D6:62:TYR:CG	28:D6:63:ALA:N	2.84	0.46
34:SR:267:PRO:HG2	34:SR:269:TYR:CE1	2.50	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
36:1:1631:C:H5"	36:1:1632:A:H5"	1.97	0.46
36:1:3013:U:H2'	36:1:3014:U:C6	2.51	0.46
41:L4:10:SER:C	41:L4:12:THR:H	2.23	0.46
41:L4:158:SER:O	41:L4:160:GLN:NE2	2.48	0.46
41:L4:338:LYS:O	41:L4:340:GLY:N	2.47	0.46
43:L6:146:ILE:O	43:L6:150:LYS:HG3	2.15	0.46
52:M6:73:PHE:CD1	52:M6:78:ARG:HD3	2.51	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
1:6:116:U:H2'	1:6:117:U:C6	2.50	0.46
1:6:1572:G:H2'	1:6:1572:G:N3	2.31	0.46
5:s3:105:MET:HG2	5:s3:122:VAL:HG21	1.97	0.46
8:s6:76:LEU:HD23	8:s6:76:LEU:HA	1.82	0.46
10:s8:36:THR:OG1	10:s8:36:THR:O	2.30	0.46
15:c3:26:PHE:CE2	15:c3:66:ILE:HD13	2.51	0.46
17:c5:130:ARG:HH22	35:sM:70:ASN:HB2	1.80	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:630:A:H2'	36:5:631:U:C6	2.49	0.46
36:5:2261:G:H21	36:5:2262:A:N6	2.13	0.46
38:8:152:G:H2'	38:8:153:U:O4'	2.15	0.46
41:l4:98:ARG:HB3	41:l4:98:ARG:CZ	2.45	0.46
41:l4:203:ARG:HD2	41:l4:226:GLU:OE2	2.16	0.46
42:l5:178:ASN:HA	42:l5:183:TRP:CG	2.49	0.46
49:m3:151:ALA:O	49:m3:153:ASP:N	2.41	0.46
54:m8:133:LYS:HB2	54:m8:135:GLN:HE22	1.80	0.46
55:m9:44:LEU:HA	55:m9:47:ASN:HB3	1.97	0.46
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
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
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
4:S2:227:PRO:HA	4:S2:230:TRP:CD2	2.50	0.46
5:S3:21:LEU:HD22	5:S3:25:PHE:HE2	1.80	0.46
20:C8:81:ILE:O	20:C8:83:ALA:N	2.49	0.46
20:C8:107:SER:O	20:C8:110:ARG:HB2	2.16	0.46
24:D2:10:ALA:HB1	24:D2:27:ILE:HD12	1.97	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
34:SR:49:GLY:O	34:SR:51:ASP:N	2.48	0.46
36:1:627:U:H4'	36:1:1399:A:O2'	2.15	0.46
36:1:1110:U:H2'	36:1:1111:U:C6	2.49	0.46
36:1:2890:A:O2'	36:1:2933:A:N3	2.39	0.46
40:L3:256:HIS:HA	40:L3:257:PRO:C	2.40	0.46
45:L8:150:LEU:HD23	45:L8:150:LEU:HA	1.81	0.46
70:O4:106:LYS:HD3	70:O4:109:THR:HB	1.97	0.46
1:6:482:U:H2'	1:6:483:A:C8	2.51	0.46
1:6:813:U:O2	1:6:813:U:H2'	2.15	0.46
1:6:1671:A:H2'	1:6:1672:G:O4'	2.16	0.46
3:s1:164:ILE:HD13	3:s1:207:LEU:HD11	1.97	0.46
4:s2:76:LEU:HD21	4:s2:104:VAL:HB	1.98	0.46
5:s3:11:LEU:HD13	22:d0:29:THR:HG23	1.98	0.46
7:s5:37:GLN:OE1	18:c6:53:LEU:HD22	2.15	0.46
8:s6:136:LYS:HG3	8:s6:173:PRO:HB3	1.97	0.46
26:d4:62:THR:HA	26:d4:69:SER:HA	1.98	0.46
36:5:119:U:C2	45:l8:138:HIS:CE1	3.03	0.46
36:5:629:U:H2'	36:5:630:A:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:928:C:H2'	36:5:929:A:C8	2.51	0.46
36:5:1257:C:H5'	81:m2:122:UNK:O	2.16	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
36:5:2746:A:H5'	42:l5:178:ASN:HD21	1.80	0.46
36:5:3006:A:H2'	36:5:3007:U:O4'	2.15	0.46
38:8:106:C:H5"	38:8:108:C:OP2	2.15	0.46
39:l2:82:VAL:HA	39:l2:86:GLN:OE1	2.15	0.46
42:l5:126:GLU:HA	42:l5:196:ARG:HD2	1.98	0.46
42:l5:155:THR:HG22	42:l5:179:ARG:NH1	2.30	0.46
48:m1:54:VAL:HG12	48:m1:57:PHE:H	1.79	0.46
50:m4:115:PHE:O	50:m4:119:GLN:HG3	2.15	0.46
55:m9:34:GLN:O	55:m9:36:ASN:ND2	2.40	0.46
63:n7:53:VAL:HA	63:n7:57:HIS:CD2	2.50	0.46
71:o5:85:THR:HB	71:o5:88:LEU:HD12	1.96	0.46
77:q1:6:ARG:O	77:q1:10:THR:HG23	2.14	0.46
78:q2:59:HIS:HA	78:q2:61:LYS:HZ1	1.78	0.46
1:2:795:U:OP2	24:D2:82:LYS:NZ	2.45	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
3:S1:39:GLU:HB3	3:S1:74:GLN:HA	1.96	0.46
22:D0:67:THR:HG21	31:D9:40:ARG:HB2	1.98	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
36:1:3049:A:H5'	36:1:3049:A:H8	1.81	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
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
1:6:416:A:H4'	1:6:417:A:OP2	2.16	0.46
1:6:1383:G:OP1	22:d0:89:ARG:NH2	2.48	0.46
1:6:1783:C:H2'	1:6:1784:C:C6	2.51	0.46
3:s1:193:ILE:HG22	3:s1:197:ILE:HD13	1.98	0.46
10:s8:62:THR:HA	10:s8:77:ARG:HA	1.97	0.46
12:c0:14:TYR:CZ	12:c0:18:GLU:HG3	2.50	0.46
12:c0:77:ARG:HE	12:c0:83:PRO:HA	1.80	0.46
15:c3:44:GLY:O	15:c3:45:LEU:HD23	2.14	0.46
20:c8:120:ARG:HD2	35:sM:58:GLU:OE2	2.15	0.46
22:d0:52:LYS:HB3	22:d0:53:LYS:H	1.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:d3:109:ARG:O	25:d3:112:LYS:HE3	2.15	0.46
34:sR:182:ASN:OD1	34:sR:184:ASN:ND2	2.48	0.46
34:sR:194:GLY:HA3	34:sR:221:MET:HE1	1.98	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
36:5:990:U:O4'	57:n1:101:CYS:HB3	2.15	0.46
36:5:1238:C:H2'	36:5:1239:C:O4'	2.15	0.46
36:5:1307:G:C4	52:m6:60:LYS:HD3	2.51	0.46
36:5:2191:U:H2'	36:5:2192:C:O4'	2.16	0.46
40:l3:331:ASN:OD1	40:l3:331:ASN:N	2.49	0.46
48:m1:16:LYS:NZ	48:m1:130:VAL:HG11	2.30	0.46
49:m3:32:LYS:HA	49:m3:35:ARG:NH1	2.30	0.46
1:2:393:C:H2'	1:2:394:C:C6	2.51	0.46
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
1:2:1089:U:O2'	1:2:1093:A:N1	2.40	0.46
2:S0:139:VAL:HG13	2:S0:141:ILE:HG13	1.97	0.46
4:S2:227:PRO:HA	4:S2:230:TRP:CD1	2.51	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
36:1:372:A:H2'	36:1:373:A:O4'	2.15	0.46
36:1:708:G:H5'	36:1:708:G:H8	1.80	0.46
36:1:1278:A:HO2'	36:1:1279:C:H6	1.61	0.46
36:1:1492:G:O3'	75:O9:48:LYS:NZ	2.48	0.46
40:L3:183:LEU:O	40:L3:191:LYS:NZ	2.48	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
63:N7:51:LEU:HB2	63:N7:65:ARG:HD2	1.97	0.46
68:O2:121:ASN:N	68:O2:121:ASN:OD1	2.48	0.46
1:6:523:G:H5'	26:d4:60:PHE:O	2.16	0.46
1:6:793:A:C3'	1:6:794:U:H5'	2.40	0.46
1:6:1305:U:H4'	1:6:1306:C:OP2	2.16	0.46
2:s0:35:PRO:O	2:s0:52:LYS:NZ	2.47	0.46
12:c0:1:MET:HG3	12:c0:2:LEU:H	1.80	0.46
20:c8:6:GLN:HA	27:d5:42:LEU:HB2	1.97	0.46
26:d4:87:PRO:HG2	26:d4:90:ARG:HG3	1.98	0.46
33:e1:77:GLY:HA2	33:e1:78:LYS:HA	1.65	0.46
34:sR:164:ASP:O	34:sR:166:SER:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:sR:193:ILE:H	34:sR:193:ILE:HD12	1.80	0.46
35:sM:54:PRO:C	35:sM:59:ALA:HB2	2.40	0.46
36:5:90:C:H2'	36:5:91:G:H5'	1.98	0.46
36:5:1050:U:OP2	57:n1:13:TYR:OH	2.26	0.46
36:5:1108:U:H2'	36:5:1109:U:H6	1.80	0.46
36:5:1844:C:O2	73:o7:9:GLY:HA2	2.16	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
40:l3:256:HIS:HA	40:l3:257:PRO:C	2.41	0.46
48:m1:28:ASP:HA	48:m1:31:THR:HG23	1.98	0.46
54:m8:122:ILE:HG22	54:m8:123:THR:O	2.15	0.46
63:n7:36:HIS:N	63:n7:37:PRO:HD3	2.31	0.46
82:p0:198:PRO:C	82:p0:275:ALA:H	2.23	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
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
12:C0:55:VAL:HA	12:C0:69:THR:HG23	1.97	0.46
18:C6:77:GLN:O	18:C6:81:ILE:HG23	2.16	0.46
34:SR:231:MET:HE2	34:SR:232:TYR:HE2	1.80	0.46
36:1:255:A:H5'	71:O5:106:LYS:HD3	1.98	0.46
36:1:1312:C:O2'	52:M6:83:ALA:O	2.32	0.46
36:1:1821:U:N3	70:O4:67:LYS:HD2	2.31	0.46
40:L3:308:MET:HE3	40:L3:308:MET:HB3	1.76	0.46
40:L3:313:HIS:O	40:L3:333:LYS:HD2	2.16	0.46
44:L7:77:VAL:HG22	57:N1:139:ARG:HG2	1.98	0.46
48:M1:54:VAL:HB	48:M1:57:PHE:HB2	1.96	0.46
79:Q3:18:TYR:O	79:Q3:22:LEU:HD12	2.15	0.46
1:6:181:A:H2'	1:6:182:A:O4'	2.15	0.46
1:6:1364:G:N2	21:c9:3:GLY:HA3	2.30	0.46
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
4:s2:103:VAL:HG22	4:s2:113:LEU:HD23	1.98	0.46
5:s3:90:ARG:HH21	5:s3:91:VAL:HG12	1.80	0.46
6:s4:9:LEU:HD12	6:s4:30:ARG:HA	1.97	0.46
12:c0:76:LEU:HD22	12:c0:79:TYR:HB3	1.96	0.46
26:d4:10:ARG:HG3	26:d4:26:ASP:OD2	2.16	0.46
34:sR:54:PHE:CE2	34:sR:312:VAL:HG11	2.50	0.46
36:5:1485:G:N2	70:o4:4:ARG:HD2	2.31	0.46
36:5:1846:C:H5'	36:5:1849:C:N4	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
38:8:37:A:H5"	38:8:39:G:O4'	2.16	0.46
40:l3:284:ARG:NH2	40:l3:293:ASN:O	2.37	0.46
41:l4:141:ARG:C	41:l4:143:GLU:H	2.23	0.46
43:l6:62:THR:HG21	43:l6:78:ARG:HB3	1.96	0.46
48:m1:140:ARG:HD2	48:m1:140:ARG:HA	1.70	0.46
81:m2:54:UNK:HA	81:m2:55:UNK:HA	1.64	0.46
57:n1:82:ASN:O	65:n9:21:ILE:N	2.44	0.46
62:n6:42:GLN:O	62:n6:125:LYS:HG3	2.16	0.46
73:o7:2:GLY:O	73:o7:7:SER:HB2	2.16	0.46
78:q2:78:LYS:O	78:q2:78:LYS:HG2	2.14	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
1:2:1487:A:H2'	1:2:1488:G:C8	2.51	0.46
1:2:1584:G:O2'	1:2:1610:G:O6	2.32	0.46
4:S2:144:TRP:NE1	24:D2:97:ARG:HD2	2.30	0.46
5:S3:93:ASP:OD2	5:S3:93:ASP:N	2.49	0.46
8:S6:78:THR:HG22	8:S6:92:ARG:HG2	1.98	0.46
36:1:729:C:H2'	36:1:730:C:H6	1.81	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
36:1:2899:C:C5	46:L9:171:ASP:HA	2.51	0.46
36:1:3276:G:OP1	36:1:3276:G:H4'	2.14	0.46
54:M8:161:LYS:O	54:M8:162:ALA:HB3	2.14	0.46
56:N0:167:ARG:HG3	56:N0:168:PRO:HD2	1.98	0.46
66:O0:42:ILE:HD11	66:O0:67:VAL:HG22	1.98	0.46
1:6:895:G:O2'	16:c4:37:GLU:HA	2.16	0.46
1:6:902:G:H2'	1:6:903:U:C6	2.50	0.46
1:6:980:G:H4'	1:6:1776:A:H4'	1.98	0.46
1:6:1079:U:H2'	1:6:1080:U:C6	2.50	0.46
3:s1:33:LYS:HB3	3:s1:232:HIS:HE1	1.81	0.46
9:s7:144:VAL:HG22	24:d2:49:GLU:HB3	1.97	0.46
24:d2:67:GLY:C	24:d2:69:LEU:H	2.23	0.46
27:d5:47:TYR:CE1	27:d5:51:LEU:HD11	2.51	0.46
34:sR:289:ALA:HA	34:sR:305:TYR:HA	1.97	0.46
36:5:114:A:H2'	36:5:115:A:O4'	2.16	0.46
36:5:585:A:H2'	36:5:586:C:C6	2.51	0.46
36:5:944:C:H4'	68:o2:33:ARG:NH1	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
39:l2:211:HIS:CD2	39:l2:219:ILE:HG23	2.51	0.46
40:l3:115:LYS:HE2	40:l3:129:ALA:HB3	1.98	0.46
77:q1:7:LYS:HE2	77:q1:11:ARG:NH2	2.31	0.46
82:p0:69:ASP:OD1	82:p0:69:ASP:N	2.36	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
1:2:959:U:C6	15:C3:61:THR:HB	2.51	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
4:S2:68:ILE:O	4:S2:72:LEU:HB2	2.15	0.46
12:C0:30:ALA:O	12:C0:38:LYS:HA	2.16	0.46
14:C2:68:GLU:O	14:C2:70:ASN:N	2.49	0.46
15:C3:99:ARG:O	15:C3:103:GLU:HG2	2.16	0.46
36:1:2724:U:H4'	57:N1:54:HIS:CD2	2.51	0.46
36:1:3362:A:H2'	36:1:3363:U:O4'	2.16	0.46
38:4:118:C:H2'	38:4:119:C:C6	2.51	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
44:L7:120:THR:HB	57:N1:132:PRO:HB2	1.98	0.46
46:L9:47:LYS:NZ	46:L9:50:ASN:OD1	2.32	0.46
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
57:N1:14:MET:HE1	57:N1:55:LYS:HB2	1.97	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
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
1:6:1229:G:C6	14:c2:47:GLU:HG2	2.50	0.46
1:6:1603:U:H2'	1:6:1604:U:C6	2.51	0.46
1:6:1608:U:O3'	18:c6:73:GLY:HA3	2.16	0.46
1:6:1655:A:N1	36:5:2291:A:O2'	2.40	0.46
7:s5:133:VAL:HG22	7:s5:198:LEU:HD13	1.97	0.46
7:s5:190:ILE:O	7:s5:194:LEU:HB2	2.16	0.46
9:s7:17:GLU:O	9:s7:21:ALA:N	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:c0:58:GLN:HB3	12:c0:65:TYR:HB2	1.97	0.46
36:5:1836:C:O2'	36:5:1842:A:N1	2.43	0.46
36:5:1942:U:OP2	55:m9:74:ARG:NH1	2.49	0.46
43:l6:170:LYS:HB3	43:l6:172:HIS:CE1	2.51	0.46
55:m9:158:GLU:HA	55:m9:161:ALA:HB3	1.96	0.46
1:2:328:A:H2'	1:2:329:G:O4'	2.16	0.46
1:2:705:U:H2'	1:2:706:A:C8	2.51	0.46
4:S2:38:VAL:O	4:S2:39:THR:OG1	2.27	0.46
13:C1:124:THR:HB	13:C1:141:LYS:HB3	1.97	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
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
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
45:L8:161:GLU:HA	45:L8:164:VAL:HG22	1.97	0.46
46:L9:22:SER:H	50:M4:8:LYS:HD2	1.80	0.46
51:M5:184:LYS:H	51:M5:186:GLY:H	1.64	0.46
54:M8:11:LYS:HB3	54:M8:11:LYS:HE2	1.63	0.46
54:M8:157:PRO:HD3	64:N8:47:LYS:HB2	1.97	0.46
58:N2:33:TYR:CE2	58:N2:63:VAL:HG21	2.50	0.46
64:N8:104:THR:OG1	64:N8:126:LYS:O	2.34	0.46
69:O3:31:LYS:NZ	69:O3:35:VAL:O	2.40	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
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
2:s0:119:ARG:HB3	2:s0:119:ARG:NH1	2.32	0.46
3:s1:232:HIS:HB3	3:s1:233:GLY:H	1.50	0.46
4:s2:152:HIS:CD2	4:s2:152:HIS:N	2.84	0.46
6:s4:31:PRO:HD2	6:s4:38:LEU:HD13	1.98	0.46
23:d1:3:ASN:ND2	23:d1:7:GLN:HB2	2.22	0.46
80:e0:14:VAL:HA	80:e0:17:GLN:HG2	1.98	0.46
36:5:1388:U:O4	41:l4:186:LYS:NZ	2.49	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
46:l9:43:VAL:CG1	46:l9:55:VAL:HG12	2.46	0.46
48:m1:8:PRO:HG2	48:m1:9:MET:H	1.81	0.46
52:m6:64:PHE:HE1	52:m6:68:ARG:NH1	2.14	0.46
56:n0:52:LYS:HE3	56:n0:52:LYS:HB2	1.60	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:543:C:H5'	1:2:543:C:O2	2.16	0.45
1:2:628:G:N1	1:2:970:A:OP2	2.36	0.45
1:2:885:G:H21	16:C4:123:SER:HB2	1.80	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
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
27:D5:57:TYR:HB3	27:D5:60:VAL:HG12	1.97	0.45
28:D6:9:GLY:HA3	28:D6:34:LYS:HE2	1.98	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
36:1:2393:G:O2'	36:1:2394:G:OP2	2.30	0.45
36:1:2424:A:N1	39:L2:230:VAL:HG21	2.31	0.45
36:1:3029:A:C5	36:1:3030:G:H1'	2.51	0.45
39:L2:10:LYS:HA	39:L2:16:PHE:CD2	2.51	0.45
40:L3:4:ARG:HD3	40:L3:7:GLU:HA	1.98	0.45
42:L5:178:ASN:OD1	42:L5:178:ASN:N	2.46	0.45
43:L6:7:PRO:HG2	43:L6:10:TYR:CZ	2.51	0.45
49:M3:122:LYS:NZ	71:O5:119:LYS:O	2.49	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
1:6:699:U:H2'	1:6:700:C:O4'	2.15	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
5:s3:75:LYS:NZ	12:c0:34:GLU:OE2	2.48	0.45
15:c3:42:ARG:HG3	15:c3:80:LEU:HD21	1.98	0.45
21:c9:33:TYR:HD1	21:c9:34:VAL:H	1.61	0.45
25:d3:78:LYS:HG3	25:d3:79:ASN:OD1	2.17	0.45
27:d5:40:VAL:HA	27:d5:75:LEU:HD13	1.98	0.45
80:e0:14:VAL:O	80:e0:18:THR:HG23	2.16	0.45
36:5:123:A:C6	36:5:150:A:C5	3.04	0.45
36:5:436:A:H3'	36:5:437:G:C8	2.51	0.45
36:5:874:U:H5"	36:5:2950:G:OP1	2.16	0.45
36:5:2228:A:H2'	36:5:2229:A:C8	2.51	0.45
38:8:108:C:H2'	38:8:109:A:O4'	2.16	0.45
38:8:141:C:OP1	51:m5:109:ARG:NH1	2.49	0.45
38:8:155:A:OP1	45:l8:181:LYS:HD2	2.17	0.45
40:l3:218:ILE:HG13	40:l3:276:THR:HG23	1.98	0.45
42:l5:106:ALA:O	42:l5:110:LEU:HD22	2.16	0.45
45:l8:231:LYS:HB2	45:l8:231:LYS:HE3	1.75	0.45
1:2:417:A:H4'	1:2:418:G:O5'	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1796:C:OP1	28:D6:87:ARG:NH1	2.50	0.45
2:S0:112:THR:HG23	2:S0:115:PHE:HB2	1.98	0.45
15:C3:61:THR:HG22	29:D7:32:PHE:CE2	2.52	0.45
27:D5:56:THR:HA	27:D5:103:ARG:HH11	1.81	0.45
35:SM:82:THR:HB	35:SM:83:LYS:H	1.36	0.45
36:1:3000:A:H2'	36:1:3001:C:C6	2.52	0.45
37:3:42:A:H2'	37:3:43:U:H6	1.81	0.45
42:L5:146:LEU:HD22	42:L5:148:ILE:HG13	1.98	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
52:M6:108:ILE:HD12	52:M6:160:ARG:CZ	2.47	0.45
57:N1:102:ARG:HG3	57:N1:106:LEU:HD23	1.98	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
1:6:1228:G:OP2	1:6:1228:G:H4'	2.17	0.45
4:s2:170:ILE:HG22	4:s2:171:PRO:HD2	1.98	0.45
6:s4:54:TYR:HD1	26:d4:15:ASN:ND2	2.15	0.45
7:s5:45:LYS:HD3	7:s5:45:LYS:HA	1.47	0.45
18:c6:102:LYS:HE2	18:c6:102:LYS:HB3	1.83	0.45
34:sR:5:GLU:HA	34:sR:317:THR:HA	1.99	0.45
44:l7:106:LEU:HD12	44:l7:130:ILE:HD12	1.98	0.45
44:l7:219:LYS:O	44:l7:228:SER:HB2	2.17	0.45
46:l9:87:LYS:HZ1	46:l9:191:LEU:HD21	1.80	0.45
49:m3:75:PHE:H	49:m3:97:VAL:HA	1.81	0.45
51:m5:98:LEU:HD12	51:m5:98:LEU:HA	1.79	0.45
51:m5:155:VAL:HG23	51:m5:156:HIS:ND1	2.31	0.45
54:m8:83:VAL:O	54:m8:85:GLY:N	2.48	0.45
60:n4:38:SER:O	60:n4:42:GLN:HG3	2.16	0.45
62:n6:83:ASP:O	62:n6:84:LYS:HB2	2.15	0.45
70:o4:10:ARG:HD2	75:o9:4:GLN:OE1	2.17	0.45
71:o5:104:GLN:OE1	71:o5:108:GLN:NE2	2.49	0.45
1:2:1504:G:OP1	21:C9:97:SER:HB2	2.15	0.45
3:S1:129:THR:HB	3:S1:180:THR:HA	1.99	0.45
5:S3:34:TYR:OH	5:S3:37:VAL:HG13	2.17	0.45
6:S4:95:THR:HG22	26:D4:16:PRO:HG2	1.98	0.45
6:S4:112:HIS:NE2	6:S4:237:SER:O	2.50	0.45
8:S6:26:VAL:HG21	8:S6:40:ALA:HB1	1.98	0.45
18:C6:115:THR:HA	18:C6:118:ILE:HG23	1.98	0.45
27:D5:43:ASP:HB2	27:D5:46:LYS:HD2	1.98	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
46:L9:16:VAL:HG12	46:L9:29:GLY:HA3	1.99	0.45
46:L9:115:ARG:HG2	46:L9:123:ILE:HG23	1.98	0.45
50:M4:105:GLN:HE22	50:M4:109:ARG:NH2	2.14	0.45
54:M8:170:ARG:HA	54:M8:174:ARG:HD2	1.98	0.45
61:N5:46:TYR:CD2	71:O5:75:TYR:HB3	2.51	0.45
64:N8:63:LYS:HE3	64:N8:68:PHE:CE2	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
3:s1:226:GLY:HA2	36:5:2536:A:H4'	1.99	0.45
6:s4:100:ARG:NH2	6:s4:122:LYS:HA	2.32	0.45
9:s7:177:THR:OG1	9:s7:178:GLY:N	2.50	0.45
20:c8:70:VAL:HG12	20:c8:74:GLN:NE2	2.31	0.45
25:d3:65:ASN:ND2	25:d3:116:ASP:OD1	2.46	0.45
26:d4:34:ASN:HB3	26:d4:35:VAL:H	1.50	0.45
27:d5:49:ARG:O	27:d5:53:GLU:HB2	2.16	0.45
33:e1:109:ASP:O	33:e1:111:GLU:N	2.50	0.45
34:sR:217:ASP:OD1	34:sR:217:ASP:N	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
36:5:375:A:OP2	62:n6:89:LYS:NZ	2.37	0.45
36:5:567:G:H2'	36:5:568:G:C8	2.51	0.45
36:5:1024:G:N2	36:5:1026:A:OP2	2.50	0.45
36:5:2582:C:H2'	36:5:2583:C:O4'	2.16	0.45
39:l2:187:HIS:ND1	39:l2:190:ARG:NH1	2.64	0.45
40:l3:21:ARG:HG2	40:l3:269:GLN:HG2	1.99	0.45
42:l5:45:ASN:OD1	57:n1:33:VAL:HG21	2.16	0.45
43:l6:41:ILE:HB	43:l6:85:ILE:HB	1.98	0.45
44:l7:43:ILE:O	44:l7:47:ARG:HG3	2.15	0.45
47:m0:16:PRO:HG3	47:m0:128:ARG:NH1	2.32	0.45
47:m0:145:LYS:HD3	47:m0:167:LEU:HD21	1.99	0.45
50:m4:16:GLU:OE2	56:n0:149:LYS:HD2	2.16	0.45
52:m6:46:GLU:HA	52:m6:135:TYR:O	2.15	0.45
63:n7:124:ALA:O	63:n7:126:LYS:N	2.49	0.45
69:o3:49:ILE:HA	69:o3:99:ARG:O	2.16	0.45
75:o9:44:TRP:O	75:o9:48:LYS:NZ	2.47	0.45
79:q3:49:ARG:HB2	79:q3:55:TRP:CH2	2.52	0.45
82:p0:25:LEU:HD13	82:p0:88:PHE:CE2	2.52	0.45
1:2:304:U:OP1	13:C1:136:ARG:HD3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:333:A:P	10:S8:48:THR:HB	2.56	0.45
1:2:1290:U:H2'	1:2:1291:G:C8	2.51	0.45
3:S1:179:SER:HB3	3:S1:183:GLN:HB2	1.99	0.45
4:S2:121:VAL:O	4:S2:125:ILE:HG13	2.16	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
7:S5:163:SER:HB3	30:D8:48:VAL:HG22	1.99	0.45
15:C3:11:ILE:HG13	15:C3:11:ILE:O	2.15	0.45
20:C8:5:VAL:HG23	27:D5:42:LEU:HD23	1.99	0.45
32:E0:41:THR:HG22	32:E0:45:VAL:HG21	1.97	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
36:1:1407:A:O3'	68:O2:33:ARG:NH2	2.50	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
42:L5:56:THR:O	42:L5:58:LYS:N	2.49	0.45
44:L7:93:ASN:OD1	44:L7:93:ASN:N	2.48	0.45
46:L9:90:MET:HE3	46:L9:181:VAL:HG23	1.99	0.45
53:M7:26:PHE:CE1	53:M7:120:ASN:HA	2.51	0.45
60:N4:39:LEU:HD12	60:N4:39:LEU:HA	1.87	0.45
1:6:200:A:H2'	1:6:201:G:C8	2.51	0.45
1:6:478:A:OP1	80:e0:37:ARG:NH1	2.49	0.45
1:6:542:A:H8	1:6:543:C:H5'	1.82	0.45
1:6:776:G:O6	26:d4:11:LYS:HE2	2.16	0.45
1:6:864:U:OP2	29:d7:26:GLN:NE2	2.49	0.45
1:6:901:G:N2	16:c4:54:GLU:OE1	2.49	0.45
1:6:924:A:H2'	1:6:925:G:C8	2.51	0.45
1:6:1417:A:H2'	1:6:1418:G:O4'	2.16	0.45
2:s0:125:ASP:O	2:s0:129:ASP:HB2	2.15	0.45
3:s1:87:ARG:NH2	3:s1:89:ASP:OD1	2.49	0.45
5:s3:62:ASN:ND2	5:s3:62:ASN:O	2.50	0.45
5:s3:67:ASN:O	5:s3:70:THR:OG1	2.23	0.45
5:s3:125:TYR:O	5:s3:129:SER:OG	2.22	0.45
6:s4:129:VAL:HG12	6:s4:156:VAL:HG23	1.98	0.45
21:c9:78:LYS:HG3	21:c9:93:HIS:NE2	2.31	0.45
28:d6:15:ARG:HD2	28:d6:18:VAL:HG12	1.99	0.45
36:5:189:G:C2	36:5:191:U:C4	3.03	0.45
36:5:938:C:H3'	64:n8:26:ARG:HH12	1.81	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
36:5:1634:G:N7	63:n7:17:ARG:NH2	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:3281:U:H5'	36:5:3282:U:OP2	2.16	0.45
41:l4:47:ARG:NH1	41:l4:109:TRP:O	2.49	0.45
51:m5:53:TYR:HB2	51:m5:133:ILE:HG21	1.99	0.45
70:o4:84:CYS:O	70:o4:88:ARG:HB2	2.16	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
4:S2:241:ASP:HA	4:S2:244:SER:HB2	1.97	0.45
5:S3:94:ARG:CZ	35:SM:134:ASP:OD1	2.60	0.45
9:S7:162:ILE:HG22	9:S7:165:LYS:HD2	1.98	0.45
11:S9:92:LYS:C	11:S9:94:ASP:H	2.24	0.45
13:C1:94:ILE:HG12	25:D3:16:ARG:HD2	1.98	0.45
17:C5:86:VAL:O	17:C5:88:GLU:N	2.50	0.45
22:D0:42:VAL:HG13	22:D0:52:LYS:NZ	2.31	0.45
24:D2:66:ASN:OD1	24:D2:68:ARG:HG3	2.16	0.45
35:SM:44:PRO:HA	36:1:2678:A:C4	2.52	0.45
35:SM:89:ARG:C	35:SM:91:THR:H	2.24	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
36:1:1895:A:O2'	36:1:3053:G:H4'	2.17	0.45
36:1:2747:A:H2'	36:1:2748:A:C8	2.51	0.45
39:L2:192:LYS:HB3	39:L2:193:ARG:NH2	2.31	0.45
48:M1:85:LYS:HE3	48:M1:85:LYS:HB2	1.75	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
59:N3:40:LYS:HG3	59:N3:57:MET:HE2	1.98	0.45
61:N5:105:VAL:HG12	61:N5:106:ASP:N	2.32	0.45
1:6:520:A:H2'	1:6:521:A:C8	2.51	0.45
1:6:1515:A:OP2	5:s3:7:LYS:HB2	2.17	0.45
5:s3:76:ARG:HG3	12:c0:65:TYR:CE1	2.51	0.45
6:s4:133:LYS:HE3	6:s4:133:LYS:HB2	1.61	0.45
7:s5:41:LYS:HE2	7:s5:41:LYS:HB3	1.67	0.45
8:s6:152:ASP:OD1	8:s6:154:ARG:NH2	2.50	0.45
15:c3:21:ASN:HB2	15:c3:22:ALA:H	1.59	0.45
16:c4:10:ASN:O	16:c4:12:GLN:HG2	2.16	0.45
18:c6:78:VAL:O	18:c6:81:ILE:HG12	2.16	0.45
29:d7:36:LYS:HE2	29:d7:43:ILE:HG22	1.97	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:l2:128:ARG:HA	39:l2:169:ILE:HD13	1.99	0.45
42:l5:226:TYR:HE1	42:l5:236:LEU:HD11	1.81	0.45
49:m3:36:ARG:HG3	49:m3:39:ARG:HH21	1.81	0.45
49:m3:74:GLY:HA3	49:m3:98:ASP:HB2	1.99	0.45
50:m4:116:GLU:O	50:m4:120:VAL:HG23	2.17	0.45
1:2:761:G:P	11:S9:54:ARG:HH12	2.36	0.45
1:2:1494:C:H2'	1:2:1495:C:H6	1.81	0.45
5:S3:176:LEU:H	5:S3:176:LEU:HD12	1.82	0.45
18:C6:82:ARG:HH22	18:C6:114:ARG:HB3	1.81	0.45
21:C9:98:GLY:O	21:C9:102:ARG:HB2	2.17	0.45
34:SR:16:HIS:HB3	34:SR:17:ASN:H	1.64	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
36:1:1128:U:OP1	47:M0:4:ARG:NH2	2.47	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
38:4:34:U:O2'	38:4:35:C:OP2	2.29	0.45
40:L3:188:ILE:HA	40:L3:191:LYS:HD2	1.98	0.45
42:L5:76:ALA:CB	42:L5:109:THR:HG22	2.47	0.45
53:M7:108:ASP:OD1	53:M7:111:LYS:NZ	2.37	0.45
54:M8:133:LYS:HB2	54:M8:135:GLN:HE22	1.82	0.45
59:N3:85:TRP:CE2	59:N3:93:LEU:HD21	2.52	0.45
70:O4:84:CYS:O	70:O4:88:ARG:HG2	2.16	0.45
1:6:75:U:O2'	1:6:76:A:O5'	2.22	0.45
1:6:1146:G:N3	1:6:1635:A:H2	2.14	0.45
5:s3:141:LYS:HA	5:s3:147:ALA:HA	1.98	0.45
7:s5:128:ASN:O	7:s5:132:VAL:HG23	2.16	0.45
8:s6:25:ARG:HA	8:s6:28:PHE:CD2	2.51	0.45
20:c8:30:TYR:HE2	20:c8:40:ARG:HD2	1.80	0.45
33:e1:120:GLU:HB3	33:e1:131:PHE:H	1.82	0.45
35:sM:33:LYS:HD2	36:5:2667:A:H5"	1.99	0.45
35:sM:65:THR:OG1	35:sM:66:ALA:N	2.50	0.45
36:5:181:U:O3'	73:o7:75:LYS:HD3	2.16	0.45
36:5:804:C:H5'	41:l4:93:MET:HE1	1.99	0.45
36:5:1021:G:N1	36:5:1032:C:O2	2.49	0.45
36:5:1322:U:OP1	56:n0:117:ARG:NH2	2.45	0.45
36:5:1875:G:OP2	55:m9:20:ARG:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:1940:G:N2	36:5:3362:A:H8	2.12	0.45
36:5:2201:G:N2	39:l2:224:THR:HG21	2.27	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
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
40:l3:41:VAL:HA	40:l3:185:GLY:CA	2.34	0.45
42:l5:219:PHE:HE1	42:l5:227:LEU:HD11	1.82	0.45
47:m0:42:THR:O	47:m0:139:ARG:NH2	2.50	0.45
50:m4:50:LYS:HD3	50:m4:85:TRP:CD1	2.51	0.45
61:n5:108:LEU:HA	61:n5:108:LEU:HD23	1.71	0.45
70:o4:47:CYS:HG	70:o4:84:CYS:HG	1.61	0.45
72:o6:42:SER:O	72:o6:46:GLU:HG2	2.16	0.45
78:q2:77:CYS:SG	78:q2:79:THR:HG23	2.56	0.45
1:2:621:A:N3	1:2:1107:G:H1'	2.32	0.45
1:2:885:G:H2'	1:2:886:U:C6	2.52	0.45
2:S0:87:LEU:HA	2:S0:87:LEU:HD12	1.74	0.45
4:S2:144:TRP:CE2	24:D2:97:ARG:HD2	2.51	0.45
5:S3:5:ILE:HG23	5:S3:9:ARG:HH11	1.81	0.45
6:S4:62:LYS:HB2	6:S4:62:LYS:NZ	2.32	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
36:1:8:C:H2'	36:1:9:U:O4'	2.17	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
38:4:24:G:OP2	62:N6:13:ARG:HD3	2.17	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:L4:205:PRO:HB3	41:L4:247:PHE:CD2	2.51	0.45
45:L8:78:PHE:O	45:L8:80:TYR:N	2.47	0.45
45:L8:149:LYS:O	45:L8:176:PRO:HG2	2.17	0.45
78:Q2:83:LEU:HD22	78:Q2:83:LEU:HA	1.78	0.45
1:6:528:U:H2'	1:6:529:A:H8	1.81	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
2:s0:79:ARG:NH1	2:s0:164:ASN:O	2.39	0.45
7:s5:109:LYS:HE3	7:s5:109:LYS:HB2	1.83	0.45
11:s9:116:LEU:O	11:s9:118:LEU:HD12	2.16	0.45
16:c4:61:MET:HE3	16:c4:61:MET:HB3	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:c5:7:ALA:C	17:c5:9:LYS:H	2.24	0.45
36:5:213:A:O4'	62:n6:2:ALA:HA	2.17	0.45
36:5:308:A:H5'	36:5:2223:A:O2'	2.16	0.45
36:5:860:G:C5	39:l2:181:LYS:HB3	2.52	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
36:5:2138:A:O2'	73:o7:3:LYS:HG2	2.17	0.45
36:5:2533:G:H22	36:5:2546:C:H42	1.64	0.45
36:5:2854:U:OP2	47:m0:3:ARG:NH2	2.49	0.45
40:l3:14:LEU:HD13	40:l3:262:TRP:CH2	2.52	0.45
41:l4:309:ARG:NH2	41:l4:312:VAL:HB	2.32	0.45
42:l5:208:MET:HE3	42:l5:223:PHE:CD2	2.52	0.45
45:l8:91:PHE:CE2	45:l8:185:ARG:HB3	2.52	0.45
50:m4:62:GLN:H	50:m4:62:GLN:HG2	1.50	0.45
69:o3:58:GLU:HG2	69:o3:63:LYS:HG3	1.98	0.45
70:o4:67:LYS:O	70:o4:71:THR:OG1	2.35	0.45
78:q2:25:VAL:HG22	78:q2:72:LEU:HD22	1.98	0.45
1:2:848:C:H2'	1:2:849:C:C6	2.51	0.45
3:S1:70:LEU:HD21	3:S1:79:HIS:CD2	2.51	0.45
8:S6:34:GLN:O	8:S6:52:ILE:HG13	2.17	0.45
17:C5:21:ASP:HB2	17:C5:24:LYS:HE3	1.98	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
36:1:22:G:H1'	38:4:104:A:N3	2.31	0.45
36:1:289:A:H5'	51:M5:95:GLN:O	2.17	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
36:1:1467:A:N1	36:1:1511:U:O2'	2.44	0.45
36:1:3360:C:N4	36:1:3361:G:O6	2.49	0.45
37:3:60:G:H2'	37:3:61:G:C8	2.52	0.45
40:L3:32:PHE:CD1	40:L3:182:GLN:HB3	2.52	0.45
52:M6:106:GLU:H	52:M6:106:GLU:HG2	1.53	0.45
53:M7:116:HIS:HB3	53:M7:149:VAL:HB	1.99	0.45
56:N0:91:TYR:O	56:N0:137:ARG:NH1	2.50	0.45
57:N1:131:GLN:HG3	57:N1:132:PRO:HD2	1.98	0.45
61:N5:142:ILE:HD13	61:N5:142:ILE:HA	1.74	0.45
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
71:O5:21:LEU:HD22	71:O5:25:LYS:HE2	1.99	0.45
1:6:542:A:C8	1:6:543:C:H5'	2.52	0.45
1:6:1228:G:N3	1:6:1228:G:H2'	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1498:G:OP1	21:c9:75:LYS:HD2	2.17	0.45
2:s0:81:PHE:HB3	2:s0:170:ILE:HD12	1.99	0.45
5:s3:195:SER:HB2	5:s3:200:LYS:HG2	1.97	0.45
8:s6:21:GLU:O	8:s6:25:ARG:HG3	2.17	0.45
9:s7:126:LEU:HB2	9:s7:173:TYR:HE2	1.82	0.45
18:c6:47:LYS:HE3	18:c6:82:ARG:NH1	2.32	0.45
21:c9:10:ALA:HB3	21:c9:13:ASP:HB2	1.99	0.45
22:d0:41:ILE:HG13	22:d0:107:THR:HG21	1.99	0.45
33:e1:88:PRO:HA	33:e1:89:LYS:HA	1.69	0.45
33:e1:113:LYS:HB3	33:e1:113:LYS:HE3	1.73	0.45
34:sR:65:SER:N	34:sR:86:ASP:OD2	2.47	0.45
36:5:584:G:H1'	69:o3:45:LEU:HD12	1.98	0.45
36:5:1137:C:H2'	36:5:1138:U:O4'	2.16	0.45
36:5:1316:C:OP2	52:m6:133:ARG:NE	2.50	0.45
36:5:2796:G:H4'	36:5:2798:C:C6	2.52	0.45
42:l5:187:THR:HG22	42:l5:189:GLU:HB2	1.98	0.45
46:l9:7:GLU:HA	46:l9:68:LEU:HD11	1.99	0.45
61:n5:53:HIS:ND1	61:n5:54:TYR:O	2.49	0.45
67:o1:70:ARG:O	67:o1:71:LEU:HD23	2.16	0.45
1:2:297:U:H5"	6:S4:37:LYS:HG2	1.98	0.45
1:2:872:G:H2'	1:2:873:U:O4'	2.17	0.45
1:2:1039:A:H5"	23:D1:62:ARG:HH21	1.81	0.45
1:2:1450:U:H2'	1:2:1451:C:C6	2.52	0.45
4:S2:238:SER:C	4:S2:240:LEU:H	2.23	0.45
9:S7:35:LYS:NZ	9:S7:39:ARG:HD2	2.32	0.45
16:C4:129:LYS:HE3	16:C4:129:LYS:HB2	1.86	0.45
36:1:617:G:H4'	53:M7:171:ARG:HH21	1.81	0.45
36:1:712:G:N2	36:1:754:G:O3'	2.50	0.45
36:1:715:A:H4'	36:1:716:A:OP1	2.16	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
40:L3:233:TRP:CD1	40:L3:265:ALA:HB1	2.52	0.45
44:L7:184:LEU:HD11	44:L7:202:LEU:HD21	1.99	0.45
61:N5:34:LEU:HD23	61:N5:35:PRO:HD2	1.99	0.45
75:O9:41:ARG:HG3	75:O9:42:ARG:H	1.81	0.45
1:6:55:A:N6	1:6:403:G:H1'	2.32	0.45
1:6:230:C:H42	1:6:235:G:H1	1.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:946:U:H2'	1:6:947:U:C6	2.52	0.45
4:s2:72:LEU:HD12	4:s2:72:LEU:HA	1.81	0.45
16:c4:135:ARG:NH1	16:c4:137:LEU:HD21	2.32	0.45
20:c8:140:THR:HA	20:c8:143:ARG:HH12	1.81	0.45
30:d8:26:THR:HB	30:d8:44:VAL:HG22	1.99	0.45
36:5:908:G:H4'	36:5:909:G:O5'	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
36:5:1805:C:H4'	70:o4:77:GLY:H	1.82	0.45
36:5:1825:G:OP1	74:o8:48:SER:HB3	2.16	0.45
38:8:44:A:H2'	38:8:45:C:C6	2.51	0.45
41:l4:60:THR:HG22	41:l4:62:ALA:N	2.32	0.45
48:m1:29:ARG:HA	48:m1:32:ARG:NH2	2.32	0.45
63:n7:46:ILE:HD13	63:n7:49:TYR:N	2.32	0.45
1:2:794:U:H1'	1:2:795:U:OP1	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
6:S4:15:PRO:HG2	6:S4:18:TRP:CE2	2.51	0.45
6:S4:23:LEU:O	6:S4:24:SER:OG	2.32	0.45
6:S4:158:ASP:OD2	6:S4:174:LYS:NZ	2.46	0.45
11:S9:34:PHE:CE1	11:S9:105:LEU:HB3	2.52	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
27:D5:74:SER:HA	27:D5:77:ARG:NH2	2.32	0.45
36:1:114:A:O2'	51:M5:50:ARG:HB3	2.17	0.45
36:1:938:C:H3'	64:N8:26:ARG:HH12	1.82	0.45
36:1:2140:U:O2'	36:1:2978:U:H5'	2.17	0.45
36:1:2210:G:OP2	36:1:2210:G:H8	2.00	0.45
36:1:2894:C:H2'	36:1:2895:G:C8	2.52	0.45
39:L2:105:GLY:HA3	39:L2:160:SER:HB3	1.99	0.45
41:L4:10:SER:O	41:L4:12:THR:N	2.50	0.45
42:L5:120:LYS:O	42:L5:248:ARG:NH2	2.49	0.45
43:L6:176:PHE:O	50:M4:113:THR:HG23	2.16	0.45
46:L9:3:TYR:HA	56:N0:142:GLN:OE1	2.16	0.45
47:M0:20:SER:H	47:M0:23:ASN:HB3	1.82	0.45
51:M5:38:ARG:CZ	51:M5:60:VAL:HG13	2.47	0.45
51:M5:150:TRP:CH2	51:M5:151:ILE:HG12	2.52	0.45
1:6:899:G:H5'	16:c4:45:GLY:O	2.17	0.45
1:6:1002:G:C6	1:6:1003:A:N7	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:c0:2:LEU:HB3	12:c0:3:MET:H	1.51	0.45
12:c0:3:MET:HE3	12:c0:8:ARG:NH1	2.32	0.45
12:c0:50:THR:HG22	12:c0:55:VAL:HG22	1.98	0.45
36:5:224:C:H2'	36:5:225:C:H6	1.82	0.45
36:5:712:G:H2'	36:5:713:U:C6	2.51	0.45
36:5:1010:G:N3	47:m0:194:GLY:HA3	2.32	0.45
36:5:1333:C:H1'	44:l7:209:ASN:ND2	2.32	0.45
36:5:1671:C:P	55:m9:60:LYS:HZ1	2.37	0.45
36:5:2140:U:O2'	36:5:2978:U:H5'	2.17	0.45
36:5:2242:A:H5'	39:l2:243:THR:HG23	1.99	0.45
36:5:2367:A:H2'	36:5:2368:A:C8	2.52	0.45
40:l3:345:ASN:OD1	40:l3:347:SER:HB2	2.17	0.45
42:l5:40:HIS:HE1	42:l5:42:ALA:HB3	1.80	0.45
43:l6:52:VAL:HA	43:l6:67:GLY:HA2	1.99	0.45
46:l9:117:PHE:HB3	46:l9:124:ARG:HH21	1.82	0.45
47:m0:65:LEU:HD23	47:m0:159:PHE:CZ	2.52	0.45
54:m8:134:GLY:O	54:m8:137:THR:OG1	2.27	0.45
55:m9:172:ARG:O	55:m9:176:ARG:HG2	2.16	0.45
74:o8:17:ARG:HG2	74:o8:19:ASP:OD2	2.17	0.45
75:o9:21:ARG:HD3	75:o9:22:PRO:O	2.17	0.45
1:2:100:A:H2'	1:2:101:U:O4'	2.16	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
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
2:S0:56:LYS:HD2	2:S0:158:VAL:HG23	1.98	0.44
3:S1:36:SER:HB3	3:S1:231:LEU:HD22	1.98	0.44
3:S1:229:MET:HA	3:S1:232:HIS:ND1	2.32	0.44
4:S2:116:LYS:HG2	4:S2:127:ALA:HB3	1.98	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
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
25:D3:107:PHE:CE1	25:D3:123:LYS:HB3	2.53	0.44
36:1:549:U:H2'	36:1:550:A:H8	1.81	0.44
36:1:1717:U:H2'	36:1:1718:G:C8	2.52	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
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
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
78:Q2:77:CYS:C	78:Q2:79:THR:H	2.25	0.44
1:6:594:A:H4'	1:6:595:G:H5'	1.98	0.44
1:6:1235:C:H5'	33:e1:146:SER:HB2	1.98	0.44
1:6:1617:U:H2'	1:6:1618:C:C6	2.52	0.44
3:s1:88:VAL:HG22	3:s1:98:THR:HG22	1.99	0.44
3:s1:149:GLN:HE22	3:s1:154:SER:HB3	1.82	0.44
8:s6:191:ARG:HD3	8:s6:191:ARG:HA	1.83	0.44
23:d1:78:LEU:HD13	23:d1:78:LEU:HA	1.81	0.44
24:d2:75:ILE:HD13	24:d2:75:ILE:HA	1.82	0.44
36:5:197:G:H2'	36:5:198:A:C8	2.52	0.44
36:5:291:C:OP1	51:m5:68:ARG:HG3	2.17	0.44
36:5:518:G:H2'	36:5:520:U:H5'	1.99	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
36:5:3268:A:O2'	36:5:3269:U:H2'	2.17	0.44
40:l3:68:HIS:CD2	40:l3:69:LYS:HG2	2.52	0.44
40:l3:211:GLN:HE21	40:l3:284:ARG:HA	1.81	0.44
41:l4:8:VAL:O	41:l4:16:THR:HG22	2.17	0.44
53:m7:31:GLU:CG	53:m7:60:PHE:HA	2.47	0.44
59:n3:23:MET:HE3	59:n3:100:GLY:HA3	1.98	0.44
71:o5:65:ALA:O	71:o5:69:LEU:HD23	2.17	0.44
1:2:947:U:H2'	1:2:948:G:C8	2.52	0.44
1:2:1597:A:OP1	31:D9:19:ARG:NH2	2.50	0.44
4:S2:150:GLN:HA	4:S2:151:PRO:HD3	1.79	0.44
4:S2:227:PRO:C	4:S2:229:LEU:H	2.26	0.44
9:S7:76:LYS:H	9:S7:76:LYS:HG2	1.54	0.44
14:C2:73:LYS:HZ2	33:E1:108:VAL:HG13	1.82	0.44
18:C6:115:THR:HB	18:C6:118:ILE:O	2.17	0.44
21:C9:28:LEU:HD12	21:C9:29:GLU:H	1.82	0.44
21:C9:111:ILE:HG23	21:C9:113:ILE:HG13	1.99	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
34:SR:274:LEU:HD13	34:SR:313:TRP:CD2	2.51	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
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
40:L3:296:THR:HG21	40:L3:356:LEU:HB2	1.98	0.44
54:M8:123:THR:OG1	54:M8:125:ASP:OD2	2.20	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:N0:14:LEU:H	56:N0:56:GLY:HA2	1.81	0.44
60:N4:52:THR:O	60:N4:56:ARG:HG3	2.17	0.44
68:O2:104:ASN:O	68:O2:108:ILE:HG13	2.17	0.44
1:6:846:G:H2'	1:6:847:A:C8	2.53	0.44
1:6:1634:C:H4'	1:6:1635:A:OP2	2.16	0.44
8:s6:93:LYS:HB2	8:s6:93:LYS:NZ	2.33	0.44
11:s9:110:GLN:OE1	11:s9:126:ARG:HG2	2.17	0.44
13:c1:78:THR:HG21	13:c1:118:GLN:HA	1.99	0.44
17:c5:96:ILE:HD13	17:c5:116:LEU:HB3	1.99	0.44
26:d4:89:TYR:O	26:d4:92:VAL:HG22	2.17	0.44
34:sR:18:GLY:O	34:sR:308:ASN:HA	2.17	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
40:l3:37:ARG:HA	40:l3:186:GLY:HA2	2.00	0.44
41:l4:193:LYS:HB2	41:l4:193:LYS:HE3	1.70	0.44
42:l5:90:HIS:NE2	42:l5:229:ASP:OD2	2.44	0.44
44:l7:68:ASP:O	44:l7:71:ALA:N	2.50	0.44
48:m1:75:LYS:O	48:m1:79:ILE:HG13	2.16	0.44
48:m1:152:HIS:O	48:m1:153:LYS:HG2	2.17	0.44
50:m4:2:SER:HB2	50:m4:6:ILE:HD11	1.98	0.44
52:m6:171:LYS:O	52:m6:175:THR:HG22	2.18	0.44
57:n1:52:MET:HA	57:n1:95:HIS:CD2	2.52	0.44
63:n7:36:HIS:H	63:n7:37:PRO:HD3	1.82	0.44
74:o8:12:LEU:HA	74:o8:12:LEU:HD13	1.86	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
4:S2:106:ASP:OD2	4:S2:110:HIS:ND1	2.49	0.44
14:C2:126:TRP:O	14:C2:128:ALA:N	2.50	0.44
19:C7:41:ILE:HD13	19:C7:47:ARG:HA	1.99	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
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
36:1:3037:U:H5"	40:L3:348:ARG:NH1	2.32	0.44
39:L2:58:LEU:HD13	39:L2:75:ILE:HG21	1.99	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
65:N9:35:VAL:HG12	65:N9:40:ARG:HG3	1.99	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:Q3:33:GLN:HB3	79:Q3:69:TYR:HB3	1.99	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
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
5:s3:122:VAL:O	5:s3:126:VAL:HG23	2.17	0.44
8:s6:175:ILE:HB	8:s6:178:LEU:HD22	1.99	0.44
19:c7:30:THR:HG22	34:sR:127:ARG:NH2	2.33	0.44
25:d3:6:PRO:HG3	25:d3:14:LYS:HG2	2.00	0.44
34:sR:112:SER:HB2	34:sR:153:GLN:HA	1.97	0.44
36:5:147:U:C4	45:l8:157:VAL:HG13	2.52	0.44
36:5:508:U:H2'	36:5:509:U:C6	2.53	0.44
36:5:1386:A:N3	41:l4:180:LYS:HA	2.33	0.44
39:l2:64:ARG:HH22	45:l8:38:GLN:HA	1.82	0.44
40:l3:138:ALA:O	40:l3:140:ASP:N	2.51	0.44
41:l4:263:GLY:HA2	41:l4:268:ALA:O	2.18	0.44
44:l7:123:THR:O	44:l7:126:LEU:HB2	2.16	0.44
47:m0:4:ARG:HG3	47:m0:8:CYS:SG	2.58	0.44
50:m4:32:LEU:HD11	50:m4:94:TRP:CG	2.52	0.44
61:n5:73:MET:HE1	61:n5:141:TYR:CE1	2.49	0.44
63:n7:14:VAL:HG23	70:o4:89:ILE:HB	2.00	0.44
65:n9:31:SER:C	65:n9:33:LYS:H	2.26	0.44
68:o2:24:ARG:HG2	68:o2:25:TYR:CZ	2.53	0.44
82:p0:46:ARG:HD3	82:p0:46:ARG:HA	1.75	0.44
1:2:76:A:N6	1:2:80:A:O2'	2.48	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
1:2:1010: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
2:S0:69:ASN:HB3	2:S0:71:GLU:CD	2.42	0.44
2:S0:175:TYR:CD1	2:S0:199:PRO:HA	2.53	0.44
7:S5:42:LEU:HD23	7:S5:42:LEU:H	1.82	0.44
8:S6:24:ILE:O	8:S6:26:VAL:N	2.50	0.44
11:S9:163:PRO:C	11:S9:165:GLY:H	2.25	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
36:1:1364:C:H5"	54:M8:3:ILE:HD13	1.99	0.44
36:1:1403:C:H5'	68:O2:67:SER:HB3	1.99	0.44
36:1:2992:U:H1'	53:M7:69:ARG:NH2	2.33	0.44
36:1:3328:G:C2	36:1:3379:C:C2	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:L7:86:VAL:HG13	44:L7:136:TYR:HB3	1.98	0.44
50:M4:21:VAL:HB	50:M4:63:VAL:HG13	1.99	0.44
55:M9:77:GLY:O	55:M9:81:ARG:HD3	2.17	0.44
67:O1:13:THR:HG23	67:O1:72:ARG:HH11	1.83	0.44
67:O1:25:PHE:HD2	67:O1:28:ARG:HD2	1.83	0.44
1:6:74:U:H5"	1:6:75:U:OP2	2.17	0.44
1:6:121:U:O2'	6:s4:33:ALA:O	2.19	0.44
1:6:187:G:OP2	10:s8:142:LYS:NZ	2.50	0.44
1:6:333:A:C6	1:6:334:G:C6	3.06	0.44
1:6:472:U:O2'	1:6:769:A:N3	2.38	0.44
1:6:804:A:C8	24:d2:107:SER:HA	2.53	0.44
1:6:1243:G:H5"	1:6:1243:G:N3	2.32	0.44
5:s3:135:GLU:HB3	5:s3:187:LYS:HB3	1.99	0.44
5:s3:167:PHE:HA	5:s3:190:ARG:HE	1.83	0.44
7:s5:99:MET:HE2	7:s5:99:MET:HB3	1.75	0.44
9:s7:50:ASP:HA	9:s7:56:LYS:HG2	1.99	0.44
24:d2:94:LEU:HD11	24:d2:102:VAL:HG23	2.00	0.44
34:sR:103:PHE:CD1	34:sR:138:GLY:HA2	2.52	0.44
35:sM:49:LYS:HG3	35:sM:50:ASN:OD1	2.18	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
38:8:97:A:OP1	71:o5:63:ARG:NH2	2.42	0.44
44:l7:31:ALA:HA	44:l7:34:LYS:HB2	1.98	0.44
45:l8:72:PRO:HA	45:l8:73:PRO:HD3	1.85	0.44
48:m1:131:MET:HE3	48:m1:131:MET:HB3	1.86	0.44
49:m3:47:ALA:HB1	49:m3:48:PRO:HD2	1.99	0.44
50:m4:115:PHE:O	50:m4:118:PHE:HB3	2.18	0.44
52:m6:10:ASP:OD1	52:m6:37:ARG:NH2	2.43	0.44
68:o2:24:ARG:HD3	68:o2:25:TYR:CZ	2.52	0.44
2:S0:126:PRO:HA	2:S0:133:ILE:HD11	1.99	0.44
9:S7:67:LEU:HD22	9:S7:71:HIS:CD2	2.52	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:D3:69:ARG:NH1	25:D3:116:ASP:OD2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:D3:88:PRO:O	25:D3:89:ASN:HB2	2.17	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
29:D7:14:SER:O	29:D7:18:LYS:HE3	2.17	0.44
34:SR:152:SER:OG	34:SR:199:ILE:O	2.32	0.44
36:1:109:A:H4'	36:1:110:G:OP1	2.18	0.44
36:1:748:U:H2'	36:1:749:C:C6	2.53	0.44
36:1:1491:A:N7	75:O9:2:ALA:HB3	2.32	0.44
36:1:1942:U:O2'	36:1:3345:G:O2'	2.12	0.44
36:1:3067:C:H3'	55:M9:62:ARG:NH1	2.33	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
46:L9:88:TYR:CZ	46:L9:184:LYS:HG2	2.53	0.44
63:N7:135:ARG:HG2	63:N7:135:ARG:HH21	1.83	0.44
64:N8:7:LYS:HA	64:N8:7:LYS:HD3	1.73	0.44
74:O8:15:THR:HG22	74:O8:45:VAL:HG11	2.00	0.44
74:O8:17:ARG:O	74:O8:20:VAL:HG23	2.18	0.44
79:Q3:3:LYS:HB3	79:Q3:3:LYS:HE2	1.74	0.44
79:Q3:37:TYR:HB2	79:Q3:47:VAL:HB	1.98	0.44
1:6:188:A:H5"	1:6:189:C:OP2	2.18	0.44
1:6:197:A:H61	10:s8:138:ASN:HD22	1.65	0.44
1:6:1689:A:H2'	1:6:1690:G:C8	2.50	0.44
1:6:1755:A:C8	25:d3:63:GLN:HG3	2.52	0.44
7:s5:79:ASN:OD1	7:s5:83:ARG:NH2	2.50	0.44
26:d4:8:ARG:NE	26:d4:28:LEU:HD11	2.33	0.44
27:d5:46:LYS:HE3	27:d5:46:LYS:HB2	1.77	0.44
28:d6:71:LEU:HD13	28:d6:73:TYR:OH	2.18	0.44
30:d8:54:LEU:HD12	30:d8:55:VAL:H	1.83	0.44
30:d8:64:ARG:HB3	30:d8:65:ARG:H	1.56	0.44
36:5:63:A:P	51:m5:172:ARG:HH22	2.40	0.44
36:5:942:U:C4	64:n8:16:SER:HA	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
36:5:3022:G:O2'	36:5:3031:G:O6	2.33	0.44
39:l2:65:ASP:HB3	39:l2:68:LYS:O	2.17	0.44
53:m7:30:ARG:HA	53:m7:119:VAL:CG1	2.48	0.44
57:n1:12:ARG:HD3	57:n1:13:TYR:CE1	2.53	0.44
61:n5:40:LEU:HB3	61:n5:41:ALA:H	1.61	0.44
71:o5:9:LEU:HB3	71:o5:17:LEU:HD21	2.00	0.44
71:o5:83:LYS:O	71:o5:85:THR:N	2.51	0.44
82:p0:11:TYR:O	82:p0:15:LEU:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
9:S7:30:SER:HB3	9:S7:34:LEU:HD12	1.98	0.44
15:C3:92:ILE:O	15:C3:96:VAL:HG23	2.17	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
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
37:3:61:G:H2'	37:3:62:U:H6	1.81	0.44
43:L6:31:ARG:HD2	69:O3:107:ILE:O	2.18	0.44
44:L7:151:ARG:HD2	44:L7:244:ASN:ND2	2.33	0.44
49:M3:164:GLU:C	49:M3:166:ALA:H	2.25	0.44
51:M5:58:GLY:HA3	51:M5:142:ILE:HD13	1.98	0.44
68:O2:55:ILE:HD12	68:O2:55:ILE:HA	1.84	0.44
70:O4:46:ASP:CG	70:O4:80:ARG:HD2	2.43	0.44
78:Q2:35:LEU:C	78:Q2:37:ALA:H	2.26	0.44
1:6:151:G:H22	1:6:163:G:N2	2.16	0.44
3:s1:76:SER:C	3:s1:78:ASP:H	2.25	0.44
4:s2:54:GLU:O	4:s2:58:LEU:HB2	2.18	0.44
5:s3:34:TYR:CE2	5:s3:37:VAL:HG13	2.51	0.44
35:sM:65:THR:O	35:sM:67:GLY:N	2.47	0.44
36:5:106:A:H2'	36:5:107:A:O4'	2.17	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
36:5:1010:G:N2	47:m0:193:ASP:OD1	2.51	0.44
36:5:1318:A:OP1	52:m6:18:ARG:NH2	2.51	0.44
36:5:1751:G:H5"	74:o8:26:LYS:HE2	1.99	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
37:7:110:G:C6	37:7:111:U:C4	3.06	0.44
38:8:41:A:O2'	73:o7:59:THR:HG22	2.17	0.44
40:l3:186:GLY:O	40:l3:190:GLU:HB2	2.16	0.44
46:l9:162:GLN:HB2	46:l9:179:ILE:O	2.18	0.44
59:n3:66:LYS:HD2	59:n3:68:GLU:HB2	2.00	0.44
76:q0:128:LYS:H	76:q0:128:LYS:HG3	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:144:U:C2	1:2:145:A:C8	3.05	0.44
1:2:830:U:O2'	1:2:831:U:H6	2.01	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
1:2:1639:C:H2'	1:2:1640:C:O4'	2.17	0.44
2:S0:184:LEU:C	2:S0:186:GLY:H	2.25	0.44
21:C9:105:LEU:HB3	21:C9:122:ARG:HE	1.83	0.44
36:1:562:C:H2'	36:1:563:U:C6	2.53	0.44
36:1:1126:G:H5"	47:M0:119:TRP:CZ3	2.53	0.44
36:1:1507:G:N7	53:M7:129:THR:HG22	2.32	0.44
36:1:1820:U:H1'	36:1:1821:U:OP2	2.17	0.44
36:1:2355:G:H4'	53:M7:139:TYR:CD2	2.52	0.44
40:L3:284:ARG:HB3	40:L3:323:MET:HB2	1.99	0.44
41:L4:291:ASN:HA	41:L4:296:GLN:NE2	2.32	0.44
53:M7:73:GLY:HA3	53:M7:78:VAL:HG12	2.00	0.44
64:N8:74:ASN:CB	64:N8:115:LYS:HB2	2.43	0.44
78:Q2:63:LYS:HE2	78:Q2:87:ARG:NH2	2.33	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
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
2:s0:3:LEU:HA	2:s0:4:PRO:HD2	1.63	0.44
7:s5:26:ALA:HB3	18:c6:28:LEU:HB3	1.98	0.44
16:c4:102:LEU:HD13	28:d6:53:LEU:HD21	1.99	0.44
19:c7:107:SER:O	19:c7:110:VAL:HG23	2.17	0.44
21:c9:28:LEU:HB3	21:c9:29:GLU:H	1.63	0.44
21:c9:35:ASP:OD2	21:c9:36:ILE:HG23	2.18	0.44
26:d4:130:ALA:HA	26:d4:133:ASN:OD1	2.18	0.44
34:sR:48:THR:HG22	34:sR:55:GLY:HA2	1.98	0.44
35:sM:88:LYS:HB3	35:sM:89:LYS:H	1.54	0.44
36:5:90:C:OP1	64:n8:59:ARG:NH1	2.50	0.44
36:5:282:G:C8	36:5:282:G:H3'	2.53	0.44
36:5:311:C:H42	36:5:2778:G:H1	1.66	0.44
36:5:525:C:H5"	50:m4:79:ALA:HB2	2.00	0.44
36:5:664:U:H2'	36:5:665:A:C8	2.53	0.44
36:5:1213:G:H4'	56:n0:90:MET:HG2	2.00	0.44
36:5:2587:U:H4'	45:l8:49:TYR:HD2	1.83	0.44
36:5:3084:C:H2'	36:5:3085:G:O4'	2.18	0.44
36:5:3242:G:H21	36:5:3245:A:H5"	1.83	0.44
40:l3:53:MET:HG2	40:l3:77:THR:HG22	1.99	0.44
40:l3:165:GLN:OE1	40:l3:167:ARG:NH2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:l4:181:VAL:HG21	41:l4:224:GLY:HA3	1.99	0.44
43:l6:51:ARG:NH1	50:m4:114:ASP:OD2	2.51	0.44
47:m0:54:SER:HA	47:m0:163:GLN:HB3	1.99	0.44
51:m5:6:TYR:CD2	72:o6:40:VAL:HG13	2.53	0.44
52:m6:23:VAL:HG13	52:m6:33:ILE:HG21	1.99	0.44
59:n3:13:ILE:HD12	59:n3:85:TRP:CG	2.52	0.44
75:o9:28:ARG:HH11	75:o9:36:ARG:HH11	1.65	0.44
1:2:67:A:C2	1:2:69:G:H1'	2.53	0.44
1:2:542:A:H5"	1:2:544:A:C8	2.53	0.44
1:2:808:U:H2'	1:2:809:A:C8	2.52	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
5:S3:82:GLY:C	5:S3:84:ILE:H	2.26	0.44
12:C0:11:ILE:HD11	12:C0:42:VAL:HG22	1.98	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
34:SR:19:TRP:HB2	34:SR:38:ARG:HD2	2.00	0.44
34:SR:61:PHE:HD1	34:SR:92:TRP:CE3	2.36	0.44
34:SR:131:ILE:HG23	34:SR:154:VAL:HG11	2.00	0.44
34:SR:240:VAL:HG22	34:SR:256:THR:HG22	1.99	0.44
36:1:116:A:OP1	72:O6:36:ARG:NH1	2.50	0.44
36:1:1064:A:H5"	36:1:1066:G:O4'	2.18	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
36:1:3267:A:H2'	43:L6:69:PHE:CZ	2.53	0.44
39:L2:183:GLY:O	39:L2:186:PHE:HB3	2.18	0.44
40:L3:3:HIS:O	40:L3:5:LYS:N	2.50	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
79:Q3:49:ARG:HB3	79:Q3:50:GLY:H	1.63	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
10:s8:72:ILE:HG12	10:s8:112:TRP:CE2	2.53	0.44
10:s8:184:LEU:HD21	10:s8:192:TYR:CD2	2.52	0.44
12:c0:53:GLY:C	12:c0:55:VAL:H	2.25	0.44
15:c3:118:ILE:HA	15:c3:121:ARG:NH1	2.32	0.44
18:c6:46:PHE:HA	18:c6:49:TYR:HB2	2.00	0.44
25:d3:30:LYS:O	25:d3:34:LEU:HG	2.18	0.44
35:sM:43:ASP:HA	35:sM:44:PRO:HD3	1.77	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:107:A:H2'	36:5:108:A:O4'	2.18	0.44
40:l3:146:ARG:HA	40:l3:146:ARG:NE	2.33	0.44
61:n5:34:LEU:HD23	61:n5:35:PRO:HD2	2.00	0.44
68:o2:16:LYS:HD2	68:o2:18:LYS:HG2	2.00	0.44
1:2:6:G:OP2	4:S2:205:ARG:HD2	2.18	0.44
1:2:576:G:OP2	35:SM:102:THR:HG21	2.17	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
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
1:2:1590:G:OP1	21:C9:91:TYR:HB2	2.18	0.44
4:S2:165:VAL:HA	4:S2:201:ASN:O	2.17	0.44
14:C2:87:PRO:HA	14:C2:140:PHE:HE1	1.83	0.44
21:C9:61:VAL:O	21:C9:65:ILE:HG13	2.17	0.44
34:SR:178:VAL:HB	34:SR:192:PHE:HB2	1.99	0.44
36:1:507:U:H2'	36:1:508:U:C6	2.53	0.44
36:1:637:C:H6	36:1:637:C:H2'	1.54	0.44
36:1:853:G:N7	79:Q3:2:ALA:N	2.65	0.44
36:1:2611:U:H2'	36:1:2612:U:C6	2.53	0.44
40:L3:332:ARG:NH1	40:L3:333:LYS:HD3	2.32	0.44
42:L5:40:HIS:HB3	42:L5:43:LYS:HG3	2.00	0.44
42:L5:86:TYR:CE1	42:L5:247:ILE:HA	2.53	0.44
46:L9:52:LEU:HD23	46:L9:52:LEU:HA	1.81	0.44
46:L9:88:TYR:CE2	46:L9:184:LYS:HG2	2.52	0.44
49:M3:94:GLY:HA3	71:O5:116:TYR:OH	2.17	0.44
51:M5:183:THR:HB	51:M5:187:ARG:HG3	1.99	0.44
72:O6:11:LEU:HD13	72:O6:11:LEU:HA	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
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
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
1:6:1795:U:O2	28:d6:10:ARG:NE	2.51	0.44
1:6:1798:U:OP2	28:d6:38:ARG:NH2	2.50	0.44
5:s3:37:VAL:HG12	5:s3:50:ILE:HA	2.00	0.44
8:s6:189:HIS:CE1	8:s6:193:LEU:HD12	2.52	0.44
9:s7:30:SER:HB2	9:s7:34:LEU:HB2	1.99	0.44
11:s9:93:LEU:O	11:s9:96:VAL:HG22	2.18	0.44
21:c9:14:PHE:HZ	21:c9:132:LEU:HD12	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:d4:83:LYS:HB2	26:d4:83:LYS:HE2	1.61	0.44
28:d6:59:TYR:HA	28:d6:60:PRO:HD3	1.90	0.44
36:5:589:A:N6	36:5:610:G:H1'	2.32	0.44
36:5:996:A:C2	36:5:1054:A:C4	3.06	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
40:l3:293:ASN:HB2	40:l3:305:ILE:H	1.82	0.44
41:l4:300:ARG:HG2	54:m8:39:ARG:O	2.18	0.44
51:m5:27:VAL:HB	51:m5:122:ASN:ND2	2.33	0.44
57:n1:105:PHE:O	57:n1:109:VAL:HG23	2.17	0.44
59:n3:38:ALA:HB3	59:n3:59:MET:HB2	2.00	0.44
71:o5:15:GLU:CD	71:o5:15:GLU:H	2.25	0.44
2:S0:162:CYS:HG	2:S0:163:ASN:H	1.56	0.43
3:S1:176:VAL:O	3:S1:177:GLN:HG2	2.18	0.43
10:S8:196:LEU:HA	10:S8:196:LEU:HD12	1.73	0.43
21:C9:31:PRO:HG3	21:C9:103:LYS:HD3	1.99	0.43
25:D3:69:ARG:HD2	25:D3:117:ILE:HG12	1.99	0.43
25:D3:126:LYS:HA	25:D3:131:SER:HA	2.00	0.43
28:D6:82:ARG:O	28:D6:84:VAL:HG12	2.18	0.43
29:D7:3:LEU:HD22	29:D7:3:LEU:HA	1.80	0.43
36:1:278:U:H2'	36:1:279:U:C6	2.53	0.43
36:1:911:C:H42	39:L2:3:ARG:HD3	1.82	0.43
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
36:1:3386:G:H2'	36:1:3387:U:H6	1.82	0.43
39:L2:113:VAL:HG12	39:L2:166:ILE:HD13	2.00	0.43
40:L3:306:THR:HA	40:L3:307:PRO:HD3	1.87	0.43
42:L5:119:TYR:OH	42:L5:141:PRO:HD3	2.18	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
52:M6:61:ALA:HA	52:M6:70:PRO:HD2	1.99	0.43
64:N8:112:ILE:HB	64:N8:130:VAL:HG12	2.00	0.43
1:6:114:C:H6	1:6:114:C:H5"	1.83	0.43
1:6:183:U:H2'	1:6:184:C:O4'	2.17	0.43
1:6:191:C:N4	10:s8:137:LYS:HE3	2.33	0.43
1:6:515:A:N6	1:6:537:G:O2'	2.45	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
2:s0:30:GLN:NE2	2:s0:32:HIS:HB2	2.33	0.43
2:s0:53:THR:HA	2:s0:161:PRO:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:s0:88:LYS:HB3	2:s0:202:TYR:CZ	2.53	0.43
7:s5:27:THR:HA	7:s5:28:PRO:HD2	1.67	0.43
11:s9:28:LEU:HD11	80:e0:39:LEU:HB3	2.00	0.43
21:c9:63:ARG:NH1	21:c9:67:MET:HE1	2.33	0.43
22:d0:53:LYS:HB2	22:d0:92:ASP:HB2	1.99	0.43
29:d7:3:LEU:HD23	29:d7:3:LEU:HA	1.77	0.43
34:sR:224:ASN:O	34:sR:228:LYS:HA	2.18	0.43
36:5:945:C:H2'	36:5:946:U:C6	2.53	0.43
36:5:1229:G:O2'	82:p0:32:ASN:HA	2.17	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
41:l4:3:ARG:O	41:l4:5:GLN:N	2.51	0.43
42:l5:276:LYS:H	42:l5:276:LYS:HG2	1.54	0.43
57:n1:101:CYS:O	57:n1:104:GLU:HG3	2.17	0.43
62:n6:37:LYS:HA	62:n6:40:ARG:HG2	2.00	0.43
63:n7:129:TRP:O	63:n7:132:SER:OG	2.31	0.43
66:o0:13:LYS:HB3	66:o0:100:ILE:HG23	2.00	0.43
66:o0:100:ILE:O	66:o0:105:ALA:HB3	2.18	0.43
78:q2:4:VAL:O	78:q2:94:GLY:N	2.37	0.43
78:q2:10:THR:O	78:q2:20:HIS:HA	2.18	0.43
87:D:3401:SPS:O1	87:D:3401:SPS:H91	2.18	0.43
1:2:814:A:C8	1:2:816:G:C8	3.06	0.43
1:2:1595:U:N3	1:2:1600:A:H2	2.14	0.43
2:S0:76:ILE:O	2:S0:124:THR:HG23	2.19	0.43
3:S1:197:ILE:O	3:S1:201:THR:OG1	2.27	0.43
4:S2:165:VAL:HG11	4:S2:210:THR:OG1	2.18	0.43
10:S8:29:LEU:HD11	10:S8:31:ARG:NH1	2.33	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
25:D3:107:PHE:HD1	25:D3:107:PHE:HA	1.68	0.43
33:E1:97:LYS:HA	33:E1:97:LYS:HD2	1.84	0.43
34:SR:192:PHE:HD1	34:SR:223:TRP:CE3	2.36	0.43
36:1:210:U:C2	36:1:230:U:H4'	2.53	0.43
36:1:305:U:C5	36:1:2776:C:H1'	2.53	0.43
36:1:655:C:H5"	68:O2:26:HIS:HB2	2.00	0.43
36:1:1177:G:C5	69:O3:20:LYS:HD3	2.53	0.43
36:1:2655:U:H4'	36:1:2656:A:O4'	2.17	0.43
36:1:3077:A:N6	36:1:3080:G:C5	2.87	0.43
36:1:3242:G:N7	40:L3:150:ARG:HD2	2.33	0.43
36:1:3364:C:H2'	36:1:3365:U:C6	2.52	0.43
40:L3:50:LYS:HD3	40:L3:331:ASN:C	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:M1:14:ILE:HD12	48:M1:77:GLU:HG2	2.00	0.43
49:M3:153:ASP:CG	49:M3:154:VAL:H	2.26	0.43
51:M5:151:ILE:HD13	51:M5:151:ILE:HA	1.85	0.43
55:M9:99:LEU:O	55:M9:103:ARG:HB2	2.18	0.43
64:N8:90:TYR:CG	64:N8:100:PRO:HG3	2.53	0.43
64:N8:104:THR:HG21	64:N8:112:ILE:HD11	2.00	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
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
1:6:1523:G:C8	21:c9:79:LEU:HD13	2.53	0.43
2:s0:74:VAL:HG12	2:s0:76:ILE:HG13	1.99	0.43
6:s4:51:ARG:HA	6:s4:51:ARG:HE	1.83	0.43
6:s4:87:MET:HE3	6:s4:226:PHE:CE1	2.53	0.43
7:s5:57:SER:HB2	30:d8:53:ILE:O	2.19	0.43
7:s5:61:TYR:OH	30:d8:49:ARG:HD3	2.17	0.43
12:c0:55:VAL:HG23	12:c0:67:THR:O	2.17	0.43
20:c8:82:PRO:HG3	21:c9:36:ILE:HD12	1.99	0.43
35:sM:25:ILE:HG12	37:7:39:C:H5'	1.99	0.43
36:5:63:A:OP1	51:m5:169:LYS:HE3	2.18	0.43
36:5:80:G:H2'	36:5:81:C:C6	2.52	0.43
36:5:191:U:H2'	36:5:192:C:C6	2.53	0.43
36:5:283:G:P	78:q2:45:ARG:HH22	2.40	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
36:5:2608:G:O2'	36:5:2609:A:H5'	2.18	0.43
36:5:3048:A:H5"	40:l3:53:MET:HE3	2.00	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
37:7:7:G:OP1	42:l5:33:ARG:HD2	2.19	0.43
42:l5:202:GLY:O	42:l5:206:GLN:HG3	2.18	0.43
47:m0:205:SER:OG	47:m0:208:ASN:OD1	2.29	0.43
1:2:637:C:OP1	24:D2:32:LYS:HG3	2.18	0.43
1:2:1389:C:O2'	19:C7:52:GLY:HA3	2.18	0.43
25:D3:86:PHE:CE1	25:D3:88:PRO:HA	2.53	0.43
32:E0:56:MET:HE3	32:E0:56:MET:HB2	1.94	0.43
36:1:689:U:O4	41:L4:209:TYR:OH	2.26	0.43
36:1:1355:A:H4'	36:1:1356:U:O5'	2.18	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
47:M0:36:LEU:HD21	47:M0:69:ARG:HD3	2.00	0.43
53:M7:168:LEU:HD22	53:M7:176:ILE:HD11	1.99	0.43
59:N3:74:MET:HE3	59:N3:102:ILE:HB	2.00	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
1:6:19:A:OP1	25:d3:112:LYS:NZ	2.50	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
1:6:1352:G:H2'	1:6:1353:U:O4'	2.17	0.43
1:6:1645:G:H1	1:6:1756[A]:A:H61	1.65	0.43
1:6:1754:A:H4'	1:6:1755:A:O5'	2.17	0.43
5:s3:179:GLN:HB3	5:s3:180:GLY:H	1.61	0.43
6:s4:31:PRO:HB2	6:s4:38:LEU:HB2	2.01	0.43
6:s4:170:THR:O	6:s4:170:THR:OG1	2.34	0.43
21:c9:137:ALA:O	21:c9:141:GLU:N	2.51	0.43
25:d3:57:LEU:HD13	80:e0:4:VAL:HG22	2.00	0.43
28:d6:51:ARG:NH2	28:d6:55:GLU:OE1	2.52	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
36:5:953:G:C8	36:5:1117:G:C8	3.06	0.43
36:5:1473:G:OP2	55:m9:8:LYS:NZ	2.51	0.43
36:5:1494:U:P	75:o9:42:ARG:HH22	2.42	0.43
36:5:1557:A:N7	36:5:1559:A:N6	2.66	0.43
36:5:1947:G:H5'	55:m9:134:HIS:HD2	1.84	0.43
36:5:2267:C:H2'	36:5:2268:U:C6	2.52	0.43
36:5:2944:U:H1'	40:l3:251:CYS:SG	2.58	0.43
36:5:2953:U:H2'	36:5:2954:U:C6	2.53	0.43
36:5:2991:A:OP1	40:l3:21:ARG:HG3	2.18	0.43
36:5:3017:A:H2'	36:5:3018:C:H6	1.83	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
37:7:93:C:H5'	47:m0:57:LEU:HD12	1.99	0.43
45:l8:78:PHE:O	45:l8:79:GLN:HB3	2.18	0.43
46:l9:70:THR:O	46:l9:74:LEU:HG	2.19	0.43
47:m0:34:TYR:O	47:m0:88:ARG:HA	2.19	0.43
47:m0:130:ASP:OD1	47:m0:131:ILE:N	2.48	0.43
49:m3:4:SER:OG	49:m3:5:LYS:HG3	2.19	0.43
49:m3:75:PHE:O	49:m3:79:GLU:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:m3:119:TYR:O	49:m3:123:ILE:HG23	2.17	0.43
52:m6:130:LYS:HD3	52:m6:131:PRO:HD2	2.00	0.43
53:m7:50:GLN:HB3	53:m7:55:GLN:HB3	2.00	0.43
75:o9:48:LYS:HA	75:o9:48:LYS:HD2	1.72	0.43
1:2:987:G:N1	39:L2:249:SER:HB2	2.34	0.43
1:2:1390:U:OP1	19:C7:5:ARG:HD2	2.18	0.43
1:2:1687:U:H1'	1:2:1715:G:N2	2.34	0.43
2:S0:52:LYS:HD2	23:D1:82:VAL:HA	1.99	0.43
3:S1:105:PHE:CD2	3:S1:213:ARG:HA	2.53	0.43
3:S1:144:ARG:HB3	3:S1:208:GLN:HB3	2.00	0.43
5:S3:148:LYS:HB2	35:SM:110:TRP:CZ2	2.54	0.43
10:S8:9:HIS:O	10:S8:10:LYS:HB2	2.18	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
22:D0:37:VAL:HG21	22:D0:109:GLU:HB2	2.00	0.43
31:D9:19:ARG:H	31:D9:19:ARG:HG2	1.54	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
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
42:L5:105:ILE:O	42:L5:109:THR:HG23	2.18	0.43
43:L6:153:PRO:O	43:L6:154:LEU:HB2	2.17	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
56:N0:2:ALA:HB3	56:N0:32:SER:HB3	2.01	0.43
65:N9:5:LYS:HG3	65:N9:6:ASN:N	2.33	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
1:6:1250:U:O2	33:e1:135:HIS:ND1	2.52	0.43
1:6:1557:U:O2'	1:6:1558:U:H2'	2.18	0.43
3:s1:157:GLN:HB2	3:s1:160:HIS:ND1	2.34	0.43
4:s2:71:THR:O	4:s2:74:PRO:HD3	2.19	0.43
8:s6:67:VAL:HG21	8:s6:99:GLY:HA2	1.99	0.43
8:s6:176:GLN:C	8:s6:178:LEU:H	2.26	0.43
8:s6:194:LYS:HE3	8:s6:194:LYS:HB2	1.76	0.43
11:s9:127:VAL:HG12	11:s9:131:GLN:CD	2.43	0.43
13:c1:121:ASP:OD1	13:c1:145:ALA:HB2	2.18	0.43
18:c6:26:LYS:HB2	18:c6:26:LYS:HE3	1.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:d4:11:LYS:HB2	26:d4:24:VAL:HG23	1.99	0.43
33:e1:82:LYS:O	33:e1:84:VAL:N	2.52	0.43
36:5:80:G:H2'	36:5:81:C:H6	1.83	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
36:5:871:U:H2'	36:5:872:U:C6	2.54	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
47:m0:175:ASN:CG	47:m0:176:LEU:H	2.23	0.43
64:n8:104:THR:HG21	64:n8:112:ILE:HD11	2.00	0.43
68:o2:77:ALA:HB3	68:o2:81:ASP:OD2	2.19	0.43
1:2:68:A:H5"	8:S6:162:VAL:HG21	2.00	0.43
1:2:952:A:H5'	15:C3:98:VAL:HG22	2.01	0.43
1:2:1002:G:N1	1:2:1761:U:OP1	2.38	0.43
3:S1:30:PHE:HD1	3:S1:96:LEU:HD22	1.83	0.43
3:S1:116:LYS:O	3:S1:117:TRP:HB2	2.19	0.43
10:S8:11:ARG:HD3	10:S8:15:GLY:O	2.17	0.43
35:SM:23:LYS:H	35:SM:23:LYS:HD2	1.84	0.43
36:1:579:G:H2'	36:1:580:C:C6	2.54	0.43
36:1:922:U:OP1	73:O7:3:LYS:NZ	2.36	0.43
36:1:1362:G:H2'	36:1:1363:A:C8	2.53	0.43
38:4:76:C:H2'	38:4:77:A:O4'	2.19	0.43
41:L4:3:ARG:O	41:L4:5:GLN:N	2.52	0.43
44:L7:244:ASN:HD22	44:L7:244:ASN:C	2.26	0.43
45:L8:146:LYS:HE2	45:L8:173:MET:HE3	1.99	0.43
46:L9:41:ILE:HD12	46:L9:67:ALA:HB1	2.01	0.43
47:M0:16:PRO:C	47:M0:18:PRO:HD3	2.44	0.43
54:M8:122:ILE:HG13	54:M8:126:GLN:HE21	1.84	0.43
62:N6:35:LEU:HD23	62:N6:106:ILE:HD12	2.01	0.43
62:N6:86:THR:HG22	62:N6:96:PRO:HA	2.01	0.43
71:O5:18:ALA:O	71:O5:22:VAL:HG23	2.19	0.43
72:O6:53:TYR:HB2	72:O6:76:ARG:HD3	2.01	0.43
79:Q3:59:CYS:C	79:Q3:61:LYS:H	2.26	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
1:6:1350:U:H2'	1:6:1351:G:H8	1.83	0.43
1:6:1565:C:OP1	20:c8:41:ARG:HD3	2.18	0.43
1:6:1691:A:H2'	1:6:1692:G:C8	2.53	0.43
3:s1:110:LEU:O	3:s1:114:VAL:HG23	2.19	0.43
5:s3:215:GLU:HG2	5:s3:215:GLU:O	2.18	0.43
5:s3:216:PRO:HB2	5:s3:217:ILE:H	1.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:c0:4:PRO:HB2	12:c0:6:GLU:CD	2.43	0.43
15:c3:125:LEU:O	15:c3:128:TYR:N	2.51	0.43
16:c4:39:ILE:HD12	16:c4:74:VAL:HG11	2.00	0.43
17:c5:68:PRO:HB2	17:c5:69:GLU:H	1.58	0.43
20:c8:88:ARG:HH12	20:c8:112:ASP:CG	2.24	0.43
21:c9:31:PRO:HB3	21:c9:103:LYS:HD3	2.00	0.43
21:c9:33:TYR:O	21:c9:34:VAL:HG12	2.18	0.43
21:c9:53:TRP:HH2	21:c9:100:ILE:HD12	1.83	0.43
28:d6:62:TYR:CG	28:d6:63:ALA:N	2.86	0.43
34:sR:294:TRP:CZ3	34:sR:301:LEU:HB2	2.53	0.43
36:5:67:A:O2'	36:5:315:C:O2	2.32	0.43
36:5:839:C:H4'	36:5:1724:U:H2'	2.01	0.43
36:5:1508:C:OP1	53:m7:127:ARG:NH2	2.50	0.43
36:5:1911:A:H2	36:5:2122:G:C8	2.37	0.43
36:5:2101:C:H2'	36:5:2102:U:C6	2.52	0.43
36:5:2245:C:O4'	39:l2:222:ALA:HA	2.19	0.43
36:5:3089:C:H2'	36:5:3090:U:O4'	2.19	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
38:8:9:A:H2'	38:8:10:A:C8	2.54	0.43
39:l2:113:VAL:HG12	39:l2:166:ILE:HD13	1.99	0.43
41:l4:186:LYS:O	41:l4:200:THR:N	2.46	0.43
41:l4:281:ILE:HG13	54:m8:125:ASP:CG	2.44	0.43
42:l5:254:LYS:NZ	42:l5:257:GLU:OE1	2.51	0.43
46:l9:105:GLU:HB2	46:l9:110:LYS:H	1.82	0.43
46:l9:111:PHE:HD1	46:l9:127:PRO:HA	1.83	0.43
46:l9:137:SER:HB2	46:l9:143:GLU:HB3	2.00	0.43
54:m8:23:ASN:HB3	54:m8:26:LEU:HB2	1.99	0.43
67:o1:10:ARG:HH12	67:o1:44:MET:HG2	1.83	0.43
71:o5:31:LEU:HD13	71:o5:47:VAL:HG11	2.00	0.43
71:o5:96:GLU:O	71:o5:99:GLN:HB2	2.18	0.43
75:o9:21:ARG:HH11	75:o9:21:ARG:HB2	1.84	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
1:2:381:C:O2'	1:2:755:A:N1	2.47	0.43
1:2:733:A:H4'	1:2:734:A:C5	2.53	0.43
1:2:827:C:H2'	1:2:828:U:C6	2.52	0.43
1:2:1211:A:H1'	17:C5:99:GLY:O	2.19	0.43
1:2:1565:C:OP1	20:C8:41:ARG:HG3	2.18	0.43
2:S0:82:GLY:O	2:S0:85:ALA:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S1:113:MET:HE2	3:S1:209:ASN:HD22	1.84	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
18:C6:32:ASN:O	18:C6:66:ARG:NH1	2.52	0.43
26:D4:112:LYS:O	26:D4:116:LYS:HG3	2.19	0.43
36:1:40:A:C2	64:N8:40:HIS:CE1	3.06	0.43
36:1:192:C:H2'	36:1:193:C:C6	2.53	0.43
36:1:501:A:H2'	36:1:502:U:C6	2.53	0.43
36:1:1230:G:H2'	36:1:1231:A:C8	2.53	0.43
36:1:1543:G:OP1	51:M5:35:VAL:HG23	2.18	0.43
36:1:1925:U:O2'	36:1:1927:G:N7	2.51	0.43
36:1:2525:G:OP2	39:L2:37:ARG:NH1	2.50	0.43
36:1:3243:A:O2'	36:1:3244:A:H8	2.02	0.43
38:4:37:A:H5"	38:4:39:G:O4'	2.17	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
42:L5:156:GLY:N	42:L5:179:ARG:O	2.48	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
1:6:78:A:H1'	8:s6:175:ILE:HG12	2.01	0.43
1:6:545:A:C6	1:6:594:A:C8	3.06	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
2:s0:66:ALA:HB1	23:d1:50:TYR:HE1	1.83	0.43
2:s0:177:LEU:HD23	2:s0:177:LEU:HA	1.91	0.43
3:s1:103:MET:HB3	3:s1:215:VAL:CG1	2.49	0.43
3:s1:138:PHE:CD2	3:s1:214:LYS:HB3	2.53	0.43
5:s3:219:ALA:HA	5:s3:220:PRO:HD2	1.78	0.43
7:s5:126:ASP:HB3	7:s5:127:GLN:H	1.51	0.43
19:c7:104:ASN:C	19:c7:106:THR:N	2.77	0.43
21:c9:67:MET:HE3	21:c9:67:MET:HB2	1.85	0.43
23:d1:13:VAL:HA	23:d1:14:PRO:HD3	1.80	0.43
26:d4:25:VAL:O	26:d4:70:VAL:HA	2.19	0.43
33:e1:95:HIS:CG	33:e1:96:LYS:H	2.37	0.43
34:sR:123:ILE:HD13	34:sR:169:ILE:HG21	2.01	0.43
34:sR:297:ASP:OD2	34:sR:297:ASP:N	2.51	0.43
36:5:142:C:H2'	36:5:143:G:O4'	2.18	0.43
36:5:260:C:H2'	36:5:261:U:C6	2.53	0.43
36:5:553:U:H2'	36:5:554:A:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:601:U:H2'	36:5:602:A: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
36:5:1581: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
36:5:2655:U:H2'	78:q2:3:ASN:O	2.19	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
37:7:11:A:N1	37:7:67:G:O2'	2.47	0.43
39:l2:66:PRO:HB2	39:l2:67:TYR:CD2	2.53	0.43
49:m3:92:THR:HG21	71:o5:111:PHE:HB3	2.00	0.43
50:m4:15:VAL:HG13	56:n0:150:PHE:O	2.18	0.43
54:m8:153:PHE:O	54:m8:161:LYS:HG2	2.19	0.43
56:n0:6:GLU:OE1	56:n0:99:ARG:NH2	2.31	0.43
5:S3:37:VAL:HG12	5:S3:50:ILE:HD13	2.01	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
15:C3:136:PRO:O	15:C3:138:ASN:N	2.44	0.43
16:C4:124:ASP:O	16:C4:125:SER:HB2	2.18	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
36:1:915:A:H8	36:1:2136:C:O2'	2.02	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
36:1:1821:U:C2	70:O4:67:LYS:HB2	2.53	0.43
36:1:2417:U:H2'	36:1:2419:A:OP2	2.19	0.43
36:1:2434:U:H5	36:1:2594:C:OP2	2.01	0.43
36:1:2534:G:H2'	36:1:2535:A:C8	2.45	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
46:L9:166:ARG:HB2	46:L9:166:ARG:HH11	1.83	0.43
50:M4:13:ARG:NH1	50:M4:65:LEU:O	2.51	0.43
52:M6:39:GLU:CD	52:M6:107:GLY:H	2.27	0.43
56:N0:80:ARG:HB2	56:N0:124:LEU:HD11	2.01	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
1:6:138:A:N6	1:6:139:C:H41	2.15	0.43
1:6:788:A:C4	6:s4:19:LEU:HD13	2.54	0.43
1:6:829:A:H1'	1:6:830:U:H5	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:903:U:H5”	16:c4:135:ARG:NH2	2.34	0.43
1:6:1257:U:O2’	1:6:1258:U:O4’	2.37	0.43
2:s0:84:ARG:NE	19:c7:82:ASP:OD1	2.51	0.43
3:s1:167:VAL:O	3:s1:171:ILE:HG13	2.19	0.43
5:s3:107:PHE:O	5:s3:111:ASN:N	2.52	0.43
15:c3:42:ARG:C	15:c3:44:GLY:H	2.27	0.43
15:c3:114:ARG:HA	15:c3:114:ARG:HD2	1.72	0.43
36:5:22:G:O4’	38:8:104:A:H1’	2.18	0.43
36:5:76:G:H3’	49:m3:73:ARG:HD2	2.01	0.43
36:5:746:A:H2’	36:5:747:A: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
36:5:2424:A:N1	39:l2:230:VAL:HG21	2.34	0.43
36:5:2746:A:C2	42:l5:146:LEU:HB3	2.50	0.43
48:m1:16:LYS:HZ2	48:m1:130:VAL:HG11	1.84	0.43
48:m1:133:ARG:HD3	48:m1:152:HIS:CD2	2.54	0.43
49:m3:100:ARG:O	49:m3:101:ARG:HB2	2.18	0.43
50:m4:18:GLY:O	50:m4:69:THR:HA	2.19	0.43
52:m6:72:HIS:O	52:m6:74:ARG:HD3	2.18	0.43
55:m9:4:LEU:O	55:m9:7:GLN:HG2	2.19	0.43
56:n0:30:PHE:CD2	56:n0:103:VAL:HG21	2.54	0.43
61:n5:100:LYS:HG2	61:n5:105:VAL:O	2.19	0.43
62:n6:102:SER:OG	62:n6:103:LYS:HE3	2.19	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
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
2:S0:185:ARG:CZ	23:D1:47:PRO:HG3	2.49	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
10:S8:48:THR:CG2	10:S8:54:LYS:HB2	2.48	0.43
13:C1:22:ASN:HD22	13:C1:25:VAL:HG23	1.83	0.43
21:C9:30:VAL:HA	21:C9:31:PRO:HD2	1.79	0.43
28:D6:11:ASN:O	28:D6:33:ASP:HB2	2.18	0.43
34:SR:112:SER:OG	34:SR:153:GLN:OE1	2.37	0.43
36:1:289:A:H2’	36:1:290:G:H8	1.84	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:1742:U:H2'	36:1:1743:G:H8	1.82	0.43
36:1:1900:A:O2'	36:1:1906:G:N7	2.40	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
36:1:3138:U:OP2	40:L3:30:LYS:HD3	2.19	0.43
37:3:61:G:H2'	37:3:62:U:C6	2.54	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
44:L7:89:ILE:HD12	44:L7:214:TRP:CH2	2.54	0.43
44:L7:179:LEU:HD22	44:L7:183:ASP:OD2	2.18	0.43
51:M5:139:HIS:O	51:M5:143:ARG:HG3	2.18	0.43
61:N5:46:TYR:HD2	71:O5:75:TYR:HB3	1.84	0.43
64:N8:6:THR:HG23	64:N8:8:THR:H	1.84	0.43
1:6:196:G:O2'	1:6:197:A:OP2	2.30	0.43
1:6:619:A:N3	1:6:1141:G:H1'	2.33	0.43
1:6:922:G:H2'	1:6:923:A:C8	2.54	0.43
1:6:1796:C:OP1	28:d6:87:ARG:HD3	2.18	0.43
2:s0:60:ALA:O	2:s0:64:ILE:HG13	2.18	0.43
4:s2:156:THR:HB	24:d2:95:PRO:HB3	2.00	0.43
7:s5:77:TYR:HB3	7:s5:84:LYS:HA	2.01	0.43
8:s6:78:THR:HG22	8:s6:79:LYS:H	1.82	0.43
15:c3:46:THR:OG1	15:c3:49:GLN:HG2	2.18	0.43
20:c8:32:LEU:HD13	20:c8:73:MET:HE1	1.99	0.43
30:d8:12:VAL:HA	30:d8:30:VAL:HG12	2.01	0.43
31:d9:4:GLU:OE1	31:d9:4:GLU:N	2.52	0.43
31:d9:16:LYS:H	31:d9:16:LYS:HG2	1.58	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
39:l2:70:ARG:HH11	39:l2:72:ARG:HE	1.66	0.43
40:l3:139:GLN:H	40:l3:139:GLN:HG3	1.51	0.43
41:l4:22:LEU:HA	41:l4:23:PRO:HD3	1.62	0.43
41:l4:326:ARG:NH2	44:l7:164:SER:O	2.50	0.43
42:l5:257:GLU:CD	42:l5:257:GLU:N	2.75	0.43
47:m0:56:GLU:C	47:m0:131:ILE:HG13	2.43	0.43
47:m0:210:ILE:HA	47:m0:217:PHE:HE2	1.83	0.43
51:m5:84:PRO:HA	51:m5:87:GLN:HB2	2.00	0.43
54:m8:143:PRO:HB2	54:m8:146:SER:OG	2.19	0.43
58:n2:37:LEU:O	58:n2:41:ILE:HG13	2.19	0.43
68:o2:20:HIS:HB2	68:o2:50:ILE:HD11	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:o2:96:ILE:N	68:o2:121:ASN:HD21	2.17	0.43
69:o3:103:TYR:HA	69:o3:104:PRO:C	2.43	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
1:2:788:A:C4	6:S4:19:LEU:HD13	2.53	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
1:2:1559:A:OP1	1:2:1559:A:H4'	2.19	0.43
2:S0:76:ILE:HD13	2:S0:98:ILE:HB	2.00	0.43
6:S4:59:ARG:NH1	26:D4:87:PRO:HG3	2.34	0.43
7:S5:63:GLN:HB3	7:S5:64:VAL:H	1.50	0.43
8:S6:58:LYS:C	8:S6:60:GLY:H	2.27	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
21:C9:77:ASN:HB3	21:C9:95:ASP:HB3	2.00	0.43
32:E0:39:LEU:HD12	32:E0:43:ARG:NH2	2.34	0.43
36:1:196:G:C2	36:1:199:A:C8	3.07	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
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
36:1:2355:G:H5'	53:M7:139:TYR:CE1	2.54	0.43
36:1:3182:G:H4'	52:M6:161:LYS:HD3	2.01	0.43
37:3:8:G:O2'	42:L5:69:ILE:O	2.33	0.43
41:L4:327:LEU:HA	44:L7:166:ASN:ND2	2.34	0.43
45:L8:158:ASP:HB3	45:L8:159:PRO:HD3	2.01	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:M6:121:PRO:HD2	56:N0:162:THR:O	2.18	0.43
1:6:119:A:H1'	1:6:397:A:C4	2.54	0.43
1:6:868:G:C2	1:6:869:A:C8	3.07	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
11:s9:171:ARG:NH2	11:s9:174:ARG:HD3	2.34	0.43
36:5:40:A:OP2	64:n8:36:GLY:N	2.51	0.43
36:5:1155:C:O2'	36:5:1197:A:N1	2.43	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
36:5:1306:G:C6	52:m6:62:THR:HA	2.54	0.43
36:5:1489:A:OP1	70:o4:10:ARG:NH1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:1947:G:H5'	55:m9:134:HIS:CD2	2.54	0.43
41:l4:170:LYS:HG3	41:l4:175:HIS:HB2	1.99	0.43
46:l9:72:LYS:HG2	46:l9:76:ASP:OD2	2.19	0.43
50:m4:45:LEU:HD21	50:m4:55:ARG:NH1	2.34	0.43
53:m7:30:ARG:HD3	53:m7:30:ARG:C	2.43	0.43
53:m7:52:LEU:HD12	53:m7:52:LEU:HA	1.76	0.43
54:m8:93:ILE:H	54:m8:93:ILE:HG13	1.64	0.43
54:m8:96:PHE:CD2	54:m8:97:PRO:HD2	2.54	0.43
57:n1:51:GLY:O	57:n1:95:HIS:HD2	2.01	0.43
78:q2:69:VAL:HG13	78:q2:84:THR:HB	2.01	0.43
1:2:119:A:H2'	1:2:120:U:O4'	2.19	0.43
1:2:704:C:H3'	1:2:704:C:OP2	2.19	0.43
1:2:816:G:H21	9:S7:110:GLN:HE22	1.67	0.43
1:2:1119:G:C6	1:2:1120:U:C4	3.07	0.43
3:S1:70:LEU:HD12	3:S1:82:ARG:O	2.19	0.43
3:S1:81:PHE:HD2	3:S1:82:ARG:HG3	1.84	0.43
8:S6:55:GLY:HA3	8:S6:63:MET:HE3	2.01	0.43
25:D3:75:GLN:HG3	25:D3:82:LYS:HD2	2.01	0.43
27:D5:70:LYS:HG3	27:D5:71:ILE:HG13	1.99	0.43
32:E0:41:THR:HA	32:E0:45:VAL:HB	2.01	0.43
34:SR:274:LEU:HD22	34:SR:313:TRP:CD1	2.54	0.43
36:1:651:G:O2'	36:1:1435:A:OP1	2.33	0.43
36:1:2309:A:N3	36:1:2961:G:O2'	2.47	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
37:3:121:U:OP2	42:L5:265:TYR:OH	2.28	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
40:L3:146:ARG:O	40:L3:150:ARG:N	2.51	0.43
42:L5:259:LYS:HE3	42:L5:259:LYS:HB3	1.65	0.43
44:L7:96:PRO:O	44:L7:100:ARG:HB2	2.19	0.43
49:M3:32:LYS:O	49:M3:36:ARG:HG3	2.19	0.43
54:M8:19:PRO:HD3	54:M8:53:PHE:CD1	2.54	0.43
62:N6:118:LEU:O	62:N6:122:LYS:HG3	2.19	0.43
63:N7:22:LYS:NZ	63:N7:132:SER:O	2.45	0.43
64:N8:91:LEU:HD13	64:N8:91:LEU:HA	1.82	0.43
1:6:320:U:H2'	1:6:321:C:H2'	2.01	0.43
1:6:600:U:OP2	25:d3:108:GLY:HA2	2.19	0.43
1:6:868:G:H1	1:6:960:U:H3	1.65	0.43
1:6:1478:G:C4	1:6:1479:A:C8	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:s3:133:GLY:HA2	5:s3:155:GLY:HA3	2.00	0.43
12:c0:31:LYS:H	12:c0:38:LYS:HA	1.83	0.43
13:c1:99:ARG:HD3	25:d3:8:GLY:O	2.19	0.43
28:d6:30:ILE:HG12	28:d6:34:LYS:HB3	2.01	0.43
33:e1:149:LYS:HE3	33:e1:149:LYS:HB2	1.81	0.43
34:sR:108:SER:OG	34:sR:109:ASP:N	2.36	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
36:5:523: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
36:5:1470:U:H2'	36:5:1471:U:C6	2.54	0.43
36:5:2710:C:H2'	36:5:2711:C:C6	2.53	0.43
38:8:71:A:H4'	38:8:72:A:O5'	2.19	0.43
39:l2:192:LYS:HB2	39:l2:193:ARG:HG2	2.01	0.43
39:l2:225:ILE:HD12	39:l2:225:ILE:N	2.34	0.43
40:l3:323:MET:HE1	40:l3:356:LEU:CD1	2.47	0.43
42:l5:41:LYS:HB2	57:n1:68:THR:O	2.18	0.43
45:l8:109:LEU:HD13	45:l8:109:LEU:HA	1.80	0.43
46:l9:4:ILE:N	56:n0:142:GLN:OE1	2.44	0.43
46:l9:109:ALA:O	46:l9:110:LYS:HB2	2.19	0.43
50:m4:54:PRO:HG2	50:m4:56:GLN:NE2	2.34	0.43
50:m4:135:LEU:HD23	50:m4:135:LEU:HA	1.85	0.43
67:o1:75:ILE:HG12	67:o1:93:VAL:HG13	2.01	0.43
73:o7:21:ARG:NH2	73:o7:41:ALA:O	2.51	0.43
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
1:2:973:A:H2'	1:2:974:A:H8	1.83	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
1:2:1229:G:HO2'	1:2:1255:G:N2	2.15	0.42
4:S2:54:GLU:H	4:S2:54:GLU:HG2	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
21:C9:13:ASP:OD2	21:C9:13:ASP:N	2.52	0.42
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
36:1:3270:U:C2	43:L6:46:ARG:HD3	2.54	0.42
39:L2:96:LEU:O	79:Q3:87:ARG:HD3	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L5:57:ASN:HA	42:L5:58:LYS:HZ2	1.83	0.42
43:L6:132:ALA:O	43:L6:136:GLU:HG2	2.18	0.42
48:M1:63:GLU:O	48:M1:64:LYS:HB2	2.19	0.42
57:N1:42:ILE:HG12	57:N1:96:ILE:HD11	2.00	0.42
62:N6:83:ASP:O	62:N6:84:LYS:HB2	2.18	0.42
64:N8:73:LEU:HD23	64:N8:112:ILE:HD12	2.01	0.42
74:O8:24:THR:HG23	74:O8:44:LYS:HB2	2.00	0.42
1:6:52:U:H2'	1:6:53:G:H8	1.83	0.42
1:6:151:G:N2	1:6:164:A:C4	2.87	0.42
1:6:1118:G:OP2	77:q1:21:ARG:NH2	2.52	0.42
1:6:1304:G:H5'	1:6:1322:A:OP2	2.19	0.42
3:s1:144:ARG:NH2	3:s1:207:LEU:O	2.52	0.42
9:s7:110:GLN:HE21	9:s7:110:GLN:HB3	1.64	0.42
18:c6:112:TYR:CZ	18:c6:114:ARG:HD2	2.54	0.42
21:c9:141:GLU:C	21:c9:143:ASP:H	2.27	0.42
29:d7:23:THR:HG21	29:d7:29:ARG:HH21	1.84	0.42
35:sM:25:ILE:HG22	48:m1:46:VAL:HG23	2.01	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
36:5:1085:A:OP1	57:n1:35:LYS:HD2	2.18	0.42
36:5:1355:A:H1'	36:5:1356:U:OP2	2.19	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
36:5:2767:U:O3'	78:q2:31:GLY:HA3	2.19	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
41:l4:6:VAL:N	41:l4:20:LEU:O	2.43	0.42
44:l7:62:ILE:O	44:l7:66:LYS:HG3	2.18	0.42
46:l9:134:ILE:HG23	46:l9:144:ILE:HD11	2.01	0.42
54:m8:89:ASP:HB2	54:m8:110:ALA:N	2.34	0.42
61:n5:80:ASN:ND2	61:n5:126:LEU:HB2	2.34	0.42
61:n5:135:ILE:HA	61:n5:138:ARG:HB3	2.00	0.42
64:n8:7:LYS:HA	64:n8:7:LYS:HD3	1.62	0.42
69:o3:59:VAL:HG23	69:o3:60:ARG:H	1.84	0.42
1:2:5:U:C2	1:2:20:G:N2	2.87	0.42
1:2:1091:A:N3	1:2:1091:A:H5"	2.34	0.42
1:2:1650:U:H2'	1:2:1651:A:C8	2.54	0.42
3:S1:131:ASP:HB3	3:S1:180:THR:CG2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
14:C2:67:THR:C	14:C2:69:ALA:H	2.27	0.42
34:SR:232:TYR:HE1	34:SR:234:LEU:HD11	1.83	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
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
40:L3:53:MET:HG2	40:L3:77:THR:HG22	2.02	0.42
41:L4:152:VAL:CG2	41:L4:172:VAL:HG21	2.49	0.42
47:M0:167:LEU:H	47:M0:167:LEU:HG	1.70	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
70:O4:71:THR:HG22	70:O4:77:GLY:HA3	2.01	0.42
77:Q1:4:LYS:HG3	77:Q1:5:TRP:N	2.34	0.42
1:6:393:C:H4'	1:6:1673:G:O2'	2.19	0.42
1:6:398:G:OP2	10:s8:47:ARG:NH1	2.41	0.42
1:6:590:C:H5'	80:e0:56:MET:HG2	2.01	0.42
1:6:683:C:H2'	1:6:684:A:O4'	2.18	0.42
1:6:1268:G:H1'	1:6:1448:G:H5"	2.01	0.42
1:6:1478:G:OP1	21:c9:39:THR:OG1	2.37	0.42
1:6:1795:U:H3'	28:d6:5:ARG:HH12	1.84	0.42
11:s9:119:ALA:O	11:s9:124:HIS:ND1	2.31	0.42
12:c0:3:MET:HE1	12:c0:45:ALA:HB2	2.01	0.42
16:c4:81:VAL:HG11	16:c4:102:LEU:HD21	2.00	0.42
17:c5:60:LEU:HD23	17:c5:60:LEU:HA	1.86	0.42
36:5:70:A:N1	36:5:313:A:O2'	2.49	0.42
36:5:1002:A:H2'	36:5:1003:A:H8	1.84	0.42
36:5:1055:A:H5"	37:7:100:C:O2'	2.19	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
37:7:77:G:H5"	56:n0:46:GLN:O	2.20	0.42
38:8:15:G:C6	38:8:16:G:C6	3.07	0.42
39:l2:144:ASN:O	39:l2:160:SER:N	2.32	0.42
40:l3:152:LYS:HE3	40:l3:192:VAL:HG22	2.01	0.42
41:l4:12:THR:HA	41:l4:171:ALA:HB1	2.02	0.42
41:l4:135:VAL:O	41:l4:140:HIS:HB2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:l5:273:ARG:O	42:l5:273:ARG:HG2	2.18	0.42
43:l6:52:VAL:HG22	43:l6:67:GLY:HA2	2.01	0.42
47:m0:185:ARG:C	47:m0:187:ALA:H	2.27	0.42
47:m0:210:ILE:HG12	47:m0:217:PHE:CZ	2.54	0.42
53:m7:28:ASN:O	53:m7:32:THR:HG23	2.19	0.42
54:m8:138:LEU:HD23	54:m8:138:LEU:HA	1.89	0.42
58:n2:20:SER:O	58:n2:24:GLU:HG2	2.19	0.42
59:n3:112:SER:HA	59:n3:132:ASN:ND2	2.34	0.42
61:n5:80:ASN:HD21	61:n5:126:LEU:HB2	1.84	0.42
66:o0:8:GLU:HB3	66:o0:13:LYS:HE2	2.01	0.42
74:o8:11:PHE:O	74:o8:15:THR:HG23	2.19	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
2:S0:96:THR:HA	2:S0:97:PRO:HD3	1.93	0.42
2:S0:128:SER:C	2:S0:130:ALA:H	2.27	0.42
3:S1:61:LEU:HD23	3:S1:62:LYS:H	1.84	0.42
18:C6:9:THR:HG21	18:C6:88:GLY:HA2	2.01	0.42
18:C6:50:GLU:OE1	18:C6:112:TYR:OH	2.37	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
29:D7:59:CYS:O	29:D7:61:THR:HG22	2.19	0.42
33:E1:96:LYS:C	33:E1:98:VAL:H	2.27	0.42
35:SM:41:SER:C	35:SM:43:ASP:H	2.27	0.42
36:1:39:A:H5"	64:N8:35:ALA:HB2	2.02	0.42
36:1:429:U:H4'	69:O3:88:ASN:O	2.20	0.42
36:1:1048:A:H2'	47:M0:22:TYR:CZ	2.54	0.42
36:1:3066:U:H2'	36:1:3067:C:C6	2.54	0.42
42:L5:106:ALA:HB2	42:L5:166:ALA:HA	2.01	0.42
43:L6:171:PRO:C	43:L6:173:MET:H	2.27	0.42
44:L7:173:LEU:HD21	44:L7:198:ALA:HA	2.01	0.42
53:M7:4:TYR:CZ	53:M7:18:ARG:HG3	2.54	0.42
72:O6:20:MET:HE2	72:O6:20:MET:HB3	1.92	0.42
72:O6:57:LEU:O	72:O6:61:ILE:HG13	2.19	0.42
79:Q3:5:THR:HB	79:Q3:8:VAL:HG22	2.01	0.42
79:Q3:84:ARG:O	79:Q3:88:GLU:HG2	2.19	0.42
1:6:152:U:C2	1:6:163:G:N2	2.87	0.42
1:6:1049:U:H2'	1:6:1050:G:C8	2.55	0.42
1:6:1184:A:O2'	1:6:1209:C:O2'	2.32	0.42
1:6:1381:U:O4	1:6:1382:A:N6	2.51	0.42
8:s6:139:ASN:HA	8:s6:142:ARG:HB2	2.01	0.42
16:c4:81:VAL:HG13	16:c4:115:ILE:HG23	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:c9:16:ASN:HA	21:c9:56:LYS:NZ	2.33	0.42
33:e1:84:VAL:HG23	33:e1:85:TYR:HD1	1.84	0.42
36:5:128:G:OP1	71:o5:74:LYS:NZ	2.52	0.42
36:5:269:G:H5'	51:m5:120:TRP:CE3	2.54	0.42
36:5:1329:U:H4'	36:5:1330:A:OP1	2.20	0.42
36:5:1591:G:O2'	36:5:1799:A:N1	2.48	0.42
36:5:1791:C:H2'	36:5:1792:C:C6	2.54	0.42
37:7:61:G:OP1	42:l5:276:LYS:HD2	2.20	0.42
42:l5:226:TYR:O	42:l5:230:ASP:N	2.52	0.42
44:l7:98:LYS:HB3	44:l7:99:PRO:HD3	2.00	0.42
44:l7:121:LYS:O	44:l7:121:LYS:HD3	2.19	0.42
45:l8:133:LYS:HD2	45:l8:138:HIS:CE1	2.54	0.42
52:m6:110:PRO:O	52:m6:111:PRO:C	2.61	0.42
55:m9:25:ASP:HB3	55:m9:28:GLU:HB2	2.01	0.42
59:n3:66:LYS:HD3	59:n3:68:GLU:OE1	2.20	0.42
67:o1:44:MET:HE3	67:o1:44:MET:HB2	1.58	0.42
70:o4:3:GLN:HE22	70:o4:30:LEU:H	1.67	0.42
75:o9:9:ILE:HG22	75:o9:13:MET:HE2	2.01	0.42
1:2:768:C:C2	11:S9:143:ILE:HG12	2.55	0.42
1:2:934:C:H1'	28:D6:11:ASN:OD1	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
2:S0:109:ASN:O	2:S0:112:THR:HG22	2.19	0.42
5:S3:5:ILE:HG23	5:S3:9:ARG:NH1	2.35	0.42
10:S8:10:LYS:HD3	13:C1:133:LYS:HE2	2.02	0.42
19:C7:23:LYS:O	19:C7:24:LEU:HB2	2.19	0.42
27:D5:70:LYS:CG	27:D5:71:ILE:H	2.32	0.42
36:1:282:G:C8	36:1:282:G:H3'	2.54	0.42
36:1:560:G:H4'	50:M4:73:PRO:HG2	2.02	0.42
36:1:997:A:H2'	36:1:998:A:O4'	2.18	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:HD11	2.00	0.42
36:1:1447:G:H3'	53:M7:67:ILE:CD1	2.49	0.42
36:1:1481:A:N3	36:1:1481:A:H2'	2.34	0.42
36:1:2529:A:OP1	45:L8:248:LYS:NZ	2.53	0.42
36:1:2883:U:H2'	36:1:2884:C:H6	1.84	0.42
39:L2:13:GLY:O	39:L2:14:SER:C	2.63	0.42
41:L4:108:LYS:HE2	41:L4:108:LYS:HB3	1.65	0.42
54:M8:176:ARG:NH1	64:N8:46:ASP:OD2	2.53	0.42
61:N5:129:ASP:HB2	61:N5:130:TYR:CD1	2.54	0.42
1:6:52:U:H2'	1:6:53:G:C8	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:506:A:OP1	1:6:506:A:H3'	2.18	0.42
1:6:558:U:OP1	80:e0:58:PRO:HA	2.19	0.42
1:6:637:C:OP1	24:d2:32:LYS:HG3	2.19	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
1:6:1078:C:H2'	1:6:1079:U:C6	2.54	0.42
2:s0:120:LEU:HD21	2:s0:144:ILE:HD11	2.02	0.42
6:s4:100:ARG:HH12	6:s4:118:GLU:HG2	1.85	0.42
8:s6:31:ARG:HH11	8:s6:34:GLN:NE2	2.18	0.42
16:c4:86:THR:HG21	16:c4:90:ARG:HD3	2.02	0.42
20:c8:116:LEU:HA	20:c8:119:ILE:HG22	2.00	0.42
22:d0:20:ILE:HG22	22:d0:21:LYS:H	1.83	0.42
33:e1:86:THR:OG1	33:e1:88:PRO:HD2	2.19	0.42
33:e1:86:THR:HG23	33:e1:87:THR:H	1.85	0.42
36:5:1222:G:H8	36:5:1222:G:OP2	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
40:l3:5:LYS:HG2	40:l3:6:TYR:CD1	2.54	0.42
41:l4:35:VAL:HG21	41:l4:244:LEU:HD21	2.01	0.42
42:l5:86:TYR:CE1	42:l5:247:ILE:HA	2.54	0.42
45:l8:52:TRP:NE1	45:l8:60:ARG:HH12	2.17	0.42
55:m9:24:LEU:HD22	55:m9:50:ILE:HG12	2.01	0.42
69:o3:41:ALA:HB3	69:o3:74:THR:HG22	2.00	0.42
69:o3:48:ARG:HG2	69:o3:103:TYR:O	2.20	0.42
1:2:867:G:C4	1:2:868:G:C8	3.08	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
3:S1:59:ASP:HA	3:S1:62:LYS:HZ2	1.84	0.42
3:S1:140:ILE:HG21	3:S1:213:ARG:HD3	2.02	0.42
6:S4:191:ARG:HD3	6:S4:245:LYS:HB2	2.02	0.42
8:S6:21:GLU:H	8:S6:21:GLU:HG2	1.48	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
13:C1:80:MET:HB2	13:C1:80:MET:HE2	1.78	0.42
28:D6:87:ARG:HB3	28:D6:91:ASP:CB	2.49	0.42
29:D7:37:CYS:HA	29:D7:38:PRO:HD3	1.90	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
36:1:1090:G:H2'	36:1:1091:A:H8	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
40:L3:199:PHE:C	40:L3:201:LYS:H	2.26	0.42
41:L4:98:ARG:CZ	41:L4:98:ARG:HB3	2.49	0.42
44:L7:88:ARG:NH1	44:L7:91:GLY:O	2.52	0.42
44:L7:92:ILE:HD11	54:M8:4:ASP:H	1.84	0.42
48:M1:47:GLN:H	48:M1:47:GLN:HG2	1.58	0.42
51:M5:9:GLU:CD	72:O6:41:ARG:HG2	2.44	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
70:O4:29:ILE:HD11	70:O4:31:ARG:HH21	1.83	0.42
71:O5:90:ARG:H	71:O5:90:ARG:HG2	1.74	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
1:6:1459:C:OP2	20:c8:138:THR:OG1	2.32	0.42
1:6:1697:G:N3	1:6:1697:G:H2'	2.34	0.42
2:s0:105:GLY:O	2:s0:109:ASN:HB3	2.20	0.42
2:s0:172:LEU:O	2:s0:176:LEU:HG	2.19	0.42
2:s0:179:ARG:HD3	2:s0:183:ARG:NH1	2.34	0.42
11:s9:75:ALA:O	11:s9:79:ARG:HG3	2.19	0.42
12:c0:61:TRP:HZ3	31:d9:22:ARG:HD2	1.82	0.42
14:c2:74:LEU:HD21	33:e1:106:TYR:HB3	2.02	0.42
18:c6:27:GLY:HA2	18:c6:60:PHE:O	2.20	0.42
24:d2:7:LEU:HD11	24:d2:37:PHE:CE2	2.54	0.42
24:d2:106:THR:HG22	24:d2:122:SER:C	2.45	0.42
27:d5:61:SER:H	27:d5:64:VAL:HB	1.83	0.42
29:d7:19:HIS:CD2	29:d7:21:LEU:H	2.36	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
36:5:3323:A:H1'	67:o1:43:HIS:HE1	1.85	0.42
36:5:3393:U:H2'	36:5:3394:U:C6	2.55	0.42
41:l4:143:GLU:HB3	41:l4:144:LYS:NZ	2.35	0.42
42:l5:109:THR:OG1	42:l5:110:LEU:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:m1:94:ARG:C	48:m1:96:PHE:N	2.76	0.42
66:o0:40:LYS:HB2	66:o0:92:ILE:O	2.20	0.42
68:o2:103:LYS:O	68:o2:106:VAL:HG22	2.20	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
1:2:1198:G:OP1	1:2:1199:G:O2'	2.34	0.42
2:S0:74:VAL:HG22	2:S0:96:THR:HG23	2.01	0.42
5:S3:23:GLU:CD	12:C0:61:TRP:HE1	2.26	0.42
9:S7:28:GLU:O	9:S7:30:SER:N	2.47	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:C6:73:GLY:H	18:C6:76:SER:HB3	1.85	0.42
27:D5:43:ASP:O	27:D5:45:GLU:N	2.53	0.42
29:D7:62:ILE:HG13	29:D7:63:LEU:H	1.82	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
36:1:1160:C:OP1	54:M8:2:GLY:N	2.53	0.42
36:1:1911:A:O5'	36:1:1911:A:H8	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
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
39:L2:187:HIS:ND1	39:L2:190:ARG:NH2	2.67	0.42
41:L4:157:GLU:HB3	41:L4:211:GLU:O	2.20	0.42
41:L4:184:SER:CB	41:L4:202:ARG:HG2	2.50	0.42
46:L9:20:ILE:HG23	46:L9:25:VAL:HG22	2.02	0.42
46:L9:69:ARG:HD2	46:L9:69:ARG:O	2.19	0.42
48:M1:94:ARG:C	48:M1:96:PHE:N	2.78	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
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
1:6:12:U:H2'	1:6:13:C:C6	2.54	0.42
1:6:329:G:H5"	10:s8:98:LYS:HB3	2.02	0.42
1:6:1176:G:C6	1:6:1464:G:C6	3.07	0.42
1:6:1191:U:H5'	18:c6:143:ARG:NH1	2.33	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)
2:s0:34:GLU:N	2:s0:35:PRO:HD2	2.33	0.42
6:s4:130:GLN:HB3	6:s4:138:TYR:CZ	2.55	0.42
6:s4:160:VAL:HG12	6:s4:162:ILE:HG13	2.01	0.42
14:c2:97:LEU:HD11	14:c2:121:VAL:HG22	2.00	0.42
20:c8:127:HIS:CD2	20:c8:133:VAL:HG11	2.54	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
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:OP1	36:5:2439:A:H4'	2.20	0.42
36:5:2902:A:P	46:l9:170:LYS:HE3	2.59	0.42
37:7:24:A:H2'	37:7:25:G:O4'	2.19	0.42
40:l3:66:LYS:HD3	40:l3:67:PHE:CD2	2.54	0.42
43:l6:142:ASP:O	43:l6:146:ILE:HG13	2.19	0.42
51:m5:155:VAL:HG23	51:m5:156:HIS:CE1	2.54	0.42
61:n5:51:VAL:HG21	71:o5:62:GLN:HB3	2.01	0.42
72:o6:98:ARG:HB3	72:o6:99:ARG:H	1.59	0.42
74:o8:46:ARG:NH1	74:o8:47:GLY:O	2.51	0.42
1:2:542:A:O2'	1:2:543:C:H2'	2.19	0.42
1:2:579:A:N1	5:S3:143:ARG:HG3	2.34	0.42
1:2:978:A:H2'	1:2:979:A:O4'	2.19	0.42
1:2:1590:G:H2'	1:2:1591:C:C6	2.54	0.42
3:S1:128:LYS:HE3	3:S1:132:ASP:OD1	2.20	0.42
5:S3:201:ALA:HB3	19:C7:42:GLN:NE2	2.34	0.42
7:S5:202:ALA:O	7:S5:203:LYS:HD2	2.20	0.42
11:S9:36:LEU:O	32:E0:33:ARG:HG3	2.19	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
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
36:1:112:U:O2'	36:1:113:C:H5"	2.19	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
36:1:1120:A:H2'	36:1:1121:U:C6	2.55	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
36:1:1895:A:HO2'	36:1:3053:G:H4'	1.84	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
48:M1:11:ASP:HB3	48:M1:12:LEU:H	1.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:M1:28:ASP:O	48:M1:32:ARG:HG3	2.20	0.42
48:M1:37:LEU:HD23	48:M1:125:MET:HE2	2.02	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
60:N4:4:GLU:HG2	60:N4:30:ARG:CD	2.48	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
78:Q2:40:LYS:HE3	78:Q2:44:ASP:OD2	2.20	0.42
1:6:488:G:N2	1:6:499:U:H3	2.18	0.42
1:6:1079:U:H2'	1:6:1080:U:H6	1.84	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
1:6:1620:C:HO2'	1:6:1621:U:P	2.41	0.42
2:s0:55:GLU:OE2	23:d1:80:LYS:HG2	2.19	0.42
5:s3:53:THR:HB	5:s3:94:ARG:HD3	2.02	0.42
7:s5:61:TYR:HE2	7:s5:164:PRO:HG2	1.83	0.42
7:s5:72:HIS:ND1	18:c6:79:TYR:OH	2.42	0.42
8:s6:72:ARG:HA	8:s6:97:VAL:O	2.19	0.42
11:s9:182:GLU:H	11:s9:182:GLU:HG3	1.67	0.42
12:c0:38:LYS:HB2	12:c0:41:TYR:CD2	2.55	0.42
16:c4:91:THR:O	16:c4:93:THR:N	2.45	0.42
25:d3:29:TYR:O	25:d3:32:ARG:N	2.51	0.42
26:d4:112:LYS:HE3	26:d4:112:LYS:HB3	1.89	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
36:5:1716:U:H6	36:5:1716:U:H5'	1.83	0.42
38:8:45:C:H2'	38:8:46:G:O4'	2.19	0.42
38:8:52:A:O4'	75:o9:21:ARG:HD2	2.19	0.42
38:8:58:G:O6	73:o7:63:ARG:NH2	2.39	0.42
41:l4:138:ARG:NH2	41:l4:240:PRO:HB2	2.34	0.42
42:l5:235:SER:O	42:l5:239:ILE:HG13	2.19	0.42
42:l5:269:SER:O	42:l5:270:LYS:HB2	2.20	0.42
45:l8:160:ILE:HG23	45:l8:164:VAL:HG13	2.01	0.42
46:l9:23:ARG:NH2	46:l9:39:LYS:O	2.52	0.42
55:m9:134:HIS:CE1	55:m9:137:ALA:HB2	2.55	0.42
56:n0:40:ARG:HA	56:n0:40:ARG:HD2	1.53	0.42
66:o0:34:LEU:HD12	66:o0:34:LEU:HA	1.85	0.42
79:q3:32:GLN:O	79:q3:37:TYR:OH	2.28	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:2:1344:A:H4'	1:2:1345:A:OP1	2.20	0.42
1:2:1381:U:H4'	22:D0:59:PRO:HG3	2.00	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
3:S1:58:SER:O	3:S1:62:LYS:HG3	2.18	0.42
4:S2:242:ILE:HG22	4:S2:243:TYR:CD1	2.55	0.42
6:S4:86:PHE:O	6:S4:87:MET:HB2	2.19	0.42
6:S4:148:ARG:NH1	8:S6:201:GLN:OE1	2.53	0.42
11:S9:4:ALA:HA	11:S9:5:PRO:HD3	1.88	0.42
16:C4:125:SER:HB3	16:C4:126:THR:H	1.48	0.42
21:C9:57:ARG:NH1	21:C9:57:ARG:HB2	2.35	0.42
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
35:SM:78:ASP:O	35:SM:82:THR:HG23	2.19	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
36:1:968:G:O2'	65:N9:15:LYS:HE3	2.19	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
36:1:2425:G:OP2	51:M5:90:ASN:ND2	2.51	0.42
36:1:2767:U:H2'	36:1:2768:U:H6	1.83	0.42
42:L5:109:THR:OG1	42:L5:110:LEU:N	2.53	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:L8:71:VAL:HG13	45:L8:234:GLY:C	2.44	0.42
47:M0:213:PHE:N	47:M0:214:PRO:HD3	2.35	0.42
52:M6:14:HIS:CD2	52:M6:124:LEU:HD13	2.55	0.42
64:N8:6:THR:HG23	64:N8:8:THR:HG23	2.01	0.42
1:6:780:A:H3'	1:6:781:U:H5'	2.02	0.42
1:6:1085:G:N2	1:6:1088:A:OP2	2.48	0.42
3:s1:39:GLU:HB3	3:s1:40:ASN:H	1.71	0.42
3:s1:67:GLU:OE2	3:s1:83:LYS:HE2	2.19	0.42
3:s1:142:PHE:O	3:s1:207:LEU:HA	2.19	0.42
7:s5:187:ILE:H	7:s5:187:ILE:HG13	1.63	0.42
14:c2:60:VAL:HG22	14:c2:122:VAL:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:c3:91:LEU:HB3	15:c3:122:ILE:HG12	2.02	0.42
22:d0:24:ILE:HD13	22:d0:41:ILE:HD13	2.02	0.42
23:d1:17:CYS:HB2	23:d1:56:SER:HB3	2.01	0.42
24:d2:15:ASN:ND2	24:d2:72:CYS:O	2.43	0.42
34:sR:40:LYS:HD2	34:sR:65:SER:O	2.20	0.42
36:5:144:A:H2'	36:5:145:G:O4'	2.19	0.42
36:5:929:A:H2'	36:5:930:U:C6	2.55	0.42
36:5:1430:U:O4	64:n8:3:SER:OG	2.28	0.42
36:5:1719:G:OP1	55:m9:110:ARG:NH1	2.52	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
37:7:22:A:C6	37:7:23:A:C6	3.07	0.42
39:l2:90:ALA:HB2	39:l2:101:VAL:HG13	2.02	0.42
81:m2:66:UNK:O	81:m2:68:UNK:N	2.52	0.42
51:m5:183:THR:O	51:m5:184:LYS:HB3	2.20	0.42
52:m6:176:LYS:O	52:m6:180:SER:N	2.53	0.42
1:2:103:A:H5'	1:2:105:A:C4	2.55	0.42
1:2:322:G:H4'	1:2:323:A:O5'	2.17	0.42
1:2:972:G:O2'	36:1:847:A:N1	2.40	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
3:S1:172:LEU:O	3:S1:176:VAL:HG23	2.19	0.42
4:S2:101:VAL:HG22	4:S2:115:ILE:HG12	2.02	0.42
5:S3:222:VAL:C	5:S3:223:LYS:HD2	2.45	0.42
8:S6:67:VAL:HG21	8:S6:99:GLY:HA2	2.02	0.42
12:C0:29:GLN:HB3	12:C0:39:ASN:HB2	2.02	0.42
20:C8:81:ILE:HA	20:C8:82:PRO:HD3	1.88	0.42
36:1:174:C:H2'	36:1:175:C:C6	2.55	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
36:1:1305:U:C2	40:L3:257:PRO:HG3	2.55	0.42
36:1:1629:U:O4	63:N7:111:LYS:HD2	2.20	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
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
48:M1:15:GLU:HB3	48:M1:130:VAL:HG22	2.01	0.42
49:M3:42:ARG:O	49:M3:46:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:O0:36:GLN:OE1	66:O0:38:LYS:HD2	2.20	0.42
66:O0:100:ILE:HG13	66:O0:101:LEU:HD22	2.02	0.42
68:O2:101:SER:HA	68:O2:125:ARG:HH21	1.84	0.42
72:O6:5:THR:HG23	72:O6:12:ASN:C	2.44	0.42
1:6:555:A:C8	1:6:555:A:H3'	2.55	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
2:s0:10:THR:O	2:s0:10:THR:OG1	2.38	0.42
2:s0:124:THR:HG22	2:s0:174:TRP:NE1	2.28	0.42
2:s0:129:ASP:O	2:s0:133:ILE:HG13	2.19	0.42
3:s1:59:ASP:C	3:s1:61:LEU:H	2.27	0.42
3:s1:144:ARG:NH1	3:s1:202:LYS:HE2	2.35	0.42
4:s2:36:VAL:HA	4:s2:37:PRO:HD2	1.92	0.42
7:s5:153:GLY:O	7:s5:155:ALA:N	2.52	0.42
14:c2:126:TRP:HD1	14:c2:128:ALA:H	1.67	0.42
15:c3:102:LEU:HD23	15:c3:102:LEU:HA	1.79	0.42
25:d3:88:PRO:O	25:d3:89:ASN:HB2	2.20	0.42
36:5:266:A:H2'	72:o6:30:LYS:HE3	2.00	0.42
36:5:618:C:H2'	36:5:619:A:C8	2.55	0.42
36:5:813:G:H5'	73:o7:47:TYR:OH	2.20	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
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
43:l6:109:GLU:CD	43:l6:109:GLU:H	2.28	0.42
45:l8:110:THR:O	45:l8:114:ALA:HB3	2.20	0.42
52:m6:106:GLU:H	52:m6:106:GLU:HG2	1.58	0.42
52:m6:119:VAL:HG11	56:n0:167:ARG:HD2	2.01	0.42
54:m8:116:LYS:C	54:m8:118:GLY:H	2.27	0.42
63:n7:34:LYS:O	63:n7:34:LYS:NZ	2.50	0.42
64:n8:47:LYS:C	64:n8:49:HIS:H	2.22	0.42
1:2:631:G:H2'	1:2:632:U:C6	2.55	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
6:S4:122:LYS:HE3	6:S4:122:LYS:HB2	1.91	0.42
23:D1:16:LYS:HE3	23:D1:16:LYS:HB2	1.73	0.42
30:D8:44:VAL:HG11	30:D8:48:VAL:HG21	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:E1:97:LYS:O	33:E1:98:VAL:HG12	2.20	0.42
34:SR:22:SER:HB3	34:SR:36:ALA:HB3	2.02	0.42
36:1:92:G:O2'	78:Q2:56:PRO:HD3	2.20	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
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
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:HD23	45:L8:186:LEU:HA	1.86	0.42
46:L9:76:ASP:O	46:L9:80:THR:HG23	2.20	0.42
46:L9:103:ILE:HD11	46:L9:134:ILE:HG22	2.01	0.42
49:M3:157:ARG:HG2	49:M3:158:ALA:N	2.33	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
65:N9:22:LYS:H	65:N9:22:LYS:HG2	1.55	0.42
68:O2:97:ALA:HB3	68:O2:100:ILE:HG12	2.01	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
1:6:553:G:OP2	1:6:554:C:O2'	2.37	0.42
1:6:737:A:H2'	1:6:738:G:O4'	2.20	0.42
1:6:1237:G:H2'	1:6:1238:A:H8	1.84	0.42
6:s4:174:LYS:HB3	6:s4:174:LYS:HE3	1.86	0.42
8:s6:31:ARG:HH11	8:s6:34:GLN:HE22	1.67	0.42
18:c6:22:VAL:HA	18:c6:64:ASP:O	2.20	0.42
20:c8:118:LYS:O	20:c8:120:ARG:HG2	2.20	0.42
23:d1:69:LEU:HD23	23:d1:69:LEU:HA	1.85	0.42
34:sR:31:ASN:HA	34:sR:47:LEU:HB2	2.01	0.42
36:5:287:G:H5'	51:m5:179:LYS:O	2.20	0.42
36:5:974:G:H2'	36:5:975:C: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
36:5:2724:U:H4'	57:n1:54:HIS:CD2	2.55	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
38:8:45:C:H4'	75:o9:11:GLN:HG3	2.02	0.42
48:m1:10:ARG:NH1	48:m1:133:ARG:HH21	2.18	0.42
53:m7:86:LYS:O	53:m7:90:PHE:HD1	2.02	0.42
59:n3:120:LYS:HB2	59:n3:137:VAL:CG2	2.50	0.42
78:q2:59:HIS:O	78:q2:61:LYS:HG2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:472:U:O2'	1:2:769:A:N3	2.44	0.41
1:2:588:U:H2'	1:2:589:C:O4'	2.20	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
4:S2:84:LYS:HA	4:S2:85:PRO:HD3	1.76	0.41
6:S4:31:PRO:HB2	6:S4:38:LEU:HD22	2.01	0.41
6:S4:240:LYS:CD	6:S4:240:LYS:H	2.33	0.41
12:C0:44:LYS:HD3	12:C0:44:LYS:HA	1.80	0.41
23:D1:11:LEU:H	23:D1:11:LEU:HG	1.68	0.41
36:1:224:C:O2	62:N6:103:LYS:NZ	2.53	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
36:1:1097:G:C8	57:N1:128:LEU:HD13	2.55	0.41
36:1:1362:G:H4'	44:L7:159:GLN:C	2.44	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
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
51:M5:63:ARG:NH2	51:M5:131:GLU:OE2	2.45	0.41
58:N2:87:ASN:HB2	58:N2:89:LEU:HG	2.02	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
73:O7:22:CYS:SG	73:O7:24:ARG:HB2	2.60	0.41
1:6:219:A:C6	1:6:843:U:H1'	2.55	0.41
1:6:512:A:O2'	11:s9:133:HIS:CE1	2.73	0.41
1:6:675:U:H2'	1:6:676:G:H8	1.84	0.41
1:6:725:U:H2'	1:6:726:C:C6	2.55	0.41
2:s0:65:ALA:C	2:s0:67:ILE:H	2.27	0.41
7:s5:225:ARG:NH2	30:d8:58:GLU:HB2	2.35	0.41
9:s7:105:THR:OG1	9:s7:106:SER:N	2.51	0.41
10:s8:81:VAL:HA	10:s8:102:VAL:HG12	2.02	0.41
13:c1:75:VAL:HG12	13:c1:119:VAL:HA	2.02	0.41
14:c2:36:LEU:HG	14:c2:41:LEU:HD12	2.02	0.41
16:c4:17:ALA:N	16:c4:80:HIS:O	2.49	0.41
17:c5:34:VAL:O	17:c5:42:ARG:HG2	2.19	0.41
19:c7:21:TYR:CD2	19:c7:58:MET:HE1	2.55	0.41
21:c9:142:GLU:H	21:c9:142:GLU:HG3	1.70	0.41
25:d3:111:GLY:O	25:d3:121:ARG:HD2	2.19	0.41
27:d5:93:SER:HB3	27:d5:100:ILE:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:655:C:H2'	36:5:656:A:C8	2.55	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
39:l2:19:HIS:CD2	39:l2:19:HIS:N	2.87	0.41
39:l2:30:ARG:HG2	39:l2:74:GLU:CD	2.45	0.41
40:l3:232:ARG:NH1	40:l3:269:GLN:O	2.51	0.41
40:l3:265:ALA:C	40:l3:266:ARG:HG2	2.45	0.41
42:l5:22:ARG:NH1	42:l5:28:THR:OG1	2.53	0.41
43:l6:82:ARG:O	69:o3:104:PRO:HA	2.20	0.41
44:l7:103:LEU:HG	44:l7:130:ILE:CG1	2.49	0.41
45:l8:210:ALA:HA	45:l8:213:LYS:HB3	2.01	0.41
53:m7:94:LEU:HD12	53:m7:94:LEU:HA	1.80	0.41
56:n0:25:PHE:HA	57:n1:149:GLN:O	2.20	0.41
57:n1:96:ILE:HD13	57:n1:96:ILE:HA	1.59	0.41
58:n2:56:VAL:HG22	58:n2:65:VAL:HG22	2.00	0.41
62:n6:125:LYS:HB3	62:n6:126:LEU:H	1.69	0.41
64:n8:45:MET:HE2	64:n8:45:MET:HA	2.02	0.41
1:2:778:G:O6	26:D4:10:ARG:HG2	2.20	0.41
1:2:1105:C:OP2	25:D3:14:LYS:NZ	2.44	0.41
1:2:1142:A:H5"	28:D6:2:PRO:HB3	2.01	0.41
1:2:1486:G:H1'	1:2:1592:A:O2'	2.21	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
5:S3:75:LYS:NZ	12:C0:34:GLU:OE2	2.43	0.41
5:S3:216:PRO:HB2	5:S3:217:ILE:H	1.62	0.41
10:S8:159:GLN:HB3	10:S8:165:LEU:HD23	2.01	0.41
11:S9:29:LYS:HG3	32:E0:44:PHE:CE2	2.55	0.41
11:S9:113:VAL:HG21	11:S9:134:ILE:HD12	2.01	0.41
11:S9:115:LYS:HD2	11:S9:115:LYS:HA	1.70	0.41
17:C5:80:MET:HE2	17:C5:80:MET:HB3	1.79	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
30:D8:13:ILE:HD11	30:D8:31:GLU:HB2	2.02	0.41
36:1:591:G:H1'	43:L6:19:LYS:HG3	2.01	0.41
36:1:789:A:H2'	36:1:790:U:C6	2.55	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
63:N7:101:PHE:HB3	63:N7:107:ARG:HH21	1.84	0.41
69:O3:89:LEU:HD23	69:O3:89:LEU:HA	1.91	0.41
79:Q3:49:ARG:HG3	79:Q3:55:TRP:CZ2	2.55	0.41
1:6:78:A:C8	8:s6:154:ARG:HD3	2.56	0.41
4:s2:152:HIS:H	4:s2:152:HIS:HD2	1.68	0.41
5:s3:207:THR:HB	19:c7:40:THR:OG1	2.20	0.41
7:s5:81:ARG:HH21	30:d8:47:PRO:HB3	1.84	0.41
9:s7:39:ARG:NH2	55:m9:185:LEU:HD22	2.33	0.41
13:c1:101:GLU:OE2	25:d3:16:ARG:NH2	2.48	0.41
18:c6:89:LEU:HG	18:c6:105:LEU:HD23	2.01	0.41
21:c9:38:LYS:O	21:c9:39:THR:OG1	2.35	0.41
36:5:213:A:OP1	62:n6:2:ALA:N	2.53	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
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
36:5:2295:A:N3	59:n3:37:ILE:HD12	2.36	0.41
36:5:2965:U:O2	39:l2:221:LYS:NZ	2.48	0.41
36:5:3047:U:O2'	40:l3:53:MET:HE1	2.20	0.41
39:l2:94:ALA:HB3	39:l2:102:LEU:HG	2.01	0.41
43:l6:62:THR:HG22	43:l6:79:VAL:O	2.20	0.41
46:l9:1:MET:HE1	56:n0:138:GLN:HG2	2.02	0.41
48:m1:164:LYS:HE3	48:m1:171:VAL:HG12	2.02	0.41
48:m1:166:LYS:C	48:m1:168:ASP:N	2.78	0.41
51:m5:135:VAL:HG13	51:m5:142:ILE:HG12	2.02	0.41
52:m6:173:ALA:O	52:m6:176:LYS:HB3	2.20	0.41
54:m8:139:ILE:O	54:m8:140:LEU:HD23	2.20	0.41
60:n4:9:SER:HB2	60:n4:51:TRP:CZ3	2.55	0.41
62:n6:52:ARG:O	62:n6:53:ASP:HB2	2.20	0.41
62:n6:56:VAL:HG22	62:n6:104:LEU:HB3	2.02	0.41
62:n6:111:LEU:HD23	62:n6:116:LYS:HG2	2.02	0.41
63:n7:15:ARG:HB2	63:n7:79:HIS:HB3	2.02	0.41
71:o5:89:ARG:HG2	71:o5:89:ARG:HH11	1.85	0.41
74:o8:36:LYS:HA	74:o8:37:PRO:HD3	1.83	0.41
75:o9:15:LYS:O	75:o9:19:GLN:HG3	2.19	0.41
1:2:312:A:C2	1:2:314:C:H2'	2.55	0.41
1:2:990:C:O2'	16:C4:127:ARG:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
8:S6:163:THR:HA	8:S6:168:THR:HA	2.03	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
15:C3:26:PHE:CE2	15:C3:66:ILE:HD13	2.55	0.41
17:C5:67:ALA:C	17:C5:69:GLU:H	2.28	0.41
18:C6:126:PRO:O	18:C6:128:LYS:HE3	2.20	0.41
27:D5:59:TYR:CZ	27:D5:100:ILE:HG12	2.56	0.41
30:D8:26:THR:HB	30:D8:44:VAL:HG22	2.03	0.41
33:E1:144:CYS:HB3	33:E1:147:VAL:HG22	2.02	0.41
34:SR:209:THR:O	34:SR:225:LEU:N	2.50	0.41
36:1:535:G:C4	36:1:554:A:C6	3.08	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
36:1:2180:G:P	39:L2:174:ARG:HH22	2.43	0.41
39:L2:117:GLU:HB3	39:L2:119:LYS:O	2.20	0.41
40:L3:257:PRO:HG2	40:L3:261:MET:HE3	2.02	0.41
40:L3:323:MET:HE1	40:L3:356:LEU:HD11	2.02	0.41
41:L4:91:GLY:O	41:L4:97:GLY:HA3	2.19	0.41
41:L4:323:VAL:HA	41:L4:326:ARG:HB3	2.02	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
47:M0:16:PRO:HG3	47:M0:128:ARG:NH1	2.35	0.41
47:M0:142:ASP:OD2	47:M0:178:ARG:NH2	2.53	0.41
49:M3:106:GLN:HB3	72:O6:18:THR:OG1	2.20	0.41
63:N7:53:VAL:HA	63:N7:57:HIS:CD2	2.55	0.41
72:O6:98:ARG:O	72:O6:99:ARG:HD2	2.20	0.41
1:6:93:A:C6	1:6:398:G:C6	3.08	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
1:6:327:U:H1'	13:c1:10:GLU:HG2	2.01	0.41
1:6:1699:G:C2'	1:6:1700:C:H5'	2.48	0.41
6:s4:71:LYS:HG2	6:s4:76:VAL:HG22	2.01	0.41
10:s8:22:ARG:HG3	10:s8:23:LYS:O	2.20	0.41
22:d0:24:ILE:HG12	22:d0:116:VAL:HG12	2.00	0.41
26:d4:23:PHE:CE2	26:d4:75:VAL:HG23	2.54	0.41
27:d5:59:TYR:HE1	27:d5:100:ILE:HG23	1.85	0.41
35:sM:124:GLU:O	35:sM:129:GLN:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:71:A:OP2	64:n8:67:HIS:NE2	2.52	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
36:5:2737:C:H4'	57:n1:68:THR:OG1	2.19	0.41
43:l6:62:THR:HG22	43:l6:79:VAL:H	1.86	0.41
55:m9:20:ARG:HH11	55:m9:21:LYS:HZ2	1.68	0.41
62:n6:45:ILE:HD12	62:n6:119:ILE:HG23	2.01	0.41
78:q2:59:HIS:HA	78:q2:61:LYS:NZ	2.35	0.41
82:p0:42:ARG:HA	82:p0:42:ARG:HD2	1.97	0.41
82:p0:80:VAL:HA	82:p0:84:VAL:HG21	2.03	0.41
1:2:142:G:H5"	8:S6:139:ASN:ND2	2.35	0.41
1:2:323:A:OP2	10:S8:10:LYS:HG2	2.21	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
1:2:912:U:H4'	1:2:913:G:O5'	2.20	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
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
12:C0:91:TYR:C	12:C0:93:GLN:H	2.28	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
27:D5:40:VAL:HA	27:D5:75:LEU:HD11	2.03	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
36:1:1134:G:O2'	36:1:2642:A:N3	2.44	0.41
36:1:1815:U:O2'	36:1:1816:A:P	2.78	0.41
36:1:2948:C:O2'	40:L3:242:THR:HG22	2.21	0.41
38:4:118:C:H2'	38:4:119:C:H6	1.85	0.41
40:L3:229:VAL:HG11	40:L3:249:VAL:HG23	2.02	0.41
41:L4:44:LYS:O	41:L4:47:ARG:HD3	2.20	0.41
46:L9:48:VAL:HG11	46:L9:52:LEU:HD13	2.03	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
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
1:6:115:G:OP1	13:c1:67:ARG:NE	2.54	0.41
1:6:247:A:H2	13:c1:65:SER:HB2	1.86	0.41
1:6:1253:U:H4'	33:e1:143:LYS:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1369:U:OP2	21:c9:69:LYS:NZ	2.44	0.41
1:6:1535:U:O2'	1:6:1536:G:OP2	2.36	0.41
4:s2:129:ILE:HG22	4:s2:133:LYS:HE3	2.02	0.41
4:s2:238:SER:O	4:s2:240:LEU:N	2.54	0.41
7:s5:184:PHE:C	7:s5:186:ASN:H	2.29	0.41
11:s9:113:VAL:O	11:s9:118:LEU:HB2	2.20	0.41
13:c1:46:LYS:HE3	13:c1:50:GLU:OE2	2.20	0.41
15:c3:4:MET:HG2	15:c3:5:HIS:CD2	2.56	0.41
17:c5:51:SER:OG	17:c5:52:LYS:N	2.53	0.41
25:d3:9:LEU:HD23	25:d3:9:LEU:HA	1.92	0.41
28:d6:10:ARG:NH1	28:d6:36:ILE:HG13	2.22	0.41
30:d8:32:PHE:HB2	30:d8:38:ARG:HB2	2.02	0.41
36:5:190:U:H2'	62:n6:60:ARG:NH2	2.35	0.41
36:5:720:A:C2	36:5:784:A:H5'	2.55	0.41
36:5:1259:A:H5'	82:p0:53:MET:O	2.20	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
36:5:2552:C:N4	66:o0:57:GLU:OE2	2.54	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
37:7:56:A:H4'	48:m1:152:HIS:HB2	2.01	0.41
38:8:94:C:H5"	73:o7:76:ASN:ND2	2.35	0.41
38:8:121:U:H2'	38:8:122:U:C6	2.55	0.41
40:l3:92:TYR:O	40:l3:156:SER:N	2.44	0.41
42:l5:261:THR:H	42:l5:264:GLN:HB2	1.85	0.41
43:l6:131:LYS:HD3	43:l6:132:ALA:N	2.34	0.41
49:m3:60:ALA:HA	49:m3:70:ARG:HH21	1.85	0.41
51:m5:42:PRO:HD3	51:m5:61:ILE:HG13	2.02	0.41
51:m5:172:ARG:CZ	51:m5:174:ILE:HD11	2.50	0.41
53:m7:16:SER:HB3	53:m7:149:VAL:HG22	2.03	0.41
55:m9:170:ARG:O	55:m9:174:ALA:N	2.52	0.41
63:n7:102:GLU:OE1	63:n7:103:GLN:N	2.53	0.41
82:p0:26:PHE:HB2	82:p0:87:VAL:HB	2.02	0.41
1:2:530:C:O2	26:D4:61:ARG:NH2	2.54	0.41
1:2:736:C:OP1	6:S4:197:HIS:NE2	2.53	0.41
1:2:850:A:C2	1:2:851:U:C2	3.09	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
1:2:1434:U:O2'	1:2:1436:A:OP1	2.32	0.41
1:2:1550:A:C6	1:2:1551:U:C4	3.08	0.41
3:S1:128:LYS:NZ	3:S1:132:ASP:HB3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S1:178:GLY:O	3:S1:180:THR:N	2.53	0.41
15:C3:27:LYS:H	15:C3:27:LYS:HE2	1.85	0.41
16:C4:19:ILE:HG12	16:C4:28:VAL:HG22	2.02	0.41
20:C8:146:ALA:N	35:SM:68:ARG:HH21	2.18	0.41
25:D3:19:ARG:O	25:D3:23:ARG:HG2	2.21	0.41
34:SR:42:LEU:HB2	34:SR:61:PHE:HB2	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
36:1:2444:C:H3'	36:1:2445:A:H5"	2.02	0.41
42:L5:236:LEU:HA	42:L5:239:ILE:HD12	2.03	0.41
44:L7:38:LYS:HE3	44:L7:38:LYS:HB2	1.81	0.41
46:L9:172:ILE:O	46:L9:176:LEU:HD23	2.21	0.41
50:M4:101:LYS:O	50:M4:105:GLN:HB2	2.20	0.41
57:N1:100:LYS:C	57:N1:102:ARG:H	2.27	0.41
1:6:588:U:OP2	80:e0:26:LYS:NZ	2.35	0.41
1:6:829:A:H1'	1:6:830:U:C5	2.56	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
2:s0:59:LEU:HD12	23:d1:79:LEU:HD11	2.01	0.41
5:s3:70:THR:HG22	5:s3:86:LEU:HB2	2.01	0.41
6:s4:121:TYR:HB2	6:s4:162:ILE:O	2.21	0.41
9:s7:31:SER:HA	9:s7:35:LYS:HB3	2.01	0.41
9:s7:91:ILE:HD12	9:s7:92:PHE:H	1.85	0.41
11:s9:87:SER:HB3	11:s9:90:LYS:HD2	2.02	0.41
18:c6:29:ILE:HA	18:c6:65:ILE:HB	2.03	0.41
20:c8:143:ARG:C	20:c8:145:ARG:H	2.28	0.41
24:d2:24:GLN:NE2	29:d7:4:VAL:HA	2.32	0.41
36:5:143:G:H4'	38:8:145:U:OP1	2.21	0.41
36:5:193:C:H2'	36:5:194:U:H6	1.85	0.41
36:5:388:G:N2	53:m7:101:ASN:OD1	2.54	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
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
36:5:2248: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
36:5:2836:C:H4'	47:m0:157:TYR:CE1	2.55	0.41
38:8:36:G:O2'	38:8:104:A:N1	2.54	0.41
40:l3:49:TYR:HE1	40:l3:177:HIS:CE1	2.39	0.41
41:l4:203:ARG:NH2	41:l4:240:PRO:HB3	2.35	0.41
42:l5:257:GLU:O	42:l5:258:LYS:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:l8:41:GLN:HG3	45:l8:42:PRO:HD2	2.01	0.41
47:m0:135:ILE:HG22	47:m0:136:PHE:CD1	2.56	0.41
53:m7:95:LEU:HD23	53:m7:95:LEU:HA	1.77	0.41
54:m8:79:LYS:HA	54:m8:136:ASN:OD1	2.20	0.41
56:n0:144:LEU:HD23	56:n0:144:LEU:HA	1.82	0.41
62:n6:108:LYS:HD3	62:n6:108:LYS:HA	1.80	0.41
63:n7:104:PRO:O	63:n7:108:GLU:HG3	2.20	0.41
71:o5:18:ALA:O	71:o5:22:VAL:HG23	2.20	0.41
78:q2:47:GLN:HE22	78:q2:53:GLN:HA	1.86	0.41
1:2:150:U:P	26:D4:123:LYS:HZ3	2.43	0.41
1:2:913:G:HO2'	1:2:914:G:P	2.42	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
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
8:S6:131:LYS:H	8:S6:131:LYS:HG3	1.67	0.41
8:S6:137:ARG:HD3	8:S6:177:ARG:HE	1.86	0.41
17:C5:60:LEU:HD11	17:C5:92:SER:OG	2.21	0.41
23:D1:28:ASP:C	23:D1:30:ALA:H	2.29	0.41
28:D6:66:LYS:HE2	28:D6:66:LYS:HB2	1.90	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
33:E1:126:CYS:O	33:E1:128:ALA:N	2.50	0.41
36:1:374:A:H4'	36:1:375:A:OP1	2.20	0.41
36:1:848:A:O5'	36:1:848:A:H8	2.04	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
37:3:64:A:H3'	47:M0:204:GLY:O	2.20	0.41
46:L9:189:GLU:C	46:L9:191:LEU:N	2.79	0.41
47:M0:52:LEU:HA	47:M0:52:LEU:HD23	1.73	0.41
49:M3:93:ILE:HG22	49:M3:93:ILE:O	2.20	0.41
66:O0:86:ARG:NH1	79:Q3:44:LYS:HG2	2.36	0.41
69:O3:69:GLY:HA2	69:O3:85:PHE:HA	2.02	0.41
72:O6:26:ILE:O	72:O6:28:TYR:N	2.51	0.41
73:O7:52:LYS:HA	73:O7:55:ARG:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:169:A:C5'	8:s6:176:GLN:HG2	2.51	0.41
1:6:291:G:H2'	1:6:292:U:C6	2.56	0.41
1:6:558:U:P	80:e0:55:ARG:HH22	2.43	0.41
1:6:1196:A:C8	1:6:1602:C:H4'	2.56	0.41
1:6:1796:C:N1	28:d6:5:ARG:HG2	2.35	0.41
1:6:1796:C:H5	28:d6:6:ALA:H	1.67	0.41
5:s3:75:LYS:HA	5:s3:75:LYS:HD3	1.85	0.41
6:s4:118:GLU:HG3	6:s4:121:TYR:CE1	2.56	0.41
11:s9:148:VAL:HG11	11:s9:156:ILE:HD11	2.01	0.41
15:c3:20:ARG:HA	15:c3:20:ARG:HD2	1.87	0.41
21:c9:73:VAL:HG12	21:c9:77:ASN:HD21	1.84	0.41
36:5:324:A:H2'	36:5:325:A:C8	2.56	0.41
36:5:326:U:OP1	49:m3:31:LYS:NZ	2.31	0.41
36:5:696:C:OP2	41:l4:119:ARG:NH2	2.43	0.41
36:5:715:A:H4'	36:5:716:A:OP1	2.20	0.41
36:5:1033:U:H2'	36:5:1034:U:H5'	2.03	0.41
36:5:1390:A:H5'	36:5:1390:A:N3	2.36	0.41
36:5:1719:G:N7	55:m9:121:HIS:HE1	2.19	0.41
36:5:2138:A:C4	73:o7:3:LYS:HB3	2.56	0.41
36:5:2726:C:O2'	36:5:2727:A:H2'	2.21	0.41
36:5:3288:G:O2'	36:5:3289:G:H8	2.04	0.41
38:8:157:U:H3'	38:8:158:U:H3'	2.02	0.41
41:l4:39:PHE:O	41:l4:43:ASN:HB2	2.21	0.41
42:l5:143:LYS:HG3	42:l5:172:TYR:HD2	1.86	0.41
45:l8:100:GLU:OE1	45:l8:108:ARG:HD3	2.21	0.41
46:l9:111:PHE:CD1	46:l9:127:PRO:HA	2.55	0.41
48:m1:77:GLU:OE2	48:m1:166:LYS:NZ	2.54	0.41
53:m7:129:THR:HG22	53:m7:137:ASN:O	2.21	0.41
63:n7:49:TYR:CE2	63:n7:133:LYS:HA	2.56	0.41
64:n8:66:ALA:C	64:n8:68:PHE:N	2.77	0.41
70:o4:54:ILE:HD11	70:o4:78:GLY:HA2	2.03	0.41
71:o5:86:ARG:O	71:o5:90:ARG:HG2	2.20	0.41
73:o7:14:LYS:HE2	75:o9:51:ILE:HG13	2.03	0.41
1:2:25:C:OP2	1:2:25:C:H4'	2.19	0.41
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
3:S1:81:PHE:HB2	3:S1:82:ARG:H	1.68	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:S5:97:LEU:HD23	7:S5:97:LEU:HA	1.95	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:S7:60:ILE:HD12	9:S7:92:PHE:CZ	2.56	0.41
9:S7:63:PRO:O	9:S7:64:VAL:HB	2.20	0.41
10:S8:199:LYS:HE3	10:S8:199:LYS:HB2	1.87	0.41
14:C2:52:LEU:O	14:C2:85:LYS:NZ	2.53	0.41
15:C3:94:LYS:HG2	15:C3:118:ILE:HD13	2.03	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
24:D2:37:PHE:CD2	24:D2:103:ILE:HD12	2.56	0.41
28:D6:41:ILE:O	28:D6:41:ILE:HG12	2.19	0.41
30:D8:5:THR:HA	30:D8:6:PRO:HD3	1.86	0.41
36:1:535:G:O2'	36:1:554:A:N1	2.39	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
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:OP2	36:1:2373:A:H3'	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
37:3:112:G:H2'	37:3:113:C:H6	1.85	0.41
38:4:85:G:O6	62:N6:112:ASP:HB3	2.20	0.41
40:L3:110:LEU:HA	40:L3:110:LEU:HD12	1.86	0.41
40:L3:331:ASN:OD1	40:L3:331:ASN:N	2.53	0.41
46:L9:72:LYS:NZ	46:L9:76:ASP:OD2	2.36	0.41
62:N6:37:LYS:H	62:N6:37:LYS:HD3	1.85	0.41
63:N7:88:ASP:HB3	63:N7:121:ARG:NH1	2.33	0.41
68:O2:126:LEU:HD23	68:O2:126:LEU:HA	1.87	0.41
70:O4:42:PRO:O	70:O4:50:ALA:HA	2.21	0.41
70:O4:106:LYS:HD3	70:O4:106:LYS:HA	1.82	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
79:Q3:55:TRP:CD1	79:Q3:66:GLY:HA3	2.56	0.41
1:6:1326:A:O3'	5:s3:156:PHE:HE1	2.03	0.41
1:6:1330:G:H2'	1:6:1331:A:O4'	2.20	0.41
1:6:1389:C:H4'	19:c7:49:LYS:HA	2.03	0.41
1:6:1603:U:H2'	1:6:1604:U:H6	1.86	0.41
2:s0:175:TYR:HE1	2:s0:197:ILE:HG22	1.86	0.41
3:s1:30:PHE:CD1	3:s1:94:LYS:HA	2.56	0.41
5:s3:64:ARG:HG2	5:s3:65:ARG:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:s3:210:GLU:HA	5:s3:211:PRO:HD3	1.75	0.41
7:s5:149:VAL:HG13	7:s5:151:GLY:N	2.36	0.41
8:s6:138:ALA:HB1	8:s6:142:ARG:NH1	2.34	0.41
11:s9:33:GLU:H	11:s9:33:GLU:HG2	1.68	0.41
16:c4:123:SER:O	16:c4:124:ASP:HB2	2.20	0.41
17:c5:89:MET:H	17:c5:89:MET:HG2	1.61	0.41
17:c5:89:MET:HE2	17:c5:89:MET:HB3	1.98	0.41
23:d1:70:ASN:N	23:d1:70:ASN:OD1	2.53	0.41
27:d5:88:ILE:HG22	27:d5:89:ILE:HG23	2.02	0.41
28:d6:64:LEU:HD23	28:d6:64:LEU:HA	1.91	0.41
34:sR:101:GLN:HG2	34:sR:137:LYS:C	2.45	0.41
35:sM:70:ASN:O	35:sM:74:LYS:HE2	2.19	0.41
36:5:3:U:H3	38:8:156:U:H3	1.68	0.41
36:5:29:C:O2'	51:m5:162:ARG:O	2.38	0.41
36:5:40:A:H5"	64:n8:35:ALA:HB1	2.03	0.41
36:5:406:G:H1'	38:8:16:G:N2	2.35	0.41
36:5:521:A:N3	56:n0:65:ASN:ND2	2.68	0.41
36:5:781:G:OP1	54:m8:151:ARG:HD2	2.21	0.41
36:5:1334:U:C1'	44:l7:208:SER:HB2	2.51	0.41
36:5:1549:U:H2'	36:5:1550:C:H6	1.85	0.41
36:5:2167:A:OP1	51:m5:72:LYS:NZ	2.43	0.41
36:5:2936:A:H2'	36:5:2937:G:C8	2.56	0.41
36:5:3124:G:H5'	46:l9:40:HIS:ND1	2.35	0.41
40:l3:43:LEU:HD11	40:l3:160:VAL:HG21	2.02	0.41
40:l3:87:VAL:HB	40:l3:110:LEU:HD11	2.01	0.41
41:l4:181:VAL:HG11	41:l4:223:PRO:C	2.45	0.41
41:l4:185:LYS:HA	41:l4:200:THR:O	2.20	0.41
42:l5:29:ASP:OD2	42:l5:29:ASP:C	2.64	0.41
42:l5:206:GLN:O	42:l5:210:GLU:HG3	2.21	0.41
45:l8:64:ILE:O	45:l8:68:ARG:HG2	2.20	0.41
46:l9:90:MET:HE2	46:l9:90:MET:HB3	1.93	0.41
46:l9:91:ARG:HD2	46:l9:143:GLU:HA	2.02	0.41
62:n6:115:ARG:O	62:n6:119:ILE:HG13	2.20	0.41
70:o4:96:GLU:HA	70:o4:99:LYS:HD2	2.01	0.41
72:o6:5:THR:OG1	72:o6:7:ILE:HG22	2.20	0.41
1:2:41:A:H2'	1:2:438:A:N7	2.36	0.41
1:2:156:A:H2'	1:2:157:A:O4'	2.20	0.41
1:2:753:A:H4'	6:S4:221:ARG:HH21	1.86	0.41
1:2:800:U:H2'	1:2:801:G:C8	2.56	0.41
1:2:1127:G:OP1	77:Q1:11:ARG:NH2	2.54	0.41
1:2:1199:G:O6	22:D0:67:THR:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S0:9:LEU:HD11	2:S0:14:ALA:HB2	2.02	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
8:S6:193:LEU:HD23	8:S6:193:LEU:HA	1.91	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
24:D2:24:GLN:OE1	29:D7:4:VAL:HA	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
36:1:911:C:H5"	39:L2:15:ILE:HD13	2.03	0.41
36:1:1051:U:H4'	57:N1:19:PHE:CG	2.54	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
43:L6:158:TYR:CE1	50:M4:115:PHE:HA	2.55	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
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
59:N3:102:ILE:O	59:N3:102:ILE:HG13	2.18	0.41
62:N6:100:HIS:HA	62:N6:101:PRO:HD2	1.84	0.41
74:O8:64:LYS:HA	74:O8:64:LYS:NZ	2.35	0.41
1:6:941:A:C5	1:6:942:G:H1'	2.55	0.41
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
3:s1:35:PRO:HB3	3:s1:231:LEU:HD21	2.03	0.41
8:s6:176:GLN:HG3	8:s6:177:ARG:N	2.35	0.41
10:s8:78:ILE:HA	10:s8:104:ILE:HG22	2.02	0.41
10:s8:103:GLN:HA	10:s8:165:LEU:O	2.21	0.41
11:s9:3:ARG:H	11:s9:3:ARG:HE	1.67	0.41
11:s9:141:VAL:HG11	11:s9:146:PHE:CD2	2.56	0.41
20:c8:119:ILE:HD12	20:c8:119:ILE:HA	1.83	0.41
28:d6:84:VAL:C	28:d6:85:ARG:HG2	2.46	0.41
30:d8:32:PHE:O	30:d8:34:GLU:N	2.54	0.41
30:d8:49:ARG:HG2	30:d8:52:ASP:OD1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:sM:46:LYS:HA	36:5:1018:G:H4'	2.03	0.41
36:5:944:C:H4'	68:o2:33:ARG:HH11	1.86	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
40:l3:119:TYR:HE2	40:l3:129:ALA:HB2	1.85	0.41
40:l3:262:TRP:HE1	52:m6:66:LYS:HE2	1.85	0.41
42:l5:111:GLN:HA	42:l5:116:ASP:CG	2.46	0.41
42:l5:160:PHE:CD2	42:l5:179:ARG:HB3	2.56	0.41
43:l6:47:PHE:O	43:l6:50:LYS:HB2	2.20	0.41
45:l8:67:ILE:HD13	45:l8:67:ILE:HA	1.87	0.41
46:l9:87:LYS:HE2	46:l9:187:ILE:HG23	2.03	0.41
49:m3:54:LEU:HD22	49:m3:54:LEU:HA	1.85	0.41
50:m4:24:LYS:HB3	50:m4:24:LYS:HE2	1.88	0.41
52:m6:125:ARG:HG3	52:m6:129:LEU:HD22	2.02	0.41
53:m7:67:ILE:HD12	53:m7:82:ARG:NH1	2.36	0.41
57:n1:147:VAL:HA	57:n1:148:PRO:HD3	1.94	0.41
60:n4:37:ALA:O	60:n4:41:LYS:HE3	2.21	0.41
1:2:1:U:O4	11:S9:54:ARG:HG3	2.21	0.41
1:2:166:C:OP1	8:S6:131:LYS:HE3	2.21	0.41
1:2:366:A:OP1	1:2:758:U:O2'	2.34	0.41
1:2:569:C:H42	25:D3:65:ASN:HD21	1.69	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
1:2:931:C:O2'	3:S1:118:GLN:O	2.33	0.41
1:2:953:G:H2'	1:2:954:G:C8	2.56	0.41
1:2:962:C:N4	1:2:963:A:C6	2.88	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
1:2:1396:U:H2'	1:2:1397:U:C6	2.56	0.41
1:2:1426:C:H5"	35:SM:93:ARG:NH1	2.35	0.41
1:2:1545:A:OP1	20:C8:133:VAL:HG12	2.21	0.41
1:2:1592:A:H2'	1:2:1593:A:H8	1.85	0.41
2:S0:56:LYS:HZ3	2:S0:158:VAL:HG23	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S1:86:LEU:HB3	3:S1:98:THR:OG1	2.21	0.41
6:S4:106:LYS:O	6:S4:108:ARG:HG3	2.21	0.41
6:S4:131:LEU:HD22	6:S4:131:LEU:HA	1.89	0.41
6:S4:246:LEU:HD21	6:S4:254:ARG:CZ	2.51	0.41
9:S7:151:LYS:HG3	9:S7:182:VAL:HG12	2.02	0.41
13:C1:98:ASN:HD22	24:D2:79:PHE:HD1	1.69	0.41
15:C3:67:THR:C	15:C3:69:ASN:H	2.27	0.41
16:C4:114:ARG:HA	28:D6:62:TYR:CZ	2.56	0.41
18:C6:114:ARG:O	18:C6:115:THR:OG1	2.28	0.41
19:C7:5:ARG:N	19:C7:5:ARG:HD3	2.36	0.41
26:D4:18:LEU:HD23	26:D4:18:LEU:HA	1.89	0.41
27:D5:41:ILE:HG13	27:D5:42:LEU:H	1.86	0.41
36:1:90:C:H2'	36:1:91:G:H5'	2.02	0.41
36:1:118:U:C5	36:1:119:U:C4	3.09	0.41
36:1:413:U:OP1	53:M7:30:ARG:NE	2.49	0.41
36:1:1657:C:O2'	36:1:1797:A:OP2	2.27	0.41
36:1:1687:U:H5"	36:1:1688:U:O5'	2.21	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
36:1:2352:A:H5"	53:M7:83:TRP:O	2.21	0.41
36:1:3084:C:H2'	36:1:3085:G:O4'	2.21	0.41
37:3:26:C:H5'	42:L5:56:THR:HB	2.03	0.41
39:L2:79:ASN:HD22	39:L2:165:VAL:HG22	1.85	0.41
39:L2:116:VAL:HG22	39:L2:126:LEU:HB2	2.02	0.41
40:L3:182:GLN:HG3	40:L3:183:LEU:N	2.36	0.41
40:L3:209:PHE:HB3	40:L3:282:ILE:HD12	2.02	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
43:L6:58:LEU:HD12	43:L6:78:ARG:HD3	2.02	0.41
46:L9:4:ILE:HG22	56:N0:142:GLN:CD	2.45	0.41
46:L9:41:ILE:HD13	46:L9:71:VAL:HG21	2.03	0.41
48:M1:32:ARG:O	48:M1:36:VAL:HG23	2.20	0.41
48:M1:141:ARG:O	48:M1:145:LYS:HE2	2.21	0.41
50:M4:19:ARG:HD2	50:M4:66:THR:O	2.20	0.41
53:M7:52:LEU:HD12	53:M7:52:LEU:HA	1.90	0.41
55:M9:130:ASN:C	55:M9:132:PHE:H	2.29	0.41
56:N0:45:LEU:HA	56:N0:45:LEU:HD22	1.82	0.41
63:N7:23:VAL:HB	63:N7:43:VAL:HB	2.02	0.41
70:O4:8:ARG:NH2	70:O4:31:ARG:HD2	2.36	0.41
1:6:119:A:H1'	1:6:397:A:C5	2.55	0.41
1:6:156:A:H2'	1:6:157:A:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:248:U:H4'	13:c1:36:LYS:HD3	2.03	0.41
1:6:1147:A:H2'	1:6:1148:C:O4'	2.20	0.41
1:6:1191:U:H5'	18:c6:143:ARG:HH11	1.86	0.41
1:6:1330:G:N2	19:c7:8:THR:HG21	2.35	0.41
1:6:1492:A:O2'	1:6:1493:A:H8	1.99	0.41
1:6:1523:G:H8	21:c9:79:LEU:HD13	1.85	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
1:6:1787:C:OP2	16:c4:132:ARG:HB3	2.21	0.41
4:s2:143:TYR:OH	4:s2:150:GLN:N	2.54	0.41
5:s3:21:LEU:HD23	5:s3:21:LEU:HA	1.82	0.41
5:s3:53:THR:O	5:s3:53:THR:OG1	2.28	0.41
7:s5:97:LEU:HD23	7:s5:97:LEU:HA	1.94	0.41
7:s5:109:LYS:O	7:s5:113:ILE:HG13	2.20	0.41
8:s6:49:VAL:HB	8:s6:115:LYS:HG2	2.03	0.41
8:s6:174:LYS:O	8:s6:175:ILE:C	2.63	0.41
10:s8:101:ILE:HA	10:s8:167:ALA:O	2.21	0.41
10:s8:151:LYS:HD2	10:s8:151:LYS:HA	1.86	0.41
15:c3:54:LEU:HB3	15:c3:60:VAL:CG1	2.50	0.41
18:c6:116:LEU:HA	18:c6:116:LEU:HD23	1.85	0.41
19:c7:33:ARG:NH2	34:sR:109:ASP:OD2	2.51	0.41
19:c7:71:PHE:CE1	19:c7:74:GLN:HB2	2.56	0.41
20:c8:62:THR:O	20:c8:66:LEU:HG	2.20	0.41
22:d0:96:PRO:O	22:d0:100:VAL:HG23	2.21	0.41
80:e0:39:LEU:HA	80:e0:39:LEU:HD13	1.85	0.41
34:sR:89:LEU:HD21	34:sR:110:VAL:HG11	2.03	0.41
36:5:279:U:H2'	36:5:280:U:C6	2.56	0.41
36:5:848:A:H2'	36:5:849:C:O4'	2.20	0.41
36:5:863:C:H2'	36:5:864:G:O4'	2.21	0.41
36:5:959:C:N4	36:5:2801:A:C8	2.88	0.41
36:5:1063:G:OP2	36:5:1097:G:H5"	2.21	0.41
36:5:1160:C:C2	68:o2:45:ARG:NH1	2.88	0.41
36:5:1160:C:O2'	36:5:1366:A:H5'	2.21	0.41
36:5:1255:C:H2'	36:5:1256:G:H8	1.86	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
36:5:1742: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
36:5:2509:U:H2'	36:5:2510:U:H5"	2.02	0.41
36:5:2730:G:H4'	54:m8:184:PHE:CD1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:2732:G:H2'	36:5:2733:A:O4'	2.19	0.41
36:5:2880:U:O2	40:l3:250:ALA:HB3	2.21	0.41
36:5:3292:A:H4'	40:l3:132:LYS:NZ	2.36	0.41
36:5:3369:G:C6	40:l3:380:MET:HE3	2.56	0.41
37:7:22:A:N6	37:7:23:A:N1	2.69	0.41
39:l2:55:GLY:O	39:l2:56:ALA:HB3	2.21	0.41
39:l2:65:ASP:OD1	39:l2:70:ARG:HD2	2.21	0.41
41:l4:31:ARG:O	41:l4:35:VAL:HG23	2.21	0.41
42:l5:92:LEU:HD23	42:l5:92:LEU:HA	1.83	0.41
42:l5:122:VAL:C	42:l5:124:GLU:H	2.28	0.41
43:l6:89:THR:HG21	50:m4:115:PHE:HB2	2.03	0.41
44:l7:176:TYR:HB3	44:l7:194:HIS:ND1	2.35	0.41
47:m0:48:LEU:O	47:m0:139:ARG:HA	2.21	0.41
51:m5:153:ASP:OD2	51:m5:155:VAL:HG22	2.21	0.41
54:m8:147:ARG:HB3	54:m8:150:VAL:HG13	2.03	0.41
54:m8:177:GLY:O	54:m8:186:VAL:N	2.42	0.41
54:m8:185:LYS:HD3	54:m8:186:VAL:HG23	2.02	0.41
55:m9:109:TYR:HB3	55:m9:115:ILE:HG12	2.02	0.41
55:m9:184:LEU:HD23	55:m9:184:LEU:HA	1.88	0.41
63:n7:4:PHE:O	63:n7:4:PHE:CG	2.74	0.41
63:n7:66:THR:O	63:n7:68:ILE:HG13	2.21	0.41
68:o2:8:LYS:HB3	68:o2:8:LYS:HE2	1.82	0.41
75:o9:27:ILE:C	75:o9:29:LEU:H	2.29	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
1:2:1241:G:H5'	17:C5:102:PHE:CZ	2.56	0.41
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:OP1	1:2:1491:U:H4'	2.20	0.41
5:S3:113:LEU:HA	5:S3:113:LEU:HD23	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:S8:8:ARG:NH1	10:S8:21:PHE:HB3	2.36	0.41
10:S8:106:ALA:HB2	10:S8:165:LEU:HG	2.03	0.41
10:S8:192:TYR:O	10:S8:196:LEU:HB2	2.21	0.41
10:S8:193:LEU:HD23	10:S8:193:LEU:HA	1.88	0.41
11:S9:108:ARG:HG2	11:S9:147:MET:HE2	2.03	0.41
21:C9:52:GLY:HA2	21:C9:55:TYR:CE2	2.55	0.41
22:D0:65:ILE:HD12	31:D9:43:PHE:CZ	2.56	0.41
25:D3:53:VAL:HG13	25:D3:72:VAL:HB	2.03	0.41
34:SR:135:THR:HG22	34:SR:141:LEU:HD23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:720:A:H2'	54:M8:69:ARG:NH2	2.36	0.41
36:1:1635:G:O6	63:N7:17:ARG:HB2	2.20	0.41
36:1:1813:A:OP1	36:1:1817:G:O2'	2.36	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
36:1:2675:C:N4	48:M1:22:SER:HB2	2.35	0.41
36:1:2880:U:O2	40:L3:250:ALA:HB3	2.21	0.41
36:1:3101:G:C2	36:1:3134:A:N3	2.89	0.41
37:3:58:C:H2'	37:3:59:U:H6	1.86	0.41
39:L2:209:HIS:CD2	39:L2:211:HIS:H	2.39	0.41
41:L4:192:GLY:HA2	41:L4:195:ARG:HB2	2.03	0.41
42:L5:143:LYS:HB3	42:L5:143:LYS:HE2	1.89	0.41
43:L6:4:GLN:HB2	68:O2:75:LEU:HB2	2.03	0.41
44:L7:140:SER:OG	44:L7:143:THR:HG23	2.21	0.41
47:M0:52:LEU:HB2	47:M0:136:PHE:HB2	2.02	0.41
47:M0:54:SER:OG	47:M0:130:ASP:O	2.39	0.41
50:M4:8:LYS:HB3	50:M4:9:ALA:H	1.61	0.41
50:M4:102:LYS:HB2	50:M4:102:LYS:HE2	1.80	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
56:N0:8:GLN:OE1	56:N0:26:ARG:NE	2.38	0.41
56:N0:66:GLU:HG3	56:N0:68:HIS:H	1.86	0.41
59:N3:80:ARG:HH21	59:N3:97:ASP:CG	2.28	0.41
63:N7:76:ASN:OD1	63:N7:77:TYR:N	2.54	0.41
69:O3:13:HIS:ND1	69:O3:93:THR:OG1	2.39	0.41
78:Q2:8:ARG:O	78:Q2:23:HIS:N	2.52	0.41
1:6:169:A:H5"	8:s6:176:GLN:HG2	2.03	0.41
1:6:1221:A:H2'	1:6:1222:C:C6	2.56	0.41
1:6:1754:A:OP2	25:d3:62:LYS:HD2	2.21	0.41
1:6:1756[B]:A:OP1	1:6:1756[B]:A:H4'	2.20	0.41
2:s0:126:PRO:HG2	2:s0:152:PRO:HD2	2.03	0.41
2:s0:184:LEU:HD13	2:s0:184:LEU:HA	1.89	0.41
11:s9:58:ASP:O	11:s9:61:THR:OG1	2.37	0.41
15:c3:132:VAL:HG23	15:c3:134:VAL:HG13	2.01	0.41
19:c7:45:ARG:O	19:c7:49:LYS:N	2.50	0.41
20:c8:4:VAL:HG11	27:d5:82:HIS:ND1	2.36	0.41
20:c8:112:ASP:O	20:c8:116:LEU:HD22	2.20	0.41
22:d0:37:VAL:HG13	22:d0:107:THR:HG22	2.03	0.41
33:e1:83:LYS:O	33:e1:84:VAL:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:28:C:O2'	36:5:29:C:H5'	2.21	0.41
36:5:281:G:C6	36:5:282:G:C6	3.09	0.41
36:5:784:A:H2'	54:m8:69:ARG:HH21	1.85	0.41
36:5:1046:A:H2'	36:5:1049:C:C5	2.55	0.41
36:5:1107:C:H5"	65:n9:25:LYS:NZ	2.36	0.41
36:5:1139:G:O6	65:n9:10:HIS:NE2	2.53	0.41
36:5:1369:A:O3'	64:n8:20:GLY:HA2	2.20	0.41
36:5:1783:U:H2'	36:5:1784:G:C8	2.56	0.41
36:5:2816:G:C8	36:5:2869:U:H3'	2.56	0.41
38:8:81:U:H1'	38:8:82:U:H5"	2.02	0.41
40:l3:74:GLU:OE2	40:l3:325:LYS:HE3	2.21	0.41
40:l3:159:ARG:HG2	40:l3:182:GLN:HA	2.02	0.41
44:l7:103:LEU:HG	44:l7:130:ILE:HG12	2.03	0.41
44:l7:203:TRP:CD1	44:l7:204:PRO:HD2	2.56	0.41
45:l8:78:PHE:C	45:l8:80:TYR:H	2.28	0.41
45:l8:230:LYS:O	45:l8:230:LYS:HG3	2.19	0.41
48:m1:155:THR:OG1	48:m1:158:ASP:HB2	2.21	0.41
50:m4:99:TRP:O	50:m4:103:ILE:HG13	2.21	0.41
52:m6:170:LYS:HE2	52:m6:170:LYS:HB3	1.81	0.41
53:m7:4:TYR:CE1	53:m7:16:SER:HB2	2.56	0.41
53:m7:52:LEU:HD13	53:m7:88:VAL:HG11	2.02	0.41
54:m8:54:LEU:HD23	54:m8:54:LEU:HA	1.89	0.41
63:n7:34:LYS:HA	63:n7:34:LYS:HD2	1.97	0.41
63:n7:41:ALA:O	63:n7:43:VAL:HG13	2.20	0.41
63:n7:81:LEU:HD22	63:n7:82:PRO:HD2	2.03	0.41
64:n8:122:PRO:HB3	64:n8:142:GLY:O	2.21	0.41
73:o7:36:SER:O	73:o7:45:ARG:HB3	2.21	0.41
73:o7:37:CYS:O	73:o7:45:ARG:N	2.53	0.41
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:H6	1:2:989:U:O5'	2.04	0.40
1:2:1559:A:N6	20:C8:134:ARG:HD2	2.36	0.40
5:S3:134:CYS:N	5:S3:157:LEU:HD11	2.36	0.40
6:S4:11:ARG:HB2	6:S4:27:TYR:C	2.47	0.40
7:S5:73:THR:HG23	18:C6:114:ARG:CD	2.51	0.40
8:S6:2:LYS:HB2	8:S6:2:LYS:HE3	1.87	0.40
19:C7:115:LEU:HB3	19:C7:116:LYS:H	1.58	0.40
25:D3:53:VAL:HG23	25:D3:100:ASP:O	2.21	0.40
33:E1:144:CYS:O	33:E1:146:SER:N	2.53	0.40
34:SR:134:TRP:N	34:SR:134:TRP:CD1	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:SM:61:ILE:H	35:SM:61:ILE:HG13	1.60	0.40
36:1:900:G:C4	36:1:901:G:C8	3.09	0.40
36:1:1257:C:H42	36:1:1261:G:H22	1.69	0.40
36:1:1477:A:H61	36:1:1876:U:H3	1.69	0.40
36:1:1480:G:H4'	36:1:1481:A:OP1	2.21	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
41:L4:316:ASN:HA	41:L4:317:PRO:HD3	1.89	0.40
56:N0:17:GLU:O	56:N0:20:PRO:HD3	2.22	0.40
56:N0:71:LYS:O	56:N0:73:LYS:NZ	2.39	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
60:N4:38:SER:O	60:N4:42:GLN:HG3	2.20	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
70:O4:106:LYS:HA	70:O4:109:THR:HB	2.02	0.40
73:O7:63:ARG:O	73:O7:68:LYS:HE2	2.21	0.40
1:6:79:C:H4'	8:s6:173:PRO:O	2.21	0.40
1:6:325:G:H4'	13:c1:80:MET:HE3	2.03	0.40
1:6:329:G:H5'	10:s8:99:ALA:HB3	2.03	0.40
1:6:678:A:H2'	1:6:679:U:O4'	2.22	0.40
1:6:1584:G:H22	1:6:1611:A:P	2.42	0.40
1:6:1755:A:H8	25:d3:63:GLN:HG3	1.85	0.40
6:s4:164:LEU:HD23	6:s4:164:LEU:HA	1.92	0.40
7:s5:149:VAL:HG12	7:s5:156:ARG:O	2.21	0.40
13:c1:84:ILE:HG13	13:c1:109:VAL:HG23	2.03	0.40
13:c1:107:VAL:HA	13:c1:108:PRO:HD2	1.90	0.40
14:c2:45:LEU:HB3	14:c2:46:ARG:H	1.50	0.40
18:c6:87:LYS:HB3	18:c6:87:LYS:HE2	1.80	0.40
22:d0:80:GLU:OE1	31:d9:44:ARG:NH1	2.47	0.40
23:d1:56:SER:O	23:d1:60:ARG:HG3	2.21	0.40
24:d2:20:THR:OG1	24:d2:22:LYS:HD3	2.20	0.40
24:d2:94:LEU:HA	24:d2:95:PRO:HD3	1.93	0.40
34:sR:177:MET:HE1	34:sR:193:ILE:HG13	2.02	0.40
36:5:294:U:H4'	72:o6:77:LEU:HD23	2.03	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:5:2730:G:H4'	54:m8:184:PHE:CG	2.56	0.40
36:5:2821:C:N1	87:D:3401:SPS:H182	2.36	0.40
36:5:3369:G:N2	40:l3:380:MET:O	2.52	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
41:l4:209:TYR:O	41:l4:230:VAL:HG22	2.22	0.40
43:l6:55:LEU:HD11	43:l6:66:SER:HB2	2.03	0.40
47:m0:76:MET:HE1	47:m0:138:VAL:HG21	2.02	0.40
56:n0:34:GLU:H	56:n0:34:GLU:HG2	1.59	0.40
66:o0:40:LYS:HD3	66:o0:93:LEU:O	2.21	0.40
68:o2:109:LEU:HD23	68:o2:109:LEU:HA	1.89	0.40
1:2:199:G:HO2'	1:2:200:A:H8	1.67	0.40
1:2:339:C:OP2	10:S8:10:LYS:NZ	2.46	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
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
3:S1:63:GLY:HA2	3:S1:88:VAL:O	2.21	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
9:S7:33:GLU:H	9:S7:33:GLU:CD	2.29	0.40
11:S9:77:ILE:HD11	11:S9:93:LEU:HB3	2.03	0.40
14:C2:81:ASP:OD1	14:C2:81:ASP:N	2.51	0.40
15:C3:135:LEU:HD22	15:C3:139:TRP:CG	2.56	0.40
17:C5:110:GLU:HB2	20:C8:119:ILE:HD11	2.03	0.40
18:C6:55:VAL:HG21	18:C6:105:LEU:HG	2.03	0.40
20:C8:86:LEU:HG	20:C8:99:HIS:HB2	2.03	0.40
20:C8:100:THR:HG21	20:C8:108:LYS:HG3	2.03	0.40
20:C8:145:ARG:HB2	35:SM:68:ARG:NH2	2.36	0.40
22:D0:106:ILE:HD12	22:D0:106:ILE:HA	1.95	0.40
25:D3:127:VAL:O	25:D3:130:VAL:HG22	2.21	0.40
32:E0:2:ALA:O	32:E0:4:VAL:HG23	2.21	0.40
35:SM:33:LYS:HA	35:SM:33:LYS:HD2	1.70	0.40
36:1:107:A:H1'	36:1:325:A:N3	2.37	0.40
36:1:709:A:O2'	64:N8:57:GLY:HA3	2.22	0.40
36:1:1340:G:H2'	36:1:1341:U:H6	1.87	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:4:45:C:H4'	75:O9:11:GLN:OE1	2.21	0.40
40:L3:117:ARG:NH1	40:L3:175:LYS:HD3	2.36	0.40
40:L3:185:GLY:H	40:L3:191:LYS:NZ	2.17	0.40
43:L6:154:LEU:HA	43:L6:154:LEU:HD23	1.85	0.40
44:L7:75:TYR:HB2	57:N1:141:VAL:HG22	2.04	0.40
44:L7:229:PHE:CD1	44:L7:229:PHE:C	2.99	0.40
46:L9:84:LYS:NZ	46:L9:191:LEU:HD22	2.36	0.40
56:N0:8:GLN:HB3	56:N0:64:ILE:HD11	2.03	0.40
57:N1:35:LYS:HB2	57:N1:35:LYS:HE3	1.88	0.40
59:N3:18:PRO:HA	59:N3:51:ALA:HA	2.03	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
1:6:727:U:H2'	1:6:728:U:H6	1.87	0.40
1:6:804:A:N3	24:d2:105:THR:HG22	2.37	0.40
1:6:959:U:C2	15:c3:17:PRO:HG3	2.56	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
2:s0:38:PHE:HD2	2:s0:49:ASN:HD22	1.68	0.40
6:s4:158:ASP:OD2	6:s4:174:LYS:NZ	2.47	0.40
11:s9:105:LEU:HD12	11:s9:105:LEU:HA	1.90	0.40
15:c3:16:ILE:HD12	15:c3:16:ILE:HA	1.78	0.40
16:c4:48:VAL:HG11	16:c4:53:ASP:HB3	2.03	0.40
19:c7:46:LEU:HD23	19:c7:46:LEU:HA	1.86	0.40
26:d4:23:PHE:HE2	26:d4:75:VAL:HG23	1.85	0.40
28:d6:23:CYS:HB3	28:d6:26:CYS:HB2	2.03	0.40
30:d8:64:ARG:NH2	30:d8:65:ARG:HB2	2.36	0.40
34:sR:144:LEU:HD21	34:sR:186:PHE:HB3	2.03	0.40
36:5:288:C:H4'	51:m5:171:SER:O	2.21	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
36:5:1195:A:H2'	36:5:1309:U:O2	2.21	0.40
36:5:1223:A:OP2	36:5:1285:G:N2	2.51	0.40
36:5:1386:A:H5"	41:l4:141:ARG:HH22	1.86	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
41:l4:3:ARG:HB3	41:l4:22:LEU:HB2	2.03	0.40
42:l5:120:LYS:H	42:l5:120:LYS:HG3	1.62	0.40
42:l5:270:LYS:HE2	42:l5:273:ARG:HA	2.02	0.40
45:l8:121:SER:O	45:l8:123:GLN:N	2.55	0.40
45:l8:152:LEU:HB3	45:l8:180:VAL:HG11	2.03	0.40
45:l8:156:ASP:OD2	45:l8:156:ASP:N	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:l9:23:ARG:NH2	46:l9:41:ILE:O	2.54	0.40
47:m0:61:SER:HB2	47:m0:63:GLU:OE2	2.21	0.40
63:n7:23:VAL:HG12	63:n7:45:GLY:HA3	2.02	0.40
64:n8:121:VAL:HA	64:n8:122:PRO:HD3	1.96	0.40
71:o5:68:GLN:C	71:o5:70:TYR:H	2.29	0.40
1:2:144:U:O2'	1:2:145:A:H8	2.05	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
1:2:1339:C:O2'	1:2:1341:A:C8	2.71	0.40
1:2:1680:G:C2	1:2:1720:G:C2	3.10	0.40
2:S0:41:ARG:HD2	2:S0:42:PRO:O	2.20	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
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
34:SR:21:THR:O	34:SR:291:SER:HB3	2.20	0.40
36:1:114:A:OP1	51:M5:54:LYS:NZ	2.55	0.40
36:1:641:C:H2'	36:1:642:U:O4'	2.21	0.40
36:1:953:G:OP1	65:N9:15:LYS:NZ	2.39	0.40
36:1:1112:A:H2'	36:1:1113:G:C8	2.56	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
38:4:141:C:OP1	51:M5:109:ARG:NH1	2.52	0.40
40:L3:10:ARG:NH1	40:L3:12:GLY:O	2.55	0.40
42:L5:153:THR:HG23	42:L5:160:PHE:CZ	2.56	0.40
44:L7:39:GLU:O	44:L7:42:ALA:HB3	2.22	0.40
49:M3:126:PHE:CD2	71:O5:115:LYS:HG2	2.56	0.40
51:M5:37:HIS:NE2	51:M5:63:ARG:HB3	2.36	0.40
51:M5:143:ARG:NH2	71:O5:92:LEU:HD23	2.36	0.40
54:M8:57:ILE:HD13	54:M8:57:ILE:HG21	1.87	0.40
56:N0:46:GLN:HG2	56:N0:51:VAL:O	2.21	0.40
68:O2:2:ALA:HB3	68:O2:90:LYS:NZ	2.37	0.40
68:O2:18:LYS:HD3	68:O2:30:GLU:HG2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:O9:21:ARG:CZ	75:O9:24:PRO:HG3	2.52	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
1:6:802:G:H21	24:d2:107:SER:HB3	1.85	0.40
1:6:837:G:H2'	1:6:838:G:H8	1.85	0.40
1:6:1733:C:H2'	1:6:1734:U:H6	1.86	0.40
4:s2:218:ILE:H	4:s2:218:ILE:HG13	1.65	0.40
17:c5:10:ARG:HB3	17:c5:11:VAL:H	1.67	0.40
36:5:266:A:C5	72:o6:30:LYS:HD2	2.56	0.40
36:5:334:A:H2'	36:5:335:G:C8	2.57	0.40
36:5:693:A:H4'	41:l4:234:ASN:OD1	2.21	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
36:5:2808:A:O2'	36:5:2969:A:OP1	2.34	0.40
36:5:3049:A:C2	40:l3:75:ALA:HB2	2.56	0.40
38:8:78:G:H2'	38:8:79:A:O4'	2.20	0.40
39:l2:104:LEU:HA	39:l2:104:LEU:HD12	1.72	0.40
40:l3:19:ARG:HB3	40:l3:232:ARG:HH12	1.83	0.40
40:l3:214:MET:HE3	40:l3:214:MET:HB3	1.82	0.40
45:l8:57:ARG:HB3	45:l8:61:GLN:NE2	2.36	0.40
81:m2:122:UNK:HA	82:p0:43:LYS:HD3	2.04	0.40
49:m3:47:ALA:HB1	49:m3:48:PRO:CD	2.52	0.40
54:m8:166:LEU:HD23	54:m8:166:LEU:HA	1.89	0.40
56:n0:94:ILE:HD11	56:n0:106:LEU:HB2	2.02	0.40
59:n3:136:VAL:HG12	59:n3:137:VAL:HG23	2.03	0.40
64:n8:94:ALA:HA	64:n8:121:VAL:HG13	2.02	0.40
65:n9:22:LYS:HB2	65:n9:23:LYS:H	1.60	0.40
73:o7:84:SER:O	73:o7:85:LYS:HB3	2.20	0.40
82:p0:27:VAL:O	82:p0:188:VAL:HG22	2.22	0.40
1:2:475:A:OP2	11:S9:126:ARG:NH1	2.54	0.40
1:2:495:C:H3'	1:2:496:G:O4'	2.22	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
6:S4:47:PHE:CZ	6:S4:90:ILE:HD12	2.56	0.40
10:S8:21:PHE:CE1	10:S8:22:ARG:HD3	2.57	0.40
10:S8:162:ALA:HA	36:1:3353:G:C5'	2.49	0.40
12:C0:33:GLU:O	12:C0:35:ILE:N	2.51	0.40
18:C6:41:PRO:C	18:C6:43:ILE:H	2.29	0.40
19:C7:57:LEU:HA	19:C7:60:ARG:HG2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:D3:5:LYS:HA	25:D3:6:PRO:HD2	1.97	0.40
34:SR:70:ASP:OD1	34:SR:71:CYS:N	2.55	0.40
36:1:607:A:H4'	36:1:608:A:OP2	2.21	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
39:L2:65:ASP:HA	39:L2:66:PRO:HD3	1.90	0.40
41:L4:269:SER:C	41:L4:271:LYS:N	2.79	0.40
45:L8:41:GLN:HG3	45:L8:42:PRO:HD2	2.04	0.40
45:L8:147:LYS:C	45:L8:201:THR:HG22	2.46	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
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
61:N5:71:THR:O	61:N5:75:LYS:HG3	2.21	0.40
72:O6:60:LEU:HD13	72:O6:64:SER:HB3	2.04	0.40
1:6:191:C:O2'	1:6:192:U:O5'	2.38	0.40
1:6:325:G:H4'	13:c1:83:THR:HG21	2.04	0.40
1:6:762:A:OP1	11:s9:79:ARG:NH1	2.39	0.40
1:6:1379:C:H5'	18:c6:10:PHE:CE2	2.56	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
1:6:1793:G:N2	28:d6:76:SER:OG	2.43	0.40
1:6:1799:U:HO2'	3:s1:152:ARG:HH12	1.58	0.40
4:s2:174:ARG:O	11:s9:97:LEU:HB3	2.21	0.40
5:s3:217:ILE:C	5:s3:219:ALA:H	2.28	0.40
6:s4:35:PRO:HB2	6:s4:36:HIS:CD2	2.56	0.40
9:s7:111:LYS:HB3	9:s7:112:ARG:H	1.53	0.40
10:s8:36:THR:HA	10:s8:58:LEU:HA	2.02	0.40
12:c0:53:GLY:O	12:c0:55:VAL:N	2.51	0.40
27:d5:78:ILE:HG13	27:d5:81:ARG:HH12	1.86	0.40
30:d8:54:LEU:HD13	30:d8:54:LEU:HA	1.95	0.40
36:5:72:C:H5'	49:m3:63:VAL:HG13	2.02	0.40
36:5:409:A:H61	38:8:15:G:H1'	1.86	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
36:5:2991:A:N3	53:m7:69:ARG:NH2	2.70	0.40
41:l4:343:LYS:HE2	41:l4:343:LYS:HB3	1.93	0.40
43:l6:145:LEU:HD23	43:l6:145:LEU:HA	1.84	0.40
47:m0:206:LEU:HD12	47:m0:206:LEU:HA	1.75	0.40
52:m6:29:ASN:ND2	69:o3:14:LEU:HD22	2.36	0.40
56:n0:132:THR:O	56:n0:133:ALA:HB3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:n7:4:PHE:HE1	63:n7:82:PRO:HB3	1.87	0.40
63:n7:64:LYS:HE2	63:n7:64:LYS:HB2	1.87	0.40
82:p0:79:PHE:CE1	82:p0:189:GLN:HG3	2.56	0.40
1:2:60:U:H5'	1:2:455:C:N4	2.36	0.40
1:2:337:G:O3'	10:S8:10:LYS:HE2	2.22	0.40
1:2:449:C:H2'	1:2:450:U:C6	2.57	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
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
4:S2:121:VAL:HB	35:SM:120:GLU:CD	2.47	0.40
5:S3:70:THR:CG2	5:S3:86:LEU:HB2	2.52	0.40
10:S8:8:ARG:HE	10:S8:21:PHE:HD1	1.70	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
27:D5:41:ILE:HG23	27:D5:42:LEU:H	1.87	0.40
29:D7:63:LEU:O	29:D7:74:SER:N	2.52	0.40
34:SR:286:GLU:HA	34:SR:287:PRO:HD3	1.83	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
36:1:1018:G:H2'	36:1:1019:G:O4'	2.21	0.40
36:1:1181:U:H2'	52:M6:122:GLN:NE2	2.37	0.40
36:1:1841:A:H2	75:O9:45:ARG:HH22	1.70	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
42:L5:104:LEU:HD11	42:L5:108:ARG:HH21	1.86	0.40
44:L7:40:LYS:HA	44:L7:43:ILE:HD12	2.04	0.40
47:M0:5:PRO:C	47:M0:7:ARG:H	2.29	0.40
48:M1:50:ALA:HB2	48:M1:65:ILE:HD12	2.04	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
68:O2:111:ARG:NH2	68:O2:115:LEU:HD21	2.37	0.40
76:Q0:111:ARG:HG3	76:Q0:112:LYS:HD2	2.02	0.40
1:6:138:A:H5"	1:6:138:A:N3	2.37	0.40
1:6:393:C:H2'	1:6:394:C:C6	2.57	0.40
1:6:424:C:O2'	1:6:426:G:OP1	2.39	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:1489:U:H5'	1:6:1494:C:H1'	2.03	0.40
3:s1:23:PRO:O	3:s1:26:ARG:HB3	2.21	0.40
4:s2:144:TRP:CZ2	4:s2:173:PRO:HG3	2.55	0.40
5:s3:72:LEU:HD22	12:c0:65:TYR:CD1	2.50	0.40
5:s3:76:ARG:HG3	12:c0:65:TYR:CZ	2.57	0.40
6:s4:131:LEU:HD22	6:s4:131:LEU:HA	1.90	0.40
9:s7:31:SER:N	9:s7:32:PRO:HD2	2.37	0.40
9:s7:63:PRO:C	9:s7:65:PRO:HD2	2.47	0.40
11:s9:156:ILE:H	11:s9:156:ILE:HG13	1.64	0.40
13:c1:76:VAL:HG12	13:c1:85:VAL:O	2.22	0.40
17:c5:22:LEU:HA	17:c5:25:LEU:HB2	2.04	0.40
24:d2:104:LEU:HD23	24:d2:125:ILE:HA	2.03	0.40
25:d3:41:SER:HA	25:d3:42:PRO:HD3	1.82	0.40
26:d4:20:ARG:HB3	26:d4:76:TYR:CD2	2.56	0.40
29:d7:19:HIS:O	29:d7:21:LEU:N	2.55	0.40
36:5:90:C:H4'	36:5:282:G:H5"	2.03	0.40
36:5:761:A:C2	36:5:771:A:H1'	2.57	0.40
36:5:1686:U:OP1	58:n2:42:LYS:NZ	2.26	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
36:5:3338:C:H2'	36:5:3339:A:O4'	2.21	0.40
40:l3:214:MET:SD	40:l3:281:LYS:HB2	2.62	0.40
44:l7:53:LYS:HE3	44:l7:57:THR:HG21	2.03	0.40
44:l7:90:LYS:HB3	44:l7:133:TYR:HB3	2.04	0.40
44:l7:96:PRO:O	44:l7:100:ARG:HB2	2.22	0.40
47:m0:16:PRO:HG3	47:m0:128:ARG:HH11	1.86	0.40
52:m6:62:THR:HG22	52:m6:65:ASN:H	1.85	0.40
52:m6:110:PRO:HB2	52:m6:111:PRO:CD	2.51	0.40
54:m8:29:LEU:HD23	54:m8:29:LEU:HA	1.90	0.40
54:m8:41:ASP:N	54:m8:41:ASP:OD1	2.54	0.40
67:o1:10:ARG:HD2	67:o1:12:TYR:OH	2.22	0.40
68:o2:22:SER:HA	68:o2:28:VAL:HG12	2.03	0.40
69:o3:26:ASN:O	69:o3:84:THR:HG22	2.22	0.40
70:o4:3:GLN:NE2	70:o4:30:LEU:H	2.19	0.40
73:o7:53:ALA:O	73:o7:56:ARG:HB2	2.21	0.40
83:p1:38:UNK:O	83:p1:42:UNK:N	2.54	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 (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	S0	204/251 (81%)	166 (81%)	26 (13%)	12 (6%)	1 8
2	s0	204/251 (81%)	162 (79%)	27 (13%)	15 (7%)	1 5
3	S1	212/254 (84%)	156 (74%)	27 (13%)	29 (14%)	0 1
3	s1	214/254 (84%)	167 (78%)	34 (16%)	13 (6%)	1 7
4	S2	215/253 (85%)	178 (83%)	27 (13%)	10 (5%)	2 11
4	s2	215/253 (85%)	185 (86%)	18 (8%)	12 (6%)	1 8
5	S3	221/239 (92%)	192 (87%)	21 (10%)	8 (4%)	2 16
5	s3	221/239 (92%)	185 (84%)	24 (11%)	12 (5%)	1 9
6	S4	258/260 (99%)	213 (83%)	31 (12%)	14 (5%)	1 9
6	s4	258/260 (99%)	209 (81%)	38 (15%)	11 (4%)	2 12
7	S5	204/224 (91%)	169 (83%)	21 (10%)	14 (7%)	1 5
7	s5	204/224 (91%)	157 (77%)	33 (16%)	14 (7%)	1 5
8	S6	224/236 (95%)	191 (85%)	21 (9%)	12 (5%)	1 9
8	s6	216/236 (92%)	190 (88%)	17 (8%)	9 (4%)	2 13
9	S7	182/189 (96%)	138 (76%)	27 (15%)	17 (9%)	0 3
9	s7	184/189 (97%)	148 (80%)	28 (15%)	8 (4%)	2 12
10	S8	184/200 (92%)	160 (87%)	18 (10%)	6 (3%)	3 17
10	s8	184/200 (92%)	161 (88%)	17 (9%)	6 (3%)	3 17
11	S9	183/196 (93%)	158 (86%)	17 (9%)	8 (4%)	2 12
11	s9	183/196 (93%)	152 (83%)	21 (12%)	10 (6%)	1 9
12	C0	94/105 (90%)	71 (76%)	16 (17%)	7 (7%)	1 5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
12	c0	92/105 (88%)	62 (67%)	14 (15%)	16 (17%)	0 0
13	C1	153/155 (99%)	129 (84%)	18 (12%)	6 (4%)	2 14
13	c1	144/155 (93%)	120 (83%)	18 (12%)	6 (4%)	2 13
14	C2	122/142 (86%)	77 (63%)	31 (25%)	14 (12%)	0 1
14	c2	122/142 (86%)	78 (64%)	30 (25%)	14 (12%)	0 1
15	C3	148/150 (99%)	126 (85%)	16 (11%)	6 (4%)	2 13
15	c3	148/150 (99%)	118 (80%)	23 (16%)	7 (5%)	2 11
16	C4	125/136 (92%)	92 (74%)	21 (17%)	12 (10%)	0 3
16	c4	126/136 (93%)	102 (81%)	18 (14%)	6 (5%)	2 11
17	C5	122/141 (86%)	90 (74%)	22 (18%)	10 (8%)	0 4
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 6
18	c6	140/142 (99%)	123 (88%)	10 (7%)	7 (5%)	1 11
19	C7	116/136 (85%)	91 (78%)	18 (16%)	7 (6%)	1 7
19	c7	113/136 (83%)	90 (80%)	13 (12%)	10 (9%)	0 3
20	C8	143/145 (99%)	121 (85%)	13 (9%)	9 (6%)	1 6
20	c8	143/145 (99%)	116 (81%)	18 (13%)	9 (6%)	1 6
21	C9	141/143 (99%)	120 (85%)	15 (11%)	6 (4%)	2 12
21	c9	141/143 (99%)	124 (88%)	13 (9%)	4 (3%)	4 20
22	D0	105/120 (88%)	90 (86%)	11 (10%)	4 (4%)	2 15
22	d0	108/120 (90%)	84 (78%)	18 (17%)	6 (6%)	1 8
23	D1	85/87 (98%)	66 (78%)	14 (16%)	5 (6%)	1 8
23	d1	85/87 (98%)	67 (79%)	13 (15%)	5 (6%)	1 8
24	D2	127/129 (98%)	119 (94%)	6 (5%)	2 (2%)	7 30
24	d2	127/129 (98%)	115 (91%)	11 (9%)	1 (1%)	16 47
25	D3	142/144 (99%)	111 (78%)	19 (13%)	12 (8%)	0 4
25	d3	142/144 (99%)	127 (89%)	10 (7%)	5 (4%)	3 16
26	D4	132/134 (98%)	110 (83%)	13 (10%)	9 (7%)	1 5
26	d4	132/134 (98%)	112 (85%)	12 (9%)	8 (6%)	1 7
27	D5	68/107 (64%)	53 (78%)	8 (12%)	7 (10%)	0 2
27	d5	67/107 (63%)	56 (84%)	9 (13%)	2 (3%)	3 19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
28	D6	95/97 (98%)	62 (65%)	19 (20%)	14 (15%)	0 0
28	d6	95/97 (98%)	71 (75%)	18 (19%)	6 (6%)	1 6
29	D7	79/81 (98%)	66 (84%)	11 (14%)	2 (2%)	4 21
29	d7	79/81 (98%)	60 (76%)	16 (20%)	3 (4%)	2 15
30	D8	61/66 (92%)	48 (79%)	12 (20%)	1 (2%)	7 30
30	d8	61/66 (92%)	46 (75%)	11 (18%)	4 (7%)	1 6
31	D9	51/55 (93%)	40 (78%)	9 (18%)	2 (4%)	2 14
31	d9	51/55 (93%)	41 (80%)	7 (14%)	3 (6%)	1 8
32	E0	58/60 (97%)	46 (79%)	10 (17%)	2 (3%)	3 16
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%)	2 13
34	sR	316/318 (99%)	268 (85%)	38 (12%)	10 (3%)	3 18
35	SM	131/263 (50%)	105 (80%)	16 (12%)	10 (8%)	1 4
35	sM	80/263 (30%)	61 (76%)	8 (10%)	11 (14%)	0 1
39	L2	250/253 (99%)	230 (92%)	15 (6%)	5 (2%)	6 25
39	l2	250/253 (99%)	209 (84%)	32 (13%)	9 (4%)	2 16
40	L3	384/386 (100%)	340 (88%)	28 (7%)	16 (4%)	2 13
40	l3	384/386 (100%)	346 (90%)	30 (8%)	8 (2%)	5 25
41	L4	359/361 (99%)	308 (86%)	32 (9%)	19 (5%)	1 10
41	l4	359/361 (99%)	297 (83%)	39 (11%)	23 (6%)	1 6
42	L5	294/296 (99%)	254 (86%)	22 (8%)	18 (6%)	1 7
42	l5	292/296 (99%)	263 (90%)	22 (8%)	7 (2%)	4 22
43	L6	152/175 (87%)	136 (90%)	14 (9%)	2 (1%)	9 35
43	l6	153/175 (87%)	128 (84%)	21 (14%)	4 (3%)	4 21
44	L7	220/243 (90%)	198 (90%)	14 (6%)	8 (4%)	2 16
44	l7	221/243 (91%)	200 (90%)	17 (8%)	4 (2%)	6 28
45	L8	231/255 (91%)	193 (84%)	29 (13%)	9 (4%)	2 14
45	l8	229/255 (90%)	197 (86%)	20 (9%)	12 (5%)	1 10
46	L9	189/191 (99%)	163 (86%)	24 (13%)	2 (1%)	11 39
46	l9	189/191 (99%)	172 (91%)	13 (7%)	4 (2%)	5 25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
47	M0	207/220 (94%)	180 (87%)	21 (10%)	6 (3%)	3 19
47	m0	209/220 (95%)	174 (83%)	27 (13%)	8 (4%)	2 15
48	M1	167/173 (96%)	134 (80%)	21 (13%)	12 (7%)	1 5
48	m1	167/173 (96%)	145 (87%)	10 (6%)	12 (7%)	1 5
49	M3	191/198 (96%)	162 (85%)	18 (9%)	11 (6%)	1 8
49	m3	192/198 (97%)	157 (82%)	22 (12%)	13 (7%)	1 5
50	M4	134/137 (98%)	117 (87%)	8 (6%)	9 (7%)	1 6
50	m4	135/137 (98%)	129 (96%)	6 (4%)	0	100 100
51	M5	201/203 (99%)	186 (92%)	8 (4%)	7 (4%)	3 16
51	m5	201/203 (99%)	179 (89%)	16 (8%)	6 (3%)	3 19
52	M6	195/198 (98%)	182 (93%)	9 (5%)	4 (2%)	5 25
52	m6	195/198 (98%)	181 (93%)	10 (5%)	4 (2%)	5 25
53	M7	181/183 (99%)	151 (83%)	21 (12%)	9 (5%)	1 11
53	m7	153/183 (84%)	141 (92%)	11 (7%)	1 (1%)	18 49
54	M8	183/185 (99%)	164 (90%)	15 (8%)	4 (2%)	5 24
54	m8	183/185 (99%)	162 (88%)	17 (9%)	4 (2%)	5 24
55	M9	186/188 (99%)	169 (91%)	16 (9%)	1 (0%)	24 57
55	m9	186/188 (99%)	168 (90%)	16 (9%)	2 (1%)	11 39
56	N0	170/172 (99%)	156 (92%)	10 (6%)	4 (2%)	4 22
56	n0	170/172 (99%)	159 (94%)	9 (5%)	2 (1%)	10 37
57	N1	157/159 (99%)	140 (89%)	15 (10%)	2 (1%)	9 35
57	n1	157/159 (99%)	145 (92%)	10 (6%)	2 (1%)	9 35
58	N2	98/120 (82%)	81 (83%)	15 (15%)	2 (2%)	6 25
58	n2	96/120 (80%)	83 (86%)	12 (12%)	1 (1%)	12 41
59	N3	134/136 (98%)	123 (92%)	10 (8%)	1 (1%)	18 49
59	n3	134/136 (98%)	126 (94%)	7 (5%)	1 (1%)	18 49
60	N4	96/155 (62%)	80 (83%)	10 (10%)	6 (6%)	1 6
60	n4	133/155 (86%)	110 (83%)	14 (10%)	9 (7%)	1 5
61	N5	119/141 (84%)	107 (90%)	8 (7%)	4 (3%)	3 16
61	n5	118/141 (84%)	98 (83%)	11 (9%)	9 (8%)	1 4
62	N6	124/126 (98%)	113 (91%)	10 (8%)	1 (1%)	16 47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
62	n6	124/126 (98%)	114 (92%)	7 (6%)	3 (2%)	4 22
63	N7	133/135 (98%)	114 (86%)	10 (8%)	9 (7%)	1 5
63	n7	133/135 (98%)	99 (74%)	21 (16%)	13 (10%)	0 3
64	N8	146/148 (99%)	120 (82%)	19 (13%)	7 (5%)	2 11
64	n8	146/148 (99%)	129 (88%)	13 (9%)	4 (3%)	4 20
65	N9	56/58 (97%)	47 (84%)	7 (12%)	2 (4%)	2 16
65	n9	56/58 (97%)	41 (73%)	11 (20%)	4 (7%)	1 5
66	O0	95/104 (91%)	89 (94%)	6 (6%)	0	100 100
66	o0	98/104 (94%)	88 (90%)	9 (9%)	1 (1%)	12 41
67	O1	107/112 (96%)	98 (92%)	3 (3%)	6 (6%)	1 8
67	o1	107/112 (96%)	91 (85%)	11 (10%)	5 (5%)	2 11
68	O2	125/129 (97%)	116 (93%)	8 (6%)	1 (1%)	16 47
68	o2	125/129 (97%)	110 (88%)	11 (9%)	4 (3%)	3 18
69	O3	104/106 (98%)	95 (91%)	9 (9%)	0	100 100
69	o3	104/106 (98%)	96 (92%)	5 (5%)	3 (3%)	3 19
70	O4	110/119 (92%)	98 (89%)	11 (10%)	1 (1%)	14 44
70	o4	110/119 (92%)	96 (87%)	11 (10%)	3 (3%)	4 20
71	O5	117/119 (98%)	106 (91%)	10 (8%)	1 (1%)	14 44
71	o5	117/119 (98%)	101 (86%)	12 (10%)	4 (3%)	3 16
72	O6	97/99 (98%)	77 (79%)	15 (16%)	5 (5%)	1 10
72	o6	97/99 (98%)	80 (82%)	13 (13%)	4 (4%)	2 13
73	O7	85/87 (98%)	74 (87%)	9 (11%)	2 (2%)	4 22
73	o7	85/87 (98%)	73 (86%)	8 (9%)	4 (5%)	2 11
74	O8	75/77 (97%)	66 (88%)	6 (8%)	3 (4%)	2 13
74	o8	75/77 (97%)	69 (92%)	5 (7%)	1 (1%)	9 35
75	O9	48/50 (96%)	43 (90%)	5 (10%)	0	100 100
75	o9	48/50 (96%)	44 (92%)	3 (6%)	1 (2%)	5 25
76	Q0	50/52 (96%)	44 (88%)	4 (8%)	2 (4%)	2 13
76	q0	50/52 (96%)	47 (94%)	2 (4%)	1 (2%)	6 25
77	Q1	23/25 (92%)	22 (96%)	1 (4%)	0	100 100
77	q1	23/25 (92%)	23 (100%)	0	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
78	Q2	103/105 (98%)	79 (77%)	21 (20%)	3 (3%)	3 19
78	q2	103/105 (98%)	96 (93%)	6 (6%)	1 (1%)	12 41
79	Q3	89/91 (98%)	76 (85%)	10 (11%)	3 (3%)	3 16
79	q3	89/91 (98%)	82 (92%)	5 (6%)	2 (2%)	5 24
80	e0	60/62 (97%)	38 (63%)	16 (27%)	6 (10%)	0 3
82	p0	139/311 (45%)	120 (86%)	15 (11%)	4 (3%)	3 19
All	All	22291/24121 (92%)	18907 (85%)	2362 (11%)	1022 (5%)	2 12

All (1022) Ramachandran outliers are listed below:

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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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 (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	S0	164/209 (78%)	145 (88%)	19 (12%)	5 22
2	s0	165/209 (79%)	139 (84%)	26 (16%)	2 12
3	S1	191/223 (86%)	164 (86%)	27 (14%)	3 15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	s1	192/223 (86%)	161 (84%)	31 (16%)	2 11
4	S2	176/204 (86%)	145 (82%)	31 (18%)	2 9
4	s2	176/204 (86%)	138 (78%)	38 (22%)	1 5
5	S3	182/194 (94%)	158 (87%)	24 (13%)	4 17
5	s3	182/194 (94%)	155 (85%)	27 (15%)	3 13
6	S4	221/221 (100%)	188 (85%)	33 (15%)	3 13
6	s4	221/221 (100%)	192 (87%)	29 (13%)	4 17
7	S5	173/190 (91%)	158 (91%)	15 (9%)	9 34
7	s5	173/190 (91%)	151 (87%)	22 (13%)	4 18
8	S6	188/201 (94%)	163 (87%)	25 (13%)	4 17
8	s6	187/201 (93%)	159 (85%)	28 (15%)	3 13
9	S7	165/169 (98%)	147 (89%)	18 (11%)	6 24
9	s7	165/169 (98%)	150 (91%)	15 (9%)	9 32
10	S8	150/161 (93%)	128 (85%)	22 (15%)	3 14
10	s8	150/161 (93%)	135 (90%)	15 (10%)	7 29
11	S9	158/165 (96%)	134 (85%)	24 (15%)	3 13
11	s9	158/165 (96%)	137 (87%)	21 (13%)	4 17
12	C0	77/98 (79%)	66 (86%)	11 (14%)	3 14
12	c0	73/98 (74%)	62 (85%)	11 (15%)	3 13
13	C1	129/136 (95%)	114 (88%)	15 (12%)	5 22
13	c1	129/136 (95%)	107 (83%)	22 (17%)	2 10
14	C2	88/118 (75%)	75 (85%)	13 (15%)	3 13
14	c2	88/118 (75%)	73 (83%)	15 (17%)	2 10
15	C3	127/127 (100%)	106 (84%)	21 (16%)	2 11
15	c3	127/127 (100%)	107 (84%)	20 (16%)	2 12
16	C4	81/104 (78%)	65 (80%)	16 (20%)	1 6
16	c4	97/104 (93%)	78 (80%)	19 (20%)	1 6
17	C5	101/117 (86%)	89 (88%)	12 (12%)	5 21
17	c5	103/117 (88%)	91 (88%)	12 (12%)	5 22
18	C6	117/118 (99%)	103 (88%)	14 (12%)	5 21
18	c6	118/118 (100%)	105 (89%)	13 (11%)	6 24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
19	C7	94/124 (76%)	76 (81%)	18 (19%)	1 7
19	c7	92/124 (74%)	80 (87%)	12 (13%)	4 18
20	C8	128/128 (100%)	111 (87%)	17 (13%)	4 17
20	c8	128/128 (100%)	106 (83%)	22 (17%)	2 10
21	C9	115/115 (100%)	95 (83%)	20 (17%)	2 9
21	c9	115/115 (100%)	97 (84%)	18 (16%)	2 12
22	D0	100/113 (88%)	84 (84%)	16 (16%)	2 12
22	d0	103/113 (91%)	88 (85%)	15 (15%)	3 14
23	D1	74/74 (100%)	64 (86%)	10 (14%)	4 16
23	d1	74/74 (100%)	61 (82%)	13 (18%)	2 9
24	D2	110/110 (100%)	90 (82%)	20 (18%)	2 8
24	d2	110/110 (100%)	100 (91%)	10 (9%)	9 32
25	D3	119/119 (100%)	97 (82%)	22 (18%)	1 8
25	d3	119/119 (100%)	105 (88%)	14 (12%)	5 21
26	D4	112/112 (100%)	98 (88%)	14 (12%)	4 19
26	d4	112/112 (100%)	104 (93%)	8 (7%)	13 41
27	D5	61/88 (69%)	48 (79%)	13 (21%)	1 5
27	d5	61/88 (69%)	51 (84%)	10 (16%)	2 11
28	D6	83/83 (100%)	68 (82%)	15 (18%)	2 8
28	d6	83/83 (100%)	74 (89%)	9 (11%)	6 25
29	D7	70/70 (100%)	62 (89%)	8 (11%)	5 23
29	d7	70/70 (100%)	61 (87%)	9 (13%)	4 18
30	D8	56/59 (95%)	44 (79%)	12 (21%)	1 5
30	d8	56/59 (95%)	45 (80%)	11 (20%)	1 6
31	D9	47/48 (98%)	39 (83%)	8 (17%)	2 10
31	d9	47/48 (98%)	41 (87%)	6 (13%)	4 18
32	E0	51/51 (100%)	44 (86%)	7 (14%)	3 15
33	E1	62/66 (94%)	44 (71%)	18 (29%)	0 1
33	e1	66/66 (100%)	53 (80%)	13 (20%)	1 6
34	SR	259/261 (99%)	240 (93%)	19 (7%)	13 40
34	sR	260/261 (100%)	248 (95%)	12 (5%)	24 55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
35	SM	97/193 (50%)	86 (89%)	11 (11%)	5 23
35	sM	54/193 (28%)	47 (87%)	7 (13%)	4 18
39	L2	193/195 (99%)	158 (82%)	35 (18%)	2 8
39	l2	192/195 (98%)	155 (81%)	37 (19%)	1 7
40	L3	321/322 (100%)	266 (83%)	55 (17%)	2 10
40	l3	319/322 (99%)	262 (82%)	57 (18%)	2 9
41	L4	288/288 (100%)	238 (83%)	50 (17%)	2 9
41	l4	288/288 (100%)	241 (84%)	47 (16%)	2 11
42	L5	244/244 (100%)	209 (86%)	35 (14%)	3 14
42	l5	243/244 (100%)	209 (86%)	34 (14%)	3 15
43	L6	134/152 (88%)	110 (82%)	24 (18%)	2 9
43	l6	135/152 (89%)	111 (82%)	24 (18%)	2 9
44	L7	186/204 (91%)	160 (86%)	26 (14%)	3 15
44	l7	187/204 (92%)	166 (89%)	21 (11%)	6 24
45	L8	187/207 (90%)	162 (87%)	25 (13%)	4 17
45	l8	177/207 (86%)	147 (83%)	30 (17%)	2 10
46	L9	171/171 (100%)	143 (84%)	28 (16%)	2 11
46	l9	171/171 (100%)	135 (79%)	36 (21%)	1 5
47	M0	177/186 (95%)	147 (83%)	30 (17%)	2 10
47	m0	179/186 (96%)	148 (83%)	31 (17%)	2 9
48	M1	147/150 (98%)	121 (82%)	26 (18%)	2 9
48	m1	147/150 (98%)	128 (87%)	19 (13%)	4 18
49	M3	154/158 (98%)	134 (87%)	20 (13%)	4 18
49	m3	154/158 (98%)	136 (88%)	18 (12%)	5 22
50	M4	107/108 (99%)	92 (86%)	15 (14%)	3 15
50	m4	108/108 (100%)	91 (84%)	17 (16%)	2 12
51	M5	175/175 (100%)	151 (86%)	24 (14%)	3 15
51	m5	175/175 (100%)	158 (90%)	17 (10%)	8 30
52	M6	160/161 (99%)	147 (92%)	13 (8%)	11 36
52	m6	160/161 (99%)	138 (86%)	22 (14%)	3 15
53	M7	140/145 (97%)	119 (85%)	21 (15%)	3 13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
53	m7	125/145 (86%)	103 (82%)	22 (18%)	2 9
54	M8	150/150 (100%)	131 (87%)	19 (13%)	4 18
54	m8	150/150 (100%)	122 (81%)	28 (19%)	1 7
55	M9	153/153 (100%)	132 (86%)	21 (14%)	3 15
55	m9	153/153 (100%)	128 (84%)	25 (16%)	2 11
56	N0	156/156 (100%)	128 (82%)	28 (18%)	2 9
56	n0	156/156 (100%)	127 (81%)	29 (19%)	1 8
57	N1	136/136 (100%)	110 (81%)	26 (19%)	1 7
57	n1	136/136 (100%)	109 (80%)	27 (20%)	1 6
58	N2	87/106 (82%)	79 (91%)	8 (9%)	8 31
58	n2	85/106 (80%)	75 (88%)	10 (12%)	5 21
59	N3	104/104 (100%)	91 (88%)	13 (12%)	4 19
59	n3	104/104 (100%)	92 (88%)	12 (12%)	5 23
60	N4	57/129 (44%)	52 (91%)	5 (9%)	9 33
60	n4	100/129 (78%)	92 (92%)	8 (8%)	11 37
61	N5	104/117 (89%)	82 (79%)	22 (21%)	1 5
61	n5	104/117 (89%)	84 (81%)	20 (19%)	1 7
62	N6	109/109 (100%)	90 (83%)	19 (17%)	2 9
62	n6	109/109 (100%)	87 (80%)	22 (20%)	1 5
63	N7	115/115 (100%)	104 (90%)	11 (10%)	8 30
63	n7	115/115 (100%)	92 (80%)	23 (20%)	1 6
64	N8	118/118 (100%)	101 (86%)	17 (14%)	3 14
64	n8	118/118 (100%)	96 (81%)	22 (19%)	1 8
65	N9	46/46 (100%)	41 (89%)	5 (11%)	6 24
65	n9	46/46 (100%)	37 (80%)	9 (20%)	1 6
66	O0	81/87 (93%)	72 (89%)	9 (11%)	6 24
66	o0	84/87 (97%)	73 (87%)	11 (13%)	4 17
67	O1	92/96 (96%)	79 (86%)	13 (14%)	3 15
67	o1	94/96 (98%)	73 (78%)	21 (22%)	1 4
68	O2	109/110 (99%)	91 (84%)	18 (16%)	2 11
68	o2	109/110 (99%)	94 (86%)	15 (14%)	3 15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
69	O3	90/90 (100%)	76 (84%)	14 (16%)	2 12
69	o3	90/90 (100%)	77 (86%)	13 (14%)	3 14
70	O4	95/101 (94%)	78 (82%)	17 (18%)	2 9
70	o4	95/101 (94%)	80 (84%)	15 (16%)	2 12
71	O5	104/104 (100%)	86 (83%)	18 (17%)	2 9
71	o5	103/104 (99%)	79 (77%)	24 (23%)	1 4
72	O6	81/81 (100%)	64 (79%)	17 (21%)	1 5
72	o6	80/81 (99%)	61 (76%)	19 (24%)	1 3
73	O7	70/70 (100%)	62 (89%)	8 (11%)	5 23
73	o7	70/70 (100%)	59 (84%)	11 (16%)	2 12
74	O8	68/68 (100%)	54 (79%)	14 (21%)	1 5
74	o8	67/68 (98%)	54 (81%)	13 (19%)	1 7
75	O9	45/45 (100%)	37 (82%)	8 (18%)	2 9
75	o9	45/45 (100%)	37 (82%)	8 (18%)	2 9
76	Q0	47/47 (100%)	39 (83%)	8 (17%)	2 10
76	q0	47/47 (100%)	41 (87%)	6 (13%)	4 18
77	Q1	23/23 (100%)	19 (83%)	4 (17%)	2 9
77	q1	23/23 (100%)	18 (78%)	5 (22%)	1 5
78	Q2	90/90 (100%)	68 (76%)	22 (24%)	1 3
78	q2	90/90 (100%)	77 (86%)	13 (14%)	3 14
79	Q3	71/71 (100%)	60 (84%)	11 (16%)	2 12
79	q3	71/71 (100%)	57 (80%)	14 (20%)	1 6
80	e0	53/53 (100%)	45 (85%)	8 (15%)	3 13
82	p0	105/253 (42%)	88 (84%)	17 (16%)	2 11
All	All	18727/20169 (93%)	15904 (85%)	2823 (15%)	3 13

All (2823) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	S0	6	THR
2	S0	9	LEU
2	S0	27	ARG
2	S0	37	VAL
2	S0	43	ASP

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Mol	Chain	Res	Type
2	S0	52	LYS
2	S0	62	ARG
2	S0	87	LEU
2	S0	88	LYS
2	S0	96	THR
2	S0	111	ILE
2	S0	137	SER
2	S0	168	HIS
2	S0	170	ILE
2	S0	172	LEU
2	S0	177	LEU
2	S0	188	LEU
2	S0	196	SER
2	S0	198	MET
3	S1	20	VAL
3	S1	21	VAL
3	S1	29	TRP
3	S1	30	PHE
3	S1	39	GLU
3	S1	46	THR
3	S1	48	VAL
3	S1	61	LEU
3	S1	70	LEU
3	S1	81	PHE
3	S1	83	LYS
3	S1	91	VAL
3	S1	97	LEU
3	S1	110	LEU
3	S1	117	TRP
3	S1	148	ASN
3	S1	176	VAL
3	S1	177	GLN
3	S1	180	THR
3	S1	181	LEU
3	S1	184	LEU
3	S1	193	ILE
3	S1	198	GLU
3	S1	202	LYS
3	S1	214	LYS
3	S1	215	VAL
3	S1	218	LEU
4	S2	41	LEU

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Mol	Chain	Res	Type
4	S2	53	ILE
4	S2	54	GLU
4	S2	55	GLU
4	S2	69	ILE
4	S2	76	LEU
4	S2	77	GLN
4	S2	80	VAL
4	S2	94	GLN
4	S2	96	THR
4	S2	97	ARG
4	S2	102	VAL
4	S2	111	VAL
4	S2	113	LEU
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	148	LEU
4	S2	159	THR
4	S2	170	ILE
4	S2	181	SER
4	S2	207	LEU
4	S2	208	GLU
4	S2	225	LEU
4	S2	226	THR
4	S2	229	LEU
4	S2	237	VAL
4	S2	245	ASP
5	S3	4	LEU
5	S3	7	LYS
5	S3	23	GLU
5	S3	41	VAL
5	S3	65	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	128	GLU

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Mol	Chain	Res	Type
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	207	THR
5	S3	212	LYS
5	S3	217	ILE
5	S3	218	LEU
6	S4	6	LYS
6	S4	7	LYS
6	S4	9	LEU
6	S4	12	LEU
6	S4	38	LEU
6	S4	42	LEU
6	S4	45	ILE
6	S4	62	LYS
6	S4	65	LEU
6	S4	70	VAL
6	S4	92	LEU
6	S4	115	THR
6	S4	116	ASP
6	S4	126	VAL
6	S4	129	VAL
6	S4	131	LEU
6	S4	133	LYS
6	S4	155	LYS
6	S4	159	THR
6	S4	174	LYS
6	S4	180	LEU
6	S4	181	VAL
6	S4	187	ARG
6	S4	189	LEU
6	S4	192	ILE
6	S4	215	ASP
6	S4	222	LEU
6	S4	227	VAL
6	S4	236	ILE
6	S4	240	LYS

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Mol	Chain	Res	Type
6	S4	248	ILE
6	S4	256	ARG
6	S4	259	GLN
7	S5	25	LEU
7	S5	32	GLU
7	S5	38	THR
7	S5	45	LYS
7	S5	53	VAL
7	S5	79	ASN
7	S5	86	GLN
7	S5	89	ILE
7	S5	93	LEU
7	S5	119	ASP
7	S5	146	THR
7	S5	156	ARG
7	S5	166	ARG
7	S5	176	THR
7	S5	194	LEU
8	S6	15	THR
8	S6	21	GLU
8	S6	71	THR
8	S6	76	LEU
8	S6	81	VAL
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	133	LEU
8	S6	155	ASP
8	S6	158	ILE
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	193	LEU
8	S6	201	GLN
8	S6	211	LEU
8	S6	212	LEU

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Mol	Chain	Res	Type
8	S6	216	LEU
9	S7	28	GLU
9	S7	38	LEU
9	S7	49	ILE
9	S7	50	ASP
9	S7	51	VAL
9	S7	60	ILE
9	S7	76	LYS
9	S7	77	LEU
9	S7	78	THR
9	S7	86	GLN
9	S7	91	ILE
9	S7	97	ARG
9	S7	114	ARG
9	S7	115	SER
9	S7	126	LEU
9	S7	130	VAL
9	S7	182	VAL
9	S7	185	ILE
10	S8	5	ARG
10	S8	7	SER
10	S8	8	ARG
10	S8	14	THR
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	66	SER
10	S8	73	SER
10	S8	74	LYS
10	S8	123	LYS
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

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Mol	Chain	Res	Type
11	S9	6	ARG
11	S9	14	THR
11	S9	28	LEU
11	S9	39	LYS
11	S9	46	SER
11	S9	49	LEU
11	S9	60	LEU
11	S9	61	THR
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	20	VAL
12	C0	22	VAL
12	C0	31	LYS
12	C0	40	LEU
12	C0	46	LEU
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	7	VAL
13	C1	8	GLN
13	C1	10	GLU
13	C1	21	ASN
13	C1	29	LYS
13	C1	40	LEU
13	C1	44	THR

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Mol	Chain	Res	Type
13	C1	54	ILE
13	C1	56	LYS
13	C1	61	THR
13	C1	67	ARG
13	C1	80	MET
13	C1	99	ARG
13	C1	109	VAL
14	C2	28	LEU
14	C2	33	ARG
14	C2	43	ARG
14	C2	50	LYS
14	C2	58	LEU
14	C2	61	VAL
14	C2	66	VAL
14	C2	71	ILE
14	C2	74	LEU
14	C2	86	VAL
14	C2	103	LEU
14	C2	129	GLU
14	C2	132	GLU
15	C3	9	LYS
15	C3	12	SER
15	C3	16	ILE
15	C3	27	LYS
15	C3	32	SER
15	C3	34	ILE
15	C3	35	GLU
15	C3	56	ASP
15	C3	64	ARG
15	C3	66	ILE
15	C3	80	LEU
15	C3	88	LEU
15	C3	102	LEU
15	C3	107	LYS
15	C3	110	ASP
15	C3	115	LEU
15	C3	125	LEU
15	C3	134	VAL
15	C3	142	GLU
15	C3	143	SER
15	C3	149	LEU
16	C4	13	VAL

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Mol	Chain	Res	Type
16	C4	26	THR
16	C4	29	HIS
16	C4	30	VAL
16	C4	39	ILE
16	C4	42	VAL
16	C4	51	ASP
16	C4	79	VAL
16	C4	81	VAL
16	C4	92	LYS
16	C4	102	LEU
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	26	LEU
17	C5	34	VAL
17	C5	35	LYS
17	C5	36	LEU
17	C5	44	ARG
17	C5	50	THR
17	C5	52	LYS
17	C5	69	GLU
17	C5	110	GLU
17	C5	126	VAL
18	C6	4	VAL
18	C6	26	LYS
18	C6	29	ILE
18	C6	43	ILE
18	C6	54	LEU
18	C6	63	ILE
18	C6	66	ARG
18	C6	69	VAL
18	C6	97	VAL
18	C6	106	LYS
18	C6	109	PHE
18	C6	116	LEU
18	C6	123	ARG
18	C6	137	ARG
19	C7	16	LEU

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Mol	Chain	Res	Type
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	46	LEU
19	C7	49	LYS
19	C7	54	THR
19	C7	62	GLN
19	C7	69	ILE
19	C7	72	LYS
19	C7	86	PRO
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	13	HIS
20	C8	14	ILE
20	C8	26	ILE
20	C8	28	ILE
20	C8	34	THR
20	C8	54	LEU
20	C8	60	GLU
20	C8	80	LYS
20	C8	88	ARG
20	C8	92	ILE
20	C8	105	VAL
20	C8	116	LEU
20	C8	136	GLN
20	C8	138	THR
21	C9	4	VAL
21	C9	6	VAL
21	C9	9	VAL
21	C9	13	ASP
21	C9	22	LEU
21	C9	23	GLN
21	C9	27	LYS
21	C9	28	LEU

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Mol	Chain	Res	Type
21	C9	35	ASP
21	C9	36	ILE
21	C9	38	LYS
21	C9	44	GLU
21	C9	64	HIS
21	C9	67	MET
21	C9	73	VAL
21	C9	94	ILE
21	C9	125	SER
21	C9	127	ASN
21	C9	131	ASP
21	C9	144	GLU
22	D0	15	GLN
22	D0	20	ILE
22	D0	23	ARG
22	D0	31	VAL
22	D0	41	ILE
22	D0	51	VAL
22	D0	61	LYS
22	D0	67	THR
22	D0	72	ASN
22	D0	76	SER
22	D0	81	THR
22	D0	89	ARG
22	D0	97	VAL
22	D0	103	ILE
22	D0	108	ILE
22	D0	116	VAL
23	D1	5	LYS
23	D1	8	LEU
23	D1	11	LEU
23	D1	32	VAL
23	D1	41	GLU
23	D1	50	TYR
23	D1	60	ARG
23	D1	62	ARG
23	D1	78	LEU
23	D1	80	LYS
24	D2	4	SER
24	D2	15	ASN
24	D2	24	GLN
24	D2	25	VAL

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Mol	Chain	Res	Type
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	81	VAL
24	D2	83	ILE
24	D2	86	ILE
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	36	THR
25	D3	41	SER
25	D3	47	SER
25	D3	69	ARG
25	D3	74	VAL
25	D3	82	LYS
25	D3	83	VAL
25	D3	84	THR
25	D3	96	VAL
25	D3	103	LEU
25	D3	107	PHE
25	D3	109	ARG
25	D3	110	LYS
25	D3	114	LYS
25	D3	117	ILE
25	D3	133	LEU
25	D3	138	GLU
25	D3	140	LYS
25	D3	144	ARG
26	D4	17	LEU
26	D4	35	VAL
26	D4	47	VAL
26	D4	52	LYS

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Mol	Chain	Res	Type
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	121	THR
26	D4	124	ARG
26	D4	127	LYS
26	D4	128	LYS
27	D5	40	VAL
27	D5	42	LEU
27	D5	48	ASP
27	D5	58	ARG
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	30	ILE
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	71	LEU
28	D6	79	ILE
28	D6	82	ARG
28	D6	84	VAL
28	D6	90	GLU
29	D7	3	LEU
29	D7	4	VAL
29	D7	23	THR
29	D7	33	LEU

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Mol	Chain	Res	Type
29	D7	48	SER
29	D7	73	LEU
29	D7	75	GLU
29	D7	80	ARG
30	D8	15	VAL
30	D8	19	THR
30	D8	28	VAL
30	D8	32	PHE
30	D8	33	LEU
30	D8	39	THR
30	D8	44	VAL
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	19	ARG
31	D9	22	ARG
31	D9	25	SER
31	D9	30	LEU
31	D9	31	ILE
31	D9	36	LEU
32	E0	8	LEU
32	E0	20	LYS
32	E0	21	VAL
32	E0	24	THR
32	E0	42	ARG
32	E0	47	VAL
32	E0	56	MET
33	E1	86	THR
33	E1	91	ILE
33	E1	93	HIS
33	E1	95	HIS
33	E1	97	LYS
33	E1	98	VAL
33	E1	102	VAL
33	E1	106	TYR
33	E1	108	VAL
33	E1	111	GLU
33	E1	113	LYS

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Mol	Chain	Res	Type
33	E1	126	CYS
33	E1	130	VAL
33	E1	135	HIS
33	E1	137	ASP
33	E1	147	VAL
33	E1	150	VAL
33	E1	151	ASN
34	SR	6	VAL
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	144	LEU
34	SR	165	ASP
34	SR	191	ASP
34	SR	202	LEU
34	SR	229	LYS
34	SR	238	ASP
34	SR	268	GLN
34	SR	314	GLN
34	SR	316	MET
35	SM	27	LYS
35	SM	33	LYS
35	SM	46	LYS
35	SM	61	ILE
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	46	LYS

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Mol	Chain	Res	Type
39	L2	48	ILE
39	L2	52	SER
39	L2	62	VAL
39	L2	70	ARG
39	L2	72	ARG
39	L2	74	GLU
39	L2	82	VAL
39	L2	84	THR
39	L2	88	ILE
39	L2	96	LEU
39	L2	101	VAL
39	L2	104	LEU
39	L2	116	VAL
39	L2	134	VAL
39	L2	135	ILE
39	L2	151	PRO
39	L2	157	VAL
39	L2	158	ILE
39	L2	165	VAL
39	L2	169	ILE
39	L2	179	LEU
39	L2	180	LEU
39	L2	202	VAL
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	39	LYS
40	L3	43	LEU
40	L3	47	LEU
40	L3	55	THR
40	L3	56	ILE
40	L3	67	PHE

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Mol	Chain	Res	Type
40	L3	73	VAL
40	L3	79	VAL
40	L3	84	VAL
40	L3	85	VAL
40	L3	103	THR
40	L3	104	THR
40	L3	110	LEU
40	L3	112	ASP
40	L3	114	VAL
40	L3	139	GLN
40	L3	148	LEU
40	L3	169	THR
40	L3	173	GLN
40	L3	183	LEU
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	244	ARG
40	L3	252	ILE
40	L3	264	VAL
40	L3	282	ILE
40	L3	296	THR
40	L3	302	LYS
40	L3	305	ILE
40	L3	308	MET
40	L3	312	VAL
40	L3	317	ILE
40	L3	324	VAL
40	L3	328	ILE
40	L3	335	ILE
40	L3	346	THR
40	L3	347	SER
40	L3	354	VAL
40	L3	355	SER
40	L3	364	LYS

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Mol	Chain	Res	Type
40	L3	375	GLU
41	L4	4	PRO
41	L4	6	VAL
41	L4	10	SER
41	L4	22	LEU
41	L4	53	SER
41	L4	67	THR
41	L4	69	ARG
41	L4	73	ARG
41	L4	74	ILE
41	L4	93	MET
41	L4	98	ARG
41	L4	133	SER
41	L4	138	ARG
41	L4	145	ILE
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	182	LEU
41	L4	185	LYS
41	L4	187	LEU
41	L4	188	ARG
41	L4	193	LYS
41	L4	200	THR
41	L4	203	ARG
41	L4	206	LEU
41	L4	216	VAL
41	L4	220	ARG
41	L4	222	VAL
41	L4	227	THR
41	L4	230	VAL
41	L4	246	ARG
41	L4	249	ILE
41	L4	258	LEU
41	L4	270	SER
41	L4	283	THR
41	L4	297	SER
41	L4	306	THR

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Mol	Chain	Res	Type
41	L4	307	GLN
41	L4	313	LEU
41	L4	323	VAL
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	73	VAL
42	L5	81	HIS
42	L5	92	LEU
42	L5	95	TRP
42	L5	103	LEU
42	L5	105	ILE
42	L5	112	LYS
42	L5	113	LEU
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
42	L5	216	GLU
42	L5	222	LEU
42	L5	236	LEU
42	L5	259	LYS
42	L5	263	GLU
42	L5	268	GLU
42	L5	277	LEU

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Mol	Chain	Res	Type
42	L5	279	LYS
42	L5	293	LEU
43	L6	5	LYS
43	L6	21	THR
43	L6	31	ARG
43	L6	52	VAL
43	L6	62	THR
43	L6	64	LEU
43	L6	65	ILE
43	L6	76	LEU
43	L6	78	ARG
43	L6	79	VAL
43	L6	84	VAL
43	L6	89	THR
43	L6	90	LYS
43	L6	98	VAL
43	L6	99	GLU
43	L6	104	GLU
43	L6	129	GLU
43	L6	130	ILE
43	L6	134	ARG
43	L6	143	LYS
43	L6	152	THR
43	L6	155	LEU
43	L6	162	SER
43	L6	173	MET
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	83	LEU
44	L7	86	VAL
44	L7	88	ARG
44	L7	89	ILE
44	L7	92	ILE
44	L7	93	ASN
44	L7	98	LYS
44	L7	100	ARG
44	L7	101	LYS
44	L7	110	ARG

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Mol	Chain	Res	Type
44	L7	121	LYS
44	L7	124	LEU
44	L7	126	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
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	92	LYS
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	201	THR
45	L8	204	ARG
45	L8	241	LYS
45	L8	246	MET
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

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Mol	Chain	Res	Type
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	134	ILE
46	L9	135	GLU
46	L9	138	THR
46	L9	149	ASN
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	168	ARG
46	L9	172	ILE
46	L9	173	ARG
47	M0	3	ARG
47	M0	24	ARG
47	M0	26	VAL
47	M0	30	LYS
47	M0	32	ARG
47	M0	33	ILE
47	M0	40	LYS
47	M0	42	THR
47	M0	48	LEU
47	M0	52	LEU
47	M0	53	VAL
47	M0	60	LEU
47	M0	63	GLU
47	M0	74	LYS
47	M0	82	ARG
47	M0	87	LEU
47	M0	91	VAL
47	M0	99	ILE
47	M0	102	MET
47	M0	129	VAL
47	M0	133	GLN

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Mol	Chain	Res	Type
47	M0	139	ARG
47	M0	143	SER
47	M0	156	ARG
47	M0	163	GLN
47	M0	165	ILE
47	M0	167	LEU
47	M0	200	LEU
47	M0	203	LYS
47	M0	207	GLU
48	M1	6	GLN
48	M1	10	ARG
48	M1	11	ASP
48	M1	12	LEU
48	M1	18	VAL
48	M1	19	LEU
48	M1	30	LEU
48	M1	31	THR
48	M1	40	LEU
48	M1	44	THR
48	M1	46	VAL
48	M1	47	GLN
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	130	VAL
48	M1	139	THR
48	M1	140	ARG
48	M1	142	LYS
48	M1	166	LYS
49	M3	5	LYS
49	M3	54	LEU
49	M3	58	VAL
49	M3	59	ARG
49	M3	63	VAL
49	M3	67	ARG
49	M3	69	VAL

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Mol	Chain	Res	Type
49	M3	85	LEU
49	M3	114	GLN
49	M3	115	ARG
49	M3	117	LYS
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	15	VAL
50	M4	20	VAL
50	M4	27	GLN
50	M4	38	ILE
50	M4	50	LYS
50	M4	53	VAL
50	M4	63	VAL
50	M4	64	VAL
50	M4	72	LEU
50	M4	78	THR
50	M4	90	VAL
50	M4	92	GLU
50	M4	130	THR
50	M4	133	LYS
50	M4	135	LEU
51	M5	10	LEU
51	M5	15	GLN
51	M5	18	VAL
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	117	ASN

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Mol	Chain	Res	Type
51	M5	133	ILE
51	M5	151	ILE
51	M5	159	ARG
51	M5	170	LYS
51	M5	182	ASN
51	M5	183	THR
51	M5	184	LYS
51	M5	190	THR
51	M5	196	THR
51	M5	204	LYS
52	M6	25	LYS
52	M6	34	VAL
52	M6	85	ARG
52	M6	89	SER
52	M6	106	GLU
52	M6	110	PRO
52	M6	116	LYS
52	M6	117	ARG
52	M6	124	LEU
52	M6	129	LEU
52	M6	134	LYS
52	M6	143	THR
52	M6	190	VAL
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	41	LEU
53	M7	42	THR
53	M7	52	LEU
53	M7	67	ILE
53	M7	78	VAL
53	M7	91	VAL
53	M7	112	LEU
53	M7	114	VAL
53	M7	119	VAL
53	M7	127	ARG
53	M7	142	SER
53	M7	154	GLU
53	M7	165	VAL

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Mol	Chain	Res	Type
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	74	GLU
54	M8	81	VAL
54	M8	86	THR
54	M8	105	ARG
54	M8	122	ILE
54	M8	127	LEU
54	M8	135	GLN
54	M8	138	LEU
54	M8	150	VAL
54	M8	170	ARG
55	M9	10	LEU
55	M9	14	VAL
55	M9	17	VAL
55	M9	41	ILE
55	M9	44	LEU
55	M9	51	VAL
55	M9	55	VAL
55	M9	74	ARG
55	M9	81	ARG
55	M9	99	LEU
55	M9	103	ARG
55	M9	104	ARG
55	M9	106	LEU
55	M9	115	ILE
55	M9	116	ASP
55	M9	125	LYS
55	M9	134	HIS
55	M9	138	LEU
55	M9	153	LYS
55	M9	175	GLN
55	M9	180	LYS

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Mol	Chain	Res	Type
56	N0	12	ARG
56	N0	14	LEU
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	92	LYS
56	N0	97	VAL
56	N0	100	VAL
56	N0	103	VAL
56	N0	105	THR
56	N0	106	LEU
56	N0	115	ARG
56	N0	125	LYS
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	169	SER
56	N0	172	TYR
57	N1	25	VAL
57	N1	27	LEU
57	N1	29	THR
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
57	N1	96	ILE

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Mol	Chain	Res	Type
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	149	GLN
58	N2	10	LYS
58	N2	52	ASN
58	N2	61	THR
58	N2	63	VAL
58	N2	66	VAL
58	N2	70	LYS
58	N2	74	LYS
58	N2	100	THR
59	N3	13	ILE
59	N3	32	ARG
59	N3	48	ARG
59	N3	64	LYS
59	N3	69	LEU
59	N3	71	LYS
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	30	ARG
60	N4	39	LEU
61	N5	26	VAL
61	N5	27	ARG
61	N5	34	LEU
61	N5	37	THR

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Mol	Chain	Res	Type
61	N5	38	LEU
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	105	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	3	LYS
62	N6	8	VAL
62	N6	10	SER
62	N6	13	ARG
62	N6	17	LYS
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	70	ILE
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	26	VAL
63	N7	30	ASP

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Mol	Chain	Res	Type
63	N7	46	ILE
63	N7	72	ILE
63	N7	75	VAL
63	N7	81	LEU
63	N7	87	LEU
63	N7	134	LEU
64	N8	6	THR
64	N8	8	THR
64	N8	12	ARG
64	N8	16	SER
64	N8	29	PRO
64	N8	34	MET
64	N8	42	ARG
64	N8	46	ASP
64	N8	73	LEU
64	N8	76	ASP
64	N8	91	LEU
64	N8	104	THR
64	N8	115	LYS
64	N8	118	ILE
64	N8	120	ASN
64	N8	130	VAL
64	N8	133	LEU
65	N9	22	LYS
65	N9	28	LYS
65	N9	38	LYS
65	N9	50	THR
65	N9	59	LYS
66	O0	14	LEU
66	O0	16	LEU
66	O0	18	ILE
66	O0	32	LYS
66	O0	34	LEU
66	O0	41	LEU
66	O0	76	GLU
66	O0	79	THR
66	O0	87	VAL
67	O1	6	ASP
67	O1	8	VAL
67	O1	16	LEU
67	O1	26	LYS
67	O1	31	ARG

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Mol	Chain	Res	Type
67	O1	55	LEU
67	O1	68	GLU
67	O1	79	ARG
67	O1	82	GLU
67	O1	84	ASP
67	O1	89	LEU
67	O1	96	VAL
67	O1	106	THR
68	O2	4	LEU
68	O2	8	LYS
68	O2	19	ARG
68	O2	31	ASN
68	O2	33	ARG
68	O2	41	VAL
68	O2	52	GLN
68	O2	54	LYS
68	O2	61	LYS
68	O2	75	LEU
68	O2	76	VAL
68	O2	82	LEU
68	O2	84	THR
68	O2	86	THR
68	O2	87	MET
68	O2	106	VAL
68	O2	125	ARG
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	57	LYS
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

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Mol	Chain	Res	Type
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
70	O4	71	THR
70	O4	85	VAL
70	O4	86	LYS
70	O4	100	ILE
70	O4	102	LYS
70	O4	104	VAL
71	O5	20	GLN
71	O5	21	LEU
71	O5	27	GLU
71	O5	28	LEU
71	O5	30	GLU
71	O5	45	LYS
71	O5	46	THR
71	O5	47	VAL
71	O5	49	LYS
71	O5	68	GLN
71	O5	71	LYS
71	O5	85	THR
71	O5	89	ARG
71	O5	90	ARG
71	O5	104	GLN
71	O5	107	LYS
71	O5	115	LYS
71	O5	119	LYS
72	O6	2	THR
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

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Mol	Chain	Res	Type
72	O6	57	LEU
72	O6	58	ILE
72	O6	60	LEU
72	O6	62	ARG
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	31	LYS
73	O7	36	SER
73	O7	44	THR
73	O7	55	ARG
73	O7	67	LEU
73	O7	85	LYS
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	64	LYS
74	O8	65	LEU
74	O8	67	GLN
74	O8	77	ARG
74	O8	78	LEU
75	O9	5	LYS
75	O9	21	ARG
75	O9	23	LEU
75	O9	27	ILE
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

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Mol	Chain	Res	Type
76	Q0	95	VAL
76	Q0	108	THR
76	Q0	113	ARG
76	Q0	127	LEU
77	Q1	2	ARG
77	Q1	9	ARG
77	Q1	10	THR
77	Q1	11	ARG
78	Q2	3	ASN
78	Q2	4	VAL
78	Q2	7	THR
78	Q2	8	ARG
78	Q2	9	LYS
78	Q2	21	THR
78	Q2	26	THR
78	Q2	29	LYS
78	Q2	35	LEU
78	Q2	45	ARG
78	Q2	46	LYS
78	Q2	47	GLN
78	Q2	60	LYS
78	Q2	61	LYS
78	Q2	64	THR
78	Q2	78	LYS
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	16	VAL
79	Q3	45	LYS
79	Q3	56	THR
79	Q3	60	CYS
79	Q3	72	SER
79	Q3	73	THR
79	Q3	78	THR
79	Q3	82	THR
79	Q3	84	ARG
79	Q3	90	VAL
2	s0	9	LEU

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Mol	Chain	Res	Type
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	83	GLN
2	s0	87	LEU
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	158	VAL
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
3	s1	21	VAL
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	74	GLN
3	s1	81	PHE
3	s1	85	LYS
3	s1	104	ASP
3	s1	110	LEU
3	s1	125	VAL

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Mol	Chain	Res	Type
3	s1	126	THR
3	s1	127	VAL
3	s1	137	ILE
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	219	LYS
3	s1	228	LEU
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	72	LEU
4	s2	80	VAL
4	s2	81	MET
4	s2	83	ILE
4	s2	90	THR
4	s2	91	ARG
4	s2	94	GLN
4	s2	97	ARG
4	s2	111	VAL
4	s2	113	LEU
4	s2	115	ILE
4	s2	117	THR
4	s2	137	ILE
4	s2	141	ARG
4	s2	146	THR
4	s2	150	GLN
4	s2	152	HIS
4	s2	158	THR
4	s2	161	LYS
4	s2	164	SER
4	s2	170	ILE

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Mol	Chain	Res	Type
4	s2	185	LYS
4	s2	187	LEU
4	s2	196	VAL
4	s2	201	ASN
4	s2	206	THR
4	s2	207	LEU
4	s2	218	ILE
4	s2	221	THR
4	s2	232	GLU
4	s2	240	LEU
5	s3	4	LEU
5	s3	7	LYS
5	s3	21	LEU
5	s3	39	VAL
5	s3	41	VAL
5	s3	44	THR
5	s3	53	THR
5	s3	55	THR
5	s3	59	LEU
5	s3	66	ILE
5	s3	67	ASN
5	s3	84	ILE
5	s3	89	GLU
5	s3	111	ASN
5	s3	115	ILE
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	175	VAL
5	s3	189	MET
5	s3	202	LEU
5	s3	213	GLU
5	s3	218	LEU
5	s3	224	ASP
6	s4	6	LYS
6	s4	9	LEU
6	s4	12	LEU
6	s4	23	LEU
6	s4	24	SER

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Mol	Chain	Res	Type
6	s4	38	LEU
6	s4	42	LEU
6	s4	49	ARG
6	s4	51	ARG
6	s4	67	GLN
6	s4	69	HIS
6	s4	70	VAL
6	s4	105	VAL
6	s4	113	ARG
6	s4	123	LEU
6	s4	129	VAL
6	s4	131	LEU
6	s4	133	LYS
6	s4	159	THR
6	s4	160	VAL
6	s4	180	LEU
6	s4	181	VAL
6	s4	191	ARG
6	s4	214	LEU
6	s4	222	LEU
6	s4	236	ILE
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	58	LEU
7	s5	59	VAL
7	s5	63	GLN
7	s5	64	VAL
7	s5	68	ILE
7	s5	89	ILE
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	162	VAL
7	s5	189	THR

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Mol	Chain	Res	Type
7	s5	194	LEU
7	s5	199	ILE
7	s5	203	LYS
7	s5	216	GLU
8	s6	21	GLU
8	s6	24	ILE
8	s6	36	VAL
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	120	GLU
8	s6	124	LEU
8	s6	125	THR
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	201	GLN
8	s6	215	ARG
8	s6	216	LEU
9	s7	11	GLN
9	s7	28	GLU
9	s7	33	GLU
9	s7	67	LEU
9	s7	80	GLU
9	s7	97	ARG
9	s7	117	THR
9	s7	129	LEU
9	s7	134	GLU
9	s7	143	LEU

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Mol	Chain	Res	Type
9	s7	144	VAL
9	s7	147	ASN
9	s7	160	GLN
9	s7	166	LEU
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	59	ARG
10	s8	72	ILE
10	s8	74	LYS
10	s8	82	VAL
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	7	THR
11	s9	9	SER
11	s9	28	LEU
11	s9	33	GLU
11	s9	37	LYS
11	s9	49	LEU
11	s9	82	ARG
11	s9	83	VAL
11	s9	93	LEU
11	s9	101	VAL
11	s9	109	LEU
11	s9	111	THR
11	s9	120	LYS
11	s9	126	ARG
11	s9	127	VAL
11	s9	130	THR
11	s9	134	ILE
11	s9	150	LEU
11	s9	156	ILE
11	s9	161	THR
11	s9	172	VAL
12	c0	2	LEU

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Mol	Chain	Res	Type
12	c0	5	LYS
12	c0	15	LEU
12	c0	20	VAL
12	c0	21	VAL
12	c0	27	PHE
12	c0	33	GLU
12	c0	49	LEU
12	c0	55	VAL
12	c0	57	THR
12	c0	76	LEU
13	c1	5	LEU
13	c1	6	THR
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	74	THR
13	c1	80	MET
13	c1	83	THR
13	c1	86	ILE
13	c1	94	ILE
13	c1	99	ARG
13	c1	118	GLN
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	71	ILE
14	c2	74	LEU
14	c2	85	LYS
14	c2	86	VAL
14	c2	89	ILE

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Mol	Chain	Res	Type
14	c2	91	VAL
14	c2	103	LEU
14	c2	132	GLU
14	c2	138	GLU
14	c2	140	PHE
15	c3	12	SER
15	c3	16	ILE
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	70	LYS
15	c3	75	LEU
15	c3	83	GLU
15	c3	84	ILE
15	c3	88	LEU
15	c3	96	VAL
15	c3	97	SER
15	c3	114	ARG
15	c3	115	LEU
15	c3	117	LEU
15	c3	134	VAL
16	c4	13	VAL
16	c4	52	ARG
16	c4	61	MET
16	c4	62	LEU
16	c4	65	GLN
16	c4	66	ASP
16	c4	73	GLU
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

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Mol	Chain	Res	Type
16	c4	136	ARG
16	c4	137	LEU
17	c5	12	PHE
17	c5	36	LEU
17	c5	52	LYS
17	c5	69	GLU
17	c5	71	GLU
17	c5	77	ARG
17	c5	106	GLU
17	c5	107	ILE
17	c5	110	GLU
17	c5	121	ILE
17	c5	124	THR
17	c5	128	HIS
18	c6	7	VAL
18	c6	28	LEU
18	c6	43	ILE
18	c6	53	LEU
18	c6	57	LEU
18	c6	63	ILE
18	c6	68	ARG
18	c6	69	VAL
18	c6	105	LEU
18	c6	114	ARG
18	c6	128	LYS
18	c6	137	ARG
18	c6	143	ARG
19	c7	8	THR
19	c7	29	GLN
19	c7	30	THR
19	c7	34	LEU
19	c7	46	LEU
19	c7	69	ILE
19	c7	77	GLU
19	c7	83	GLN
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

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Mol	Chain	Res	Type
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
20	c8	120	ARG
20	c8	133	VAL
20	c8	136	GLN
20	c8	138	THR
20	c8	144	ARG
21	c9	6	VAL
21	c9	9	VAL
21	c9	27	LYS
21	c9	28	LEU
21	c9	34	VAL
21	c9	37	VAL
21	c9	51	GLU
21	c9	68	ARG
21	c9	70	GLN
21	c9	71	VAL
21	c9	88	VAL
21	c9	94	ILE
21	c9	111	ILE
21	c9	116	ILE
21	c9	123	ARG
21	c9	126	GLU
21	c9	131	ASP
21	c9	139	THR
22	d0	20	ILE
22	d0	22	ILE
22	d0	34	LEU
22	d0	44	ASN
22	d0	52	LYS

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Mol	Chain	Res	Type
22	d0	57	ARG
22	d0	60	THR
22	d0	70	THR
22	d0	81	THR
22	d0	97	VAL
22	d0	99	ILE
22	d0	103	ILE
22	d0	105	GLN
22	d0	115	GLU
22	d0	118	VAL
23	d1	2	GLU
23	d1	5	LYS
23	d1	8	LEU
23	d1	10	GLU
23	d1	25	LYS
23	d1	32	VAL
23	d1	34	ILE
23	d1	38	LYS
23	d1	49	GLU
23	d1	52	THR
23	d1	62	ARG
23	d1	78	LEU
23	d1	81	ASN
24	d2	7	LEU
24	d2	9	ASP
24	d2	23	ARG
24	d2	25	VAL
24	d2	43	LYS
24	d2	47	ILE
24	d2	65	LEU
24	d2	83	ILE
24	d2	98	GLN
24	d2	103	ILE
25	d3	9	LEU
25	d3	14	LYS
25	d3	19	ARG
25	d3	27	ASN
25	d3	28	ASN
25	d3	73	ARG
25	d3	84	THR
25	d3	96	VAL
25	d3	100	ASP

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Mol	Chain	Res	Type
25	d3	103	LEU
25	d3	107	PHE
25	d3	114	LYS
25	d3	131	SER
25	d3	144	ARG
26	d4	26	ASP
26	d4	28	LEU
26	d4	47	VAL
26	d4	62	THR
26	d4	88	THR
26	d4	114	ARG
26	d4	125	LEU
26	d4	128	LYS
27	d5	41	ILE
27	d5	45	GLU
27	d5	53	GLU
27	d5	57	TYR
27	d5	60	VAL
27	d5	81	ARG
27	d5	88	ILE
27	d5	90	LYS
27	d5	97	LYS
27	d5	102	THR
28	d6	12	LYS
28	d6	18	VAL
28	d6	26	CYS
28	d6	28	LYS
28	d6	44	ILE
28	d6	46	GLU
28	d6	53	LEU
28	d6	61	GLU
28	d6	90	GLU
29	d7	3	LEU
29	d7	14	SER
29	d7	41	LEU
29	d7	43	ILE
29	d7	46	VAL
29	d7	52	THR
29	d7	56	CYS
29	d7	72	LYS
29	d7	82	LYS
30	d8	15	VAL

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Mol	Chain	Res	Type
30	d8	22	ARG
30	d8	32	PHE
30	d8	33	LEU
30	d8	36	THR
30	d8	39	THR
30	d8	40	ILE
30	d8	44	VAL
30	d8	54	LEU
30	d8	61	ARG
30	d8	64	ARG
31	d9	10	HIS
31	d9	19	ARG
31	d9	30	LEU
31	d9	32	ARG
31	d9	36	LEU
31	d9	54	LYS
80	e0	4	VAL
80	e0	13	LYS
80	e0	21	VAL
80	e0	28	LYS
80	e0	29	LYS
80	e0	39	LEU
80	e0	54	ARG
80	e0	56	MET
33	e1	84	VAL
33	e1	86	THR
33	e1	90	LYS
33	e1	96	LYS
33	e1	97	LYS
33	e1	98	VAL
33	e1	102	VAL
33	e1	106	TYR
33	e1	107	LYS
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

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Mol	Chain	Res	Type
34	sR	76	ASP
34	sR	96	THR
34	sR	167	VAL
34	sR	202	LEU
34	sR	232	TYR
34	sR	297	ASP
34	sR	300	THR
35	sM	23	LYS
35	sM	33	LYS
35	sM	43	ASP
35	sM	49	LYS
35	sM	50	ASN
35	sM	74	LYS
35	sM	75	ASP
39	l2	15	ILE
39	l2	22	LEU
39	l2	32	LEU
39	l2	44	ILE
39	l2	45	VAL
39	l2	48	ILE
39	l2	61	VAL
39	l2	62	VAL
39	l2	71	LEU
39	l2	79	ASN
39	l2	82	VAL
39	l2	98	VAL
39	l2	101	VAL
39	l2	104	LEU
39	l2	107	VAL
39	l2	109	GLU
39	l2	116	VAL
39	l2	118	GLU
39	l2	119	LYS
39	l2	128	ARG
39	l2	134	VAL
39	l2	137	ILE
39	l2	147	ARG
39	l2	155	LYS
39	l2	157	VAL
39	l2	158	ILE
39	l2	165	VAL
39	l2	169	ILE

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Mol	Chain	Res	Type
39	l2	179	LEU
39	l2	202	VAL
39	l2	204	MET
39	l2	207	VAL
39	l2	230	VAL
39	l2	246	LEU
39	l2	247	ARG
39	l2	249	SER
39	l2	250	GLN
40	l3	3	HIS
40	l3	10	ARG
40	l3	17	LEU
40	l3	19	ARG
40	l3	30	LYS
40	l3	37	ARG
40	l3	43	LEU
40	l3	47	LEU
40	l3	50	LYS
40	l3	56	ILE
40	l3	70	ARG
40	l3	73	VAL
40	l3	77	THR
40	l3	81	THR
40	l3	84	VAL
40	l3	85	VAL
40	l3	95	THR
40	l3	104	THR
40	l3	108	GLU
40	l3	110	LEU
40	l3	114	VAL
40	l3	125	SER
40	l3	139	GLN
40	l3	146	ARG
40	l3	148	LEU
40	l3	152	LYS
40	l3	153	LYS
40	l3	157	VAL
40	l3	167	ARG
40	l3	169	THR
40	l3	178	LEU
40	l3	183	LEU
40	l3	188	ILE

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Mol	Chain	Res	Type
40	l3	192	VAL
40	l3	202	THR
40	l3	205	VAL
40	l3	212	ASN
40	l3	221	THR
40	l3	227	GLU
40	l3	232	ARG
40	l3	235	THR
40	l3	238	LEU
40	l3	244	ARG
40	l3	246	LEU
40	l3	248	LYS
40	l3	249	VAL
40	l3	252	ILE
40	l3	264	VAL
40	l3	266	ARG
40	l3	275	ARG
40	l3	287	LYS
40	l3	304	THR
40	l3	324	VAL
40	l3	328	ILE
40	l3	338	LEU
40	l3	340	LYS
40	l3	386	ASP
41	l4	2	SER
41	l4	3	ARG
41	l4	6	VAL
41	l4	14	GLU
41	l4	22	LEU
41	l4	25	VAL
41	l4	47	ARG
41	l4	55	LYS
41	l4	69	ARG
41	l4	73	ARG
41	l4	92	ASN
41	l4	93	MET
41	l4	98	ARG
41	l4	99	MET
41	l4	122	THR
41	l4	134	LEU
41	l4	144	LYS
41	l4	145	ILE

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Mol	Chain	Res	Type
41	l4	148	ILE
41	l4	150	LEU
41	l4	156	LEU
41	l4	160	GLN
41	l4	170	LYS
41	l4	177	ASP
41	l4	179	LEU
41	l4	182	LEU
41	l4	186	LYS
41	l4	187	LEU
41	l4	200	THR
41	l4	206	LEU
41	l4	220	ARG
41	l4	222	VAL
41	l4	230	VAL
41	l4	246	ARG
41	l4	258	LEU
41	l4	266	THR
41	l4	286	VAL
41	l4	301	PRO
41	l4	307	GLN
41	l4	313	LEU
41	l4	319	LYS
41	l4	327	LEU
41	l4	333	VAL
41	l4	338	LYS
41	l4	342	LYS
41	l4	345	GLU
41	l4	347	THR
42	l5	4	GLN
42	l5	25	GLU
42	l5	34	LYS
42	l5	41	LYS
42	l5	51	LEU
42	l5	61	ILE
42	l5	65	ILE
42	l5	68	THR
42	l5	70	THR
42	l5	74	VAL
42	l5	75	LEU
42	l5	93	THR
42	l5	110	LEU

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Mol	Chain	Res	Type
42	l5	112	LYS
42	l5	113	LEU
42	l5	115	LEU
42	l5	118	THR
42	l5	120	LYS
42	l5	136	GLU
42	l5	144	VAL
42	l5	146	LEU
42	l5	148	ILE
42	l5	152	ARG
42	l5	155	THR
42	l5	164	LYS
42	l5	177	GLU
42	l5	185	PHE
42	l5	194	LEU
42	l5	227	LEU
42	l5	236	LEU
42	l5	268	GLU
42	l5	273	ARG
42	l5	275	THR
42	l5	282	ARG
43	l6	8	LYS
43	l6	18	LEU
43	l6	20	LYS
43	l6	21	THR
43	l6	35	VAL
43	l6	50	LYS
43	l6	52	VAL
43	l6	62	THR
43	l6	64	LEU
43	l6	65	ILE
43	l6	78	ARG
43	l6	79	VAL
43	l6	82	ARG
43	l6	89	THR
43	l6	93	VAL
43	l6	98	VAL
43	l6	99	GLU
43	l6	108	LYS
43	l6	109	GLU
43	l6	131	LYS
43	l6	143	LYS

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Mol	Chain	Res	Type
43	l6	152	THR
43	l6	155	LEU
43	l6	162	SER
44	l7	26	VAL
44	l7	41	ARG
44	l7	45	LEU
44	l7	64	GLN
44	l7	77	VAL
44	l7	83	LEU
44	l7	87	VAL
44	l7	88	ARG
44	l7	101	LYS
44	l7	110	ARG
44	l7	121	LYS
44	l7	124	LEU
44	l7	130	ILE
44	l7	147	LEU
44	l7	158	LYS
44	l7	178	ILE
44	l7	179	LEU
44	l7	184	LEU
44	l7	225	GLN
44	l7	229	PHE
44	l7	239	LEU
45	l8	26	LEU
45	l8	41	GLN
45	l8	50	VAL
45	l8	68	ARG
45	l8	71	VAL
45	l8	74	THR
45	l8	79	GLN
45	l8	81	THR
45	l8	95	ASN
45	l8	109	LEU
45	l8	136	LEU
45	l8	149	LYS
45	l8	150	LEU
45	l8	160	ILE
45	l8	163	VAL
45	l8	164	VAL
45	l8	169	LEU
45	l8	172	LYS

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Mol	Chain	Res	Type
45	l8	183	LYS
45	l8	189	LEU
45	l8	190	VAL
45	l8	195	SER
45	l8	200	LEU
45	l8	206	GLU
45	l8	213	LYS
45	l8	214	LEU
45	l8	230	LYS
45	l8	238	LEU
45	l8	241	LYS
45	l8	248	LYS
46	l9	5	GLN
46	l9	6	THR
46	l9	16	VAL
46	l9	17	THR
46	l9	18	VAL
46	l9	19	SER
46	l9	21	LYS
46	l9	24	ILE
46	l9	33	THR
46	l9	39	LYS
46	l9	44	THR
46	l9	55	VAL
46	l9	62	ARG
46	l9	68	LEU
46	l9	69	ARG
46	l9	70	THR
46	l9	80	THR
46	l9	82	VAL
46	l9	100	ASN
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

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Mol	Chain	Res	Type
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	26	VAL
47	m0	38	LYS
47	m0	42	THR
47	m0	48	LEU
47	m0	52	LEU
47	m0	57	LEU
47	m0	63	GLU
47	m0	70	ILE
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	131	ILE
47	m0	137	SER
47	m0	142	ASP
47	m0	148	VAL
47	m0	156	ARG
47	m0	167	LEU
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

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Mol	Chain	Res	Type
48	m1	32	ARG
48	m1	46	VAL
48	m1	56	THR
48	m1	80	LEU
48	m1	106	ILE
48	m1	112	LEU
48	m1	129	VAL
48	m1	130	VAL
48	m1	145	LYS
48	m1	147	THR
48	m1	159	THR
48	m1	160	VAL
48	m1	166	LYS
48	m1	171	VAL
49	m3	54	LEU
49	m3	58	VAL
49	m3	67	ARG
49	m3	68	LYS
49	m3	69	VAL
49	m3	73	ARG
49	m3	107	GLU
49	m3	118	GLU
49	m3	123	ILE
49	m3	131	LYS
49	m3	138	VAL
49	m3	149	GLN
49	m3	162	ASN
49	m3	164	GLU
49	m3	176	GLU
49	m3	183	ARG
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	43	LYS
50	m4	53	VAL
50	m4	62	GLN
50	m4	64	VAL
50	m4	66	THR
50	m4	69	THR

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Mol	Chain	Res	Type
50	m4	72	LEU
50	m4	80	THR
50	m4	108	ARG
50	m4	124	ARG
50	m4	130	THR
50	m4	132	LYS
50	m4	135	LEU
51	m5	5	LYS
51	m5	10	LEU
51	m5	22	LEU
51	m5	24	ARG
51	m5	68	ARG
51	m5	76	PRO
51	m5	80	THR
51	m5	83	LYS
51	m5	85	THR
51	m5	93	LYS
51	m5	98	LEU
51	m5	105	ARG
51	m5	117	ASN
51	m5	138	GLN
51	m5	142	ILE
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	62	THR
52	m6	67	THR
52	m6	78	ARG
52	m6	85	ARG
52	m6	89	SER
52	m6	106	GLU
52	m6	110	PRO
52	m6	117	ARG
52	m6	124	LEU
52	m6	129	LEU
52	m6	130	LYS
52	m6	134	LYS
52	m6	160	ARG
52	m6	171	LYS

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Mol	Chain	Res	Type
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	29	THR
53	m7	32	THR
53	m7	52	LEU
53	m7	65	SER
53	m7	69	ARG
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	114	VAL
53	m7	118	GLN
53	m7	119	VAL
53	m7	127	ARG
53	m7	148	LEU
53	m7	155	GLU
54	m8	3	ILE
54	m8	7	SER
54	m8	12	ARG
54	m8	17	THR
54	m8	26	LEU
54	m8	32	LEU
54	m8	34	THR
54	m8	39	ARG
54	m8	49	LEU
54	m8	62	VAL
54	m8	64	VAL
54	m8	80	THR
54	m8	81	VAL
54	m8	86	THR
54	m8	93	ILE
54	m8	113	LYS

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Mol	Chain	Res	Type
54	m8	127	LEU
54	m8	135	GLN
54	m8	138	LEU
54	m8	141	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	182	LYS
54	m8	185	LYS
55	m9	5	ARG
55	m9	7	GLN
55	m9	10	LEU
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	74	ARG
55	m9	88	ARG
55	m9	93	VAL
55	m9	99	LEU
55	m9	106	LEU
55	m9	117	LYS
55	m9	128	LYS
55	m9	134	HIS
55	m9	138	LEU
55	m9	143	ILE
55	m9	152	GLU
55	m9	153	LYS
55	m9	156	ASN
55	m9	164	LEU
55	m9	171	ASP
55	m9	173	ARG
56	n0	1	MET
56	n0	17	GLU
56	n0	21	GLU
56	n0	23	LYS
56	n0	32	SER

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Mol	Chain	Res	Type
56	n0	34	GLU
56	n0	40	ARG
56	n0	50	LYS
56	n0	71	LYS
56	n0	79	VAL
56	n0	80	ARG
56	n0	87	THR
56	n0	96	ASP
56	n0	97	VAL
56	n0	100	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	142	GLN
56	n0	148	LEU
56	n0	155	ARG
56	n0	157	GLN
56	n0	160	THR
56	n0	162	THR
56	n0	172	TYR
57	n1	9	SER
57	n1	12	ARG
57	n1	18	ASP
57	n1	25	VAL
57	n1	35	LYS
57	n1	68	THR
57	n1	69	LYS
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	103	GLN
57	n1	118	GLU
57	n1	124	VAL
57	n1	126	VAL

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Mol	Chain	Res	Type
57	n1	129	LYS
57	n1	130	ARG
57	n1	131	GLN
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
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	90	ARG
58	n2	96	VAL
59	n3	7	GLN
59	n3	13	ILE
59	n3	40	LYS
59	n3	48	ARG
59	n3	64	LYS
59	n3	69	LEU
59	n3	73	VAL
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	5	ILE
60	n4	19	THR
60	n4	39	LEU
60	n4	63	ILE
60	n4	96	LEU
60	n4	99	GLU
60	n4	126	GLU
61	n5	24	LEU
61	n5	27	ARG
61	n5	34	LEU

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Mol	Chain	Res	Type
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	97	LYS
61	n5	109	LYS
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	64	LYS
62	n6	66	GLN
62	n6	69	LYS
62	n6	83	ASP
62	n6	94	SER
62	n6	108	LYS
62	n6	115	ARG
62	n6	120	GLN
62	n6	122	LYS
63	n7	3	LYS
63	n7	5	LEU
63	n7	12	VAL

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Mol	Chain	Res	Type
63	n7	17	ARG
63	n7	24	VAL
63	n7	26	VAL
63	n7	34	LYS
63	n7	36	HIS
63	n7	46	ILE
63	n7	54	THR
63	n7	72	ILE
63	n7	75	VAL
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	111	LYS
63	n7	121	ARG
63	n7	126	LYS
63	n7	134	LEU
64	n8	4	ARG
64	n8	6	THR
64	n8	7	LYS
64	n8	8	THR
64	n8	12	ARG
64	n8	15	VAL
64	n8	27	LYS
64	n8	42	ARG
64	n8	46	ASP
64	n8	64	GLN
64	n8	65	GLN
64	n8	73	LEU
64	n8	78	LEU
64	n8	80	THR
64	n8	85	ASP
64	n8	97	GLU
64	n8	98	THR
64	n8	115	LYS
64	n8	124	ILE
64	n8	128	ARG
64	n8	133	LEU
64	n8	139	ARG

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Mol	Chain	Res	Type
65	n9	3	LYS
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	17	VAL
66	o0	18	ILE
66	o0	32	LYS
66	o0	41	LEU
66	o0	61	MET
66	o0	66	LYS
66	o0	76	GLU
66	o0	86	ARG
66	o0	87	VAL
66	o0	100	ILE
67	o1	8	VAL
67	o1	13	THR
67	o1	16	LEU
67	o1	24	SER
67	o1	26	LYS
67	o1	31	ARG
67	o1	36	ILE
67	o1	44	MET
67	o1	55	LEU
67	o1	68	GLU
67	o1	76	SER
67	o1	81	GLU
67	o1	83	GLU
67	o1	84	ASP
67	o1	93	VAL
67	o1	96	VAL
67	o1	98	VAL
67	o1	102	LYS
67	o1	106	THR
67	o1	107	VAL
67	o1	110	GLU
68	o2	4	LEU

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Mol	Chain	Res	Type
68	o2	16	LYS
68	o2	19	ARG
68	o2	33	ARG
68	o2	35	GLN
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	95	GLU
68	o2	106	VAL
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	107	ILE
70	o4	5	VAL
70	o4	20	ILE
70	o4	21	LYS
70	o4	24	LYS
70	o4	29	ILE
70	o4	31	ARG
70	o4	54	ILE
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
70	o4	104	VAL

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Mol	Chain	Res	Type
71	o5	4	VAL
71	o5	15	GLU
71	o5	20	GLN
71	o5	21	LEU
71	o5	27	GLU
71	o5	28	LEU
71	o5	36	LEU
71	o5	37	SER
71	o5	38	ARG
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
71	o5	119	LYS
72	o6	7	ILE
72	o6	9	ILE
72	o6	11	LEU
72	o6	17	VAL
72	o6	21	THR
72	o6	26	ILE
72	o6	35	ASN
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	84	LYS
72	o6	88	GLU
72	o6	94	ILE

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Mol	Chain	Res	Type
72	o6	98	ARG
73	o7	17	THR
73	o7	25	ARG
73	o7	33	THR
73	o7	36	SER
73	o7	44	THR
73	o7	55	ARG
73	o7	59	THR
73	o7	65	ARG
73	o7	67	LEU
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	50	SER
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	12	LYS
75	o9	21	ARG
75	o9	23	LEU
75	o9	29	LEU
75	o9	45	ARG
75	o9	48	LYS
75	o9	51	ILE
76	q0	79	GLU
76	q0	83	LYS
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

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Mol	Chain	Res	Type
77	q1	13	LEU
77	q1	21	ARG
78	q2	8	ARG
78	q2	15	LYS
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	104	LEU
78	q2	105	GLN
79	q3	3	LYS
79	q3	4	ARG
79	q3	17	ARG
79	q3	20	SER
79	q3	24	ARG
79	q3	41	PHE
79	q3	46	THR
79	q3	49	ARG
79	q3	54	ILE
79	q3	56	THR
79	q3	59	CYS
79	q3	64	VAL
79	q3	73	THR
79	q3	79	VAL
82	p0	4	ILE
82	p0	10	GLU
82	p0	15	LEU
82	p0	39	HIS
82	p0	51	VAL
82	p0	52	LEU
82	p0	55	LYS
82	p0	67	LEU
82	p0	68	SER
82	p0	69	ASP
82	p0	70	LEU
82	p0	81	LYS
82	p0	91	GLU

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Mol	Chain	Res	Type
82	p0	93	LEU
82	p0	97	LYS
82	p0	99	VAL
82	p0	104	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (185) such sidechains are listed below:

Mol	Chain	Res	Type
3	S1	146	GLN
3	S1	148	ASN
3	S1	209	ASN
4	S2	59	HIS
4	S2	189	GLN
4	S2	199	GLN
6	S4	98	ASN
7	S5	104	ASN
8	S6	10	ASN
8	S6	190	GLN
9	S7	147	ASN
9	S7	170	GLN
9	S7	174	ASN
10	S8	52	ASN
10	S8	88	ASN
10	S8	116	HIS
11	S9	139	GLN
13	C1	81	HIS
14	C2	70	ASN
15	C3	151	ASN
16	C4	12	GLN
18	C6	21	HIS
18	C6	103	ASN
19	C7	48	ASN
19	C7	56	HIS
19	C7	62	GLN
20	C8	104	ASN
21	C9	23	GLN
22	D0	48	HIS
23	D1	74	GLN
24	D2	12	ASN
24	D2	44	HIS
25	D3	10	ASN
25	D3	27	ASN

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Mol	Chain	Res	Type
25	D3	65	ASN
26	D4	63	GLN
27	D5	82	HIS
28	D6	8	ASN
28	D6	69	ASN
29	D7	19	HIS
30	D8	51	ASN
31	D9	37	ASN
31	D9	53	ASN
33	E1	135	HIS
33	E1	145	HIS
34	SR	196	ASN
34	SR	308	ASN
35	SM	70	ASN
39	L2	209	HIS
39	L2	250	GLN
41	L4	5	GLN
41	L4	260	GLN
41	L4	296	GLN
42	L5	40	HIS
42	L5	244	HIS
42	L5	264	GLN
43	L6	80	ASN
43	L6	157	GLN
44	L7	157	ASN
44	L7	244	ASN
47	M0	59	GLN
47	M0	123	HIS
48	M1	43	GLN
49	M3	19	GLN
49	M3	114	GLN
50	M4	105	GLN
52	M6	90	HIS
52	M6	193	GLN
53	M7	34	GLN
54	M8	9	GLN
56	N0	108	GLN
57	N1	16	GLN
57	N1	103	GLN
58	N2	87	ASN
59	N3	98	ASN
60	N4	58	HIS

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Mol	Chain	Res	Type
60	N4	59	HIS
61	N5	85	GLN
61	N5	94	GLN
63	N7	128	GLN
64	N8	67	HIS
65	N9	45	HIS
68	O2	49	ASN
68	O2	52	GLN
68	O2	71	HIS
71	O5	68	GLN
71	O5	99	GLN
73	O7	30	GLN
74	O8	32	ASN
78	Q2	82	GLN
2	s0	49	ASN
2	s0	69	ASN
3	s1	74	GLN
3	s1	149	GLN
4	s2	82	ASN
5	s3	159	HIS
6	s4	188	ASN
7	s5	104	ASN
7	s5	224	ASN
8	s6	65	GLN
8	s6	197	ASN
10	s8	87	ASN
10	s8	94	ASN
13	c1	37	ASN
13	c1	81	HIS
13	c1	127	GLN
14	c2	125	ASN
14	c2	142	GLN
15	c3	5	HIS
15	c3	105	ASN
16	c4	10	ASN
16	c4	65	GLN
18	c6	21	HIS
18	c6	74	HIS
20	c8	6	GLN
20	c8	74	GLN
21	c9	43	ASN
21	c9	64	HIS

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Mol	Chain	Res	Type
22	d0	47	GLN
22	d0	105	GLN
25	d3	18	HIS
26	d4	31	ASN
26	d4	106	GLN
29	d7	49	HIS
31	d9	27	HIS
31	d9	53	ASN
80	e0	17	GLN
34	sR	29	GLN
34	sR	52	GLN
34	sR	288	HIS
39	l2	205	ASN
40	l3	11	HIS
40	l3	211	GLN
41	l4	116	ASN
41	l4	213	ASN
41	l4	322	GLN
42	l5	63	GLN
43	l6	61	ASN
44	l7	64	GLN
44	l7	157	ASN
44	l7	172	ASN
44	l7	186	HIS
45	l8	61	GLN
46	l9	96	HIS
46	l9	100	ASN
46	l9	156	GLN
47	m0	55	ASN
47	m0	92	HIS
48	m1	132	ASN
48	m1	150	ASN
49	m3	99	HIS
51	m5	123	GLN
51	m5	182	ASN
52	m6	50	ASN
52	m6	90	HIS
52	m6	182	ASN
53	m7	50	GLN
53	m7	121	GLN
53	m7	137	ASN
54	m8	45	ASN

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Mol	Chain	Res	Type
55	m9	121	HIS
55	m9	141	HIS
56	n0	63	GLN
56	n0	65	ASN
56	n0	138	GLN
57	n1	5	HIS
57	n1	95	HIS
57	n1	103	GLN
60	n4	59	HIS
60	n4	112	ASN
61	n5	55	ASN
62	n6	81	GLN
64	n8	11	HIS
64	n8	44	ASN
64	n8	65	GLN
69	o3	106	ASN
70	o4	3	GLN
71	o5	68	GLN
71	o5	99	GLN
71	o5	113	GLN
75	o9	25	GLN
78	q2	47	GLN
78	q2	90	HIS
78	q2	102	GLN
82	p0	98	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1778/1800 (98%)	439 (24%)	50 (2%)
1	6	1792/1800 (99%)	419 (23%)	43 (2%)
36	1	3143/3396 (92%)	621 (19%)	66 (2%)
36	5	3143/3396 (92%)	609 (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%)	33 (21%)	2 (1%)
38	8	157/158 (99%)	31 (19%)	0
85	C	1/5 (20%)	0	0
85	D	1/5 (20%)	0	0
All	All	10412/10960 (95%)	2181 (20%)	225 (2%)

All (2181) 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	46	A
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
1	2	158	U
1	2	159	U
1	2	178	U
1	2	185	U
1	2	186	C

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Mol	Chain	Res	Type
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
1	2	275	C
1	2	276	C
1	2	277	U
1	2	278	U
1	2	279	G

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Mol	Chain	Res	Type
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
1	2	428	A
1	2	434	G
1	2	437	A
1	2	439	U
1	2	444	C

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Mol	Chain	Res	Type
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
1	2	544	A
1	2	548	G
1	2	555	A
1	2	556	A
1	2	557	G

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Mol	Chain	Res	Type
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
1	2	705	U
1	2	707	A
1	2	709	C
1	2	710	U
1	2	712	G

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Mol	Chain	Res	Type
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
1	2	794	U
1	2	795	U
1	2	807	A
1	2	812	A
1	2	815	G

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Mol	Chain	Res	Type
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
1	2	1005	A
1	2	1020	A
1	2	1021	C
1	2	1026	A
1	2	1028	C

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Mol	Chain	Res	Type
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
1	2	1229	G
1	2	1243	G
1	2	1244	A
1	2	1245	G
1	2	1251	U

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Mol	Chain	Res	Type
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
1	2	1482	C
1	2	1486	G
1	2	1489	U
1	2	1490	C
1	2	1491	U

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Mol	Chain	Res	Type
1	2	1492	A
1	2	1493	A
1	2	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
1	2	1699	G
1	2	1700	C
1	2	1701	A
1	2	1702	A
1	2	1703	C

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Mol	Chain	Res	Type
1	2	1711	C
1	2	1712	A
1	2	1713	G
1	2	1715	G
1	2	1717	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
36	1	133	U
36	1	136	G
36	1	147	U
36	1	148	G

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Mol	Chain	Res	Type
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
36	1	376	G
36	1	398	A
36	1	399	A
36	1	401	U

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Mol	Chain	Res	Type
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
36	1	638	C
36	1	649	A
36	1	651	G
36	1	654	C

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Mol	Chain	Res	Type
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
36	1	923	C
36	1	924	G
36	1	925	A
36	1	937	G

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Mol	Chain	Res	Type
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	993	G
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
36	1	1098	A
36	1	1103	A
36	1	1104	G

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Mol	Chain	Res	Type
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
36	1	1278	A
36	1	1279	C
36	1	1285	G

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Mol	Chain	Res	Type
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
36	1	1508	C
36	1	1527	C
36	1	1533	U

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Mol	Chain	Res	Type
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
36	1	1750	A
36	1	1751	G
36	1	1762	C

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Mol	Chain	Res	Type
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	1847	A
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
36	1	2120	A
36	1	2121	G

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Mol	Chain	Res	Type
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
36	1	2375	G
36	1	2385	G

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Mol	Chain	Res	Type
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
36	1	2570	U
36	1	2571	U

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Mol	Chain	Res	Type
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
36	1	2801	A
36	1	2802	A

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Mol	Chain	Res	Type
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	2819	A
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
36	1	3006	A

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Mol	Chain	Res	Type
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
36	1	3208	G

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Mol	Chain	Res	Type
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
36	1	3368	U

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Mol	Chain	Res	Type
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
38	4	95	G

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Mol	Chain	Res	Type
38	4	104	A
38	4	105	A
38	4	106	C
38	4	111	A
38	4	112	U
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	211	A
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

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Mol	Chain	Res	Type
36	5	285	A
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

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Mol	Chain	Res	Type
36	5	604	G
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

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Mol	Chain	Res	Type
36	5	861	C
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

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Mol	Chain	Res	Type
36	5	1032	C
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

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Mol	Chain	Res	Type
36	5	1241	U
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	1331	U
36	5	1332	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

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Mol	Chain	Res	Type
36	5	1508	C
36	5	1527	C
36	5	1536	G
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

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Mol	Chain	Res	Type
36	5	1683	A
36	5	1687	U
36	5	1716	U
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

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Mol	Chain	Res	Type
36	5	2101	C
36	5	2102	U
36	5	2111	G
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

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Mol	Chain	Res	Type
36	5	2336	U
36	5	2366	C
36	5	2367	A
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

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Mol	Chain	Res	Type
36	5	2568	C
36	5	2569	A
36	5	2570	U
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

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Mol	Chain	Res	Type
36	5	2800	G
36	5	2801	A
36	5	2802	A
36	5	2810	C
36	5	2814	G
36	5	2816	G
36	5	2817	A
36	5	2818	U
36	5	2819	A
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	2955	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

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Mol	Chain	Res	Type
36	5	3092	C
36	5	3113	A
36	5	3116	G
36	5	3122	A
36	5	3130	A
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

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Mol	Chain	Res	Type
36	5	3276	G
36	5	3277	U
36	5	3278	C
36	5	3279	A
36	5	3280	U
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

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Mol	Chain	Res	Type
37	7	76	A
37	7	93	C
37	7	99	G
37	7	102	A
37	7	103	A
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:

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Mol	Chain	Res	Type

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

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Mol	Chain	Res	Type
1	2	1481	C
1	2	1489	U
1	2	1490	C
1	2	1568	C
1	2	1573	A
1	2	1615	C
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

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Mol	Chain	Res	Type
36	1	1846	C
36	1	1849	C
36	1	2101	C
36	1	2112	U
36	1	2209	U
36	1	2227	C
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

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Mol	Chain	Res	Type
1	6	145	A
1	6	158	U
1	6	187	G
1	6	217	A
1	6	240	U
1	6	272	U
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

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Mol	Chain	Res	Type
36	5	240	U
36	5	282	G
36	5	397	A
36	5	438	A
36	5	588	G
36	5	715	A
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

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Mol	Chain	Res	Type
36	5	2817	A
36	5	2818	U
36	5	2954	U
36	5	3078	U
36	5	3121	U
36	5	3154	C
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 (i)

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	21,24,25	1.58	4 (19%)	26,35,38	2.28	10 (38%)
85	8AN	D	76	88,85	21,24,25	1.55	4 (19%)	26,35,38	2.26	10 (38%)

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	-	1/7/25/26	0/3/3/3
85	8AN	D	76	88,85	-	1/7/25/26	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	D	76	8AN	C5-C4	4.55	1.47	1.39
85	C	76	8AN	C5-C4	4.51	1.47	1.39
85	C	76	8AN	C5-C6	2.75	1.48	1.41
85	D	76	8AN	C5-N7	-2.62	1.34	1.39
85	C	76	8AN	C8-N7	2.50	1.36	1.31
85	D	76	8AN	C8-N7	2.28	1.36	1.31
85	D	76	8AN	C5-C6	2.18	1.47	1.41
85	C	76	8AN	C5-N7	-2.15	1.35	1.39

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
85	C	76	8AN	C5-C4-N3	-5.95	118.53	126.72
85	D	76	8AN	C5-C4-N3	-5.87	118.63	126.72
85	D	76	8AN	N3-C4-N9	5.00	135.67	127.17
85	C	76	8AN	N3-C4-N9	4.28	134.45	127.17
85	C	76	8AN	C4-C5-N7	-4.04	105.96	110.58
85	C	76	8AN	C2-N3-C4	3.73	120.94	111.83
85	D	76	8AN	C2-N3-C4	3.24	119.75	111.83
85	D	76	8AN	C4-N9-C8	3.07	108.96	105.74
85	C	76	8AN	N1-C2-N3	-3.03	123.99	128.58
85	D	76	8AN	C4-C5-N7	-3.01	107.14	110.58
85	C	76	8AN	C5-N7-C8	2.77	107.80	103.45
85	D	76	8AN	N1-C2-N3	-2.70	124.50	128.58
85	C	76	8AN	C6-C5-N7	2.49	136.89	132.09
85	D	76	8AN	O4'-C1'-N9	-2.48	103.32	108.09
85	D	76	8AN	C5-N7-C8	2.41	107.24	103.45
85	C	76	8AN	C4-N9-C8	2.40	108.26	105.74
85	C	76	8AN	C2'-C3'-C4'	2.25	105.78	102.70
85	D	76	8AN	C2'-C3'-C4'	2.19	105.69	102.70
85	C	76	8AN	N9-C8-N7	-2.11	110.94	113.94
85	D	76	8AN	N9-C8-N7	-2.11	110.94	113.94

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
85	C	76	8AN	C4'-C5'-O5'-P
85	D	76	8AN	C4'-C5'-O5'-P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no oligosaccharides 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	20,23,23	3.56	15 (75%)	23,30,30	2.73	12 (52%)
87	SPS	D	3401	88	20,23,23	3.58	14 (70%)	23,30,30	2.98	14 (60%)

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	-	2/15/18/18	0/1/1/1
87	SPS	D	3401	88	-	5/15/18/18	0/1/1/1

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	D	3401	SPS	C9-C10	-7.95	1.31	1.48
87	C	3401	SPS	C9-C10	-7.87	1.31	1.48
87	C	3401	SPS	C9-C8	6.61	1.52	1.33
87	D	3401	SPS	C9-C8	6.60	1.52	1.33
87	D	3401	SPS	O13-C13	-5.75	1.18	1.42
87	C	3401	SPS	O13-C13	-5.36	1.19	1.42
87	C	3401	SPS	C10-N11	4.86	1.45	1.34
87	C	3401	SPS	O15-S15	4.24	1.65	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	D	3401	SPS	O15-S15	4.11	1.64	1.50
87	D	3401	SPS	C10-N11	3.96	1.43	1.34
87	D	3401	SPS	C6-C1	-3.79	1.37	1.45
87	D	3401	SPS	C5-N4	-3.76	1.33	1.38
87	C	3401	SPS	C5-N4	-3.65	1.33	1.38
87	C	3401	SPS	C6-C1	-3.19	1.39	1.45
87	C	3401	SPS	O10-C10	-3.07	1.18	1.24
87	D	3401	SPS	O10-C10	-3.05	1.18	1.24
87	C	3401	SPS	C1-N2	-2.95	1.33	1.38
87	D	3401	SPS	C1-N2	-2.90	1.33	1.38
87	D	3401	SPS	O1-C1	-2.67	1.18	1.23
87	C	3401	SPS	C8-C6	2.66	1.54	1.46
87	C	3401	SPS	O1-C1	-2.56	1.18	1.23
87	D	3401	SPS	O3-C3	-2.44	1.18	1.23
87	D	3401	SPS	C3-N4	-2.44	1.33	1.37
87	C	3401	SPS	C3-N4	-2.35	1.33	1.37
87	C	3401	SPS	C7-C5	2.32	1.53	1.49
87	C	3401	SPS	O3-C3	-2.27	1.18	1.23
87	D	3401	SPS	C3-N2	-2.24	1.33	1.37
87	D	3401	SPS	C7-C5	2.09	1.53	1.49
87	C	3401	SPS	C3-N2	-2.06	1.34	1.37

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
87	D	3401	SPS	C7-C5-C6	-5.50	119.35	126.47
87	C	3401	SPS	C7-C5-C6	-5.45	119.41	126.47
87	C	3401	SPS	C7-C5-N4	5.40	119.70	113.42
87	D	3401	SPS	O15-S15-C14	5.32	113.26	106.12
87	D	3401	SPS	C7-C5-N4	5.25	119.53	113.42
87	D	3401	SPS	C1-N2-C3	-4.08	120.75	126.37
87	D	3401	SPS	C5-N4-C3	-3.87	120.71	123.70
87	C	3401	SPS	C18-S17-C16	3.82	110.32	100.14
87	D	3401	SPS	C6-C1-N2	3.76	121.02	114.45
87	C	3401	SPS	C9-C10-N11	3.54	120.66	114.61
87	C	3401	SPS	C5-N4-C3	-3.38	121.09	123.70
87	D	3401	SPS	C9-C10-N11	3.33	120.30	114.61
87	D	3401	SPS	O13-C13-C12	3.26	119.92	111.73
87	D	3401	SPS	O10-C10-N11	-3.21	118.25	122.44
87	C	3401	SPS	O15-S15-C14	3.20	110.41	106.12
87	C	3401	SPS	C6-C1-N2	3.18	120.01	114.45
87	C	3401	SPS	C1-N2-C3	-3.13	122.05	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
87	C	3401	SPS	O13-C13-C12	3.07	119.44	111.73
87	C	3401	SPS	O10-C10-N11	-2.72	118.88	122.44
87	D	3401	SPS	C18-S17-C16	2.70	107.34	100.14
87	D	3401	SPS	N4-C3-N2	2.61	119.84	115.74
87	D	3401	SPS	C14-C12-C13	-2.57	106.43	111.72
87	C	3401	SPS	N4-C3-N2	2.25	119.27	115.74
87	D	3401	SPS	C6-C5-N4	2.11	121.12	118.62
87	D	3401	SPS	O1-C1-C6	-2.10	121.35	125.98
87	C	3401	SPS	O15-S15-C16	2.02	108.87	106.47

There are no chirality outliers.

All (7) torsion outliers are listed below:

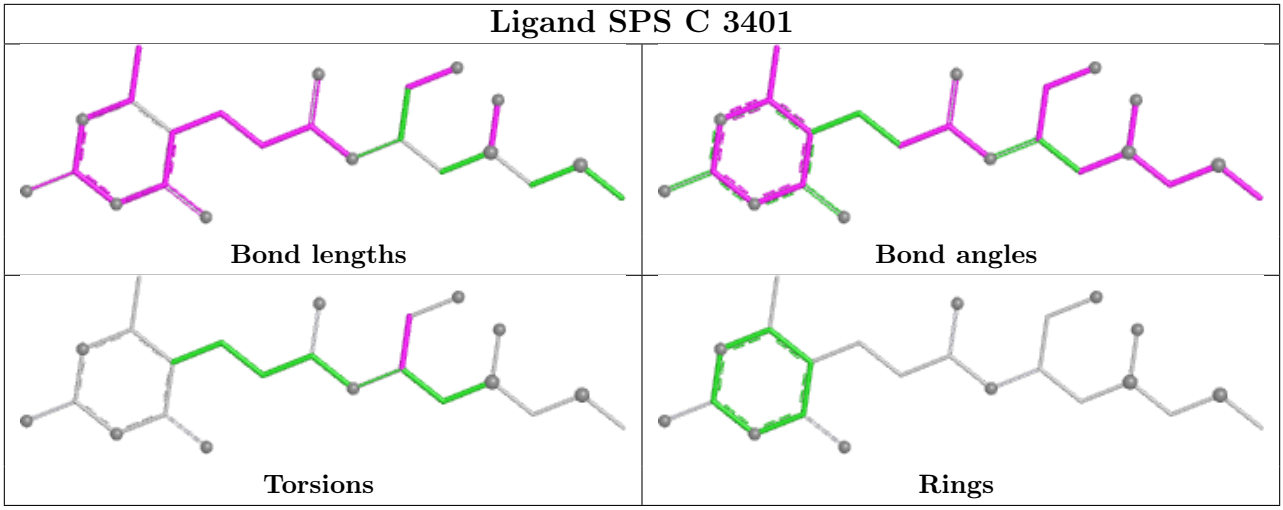
Mol	Chain	Res	Type	Atoms
87	C	3401	SPS	C14-C12-C13-O13
87	D	3401	SPS	C14-C12-C13-O13
87	D	3401	SPS	C12-C14-S15-O15
87	D	3401	SPS	C12-C14-S15-C16
87	C	3401	SPS	N11-C12-C13-O13
87	D	3401	SPS	N11-C12-C14-S15
87	D	3401	SPS	C5-C6-C8-C9

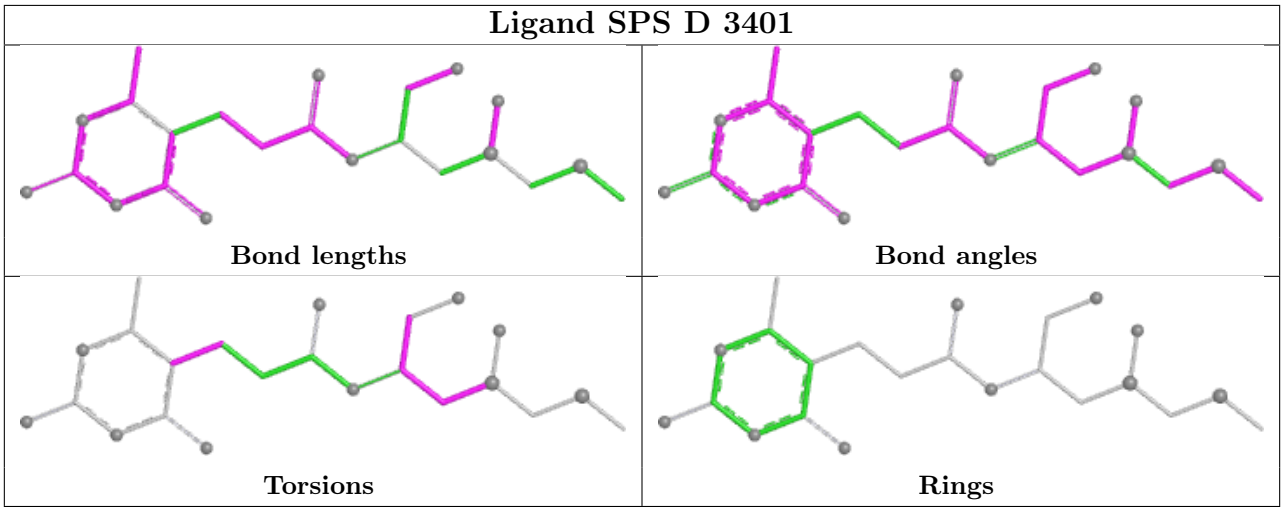
There are no ring outliers.

1 monomer is involved in 6 short contacts:

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

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





5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
81	m2	2
1	2	2
35	sM	1
35	SM	1
12	c0	1
85	C	1
85	D	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	C	77:PRO	C	78:PRO	N	5.78
1	D	77:PRO	C	78:PRO	N	5.62
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, 95^{th} 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%)	0.75	120 (6%) 24 13	35, 88, 194, 293	1 (0%)
1	6	1795/1800 (99%)	0.59	84 (4%) 36 19	28, 78, 178, 271	1 (0%)
2	S0	206/251 (82%)	1.77	73 (35%) 1 0	98, 124, 141, 156	0
2	s0	206/251 (82%)	1.31	34 (16%) 4 2	77, 102, 120, 127	0
3	S1	214/254 (84%)	2.06	100 (46%) 0 0	101, 160, 206, 217	0
3	s1	216/254 (85%)	0.89	17 (7%) 18 10	68, 87, 112, 120	0
4	S2	217/253 (85%)	1.21	30 (13%) 6 4	74, 95, 116, 124	0
4	s2	217/253 (85%)	1.04	24 (11%) 10 5	60, 80, 95, 112	0
5	S3	223/239 (93%)	1.28	32 (14%) 6 3	80, 99, 136, 152	0
5	s3	223/239 (93%)	1.45	47 (21%) 2 1	78, 121, 152, 164	0
6	S4	260/260 (100%)	1.18	32 (12%) 8 5	60, 95, 109, 144	0
6	s4	260/260 (100%)	1.08	26 (10%) 12 6	52, 85, 99, 129	0
7	S5	206/224 (91%)	1.75	72 (34%) 1 0	103, 134, 153, 168	0
7	s5	206/224 (91%)	1.75	68 (33%) 1 0	87, 120, 139, 153	0
8	S6	226/236 (95%)	1.75	76 (33%) 1 0	63, 105, 134, 163	0
8	s6	218/236 (92%)	1.17	42 (19%) 3 1	50, 87, 112, 126	0
9	S7	184/189 (97%)	1.89	71 (38%) 1 0	94, 134, 175, 186	0
9	s7	186/189 (98%)	1.46	41 (22%) 2 1	74, 118, 168, 174	0
10	S8	188/200 (94%)	1.07	19 (10%) 12 6	56, 77, 118, 130	0
10	s8	188/200 (94%)	1.13	30 (15%) 5 2	47, 71, 117, 137	0
11	S9	185/196 (94%)	1.44	46 (24%) 2 1	78, 106, 152, 185	0
11	s9	185/196 (94%)	1.26	27 (14%) 6 3	67, 89, 135, 160	0
12	C0	96/105 (91%)	1.67	33 (34%) 1 0	88, 122, 166, 181	0
12	c0	96/105 (91%)	1.90	42 (43%) 0 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%)	1.13	23 (14%)	5	3	61, 74, 133, 148	0
13	c1	146/155 (94%)	1.10	21 (14%)	6	3	52, 69, 101, 130	0
14	C2	124/142 (87%)	1.87	49 (39%)	1	0	162, 188, 207, 214	0
14	c2	124/142 (87%)	2.35	69 (55%)	0	0	211, 238, 259, 264	0
15	C3	150/150 (100%)	1.25	22 (14%)	6	3	70, 89, 114, 119	0
15	c3	150/150 (100%)	0.81	10 (6%)	24	13	56, 74, 96, 99	0
16	C4	127/136 (93%)	2.22	70 (55%)	0	0	68, 155, 181, 187	0
16	c4	128/136 (94%)	0.85	10 (7%)	19	10	48, 90, 104, 109	0
17	C5	124/141 (87%)	1.46	23 (18%)	3	1	82, 102, 124, 162	0
17	c5	135/141 (95%)	1.47	31 (22%)	2	1	73, 105, 118, 128	0
18	C6	141/142 (99%)	1.80	50 (35%)	1	0	83, 118, 125, 128	0
18	c6	142/142 (100%)	1.93	52 (36%)	1	0	74, 113, 131, 136	0
19	C7	120/136 (88%)	1.70	42 (35%)	1	0	91, 114, 151, 157	0
19	c7	117/136 (86%)	1.77	45 (38%)	1	0	80, 106, 135, 150	0
20	C8	145/145 (100%)	1.59	39 (26%)	1	1	77, 114, 154, 160	0
20	c8	145/145 (100%)	1.31	21 (14%)	6	3	87, 102, 141, 147	0
21	C9	143/143 (100%)	1.73	46 (32%)	1	0	87, 114, 133, 142	0
21	c9	143/143 (100%)	1.34	27 (18%)	3	1	81, 103, 127, 136	0
22	D0	107/120 (89%)	1.87	46 (42%)	0	0	74, 120, 154, 157	0
22	d0	110/120 (91%)	1.67	32 (29%)	1	1	75, 132, 171, 177	0
23	D1	87/87 (100%)	1.27	16 (18%)	3	1	98, 107, 135, 144	0
23	d1	87/87 (100%)	0.92	8 (9%)	14	8	75, 89, 116, 124	0
24	D2	129/129 (100%)	1.39	23 (17%)	4	2	70, 88, 96, 104	0
24	d2	129/129 (100%)	0.75	5 (3%)	43	24	58, 71, 78, 87	0
25	D3	144/144 (100%)	0.96	18 (12%)	8	5	61, 67, 77, 101	0
25	d3	144/144 (100%)	0.64	7 (4%)	35	18	50, 56, 71, 91	0
26	D4	134/134 (100%)	1.20	17 (12%)	8	4	73, 107, 120, 134	0
26	d4	134/134 (100%)	1.34	28 (20%)	2	1	61, 92, 108, 118	0
27	D5	70/107 (65%)	1.77	23 (32%)	1	0	130, 149, 160, 161	0
27	d5	69/107 (64%)	1.76	21 (30%)	1	1	106, 132, 148, 150	0
28	D6	97/97 (100%)	2.01	47 (48%)	0	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%)	0.84	6 (6%) 26 14	53, 65, 110, 117	0
29	D7	81/81 (100%)	1.55	19 (23%) 2 1	90, 108, 149, 151	0
29	d7	81/81 (100%)	1.04	4 (4%) 35 18	72, 88, 139, 143	0
30	D8	63/66 (95%)	2.09	26 (41%) 0 0	114, 147, 161, 164	0
30	d8	63/66 (95%)	1.64	20 (31%) 1 1	102, 129, 141, 144	0
31	D9	53/55 (96%)	1.20	7 (13%) 7 4	77, 82, 101, 110	0
31	d9	53/55 (96%)	1.30	10 (18%) 3 1	74, 86, 131, 153	0
32	E0	60/60 (100%)	1.59	24 (40%) 1 0	72, 106, 148, 150	0
33	E1	71/76 (93%)	2.05	32 (45%) 0 0	114, 147, 184, 189	0
33	e1	76/76 (100%)	2.84	47 (61%) 0 0	110, 188, 229, 231	0
34	SR	318/318 (100%)	1.44	66 (20%) 2 1	111, 133, 149, 177	0
34	sR	318/318 (100%)	1.62	86 (27%) 1 1	122, 149, 166, 179	0
35	SM	133/263 (50%)	1.47	40 (30%) 1 1	53, 92, 148, 165	0
35	sM	84/263 (31%)	1.94	36 (42%) 0 0	45, 107, 147, 150	0
36	1	3148/3396 (92%)	0.04	75 (2%) 59 38	29, 49, 128, 262	0
36	5	3149/3396 (92%)	-0.06	66 (2%) 63 42	26, 46, 119, 209	0
37	3	121/121 (100%)	0.17	0 100 100	37, 69, 84, 91	0
37	7	121/121 (100%)	-0.24	1 (0%) 82 65	30, 49, 60, 72	0
38	4	158/158 (100%)	-0.07	1 (0%) 85 70	34, 49, 87, 132	0
38	8	158/158 (100%)	0.08	4 (2%) 58 37	37, 55, 91, 120	0
39	L2	252/253 (99%)	0.37	7 (2%) 55 34	33, 51, 66, 86	0
39	l2	252/253 (99%)	0.36	7 (2%) 55 34	32, 53, 70, 75	0
40	L3	386/386 (100%)	0.42	9 (2%) 61 39	32, 56, 69, 83	0
40	l3	386/386 (100%)	0.17	6 (1%) 70 49	26, 44, 57, 80	0
41	L4	361/361 (100%)	0.22	7 (1%) 66 45	30, 49, 68, 75	0
41	l4	361/361 (100%)	0.34	4 (1%) 78 59	30, 53, 73, 85	0
42	L5	296/296 (100%)	0.86	18 (6%) 27 15	51, 81, 100, 123	0
42	l5	294/296 (99%)	0.55	15 (5%) 33 18	39, 56, 78, 92	0
43	L6	156/175 (89%)	0.32	4 (2%) 57 36	44, 52, 70, 83	0
43	l6	157/175 (89%)	0.46	8 (5%) 33 18	45, 52, 76, 88	0
44	L7	222/243 (91%)	0.11	6 (2%) 56 35	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%)	0.09	0 100 100	32, 42, 82, 119	0
45	L8	233/255 (91%)	0.94	20 (8%) 16 9	61, 75, 118, 126	0
45	l8	231/255 (90%)	1.01	30 (12%) 7 4	67, 81, 112, 123	0
46	L9	191/191 (100%)	0.59	5 (2%) 57 36	52, 65, 79, 94	0
46	l9	191/191 (100%)	0.25	2 (1%) 79 61	40, 52, 72, 82	0
47	M0	211/220 (95%)	0.52	9 (4%) 40 22	39, 61, 96, 108	0
47	m0	213/220 (96%)	0.57	12 (5%) 30 16	33, 54, 75, 96	0
48	M1	169/173 (97%)	0.85	10 (5%) 28 15	63, 84, 99, 104	0
48	m1	169/173 (97%)	0.37	1 (0%) 85 70	42, 60, 72, 78	0
49	M3	193/198 (97%)	0.41	7 (3%) 46 26	33, 58, 97, 118	0
49	m3	194/198 (97%)	0.56	7 (3%) 46 26	36, 64, 106, 125	0
50	M4	136/137 (99%)	0.34	7 (5%) 33 18	49, 55, 69, 80	0
50	m4	137/137 (100%)	0.30	4 (2%) 53 32	44, 50, 66, 87	0
51	M5	203/203 (100%)	0.37	5 (2%) 58 37	31, 48, 58, 62	0
51	m5	203/203 (100%)	0.53	6 (2%) 52 31	35, 53, 66, 69	0
52	M6	197/198 (99%)	0.70	17 (8%) 16 9	35, 42, 57, 59	0
52	m6	197/198 (99%)	0.72	21 (10%) 11 6	30, 36, 55, 58	0
53	M7	183/183 (100%)	0.52	16 (8%) 16 9	36, 47, 115, 160	0
53	m7	155/183 (84%)	0.12	1 (0%) 85 70	33, 41, 58, 78	0
54	M8	185/185 (100%)	0.26	6 (3%) 50 30	37, 49, 66, 79	0
54	m8	185/185 (100%)	0.35	2 (1%) 78 59	36, 52, 62, 67	0
55	M9	188/188 (100%)	0.98	22 (11%) 9 5	51, 67, 166, 188	0
55	m9	188/188 (100%)	0.75	11 (5%) 28 15	46, 60, 154, 171	0
56	N0	172/172 (100%)	0.40	8 (4%) 36 19	43, 53, 68, 72	0
56	n0	172/172 (100%)	0.20	7 (4%) 41 23	37, 45, 58, 67	0
57	N1	159/159 (100%)	0.63	12 (7%) 20 11	37, 52, 95, 105	0
57	n1	159/159 (100%)	0.37	6 (3%) 44 25	32, 42, 77, 85	0
58	N2	100/120 (83%)	1.25	17 (17%) 4 2	86, 104, 112, 116	0
58	n2	98/120 (81%)	1.09	10 (10%) 12 6	74, 91, 101, 106	0
59	N3	136/136 (100%)	0.36	3 (2%) 62 41	40, 52, 66, 76	0
59	n3	136/136 (100%)	0.09	3 (2%) 62 41	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%)	1.41	28 (28%) 1 1	52, 64, 164, 171	0
60	n4	135/155 (87%)	1.02	23 (17%) 4 2	42, 96, 146, 170	0
61	N5	121/141 (85%)	0.59	5 (4%) 41 23	49, 62, 75, 108	0
61	n5	120/141 (85%)	0.69	8 (6%) 24 13	49, 63, 79, 92	0
62	N6	126/126 (100%)	0.33	2 (1%) 70 49	40, 58, 69, 76	0
62	n6	126/126 (100%)	0.49	3 (2%) 59 38	43, 59, 74, 81	0
63	N7	135/135 (100%)	0.77	8 (5%) 28 15	71, 88, 99, 102	0
63	n7	135/135 (100%)	1.13	20 (14%) 5 3	75, 91, 103, 108	0
64	N8	148/148 (100%)	0.31	1 (0%) 84 68	28, 50, 72, 83	0
64	n8	148/148 (100%)	0.31	0 100 100	27, 53, 72, 76	0
65	N9	58/58 (100%)	0.57	4 (6%) 23 12	32, 58, 105, 120	0
65	n9	58/58 (100%)	0.69	7 (12%) 8 5	31, 53, 78, 87	0
66	O0	97/104 (93%)	0.80	6 (6%) 26 14	70, 82, 105, 111	0
66	o0	100/104 (96%)	0.77	7 (7%) 22 12	69, 84, 112, 120	0
67	O1	109/112 (97%)	0.66	5 (4%) 37 20	50, 65, 98, 109	0
67	o1	109/112 (97%)	0.42	5 (4%) 37 20	41, 54, 89, 100	0
68	O2	127/129 (98%)	0.12	3 (2%) 59 38	30, 44, 58, 78	0
68	o2	127/129 (98%)	0.31	5 (3%) 43 24	27, 48, 63, 74	0
69	O3	106/106 (100%)	0.24	4 (3%) 44 25	36, 42, 67, 80	0
69	o3	106/106 (100%)	0.17	2 (1%) 66 45	33, 42, 65, 79	0
70	O4	112/119 (94%)	0.89	10 (8%) 15 8	45, 62, 102, 109	0
70	o4	112/119 (94%)	0.84	6 (5%) 31 17	45, 61, 107, 115	0
71	O5	119/119 (100%)	0.63	4 (3%) 48 28	44, 65, 72, 75	0
71	o5	119/119 (100%)	0.84	14 (11%) 9 5	49, 67, 82, 95	0
72	O6	99/99 (100%)	0.79	6 (6%) 27 15	55, 64, 97, 112	0
72	o6	99/99 (100%)	0.64	2 (2%) 65 44	58, 70, 95, 115	0
73	O7	87/87 (100%)	0.29	3 (3%) 48 28	33, 39, 59, 68	0
73	o7	87/87 (100%)	0.42	5 (5%) 29 16	34, 43, 69, 81	0
74	O8	77/77 (100%)	1.04	8 (10%) 11 6	72, 87, 111, 117	0
74	o8	77/77 (100%)	1.00	8 (10%) 11 6	71, 87, 102, 105	0
75	O9	50/50 (100%)	0.63	4 (8%) 18 10	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%)	0.45	1 (2%) 65 44	43, 49, 57, 59	0
76	Q0	52/52 (100%)	0.44	2 (3%) 44 25	43, 50, 71, 79	0
76	q0	52/52 (100%)	-0.02	0 100 100	34, 39, 54, 57	0
77	Q1	25/25 (100%)	0.73	1 (4%) 42 23	51, 56, 58, 60	0
77	q1	25/25 (100%)	0.44	0 100 100	43, 46, 48, 49	0
78	Q2	105/105 (100%)	0.25	4 (3%) 44 25	34, 51, 76, 103	0
78	q2	105/105 (100%)	0.21	2 (1%) 66 45	35, 46, 64, 97	0
79	Q3	91/91 (100%)	0.36	0 100 100	41, 56, 73, 81	0
79	q3	91/91 (100%)	0.39	1 (1%) 78 59	37, 53, 67, 78	0
80	e0	62/62 (100%)	0.92	7 (11%) 10 5	57, 88, 121, 129	0
81	m2	0/160	-	-	-	-
82	p0	143/311 (45%)	1.82	54 (37%) 1 0	98, 131, 238, 246	0
83	p1	0/47	-	-	-	-
84	p2	0/46	-	-	-	-
85	C	4/5 (80%)	0.32	0 100 100	34, 36, 37, 37	0
85	D	4/5 (80%)	-0.41	0 100 100	33, 34, 34, 39	0
All	All	33054/35334 (93%)	0.70	3363 (10%) 12 6	26, 68, 150, 293	2 (0%)

All (3363) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
73	o7	88	ALA	10.4
60	N4	83	THR	10.0
8	S6	80	ASN	9.3
60	N4	86	SER	9.0
33	e1	89	LYS	8.3
22	d0	64	LYS	8.3
7	S5	75	GLY	8.2
33	e1	85	TYR	8.1
33	e1	86	THR	8.0
13	C1	146	ALA	7.9
42	L5	6	ASP	7.1
8	S6	77	LEU	7.1
8	S6	79	LYS	7.0
39	L2	253	GLN	7.0
73	O7	88	ALA	7.0
60	N4	84	GLY	6.9

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Mol	Chain	Res	Type	RSRZ
14	c2	136	ILE	6.9
18	c6	124	PRO	6.8
33	e1	77	GLY	6.7
18	c6	83	GLN	6.6
33	e1	87	THR	6.5
3	S1	32	ILE	6.5
4	s2	90	THR	6.5
60	N4	82	ILE	6.5
1	2	1699	G	6.4
7	S5	37	GLN	6.3
9	S7	98	ILE	6.3
7	S5	71	ALA	6.3
33	e1	88	PRO	6.3
15	C3	14	SER	6.3
53	M7	184	ALA	6.1
8	S6	148	SER	6.1
3	S1	92	GLN	6.1
28	D6	2	PRO	6.1
7	s5	77	TYR	6.0
9	S7	108	GLN	5.9
27	d5	50	ILE	5.9
30	D8	16	LEU	5.9
30	D8	28	VAL	5.9
16	C4	18	ARG	5.9
5	s3	208	ILE	5.8
75	O9	2	ALA	5.8
11	s9	145	SER	5.8
9	S7	109	VAL	5.7
21	c9	55	TYR	5.7
12	C0	39	ASN	5.7
1	6	678	A	5.7
12	c0	84	GLU	5.7
52	m6	184	THR	5.7
8	S6	75	LEU	5.7
30	D8	24	GLY	5.6
1	2	1756[A]	A	5.6
14	c2	123	VAL	5.6
18	c6	44	LEU	5.6
8	S6	78	THR	5.6
20	c8	18	LEU	5.6
82	p0	192	ASP	5.5
3	S1	91	VAL	5.5

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Mol	Chain	Res	Type	RSRZ
14	c2	126	TRP	5.5
35	sM	34	LYS	5.5
22	d0	54	GLY	5.5
1	2	1708	U	5.5
33	e1	84	VAL	5.4
33	E1	87	THR	5.4
9	S7	115	SER	5.4
53	M7	162	GLU	5.3
34	SR	115	ILE	5.3
53	M7	182	ILE	5.3
1	2	1696	G	5.3
60	N4	88	ASP	5.3
2	S0	99	ALA	5.3
42	L5	3	PHE	5.2
7	s5	133	VAL	5.2
1	2	656	G	5.2
14	c2	102	GLY	5.2
45	l8	109	LEU	5.2
60	N4	87	LEU	5.2
1	2	173	A	5.1
33	e1	80	ARG	5.1
1	6	679	U	5.1
3	S1	46	THR	5.1
47	M0	221	ALA	5.1
36	1	2205	U	5.1
17	C5	104	GLN	5.1
34	sR	158	PRO	5.1
60	N4	75	THR	5.1
14	c2	59	LEU	5.1
7	S5	70	VAL	5.0
8	s6	162	VAL	5.0
13	C1	3	THR	5.0
1	2	1370	U	5.0
6	s4	13	ALA	5.0
42	L5	2	ALA	5.0
13	C1	150	ASN	5.0
13	c1	3	THR	5.0
34	sR	115	ILE	5.0
60	N4	85	ALA	5.0
28	D6	3	LYS	5.0
6	S4	26	CYS	5.0
3	S1	131	ASP	4.9

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Mol	Chain	Res	Type	RSRZ
39	l2	253	GLN	4.9
3	S1	98	THR	4.9
27	D5	73	GLY	4.9
18	C6	17	THR	4.9
53	M7	161	ALA	4.9
14	c2	93	ASP	4.9
18	C6	40	GLU	4.8
56	n0	1	MET	4.8
60	N4	89	LEU	4.8
1	2	1707	A	4.8
16	C4	89	THR	4.8
17	c5	134	THR	4.8
7	S5	36	ALA	4.8
15	C3	15	ALA	4.8
11	s9	2	PRO	4.8
3	S1	54	LEU	4.8
16	C4	75	GLY	4.8
10	s8	61	GLU	4.8
60	n4	66	GLU	4.8
7	S5	172	ILE	4.8
5	s3	205	ALA	4.8
20	C8	146	ALA	4.8
34	SR	284	ALA	4.8
34	sR	27	ALA	4.8
16	C4	39	ILE	4.8
19	c7	42	GLN	4.7
33	e1	93	HIS	4.7
18	c6	79	TYR	4.7
14	C2	59	LEU	4.7
14	c2	64	SER	4.7
33	e1	105	TYR	4.7
7	s5	108	LEU	4.7
17	C5	101	ALA	4.7
1	2	261	U	4.7
10	s8	176	SER	4.7
7	s5	75	GLY	4.7
14	c2	75	VAL	4.7
19	c7	65	PRO	4.7
33	E1	103	LEU	4.7
16	C4	120	PRO	4.6
3	s1	54	LEU	4.6
18	c6	2	SER	4.6

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Mol	Chain	Res	Type	RSRZ
1	2	913	G	4.6
30	D8	53	ILE	4.6
3	S1	55	LYS	4.6
30	d8	24	GLY	4.6
3	S1	20	VAL	4.6
57	n1	86	GLU	4.6
20	C8	18	LEU	4.6
22	D0	81	THR	4.6
18	c6	11	GLY	4.6
36	5	1565	G	4.6
2	S0	158	VAL	4.6
14	c2	92	ALA	4.6
35	SM	85	SER	4.6
14	C2	136	ILE	4.6
2	S0	207	PRO	4.6
45	l8	123	GLN	4.6
4	S2	62	PRO	4.5
1	2	1702	A	4.5
13	C1	145	ALA	4.5
9	S7	100	PRO	4.5
9	s7	108	GLN	4.5
16	C4	15	GLY	4.5
58	N2	89	LEU	4.5
45	l8	104	GLU	4.5
18	c6	115	THR	4.5
35	SM	87	THR	4.5
34	sR	136	ILE	4.5
8	S6	145	PHE	4.5
30	D8	49	ARG	4.5
34	SR	131	ILE	4.5
33	E1	147	VAL	4.5
9	S7	123	ASP	4.4
18	c6	119	ALA	4.4
19	c7	97	ASN	4.4
15	C3	16	ILE	4.4
29	d7	24	LEU	4.4
1	2	1697	G	4.4
9	s7	43	PHE	4.4
13	C1	152	GLN	4.4
1	2	1686	C	4.4
2	S0	126	PRO	4.4
16	C4	16	VAL	4.4

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Mol	Chain	Res	Type	RSRZ
17	c5	74	ALA	4.4
71	o5	118	ILE	4.4
18	C6	74	HIS	4.4
8	s6	88	ARG	4.4
56	N0	1	MET	4.4
1	2	657	U	4.4
35	sM	25	ILE	4.4
7	s5	92	ARG	4.4
7	s5	94	THR	4.4
10	S8	152	ILE	4.4
13	C1	151	LYS	4.4
33	E1	90	LYS	4.4
14	C2	107	ASP	4.4
30	D8	48	VAL	4.4
14	c2	128	ALA	4.3
43	l6	3	ALA	4.3
7	s5	76	ARG	4.3
32	E0	60	PRO	4.3
7	s5	36	ALA	4.3
16	C4	40	ALA	4.3
8	S6	149	LYS	4.3
33	e1	100	LEU	4.3
40	L3	387	LEU	4.3
13	c1	2	SER	4.3
3	S1	84	ILE	4.3
31	d9	29	GLY	4.3
45	l8	110	THR	4.3
52	m6	63	ALA	4.3
8	S6	226	ILE	4.3
1	2	1698	G	4.3
36	5	1566	A	4.3
21	C9	38	LYS	4.3
53	M7	160	ALA	4.3
7	S5	77	TYR	4.3
9	s7	63	PRO	4.2
10	s8	58	LEU	4.2
34	SR	279	ALA	4.2
35	SM	15	ALA	4.2
22	D0	19	ILE	4.2
31	d9	55	PHE	4.2
55	M9	78	TYR	4.2
35	sM	95	LYS	4.2

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Mol	Chain	Res	Type	RSRZ
8	S6	99	GLY	4.2
7	s5	84	LYS	4.2
56	n0	130	GLU	4.2
9	s7	103	SER	4.2
1	6	1082	C	4.2
18	c6	46	PHE	4.2
20	c8	121	ALA	4.2
60	n4	68	ALA	4.2
33	e1	79	LYS	4.2
49	M3	41	THR	4.2
45	L8	116	VAL	4.2
52	M6	52	LEU	4.2
6	s4	26	CYS	4.2
1	2	506	A	4.2
4	s2	92	ALA	4.2
34	sR	257	ALA	4.2
35	sM	35	ALA	4.2
9	S7	103	SER	4.1
19	c7	60	ARG	4.1
20	c8	3	LEU	4.1
7	S5	98	MET	4.1
3	S1	89	ASP	4.1
58	N2	48	GLY	4.1
22	d0	20	ILE	4.1
12	C0	96	ASN	4.1
4	s2	91	ARG	4.1
35	SM	14	ASP	4.1
45	l8	124	ASP	4.1
8	S6	66	GLY	4.1
18	c6	57	LEU	4.1
63	n7	75	VAL	4.1
18	C6	70	THR	4.1
33	e1	92	LYS	4.1
55	M9	189	ALA	4.1
14	C2	126	TRP	4.1
32	E0	61	SER	4.1
3	S1	114	VAL	4.1
18	c6	132	LYS	4.1
33	e1	81	LYS	4.1
18	C6	118	ILE	4.1
42	l5	297	GLN	4.1
26	D4	70	VAL	4.0

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Mol	Chain	Res	Type	RSRZ
47	m0	103	LEU	4.0
16	C4	119	THR	4.0
22	d0	67	THR	4.0
80	e0	62	VAL	4.0
10	S8	106	ALA	4.0
28	D6	6	ALA	4.0
26	d4	128	LYS	4.0
30	D8	45	LYS	4.0
52	M6	3	VAL	4.0
6	S4	253	ASP	4.0
8	S6	89	ASP	4.0
21	C9	8	ASP	4.0
33	E1	104	SER	4.0
20	c8	20	THR	4.0
18	c6	12	LYS	4.0
17	c5	103	ASN	4.0
18	c6	121	SER	4.0
79	q3	2	ALA	4.0
15	C3	62	GLN	4.0
17	c5	137	ARG	4.0
50	m4	40	ASP	4.0
20	C8	17	LEU	4.0
22	d0	93	LEU	4.0
31	D9	6	VAL	3.9
58	N2	27	VAL	3.9
30	D8	27	GLN	3.9
8	S6	73	ILE	3.9
10	s8	34	ALA	3.9
28	D6	47	ALA	3.9
47	m0	221	ALA	3.9
19	c7	59	LYS	3.9
1	6	1584	G	3.9
17	c5	78	THR	3.9
82	p0	281	THR	3.9
36	5	440	A	3.9
17	c5	104	GLN	3.9
33	E1	145	HIS	3.9
34	sR	296	ALA	3.9
71	o5	120	ALA	3.9
3	S1	188	LEU	3.9
18	c6	38	LEU	3.9
19	c7	57	LEU	3.9

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Mol	Chain	Res	Type	RSRZ
55	M9	184	LEU	3.9
8	S6	222	GLU	3.9
8	s6	80	ASN	3.9
33	e1	98	VAL	3.9
18	C6	114	ARG	3.9
14	c2	103	LEU	3.9
47	m0	195	ALA	3.9
18	C6	123	ARG	3.9
14	c2	65	SER	3.9
2	s0	162	CYS	3.9
22	D0	119	ALA	3.9
7	S5	76	ARG	3.9
16	C4	133	ARG	3.9
21	C9	114	VAL	3.9
55	M9	51	VAL	3.9
19	c7	25	THR	3.9
1	2	174	U	3.9
4	s2	93	GLY	3.9
19	C7	2	GLY	3.9
22	D0	20	ILE	3.9
55	M9	52	LYS	3.9
60	N4	90	ILE	3.9
21	c9	37	VAL	3.8
33	e1	78	LYS	3.8
1	6	659	C	3.8
36	1	1581	C	3.8
1	6	676	G	3.8
7	S5	96	SER	3.8
5	S3	21	LEU	3.8
33	e1	103	LEU	3.8
2	S0	32	HIS	3.8
33	e1	152	ALA	3.8
52	m6	59	ARG	3.8
60	N4	93	ARG	3.8
33	E1	114	VAL	3.8
34	SR	283	LYS	3.8
11	S9	130	THR	3.8
16	C4	23	PHE	3.8
9	S7	68	ALA	3.8
1	2	696	C	3.8
27	d5	59	TYR	3.8
33	e1	115	THR	3.8

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Mol	Chain	Res	Type	RSRZ
26	D4	61	ARG	3.8
10	s8	40	ALA	3.8
58	N2	46	ALA	3.8
33	e1	104	SER	3.8
7	s5	68	ILE	3.8
9	s7	102	PRO	3.8
13	c1	4	GLU	3.8
73	o7	23	GLY	3.8
3	S1	217	LEU	3.8
29	D7	61	THR	3.8
32	E0	41	THR	3.8
1	2	1695	G	3.8
20	C8	44	ASN	3.8
45	l8	114	ALA	3.8
8	S6	81	VAL	3.8
24	D2	60	LYS	3.8
27	D5	97	LYS	3.8
3	S1	190	PRO	3.8
14	C2	103	LEU	3.8
82	p0	78	PRO	3.8
1	6	470	A	3.8
16	C4	121	VAL	3.7
11	s9	134	ILE	3.7
8	S6	193	LEU	3.7
80	e0	49	LEU	3.7
82	p0	93	LEU	3.7
23	D1	10	GLU	3.7
11	S9	29	LYS	3.7
8	s6	182	GLN	3.7
1	2	658	C	3.7
2	S0	174	TRP	3.7
11	S9	6	ARG	3.7
20	c8	14	ILE	3.7
35	sM	90	SER	3.7
7	s5	82	PHE	3.7
35	SM	58	GLU	3.7
55	M9	72	GLU	3.7
1	6	1610	G	3.7
36	5	2533	G	3.7
56	N0	2	ALA	3.7
70	O4	2	ALA	3.7
23	D1	32	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
2	S0	193	GLN	3.7
26	d4	106	GLN	3.7
11	S9	38	ASN	3.7
2	s0	98	ILE	3.7
2	S0	2	SER	3.7
3	S1	93	GLY	3.7
78	Q2	106	PHE	3.7
4	S2	88	LYS	3.7
7	S5	41	LYS	3.7
34	sR	72	THR	3.7
2	s0	101	ARG	3.7
10	S8	179	CYS	3.7
33	e1	91	ILE	3.7
9	S7	67	LEU	3.7
34	sR	62	LYS	3.7
15	c3	14	SER	3.7
2	S0	190	ASP	3.7
45	l8	194	THR	3.7
32	E0	56	MET	3.7
42	L5	148	ILE	3.7
56	n0	129	ILE	3.7
14	C2	36	LEU	3.7
14	c2	58	LEU	3.7
7	s5	44	ASN	3.7
82	p0	43	LYS	3.7
34	sR	241	PHE	3.7
9	S7	132	PRO	3.6
36	5	3275	U	3.6
34	SR	96	THR	3.6
2	S0	98	ILE	3.6
3	S1	110	LEU	3.6
9	S7	41	LEU	3.6
45	l8	192	GLN	3.6
9	S7	111	LYS	3.6
28	D6	9	GLY	3.6
9	S7	113	PRO	3.6
35	sM	38	PRO	3.6
19	c7	96	SER	3.6
82	p0	285	SER	3.6
9	S7	119	THR	3.6
16	C4	86	THR	3.6
19	C7	62	GLN	3.6

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Mol	Chain	Res	Type	RSRZ
8	S6	156	PHE	3.6
60	N4	81	PRO	3.6
33	E1	150	VAL	3.6
2	S0	170	ILE	3.6
8	S6	147	LEU	3.6
33	E1	91	ILE	3.6
43	L6	8	LYS	3.6
47	m0	166	ILE	3.6
74	O8	51	LEU	3.6
75	o9	11	GLN	3.6
1	2	134	U	3.6
8	s6	134	GLY	3.6
35	sM	56	GLY	3.6
12	C0	42	VAL	3.6
12	c0	23	ALA	3.6
19	c7	90	ALA	3.6
22	D0	51	VAL	3.6
27	D5	62	VAL	3.6
33	E1	102	VAL	3.6
19	c7	35	CYS	3.6
1	2	1694	A	3.6
36	5	1025	A	3.6
22	D0	108	ILE	3.6
28	D6	76	SER	3.6
60	N4	64	THR	3.6
9	S7	150	GLN	3.6
5	S3	149	ALA	3.6
13	c1	142	VAL	3.6
25	d3	21	ASN	3.6
35	SM	10	ASN	3.6
20	C8	32	LEU	3.6
23	D1	8	LEU	3.6
82	p0	70	LEU	3.6
14	c2	71	ILE	3.6
9	s7	66	SER	3.6
34	sR	166	SER	3.6
82	p0	69	ASP	3.6
82	p0	107	ALA	3.5
20	C8	3	LEU	3.5
33	E1	100	LEU	3.5
9	S7	142	TYR	3.5
36	1	1564	U	3.5

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Mol	Chain	Res	Type	RSRZ
36	1	1955	U	3.5
54	M8	167	SER	3.5
19	c7	62	GLN	3.5
14	C2	101	ALA	3.5
17	c5	4	ALA	3.5
33	e1	82	LYS	3.5
35	sM	128	ALA	3.5
1	2	169	A	3.5
15	C3	53	LEU	3.5
1	6	38	C	3.5
13	c1	42	PHE	3.5
36	1	3155	U	3.5
8	s6	171	LYS	3.5
14	c2	37	VAL	3.5
14	c2	107	ASP	3.5
25	D3	31	LYS	3.5
25	D3	48	HIS	3.5
35	SM	19	VAL	3.5
13	c1	145	ALA	3.5
9	S7	4	PRO	3.5
14	c2	41	LEU	3.5
72	o6	58	ILE	3.5
11	s9	8	TYR	3.5
14	c2	111	ASN	3.5
35	SM	86	ASN	3.5
5	S3	152	PHE	3.5
1	6	720	G	3.5
7	S5	73	THR	3.5
10	s8	179	CYS	3.5
16	C4	38	THR	3.5
14	c2	121	VAL	3.5
42	l5	4	GLN	3.5
44	L7	26	VAL	3.5
6	s4	14	ALA	3.5
16	C4	96	PRO	3.5
5	s3	158	ILE	3.5
5	s3	184	ILE	3.5
16	C4	83	ILE	3.5
19	c7	95	ARG	3.5
8	S6	225	GLU	3.5
6	S4	57	ASN	3.5
8	s6	79	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
12	C0	24	LYS	3.5
27	d5	97	LYS	3.5
82	p0	26	PHE	3.5
19	C7	123	ASN	3.5
7	s5	73	THR	3.5
1	2	1719	A	3.5
14	c2	22	VAL	3.5
20	C8	5	VAL	3.5
16	C4	71	CYS	3.5
13	c1	144	ALA	3.5
16	C4	34	SER	3.5
23	D1	78	LEU	3.5
27	d5	75	LEU	3.5
11	S9	5	PRO	3.5
2	s0	170	ILE	3.5
28	D6	83	ILE	3.5
52	M6	59	ARG	3.5
60	N4	65	GLU	3.4
29	D7	70	LYS	3.4
3	S1	142	PHE	3.4
12	c0	27	PHE	3.4
18	C6	10	PHE	3.4
11	s9	148	VAL	3.4
12	c0	98	ASN	3.4
26	d4	34	ASN	3.4
33	e1	134	ASN	3.4
11	s9	111	THR	3.4
18	c6	54	LEU	3.4
33	E1	86	THR	3.4
74	O8	34	ALA	3.4
19	c7	103	ASP	3.4
26	D4	26	ASP	3.4
31	d9	7	TRP	3.4
34	sR	297	ASP	3.4
18	c6	14	LYS	3.4
3	S1	90	GLU	3.4
36	5	2444	C	3.4
34	SR	186	PHE	3.4
7	S5	74	ALA	3.4
14	c2	23	THR	3.4
22	D0	121	ASN	3.4
47	M0	112	GLN	3.4

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Mol	Chain	Res	Type	RSRZ
20	C8	2	SER	3.4
41	l4	345	GLU	3.4
22	D0	82	TYR	3.4
23	D1	53	TYR	3.4
7	s5	134	VAL	3.4
3	S1	86	LEU	3.4
11	S9	171	ARG	3.4
24	D2	34	ILE	3.4
34	SR	66	HIS	3.4
6	s4	22	LYS	3.4
13	C1	153	PHE	3.4
3	S1	43	VAL	3.4
21	C9	37	VAL	3.4
31	d9	6	VAL	3.4
5	S3	161	GLY	3.4
12	C0	89	ALA	3.4
14	C2	89	ILE	3.4
14	c2	34	THR	3.4
15	c3	66	ILE	3.4
36	1	2207	A	3.4
35	sM	33	LYS	3.4
36	1	1192	C	3.4
22	D0	120	SER	3.4
27	D5	93	SER	3.4
2	s0	146	LEU	3.4
3	S1	88	VAL	3.4
7	s5	70	VAL	3.4
8	S6	137	ARG	3.4
27	D5	103	ARG	3.4
28	D6	33	ASP	3.4
16	C4	92	LYS	3.4
29	D7	62	ILE	3.4
7	s5	30	PRO	3.4
22	D0	70	THR	3.4
28	D6	31	PRO	3.4
33	e1	95	HIS	3.4
35	SM	97	THR	3.4
36	5	2872	A	3.3
7	S5	43	PHE	3.3
17	c5	136	SER	3.3
53	M7	165	VAL	3.3
7	s5	161	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
15	c3	7	ALA	3.3
20	c8	124	GLY	3.3
7	s5	129	PRO	3.3
11	S9	2	PRO	3.3
1	6	656	G	3.3
15	c3	151	ASN	3.3
4	S2	63	VAL	3.3
6	s4	23	LEU	3.3
82	p0	25	LEU	3.3
5	s3	160	SER	3.3
33	e1	94	LYS	3.3
52	m6	89	SER	3.3
55	M9	180	LYS	3.3
6	S4	54	TYR	3.3
13	C1	147	GLY	3.3
76	Q0	77	ILE	3.3
82	p0	276	ALA	3.3
35	sM	39	PRO	3.3
6	s4	9	LEU	3.3
9	S7	93	LEU	3.3
14	c2	36	LEU	3.3
26	d4	125	LEU	3.3
27	D5	69	LEU	3.3
34	SR	61	PHE	3.3
34	sR	81	LEU	3.3
45	L8	240	ASN	3.3
61	n5	24	LEU	3.3
28	D6	18	VAL	3.3
14	c2	25	GLU	3.3
18	c6	40	GLU	3.3
5	s3	193	ALA	3.3
14	c2	89	ILE	3.3
33	E1	152	ALA	3.3
60	n4	122	ALA	3.3
69	o3	107	ILE	3.3
8	S6	169	TYR	3.3
18	c6	49	TYR	3.3
52	m6	56	ASP	3.3
4	s2	89	GLN	3.3
19	c7	67	ARG	3.3
20	C8	16	ARG	3.3
23	d1	87	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
29	D7	26	GLN	3.3
36	5	1567	U	3.3
53	M7	167	ARG	3.3
1	2	697	C	3.3
1	2	870	C	3.3
2	s0	57	LEU	3.3
2	s0	87	LEU	3.3
3	S1	138	PHE	3.3
33	e1	83	LYS	3.3
34	sR	157	VAL	3.3
41	l4	186	LYS	3.3
18	C6	36	ILE	3.3
56	n0	2	ALA	3.3
12	c0	54	TYR	3.3
16	C4	22	SER	3.3
60	N4	72	SER	3.3
2	S0	206	ASP	3.3
34	SR	102	ARG	3.3
7	s5	37	GLN	3.3
34	sR	145	LEU	3.3
36	1	1349	G	3.3
3	S1	151	LYS	3.3
1	6	40	A	3.3
36	5	1764	U	3.3
28	d6	11	ASN	3.3
14	C2	137	MET	3.3
21	C9	67	MET	3.3
36	5	1192	C	3.3
43	l6	130	ILE	3.3
45	l8	100	GLU	3.3
6	S4	203	GLY	3.3
58	n2	48	GLY	3.3
15	C3	13	SER	3.2
16	C4	57	PRO	3.2
3	S1	96	LEU	3.2
8	S6	83	CYS	3.2
8	S6	74	LYS	3.2
28	d6	19	LYS	3.2
9	S7	105	THR	3.2
33	e1	150	VAL	3.2
70	O4	64	THR	3.2
34	SR	180	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
34	sR	284	ALA	3.2
53	M7	183	ALA	3.2
61	n5	50	ALA	3.2
36	1	2095	G	3.2
36	5	1576	G	3.2
38	8	81	U	3.2
39	l2	143	GLU	3.2
49	M3	130	GLY	3.2
14	c2	43	ARG	3.2
1	2	1709	C	3.2
9	S7	99	LEU	3.2
9	s7	16	LEU	3.2
17	C5	53	PRO	3.2
43	l6	11	PRO	3.2
8	S6	144	PHE	3.2
26	d4	72	PHE	3.2
82	p0	86	PHE	3.2
2	S0	30	GLN	3.2
2	S0	162	CYS	3.2
17	C5	105	VAL	3.2
30	d8	48	VAL	3.2
34	SR	6	VAL	3.2
53	M7	166	VAL	3.2
27	d5	56	THR	3.2
18	c6	118	ILE	3.2
22	d0	99	ILE	3.2
46	l9	1	MET	3.2
18	C6	3	ALA	3.2
27	D5	36	ALA	3.2
34	sR	251	TRP	3.2
35	sM	60	ALA	3.2
82	p0	288	ALA	3.2
15	C3	151	ASN	3.2
35	SM	89	ARG	3.2
12	c0	25	LYS	3.2
50	M4	43	LYS	3.2
34	SR	57	PRO	3.2
1	2	145	A	3.2
8	s6	144	PHE	3.2
16	C4	29	HIS	3.2
28	D6	17	HIS	3.2
1	2	172	C	3.2

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Mol	Chain	Res	Type	RSRZ
35	SM	11	ASP	3.2
2	S0	159	ALA	3.2
82	p0	184	GLY	3.2
8	S6	91	GLU	3.2
22	d0	83	GLU	3.2
43	l6	129	GLU	3.2
18	C6	12	LYS	3.2
18	C6	79	TYR	3.2
21	c9	18	TYR	3.2
14	C2	82	PRO	3.2
70	O4	5	VAL	3.2
20	c8	2	SER	3.2
2	s0	190	ASP	3.2
17	C5	81	ARG	3.2
21	C9	57	ARG	3.2
34	sR	122	ILE	3.2
34	sR	168	THR	3.2
15	C3	57	ALA	3.2
36	1	1103	A	3.2
38	8	80	A	3.2
52	m6	61	ALA	3.2
19	c7	68	GLY	3.2
33	e1	99	LYS	3.2
36	5	1349	G	3.2
57	N1	62	GLY	3.2
65	n9	23	LYS	3.2
3	s1	228	LEU	3.2
7	s5	174	LEU	3.2
9	S7	38	LEU	3.2
12	C0	84	GLU	3.2
17	C5	69	GLU	3.2
36	5	1016	C	3.2
36	5	1582	C	3.2
20	C8	15	LEU	3.2
45	l8	107	GLU	3.2
2	S0	28	ASN	3.2
35	sM	29	ASN	3.2
13	c1	97	TYR	3.2
5	s3	163	PRO	3.2
9	S7	73	VAL	3.2
21	C9	2	PRO	3.2
30	D8	15	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
82	p0	188	VAL	3.2
7	S5	72	HIS	3.2
2	S0	122	ILE	3.2
7	s5	130	ILE	3.2
8	S6	87	ARG	3.2
21	C9	7	ARG	3.2
60	N4	63	ILE	3.2
82	p0	68	SER	3.2
34	SR	257	ALA	3.2
18	C6	132	LYS	3.1
35	SM	16	ASP	3.1
36	1	1568	U	3.1
28	D6	16	GLY	3.1
5	s3	11	LEU	3.1
36	5	2404	A	3.1
2	S0	189	VAL	3.1
7	s5	79	ASN	3.1
18	c6	10	PHE	3.1
42	L5	20	PHE	3.1
82	p0	27	VAL	3.1
1	6	1588	G	3.1
36	5	3276	G	3.1
8	S6	219	ARG	3.1
3	S1	101	HIS	3.1
18	C6	21	HIS	3.1
19	c7	122	ILE	3.1
27	D5	50	ILE	3.1
7	S5	66	GLN	3.1
34	SR	27	ALA	3.1
35	SM	141	ALA	3.1
82	p0	282	SER	3.1
8	S6	68	LEU	3.1
10	s8	39	GLY	3.1
12	C0	40	LEU	3.1
42	L5	150	LEU	3.1
55	m9	185	LEU	3.1
31	D9	7	TRP	3.1
8	S6	150	GLU	3.1
21	C9	115	GLU	3.1
32	E0	50	VAL	3.1
19	c7	118	PRO	3.1
55	M9	85	ARG	3.1

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Mol	Chain	Res	Type	RSRZ
1	6	1701	A	3.1
8	S6	175	ILE	3.1
36	5	1350	A	3.1
26	D4	117	LYS	3.1
34	SR	40	LYS	3.1
5	S3	153	ALA	3.1
10	S8	150	ALA	3.1
24	D2	17	ALA	3.1
2	s0	151	SER	3.1
7	s5	42	LEU	3.1
14	C2	45	LEU	3.1
1	6	651	G	3.1
19	C7	103	ASP	3.1
32	E0	25	GLU	3.1
70	o4	96	GLU	3.1
5	s3	137	VAL	3.1
16	C4	67	VAL	3.1
46	L9	43	VAL	3.1
3	S1	140	ILE	3.1
8	S6	139	ASN	3.1
8	S6	187	LYS	3.1
8	s6	164	LYS	3.1
25	D3	27	ASN	3.1
34	SR	121	MET	3.1
36	5	3155	U	3.1
45	l8	122	LYS	3.1
49	M3	46	ILE	3.1
55	m9	165	LYS	3.1
8	S6	100	ALA	3.1
21	C9	50	ALA	3.1
3	S1	228	LEU	3.1
7	S5	108	LEU	3.1
4	s2	105	GLY	3.1
15	C3	59	GLY	3.1
17	C5	129	GLY	3.1
20	c8	142	GLY	3.1
35	SM	9	GLY	3.1
11	S9	145	SER	3.1
33	E1	146	SER	3.1
60	n4	95	SER	3.1
73	O7	87	SER	3.1
74	o8	48	SER	3.1

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Mol	Chain	Res	Type	RSRZ
2	S0	29	VAL	3.1
3	s1	89	ASP	3.1
8	S6	153	VAL	3.1
8	s6	195	VAL	3.1
9	S7	107	ARG	3.1
14	C2	121	VAL	3.1
16	C4	28	VAL	3.1
18	C6	4	VAL	3.1
4	s2	88	LYS	3.1
7	S5	84	LYS	3.1
19	C7	59	LYS	3.1
18	c6	43	ILE	3.1
52	m6	182	ASN	3.1
5	s3	201	ALA	3.1
18	C6	119	ALA	3.1
1	6	277	U	3.1
5	s3	202	LEU	3.1
9	s7	18	LEU	3.1
14	C2	32	LEU	3.1
22	d0	26	LEU	3.1
74	O8	24	THR	3.1
8	S6	67	VAL	3.1
11	S9	101	VAL	3.1
13	c1	117	VAL	3.1
18	C6	39	VAL	3.1
21	C9	34	VAL	3.1
30	D8	44	VAL	3.1
60	n4	72	SER	3.1
1	6	1337	A	3.1
10	s8	200	LYS	3.1
35	sM	46	LYS	3.1
3	S1	59	ASP	3.1
8	s6	89	ASP	3.1
7	s5	172	ILE	3.1
22	d0	22	ILE	3.1
28	D6	65	PRO	3.1
35	SM	61	ILE	3.1
37	7	73	C	3.0
8	s6	216	LEU	3.0
13	C1	154	ALA	3.0
14	c2	57	ALA	3.0
30	d8	43	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
55	M9	131	ALA	3.0
1	2	730	G	3.0
10	s8	42	ARG	3.0
16	C4	41	ARG	3.0
18	C6	115	THR	3.0
34	SR	25	THR	3.0
7	S5	24	VAL	3.0
34	sR	104	VAL	3.0
58	N2	47	VAL	3.0
8	S6	93	LYS	3.0
16	C4	70	LYS	3.0
52	m6	66	LYS	3.0
18	C6	15	SER	3.0
19	C7	125	SER	3.0
21	C9	117	SER	3.0
35	sM	124	GLU	3.0
69	O3	56	SER	3.0
2	S0	97	PRO	3.0
16	C4	94	PRO	3.0
56	N0	96	ASP	3.0
33	e1	106	TYR	3.0
3	S1	231	LEU	3.0
6	s4	12	LEU	3.0
6	s4	261	LEU	3.0
14	c2	78	LEU	3.0
3	S1	49	ASN	3.0
8	S6	177	ARG	3.0
11	s9	48	GLN	3.0
14	c2	33	ARG	3.0
36	5	3278	C	3.0
52	m6	69	GLY	3.0
71	O5	20	GLN	3.0
6	s4	245	LYS	3.0
14	C2	115	VAL	3.0
60	n4	75	THR	3.0
17	c5	138	PHE	3.0
58	N2	28	PHE	3.0
7	S5	91	GLU	3.0
10	s8	143	TRP	3.0
9	S7	49	ILE	3.0
19	C7	96	SER	3.0
34	sR	123	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
28	D6	98	PRO	3.0
34	sR	30	PRO	3.0
13	c1	5	LEU	3.0
24	D2	55	ASP	3.0
39	L2	176	ASP	3.0
47	M0	218	ALA	3.0
67	O1	112	ASP	3.0
16	C4	90	ARG	3.0
18	c6	82	ARG	3.0
19	c7	3	ARG	3.0
23	d1	22	ARG	3.0
10	S8	44	HIS	3.0
33	E1	93	HIS	3.0
19	C7	74	GLN	3.0
35	SM	64	LYS	3.0
1	6	754	A	3.0
11	S9	136	VAL	3.0
16	C4	74	VAL	3.0
5	s3	170	THR	3.0
16	C4	14	PHE	3.0
16	C4	27	PHE	3.0
27	d5	88	ILE	3.0
42	l5	216	GLU	3.0
60	N4	92	GLU	3.0
14	C2	43	ARG	3.0
75	O9	21	ARG	3.0
1	2	144	U	3.0
1	6	794	U	3.0
2	S0	129	ASP	3.0
33	e1	90	LYS	3.0
65	N9	25	LYS	3.0
14	C2	102	GLY	3.0
21	C9	139	THR	3.0
65	n9	26	THR	3.0
21	c9	116	ILE	3.0
21	C9	90	PRO	3.0
34	SR	73	LEU	3.0
54	M8	74	GLU	3.0
1	2	713	A	3.0
2	S0	152	PRO	3.0
36	1	2208	A	3.0
11	s9	6	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
20	C8	145	ARG	3.0
8	S6	138	ALA	3.0
19	C7	70	SER	3.0
20	C8	83	ALA	3.0
44	L7	27	ALA	3.0
5	s3	10	LYS	3.0
5	s3	206	VAL	3.0
6	S4	8	HIS	3.0
16	C4	98	GLY	3.0
43	l6	67	GLY	3.0
51	M5	155	VAL	3.0
1	2	718	U	3.0
1	6	261	U	3.0
11	S9	146	PHE	3.0
25	D3	28	ASN	3.0
7	s5	137	ILE	3.0
46	L9	191	LEU	2.9
2	s0	199	PRO	2.9
9	s7	40	PRO	2.9
12	c0	83	PRO	2.9
15	C3	76	LYS	2.9
32	E0	2	ALA	2.9
71	o5	107	LYS	2.9
19	C7	53	TYR	2.9
39	l2	249	SER	2.9
2	S0	168	HIS	2.9
6	S4	208	VAL	2.9
12	C0	53	GLY	2.9
12	c0	22	VAL	2.9
14	C2	30	VAL	2.9
33	e1	102	VAL	2.9
10	S8	109	PHE	2.9
11	s9	104	PHE	2.9
71	o5	104	GLN	2.9
74	o8	11	PHE	2.9
1	6	1355	C	2.9
27	d5	41	ILE	2.9
3	S1	218	LEU	2.9
12	C0	28	ASN	2.9
14	C2	111	ASN	2.9
17	C5	50	THR	2.9
19	c7	46	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
26	D4	125	LEU	2.9
36	5	3277	U	2.9
39	L2	252	THR	2.9
42	L5	28	THR	2.9
61	N5	108	LEU	2.9
5	s3	199	PRO	2.9
13	c1	29	LYS	2.9
21	C9	92	LYS	2.9
43	l6	128	LYS	2.9
60	n4	65	GLU	2.9
71	O5	64	GLU	2.9
3	S1	141	ALA	2.9
12	C0	30	ALA	2.9
47	M0	2	ALA	2.9
2	s0	2	SER	2.9
3	S1	66	VAL	2.9
7	s5	33	VAL	2.9
28	D6	58	VAL	2.9
35	SM	41	SER	2.9
73	O7	84	SER	2.9
1	6	677	G	2.9
36	5	1268	G	2.9
34	sR	310	ILE	2.9
42	L5	4	GLN	2.9
56	N0	129	ILE	2.9
16	C4	33	LEU	2.9
22	d0	58	LEU	2.9
30	d8	16	LEU	2.9
3	S1	219	LYS	2.9
22	D0	64	LYS	2.9
27	d5	46	LYS	2.9
1	6	1700	C	2.9
8	s6	91	GLU	2.9
13	C1	4	GLU	2.9
10	s8	67	TRP	2.9
27	d5	99	ALA	2.9
34	SR	181	TRP	2.9
34	sR	119	ALA	2.9
36	1	1562	C	2.9
45	l8	196	ALA	2.9
53	m7	156	ALA	2.9
9	S7	90	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
21	C9	6	VAL	2.9
3	S1	24	PHE	2.9
7	S5	82	PHE	2.9
9	S7	31	SER	2.9
34	sR	186	PHE	2.9
70	O4	66	SER	2.9
6	S4	66	MET	2.9
6	S4	195	ILE	2.9
6	s4	162	ILE	2.9
7	s5	198	LEU	2.9
8	S6	142	ARG	2.9
8	s6	147	LEU	2.9
14	c2	137	MET	2.9
32	E0	39	LEU	2.9
34	SR	141	LEU	2.9
26	d4	99	LYS	2.9
65	n9	22	LYS	2.9
82	p0	23	LYS	2.9
22	d0	29	THR	2.9
2	S0	5	ALA	2.9
7	s5	154	ALA	2.9
14	C2	69	ALA	2.9
30	D8	43	ASN	2.9
82	p0	284	ALA	2.9
36	5	1580	A	2.9
18	C6	7	VAL	2.9
18	C6	75	VAL	2.9
60	N4	67	VAL	2.9
1	6	1708	U	2.9
13	c1	115	PHE	2.9
40	l3	225	GLY	2.9
58	N2	60	GLY	2.9
28	D6	82	ARG	2.9
31	d9	56	ARG	2.9
7	s5	90	ILE	2.9
14	c2	106	ILE	2.9
9	S7	138	LYS	2.9
12	c0	2	LEU	2.9
12	c0	40	LEU	2.9
16	C4	36	LYS	2.9
16	C4	102	LEU	2.9
20	c8	54	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
33	e1	145	HIS	2.9
33	e1	96	LYS	2.9
45	l8	43	LYS	2.9
4	s2	94	GLN	2.9
8	S6	65	GLN	2.9
9	s7	119	THR	2.9
10	s8	150	ALA	2.9
11	S9	67	PRO	2.9
18	C6	20	ALA	2.9
35	SM	38	PRO	2.9
40	L3	250	ALA	2.9
50	M4	138	ALA	2.9
57	N1	61	THR	2.9
74	o8	2	ALA	2.9
8	s6	166	GLU	2.9
27	D5	40	VAL	2.9
34	sR	8	VAL	2.9
7	s5	150	GLY	2.9
9	S7	97	ARG	2.9
19	c7	47	ARG	2.9
32	E0	35	TYR	2.9
59	N3	3	GLY	2.9
1	2	740	A	2.9
1	2	1584	G	2.9
2	S0	146	LEU	2.9
3	S1	222	LYS	2.9
4	S2	225	LEU	2.9
13	c1	32	LYS	2.9
36	1	1605	A	2.9
27	D5	83	LEU	2.9
34	sR	301	LEU	2.9
36	5	437	G	2.9
36	5	443	G	2.9
53	M7	176	ILE	2.9
1	2	137	U	2.8
1	2	320	U	2.8
7	s5	47	SER	2.8
72	O6	27	SER	2.8
1	6	658	C	2.8
6	s4	15	PRO	2.8
14	C2	104	ALA	2.8
17	c5	131	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
35	SM	134	ASP	2.8
35	sM	40	PRO	2.8
58	N2	100	THR	2.8
57	n1	104	GLU	2.8
30	D8	55	VAL	2.8
33	e1	147	VAL	2.8
3	S1	64	ARG	2.8
11	s9	3	ARG	2.8
7	S5	187	ILE	2.8
14	C2	88	LEU	2.8
22	D0	54	GLY	2.8
33	e1	117	LEU	2.8
63	n7	118	PHE	2.8
1	2	1583	A	2.8
16	C4	56	SER	2.8
5	s3	88	ALA	2.8
1	2	540	G	2.8
1	6	833	U	2.8
22	D0	110	PRO	2.8
36	5	170	G	2.8
1	2	1096	C	2.8
1	2	1700	C	2.8
1	2	1706	C	2.8
6	s4	183	VAL	2.8
14	C2	21	GLU	2.8
19	c7	55	THR	2.8
48	M1	147	THR	2.8
36	1	1563	C	2.8
40	L3	316	GLU	2.8
53	M7	157	VAL	2.8
34	sR	294	TRP	2.8
9	s7	44	LYS	2.8
12	c0	28	ASN	2.8
28	D6	8	ASN	2.8
60	n4	115	LYS	2.8
5	s3	182	LEU	2.8
7	S5	48	PHE	2.8
12	C0	43	ILE	2.8
14	c2	28	LEU	2.8
14	c2	74	LEU	2.8
19	c7	69	ILE	2.8
21	c9	15	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
24	D2	26	LEU	2.8
27	d5	89	ILE	2.8
64	N8	116	GLY	2.8
30	D8	57	MET	2.8
42	L5	62	CYS	2.8
45	L8	130	TYR	2.8
16	C4	80	HIS	2.8
47	m0	220	GLN	2.8
3	S1	130	SER	2.8
16	C4	108	SER	2.8
18	c6	3	ALA	2.8
30	d8	21	SER	2.8
2	S0	205	ARG	2.8
2	S0	192	THR	2.8
2	s0	189	VAL	2.8
7	s5	149	VAL	2.8
18	c6	48	VAL	2.8
18	c6	97	VAL	2.8
19	C7	9	VAL	2.8
19	c7	121	VAL	2.8
27	d5	94	LYS	2.8
35	sM	87	THR	2.8
63	n7	96	VAL	2.8
4	S2	84	LYS	2.8
16	C4	116	GLU	2.8
60	n4	69	LYS	2.8
60	n4	74	LYS	2.8
82	p0	44	GLU	2.8
1	2	1346	A	2.8
36	1	2872	A	2.8
3	S1	29	TRP	2.8
4	S2	207	LEU	2.8
9	S7	154	LEU	2.8
3	S1	53	GLY	2.8
4	s2	75	GLY	2.8
21	C9	124	ILE	2.8
27	D5	88	ILE	2.8
28	D6	41	ILE	2.8
1	6	654	C	2.8
2	S0	75	ALA	2.8
8	S6	182	GLN	2.8
11	s9	167	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
14	C2	42	ALA	2.8
33	e1	101	ALA	2.8
34	SR	78	ALA	2.8
35	sM	153	ALA	2.8
60	n4	121	ALA	2.8
27	D5	58	ARG	2.8
34	sR	117	LYS	2.8
4	S2	232	GLU	2.8
8	S6	163	THR	2.8
14	C2	109	GLU	2.8
19	C7	100	LEU	2.8
22	D0	60	THR	2.8
22	D0	94	GLU	2.8
26	d4	18	LEU	2.8
28	D6	90	GLU	2.8
34	SR	183	LEU	2.8
82	p0	20	GLU	2.8
2	s0	173	ILE	2.8
9	s7	135	ILE	2.8
27	D5	71	ILE	2.8
45	L8	158	ASP	2.8
48	M1	127	PHE	2.8
34	sR	105	GLY	2.8
60	N4	62	GLY	2.8
11	s9	142	ASN	2.8
1	6	1491	U	2.8
12	C0	64	TYR	2.8
36	1	1764	U	2.8
33	E1	95	HIS	2.8
45	L8	28	HIS	2.8
1	6	1447	C	2.8
2	S0	132	ALA	2.8
6	S4	2	ALA	2.8
18	C6	24	ALA	2.8
18	C6	134	ALA	2.8
42	L5	151	GLN	2.8
45	l8	113	ALA	2.8
8	S6	164	LYS	2.8
9	S7	101	LYS	2.8
20	C8	36	LYS	2.8
34	sR	118	LYS	2.8
35	sM	88	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	6	1607	G	2.8
8	s6	173	PRO	2.8
14	c2	122	VAL	2.8
22	d0	97	VAL	2.8
63	n7	10	VAL	2.8
8	s6	193	LEU	2.8
10	S8	96	LEU	2.8
15	C3	147	SER	2.8
17	c5	36	LEU	2.8
29	D7	30	SER	2.8
63	n7	80	LEU	2.8
4	S2	208	GLU	2.8
14	c2	76	GLU	2.8
16	C4	37	GLU	2.8
2	S0	102	PHE	2.7
7	S5	38	THR	2.8
7	S5	69	PHE	2.7
9	S7	92	PHE	2.7
9	s7	70	PHE	2.7
52	M6	71	PHE	2.7
61	n5	71	THR	2.8
11	s9	147	MET	2.7
7	S5	153	GLY	2.7
15	C3	25	TRP	2.7
7	s5	126	ASP	2.7
47	m0	204	GLY	2.7
12	c0	65	TYR	2.7
42	L5	30	TYR	2.7
18	C6	128	LYS	2.7
19	c7	116	LYS	2.7
21	C9	110	LYS	2.7
55	m9	153	LYS	2.7
1	6	39	A	2.7
1	6	1526	A	2.7
3	S1	212	VAL	2.7
3	s1	20	VAL	2.7
6	s4	196	VAL	2.7
12	C0	13	GLN	2.7
22	D0	100	VAL	2.7
26	d4	35	VAL	2.7
2	s0	207	PRO	2.7
11	S9	144	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
12	c0	4	PRO	2.7
5	s3	59	LEU	2.7
19	c7	100	LEU	2.7
45	L8	46	LEU	2.7
3	S1	223	PHE	2.7
4	s2	164	SER	2.7
9	S7	181	ILE	2.7
9	s7	181	ILE	2.7
21	C9	116	ILE	2.7
22	d0	19	ILE	2.7
26	d4	58	PHE	2.7
31	d9	8	PHE	2.7
35	sM	28	SER	2.7
22	d0	25	THR	2.7
36	1	1016	C	2.7
42	L5	221	GLU	2.7
9	S7	53	GLY	2.7
10	s8	177	GLY	2.7
21	C9	35	ASP	2.7
35	sM	131	ASP	2.7
6	s4	39	ARG	2.7
45	L8	84	ARG	2.7
14	c2	105	LYS	2.7
18	C6	14	LYS	2.7
22	D0	53	LYS	2.7
34	sR	24	ALA	2.7
12	c0	73	VAL	2.7
28	D6	50	VAL	2.7
82	p0	187	VAL	2.7
2	S0	161	PRO	2.7
19	C7	26	LEU	2.7
19	C7	119	LEU	2.7
27	D5	75	LEU	2.7
45	l8	238	LEU	2.7
1	6	680	U	2.7
9	S7	8	ILE	2.7
13	C1	156	PHE	2.7
36	5	252	U	2.7
36	5	3319	U	2.7
57	N1	160	ILE	2.7
2	S0	135	GLU	2.7
68	o2	95	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
2	s0	80	THR	2.7
7	s5	138	THR	2.7
13	C1	2	SER	2.7
17	c5	135	THR	2.7
18	c6	61	SER	2.7
25	d3	2	GLY	2.7
45	l8	121	SER	2.7
71	o5	72	GLY	2.7
30	d8	65	ARG	2.7
28	D6	4	LYS	2.7
35	SM	84	LYS	2.7
1	2	1703	C	2.7
38	8	84	C	2.7
12	c0	75	TYR	2.7
21	C9	18	TYR	2.7
3	S1	99	ASN	2.7
14	C2	112	ALA	2.7
17	c5	79	HIS	2.7
45	L8	119	ALA	2.7
63	N7	124	ALA	2.7
82	p0	103	ASN	2.7
8	s6	179	VAL	2.7
12	C0	22	VAL	2.7
19	C7	99	VAL	2.7
2	S0	87	LEU	2.7
6	S4	261	LEU	2.7
28	D6	53	LEU	2.7
1	2	175	G	2.7
1	6	660	G	2.7
10	s8	33	PRO	2.7
21	C9	129	GLN	2.7
66	o0	12	GLN	2.7
5	s3	167	PHE	2.7
40	l3	188	ILE	2.7
16	C4	87	GLY	2.7
22	D0	67	THR	2.7
23	d1	62	ARG	2.7
25	D3	4	GLY	2.7
26	d4	73	GLY	2.7
82	p0	91	GLU	2.7
17	C5	47	ARG	2.7
34	sR	74	THR	2.7

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Mol	Chain	Res	Type	RSRZ
59	N3	32	ARG	2.7
8	S6	82	SER	2.7
8	s6	167	LYS	2.7
17	C5	52	LYS	2.7
34	sR	65	SER	2.7
35	sM	55	SER	2.7
35	sM	89	LYS	2.7
45	l8	106	LYS	2.7
36	5	3157	U	2.7
2	S0	40	ALA	2.7
12	c0	26	ASP	2.7
18	c6	24	ALA	2.7
31	d9	14	TYR	2.7
60	N4	68	ALA	2.7
82	p0	296	ALA	2.7
2	s0	45	VAL	2.7
2	s0	176	LEU	2.7
6	S4	102	VAL	2.7
8	S6	179	VAL	2.7
9	S7	62	VAL	2.7
12	c0	87	HIS	2.7
14	c2	88	LEU	2.7
17	C5	126	VAL	2.7
19	c7	26	LEU	2.7
19	c7	115	LEU	2.7
22	D0	118	VAL	2.7
26	D4	100	VAL	2.7
28	D6	11	ASN	2.7
30	d8	9	LEU	2.7
32	E0	38	LEU	2.7
34	sR	31	ASN	2.7
40	l3	387	LEU	2.7
1	2	768	C	2.7
2	S0	35	PRO	2.7
7	s5	177	ILE	2.7
14	c2	96	GLN	2.7
21	C9	118	PRO	2.7
35	SM	39	PRO	2.7
2	S0	7	PHE	2.7
9	S7	70	PHE	2.7
34	sR	121	MET	2.7
3	S1	44	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
5	S3	210	GLU	2.7
5	s3	61	GLU	2.7
8	s6	146	GLY	2.7
14	c2	127	GLY	2.7
18	C6	13	LYS	2.7
19	C7	18	GLU	2.7
34	SR	161	LYS	2.7
51	M5	2	GLY	2.7
55	m9	186	LYS	2.7
9	S7	133	THR	2.7
18	C6	141	SER	2.7
22	D0	66	SER	2.7
8	s6	172	ALA	2.7
82	p0	275	ALA	2.7
3	S1	181	LEU	2.7
5	s3	86	LEU	2.7
6	S4	180	LEU	2.7
9	s7	81	LEU	2.7
12	c0	66	TYR	2.7
14	C2	66	VAL	2.7
16	C4	30	VAL	2.7
20	c8	42	TYR	2.7
22	d0	100	VAL	2.7
27	d5	54	VAL	2.7
28	D6	86	VAL	2.7
34	sR	100	TYR	2.7
34	sR	144	LEU	2.7
34	sR	167	VAL	2.7
36	5	2506	U	2.7
52	M6	112	TYR	2.7
58	n2	66	VAL	2.7
1	6	1756[A]	A	2.6
28	d6	98	PRO	2.6
35	sM	129	GLN	2.6
36	1	440	A	2.6
36	5	2099	A	2.6
45	l8	25	PRO	2.6
4	S2	91	ARG	2.6
7	S5	184	PHE	2.6
51	M5	95	GLN	2.6
60	N4	71	ARG	2.6
60	n4	80	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
22	D0	52	LYS	2.6
13	c1	68	GLY	2.6
36	1	1196	C	2.6
47	M0	186	GLU	2.6
52	M6	100	GLU	2.6
54	m8	154	GLY	2.6
71	o5	27	GLU	2.6
19	c7	106	THR	2.6
3	S1	139	ALA	2.6
3	S1	227	ALA	2.6
5	s3	138	VAL	2.6
7	S5	93	LEU	2.6
9	S7	12	ALA	2.6
9	s7	12	ALA	2.6
9	s7	176	LEU	2.6
11	S9	116	LEU	2.6
14	c2	115	VAL	2.6
15	c3	125	LEU	2.6
17	C5	76	VAL	2.6
20	c8	146	ALA	2.6
21	C9	140	LEU	2.6
22	d0	66	SER	2.6
30	D8	41	VAL	2.6
45	l8	253	SER	2.6
74	o8	54	LEU	2.6
25	d3	18	HIS	2.6
3	S1	22	ASP	2.6
57	n1	160	ILE	2.6
1	2	194	U	2.6
5	s3	151	LYS	2.6
7	s5	45	LYS	2.6
8	S6	140	ASN	2.6
36	1	1820	U	2.6
36	5	2954	U	2.6
52	M6	80	PHE	2.6
6	s4	203	GLY	2.6
3	S1	107	THR	2.6
8	s6	78	THR	2.6
12	c0	67	THR	2.6
27	d5	102	THR	2.6
2	S0	18	LEU	2.6
3	S1	61	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
7	S5	124	LEU	2.6
10	S8	144	ALA	2.6
13	c1	140	VAL	2.6
13	c1	146	ALA	2.6
17	c5	101	ALA	2.6
18	C6	78	VAL	2.6
20	C8	58	ALA	2.6
21	c9	17	ALA	2.6
32	E0	49	LEU	2.6
49	m3	195	ALA	2.6
63	n7	13	VAL	2.6
19	c7	13	SER	2.6
19	c7	120	SER	2.6
36	1	2685	C	2.6
82	p0	102	SER	2.6
33	E1	105	TYR	2.6
34	sR	250	TYR	2.6
9	s7	60	ILE	2.6
3	s1	103	MET	2.6
8	S6	95	LYS	2.6
16	C4	82	LYS	2.6
21	C9	63	ARG	2.6
22	D0	91	ILE	2.6
34	sR	161	LYS	2.6
39	l2	251	LYS	2.6
55	M9	176	ARG	2.6
57	n1	76	ILE	2.6
65	N9	59	LYS	2.6
48	M1	104	PHE	2.6
58	N2	95	PHE	2.6
3	S1	42	ASN	2.6
4	s2	201	ASN	2.6
7	S5	86	GLN	2.6
17	C5	103	ASN	2.6
21	c9	12	GLN	2.6
47	m0	112	GLN	2.6
70	O4	3	GLN	2.6
2	S0	100	GLY	2.6
2	s0	100	GLY	2.6
8	S6	54	GLY	2.6
19	c7	98	GLY	2.6
35	sM	24	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
36	5	1028	U	2.6
1	2	914	G	2.6
9	S7	118	LEU	2.6
9	S7	129	LEU	2.6
14	C2	41	LEU	2.6
2	S0	143	VAL	2.6
7	s5	27	THR	2.6
14	C2	110	ALA	2.6
14	c2	101	ALA	2.6
18	c6	69	VAL	2.6
19	c7	8	THR	2.6
30	D8	66	LEU	2.6
62	n6	126	LEU	2.6
66	O0	104	LEU	2.6
19	c7	66	VAL	2.6
21	c9	4	VAL	2.6
26	d4	80	ALA	2.6
50	m4	138	ALA	2.6
60	n4	67	VAL	2.6
61	n5	23	ALA	2.6
80	e0	50	VAL	2.6
1	2	138	A	2.6
1	2	1611	A	2.6
1	6	538	A	2.6
5	S3	187	LYS	2.6
7	s5	83	ARG	2.6
5	S3	35	SER	2.6
9	S7	91	ILE	2.6
45	l8	111	LYS	2.6
15	c3	90	TYR	2.6
24	d2	130	TYR	2.6
25	D3	145	SER	2.6
28	D6	73	TYR	2.6
2	S0	118	PRO	2.6
8	s6	86	PRO	2.6
32	E0	44	PHE	2.6
82	p0	88	PHE	2.6
2	S0	72	ASP	2.6
18	c6	113	ASP	2.6
3	S1	120	LEU	2.6
8	S6	76	LEU	2.6
26	D4	28	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
34	sR	7	LEU	2.6
34	sR	141	LEU	2.6
45	L8	202	GLU	2.6
48	M1	108	GLU	2.6
49	m3	79	GLU	2.6
52	m6	4	GLU	2.6
82	p0	45	LEU	2.6
11	S9	148	VAL	2.6
5	s3	172	THR	2.6
5	s3	219	ALA	2.6
7	S5	176	THR	2.6
7	s5	202	ALA	2.6
16	C4	21	ALA	2.6
22	d0	62	VAL	2.6
26	d4	27	VAL	2.6
29	D7	52	THR	2.6
34	sR	143	THR	2.6
82	p0	277	ALA	2.6
3	S1	94	LYS	2.6
18	c6	68	ARG	2.6
25	d3	31	LYS	2.6
36	1	3079	U	2.6
36	5	1568	U	2.6
5	s3	115	ILE	2.6
43	L6	130	ILE	2.6
12	c0	79	TYR	2.6
16	c4	125	SER	2.6
17	C5	128	HIS	2.6
19	C7	65	PRO	2.6
27	d5	74	SER	2.6
1	2	1410	A	2.6
3	S1	74	GLN	2.6
31	D9	20	GLN	2.6
78	Q2	99	GLN	2.6
7	S5	151	GLY	2.6
19	c7	114	GLY	2.6
22	D0	92	ASP	2.6
67	o1	45	GLY	2.6
31	D9	5	ASN	2.6
8	s6	76	LEU	2.6
26	d4	28	LEU	2.6
27	d5	51	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
42	L5	92	LEU	2.6
74	O8	78	LEU	2.6
74	o8	78	LEU	2.6
1	2	321	C	2.6
38	8	83	C	2.6
42	l5	281	GLU	2.6
9	S7	152	VAL	2.6
3	S1	128	LYS	2.6
10	s8	8	ARG	2.6
20	C8	105	VAL	2.6
13	C1	148	LYS	2.6
25	D3	123	LYS	2.6
29	D7	71	ALA	2.6
34	sR	87	LYS	2.6
45	L8	141	ALA	2.6
63	N7	2	ALA	2.6
40	l3	233	TRP	2.5
4	S2	242	ILE	2.5
19	c7	17	ILE	2.5
21	c9	111	ILE	2.5
28	D6	44	ILE	2.5
2	S0	203	PHE	2.5
5	S3	17	PHE	2.5
6	S4	205	PHE	2.5
45	l8	34	PHE	2.5
1	2	74	U	2.5
1	2	240	U	2.5
1	6	681	U	2.5
5	s3	87	TYR	2.5
18	C6	93	HIS	2.5
2	s0	97	PRO	2.5
28	D6	20	PRO	2.5
26	d4	2	SER	2.5
74	O8	49	SER	2.5
2	S0	171	GLY	2.5
12	C0	62	GLN	2.5
22	d0	98	GLN	2.5
39	l2	248	GLY	2.5
48	M1	6	GLN	2.5
72	O6	31	GLY	2.5
3	S1	135	LEU	2.5
9	S7	166	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
41	L4	179	LEU	2.5
42	l5	293	LEU	2.5
1	2	143	G	2.5
1	6	540	G	2.5
2	s0	116	LYS	2.5
3	S1	209	ASN	2.5
6	S4	11	ARG	2.5
7	s5	224	ASN	2.5
9	S7	172	VAL	2.5
9	s7	112	ARG	2.5
16	C4	13	VAL	2.5
16	c4	124	ASP	2.5
18	C6	106	LYS	2.5
26	d4	24	VAL	2.5
48	M1	164	LYS	2.5
36	5	1352	A	2.5
41	L4	63	GLU	2.5
52	m6	100	GLU	2.5
60	n4	113	LYS	2.5
1	2	505	A	2.5
1	2	793	A	2.5
7	S5	26	ALA	2.5
19	c7	12	ALA	2.5
34	sR	214	ALA	2.5
60	n4	131	ALA	2.5
63	n7	59	ALA	2.5
3	S1	25	THR	2.5
4	S2	178	ILE	2.5
6	S4	162	ILE	2.5
10	S8	62	THR	2.5
10	s8	36	THR	2.5
14	C2	71	ILE	2.5
20	c8	35	ILE	2.5
21	c9	65	ILE	2.5
22	D0	78	THR	2.5
34	SR	306	THR	2.5
39	l2	252	THR	2.5
58	N2	68	THR	2.5
9	s7	24	PHE	2.5
10	s8	27	PHE	2.5
31	d9	43	PHE	2.5
6	s4	182	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
8	S6	135	PRO	2.5
27	d5	55	PRO	2.5
42	l5	12	TYR	2.5
2	S0	77	SER	2.5
4	s2	202	GLY	2.5
8	s6	201	GLN	2.5
8	s6	212	LEU	2.5
9	s7	11	GLN	2.5
10	s8	122	GLY	2.5
11	S9	93	LEU	2.5
12	c0	19	GLY	2.5
14	c2	77	GLY	2.5
14	c2	133	LEU	2.5
16	c4	35	GLY	2.5
34	SR	65	SER	2.5
35	SM	20	LEU	2.5
36	1	1569	U	2.5
41	L4	81	GLY	2.5
63	n7	5	LEU	2.5
65	n9	34	GLY	2.5
71	o5	98	SER	2.5
3	S1	216	LYS	2.5
7	s5	81	ARG	2.5
8	S6	154	ARG	2.5
33	E1	143	LYS	2.5
40	l3	19	ARG	2.5
63	n7	52	LYS	2.5
66	o0	32	LYS	2.5
67	O1	5	LYS	2.5
18	c6	55	VAL	2.5
55	M9	177	VAL	2.5
57	N1	124	VAL	2.5
63	n7	14	VAL	2.5
82	p0	87	VAL	2.5
3	S1	182	ALA	2.5
14	c2	109	GLU	2.5
17	c5	66	ALA	2.5
21	C9	58	ALA	2.5
50	M4	9	ALA	2.5
51	m5	111	ALA	2.5
52	M6	151	ASP	2.5
52	m6	183	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
66	O0	15	ALA	2.5
8	S6	158	ILE	2.5
21	C9	135	ILE	2.5
58	N2	38	ILE	2.5
34	sR	313	TRP	2.5
35	sM	30	THR	2.5
21	C9	54	PHE	2.5
63	n7	92	PHE	2.5
1	6	1559	A	2.5
1	2	1718	G	2.5
1	2	1777	G	2.5
36	1	2573	G	2.5
13	c1	23	PRO	2.5
21	c9	118	PRO	2.5
30	d8	47	PRO	2.5
82	p0	290	PRO	2.5
5	S3	157	LEU	2.5
6	s4	101	LEU	2.5
7	S5	174	LEU	2.5
1	2	1338	C	2.5
1	2	1705	C	2.5
6	S4	260	GLY	2.5
9	S7	69	GLY	2.5
9	S7	151	LYS	2.5
22	d0	50	LEU	2.5
32	E0	53	LYS	2.5
34	SR	117	LYS	2.5
34	SR	225	LEU	2.5
15	C3	51	GLY	2.5
18	c6	73	GLY	2.5
24	D2	59	GLY	2.5
36	1	2772	C	2.5
3	S1	220	GLN	2.5
16	C4	11	SER	2.5
28	D6	7	SER	2.5
47	M0	220	GLN	2.5
5	S3	186	VAL	2.5
6	S4	111	VAL	2.5
11	s9	101	VAL	2.5
13	c1	139	VAL	2.5
22	D0	117	VAL	2.5
70	O4	22	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
7	s5	74	ALA	2.5
7	s5	155	ALA	2.5
14	c2	118	ALA	2.5
28	D6	81	ALA	2.5
60	n4	128	ALA	2.5
1	2	701	U	2.5
1	6	1285	U	2.5
12	c0	96	GLU	2.5
5	S3	166	ASP	2.5
5	S3	217	ILE	2.5
7	S5	89	ILE	2.5
34	SR	136	ILE	2.5
34	SR	148	ASN	2.5
34	SR	199	ILE	2.5
24	D2	111	MET	2.5
5	s3	55	THR	2.5
11	S9	14	THR	2.5
12	C0	59	PHE	2.5
35	SM	65	THR	2.5
78	Q2	36	PHE	2.5
82	p0	79	PHE	2.5
2	s0	168	HIS	2.5
9	S7	102	PRO	2.5
32	E0	27	PRO	2.5
35	SM	21	PRO	2.5
3	S1	213	ARG	2.5
14	c2	52	LEU	2.5
17	C5	9	LYS	2.5
21	c9	103	LYS	2.5
22	D0	61	LYS	2.5
28	D6	92	ARG	2.5
32	E0	29	LYS	2.5
33	e1	139	LEU	2.5
3	s1	233	GLY	2.5
18	c6	56	GLY	2.5
47	m0	114	GLY	2.5
2	S0	86	VAL	2.5
2	s0	73	VAL	2.5
3	S1	65	VAL	2.5
5	s3	41	VAL	2.5
6	s4	208	VAL	2.5
78	Q2	102	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	2	142	G	2.5
1	6	652	G	2.5
2	S0	20	ALA	2.5
4	s2	47	ALA	2.5
5	S3	6	SER	2.5
6	S4	24	SER	2.5
14	c2	42	ALA	2.5
34	sR	213	SER	2.5
36	1	1354	G	2.5
57	N1	125	ALA	2.5
1	2	1339	C	2.5
9	s7	127	GLU	2.5
11	S9	41	GLU	2.5
27	D5	41	ILE	2.5
35	sM	146	GLU	2.5
76	Q0	78	ILE	2.5
36	1	1017	C	2.5
10	S8	160	PHE	2.5
17	c5	102	PHE	2.5
26	d4	26	ASP	2.5
31	d9	52	PHE	2.5
34	sR	116	ASP	2.5
6	S4	159	THR	2.5
30	D8	26	THR	2.5
33	e1	125	THR	2.5
36	1	1570	U	2.5
36	1	2209	U	2.5
8	S6	174	LYS	2.5
10	s8	135	LYS	2.5
3	s1	207	LEU	2.5
5	S3	220	PRO	2.5
8	S6	212	LEU	2.5
19	C7	73	LEU	2.5
20	c8	17	LEU	2.5
27	d5	68	ARG	2.5
68	O2	128	LEU	2.5
82	p0	278	PRO	2.5
41	L4	194	TYR	2.5
25	D3	129	GLY	2.5
34	sR	298	GLY	2.5
7	S5	33	VAL	2.5
11	S9	85	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
14	c2	30	VAL	2.5
18	C6	22	VAL	2.5
7	S5	159	ALA	2.4
8	S6	224	ALA	2.4
61	N5	23	ALA	2.4
11	s9	13	SER	2.4
34	sR	170	ILE	2.4
70	o4	29	ILE	2.4
24	d2	114	GLU	2.4
45	l8	118	GLU	2.4
8	s6	156	PHE	2.4
14	C2	26	ASP	2.4
21	C9	119	LYS	2.4
26	d4	133	ASN	2.4
34	sR	159	ASN	2.4
35	SM	50	ASN	2.4
35	SM	53	ARG	2.4
35	sM	141	ASP	2.4
53	M7	159	LYS	2.4
55	m9	42	ARG	2.4
1	6	1418	G	2.4
4	S2	117	THR	2.4
4	s2	117	THR	2.4
7	S5	165	LEU	2.4
18	c6	37	THR	2.4
36	1	1949	G	2.4
36	5	1354	G	2.4
41	L4	60	THR	2.4
62	n6	83	ASP	2.4
34	sR	34	LEU	2.4
42	L5	146	LEU	2.4
55	M9	155	LEU	2.4
58	n2	79	LEU	2.4
66	o0	104	LEU	2.4
2	s0	126	PRO	2.4
9	S7	65	PRO	2.4
35	sM	52	PRO	2.4
1	2	912	U	2.4
28	D6	62	TYR	2.4
36	5	1564	U	2.4
36	5	2875	U	2.4
11	s9	127	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
20	c8	9	GLY	2.4
24	D2	25	VAL	2.4
59	n3	3	GLY	2.4
60	n4	84	GLY	2.4
5	s3	3	ALA	2.4
7	s5	86	GLN	2.4
52	m6	196	ALA	2.4
82	p0	283	ALA	2.4
82	p0	291	ALA	2.4
14	c2	24	ILE	2.4
24	D2	27	ILE	2.4
26	d4	7	ILE	2.4
45	L8	246	MET	2.4
7	s5	196	GLU	2.4
9	S7	48	GLU	2.4
15	c3	83	GLU	2.4
16	C4	73	GLU	2.4
19	c7	87	GLU	2.4
19	c7	89	SER	2.4
21	c9	125	SER	2.4
34	SR	160	GLU	2.4
47	m0	207	GLU	2.4
63	N7	132	SER	2.4
8	s6	188	ARG	2.4
9	S7	157	LYS	2.4
21	C9	69	LYS	2.4
22	D0	21	LYS	2.4
60	N4	74	LYS	2.4
78	q2	106	PHE	2.4
19	C7	78	ARG	2.4
3	s1	217	LEU	2.4
5	s3	176	LEU	2.4
7	s5	124	LEU	2.4
9	S7	176	LEU	2.4
14	C2	74	LEU	2.4
3	S1	95	ASN	2.4
26	D4	34	ASN	2.4
34	sR	88	THR	2.4
35	sM	57	ASN	2.4
52	M6	50	ASN	2.4
24	D2	29	PRO	2.4
36	5	1575	A	2.4

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Mol	Chain	Res	Type	RSRZ
36	5	2971	A	2.4
67	o1	88	PRO	2.4
6	S4	27	TYR	2.4
17	c5	113	GLY	2.4
19	C7	110	VAL	2.4
22	d0	118	VAL	2.4
24	D2	62	VAL	2.4
34	SR	55	GLY	2.4
1	6	1709	C	2.4
8	s6	213	ALA	2.4
1	2	133	U	2.4
1	2	280	U	2.4
4	s2	87	GLN	2.4
8	S6	24	ILE	2.4
9	s7	91	ILE	2.4
10	s8	60	ILE	2.4
14	c2	35	ALA	2.4
29	D7	12	ALA	2.4
34	sR	80	ALA	2.4
35	SM	135	ALA	2.4
45	L8	256	ALA	2.4
55	m9	183	ALA	2.4
36	1	2954	U	2.4
71	O5	113	GLN	2.4
5	s3	185	LYS	2.4
10	S8	21	PHE	2.4
12	c0	78	GLU	2.4
19	C7	60	ARG	2.4
28	D6	5	ARG	2.4
30	D8	50	GLU	2.4
30	d8	67	ARG	2.4
35	sM	58	GLU	2.4
7	S5	206	SER	2.4
15	c3	12	SER	2.4
19	C7	89	SER	2.4
23	D1	61	SER	2.4
9	s7	126	LEU	2.4
21	C9	22	LEU	2.4
82	p0	77	LEU	2.4
4	S2	51	THR	2.4
13	c1	44	THR	2.4
19	C7	48	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
23	D1	35	ASN	2.4
28	d6	65	PRO	2.4
72	O6	22	PRO	2.4
7	S5	53	VAL	2.4
14	c2	120	VAL	2.4
43	l6	14	ASP	2.4
78	q2	44	ASP	2.4
7	s5	72	HIS	2.4
10	S8	63	GLY	2.4
18	c6	92	TYR	2.4
22	D0	87	HIS	2.4
22	D0	90	TYR	2.4
30	d8	46	GLY	2.4
9	S7	57	ALA	2.4
19	C7	12	ALA	2.4
1	2	856	A	2.4
1	6	1719	A	2.4
5	s3	217	ILE	2.4
21	C9	36	ILE	2.4
29	D7	13	ALA	2.4
53	M7	156	ALA	2.4
3	S1	85	LYS	2.4
5	s3	148	LYS	2.4
12	C0	5	LYS	2.4
16	C4	99	GLN	2.4
28	D6	13	LYS	2.4
33	E1	99	LYS	2.4
34	sR	137	LYS	2.4
51	m5	15	GLN	2.4
35	sM	69	ARG	2.4
60	n4	110	LYS	2.4
65	n9	28	LYS	2.4
4	S2	66	PHE	2.4
17	C5	119	PHE	2.4
71	o5	95	PHE	2.4
1	2	700	C	2.4
1	2	1527	C	2.4
7	S5	175	LEU	2.4
12	c0	82	LEU	2.4
14	c2	32	LEU	2.4
34	sR	265	LEU	2.4
36	1	1014	U	2.4

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Mol	Chain	Res	Type	RSRZ
50	M4	60	LEU	2.4
33	e1	122	SER	2.4
35	sM	31	SER	2.4
49	M3	140	SER	2.4
1	2	1367	G	2.4
1	6	142	G	2.4
36	1	241	G	2.4
3	S1	21	VAL	2.4
3	S1	37	THR	2.4
5	s3	43	PRO	2.4
14	c2	49	THR	2.4
22	d0	56	VAL	2.4
23	d1	36	VAL	2.4
29	D7	45	THR	2.4
30	d8	44	VAL	2.4
34	SR	56	VAL	2.4
34	sR	247	PRO	2.4
55	m9	177	VAL	2.4
60	N4	98	PRO	2.4
26	d4	113	ASN	2.4
34	sR	200	ASN	2.4
59	n3	4	ASN	2.4
70	O4	78	GLY	2.4
3	s1	189	ILE	2.4
9	S7	135	ILE	2.4
10	s8	38	ILE	2.4
12	C0	65	TYR	2.4
12	c0	30	ALA	2.4
15	C3	66	ILE	2.4
15	c3	24	ALA	2.4
19	C7	69	ILE	2.4
29	d7	43	ILE	2.4
30	D8	13	ILE	2.4
30	D8	63	ALA	2.4
33	E1	101	ALA	2.4
55	M9	54	ALA	2.4
68	o2	77	ALA	2.4
8	S6	64	LYS	2.4
12	c0	38	LYS	2.4
28	D6	93	LYS	2.4
7	S5	92	ARG	2.4
55	M9	74	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
18	C6	83	GLN	2.4
49	m3	145	PHE	2.4
2	S0	57	LEU	2.4
14	c2	45	LEU	2.4
21	c9	22	LEU	2.4
34	SR	145	LEU	2.4
34	sR	33	LEU	2.4
1	2	135	A	2.4
1	2	1701	A	2.4
1	2	1721	A	2.4
1	6	1371	A	2.4
8	s6	150	GLU	2.4
36	1	1352	A	2.4
36	1	2971	A	2.4
52	M6	4	GLU	2.4
55	M9	179	GLU	2.4
11	S9	13	SER	2.4
59	n3	2	SER	2.4
82	p0	24	SER	2.4
1	2	260	U	2.4
1	2	639	U	2.4
12	C0	61	TRP	2.4
27	d5	62	VAL	2.4
32	E0	47	VAL	2.4
33	E1	88	PRO	2.4
34	sR	19	TRP	2.4
34	sR	206	PRO	2.4
35	SM	18	VAL	2.4
36	1	979	U	2.4
36	5	250	U	2.4
6	s4	74	GLY	2.3
7	S5	94	THR	2.3
8	S6	180	THR	2.3
8	s6	168	THR	2.3
10	s8	51	GLY	2.3
11	s9	11	THR	2.3
26	D4	88	THR	2.3
34	sR	12	THR	2.3
34	sR	15	GLY	2.3
61	n5	31	THR	2.3
2	s0	64	ILE	2.3
7	S5	80	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
7	S5	95	ASN	2.3
8	s6	189	HIS	2.3
18	c6	23	LYS	2.3
18	c6	140	LYS	2.3
19	C7	97	ASN	2.3
3	S1	111	ARG	2.3
3	S1	189	ILE	2.3
7	S5	112	ARG	2.3
9	s7	142	TYR	2.3
10	S8	148	ALA	2.3
10	s8	79	ALA	2.3
20	C8	35	ILE	2.3
45	L8	114	ALA	2.3
56	N0	95	ARG	2.3
58	N2	12	ALA	2.3
58	n2	70	LYS	2.3
12	C0	79	TYR	2.3
12	c0	64	TYR	2.3
19	C7	95	ARG	2.3
21	C9	123	ARG	2.3
63	n7	124	ALA	2.3
66	o0	23	TYR	2.3
1	2	1610	G	2.3
1	6	1774	G	2.3
36	5	2574	G	2.3
3	S1	100	PHE	2.3
9	S7	11	GLN	2.3
67	o1	4	LEU	2.3
71	o5	92	LEU	2.3
45	l8	112	GLU	2.3
49	M3	134	GLU	2.3
49	M3	164	GLU	2.3
71	o5	102	GLU	2.3
5	S3	126	VAL	2.3
5	s3	39	VAL	2.3
7	S5	23	VAL	2.3
13	C1	25	VAL	2.3
14	c2	63	VAL	2.3
16	C4	118	VAL	2.3
25	D3	130	VAL	2.3
28	D6	84	VAL	2.3
30	d8	41	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
35	SM	17	VAL	2.3
57	n1	126	VAL	2.3
63	N7	14	VAL	2.3
4	S2	236	PRO	2.3
9	S7	13	PRO	2.3
17	c5	68	PRO	2.3
1	2	1790	A	2.3
1	6	793	A	2.3
1	6	1516	A	2.3
3	S1	56	SER	2.3
3	S1	169	SER	2.3
22	d0	55	PRO	2.3
52	m6	110	PRO	2.3
36	1	3359	A	2.3
40	L3	277	SER	2.3
59	N3	2	SER	2.3
2	S0	101	ARG	2.3
8	s6	90	GLY	2.3
20	C8	108	LYS	2.3
30	d8	29	ARG	2.3
33	e1	118	ARG	2.3
35	SM	100	THR	2.3
42	L5	279	LYS	2.3
5	S3	88	ALA	2.3
5	S3	208	ILE	2.3
7	s5	195	ALA	2.3
9	S7	125	ILE	2.3
39	l2	247	ARG	2.3
60	n4	64	THR	2.3
71	O5	11	THR	2.3
27	D5	82	HIS	2.3
70	o4	2	ALA	2.3
1	2	1710	U	2.3
2	S0	198	MET	2.3
2	s0	49	ASN	2.3
13	c1	37	ASN	2.3
21	C9	45	MET	2.3
33	E1	106	TYR	2.3
36	1	719	U	2.3
36	1	3319	U	2.3
72	O6	28	TYR	2.3
1	6	682	C	2.3

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Mol	Chain	Res	Type	RSRZ
7	S5	161	ASP	2.3
11	s9	151	ASP	2.3
18	C6	120	ASP	2.3
34	SR	165	ASP	2.3
6	S4	92	LEU	2.3
11	S9	128	LEU	2.3
18	C6	89	LEU	2.3
19	c7	24	LEU	2.3
20	C8	101	LEU	2.3
27	d5	80	LEU	2.3
36	1	1574	C	2.3
36	1	1762	C	2.3
36	1	2444	C	2.3
49	m3	54	LEU	2.3
20	C8	71	GLN	2.3
42	L5	17	GLN	2.3
12	C0	94	GLU	2.3
33	e1	120	GLU	2.3
34	SR	98	GLU	2.3
52	M6	187	GLU	2.3
52	m6	40	GLU	2.3
6	S4	196	VAL	2.3
18	C6	48	VAL	2.3
23	D1	9	VAL	2.3
34	SR	20	VAL	2.3
2	S0	134	LYS	2.3
26	d4	123	LYS	2.3
30	d8	45	LYS	2.3
33	E1	83	LYS	2.3
60	N4	69	LYS	2.3
4	S2	171	PRO	2.3
21	c9	2	PRO	2.3
27	D5	91	PRO	2.3
35	SM	88	ARG	2.3
55	m9	173	ARG	2.3
5	s3	5	ILE	2.3
3	S1	123	ALA	2.3
4	S2	155	ALA	2.3
7	s5	146	THR	2.3
9	s7	106	SER	2.3
11	S9	84	GLY	2.3
17	C5	117	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
14	C2	53	THR	2.3
14	C2	119	SER	2.3
22	d0	24	ILE	2.3
40	L3	253	GLY	2.3
52	m6	144	SER	2.3
67	O1	36	ILE	2.3
18	c6	17	THR	2.3
27	D5	102	THR	2.3
27	D5	105	THR	2.3
34	sR	227	ALA	2.3
58	n2	14	THR	2.3
82	p0	280	ALA	2.3
3	S1	103	MET	2.3
28	D6	72	HIS	2.3
82	p0	38	MET	2.3
12	C0	63	TYR	2.3
21	C9	66	TYR	2.3
82	p0	22	TYR	2.3
3	S1	47	LEU	2.3
4	S2	201	ASN	2.3
7	S5	104	ASN	2.3
14	C2	70	ASN	2.3
16	C4	62	LEU	2.3
19	C7	115	LEU	2.3
25	D3	22	ASN	2.3
33	E1	117	LEU	2.3
55	m9	36	ASN	2.3
57	N1	90	ASN	2.3
62	N6	99	LEU	2.3
4	S2	57	PHE	2.3
35	SM	75	ASP	2.3
82	p0	287	ASP	2.3
1	2	1362	U	2.3
1	6	719	U	2.3
1	6	1609	U	2.3
36	5	3079	U	2.3
15	c3	35	GLU	2.3
1	6	1481	C	2.3
2	S0	50	VAL	2.3
12	c0	52	LYS	2.3
17	C5	8	LYS	2.3
18	c6	4	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
20	C8	48	LYS	2.3
22	D0	31	VAL	2.3
36	5	439	C	2.3
36	5	1581	C	2.3
57	N1	126	VAL	2.3
61	N5	22	LYS	2.3
18	c6	114	ARG	2.3
9	S7	32	PRO	2.3
3	S1	63	GLY	2.3
7	s5	187	ILE	2.3
8	S6	33	GLY	2.3
8	s6	18	ILE	2.3
20	C8	81	ILE	2.3
20	C8	92	ILE	2.3
21	C9	112	GLY	2.3
24	D2	53	ILE	2.3
30	d8	53	ILE	2.3
16	C4	78	ALA	2.3
51	m5	39	ALA	2.3
53	M7	158	ALA	2.3
2	S0	93	THR	2.3
8	S6	96	SER	2.3
14	c2	48	SER	2.3
19	C7	25	THR	2.3
23	d1	56	SER	2.3
26	d4	88	THR	2.3
31	D9	9	SER	2.3
35	SM	28	SER	2.3
66	o0	9	SER	2.3
80	e0	41	THR	2.3
7	S5	97	LEU	2.3
8	S6	189	HIS	2.3
11	S9	109	LEU	2.3
11	s9	109	LEU	2.3
34	SR	144	LEU	2.3
63	N7	80	LEU	2.3
1	2	1685	G	2.3
2	S0	138	TYR	2.3
16	C4	58	TYR	2.3
9	S7	131	PHE	2.3
36	1	1573	G	2.3
36	1	2669	G	2.3

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Mol	Chain	Res	Type	RSRZ
36	5	251	G	2.3
8	s6	140	ASN	2.3
13	C1	22	ASN	2.3
19	C7	31	ASN	2.3
63	n7	76	ASN	2.3
82	p0	98	ASN	2.3
8	S6	20	ASP	2.3
11	S9	94	ASP	2.3
18	C6	77	GLN	2.3
49	m3	137	GLN	2.3
5	s3	223	LYS	2.3
1	2	541	A	2.3
1	6	1593	A	2.3
3	S1	127	VAL	2.3
4	s2	205	ARG	2.3
7	s5	64	VAL	2.3
14	C2	108	ARG	2.3
18	c6	90	VAL	2.3
23	D1	39	VAL	2.3
31	D9	56	ARG	2.3
56	n0	103	VAL	2.3
1	2	909	U	2.3
3	S1	206	PRO	2.3
7	S5	68	ILE	2.3
7	S5	121	ILE	2.3
11	S9	15	PRO	2.3
11	S9	143	ILE	2.3
12	C0	83	PRO	2.3
12	C0	88	PRO	2.3
18	C6	65	ILE	2.3
20	C8	69	ILE	2.3
42	l5	247	ILE	2.3
61	n5	142	ILE	2.3
5	S3	114	ALA	2.3
10	s8	71	GLY	2.3
13	C1	149	ALA	2.3
20	C8	39	GLY	2.3
20	c8	130	GLY	2.3
17	C5	49	MET	2.3
21	c9	107	ALA	2.3
36	1	3164	C	2.3
3	S1	70	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
4	S2	41	LEU	2.3
7	S5	58	LEU	2.3
10	s8	44	HIS	2.3
11	S9	123	HIS	2.3
19	C7	8	THR	2.3
20	C8	77	THR	2.3
20	C8	86	LEU	2.3
22	D0	27	THR	2.3
22	D0	58	LEU	2.3
22	d0	70	THR	2.3
33	E1	125	THR	2.3
34	SR	7	LEU	2.3
66	O0	62	LEU	2.3
71	o5	55	LEU	2.3
58	N2	108	TYR	2.3
2	s0	134	LYS	2.3
9	S7	124	LYS	2.3
13	C1	46	LYS	2.3
19	C7	14	LYS	2.3
52	M6	42	ASN	2.3
11	S9	3	ARG	2.3
18	C6	68	ARG	2.3
20	C8	126	ARG	2.3
32	E0	54	ARG	2.3
34	sR	90	ARG	2.3
55	M9	81	ARG	2.3
60	N4	73	ARG	2.3
22	d0	117	VAL	2.3
26	D4	25	VAL	2.3
34	sR	240	VAL	2.3
35	sM	152	ASP	2.3
48	M1	171	VAL	2.3
52	M6	16	VAL	2.3
12	c0	33	GLU	2.2
1	2	234	G	2.2
1	6	913	G	2.2
36	5	1233	G	2.2
6	s4	64	ILE	2.2
7	S5	199	ILE	2.2
13	C1	54	ILE	2.2
24	D2	83	ILE	2.2
28	D6	60	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
34	SR	30	PRO	2.2
7	S5	78	ALA	2.2
7	s5	26	ALA	2.2
8	s6	192	ALA	2.2
56	n0	102	ALA	2.2
61	N5	118	GLY	2.2
68	o2	127	ALA	2.2
74	O8	18	ALA	2.2
1	2	231	U	2.2
1	2	705	U	2.2
1	6	1259	U	2.2
2	s0	9	LEU	2.2
14	C2	52	LEU	2.2
18	c6	116	LEU	2.2
29	D7	73	LEU	2.2
34	SR	81	LEU	2.2
36	1	1269	U	2.2
36	1	1350	A	2.2
36	1	2404	A	2.2
36	5	1103	A	2.2
53	M7	168	LEU	2.2
3	S1	30	PHE	2.2
25	D3	122	PHE	2.2
39	L2	20	THR	2.2
42	l5	275	THR	2.2
77	Q1	10	THR	2.2
8	S6	53	SER	2.2
14	c2	119	SER	2.2
21	C9	27	LYS	2.2
66	O0	20	SER	2.2
1	2	1379	C	2.2
3	S1	136	ARG	2.2
18	C6	143	ARG	2.2
26	d4	132	ARG	2.2
36	1	1254	C	2.2
5	S3	41	VAL	2.2
8	S6	9	VAL	2.2
11	S9	142	ASN	2.2
16	c4	48	VAL	2.2
18	c6	8	GLN	2.2
19	c7	102	VAL	2.2
22	D0	37	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
24	D2	129	VAL	2.2
26	D4	106	GLN	2.2
61	n5	114	VAL	2.2
71	o5	113	GLN	2.2
7	S5	181	GLU	2.2
43	L6	129	GLU	2.2
46	L9	143	GLU	2.2
69	O3	3	GLU	2.2
11	s9	52	ILE	2.2
3	s1	53	GLY	2.2
5	S3	171	ALA	2.2
7	s5	173	ALA	2.2
8	S6	134	GLY	2.2
10	S8	80	GLY	2.2
11	S9	26	ALA	2.2
16	C4	97	GLY	2.2
18	c6	18	ALA	2.2
20	C8	76	PRO	2.2
25	D3	42	PRO	2.2
20	C8	54	LEU	2.2
24	D2	11	LEU	2.2
26	d4	130	ALA	2.2
28	D6	64	LEU	2.2
29	D7	69	GLY	2.2
42	L5	227	LEU	2.2
44	L7	49	ALA	2.2
45	L8	211	LEU	2.2
52	m6	195	ALA	2.2
58	N2	76	LEU	2.2
9	S7	24	PHE	2.2
10	s8	21	PHE	2.2
1	2	461	G	2.2
1	2	497	G	2.2
1	2	702	G	2.2
2	S0	108	THR	2.2
3	S1	50	LYS	2.2
11	S9	16	LYS	2.2
12	C0	90	THR	2.2
16	c4	86	THR	2.2
18	c6	110	THR	2.2
24	D2	22	LYS	2.2
33	E1	116	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
34	SR	99	THR	2.2
34	sR	99	THR	2.2
52	M6	184	THR	2.2
61	N5	37	THR	2.2
1	2	742	U	2.2
1	6	395	U	2.2
1	6	744	U	2.2
34	SR	79	TYR	2.2
36	1	2102	U	2.2
36	1	2314	U	2.2
36	1	3156	U	2.2
36	5	1555	U	2.2
46	l9	3	TYR	2.2
82	p0	18	TYR	2.2
1	2	217	A	2.2
1	2	733	A	2.2
1	6	1707	A	2.2
11	S9	184	SER	2.2
22	D0	38	SER	2.2
25	d3	40	SER	2.2
25	d3	47	SER	2.2
34	sR	82	SER	2.2
42	l5	10	SER	2.2
62	n6	62	SER	2.2
66	o0	6	SER	2.2
3	S1	167	VAL	2.2
7	S5	168	VAL	2.2
16	C4	42	VAL	2.2
17	c5	94	VAL	2.2
33	e1	114	VAL	2.2
34	SR	167	VAL	2.2
35	SM	106	VAL	2.2
58	n2	47	VAL	2.2
82	p0	41	VAL	2.2
34	sR	185	GLN	2.2
4	s2	82	ASN	2.2
6	S4	157	ASN	2.2
45	l8	33	ASN	2.2
47	M0	55	ASN	2.2
3	S1	196	GLU	2.2
7	s5	89	ILE	2.2
12	c0	43	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
17	c5	84	ILE	2.2
27	D5	92	ILE	2.2
1	2	1332	C	2.2
1	2	1399	C	2.2
2	s0	206	ASP	2.2
36	1	1582	C	2.2
2	s0	99	ALA	2.2
6	S4	107	GLY	2.2
7	S5	182	ALA	2.2
7	s5	78	ALA	2.2
14	C2	128	ALA	2.2
16	C4	137	LEU	2.2
19	c7	117	LEU	2.2
24	d2	73	GLY	2.2
26	D4	18	LEU	2.2
28	D6	48	ALA	2.2
34	sR	91	LEU	2.2
42	l5	230	ASP	2.2
74	o8	19	ASP	2.2
45	l8	154	ALA	2.2
48	m1	8	PRO	2.2
68	O2	2	ALA	2.2
72	O6	96	ALA	2.2
74	o8	69	LEU	2.2
4	s2	84	LYS	2.2
20	C8	80	LYS	2.2
22	d0	32	LYS	2.2
49	M3	131	LYS	2.2
52	m6	60	LYS	2.2
54	M8	72	LYS	2.2
10	s8	113	PHE	2.2
25	D3	107	PHE	2.2
16	c4	133	ARG	2.2
28	D6	15	ARG	2.2
28	d6	10	ARG	2.2
7	s5	38	THR	2.2
19	C7	30	THR	2.2
32	E0	48	THR	2.2
57	N1	29	THR	2.2
8	S6	208	TYR	2.2
71	o5	70	TYR	2.2
4	S2	237	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
5	S3	99	VAL	2.2
11	s9	141	VAL	2.2
20	c8	5	VAL	2.2
30	d8	15	VAL	2.2
3	S1	186	SER	2.2
26	d4	69	SER	2.2
28	D6	57	SER	2.2
28	d6	29	SER	2.2
73	o7	84	SER	2.2
1	2	1473	U	2.2
4	S2	250	GLN	2.2
36	1	2538	U	2.2
70	o4	33	GLN	2.2
2	S0	111	ILE	2.2
7	S5	29	ILE	2.2
9	s7	98	ILE	2.2
18	C6	43	ILE	2.2
54	M8	93	ILE	2.2
1	2	538	A	2.2
1	2	542	A	2.2
1	2	810	G	2.2
1	2	1048	G	2.2
1	6	225	A	2.2
2	s0	188	LEU	2.2
4	S2	134	LEU	2.2
13	c1	40	LEU	2.2
14	c2	47	GLU	2.2
16	C4	24	ASN	2.2
18	C6	116	LEU	2.2
29	D7	3	LEU	2.2
30	D8	54	LEU	2.2
30	D8	58	GLU	2.2
36	1	2445	A	2.2
41	L4	143	GLU	2.2
45	L8	93	LEU	2.2
69	O3	58	GLU	2.2
82	p0	40	GLU	2.2
2	S0	145	ALA	2.2
4	S2	151	PRO	2.2
9	s7	32	PRO	2.2
19	C7	126	ALA	2.2
20	c8	73	MET	2.2

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Mol	Chain	Res	Type	RSRZ
22	D0	95	ALA	2.2
27	d5	79	ALA	2.2
29	D7	53	ALA	2.2
33	e1	124	PRO	2.2
34	SR	255	ALA	2.2
34	SR	280	GLY	2.2
55	M9	183	ALA	2.2
70	o4	78	GLY	2.2
74	o8	18	ALA	2.2
2	S0	88	LYS	2.2
2	S0	167	LYS	2.2
3	S1	224	ASP	2.2
7	s5	213	LYS	2.2
8	S6	223	LYS	2.2
25	D3	3	LYS	2.2
33	e1	143	LYS	2.2
48	M1	174	LYS	2.2
60	N4	70	LYS	2.2
60	N4	77	LYS	2.2
2	S0	107	PHE	2.2
2	S0	113	ARG	2.2
5	S3	25	PHE	2.2
7	S5	185	ARG	2.2
11	S9	104	PHE	2.2
20	C8	40	ARG	2.2
73	o7	65	ARG	2.2
1	2	1082	C	2.2
1	2	1481	C	2.2
3	S1	52	THR	2.2
8	s6	163	THR	2.2
14	C2	139	HIS	2.2
14	c2	53	THR	2.2
17	c5	128	HIS	2.2
40	L3	337	THR	2.2
45	l8	74	THR	2.2
48	M1	53	THR	2.2
65	N9	26	THR	2.2
3	S1	192	VAL	2.2
5	s3	12	VAL	2.2
8	S6	84	TYR	2.2
12	C0	75	TYR	2.2
4	s2	250	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
9	s7	49	ILE	2.2
13	C1	16	GLN	2.2
15	C3	143	SER	2.2
19	c7	41	ILE	2.2
21	C9	41	SER	2.2
21	c9	100	ILE	2.2
43	l6	2	SER	2.2
50	M4	10	SER	2.2
63	n7	68	ILE	2.2
3	s1	218	LEU	2.2
11	S9	118	LEU	2.2
34	sR	13	LEU	2.2
34	sR	23	LEU	2.2
5	s3	80	ALA	2.2
14	c2	132	GLU	2.2
8	s6	174	LYS	2.2
9	s7	3	ALA	2.2
24	d2	29	PRO	2.2
25	D3	110	LYS	2.2
30	d8	63	ALA	2.2
34	SR	285	ALA	2.2
35	sM	70	ASN	2.2
40	L3	22	ALA	2.2
43	L6	13	GLU	2.2
1	2	493	U	2.2
1	6	1398	U	2.2
3	s1	44	GLY	2.2
7	S5	67	PRO	2.2
9	s7	69	GLY	2.2
16	C4	109	GLY	2.2
18	C6	130	GLY	2.2
19	C7	10	LYS	2.2
45	l8	117	ALA	2.2
51	M5	90	ASN	2.2
55	M9	178	ALA	2.2
60	n4	116	LYS	2.2
63	n7	64	LYS	2.2
71	o5	115	LYS	2.2
73	o7	86	ALA	2.2
36	1	1765	U	2.2
36	1	3287	U	2.2
36	5	1353	U	2.2

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Mol	Chain	Res	Type	RSRZ
36	5	1569	U	2.2
48	M1	8	PRO	2.2
74	O8	35	GLY	2.2
14	C2	33	ARG	2.2
17	C5	127	ARG	2.2
3	s1	100	PHE	2.2
7	s5	60	ASP	2.2
1	6	979	A	2.2
1	6	496	G	2.2
21	C9	53	TRP	2.2
36	1	1576	G	2.2
29	D7	19	HIS	2.2
12	C0	87	VAL	2.1
17	c5	124	THR	2.1
19	C7	124	VAL	2.1
20	C8	70	VAL	2.1
22	D0	62	VAL	2.1
22	d0	31	VAL	2.1
23	D1	52	THR	2.1
26	D4	5	VAL	2.1
66	O0	48	THR	2.1
11	S9	8	TYR	2.1
33	E1	85	TYR	2.1
1	2	716	C	2.1
1	2	1365	C	2.1
3	S1	161	ILE	2.1
6	s4	147	ILE	2.1
27	d5	92	ILE	2.1
34	SR	43	ILE	2.1
36	1	2507	C	2.1
36	5	1017	C	2.1
42	l5	69	ILE	2.1
3	S1	97	LEU	2.1
8	s6	199	GLN	2.1
19	C7	57	LEU	2.1
27	D5	51	LEU	2.1
30	d8	54	LEU	2.1
6	s4	6	LYS	2.1
17	c5	9	LYS	2.1
8	S6	204	ALA	2.1
18	C6	121	SER	2.1
21	c9	69	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
21	c9	85	SER	2.1
34	SR	87	LYS	2.1
21	C9	82	GLY	2.1
23	D1	62	ARG	2.1
23	d1	42	GLU	2.1
26	D4	50	ALA	2.1
32	E0	34	ALA	2.1
34	sR	60	SER	2.1
34	sR	120	SER	2.1
44	L7	23	ALA	2.1
47	M0	219	ALA	2.1
50	M4	5	SER	2.1
53	M7	163	LYS	2.1
68	o2	16	LYS	2.1
12	C0	6	GLU	2.1
28	D6	46	GLU	2.1
51	M5	71	ARG	2.1
52	m6	46	GLU	2.1
55	m9	189	ALA	2.1
68	O2	127	ALA	2.1
6	S4	15	PRO	2.1
6	S4	152	PRO	2.1
8	S6	186	ARG	2.1
14	C2	55	GLY	2.1
28	D6	85	ARG	2.1
51	m5	2	GLY	2.1
7	S5	44	ASN	2.1
34	SR	174	ASN	2.1
58	N2	30	PRO	2.1
67	O1	53	PRO	2.1
11	s9	146	PHE	2.1
18	C6	46	PHE	2.1
18	C6	60	PHE	2.1
29	D7	47	PHE	2.1
14	c2	39	ASP	2.1
34	SR	217	ASP	2.1
34	sR	165	ASP	2.1
36	5	981	U	2.1
46	L9	190	ASP	2.1
3	S1	225	VAL	2.1
4	S2	86	VAL	2.1
18	c6	39	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
20	C8	4	VAL	2.1
24	D2	121	VAL	2.1
28	D6	24	VAL	2.1
34	sR	20	VAL	2.1
70	O4	23	VAL	2.1
82	p0	59	VAL	2.1
12	c0	57	THR	2.1
14	C2	34	THR	2.1
22	d0	27	THR	2.1
1	6	579	A	2.1
1	6	1336	A	2.1
11	s9	140	ILE	2.1
7	S5	107	LYS	2.1
7	s5	106	LYS	2.1
11	S9	59	LEU	2.1
14	C2	95	LYS	2.1
14	c2	90	LYS	2.1
22	d0	34	LEU	2.1
23	D1	55	LEU	2.1
25	d3	3	LYS	2.1
29	d7	41	LEU	2.1
30	D8	9	LEU	2.1
58	N2	13	LYS	2.1
58	n2	89	LEU	2.1
68	o2	4	LEU	2.1
1	2	687	G	2.1
1	2	1354	G	2.1
1	6	823	G	2.1
12	c0	1	MET	2.1
8	S6	88	ARG	2.1
8	S6	176	GLN	2.1
8	s6	204	ALA	2.1
15	C3	144	ALA	2.1
16	C4	100	ALA	2.1
16	C4	127	ARG	2.1
24	D2	10	ALA	2.1
28	D6	10	ARG	2.1
34	SR	52	GLN	2.1
61	n5	47	ALA	2.1
82	p0	106	ALA	2.1
9	S7	95	GLU	2.1
9	s7	187	SER	2.1

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Mol	Chain	Res	Type	RSRZ
10	S8	118	GLY	2.1
10	s8	7	SER	2.1
14	c2	55	GLY	2.1
14	c2	117	GLY	2.1
15	C3	68	GLY	2.1
1	2	910	C	2.1
1	2	1494	C	2.1
7	S5	30	PRO	2.1
7	S5	88	PRO	2.1
7	s5	28	PRO	2.1
15	C3	137	PRO	2.1
20	C8	106	GLU	2.1
24	D2	67	GLY	2.1
25	D3	44	GLY	2.1
34	sR	160	GLU	2.1
52	m6	146	GLY	2.1
55	M9	79	GLY	2.1
36	1	2101	C	2.1
36	5	180	C	2.1
2	S0	89	PHE	2.1
5	s3	156	PHE	2.1
7	s5	122	ASN	2.1
12	c0	39	ASN	2.1
30	D8	51	ASN	2.1
4	S2	36	VAL	2.1
9	S7	20	VAL	2.1
9	s7	20	VAL	2.1
11	S9	172	VAL	2.1
12	c0	89	VAL	2.1
14	C2	86	VAL	2.1
17	c5	11	VAL	2.1
20	c8	129	TRP	2.1
26	D4	24	VAL	2.1
57	N1	18	ASP	2.1
70	o4	101	VAL	2.1
3	S1	153	HIS	2.1
1	2	1657	U	2.1
1	6	1029	U	2.1
2	S0	17	LEU	2.1
2	S0	64	ILE	2.1
3	S1	171	ILE	2.1
9	S7	117	THR	2.1

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Mol	Chain	Res	Type	RSRZ
2	S0	110	TYR	2.1
6	S4	127	LYS	2.1
7	S5	42	LEU	2.1
7	S5	217	LEU	2.1
7	s5	209	TYR	2.1
9	s7	41	LEU	2.1
10	s8	78	ILE	2.1
12	c0	92	THR	2.1
12	c0	94	ILE	2.1
13	C1	56	LYS	2.1
18	c6	117	LEU	2.1
23	d1	69	LEU	2.1
24	D2	35	ILE	2.1
29	D7	44	THR	2.1
33	e1	107	LYS	2.1
36	1	2501	U	2.1
36	5	249	U	2.1
41	l4	7	THR	2.1
50	m4	25	LYS	2.1
63	N7	54	THR	2.1
5	s3	150	MET	2.1
21	c9	57	ARG	2.1
40	L3	261	MET	2.1
69	o3	60	ARG	2.1
80	e0	56	MET	2.1
6	s4	28	ALA	2.1
11	s9	139	GLN	2.1
21	C9	59	ALA	2.1
21	c9	19	ALA	2.1
35	SM	42	ALA	2.1
50	m4	27	GLN	2.1
1	6	684	A	2.1
1	6	829	A	2.1
4	S2	55	GLU	2.1
5	S3	130	GLY	2.1
9	S7	40	PRO	2.1
12	C0	4	PRO	2.1
16	C4	88	GLY	2.1
18	c6	5	PRO	2.1
26	d4	30	PRO	2.1
33	E1	124	PRO	2.1
36	1	2096	A	2.1

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Mol	Chain	Res	Type	RSRZ
36	1	2100	A	2.1
36	1	3163	A	2.1
39	L2	201	GLY	2.1
60	n4	99	GLU	2.1
66	o0	8	GLU	2.1
2	S0	151	SER	2.1
2	s0	114	SER	2.1
6	s4	24	SER	2.1
17	c5	51	SER	2.1
19	c7	43	SER	2.1
29	d7	60	SER	2.1
34	sR	61	PHE	2.1
42	l5	220	SER	2.1
63	n7	130	PHE	2.1
21	C9	43	ASN	2.1
33	E1	151	ASN	2.1
34	SR	17	ASN	2.1
34	sR	248	ASN	2.1
56	N0	74	ASN	2.1
56	n0	74	ASN	2.1
1	2	1241	G	2.1
1	6	738	G	2.1
1	6	1695	G	2.1
12	c0	20	VAL	2.1
14	C2	60	VAL	2.1
20	c8	22	VAL	2.1
23	D1	13	VAL	2.1
30	d8	55	VAL	2.1
36	1	1242	G	2.1
36	5	1560	G	2.1
36	5	2503	G	2.1
36	5	3290	G	2.1
40	L3	336	VAL	2.1
52	m6	3	VAL	2.1
36	5	2507	C	2.1
2	S0	188	LEU	2.1
5	s3	109	LEU	2.1
6	s4	253	ASP	2.1
9	S7	89	HIS	2.1
34	SR	137	LYS	2.1
34	SR	149	ASP	2.1
35	SM	27	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
42	l5	41	LYS	2.1
45	L8	43	LYS	2.1
9	s7	9	LEU	2.1
11	S9	28	LEU	2.1
11	S9	45	ILE	2.1
15	C3	54	LEU	2.1
19	c7	38	ILE	2.1
21	c9	113	ILE	2.1
27	D5	80	LEU	2.1
47	M0	71	CYS	2.1
55	M9	25	ASP	2.1
58	n2	41	ILE	2.1
74	O8	8	ILE	2.1
9	S7	104	ARG	2.1
16	C4	26	THR	2.1
16	C4	84	ARG	2.1
21	c9	139	THR	2.1
30	D8	64	ARG	2.1
20	C8	73	MET	2.1
24	D2	46	TYR	2.1
34	SR	12	THR	2.1
39	L2	243	THR	2.1
44	L7	30	ARG	2.1
45	L8	217	THR	2.1
45	l8	177	TYR	2.1
70	O4	71	THR	2.1
34	SR	231	MET	2.1
3	S1	57	ALA	2.1
8	S6	205	ALA	2.1
16	C4	59	ALA	2.1
18	C6	86	ALA	2.1
34	SR	172	ALA	2.1
80	e0	2	ALA	2.1
1	2	232	U	2.1
1	2	1704	U	2.1
7	s5	170	GLN	2.1
36	5	182	U	2.1
44	L7	25	GLN	2.1
2	s0	51	GLY	2.1
3	S1	233	GLY	2.1
23	d1	43	GLY	2.1
32	E0	32	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
55	m9	83	GLY	2.1
2	S0	155	PHE	2.1
2	s0	35	PRO	2.1
9	s7	4	PRO	2.1
9	s7	95	GLU	2.1
31	D9	8	PHE	2.1
34	SR	206	PRO	2.1
49	m3	192	GLU	2.1
52	M6	40	GLU	2.1
54	M8	95	GLU	2.1
63	N7	131	PHE	2.1
63	n7	82	PRO	2.1
67	o1	90	PHE	2.1
82	p0	74	GLU	2.1
6	s4	41	SER	2.1
12	C0	48	SER	2.1
14	C2	134	SER	2.1
23	D1	68	SER	2.1
50	M4	28	SER	2.1
16	c4	13	VAL	2.1
20	C8	52	VAL	2.1
22	d0	37	VAL	2.1
34	sR	94	VAL	2.1
34	sR	113	VAL	2.1
1	6	755	A	2.1
3	S1	33	LYS	2.1
8	s6	187	LYS	2.1
14	C2	50	LYS	2.1
17	c5	8	LYS	2.1
33	E1	134	ASN	2.1
33	e1	97	LYS	2.1
45	l8	137	ASN	2.1
63	n7	55	LYS	2.1
75	O9	32	ASN	2.1
3	S1	184	LEU	2.1
3	S1	207	LEU	2.1
5	S3	176	LEU	2.1
6	S4	173	ILE	2.1
9	S7	126	LEU	2.1
5	s3	159	HIS	2.1
9	s7	104	ARG	2.1
10	S8	67	TRP	2.1

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Mol	Chain	Res	Type	RSRZ
12	C0	95	ARG	2.1
16	C4	115	ILE	2.1
17	c5	22	LEU	2.1
19	C7	46	LEU	2.1
19	C7	117	LEU	2.1
21	C9	65	ILE	2.1
29	D7	41	LEU	2.1
42	l5	277	LEU	2.1
46	L9	134	ILE	2.1
52	M6	79	ILE	2.1
70	O4	54	ILE	2.1
15	C3	4	MET	2.1
5	S3	34	TYR	2.1
7	s5	140	THR	2.1
11	S9	12	TYR	2.1
16	C4	20	TYR	2.1
20	C8	47	CYS	2.1
30	d8	26	THR	2.1
75	O9	34	THR	2.1
1	6	1379	C	2.1
1	2	1114	G	2.1
1	2	1486	G	2.1
1	2	1720	G	2.1
1	6	34	G	2.1
1	6	1696	G	2.1
4	S2	92	ALA	2.1
16	c4	50	ALA	2.1
21	C9	11	ALA	2.1
36	1	1262	G	2.1
36	1	1268	G	2.1
36	1	1952	G	2.1
36	5	173	G	2.1
36	5	1953	G	2.1
63	N7	7	ALA	2.1
66	O0	95	ALA	2.1
9	s7	54	GLY	2.1
12	c0	62	GLN	2.1
12	c0	95	GLN	2.1
16	C4	95	GLY	2.1
20	C8	9	GLY	2.1
21	C9	106	GLN	2.1
21	c9	23	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
22	D0	111	GLY	2.1
29	D7	51	GLN	2.1
35	SM	111	GLY	2.1
39	L2	250	GLN	2.1
42	l5	151	GLN	2.1
72	O6	14	GLY	2.1
5	S3	43	PRO	2.1
5	S3	203	PRO	2.1
11	s9	164	PHE	2.1
14	c2	56	GLU	2.1
15	C3	26	PHE	2.1
17	c5	118	GLU	2.1
19	C7	22	PRO	2.1
26	D4	119	PHE	2.1
26	d4	23	PHE	2.1
80	e0	60	PRO	2.1
5	s3	181	VAL	2.0
11	S9	96	VAL	2.0
14	C2	105	LYS	2.0
18	C6	140	LYS	2.0
19	c7	110	VAL	2.0
21	c9	30	VAL	2.0
22	D0	97	VAL	2.0
22	d0	101	LYS	2.0
34	SR	262	VAL	2.0
35	sM	23	LYS	2.0
36	1	1555	U	2.0
36	1	2508	U	2.0
36	1	2875	U	2.0
42	L5	5	LYS	2.0
60	n4	117	LYS	2.0
14	c2	134	SER	2.0
34	sR	108	SER	2.0
2	S0	120	LEU	2.0
8	S6	196	ARG	2.0
8	s6	215	ARG	2.0
9	S7	116	ARG	2.0
11	S9	105	LEU	2.0
11	S9	150	LEU	2.0
12	c0	15	LEU	2.0
13	C1	49	ILE	2.0
14	c2	108	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
18	C6	54	LEU	2.0
24	D2	80	ASN	2.0
25	D3	7	ARG	2.0
32	E0	42	ARG	2.0
32	E0	46	ASN	2.0
35	sM	51	ARG	2.0
55	M9	138	LEU	2.0
55	M9	143	ILE	2.0
57	N1	85	LEU	2.0
58	n2	38	ILE	2.0
65	n9	21	ILE	2.0
67	O1	4	LEU	2.0
9	S7	122	HIS	2.0
20	C8	13	HIS	2.0
20	c8	55	HIS	2.0
41	l4	65	TRP	2.0
1	2	623	A	2.0
3	S1	180	THR	2.0
4	s2	124	ALA	2.0
4	s2	183	ALA	2.0
4	s2	245	ASP	2.0
9	s7	23	ALA	2.0
11	s9	61	THR	2.0
16	C4	66	ASP	2.0
16	c4	91	THR	2.0
21	c9	80	TYR	2.0
22	D0	107	THR	2.0
26	D4	80	ALA	2.0
34	sR	266	ASP	2.0
41	L4	17	ALA	2.0
56	N0	147	ASP	2.0
63	n7	49	TYR	2.0
63	n7	86	THR	2.0
65	n9	27	TYR	2.0
67	o1	85	ALA	2.0
6	S4	74	GLY	2.0
17	c5	129	GLY	2.0
32	E0	6	GLY	2.0
33	e1	129	GLY	2.0
34	SR	29	GLN	2.0
51	m5	52	GLY	2.0
54	M8	183	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
13	C1	45	PRO	2.0
22	D0	96	PRO	2.0
49	m3	133	PRO	2.0
58	N2	15	PHE	2.0
3	s1	234	GLU	2.0
1	2	708	C	2.0
5	s3	194	LYS	2.0
10	s8	199	LYS	2.0
16	C4	47	LYS	2.0
18	c6	47	LYS	2.0
28	D6	70	LYS	2.0
33	E1	94	LYS	2.0
45	L8	92	LYS	2.0
82	p0	292	GLU	2.0
2	S0	139	VAL	2.0
8	S6	157	VAL	2.0
10	S8	156	VAL	2.0
14	C2	75	VAL	2.0
17	C5	11	VAL	2.0
21	C9	73	VAL	2.0
30	D8	25	VAL	2.0
34	sR	56	VAL	2.0
54	m8	115	VAL	2.0
1	2	732	G	2.0
1	6	722	G	2.0
1	6	1199	G	2.0
2	S0	149	LEU	2.0
3	s1	97	LEU	2.0
3	s1	231	LEU	2.0
7	s5	148	ARG	2.0
9	S7	27	LEU	2.0
11	S9	49	LEU	2.0
13	C1	30	ARG	2.0
19	C7	11	ARG	2.0
23	D1	79	LEU	2.0
26	d4	44	LEU	2.0
27	D5	65	LEU	2.0
36	1	1565	G	2.0
36	1	2522	G	2.0
57	n1	31	LEU	2.0
65	N9	54	LEU	2.0
82	p0	16	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
2	S0	133	ILE	2.0
2	S0	173	ILE	2.0
5	S3	209	ILE	2.0
7	s5	40	ILE	2.0
12	C0	35	ILE	2.0
12	c0	51	SER	2.0
18	c6	141	SER	2.0
22	D0	86	ILE	2.0
22	D0	99	ILE	2.0
22	d0	106	ILE	2.0
34	sR	211	ILE	2.0
35	SM	95	SER	2.0
52	M6	43	ILE	2.0
72	o6	19	SER	2.0
1	6	241	U	2.0
1	6	657	U	2.0
1	6	667	U	2.0
1	6	1340	U	2.0
7	S5	79	ASN	2.0
22	D0	84	MET	2.0
23	D1	75	ASN	2.0
25	D3	18	HIS	2.0
28	D6	39	MET	2.0
31	d9	5	ASN	2.0
36	1	252	U	2.0
36	5	441	U	2.0
36	5	1356	U	2.0
38	4	125	U	2.0
57	N1	77	ASN	2.0
7	s5	46	TRP	2.0
10	S8	9	HIS	2.0
17	c5	15	HIS	2.0
57	N1	79	MET	2.0
4	S2	206	THR	2.0
14	C2	92	ALA	2.0
7	S5	209	TYR	2.0
17	C5	115	TYR	2.0
18	C6	110	THR	2.0
19	C7	15	ALA	2.0
21	c9	83	ALA	2.0
22	D0	29	THR	2.0
34	sR	279	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
47	m0	68	ALA	2.0
82	p0	289	ALA	2.0
18	c6	96	TYR	2.0
33	E1	148	TYR	2.0
6	S4	79	ASP	2.0
11	S9	151	ASP	2.0
35	SM	36	ASP	2.0
35	SM	101	ASP	2.0
45	L8	83	ASP	2.0
2	s0	186	GLY	2.0
14	c2	40	GLY	2.0
4	S2	46	LYS	2.0
5	s3	134	CYS	2.0
7	S5	105	GLY	2.0
24	D2	100	GLY	2.0
32	E0	59	GLY	2.0
34	SR	192	PHE	2.0
34	SR	245	PHE	2.0
4	s2	199	GLN	2.0
5	S3	7	LYS	2.0
5	S3	223	LYS	2.0
11	s9	144	PRO	2.0
12	C0	93	GLN	2.0
16	C4	49	LYS	2.0
16	C4	65	GLN	2.0
16	c4	49	LYS	2.0
18	c6	127	LYS	2.0
51	m5	152	CYS	2.0
56	N0	138	GLN	2.0
60	n4	70	LYS	2.0
1	6	197	A	2.0
1	6	1583	A	2.0
1	6	1800	A	2.0
5	S3	206	VAL	2.0
9	s7	109	VAL	2.0
14	c2	83	GLU	2.0
10	S8	18	ARG	2.0
11	S9	83	VAL	2.0
15	C3	3	ARG	2.0
17	C5	94	VAL	2.0
17	c5	5	VAL	2.0
22	D0	115	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
20	c8	132	ARG	2.0
26	d4	12	VAL	2.0
34	SR	58	VAL	2.0
40	l3	227	GLU	2.0
47	m0	212	GLU	2.0
45	l8	44	ARG	2.0
60	N4	76	VAL	2.0
69	O3	60	ARG	2.0
3	s1	135	LEU	2.0
4	s2	235	LEU	2.0
6	S4	12	LEU	2.0
7	S5	194	LEU	2.0
9	S7	58	LEU	2.0
12	c0	49	LEU	2.0
30	D8	33	LEU	2.0
47	m0	111	LEU	2.0
62	N6	126	LEU	2.0
2	S0	141	ILE	2.0
7	S5	190	ILE	2.0
7	s5	190	ILE	2.0
8	S6	141	ILE	2.0
22	D0	24	ILE	2.0
24	d2	103	ILE	2.0
34	SR	169	ILE	2.0
45	L8	36	ILE	2.0
58	n2	11	ILE	2.0
1	2	239	C	2.0
36	5	1563	C	2.0
36	5	3166	C	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
85	8AN	D	76	22/23	0.96	0.08	32,33,34,35	0
85	8AN	C	76	22/23	0.98	0.06	34,34,34,34	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
86	ZN	D7	101	1/1	0.81	0.14	165,165,165,165	0
86	ZN	d7	101	1/1	0.82	0.14	148,148,148,148	0
88	MG	C	3402	1/1	0.90	0.20	34,34,34,34	0
86	ZN	e1	501	1/1	0.91	0.14	200,200,200,200	0
88	MG	D	3402	1/1	0.91	0.18	33,33,33,33	0
87	SPS	D	3401	23/23	0.92	0.13	29,32,45,48	0
86	ZN	E1	501	1/1	0.93	0.08	155,155,155,155	0
87	SPS	C	3401	23/23	0.96	0.09	29,32,46,48	0
86	ZN	Q2	501	1/1	0.97	0.11	75,75,75,75	0
86	ZN	q2	501	1/1	0.97	0.12	72,72,72,72	0
86	ZN	D6	500	1/1	0.98	0.03	88,88,88,88	0
86	ZN	q0	500	1/1	0.99	0.02	38,38,38,38	0
86	ZN	Q3	501	1/1	0.99	0.04	66,66,66,66	0
86	ZN	q3	501	1/1	0.99	0.05	60,60,60,60	0
86	ZN	d6	500	1/1	0.99	0.03	57,57,57,57	0
86	ZN	Q0	500	1/1	0.99	0.03	46,46,46,46	0
86	ZN	d9	101	1/1	0.99	0.04	85,85,85,85	0
86	ZN	D9	101	1/1	0.99	0.03	85,85,85,85	0
86	ZN	o7	501	1/1	1.00	0.03	46,46,46,46	0
86	ZN	O7	100	1/1	1.00	0.01	44,44,44,44	0

6.5 Other polymers (i)

There are no such residues in this entry.