



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 7, 2016 – 03:30 AM EDT

PDB ID : 5J3C
Title : Thermus thermophilus 70S termination complex containing E. coli RF1
Authors : Hoffer, E.D.; Dunham, C.M.
Deposited on : 2016-03-30
Resolution : 3.04 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : **FAILED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027939

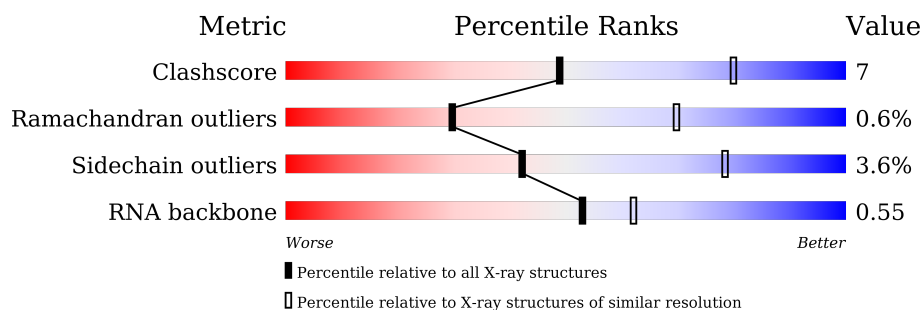
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.04 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	2351 (3.08-3.00)
Ramachandran outliers	100387	2272 (3.08-3.00)
Sidechain outliers	100360	2275 (3.08-3.00)
RNA backbone	2183	1061 (3.48-2.60)











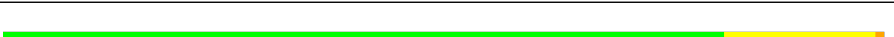


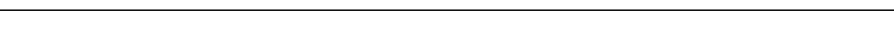
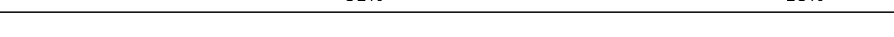
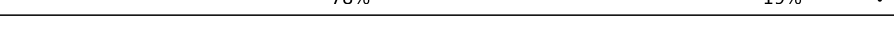



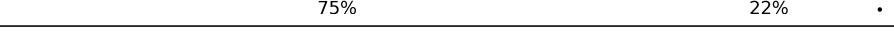





The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey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

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	RA	2915	
1	YA	2915	
2	RB	122	
2	YB	122	
3	RD	276	
3	YD	276	









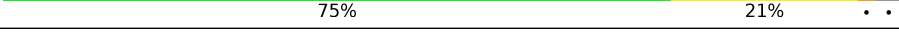

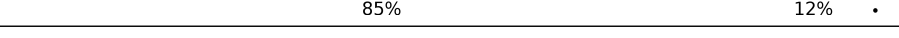
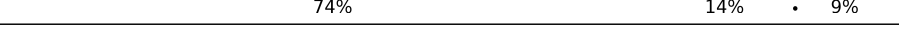

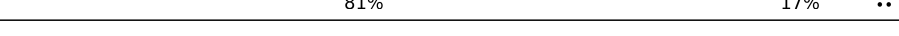


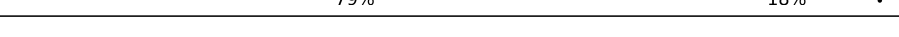

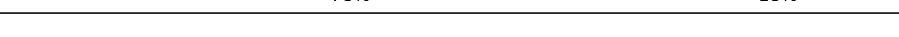






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Mol	Chain	Length	Quality of chain
4	RE	206	 77%20%..
4	YE	206	 76%21%..
5	RF	210	 73%21%..
5	YF	210	 69%27%..
6	RG	182	 75%25%.
6	YG	182	 71%25%..
7	RH	180	 82%14%..
7	YH	180	 68%28%..
8	RI	148	 80%18%..
8	YI	148	 80%15%..
9	RN	140	 81%17%.
9	YN	140	 83%14%.
10	RO	122	 76%24%
10	YO	122	 81%18%.
11	RP	150	 78%19%..
11	YP	150	 75%21%..
12	RQ	141	 81%18%.
12	YQ	141	 77%21%.
13	RR	118	 75%22%.
13	YR	118	 81%19%
14	RS	112	 80%15%..
14	YS	112	 81%16%..
15	RT	146	 66%20%.10%
15	YT	146	 71%17%.10%
16	RU	118	 81%16%..


























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Mol	Chain	Length	Quality of chain
16	YU	118	 83% 15% .
17	RV	101	 83% 15% .
17	YV	101	 79% 19% ..
18	RW	113	 84% 14% ..
18	YW	113	 81% 18% ..
19	RX	96	 76% 23% .
19	YX	96	 88% 11% .
20	RY	110	 76% 20% ..
20	YY	110	 75% 21% . .
21	RZ	206	 83% 14% ..
21	YZ	206	 85% 12% .
22	R0	85	 74% 14% . 9%
22	Y0	85	 73% 16% . 9%
23	R1	98	 81% 17% ..
23	Y1	98	 76% 21% ..
24	R2	72	 75% 22% .
24	Y2	72	 79% 18% .
25	R3	60	 87% 12% .
25	Y3	60	 78% 18% ..
26	R4	71	 58% 35% . . .
26	Y4	71	 63% 30% . . .
27	R5	60	 73% 22% ..
27	Y5	60	 83% 13% ..
28	R6	54	 76% 22% .
28	Y6	54	 80% 19% .

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Mol	Chain	Length	Quality of chain
29	R7	49	 71% 27% .
29	Y7	49	 69% 29% .
30	R8	65	 72% 23% . .
30	Y8	65	 69% 29% .
31	R9	37	 59% 41%
31	Y9	37	 68% 32%
32	QA	1521	 61% 32% 5% .
32	XA	1521	 61% 32% 6% .
33	QB	256	 59% 27% . . 10%
33	XB	256	 55% 30% 5% 10%
34	QC	239	 67% 18% . 14%
34	XC	239	 66% 19% . 14%
35	QD	209	 64% 34% .
35	XD	209	 72% 26% .
36	QE	162	 65% 26% 9%
36	XE	162	 69% 22% . 9%
37	QF	101	 71% 28% .
37	XF	101	 86% 12% ..
38	QG	156	 83% 15% ..
38	XG	156	 83% 15% ..
39	QH	138	 78% 21% ..
39	XH	138	 78% 21% ..
40	QI	128	 68% 29% ..
40	XI	128	 62% 34% . .
41	QJ	105	 57% 33% . 8%

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Mol	Chain	Length	Quality of chain
41	XJ	105	
42	QK	129	
42	XK	129	
43	QL	132	
43	XL	132	
44	QM	126	
44	XM	126	
45	QN	61	
45	XN	61	
46	QO	89	
46	XO	89	
47	QP	88	
47	XP	88	
48	QQ	105	
48	XQ	105	
49	QR	88	
49	XR	88	
50	QS	93	
50	XS	93	
51	QT	106	
51	XT	106	
52	QU	27	
52	XU	27	
53	QV	77	
53	XV	77	

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Mol	Chain	Length	Quality of chain
54	QX	25	
54	XX	25	
55	QY	360	
55	XY	360	

2 Entry composition [i](#)

There are 58 unique types of molecules in this entry. The entry contains 294929 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 23S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	RA	2867	Total	C	N	O	P	0	0	0
			61758	27491	11552	19850	2865			
1	YA	2867	Total	C	N	O	P	0	0	0
			61758	27491	11552	19850	2865			

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	RB	120	Total	C	N	O	P	0	0	0
			2572	1145	476	832	119			
2	YB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	RD	275	Total	C	N	O	S	0	0	0
			2131	1346	422	360	3			
3	YD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	RE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			
4	YE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	RF	203	Total	C	N	O	S	0	0	1
			1584	1009	298	275	2			
5	YF	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	RG	181	Total	C	N	O	S	0	0	0
			1426	916	253	253	4			
6	YG	181	Total	C	N	O	S	0	0	0
			1424	912	259	249	4			

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	RH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			
7	YH	173	Total	C	N	O	S	0	0	0
			1324	842	247	234	1			

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	RI	147	Total	C	N	O	S	0	0	0
			1094	699	191	203	1			
8	YI	146	Total	C	N	O	S	0	0	0
			1076	687	186	202	1			

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	RN	140	Total	C	N	O	S	0	0	0
			1121	722	208	187	4			
9	YN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	RO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	YO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	RP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			
11	YP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	RQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
12	YQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	RR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			
13	YR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	RS	110	Total	C	N	O	0	0	0
			877	553	175	149			
14	YS	110	Total	C	N	O	0	0	0
			870	549	173	148			

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	RT	131	Total	C	N	O	S	0	0	0
			1091	680	225	185	1			
15	YT	131	Total	C	N	O	S	0	0	0
			1083	675	224	183	1			

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	RU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			
16	YU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	RV	101	Total	C	N	O	S	0	0	0
			775	498	141	135	1			
17	YV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	RW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			
18	YW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	RX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
19	YX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	RY	107	Total	C	N	O	S	0	0	0
			810	520	153	131	6			
20	YY	107	Total	C	N	O	S	0	0	0
			810	519	153	132	6			

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	RZ	203	Total	C	N	O	S	0	0	0
			1587	1011	282	292	2			
21	YZ	201	Total	C	N	O	S	0	0	0
			1557	995	274	286	2			

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	R0	77	Total	C	N	O	S	0	0	0
			608	375	129	103	1			
22	Y0	77	Total	C	N	O	S	0	0	0
			608	375	129	103	1			

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	R1	97	Total	C	N	O	S	0	0	0
			754	475	148	130	1			
23	Y1	97	Total	C	N	O	S	0	0	0
			759	478	149	131	1			

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	R2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			
24	Y2	70	Total	C	N	O	S	0	0	0
			592	368	119	103	2			

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
25	R3	59	Total	C	N	O	0	0	0
			469	298	90	81			
25	Y3	59	Total	C	N	O	0	0	0
			464	296	90	78			

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	R4	69	Total	C	N	O	S	0	0	0
			546	346	96	99	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	Y4	69	Total	C	N	O	S	0	0	0
			536	342	98	91	5			

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	R5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			
27	Y5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	R6	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			
28	Y6	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	R7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			
29	Y7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	R8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			
30	Y8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	R9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
31	Y9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 32 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	QA	1500	Total	C	N	O	P	0	0	0
			32246	14358	5975	10413	1500			
32	XA	1504	Total	C	N	O	P	0	0	0
			32331	14396	5990	10441	1504			

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	QB	231	Total	C	N	O	S	0	0	0
			1842	1175	330	332	5			
33	XB	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	5			

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	QC	206	Total	C	N	O	S	0	0	0
			1558	979	305	273	1			
34	XC	206	Total	C	N	O	S	0	0	0
			1542	968	300	273	1			

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	QD	208	Total	C	N	O	S	0	0	0
			1665	1043	329	286	7			
35	XD	208	Total	C	N	O	S	0	0	0
			1668	1047	330	284	7			

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	QE	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			
36	XE	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	QF	100	Total	C	N	O	S	0	0	0
			814	516	144	151	3			
37	XF	100	Total	C	N	O	S	0	0	0
			816	516	146	151	3			

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	QG	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			
38	XG	155	Total	C	N	O	S	0	0	0
			1229	766	241	216	6			

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	QH	137	Total	C	N	O	S	0	0	0
			1098	694	210	192	2			
39	XH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
40	QI	127	Total	C	N	O	0	0	0
			986	625	193	168			
40	XI	126	Total	C	N	O	0	0	0
			966	613	186	167			

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
41	QJ	97	Total	C	N	O	0	0	0
			719	446	142	131			
41	XJ	96	Total	C	N	O	0	0	0
			710	442	137	131			

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	QK	114	Total	C	N	O	S	0	0	0
			834	520	156	155	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	XK	114	Total	C	N	O	S	0	0	0
			833	519	156	155	3			

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	QL	122	Total	C	N	O	S	0	0	0
			932	586	185	159	2			
43	XL	122	Total	C	N	O	S	0	0	0
			932	586	185	159	2			

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	QM	116	Total	C	N	O	S	0	0	0
			914	564	189	159	2			
44	XM	114	Total	C	N	O	S	0	0	0
			895	550	186	157	2			

- Molecule 45 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	QN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			
45	XN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	QO	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			
46	XO	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	QP	82	Total	C	N	O	S	0	0	0
			681	433	134	113	1			
47	XP	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	QQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			
48	XQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	QR	68	Total	C	N	O		0	0	0
			555	355	108	92				
49	XR	68	Total	C	N	O		0	0	0
			555	355	108	92				

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	QS	83	Total	C	N	O	S	0	0	0
			648	415	120	111	2			
50	XS	83	Total	C	N	O	S	0	0	0
			645	410	118	115	2			

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	QT	96	Total	C	N	O	S	0	0	0
			732	449	157	124	2			
51	XT	98	Total	C	N	O	S	0	0	0
			733	451	154	126	2			

- Molecule 52 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	QU	23	Total	C	N	O		0	0	0
			199	122	48	29				
52	XU	23	Total	C	N	O		0	0	0
			199	122	48	29				

- Molecule 53 is a RNA chain called Escherichia coli JJ1887, complete genome.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	QV	77	Total	C	N	O	P	0	0	0
			1640	732	297	535	76			
53	XV	77	Total	C	N	O	P	0	0	0
			1644	732	297	538	77			

- Molecule 54 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	QX	9	Total	C	N	O	P	0	0	0
			193	87	37	60	9			
54	XX	10	Total	C	N	O	P	0	0	0
			215	97	42	66	10			

- Molecule 55 is a protein called Peptide chain release factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	QY	259	Total	C	N	O	S	0	0	0
			2014	1235	382	389	8			
55	XY	260	Total	C	N	O	S	0	0	0
			2022	1241	383	390	8			

- Molecule 56 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	QA	262	Total	Mg	0	0
			262	262		
56	YV	1	Total	Mg	0	0
			1	1		
56	RP	2	Total	Mg	0	0
			2	2		
56	R7	3	Total	Mg	0	0
			3	3		
56	YA	749	Total	Mg	0	0
			749	749		
56	Y5	2	Total	Mg	0	0
			2	2		
56	YR	1	Total	Mg	0	0
			1	1		
56	RT	3	Total	Mg	0	0
			3	3		
56	QD	2	Total	Mg	0	0
			2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	RN	2	Total Mg 2 2	0	0
56	XE	2	Total Mg 2 2	0	0
56	RG	4	Total Mg 4 4	0	0
56	QI	1	Total Mg 1 1	0	0
56	YD	9	Total Mg 9 9	0	0
56	QV	6	Total Mg 6 6	0	0
56	RX	1	Total Mg 1 1	0	0
56	Y8	2	Total Mg 2 2	0	0
56	YO	1	Total Mg 1 1	0	0
56	XA	187	Total Mg 187 187	0	0
56	Y1	1	Total Mg 1 1	0	0
56	RQ	5	Total Mg 5 5	0	0
56	R0	7	Total Mg 7 7	0	0
56	XT	1	Total Mg 1 1	0	0
56	QR	1	Total Mg 1 1	0	0
56	QL	2	Total Mg 2 2	0	0
56	RU	3	Total Mg 3 3	0	0
56	QG	3	Total Mg 3 3	0	0
56	RO	1	Total Mg 1 1	0	0
56	XJ	1	Total Mg 1 1	0	0
56	Y7	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	QH	1	Total 1	Mg 1	0	0
56	YG	2	Total 2	Mg 2	0	0
56	XY	1	Total 1	Mg 1	0	0
56	YQ	3	Total 3	Mg 3	0	0
56	RY	1	Total 1	Mg 1	0	0
56	YN	1	Total 1	Mg 1	0	0
56	XF	4	Total 4	Mg 4	0	0
56	YX	1	Total 1	Mg 1	0	0
56	RR	4	Total 4	Mg 4	0	0
56	RD	15	Total 15	Mg 15	0	0
56	R1	5	Total 5	Mg 5	0	0
56	QO	1	Total 1	Mg 1	0	0
56	YT	3	Total 3	Mg 3	0	0
56	RV	3	Total 3	Mg 3	0	0
56	QF	1	Total 1	Mg 1	0	0
56	R5	1	Total 1	Mg 1	0	0
56	Y0	1	Total 1	Mg 1	0	0
56	QQ	1	Total 1	Mg 1	0	0
56	RA	1032	Total 1032	Mg 1032	0	0
56	YF	2	Total 2	Mg 2	0	0
56	YP	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	QB	1	Total Mg 1 1	0	0
56	R9	1	Total Mg 1 1	0	0
56	RS	1	Total Mg 1 1	0	0
56	RE	7	Total Mg 7 7	0	0
56	XL	1	Total Mg 1 1	0	0
56	YB	20	Total Mg 20 20	0	0
56	QT	1	Total Mg 1 1	0	0
56	QN	1	Total Mg 1 1	0	0
56	YW	2	Total Mg 2 2	0	0
56	RW	2	Total Mg 2 2	0	0
56	XV	4	Total Mg 4 4	0	0
56	RB	22	Total Mg 22 22	0	0
56	QJ	1	Total Mg 1 1	0	0
56	YI	1	Total Mg 1 1	0	0
56	QE	2	Total Mg 2 2	0	0
56	RF	11	Total Mg 11 11	0	0
56	R3	2	Total Mg 2 2	0	0
56	YE	6	Total Mg 6 6	0	0

- Molecule 57 is ZINC ION (three-letter code: ZN) (formula: Zn).

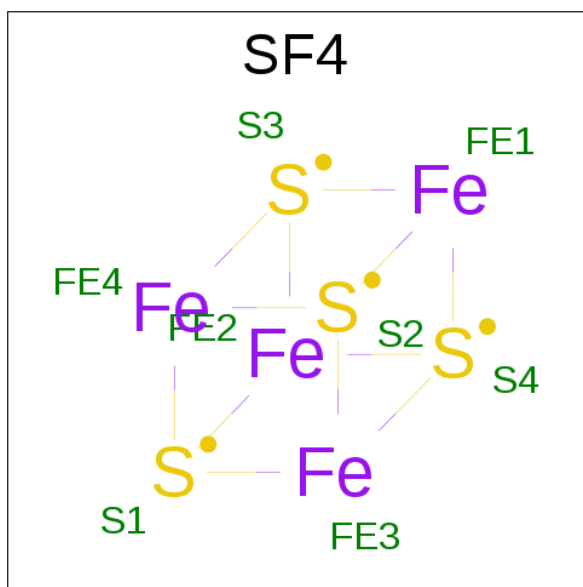
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	Y9	1	Total Zn 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	YY	1	Total	Zn	0	0
			1	1		
57	Y6	1	Total	Zn	0	0
			1	1		
57	QN	1	Total	Zn	0	0
			1	1		
57	XN	1	Total	Zn	0	0
			1	1		
57	RY	1	Total	Zn	0	0
			1	1		
57	Y4	1	Total	Zn	0	0
			1	1		
57	R6	1	Total	Zn	0	0
			1	1		
57	Y5	1	Total	Zn	0	0
			1	1		
57	R5	1	Total	Zn	0	0
			1	1		
57	R4	1	Total	Zn	0	0
			1	1		
57	R9	1	Total	Zn	0	0
			1	1		

- Molecule 58 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



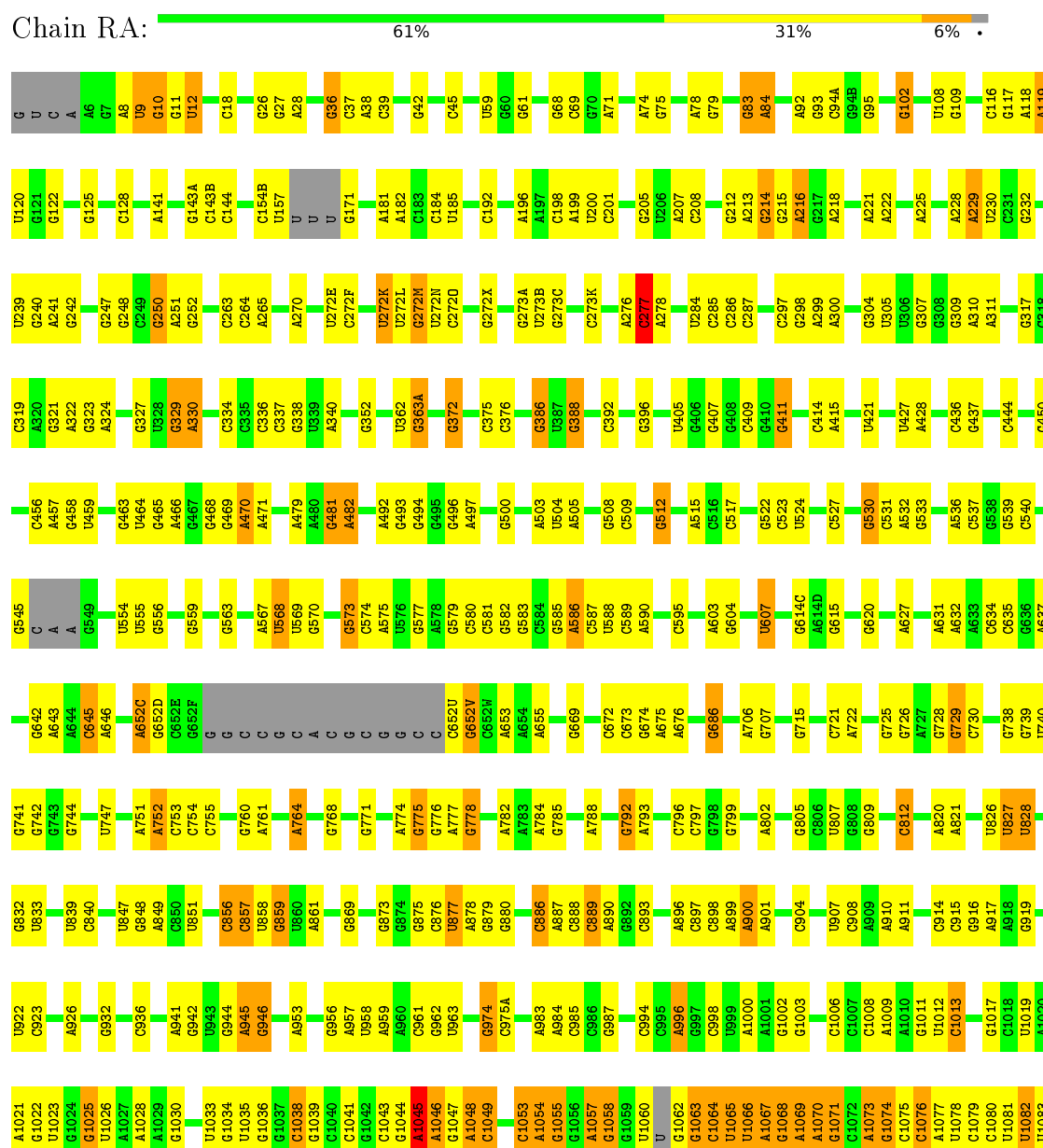
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
58	QD	1	Total 8	Fe 4	S 4	0	0
58	XD	1	Total 8	Fe 4	S 4	0	0

3 Residue-property plots

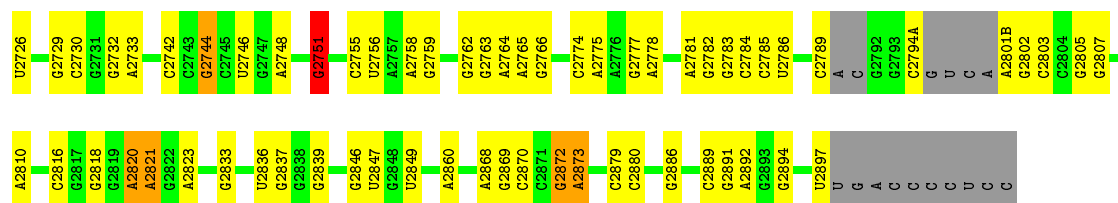
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

Note EDS failed to run properly.

• Molecule 1: 23S rRNA

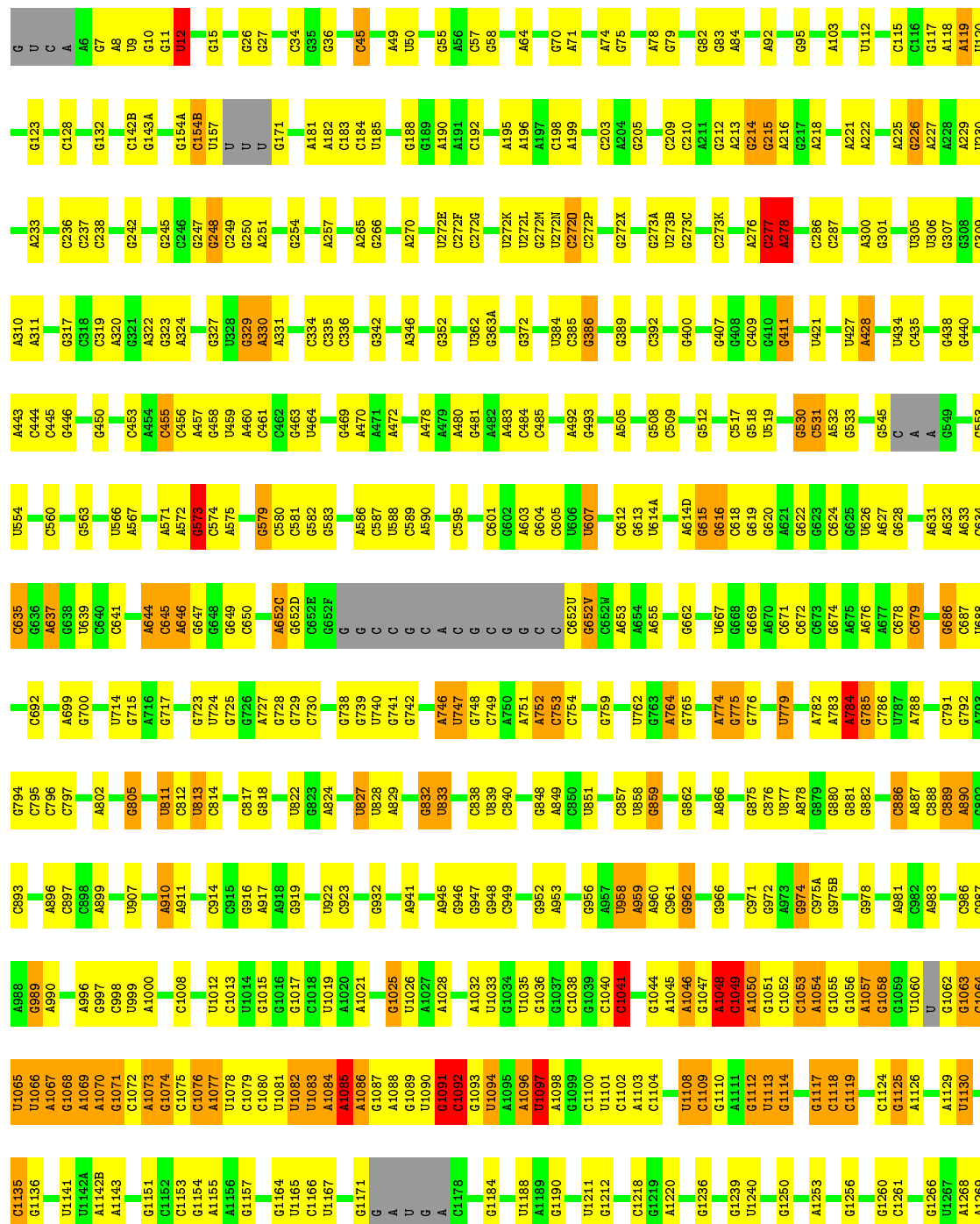


U2613	G2612	G2315	G2219	G2131	C2043	A1937	U1798	A1676	A	G1413	G1277	G1170	A1084
A2614	G2502	G2316	G2219	U2132	C2043	A1938	U1799	A1676	C1536	G1413	G1277	G1170	A1085
U2615	U2504	C2317	G2223	G2133	G2046	U1939	C1800	C1686	G	G1416	A1278	G1171	A1086
C2616	G2505	G2318	G2224	A2134	G2046	U1940	G1801	G1687	A	C1417	C1289	G	A1087
C2617	U2506	G2319	C2225	A2135	A2051	C1941	A1802	U1688	U	G1418	C1290	U	A1088
G2618	C2507	G2320	C2226	C2136	C2055	C1942	A1803	A1689	G	A1419	C1291	G	G1089
C2619	G2508	G2321	A2227	G2137	G2056	U1955	A1812	U1693	A	U1420	U1282	A	U1090
A2629	C2512	A2322	G2228	C2138	G2056	U1955	A1812	U1693	C1178	G1421	C1293	C1092	C1091
G2630	G2513	G2325	U2232	C2139	A2060	U1958	A1815	G1696	C1179	G1422	U1300	C1092	C1092
G2631	U2514	G2326	U2233	G2140	G2061	G1959	A1816	G1697	C1180	G1423	A1301	C1180	U1093
A2632	G2516	C2327	G2234	C2141	A2062	A1960	A1817	U1698	U1094	G1424	U1301	U1094	U1094
U2636	C2517	A2328	C2238	C2142	C2063	U1961	U1818	U1699	U1188	G1425	C1306	U1187	A1095
G2643	A2518	A2422	G2239	U2144	U2063	C1962	G1826	A1700	A1096	G1426	U1306	U1188	A1096
G2644	U2519	U2423	G2239	G2145	G2069	U1963	C1827	A1701	U1097	A1427	G1309	A1189	U1097
G2645	C2520	A2325	U2242	C2146	G2070	U1964	C1827	G1702	A1098	G1428	U1309	U1205	A1098
G2646	G2521	A2326	U2243	G2147	A2071	G1967	G1828	G1703	C1100	G1429	U1313	U1205	G1100
U2647	G2522	A2336	U2244	G2148	A2071	C1967	U1833	A1741	C1101	G1430	C1314	A1210	U1101
U2648	G2523	C2342	U2245	G2149	U2074	U1968	U1834	G1721	C1102	G1431	U1341	U1211	C1102
A2654	G2524	C2343	U2246	U2150	U2075	A1969	U1835	A1722	A1103	U1431	C1320	U1212	A1103
G2659	U2537	U2344	G2246	G2151	U2076	A1970	G1836	A1722	C1104	U1449	A1321	G1212	C1104
U2659	C2538	A2345	U2247	G2152	A2077	A1971	A1876	G1756	U1105	G1450	U1322	U1213	U1105
G2659	G2539	A2346	G2251	G2153	C2078	A1972	A1877	U1757	U1106	G1451	A1323	G1219	G1106
A2679	G2540	C2347	U2262	G2154	G2087	U1975	A1849	G1746	U1107	G1455	U1341	G1223	G1107
C2680	A2541	C2350	U2267	G2155	G2087	U1975	A1849	G1746	C1108	G1455	U1341	G1223	U1108
C2680	A2542	G2351	A2267	G2156	G2094	U1991	U1864	G1750	C1109	G1459	U1351	C1224	G1109
C2683	G2549	A2352	A2268	G2157	C2095	G1992	C1865	G1750	C1110	G1459	C1351	G1225	G1110
U2689	U2552	C2353	A2269	G2158	U2096	U1993	A1876	U1756	C1111	A1460	U1352	G1226	A1111
C2690	C2553	G2354	G2270	G2159	C2097	U1993	A1877	U1757	C1112	C1467	G1356	G1236	U1112
C2691	U2554	A2355	G2271	G2160	U2098	G1997	G1878	G1758	U1113	C1467	U1357	U1237	G1113
A2694	G2555	C2356	U2275	G2161	U2099	G1998	U1889	A1762	C1114	A1471	U1358	G1238	G1114
U2697	U2556	U2357	C2275	G2162	C2103	C1999	A1889	A1762	C1115	G1482	A1359	G1239	C1117
C2699	G2557	C2358	A2278	G2163	G2104	A2001	C1895	G1764	C1116	G1482	A1360	U1240	C1118
C2700	U2558	G2359	G2282	G2164	C2105	G2002	C1895	G1764	C1117	A1490	A1365	A1241	C1119
U2701	G2559	A2360	U2283	G2165	G2106	C2006	G1899	G1769	C1118	A1490	A1365	G1248	C1123
U2702	C2573	C2372	C2283	A2171	C2107	C2006	A1900	G1773	C1119	C1493	G1368	U1249	U127
C2703	G2574	G2373	C2284	U2172	C2108	A2014	G1903	A1773	C1120	A1494	U1372	U1250	A1127
C2704	C2575	C2374	C2285	A2173	U2109	A2015	G1906	U1776	C1121	A1495	U1372	C1251	A1128
U2712A	G2576	G2375	A2287	C2174	G2110	A2015	G1907	U1777	C1122	A1496	C1376	A1252	A1129
A2713B	C2577	G2376	G2288	C2175	C2111	G2018	G1907	U1778	C1123	U1497	U1376	A1253	U1130
G2719	C2578	A2377	U2291	A2176	U2112	G2018	G1907	U1778	C1124	C1504	G1377	U1254	U1133
C2723	G2579	G2378	C2292	G2180	G2113	U2022	A1913	A1780	C1125	C1505	A1378	U1255	C1135
C2724	C2580	C2379	C2293	G2181	A2114	G2023	A1914	A1780	C1126	C1506	A1379	G1256	C1136
U2712A	A2581	G2382	U2296	G2182	G2115	G2023	A1915	C1782	C1127	A1507	G1380	G1259	G1137
A2713B	G2582	C2383	C2297	G2183	G2116	C2026	U1916	C1782	C1128	A1508	A1384	G1260	G1138
G2719	C2583	G2384	A2298	G2184	A2117	C2027	A1917	A1783	C1129	A1509A	G1385	U1263	C1139
C2723	C2601	C2385	G2304	U2189	A2119	U2028	U1917	A1785	C1130	A1509B	U1388	U1264	C1140
C2724	A2602	C2386	A2305	G2190	A2120	G2029	A1918	A1786	C1131	A1509C	G1388	U1265	U1141
U2719	G2603	C2387	G2306	G2191	G2121	A2030	A1919	A1786	C1132	A1509C	U1388	A1265	U1142A
C2725	U2609	A2388	A2310	G2192	U2122	A2031	C1920	A1789	C1133	G1525	U1394	A1266	A1142B
C2726	U2611	C2394	A2311	G2193	U2123	A2032	C1921	A1790	C1134	G1526	C1395	U1267	A1143
A2725	C2612	G2397	U2312	G2194	G2123	A2033	G1929	A1791	C1135	G1529	U1396	A1268	A1143
				A2126	A2126	U2034	G1930	A1791	C1136	C1530	A1269	U1269	A1155
				G2127	G2127	G2035	G1934	U1794	C1137	C1531	C1404	G1270	U1165
				C2037	C2037	G2037	C1935	U1795	C1138	C1532	U1405	G1271	C1166
				U2130	U2130		A1936	C1797	C1139	C1533	A1412	A1272	

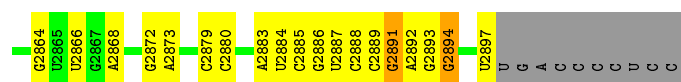


• Molecule 1: 23S rRNA

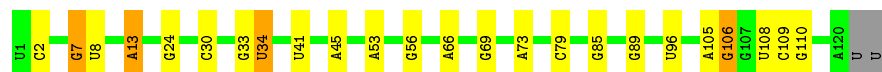
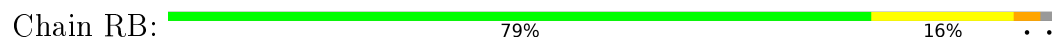
Chain YA: 59% 31% 7% ..



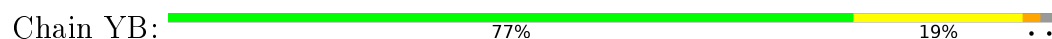
A2753	A2754	A2755	A2756	A2757	A2758	A2759	G2762	G2763	A2764	A2765	C2769	A2778	G2779	G2780	A2781	C2785	G2786	G2787	G2788	G2789	A	C	G2792	G2793	G2794	G	U	C	A	A2801B	G2802	G2805	G2807	G2808	G2811	G2818	G2819	A2820	A2821	A2822	A2823	U2832	G2833	A2835	U2836	G2837	G2838	G2839	U2849		
C2648	A2654	A2654	G2659	A2660	G2661	A2662	G2663	G2667	G2668	A2668	A2668	A2679	C2680	G2680	G2681	U2682	G2683	U2687	U2688	U2689	U2690	C2691	C2692	U2698	C2699	U2702	C2703	G2704	A2705	G2709	G2710	A2711	A2712A	A2712B	A2713	G2714	G2715	U2716	G2717	U2726	G2732	G2733	A2734	G2735	G2735	G2744	G2747	A2748	A2749	G2750	G2752
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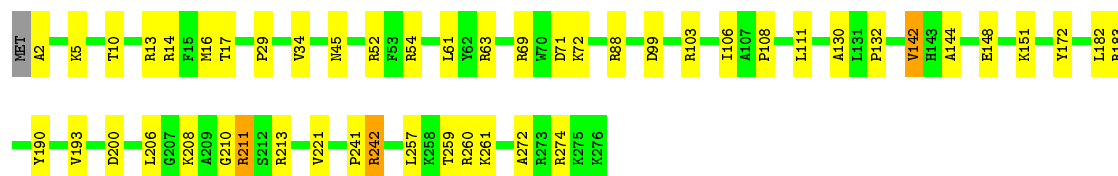
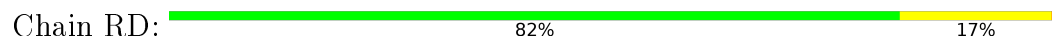
- Molecule 2: 5S rRNA



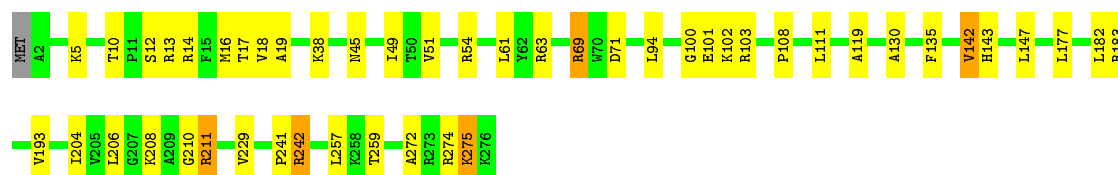
- Molecule 2: 5S rRNA



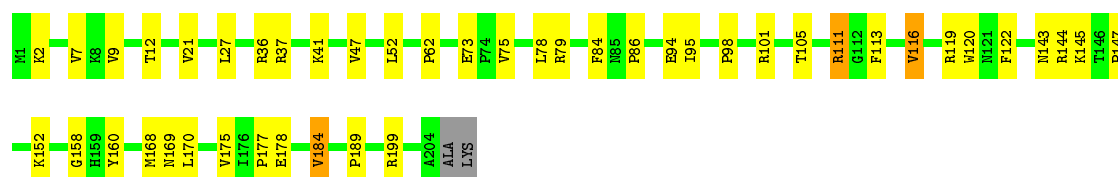
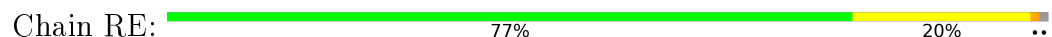
- Molecule 3: 50S ribosomal protein L2



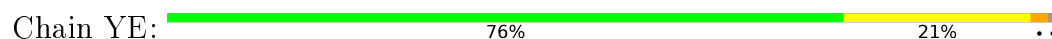
- Molecule 3: 50S ribosomal protein L2

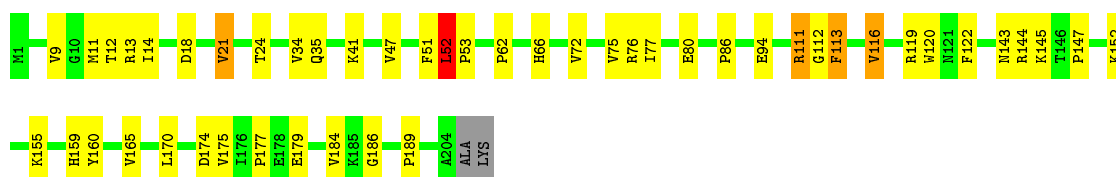


- Molecule 4: 50S ribosomal protein L3



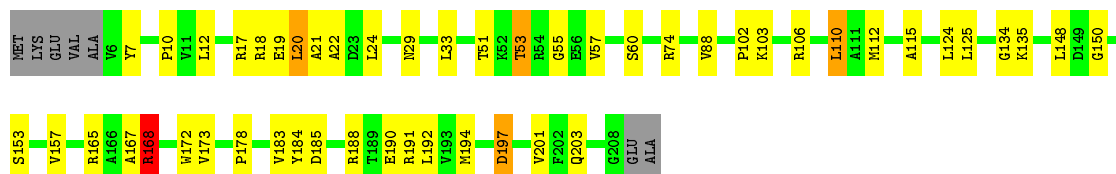
- Molecule 4: 50S ribosomal protein L3





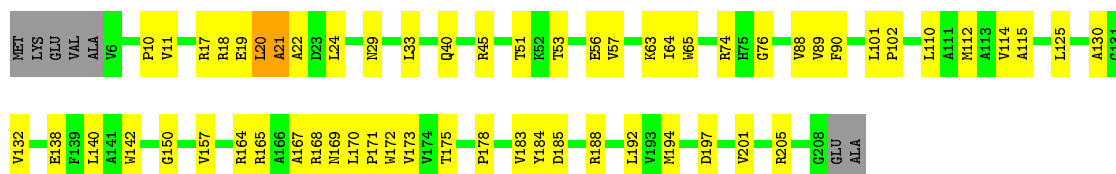
- Molecule 5: 50S ribosomal protein L4

Chain RF: 73% 21% ..



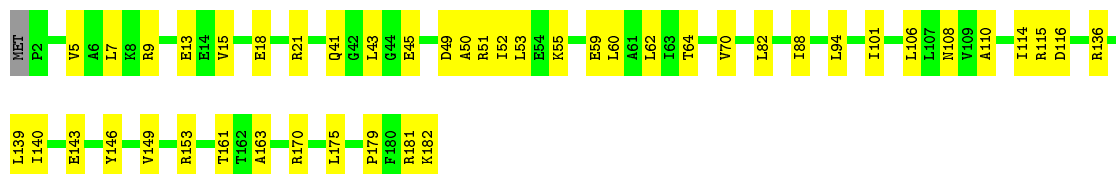
- Molecule 5: 50S ribosomal protein L4

Chain YF: 69% 27% ..



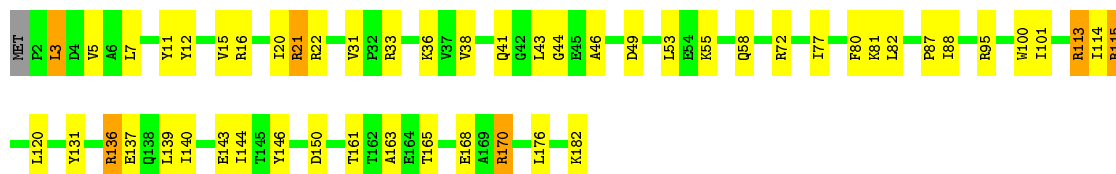
- Molecule 6: 50S ribosomal protein L5

Chain RG: 75% 25% ..



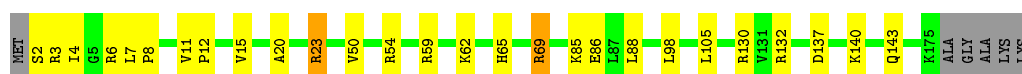
- Molecule 6: 50S ribosomal protein L5

Chain YG: 71% 25% ..



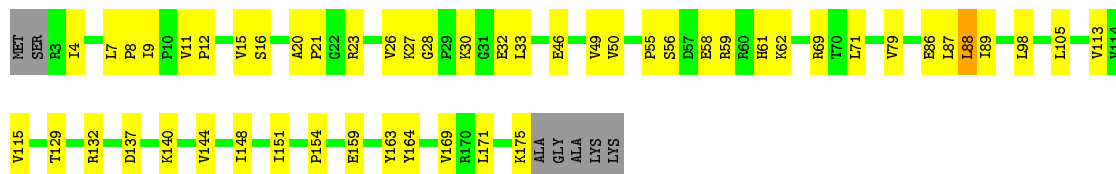
- Molecule 7: 50S ribosomal protein L6

Chain RH: 82% 14% ..



- Molecule 7: 50S ribosomal protein L6

Chain YH: 68% 28% . .



- Molecule 8: 50S ribosomal protein L9

Chain RI: 80% 18% . .



- Molecule 8: 50S ribosomal protein L9

Chain YI: 80% 15% . .



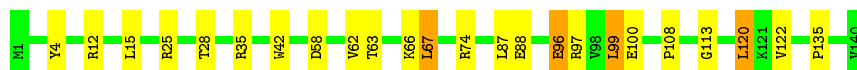
- Molecule 9: 50S ribosomal protein L13

Chain RN: 81% 17% .



- Molecule 9: 50S ribosomal protein L13

Chain YN: 83% 14% .



- Molecule 10: 50S ribosomal protein L14

Chain RO: 76% 24%



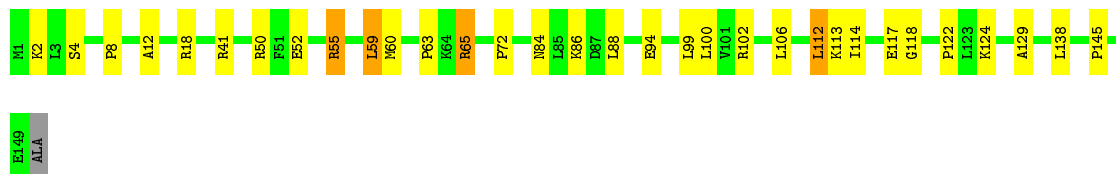
- Molecule 10: 50S ribosomal protein L14

Chain YO: 81% 18%



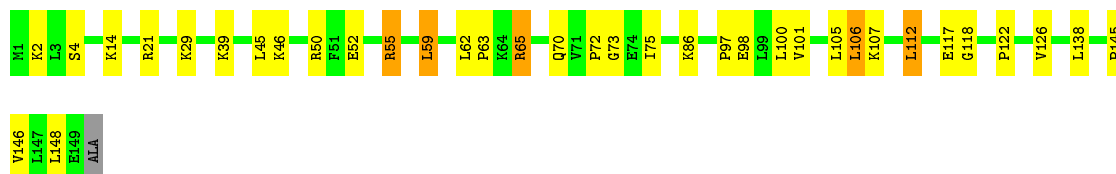
- Molecule 11: 50S ribosomal protein L15

Chain RP: 78% 19% ..



- Molecule 11: 50S ribosomal protein L15

Chain YP: 75% 21% ..



- Molecule 12: 50S ribosomal protein L16

Chain RQ: 81% 18% .



- Molecule 12: 50S ribosomal protein L16

Chain YQ: 77% 21% .



- Molecule 13: 50S ribosomal protein L17

Chain RR: 75% 22% .




- Molecule 13: 50S ribosomal protein L17

Chain YR: 81% 19%




- Molecule 14: 50S ribosomal protein L18

Chain RS:  80% 15% ..



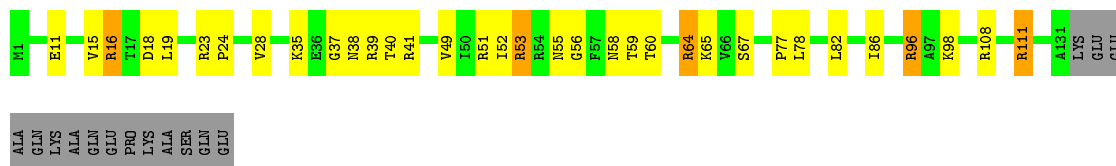
- Molecule 14: 50S ribosomal protein L18

Chain YS:  81% 16% ..



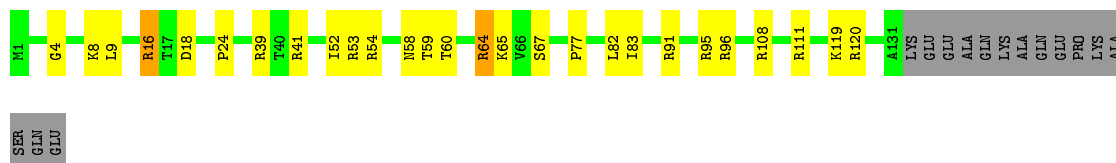
- Molecule 15: 50S ribosomal protein L19

Chain RT:  66% 20% • 10%




- Molecule 15: 50S ribosomal protein L19

Chain YT:  71% 17% • 10%




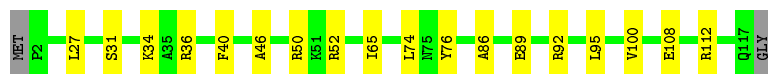
- Molecule 16: 50S ribosomal protein L20

Chain RU:  81% 16% ..




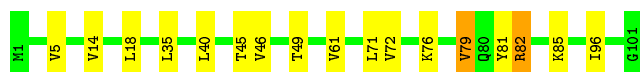
- Molecule 16: 50S ribosomal protein L20

Chain YU:  83% 15% •



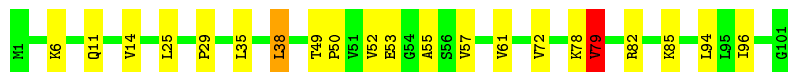
- Molecule 17: 50S ribosomal protein L21

Chain RV:  83% 15% •



- Molecule 17: 50S ribosomal protein L21

Chain YV: 79% 19% ..



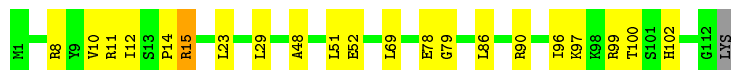
- Molecule 18: 50S ribosomal protein L22

Chain RW: 84% 14% ..



- Molecule 18: 50S ribosomal protein L22

Chain YW: 81% 18% ..



- Molecule 19: 50S ribosomal protein L23

Chain RX: 76% 23% .



- Molecule 19: 50S ribosomal protein L23

Chain YX: 88% 11% .



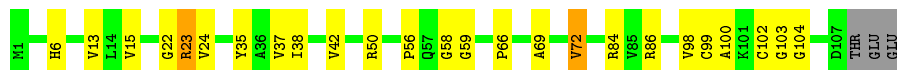
- Molecule 20: 50S ribosomal protein L24

Chain RY: 76% 20% ..

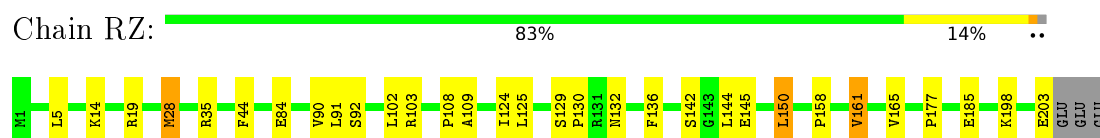


- Molecule 20: 50S ribosomal protein L24

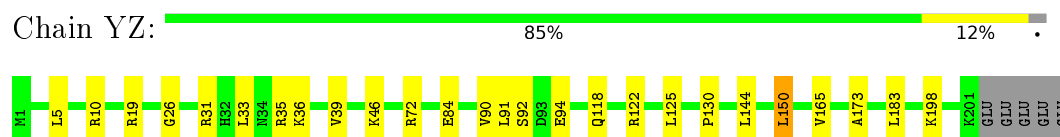
Chain YY: 75% 21% . .



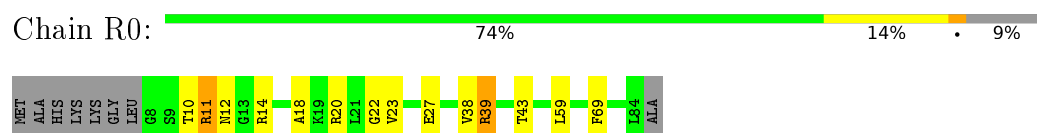
- Molecule 21: 50S ribosomal protein L25



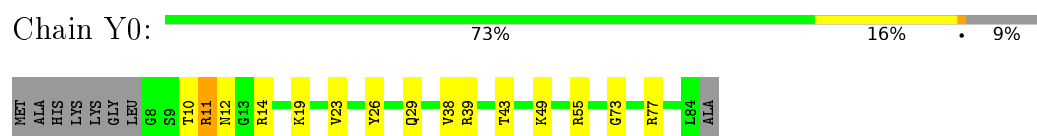
- Molecule 21: 50S ribosomal protein L25



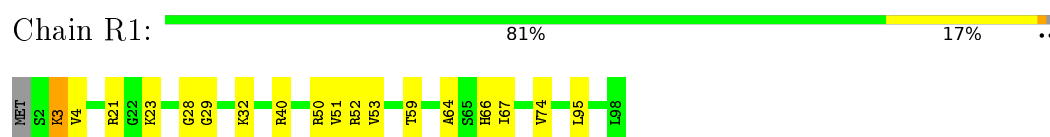
- Molecule 22: 50S ribosomal protein L27



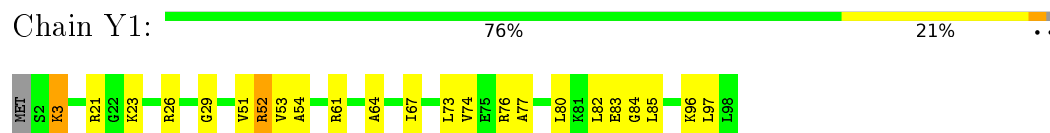
- Molecule 22: 50S ribosomal protein L27



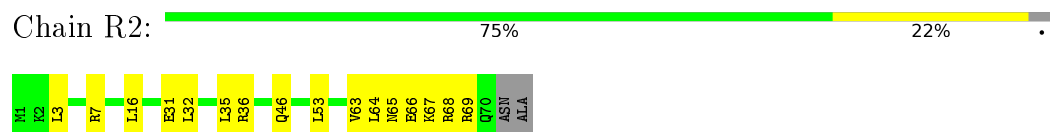
- Molecule 23: 50S ribosomal protein L28




- Molecule 23: 50S ribosomal protein L28

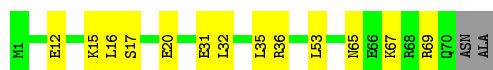


- Molecule 24: 50S ribosomal protein L29




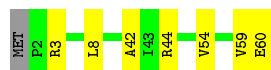
- Molecule 24: 50S ribosomal protein L29

Chain Y2:  79% 18% .




- Molecule 25: 50S ribosomal protein L30

Chain R3:  87% 12% .



- Molecule 25: 50S ribosomal protein L30

Chain Y3:  78% 18% ..



- Molecule 26: 50S ribosomal protein L31

Chain R4:  58% 35% ...



- Molecule 26: 50S ribosomal protein L31

Chain Y4:  63% 30% ...




- Molecule 27: 50S ribosomal protein L32

Chain R5:  73% 22% ..




- Molecule 27: 50S ribosomal protein L32

Chain Y5:  83% 13% ..

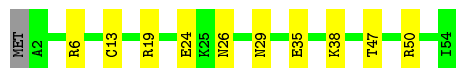
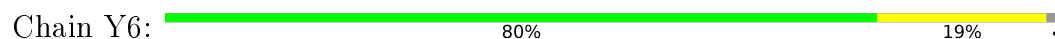


- Molecule 28: 50S ribosomal protein L33

Chain R6:  76% 22% .



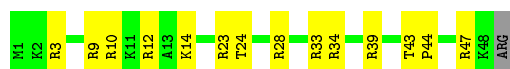
- Molecule 28: 50S ribosomal protein L33



- Molecule 29: 50S ribosomal protein L34



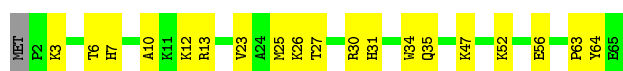
- Molecule 29: 50S ribosomal protein L34



- Molecule 30: 50S ribosomal protein L35



- Molecule 30: 50S ribosomal protein L35



- Molecule 31: 50S ribosomal protein L36

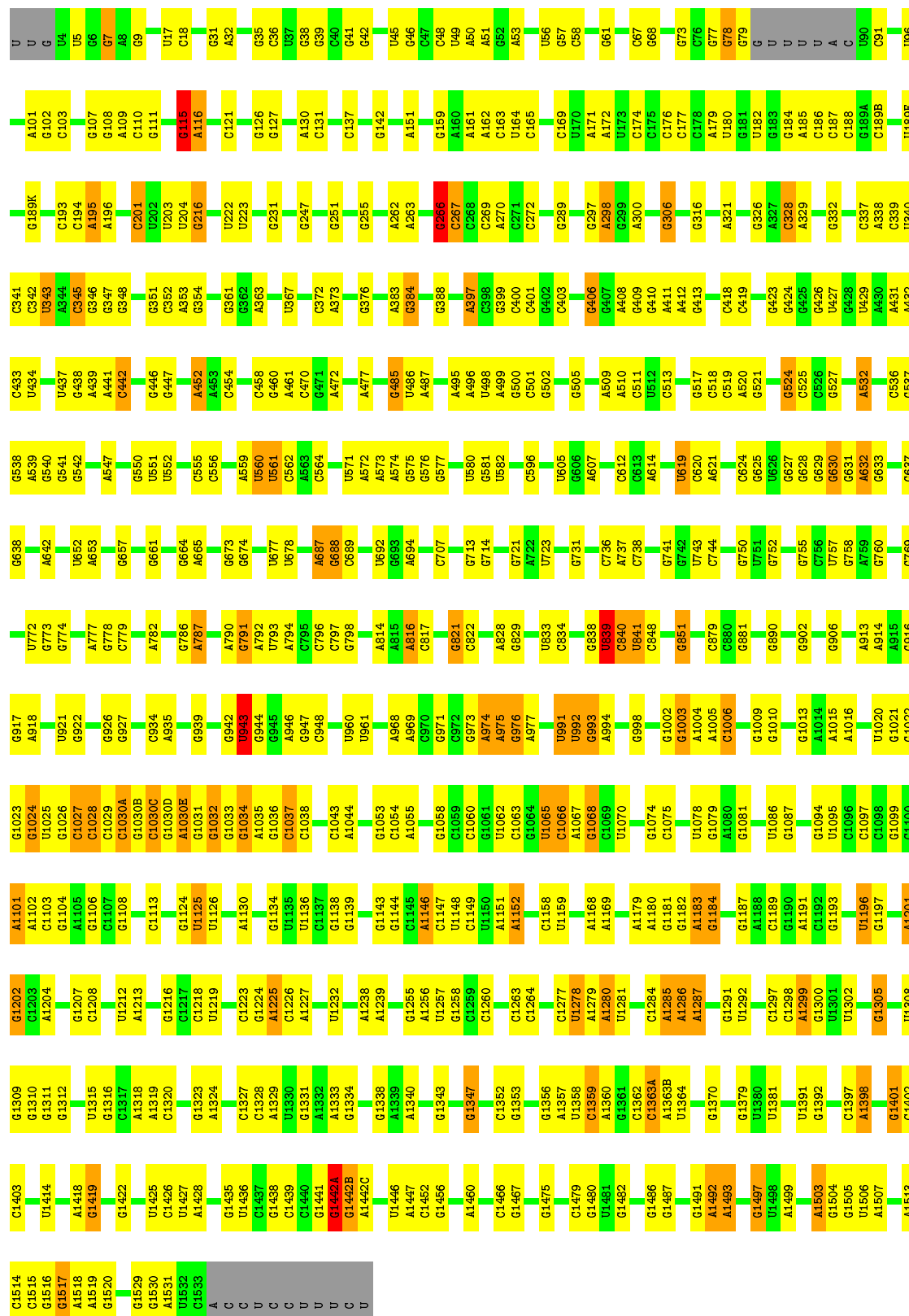


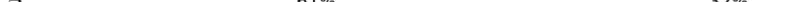
- Molecule 31: 50S ribosomal protein L36



- Molecule 32: 16S rRNA

Chain QA:  61% 32% 5%

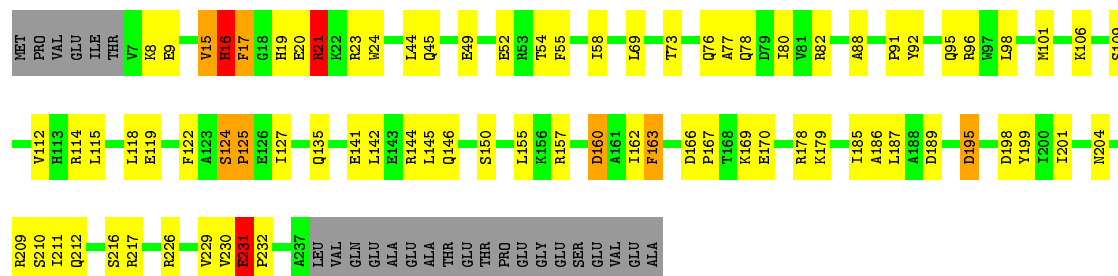


Chain XA:  61% 32% 6%



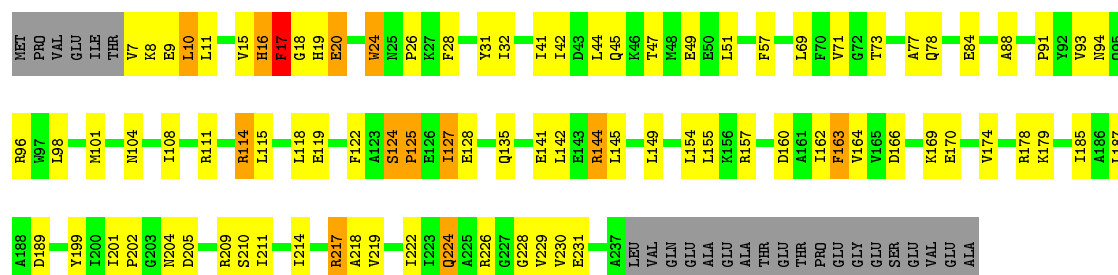
- Molecule 33: 30S ribosomal protein S2

Chain QB:  59% 27% 10%



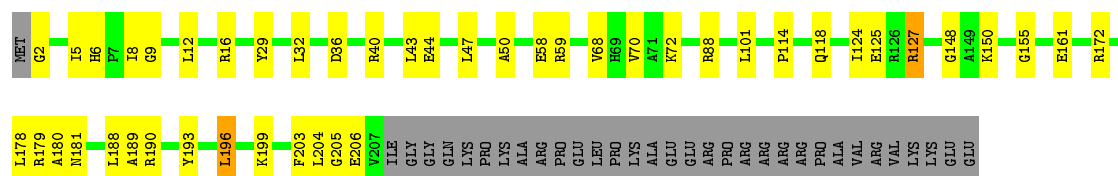
- Molecule 33: 30S ribosomal protein S2

Chain XB:



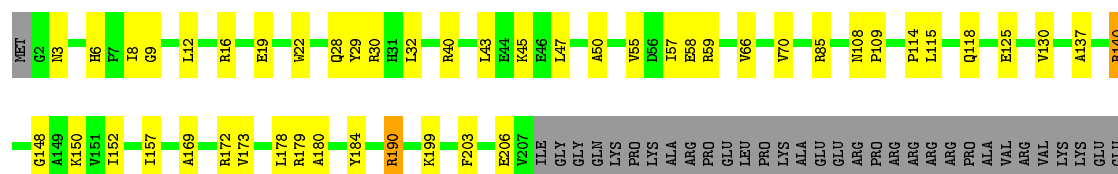
- Molecule 34: 30S ribosomal protein S3

Chain QC: 67% 18% 14%



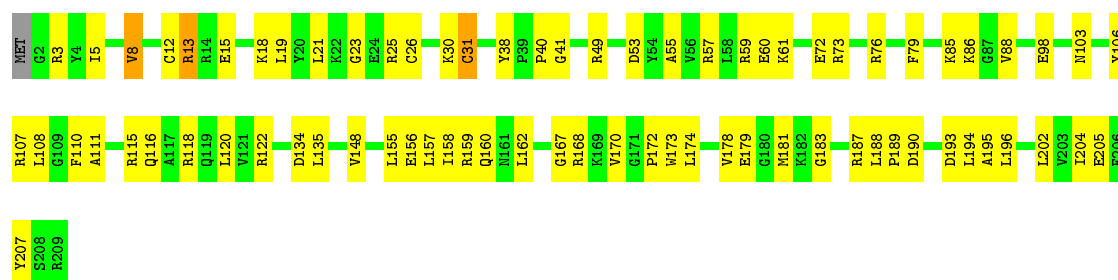
- Molecule 34: 30S ribosomal protein S3

Chain XC:  66% 19% • 14%



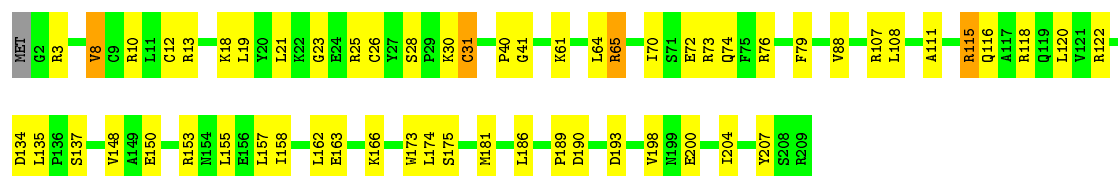
- Molecule 35: 30S ribosomal protein S4

Chain QD: 64% 34%



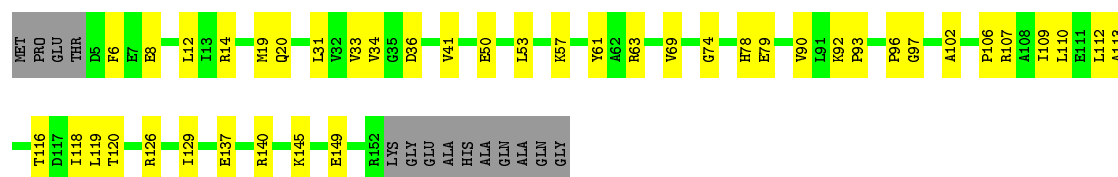
- Molecule 35: 30S ribosomal protein S4

Chain XD: 72% 26% .



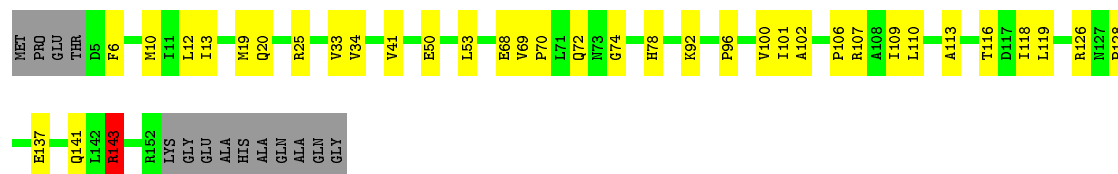
- Molecule 36: 30S ribosomal protein S5

Chain QE: 65% 26% 9%



- Molecule 36: 30S ribosomal protein S5

Chain XE: 69% 22% 9%



- Molecule 37: 30S ribosomal protein S6

Chain QF: 71% 28% .



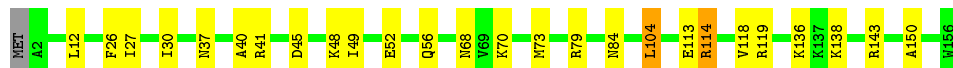
- Molecule 37: 30S ribosomal protein S6

Chain XF: 86% 12% ..



- Molecule 38: 30S ribosomal protein S7

Chain QG: 83% 15% ..



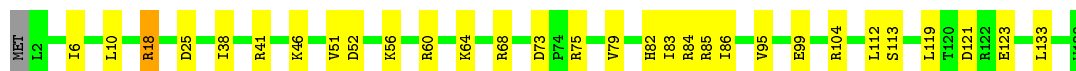
- Molecule 38: 30S ribosomal protein S7

Chain XG: 83% 15% ..



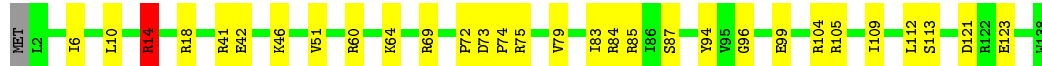
- Molecule 39: 30S ribosomal protein S8

Chain QH: 78% 21% ..



- Molecule 39: 30S ribosomal protein S8

Chain XH: 78% 21% ..



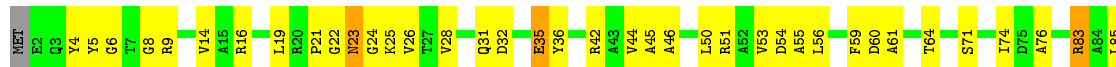
- Molecule 40: 30S ribosomal protein S9

Chain QI: 68% 29% ..

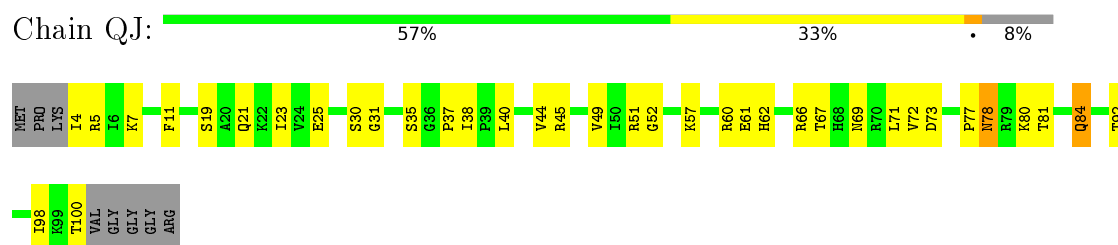


- Molecule 40: 30S ribosomal protein S9

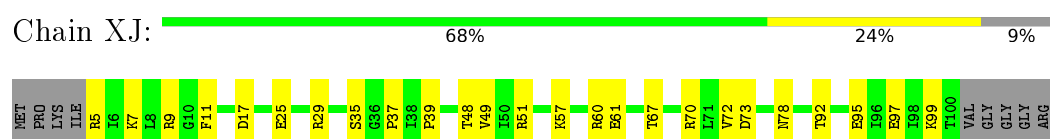
Chain XI: 62% 34% ..



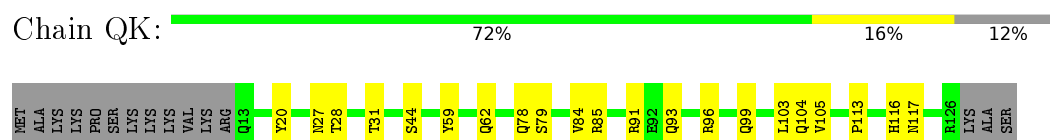
- Molecule 41: 30S ribosomal protein S10



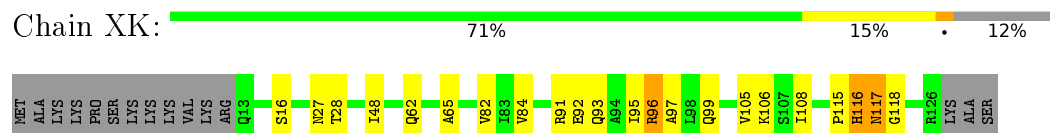
- Molecule 41: 30S ribosomal protein S10



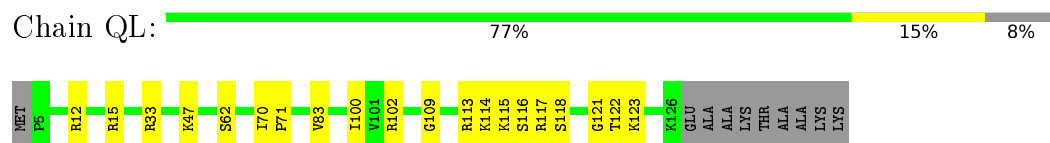
- Molecule 42: 30S ribosomal protein S11



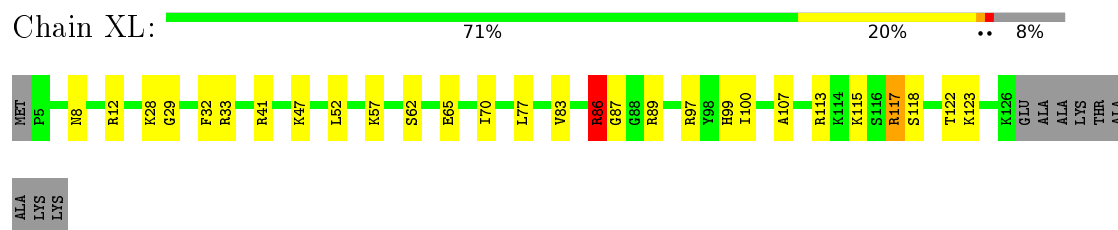
- Molecule 42: 30S ribosomal protein S11



- Molecule 43: 30S ribosomal protein S12



- Molecule 43: 30S ribosomal protein S12



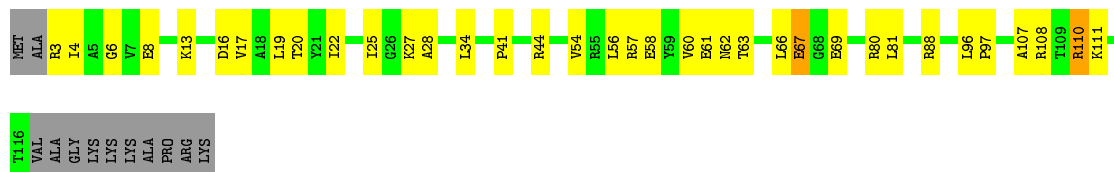
- Molecule 44: 30S ribosomal protein S13





- Molecule 44: 30S ribosomal protein S13

Chain XM: 62% 27% 10%



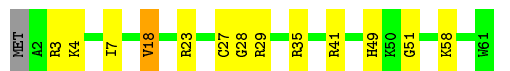
- Molecule 45: 30S ribosomal protein S14 type Z

Chain QN: 77% 20% 3%



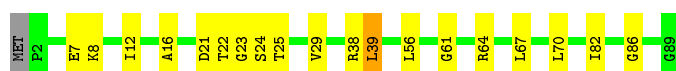
- Molecule 45: 30S ribosomal protein S14 type Z

Chain XN: 77% 20% 3%



- Molecule 46: 30S ribosomal protein S15

Chain QO: 78% 20% 2%



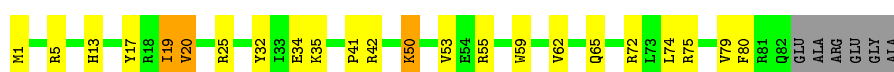
- Molecule 46: 30S ribosomal protein S15

Chain XO: 79% 19% 2%



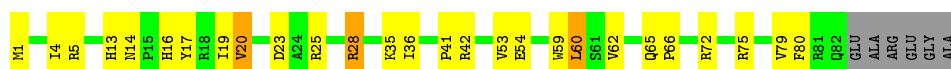
- Molecule 47: 30S ribosomal protein S16

Chain QP: 67% 23% 10%



- Molecule 47: 30S ribosomal protein S16

Chain XP: 63% 27% 10%



- Molecule 48: 30S ribosomal protein S17

Chain QQ: 84% 10% 6%



- Molecule 48: 30S ribosomal protein S17

Chain XQ: 83% 11% 6%



- Molecule 49: 30S ribosomal protein S18

Chain QR: 64% 13% 23%



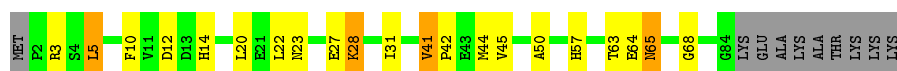
- Molecule 49: 30S ribosomal protein S18

Chain XR: 64% 13% 23%



- Molecule 50: 30S ribosomal protein S19

Chain QS: 67% 18% 11%



- Molecule 50: 30S ribosomal protein S19

Chain XS: 72% 17% 11%



- Molecule 51: 30S ribosomal protein S20

Chain QT: 68% 21% 9%



- Molecule 51: 30S ribosomal protein S20

Chain XT: 74% 17% 8%



- Molecule 52: 30S ribosomal protein Thx

Chain QU: 70% 15% 15%



- Molecule 52: 30S ribosomal protein Thx

Chain XU: 74% 11% 15%



- Molecule 53: Escherichia coli JJ1887, complete genome

Chain QV: 62% 32% 5%



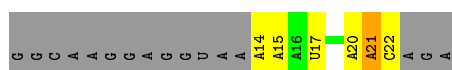
- Molecule 53: Escherichia coli JJ1887, complete genome

Chain XV: 64% 26% 9%



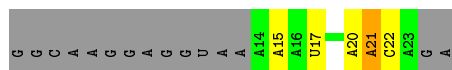
- Molecule 54: messenger RNA

Chain QX: 12% 20% 64%



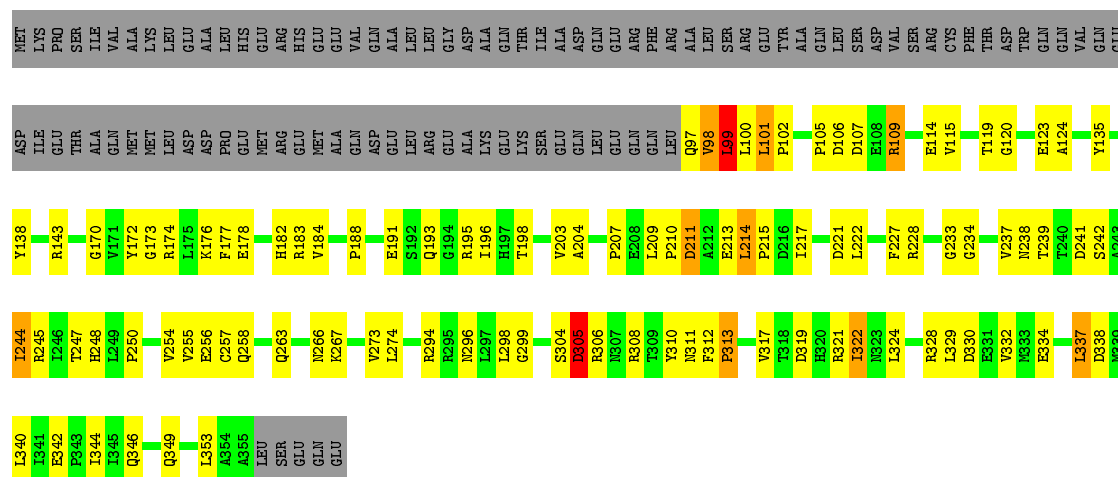
- Molecule 54: messenger RNA

Chain XX: 20% 16% 60%



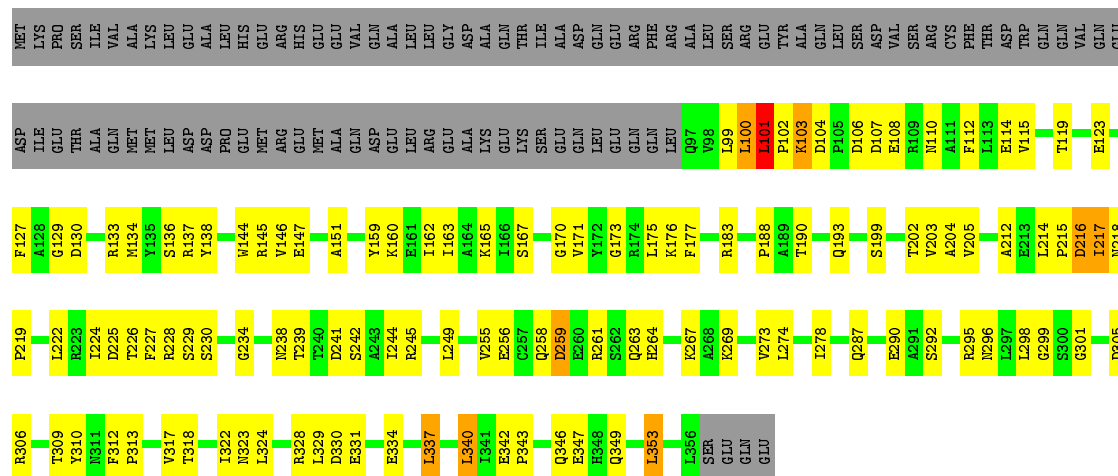
• Molecule 55: Peptide chain release factor 1

Chain QY: 44% 25% 28%



• Molecule 55: Peptide chain release factor 1

Chain XY: 40% 30% 28%



4 Data and refinement statistics

EDS failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.51Å 450.89Å 622.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.86 – 3.04	Depositor
% Data completeness (in resolution range)	99.3 (49.86-3.04)	Depositor
R_{merge}	0.35	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 3.07Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.246 , 0.279	Depositor
Wilson B-factor (Å ²)	65.2	Xtriage
Anisotropy	0.225	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	294929	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, ZN, OMG, MA6, SF4, 0TD, MG, 2MA, 2MU, 2MG, 5MC, UR3, 4OC, M2G, 7MG, PSU

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	RA	0.43	0/68901	1.00	55/107544 (0.1%)
1	YA	0.51	1/68901 (0.0%)	1.10	180/107544 (0.2%)
2	RB	0.35	0/2876	0.90	0/4486
2	YB	0.43	0/2878	1.00	1/4490 (0.0%)
3	RD	0.38	0/2181	0.64	1/2940 (0.0%)
3	YD	0.40	0/2186	0.66	1/2944 (0.0%)
4	RE	0.37	0/1592	0.60	0/2149
4	YE	0.38	0/1592	0.65	1/2149 (0.0%)
5	RF	0.36	0/1619	0.61	2/2193 (0.1%)
5	YF	0.42	0/1615	0.61	0/2188
6	RG	0.29	0/1451	0.54	0/1961
6	YG	0.34	0/1449	0.57	0/1957
7	RH	0.31	0/1356	0.54	1/1834 (0.1%)
7	YH	0.35	0/1350	0.57	1/1826 (0.1%)
8	RI	0.29	0/1109	0.57	0/1512
8	YI	0.34	0/1091	0.60	1/1490 (0.1%)
9	RN	0.36	0/1148	0.56	0/1547
9	YN	0.35	0/1144	0.55	0/1543
10	RO	0.34	0/943	0.58	0/1269
10	YO	0.42	1/943 (0.1%)	0.61	0/1269
11	RP	0.35	0/1152	0.60	0/1533
11	YP	0.41	0/1152	0.66	0/1533
12	RQ	0.35	0/1143	0.62	0/1527
12	YQ	0.40	0/1143	0.66	0/1527
13	RR	0.34	0/982	0.62	0/1312
13	YR	0.34	0/982	0.62	0/1312
14	RS	0.35	0/887	0.59	0/1180
14	YS	0.37	0/880	0.62	0/1172
15	RT	0.36	0/1105	0.67	1/1477 (0.1%)
15	YT	0.35	0/1097	0.63	1/1468 (0.1%)
16	RU	0.32	0/977	0.55	0/1301
16	YU	0.37	0/977	0.54	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	RV	0.35	0/786	0.57	0/1053
17	YV	0.37	0/782	0.61	0/1049
18	RW	0.35	0/897	0.57	0/1205
18	YW	0.37	0/897	0.57	0/1205
19	RX	0.39	0/764	0.59	0/1025
19	YX	0.39	0/764	0.61	0/1025
20	RY	0.34	0/823	0.64	0/1099
20	YY	0.39	0/823	0.63	0/1100
21	RZ	0.33	0/1620	0.55	0/2200
21	YZ	0.35	0/1590	0.59	0/2162
22	R0	0.39	0/616	0.70	1/821 (0.1%)
22	Y0	0.42	0/616	0.77	2/821 (0.2%)
23	R1	0.37	0/761	0.59	0/1013
23	Y1	0.38	0/766	0.64	0/1018
24	R2	0.29	0/590	0.50	0/781
24	Y2	0.35	0/594	0.54	0/785
25	R3	0.35	0/474	0.59	0/635
25	Y3	0.36	0/469	0.58	0/630
26	R4	0.37	0/559	0.70	0/754
26	Y4	0.40	0/549	0.70	1/741 (0.1%)
27	R5	0.44	0/473	0.64	0/639
27	Y5	0.41	0/469	0.60	0/635
28	R6	0.30	0/460	0.54	0/613
28	Y6	0.30	0/456	0.53	0/608
29	R7	0.40	0/426	0.67	0/561
29	Y7	0.42	0/426	0.69	0/561
30	R8	0.38	0/525	0.61	0/691
30	Y8	0.39	0/525	0.61	0/691
31	R9	0.32	0/310	0.68	0/407
31	Y9	0.33	0/310	0.68	0/407
32	QA	0.34	0/35795	0.88	12/55864 (0.0%)
32	XA	0.36	1/35890 (0.0%)	0.90	29/56012 (0.1%)
33	QB	0.34	0/1876	0.59	0/2533
33	XB	0.34	0/1860	0.60	1/2518 (0.0%)
34	QC	0.30	0/1582	0.53	0/2137
34	XC	0.36	1/1566 (0.1%)	0.61	0/2119
35	QD	0.33	0/1695	0.59	1/2274 (0.0%)
35	XD	0.32	0/1698	0.57	0/2277
36	QE	0.34	0/1149	0.55	0/1548
36	XE	0.32	0/1149	0.57	1/1548 (0.1%)
37	QF	0.31	0/827	0.55	0/1120
37	XF	0.33	0/829	0.64	1/1123 (0.1%)
38	QG	0.31	0/1254	0.46	0/1683

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	XG	0.31	0/1248	0.51	0/1676
39	QH	0.30	0/1118	0.53	0/1506
39	XH	0.32	0/1108	0.58	1/1494 (0.1%)
40	QI	0.32	0/1005	0.60	1/1351 (0.1%)
40	XI	0.31	0/985	0.54	0/1329
41	QJ	0.28	0/732	0.51	0/993
41	XJ	0.29	0/723	0.52	0/984
42	QK	0.30	0/849	0.55	0/1150
42	XK	0.30	0/848	0.57	0/1149
43	QL	0.39	0/937	0.61	0/1260
43	XL	0.36	0/937	0.67	0/1260
44	QM	0.30	0/924	0.57	0/1242
44	XM	0.31	0/905	0.55	0/1217
45	QN	0.34	0/501	0.59	1/664 (0.2%)
45	XN	0.35	0/501	0.58	0/664
46	QO	0.32	0/739	0.52	0/985
46	XO	0.35	0/739	0.56	0/985
47	QP	0.32	0/697	0.54	0/939
47	XP	0.30	0/693	0.57	0/935
48	QQ	0.33	0/836	0.55	0/1117
48	XQ	0.32	0/836	0.54	0/1117
49	QR	0.31	0/560	0.54	0/746
49	XR	0.32	0/560	0.59	0/746
50	QS	0.29	0/663	0.58	1/895 (0.1%)
50	XS	0.27	0/660	0.54	0/893
51	QT	0.31	0/734	0.51	0/969
51	XT	0.29	0/736	0.47	0/976
52	QU	0.30	0/203	0.58	0/266
52	XU	0.31	0/203	0.70	0/266
53	QV	0.34	0/1832	0.92	0/2855
53	XV	0.42	1/1836 (0.1%)	0.91	2/2859 (0.1%)
54	QX	0.39	0/216	0.83	0/334
54	XX	0.46	0/241	0.92	0/373
55	QY	0.36	0/2046	0.65	1/2759 (0.0%)
55	XY	0.40	0/2054	0.69	2/2770 (0.1%)
All	All	0.41	5/316497 (0.0%)	0.90	304/472893 (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
14	RS	0	1
33	QB	0	1
43	XL	0	1
55	QY	0	1
All	All	0	4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	XV	1	C	OP3-P	-10.47	1.48	1.61
32	XA	68	G	O3'-P	-6.54	1.53	1.61
34	XC	173	VAL	C-N	6.47	1.46	1.34
10	YO	21	CYS	CB-SG	-5.52	1.72	1.81
1	YA	1046	A	N3-C4	-5.10	1.31	1.34

All (304) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	277	C	N1-C2-O2	17.75	129.55	118.90
1	YA	210	C	C6-N1-C2	12.43	125.27	120.30
1	YA	277	C	N3-C2-O2	-11.59	113.79	121.90
1	YA	277	C	N3-C4-N4	-11.48	109.96	118.00
1	YA	277	C	C5-C4-N4	10.97	127.88	120.20
1	YA	1083	U	N3-C4-O4	10.39	126.67	119.40
1	YA	210	C	N3-C4-C5	10.22	125.99	121.90
1	YA	1046	A	C5-C6-N1	-9.13	113.14	117.70
32	XA	1158	C	N1-C2-O2	8.82	124.19	118.90
32	XA	1158	C	C2-N1-C1'	8.07	127.68	118.80
1	YA	203	C	N1-C2-O2	7.83	123.59	118.90
1	YA	635	C	C6-N1-C2	-7.82	117.17	120.30
22	R0	11	ARG	NE-CZ-NH1	-7.79	116.41	120.30
1	RA	1097	U	C2-N1-C1'	7.74	126.99	117.70
1	YA	966	G	N1-C6-O6	-7.61	115.33	119.90
1	YA	512	G	O4'-C1'-N9	7.40	114.12	108.20
1	YA	966	G	C5-C6-O6	7.20	132.92	128.60
1	YA	2516	G	C5-C6-O6	-7.17	124.30	128.60
32	XA	266	G	P-O3'-C3'	7.17	128.30	119.70
1	RA	1092	C	N1-C2-O2	7.17	123.20	118.90
1	YA	277	C	C2-N3-C4	7.15	123.47	119.90
1	YA	12	U	N3-C2-O2	-7.13	117.21	122.20
55	XY	353	LEU	CA-CB-CG	7.12	131.67	115.30
1	YA	1372	U	N1-C2-O2	7.06	127.74	122.80
1	YA	1083	U	C6-N1-C2	-7.04	116.77	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	Y0	11	ARG	NE-CZ-NH1	7.03	123.82	120.30
1	YA	2506	U	C5-C4-O4	7.01	130.11	125.90
1	YA	676	A	C8-N9-C4	7.01	108.60	105.80
32	XA	1183	A	P-O3'-C3'	6.98	128.07	119.70
1	YA	813	U	N3-C2-O2	-6.97	117.32	122.20
1	YA	2463	C	N1-C2-O2	-6.94	114.74	118.90
1	YA	1820	U	N3-C2-O2	-6.90	117.37	122.20
1	RA	1640	C	C6-N1-C2	-6.87	117.55	120.30
1	YA	1625	C	N3-C4-N4	-6.86	113.20	118.00
1	YA	12	U	N1-C2-O2	6.86	127.60	122.80
1	YA	2751	G	N1-C6-O6	-6.86	115.78	119.90
32	XA	758	G	N1-C6-O6	6.85	124.01	119.90
1	YA	2506	U	N3-C2-O2	-6.78	117.45	122.20
1	YA	1083	U	N3-C4-C5	-6.76	110.55	114.60
8	YI	75	LEU	CA-CB-CG	6.75	130.83	115.30
15	RT	111	ARG	NE-CZ-NH1	6.73	123.67	120.30
1	YA	783	A	C8-N9-C4	-6.70	103.12	105.80
1	YA	2201	C	C6-N1-C2	6.70	122.98	120.30
1	YA	628	G	N1-C6-O6	-6.70	115.88	119.90
1	RA	1097	U	N3-C2-O2	-6.67	117.53	122.20
1	RA	799	G	N1-C6-O6	6.66	123.90	119.90
39	XH	14	ARG	NE-CZ-NH1	-6.66	116.97	120.30
32	XA	1158	C	N3-C2-O2	-6.64	117.25	121.90
5	RF	168	ARG	NE-CZ-NH1	6.61	123.61	120.30
1	RA	1097	U	N1-C2-O2	6.57	127.40	122.80
1	YA	1190	G	N1-C6-O6	-6.55	115.97	119.90
53	XV	13	C	C6-N1-C2	-6.54	117.68	120.30
1	YA	1369	G	N1-C6-O6	-6.51	116.00	119.90
1	YA	2435	A	N1-C6-N6	-6.51	114.70	118.60
1	YA	989	G	C5-C6-O6	-6.49	124.70	128.60
1	YA	974	G	C5-C6-O6	-6.49	124.71	128.60
55	QY	99	LEU	CA-CB-CG	6.48	130.21	115.30
1	YA	2237	G	C8-N9-C4	-6.47	103.81	106.40
1	YA	2440	C	O5'-P-OP2	-6.46	99.89	105.70
1	YA	1049	C	N1-C2-O2	6.43	122.76	118.90
22	Y0	11	ARG	NE-CZ-NH2	-6.42	117.09	120.30
32	QA	1030(C)	C	N1-C2-O2	6.42	122.75	118.90
1	YA	2554	U	O5'-P-OP1	-6.41	99.93	105.70
1	YA	2571	C	C6-N1-C2	6.39	122.86	120.30
5	RF	168	ARG	NE-CZ-NH2	-6.39	117.11	120.30
1	YA	1672	C	C6-N1-C2	6.37	122.85	120.30
1	YA	1097	U	C2-N1-C1'	6.36	125.33	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	1611	C	C6-N1-C2	6.33	122.83	120.30
1	YA	1097	U	N1-C2-O2	6.32	127.23	122.80
1	YA	2242	G	O5'-P-OP1	-6.32	100.02	105.70
1	RA	1934	C	N1-C2-O2	6.31	122.69	118.90
1	YA	2047	U	N1-C2-O2	6.29	127.20	122.80
32	XA	1054	C	C6-N1-C2	-6.26	117.79	120.30
1	YA	1992	G	P-O3'-C3'	6.25	127.20	119.70
1	YA	2253	G	N1-C6-O6	6.24	123.64	119.90
32	XA	754	C	C2-N1-C1'	6.24	125.66	118.80
55	XY	100	LEU	CA-CB-CG	6.22	129.61	115.30
1	YA	1097	U	N3-C2-O2	-6.22	117.85	122.20
32	QA	115	G	P-O3'-C3'	6.20	127.14	119.70
32	QA	1030(C)	C	C2-N1-C1'	6.19	125.61	118.80
1	YA	277	C	P-O3'-C3'	6.19	127.13	119.70
1	YA	2501	C	C2-N1-C1'	-6.18	112.00	118.80
1	YA	2385	C	N3-C4-C5	6.18	124.37	121.90
1	RA	832	G	N1-C6-O6	-6.17	116.20	119.90
1	YA	2385	C	C6-N1-C2	6.17	122.77	120.30
1	RA	2386	C	C6-N1-C2	6.14	122.76	120.30
32	XA	1003	G	C4-N9-C1'	6.13	134.47	126.50
1	RA	778	G	C5-C6-O6	6.12	132.27	128.60
32	XA	1003	G	N3-C4-C5	-6.12	125.54	128.60
2	YB	6	C	C6-N1-C2	6.12	122.75	120.30
1	RA	1092	C	N3-C2-O2	-6.11	117.63	121.90
1	RA	1092	C	C2-N1-C1'	6.10	125.51	118.80
15	YT	111	ARG	NE-CZ-NH1	-6.10	117.25	120.30
1	YA	2524	G	N1-C6-O6	-6.08	116.25	119.90
1	YA	2569	G	N1-C6-O6	6.08	123.55	119.90
1	YA	1780	A	N1-C6-N6	-6.07	114.96	118.60
1	YA	1046	A	C6-N1-C2	6.07	122.24	118.60
1	RA	1940	U	N1-C2-O2	-6.06	118.56	122.80
1	YA	2573	C	N3-C4-N4	-6.06	113.76	118.00
1	RA	2445	G	N1-C6-O6	-6.04	116.28	119.90
1	YA	1083	U	C2-N1-C1'	6.02	124.92	117.70
32	XA	1183	A	OP1-P-O3'	6.01	118.43	105.20
32	XA	1003	G	C8-N9-C4	-5.99	104.00	106.40
1	YA	1530	C	P-O3'-C3'	5.98	126.88	119.70
1	YA	1806	C	C6-N1-C2	5.97	122.69	120.30
1	YA	203	C	N3-C4-N4	-5.97	113.82	118.00
4	YE	52	LEU	CA-CB-CG	5.97	129.03	115.30
1	RA	1045	A	P-O3'-C3'	5.97	126.86	119.70
32	QA	1442(A)	G	P-O3'-C3'	5.95	126.83	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	RA	728	G	N1-C6-O6	-5.92	116.35	119.90
1	YA	2699	C	N1-C2-O2	-5.91	115.35	118.90
1	RA	778	G	N1-C6-O6	-5.89	116.36	119.90
1	YA	1270	C	C6-N1-C2	5.88	122.65	120.30
1	YA	1811	G	C8-N9-C4	5.88	108.75	106.40
7	RH	69	ARG	NE-CZ-NH1	-5.87	117.36	120.30
1	YA	1046	A	N1-C6-N6	5.86	122.12	118.60
1	YA	1372	U	N3-C2-O2	-5.85	118.11	122.20
1	YA	209	C	C5-C4-N4	-5.84	116.11	120.20
1	YA	573	G	C8-N9-C4	-5.84	104.06	106.40
1	RA	744	G	N1-C6-O6	5.81	123.39	119.90
32	XA	1158	C	C6-N1-C1'	-5.78	113.86	120.80
1	RA	1530	C	P-O3'-C3'	5.78	126.64	119.70
1	YA	779	U	N3-C4-O4	5.77	123.44	119.40
1	YA	2047	U	N3-C2-O2	-5.76	118.17	122.20
1	RA	277	C	N1-C2-O2	5.75	122.35	118.90
7	YH	88	LEU	CA-CB-CG	5.75	128.51	115.30
1	YA	679	C	C6-N1-C2	5.74	122.60	120.30
1	RA	2061	G	N1-C6-O6	-5.72	116.47	119.90
1	YA	805	G	C5-C6-O6	-5.72	125.17	128.60
1	YA	1082	U	C5-C4-O4	-5.71	122.47	125.90
32	XA	803	G	C5-C6-O6	5.71	132.02	128.60
1	YA	1769	G	C2-N3-C4	5.70	114.75	111.90
1	YA	1854	A	C8-N9-C4	5.69	108.08	105.80
32	QA	943	U	P-O3'-C3'	5.69	126.53	119.70
3	YD	242	ARG	CG-CD-NE	5.68	123.74	111.80
26	Y4	60	GLN	N-CA-C	5.68	126.33	111.00
1	RA	1992	G	P-O3'-C3'	5.67	126.51	119.70
1	YA	2509	G	N3-C4-N9	5.67	129.40	126.00
1	YA	2056	G	N3-C4-N9	5.66	129.40	126.00
1	YA	1670	C	C5-C6-N1	5.65	123.82	121.00
1	YA	2385	C	C2-N3-C4	-5.65	117.08	119.90
1	RA	799	G	C5-C6-O6	-5.65	125.21	128.60
1	YA	2561	A	N1-C6-N6	5.64	121.98	118.60
32	QA	991	U	OP2-P-O3'	5.64	117.60	105.20
1	RA	2028	U	N1-C2-N3	5.63	118.28	114.90
1	YA	1625	C	N1-C2-O2	5.63	122.28	118.90
1	RA	2700	C	C6-N1-C2	5.62	122.55	120.30
32	XA	1003	G	N7-C8-N9	5.62	115.91	113.10
1	YA	2083	G	N1-C6-O6	5.62	123.27	119.90
1	RA	1092	C	C6-N1-C2	-5.61	118.05	120.30
1	YA	2501	C	C6-N1-C2	5.60	122.54	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	2573	C	C6-N1-C2	5.60	122.54	120.30
1	RA	512	G	O4'-C1'-N9	5.59	112.68	108.20
1	YA	1046	A	C2-N3-C4	-5.59	107.81	110.60
1	RA	847	U	C2-N1-C1'	5.58	124.39	117.70
1	YA	2036	C	C6-N1-C2	-5.58	118.07	120.30
1	YA	2237	G	N9-C4-C5	5.57	107.63	105.40
1	YA	198	C	N3-C4-N4	-5.56	114.11	118.00
1	YA	210	C	C5-C6-N1	-5.55	118.22	121.00
1	YA	2689	U	P-O3'-C3'	5.55	126.36	119.70
1	YA	277	C	OP1-P-O3'	5.53	117.36	105.20
1	YA	1092	C	N1-C2-O2	5.52	122.21	118.90
1	YA	2496	C	C6-N1-C2	5.52	122.51	120.30
1	YA	1369	G	C5-C6-O6	5.52	131.91	128.60
1	YA	765	G	N1-C6-O6	-5.52	116.59	119.90
1	YA	2072	G	C5-C6-O6	5.52	131.91	128.60
1	YA	1798	U	N3-C4-O4	-5.51	115.54	119.40
1	RA	1789	A	C8-N9-C4	5.51	108.00	105.80
1	YA	579	G	N1-C6-O6	5.51	123.21	119.90
1	RA	1640	C	C5-C6-N1	5.50	123.75	121.00
1	RA	1277	G	C8-N9-C4	5.50	108.60	106.40
1	YA	2571	C	C5-C6-N1	-5.50	118.25	121.00
1	YA	278	A	O5'-P-OP1	-5.50	100.75	105.70
1	YA	1048	A	N1-C6-N6	-5.50	115.30	118.60
1	RA	436	C	N3-C2-O2	-5.49	118.06	121.90
1	YA	1083	U	C4-C5-C6	5.49	123.00	119.70
32	XA	284	G	N1-C6-O6	-5.49	116.61	119.90
1	YA	1092	C	C2-N1-C1'	5.49	124.84	118.80
32	XA	963	G	N1-C6-O6	-5.49	116.61	119.90
1	YA	128	C	C6-N1-C2	5.48	122.49	120.30
1	YA	746	A	O4'-C1'-N9	5.47	112.58	108.20
1	YA	678	C	C6-N1-C2	5.47	122.49	120.30
1	YA	1670	C	C6-N1-C2	-5.46	118.11	120.30
1	YA	1218	C	C6-N1-C2	5.45	122.48	120.30
1	YA	1083	U	N3-C2-O2	-5.45	118.39	122.20
1	YA	1063	G	C4-N9-C1'	5.43	133.56	126.50
32	XA	1067	A	P-O3'-C3'	5.43	126.22	119.70
1	YA	1807	G	C2-N3-C4	-5.43	109.19	111.90
1	RA	673	C	C6-N1-C2	-5.42	118.13	120.30
1	YA	624	C	C6-N1-C2	5.42	122.47	120.30
1	YA	2509	G	N3-C4-C5	-5.41	125.89	128.60
1	YA	1041	C	N1-C2-O2	5.41	122.14	118.90
1	YA	2569	G	C5-C6-O6	-5.41	125.36	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	2004	G	C5-C6-O6	5.40	131.84	128.60
1	YA	692	C	C6-N1-C2	5.39	122.45	120.30
1	RA	1210	A	P-O3'-C3'	5.38	126.15	119.70
36	XE	143	ARG	NE-CZ-NH2	-5.37	117.62	120.30
1	YA	2247	A	C2-N3-C4	-5.36	107.92	110.60
32	XA	1054	C	C2-N1-C1'	5.36	124.70	118.80
32	XA	266	G	OP2-P-O3'	5.36	116.99	105.20
1	YA	974	G	N1-C6-O6	5.35	123.11	119.90
50	QS	28	LYS	CB-CA-C	-5.34	99.71	110.40
1	YA	531	C	N1-C2-O2	-5.34	115.70	118.90
1	RA	672	C	N1-C2-O2	5.33	122.10	118.90
1	RA	585	G	C6-C5-N7	-5.33	127.20	130.40
1	RA	1940	U	N3-C4-O4	5.33	123.13	119.40
1	RA	1763	G	C8-N9-C4	5.33	108.53	106.40
1	YA	1328	G	C5-C6-O6	-5.33	125.40	128.60
32	QA	839	U	P-O3'-C3'	5.32	126.08	119.70
1	YA	1313	U	C2-N1-C1'	5.32	124.08	117.70
1	YA	2447	G	C2-N3-C4	-5.31	109.25	111.90
1	YA	1091	G	N3-C4-C5	-5.31	125.95	128.60
1	YA	2072	G	N1-C6-O6	-5.31	116.72	119.90
1	RA	122	G	C8-N9-C4	5.31	108.52	106.40
1	YA	226	G	O4'-C1'-N9	5.30	112.44	108.20
1	YA	862	G	N1-C6-O6	-5.30	116.72	119.90
1	YA	678	C	O5'-P-OP2	-5.30	100.93	105.70
37	XF	82	ARG	NE-CZ-NH1	5.30	122.95	120.30
1	RA	388	G	C6-C5-N7	5.29	133.57	130.40
32	QA	1030(C)	C	N3-C2-O2	-5.29	118.20	121.90
32	XA	748	C	P-O3'-C3'	5.28	126.04	119.70
32	XA	1065	U	P-O3'-C3'	5.27	126.03	119.70
1	RA	778	G	C4-C5-N7	-5.27	108.69	110.80
32	QA	1419	G	N1-C6-O6	5.27	123.06	119.90
1	YA	2272	U	N3-C2-O2	5.27	125.89	122.20
32	XA	115	G	P-O3'-C3'	5.26	126.01	119.70
1	YA	966	G	N3-C2-N2	5.26	123.58	119.90
1	YA	132	G	C8-N9-C4	5.25	108.50	106.40
1	YA	2226	C	C6-N1-C2	5.25	122.40	120.30
1	YA	2070	G	C8-N9-C4	5.25	108.50	106.40
32	XA	1442(A)	G	P-O3'-C3'	5.25	126.00	119.70
1	YA	2506	U	N3-C4-O4	-5.25	115.73	119.40
1	RA	2751	G	C2-N3-C4	5.24	114.52	111.90
1	YA	1049	C	N3-C2-O2	-5.24	118.23	121.90
1	YA	1083	U	C5-C4-O4	-5.23	122.76	125.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	RA	585	G	N1-C6-O6	5.23	123.04	119.90
35	QD	13	ARG	NE-CZ-NH1	5.22	122.91	120.30
40	QI	42	ARG	NE-CZ-NH2	-5.22	117.69	120.30
1	RA	1790	C	N3-C4-C5	5.22	123.99	121.90
1	YA	2081	C	N1-C2-O2	5.22	122.03	118.90
1	YA	123	G	N1-C6-O6	5.21	123.03	119.90
1	RA	1082	U	C2-N1-C1'	5.20	123.94	117.70
32	XA	803	G	N1-C6-O6	-5.20	116.78	119.90
32	XA	1004	A	O4'-C1'-N9	5.20	112.36	108.20
33	XB	144	ARG	NE-CZ-NH1	-5.20	117.70	120.30
1	YA	2237	G	C5-C6-O6	5.19	131.72	128.60
1	YA	949	C	N3-C2-O2	5.18	125.53	121.90
1	YA	1314	C	C2-N1-C1'	5.17	124.49	118.80
1	YA	400	G	N1-C6-O6	5.17	123.00	119.90
32	XA	916	G	N1-C6-O6	-5.16	116.80	119.90
32	XA	766	A	C8-N9-C4	5.16	107.86	105.80
1	RA	1323	U	N3-C2-O2	5.15	125.81	122.20
3	RD	242	ARG	NE-CZ-NH1	5.15	122.88	120.30
1	YA	2689	U	N3-C2-O2	-5.15	118.59	122.20
1	YA	822	U	N3-C2-O2	-5.15	118.59	122.20
1	YA	2056	G	N3-C4-C5	-5.15	126.03	128.60
1	YA	2751	G	C5-C6-O6	5.15	131.69	128.60
1	YA	2751	G	C6-C5-N7	5.15	133.49	130.40
1	RA	1993	U	O5'-P-OP1	-5.14	101.07	105.70
1	YA	989	G	N1-C6-O6	5.14	122.98	119.90
1	YA	2249	U	N1-C2-O2	5.13	126.39	122.80
1	YA	1092	C	C5-C6-N1	5.13	123.56	121.00
1	YA	1611	C	N3-C4-C5	5.13	123.95	121.90
1	YA	209	C	N3-C4-N4	5.13	121.59	118.00
1	YA	2441	C	N3-C4-N4	-5.13	114.41	118.00
1	YA	2087	G	N1-C6-O6	5.12	122.97	119.90
1	YA	2068	U	N1-C2-O2	-5.12	119.22	122.80
32	XA	773	G	N1-C6-O6	-5.12	116.83	119.90
1	RA	2029	G	N1-C6-O6	-5.12	116.83	119.90
1	YA	238	C	C6-N1-C2	5.12	122.35	120.30
1	RA	388	G	N3-C4-N9	-5.11	122.93	126.00
1	YA	2336	A	C5-C6-N1	5.10	120.25	117.70
1	RA	752	A	P-O3'-C3'	5.10	125.82	119.70
1	RA	1636	C	C6-N1-C2	5.09	122.33	120.30
1	YA	791	C	C6-N1-C2	5.08	122.33	120.30
1	YA	1085	A	C2-N3-C4	5.08	113.14	110.60
1	YA	115	C	C5-C4-N4	-5.08	116.64	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	214	G	O4'-C1'-N9	5.08	112.26	108.20
1	YA	667	U	N3-C4-O4	5.08	122.95	119.40
1	RA	775	G	N1-C6-O6	-5.07	116.86	119.90
1	YA	748	G	N3-C2-N2	-5.07	116.35	119.90
1	YA	783	A	C4-C5-C6	5.06	119.53	117.00
53	XV	53	G	P-O3'-C3'	5.06	125.77	119.70
1	YA	784	A	O4'-C1'-N9	5.06	112.25	108.20
1	YA	2318	G	C4-N9-C1'	5.06	133.07	126.50
32	QA	266	G	P-O3'-C3'	5.05	125.76	119.70
1	RA	2029	G	C6-C5-N7	5.05	133.43	130.40
1	YA	742	G	N1-C6-O6	5.05	122.93	119.90
1	YA	2440	C	N3-C4-C5	-5.05	119.88	121.90
1	YA	2525	G	C8-N9-C4	5.05	108.42	106.40
1	YA	2571	C	N3-C4-C5	5.04	123.92	121.90
32	QA	1285	A	P-O3'-C3'	5.04	125.75	119.70
1	YA	832	G	P-O3'-C3'	5.03	125.74	119.70
1	YA	2495	G	C8-N9-C4	5.03	108.41	106.40
32	QA	791	G	N3-C2-N2	-5.02	116.39	119.90
1	YA	1125	G	C5-C6-O6	5.02	131.61	128.60
1	YA	1671	U	C5-C4-O4	-5.02	122.89	125.90
1	RA	2751	G	N1-C2-N2	5.01	120.71	116.20
45	QN	31	ARG	NE-CZ-NH2	-5.01	117.79	120.30
1	YA	2509	G	C2-N3-C4	5.01	114.41	111.90
1	YA	2692	C	N3-C2-O2	-5.01	118.39	121.90
1	YA	622	G	C8-N9-C4	5.01	108.40	106.40
1	RA	2075	U	O5'-P-OP1	-5.01	101.19	105.70
1	YA	1602	U	N1-C2-O2	-5.00	119.30	122.80

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	QB	231	GLU	Peptide
55	QY	305	ASP	Peptide
14	RS	58	LEU	Peptide
43	XL	86	ARG	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	RA	61758	0	31144	585	0
1	YA	61758	0	31147	608	1
2	RB	2572	0	1305	11	0
2	YB	2573	0	1306	12	0
3	RD	2131	0	2207	49	0
3	YD	2136	0	2218	49	0
4	RE	1559	0	1618	34	0
4	YE	1559	0	1618	40	0
5	RF	1584	0	1625	37	0
5	YF	1580	0	1619	46	0
6	RG	1426	0	1445	30	0
6	YG	1424	0	1441	38	0
7	RH	1330	0	1407	20	0
7	YH	1324	0	1402	33	0
8	RI	1094	0	1127	22	0
8	YI	1076	0	1093	14	0
9	RN	1121	0	1195	16	0
9	YN	1117	0	1184	16	0
10	RO	933	0	996	17	0
10	YO	933	0	996	14	0
11	RP	1135	0	1212	22	0
11	YP	1135	0	1212	32	0
12	RQ	1122	0	1179	20	0
12	YQ	1122	0	1179	20	0
13	RR	968	0	1033	21	0
13	YR	968	0	1033	13	0
14	RS	877	0	938	12	0
14	YS	870	0	923	13	0
15	RT	1091	0	1151	25	0
15	YT	1083	0	1136	19	0
16	RU	959	0	1019	16	0
16	YU	959	0	1019	18	0
17	RV	775	0	841	13	0
17	YV	771	0	830	13	0
18	RW	886	0	940	12	0
18	YW	886	0	940	12	0
19	RX	750	0	814	16	0
19	YX	750	0	814	6	0
20	RY	810	0	894	15	0
20	YY	810	0	891	17	0
21	RZ	1587	0	1598	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	YZ	1557	0	1564	24	0
22	R0	608	0	622	12	0
22	Y0	608	0	622	15	0
23	R1	754	0	823	10	0
23	Y1	759	0	837	18	0
24	R2	588	0	643	11	1
24	Y2	592	0	654	7	0
25	R3	469	0	518	5	0
25	Y3	464	0	514	6	0
26	R4	546	0	523	27	0
26	Y4	536	0	516	26	0
27	R5	459	0	477	12	0
27	Y5	455	0	467	5	0
28	R6	453	0	475	7	0
28	Y6	449	0	471	7	0
29	R7	418	0	467	11	0
29	Y7	418	0	467	8	0
30	R8	517	0	582	17	0
30	Y8	517	0	582	19	0
31	R9	307	0	336	14	0
31	Y9	307	0	336	11	0
32	QA	32246	0	16294	306	0
32	XA	32331	0	16338	343	0
33	QB	1842	0	1862	54	0
33	XB	1825	0	1828	62	0
34	QC	1558	0	1557	33	0
34	XC	1542	0	1517	32	0
35	QD	1665	0	1690	60	0
35	XD	1668	0	1706	44	0
36	QE	1133	0	1191	28	0
36	XE	1133	0	1191	25	0
37	QF	814	0	808	20	0
37	XF	816	0	807	8	0
38	QG	1235	0	1249	18	0
38	XG	1229	0	1238	15	0
39	QH	1098	0	1143	20	0
39	XH	1088	0	1126	21	0
40	QI	986	0	990	28	0
40	XI	966	0	953	35	0
41	QJ	719	0	672	27	0
41	XJ	710	0	661	20	0
42	QK	834	0	838	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	XK	833	0	836	13	0
43	QL	932	0	981	18	0
43	XL	932	0	981	26	0
44	QM	914	0	954	23	0
44	XM	895	0	920	24	0
45	QN	492	0	529	11	0
45	XN	492	0	529	14	0
46	QO	728	0	760	12	0
46	XO	728	0	760	13	0
47	QP	681	0	697	19	0
47	XP	677	0	686	19	0
48	QQ	823	0	891	8	0
48	XQ	823	0	891	9	0
49	QR	555	0	618	11	0
49	XR	555	0	618	9	0
50	QS	648	0	658	17	0
50	XS	645	0	635	19	0
51	QT	732	0	809	15	0
51	XT	733	0	795	13	0
52	QU	199	0	208	3	0
52	XU	199	0	208	1	0
53	QV	1640	0	837	15	0
53	XV	1644	0	836	15	0
54	QX	193	0	98	5	0
54	XX	215	0	108	2	0
55	QY	2014	0	1980	73	0
55	XY	2022	0	1991	85	0
56	QA	262	0	0	0	0
56	QB	1	0	0	0	0
56	QD	2	0	0	0	0
56	QE	2	0	0	0	0
56	QF	1	0	0	0	0
56	QG	3	0	0	0	0
56	QH	1	0	0	0	0
56	QI	1	0	0	0	0
56	QJ	1	0	0	0	0
56	QL	2	0	0	0	0
56	QN	1	0	0	0	0
56	QO	1	0	0	0	0
56	QQ	1	0	0	0	0
56	QR	1	0	0	0	0
56	QT	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	QV	6	0	0	0	0
56	R0	7	0	0	0	0
56	R1	5	0	0	0	0
56	R3	2	0	0	0	0
56	R5	1	0	0	0	0
56	R7	3	0	0	0	0
56	R9	1	0	0	0	0
56	RA	1032	0	0	0	0
56	RB	22	0	0	0	0
56	RD	15	0	0	0	0
56	RE	7	0	0	0	0
56	RF	11	0	0	0	0
56	RG	4	0	0	0	0
56	RN	2	0	0	0	0
56	RO	1	0	0	0	0
56	RP	2	0	0	0	0
56	RQ	5	0	0	0	0
56	RR	4	0	0	0	0
56	RS	1	0	0	0	0
56	RT	3	0	0	0	0
56	RU	3	0	0	0	0
56	RV	3	0	0	0	0
56	RW	2	0	0	0	0
56	RX	1	0	0	0	0
56	RY	1	0	0	0	0
56	XA	187	0	0	0	0
56	XE	2	0	0	0	0
56	XF	4	0	0	0	0
56	XJ	1	0	0	0	0
56	XL	1	0	0	0	0
56	XT	1	0	0	0	0
56	XV	4	0	0	0	0
56	XY	1	0	0	0	0
56	Y0	1	0	0	0	0
56	Y1	1	0	0	0	0
56	Y5	2	0	0	0	0
56	Y7	1	0	0	0	0
56	Y8	2	0	0	0	0
56	YA	749	0	0	0	0
56	YB	20	0	0	0	0
56	YD	9	0	0	0	0
56	YE	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	YF	2	0	0	0	0
56	YG	2	0	0	0	0
56	YI	1	0	0	0	0
56	YN	1	0	0	0	0
56	YO	1	0	0	0	0
56	YP	1	0	0	0	0
56	YQ	3	0	0	0	0
56	YR	1	0	0	0	0
56	YT	3	0	0	0	0
56	YV	1	0	0	0	0
56	YW	2	0	0	0	0
56	YX	1	0	0	0	0
57	QN	1	0	0	0	0
57	R4	1	0	0	0	0
57	R5	1	0	0	0	0
57	R6	1	0	0	0	0
57	R9	1	0	0	0	0
57	RY	1	0	0	0	0
57	XN	1	0	0	0	0
57	Y4	1	0	0	0	0
57	Y5	1	0	0	0	0
57	Y6	1	0	0	0	0
57	Y9	1	0	0	0	0
57	YY	1	0	0	0	0
58	QD	8	0	0	0	0
58	XD	8	0	0	0	0
All	All	294929	0	198658	3417	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 7.

All (3417) 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)
1:RA:2552:2MU:C4	1:RA:2552:2MU:C5	1.74	1.65
1:YA:2552:2MU:C5	1:YA:2552:2MU:C4	1.75	1.56
32:XA:1003:G:H2'	32:XA:1004:A:H4'	1.40	1.03
1:YA:2131:G:H5''	1:YA:2132:U:H5'	1.46	0.98
26:Y4:59:PHE:HA	26:Y4:61:ARG:H	1.26	0.97
1:RA:2131:G:H5''	1:RA:2132:U:H5'	1.45	0.96
15:RT:55:ASN:H	15:RT:59:THR:HG22	1.30	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y4:59:PHE:HA	26:Y4:61:ARG:N	1.80	0.96
33:QB:82:ARG:NH1	33:QB:92:TYR:OH	2.01	0.93
12:RQ:21:THR:HG21	12:RQ:101:ARG:HB2	1.52	0.92
55:XY:242:SER:HA	55:XY:263:GLN:HB3	1.53	0.90
35:QD:3:ARG:HD3	35:QD:118:ARG:HE	1.37	0.89
29:Y7:34:ARG:HG2	29:Y7:39:ARG:HG3	1.53	0.89
14:RS:59:LYS:HD2	14:RS:60:GLY:H	1.37	0.89
1:YA:2552:2MU:C6	1:YA:2552:2MU:C4	2.48	0.88
8:YI:92:VAL:HG23	8:YI:120:ILE:HB	1.56	0.88
1:YA:2785:C:OP1	4:YE:41:LYS:NZ	2.08	0.87
10:YO:48:PRO:HB3	32:XA:1422:G:H5'	1.57	0.86
7:RH:7:LEU:O	7:RH:69:ARG:NH1	2.09	0.85
55:XY:212:ALA:HB1	55:XY:214:LEU:HG	1.59	0.85
55:QY:242:SER:HA	55:QY:263:GLN:HB3	1.59	0.84
40:QI:17:VAL:HG21	40:QI:81:ILE:HG22	1.60	0.84
33:QB:231:GLU:HB3	33:QB:232:PRO:HD3	1.58	0.83
33:XB:15:VAL:HB	33:XB:209:ARG:HB3	1.60	0.83
10:RO:35:VAL:HG11	10:RO:103:ALA:HB3	1.62	0.82
21:YZ:198:LYS:HE3	53:XV:52:G:H2'	1.61	0.82
55:QY:123:GLU:HG3	55:QY:188:PRO:HB3	1.59	0.82
1:YA:301:G:OP2	20:YY:84:ARG:NH2	2.13	0.82
32:XA:664:G:H22	32:XA:741:G:H1	1.27	0.82
32:QA:1103:C:OP1	33:QB:96:ARG:NH2	2.12	0.81
1:RA:143(A):G:H4'	19:RX:35:THR:HG21	1.60	0.81
5:YF:10:PRO:HB3	5:YF:17:ARG:HE	1.45	0.81
15:YT:65:LYS:HE3	15:YT:67:SER:HB2	1.62	0.81
32:QA:78:G:H1	32:QA:91:C:H42	1.27	0.81
3:YD:17:THR:O	3:YD:211:ARG:NH2	2.14	0.80
1:RA:2573:C:N4	55:QY:239:THR:HA	1.96	0.80
1:YA:2573:C:N4	55:XY:239:THR:O	2.13	0.80
32:QA:343:U:O2'	32:QA:346:G:O6	2.00	0.80
55:XY:101:LEU:HD11	55:XY:353:LEU:HD23	1.62	0.80
41:QJ:35:SER:HB3	41:QJ:73:ASP:HB2	1.63	0.80
1:RA:2529:G:O6	31:R9:31:LYS:NZ	2.14	0.80
32:XA:1398:A:OP1	55:XY:193:GLN:NE2	2.15	0.80
32:XA:582:U:OP1	46:XO:68:ARG:NH2	2.14	0.80
32:XA:559:A:OP1	36:XE:126:ARG:NH2	2.14	0.79
41:XJ:49:VAL:HG23	45:XN:41:ARG:HB2	1.64	0.79
1:YA:631:A:OP1	11:YP:65:ARG:NH1	2.14	0.79
1:RA:987:G:O2'	1:RA:1000:A:N3	2.16	0.79
50:XS:50:ALA:HB1	50:XS:57:HIS:HB3	1.64	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1798:U:H5'	3:YD:259:THR:HG22	1.63	0.79
42:XK:99:GLN:HG2	42:XK:105:VAL:HG21	1.63	0.79
1:RA:833:U:O2	11:RP:55:ARG:NH2	2.15	0.78
29:R7:24:THR:HG23	29:R7:27:GLY:H	1.48	0.78
1:RA:2140:C:H2'	1:RA:2141:G:H8	1.49	0.78
10:RO:48:PRO:HB3	32:QA:1422:G:H5''	1.64	0.78
1:RA:1798:U:OP2	3:RD:274:ARG:NH2	2.17	0.78
1:RA:1048:A:N6	1:RA:2751:G:O6	2.17	0.78
1:YA:2128:C:H42	1:YA:2160:G:H1	1.32	0.77
40:XI:53:VAL:O	40:XI:55:ALA:N	2.17	0.77
55:XY:263:GLN:O	55:XY:267:LYS:N	2.17	0.77
10:YO:35:VAL:HG11	10:YO:103:ALA:HB3	1.65	0.77
6:RG:179:PRO:HB2	26:R4:42:PHE:HE2	1.49	0.77
1:RA:250:G:OP2	30:R8:13:ARG:NH2	2.18	0.77
1:RA:1057:A:N6	1:RA:1087:G:OP1	2.17	0.77
55:QY:102:PRO:HG3	55:QY:353:LEU:HD21	1.65	0.77
1:RA:2478:A:OP2	31:R9:2:LYS:NZ	2.17	0.77
1:YA:2469:A:O2'	12:YQ:56:ARG:NH1	2.17	0.77
1:RA:1041:C:H42	1:RA:1114:G:H1	1.31	0.77
1:RA:1141:U:OP1	9:RN:25:ARG:NH1	2.18	0.77
32:XA:390:C:O3'	47:XP:28:ARG:NH2	2.18	0.77
1:RA:2128:C:H42	1:RA:2160:G:H1	1.30	0.76
53:XV:75:C:OP2	55:XY:261:ARG:NH2	2.17	0.76
22:R0:10:THR:HG22	22:R0:12:ASN:H	1.50	0.76
11:YP:59:LEU:HD11	30:Y8:10:ALA:HB2	1.66	0.76
32:QA:1189:C:OP1	41:QJ:51:ARG:NH2	2.19	0.76
32:XA:975:A:H4'	32:XA:976:G:H5''	1.67	0.76
1:YA:1048:A:N6	1:YA:2751:G:O6	2.18	0.76
32:XA:401:C:OP2	35:XD:73:ARG:NH2	2.15	0.76
23:Y1:51:VAL:HG11	23:Y1:74:VAL:HG21	1.68	0.76
1:RA:1530:C:O2'	1:RA:1531:C:O5'	2.03	0.76
6:YG:113:ARG:HH21	26:Y4:33:VAL:HG12	1.51	0.76
1:RA:2552:2MU:C6	1:RA:2552:2MU:C4	2.49	0.76
55:XY:214:LEU:HB2	55:XY:215:PRO:HA	1.67	0.76
20:RY:92:ASN:HB2	20:RY:94:LYS:H	1.51	0.76
4:YE:47:VAL:HG11	4:YE:86:PRO:HD2	1.67	0.76
19:RX:60:ARG:HH22	29:R7:47:ARG:HH22	1.31	0.75
55:QY:209:LEU:O	55:QY:211:ASP:N	2.19	0.75
5:RF:53:THR:HG22	5:RF:55:GLY:H	1.51	0.75
11:RP:59:LEU:HD11	30:R8:10:ALA:HB2	1.68	0.75
33:QB:15:VAL:HG23	33:QB:209:ARG:HB3	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:R7:34:ARG:NH1	29:R7:41:ARG:O	2.19	0.75
33:XB:17:PHE:HD1	33:XB:18:GLY:H	1.35	0.75
1:YA:574:C:N3	4:YE:145:LYS:NZ	2.34	0.75
32:XA:1310:G:OP2	44:XM:88:ARG:NH1	2.19	0.75
1:RA:1038:C:H42	1:RA:1117:G:H1	1.34	0.75
4:RE:47:VAL:HG21	4:RE:86:PRO:HD2	1.67	0.75
32:XA:677:U:H3	32:XA:713:G:H22	1.33	0.75
20:RY:102:CYS:SG	20:RY:103:GLY:N	2.59	0.74
1:YA:250:G:OP2	30:Y8:13:ARG:NH2	2.21	0.74
1:RA:2285:C:OP1	28:R6:29:ASN:ND2	2.20	0.74
1:YA:587:C:OP2	11:YP:21:ARG:NH2	2.20	0.74
33:QB:21:ARG:HH22	33:QB:23:ARG:HE	1.35	0.74
26:Y4:59:PHE:CE1	50:XS:64:GLU:HB2	2.23	0.74
1:YA:2285:C:OP2	28:Y6:26:ASN:ND2	2.18	0.74
5:YF:178:PRO:HB2	5:YF:201:VAL:HG21	1.68	0.74
48:XQ:66:SER:O	48:XQ:70:ARG:NH1	2.21	0.74
6:RG:139:LEU:HD21	6:RG:149:VAL:HG11	1.70	0.73
3:RD:69:ARG:HH11	3:RD:69:ARG:HG2	1.53	0.73
33:XB:88:ALA:HB1	33:XB:222:ILE:HD11	1.70	0.73
21:YZ:144:LEU:HD21	21:YZ:150:LEU:HD13	1.69	0.73
1:YA:1971:A:OP2	3:YD:242:ARG:NH2	2.20	0.73
32:QA:201:C:H42	32:QA:216:G:H1	1.36	0.73
34:XC:40:ARG:NH2	34:XC:55:VAL:O	2.19	0.73
47:QP:53:VAL:HG13	47:QP:79:VAL:HG12	1.70	0.73
55:XY:217:ILE:HD12	55:XY:222:LEU:HD11	1.69	0.73
1:YA:2134:A:N6	1:YA:2156:G:O2'	2.22	0.73
1:RA:2746:U:OP1	7:RH:85:LYS:NZ	2.22	0.72
32:QA:677:U:H3	32:QA:713:G:H22	1.33	0.72
40:QI:121:ARG:NH1	40:QI:122:ALA:O	2.22	0.72
32:QA:975:A:H4'	32:QA:976:G:H5''	1.70	0.72
35:QD:53:ASP:HB3	35:QD:57:ARG:HH12	1.54	0.72
32:QA:1352:C:OP1	52:QU:3:LYS:NZ	2.21	0.72
32:XA:1518:MA6:H93	32:XA:1519:MA6:H102	1.71	0.72
40:XI:16:ARG:HB2	40:XI:64:THR:HG22	1.71	0.72
31:Y9:16:VAL:HG22	31:Y9:25:VAL:HG22	1.72	0.72
33:QB:88:ALA:O	33:QB:226:ARG:NH2	2.21	0.72
1:RA:2206:G:H3'	1:RA:2207:G:C8	2.25	0.72
1:YA:270:A:OP2	1:YA:272(X):G:N1	2.20	0.72
6:RG:161:THR:HG22	6:RG:163:ALA:H	1.55	0.72
1:RA:463:G:N2	1:RA:466:A:OP2	2.20	0.72
44:XM:58:GLU:O	44:XM:62:ASN:ND2	2.21	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1359:A:H61	1:YA:1372:U:H3	1.38	0.72
1:YA:2140:C:H2'	1:YA:2141:G:H8	1.53	0.72
8:YI:9:LEU:HD12	8:YI:12:LEU:HD12	1.72	0.72
1:YA:1530:C:O2'	1:YA:1531:C:O5'	2.06	0.72
1:YA:1593:G:H2'	1:YA:1594:G:C8	2.25	0.72
20:YY:102:CYS:SG	20:YY:103:GLY:N	2.63	0.72
32:QA:38:G:H22	32:QA:397:A:H5'	1.55	0.72
1:RA:631:A:OP1	11:RP:65:ARG:NH1	2.23	0.71
44:XM:107:ALA:HB3	44:XM:111:LYS:HD2	1.71	0.71
51:XT:56:MET:HE1	51:XT:85:MET:HG2	1.72	0.71
5:YF:18:ARG:HG2	5:YF:19:GLU:H	1.54	0.71
34:XC:58:GLU:HB3	41:XJ:92:THR:HG21	1.70	0.71
44:QM:19:LEU:HD21	44:QM:56:LEU:HD21	1.73	0.71
11:YP:2:LYS:NZ	11:YP:4:SER:OG	2.23	0.71
55:XY:123:GLU:OE1	55:XY:199:SER:OG	2.07	0.71
22:R0:23:VAL:HG22	22:R0:38:VAL:HG22	1.70	0.71
32:XA:642:A:N3	39:XH:113:SER:OG	2.23	0.71
1:YA:1815:A:OP2	3:YD:54:ARG:NH2	2.24	0.71
33:XB:128:GLU:OE1	33:XB:135:GLN:NE2	2.21	0.70
55:XY:245:ARG:HG3	55:XY:256:GLU:HG2	1.71	0.70
1:YA:1064:C:H3'	1:YA:1065:U:H5'	1.72	0.70
36:QE:126:ARG:HG3	36:QE:126:ARG:HH11	1.57	0.70
21:RZ:158:PRO:HG2	21:RZ:161:VAL:HG11	1.74	0.70
32:XA:1360:A:OP2	45:XN:35:ARG:NH2	2.25	0.70
50:QS:50:ALA:HB1	50:QS:57:HIS:HB3	1.73	0.70
1:YA:1041:C:H42	1:YA:1114:G:H1	1.39	0.70
13:YR:96:ARG:NH1	13:YR:115:GLU:OE1	2.24	0.70
36:QE:79:GLU:HG3	36:QE:93:PRO:HD2	1.73	0.70
32:QA:538:G:H5''	43:QL:114:LYS:HB2	1.74	0.70
11:YP:86:LYS:HB3	11:YP:118:GLY:HA3	1.74	0.70
32:QA:1003:G:N2	32:QA:1004:A:N3	2.39	0.70
55:QY:328:ARG:HD2	55:QY:340:LEU:HD21	1.72	0.70
1:YA:1798:U:OP2	3:YD:274:ARG:NH2	2.24	0.70
32:XA:1292:U:OP2	38:XG:41:ARG:NH2	2.24	0.70
55:XY:255:VAL:HG12	55:XY:274:LEU:HG	1.73	0.70
1:YA:1914:C:C2	55:XY:295:ARG:HD3	2.27	0.70
32:QA:1360:A:OP2	45:QN:35:ARG:NH2	2.24	0.70
26:R4:57:GLU:HB2	26:R4:58:ARG:HA	1.72	0.70
6:RG:41:GLN:HB3	6:RG:43:LEU:HD13	1.73	0.69
32:XA:696:A:N1	32:XA:797:C:O2'	2.22	0.69
32:QA:189(B):C:H42	32:QA:189(K):G:H1	1.39	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:QY:114:GLU:HB2	55:QY:204:ALA:HB3	1.74	0.69
1:RA:2785:C:OP1	4:RE:41:LYS:NZ	2.24	0.69
32:XA:474:G:H2'	32:XA:475:G:H8	1.56	0.69
1:YA:2640:G:O3'	9:YN:74:ARG:NH2	2.19	0.69
32:XA:427:U:OP1	35:XD:13:ARG:NH2	2.25	0.69
41:XJ:17:ASP:OD1	41:XJ:70:ARG:NH1	2.25	0.69
36:XE:50:GLU:HB2	36:XE:53:LEU:HD13	1.74	0.69
22:Y0:11:ARG:O	22:Y0:14:ARG:NH2	2.25	0.69
6:YG:161:THR:HG22	6:YG:163:ALA:H	1.56	0.69
40:QI:50:LEU:HD13	40:QI:56:LEU:HA	1.72	0.69
13:YR:67:LEU:HD13	13:YR:76:VAL:HG21	1.75	0.69
1:RA:1071:G:N2	1:RA:1089:G:O6	2.17	0.69
1:RA:1378:A:OP1	29:R7:10:ARG:NH2	2.26	0.69
1:RA:652(C):A:H61	1:RA:655:A:H1'	1.57	0.69
15:YT:16:ARG:NH2	15:YT:83:ILE:O	2.26	0.69
1:RA:1009:A:OP2	9:RN:37:LYS:NZ	2.24	0.69
1:RA:2748:A:H5'	7:RH:4:ILE:HD12	1.75	0.69
1:YA:2748:A:H5'	7:YH:4:ILE:HD12	1.74	0.69
44:QM:3:ARG:HD2	44:QM:9:ILE:HG12	1.75	0.68
32:XA:486:U:H2'	32:XA:487:A:H8	1.57	0.68
50:XS:41:VAL:HG12	50:XS:44:MET:HG3	1.74	0.68
4:YE:12:THR:HG23	15:YT:58:ASN:HD21	1.56	0.68
1:YA:1071:G:N2	1:YA:1089:G:O6	2.18	0.68
27:R5:16:ARG:NH1	27:R5:17:ASP:OD1	2.26	0.68
36:XE:69:VAL:HG11	36:XE:113:ALA:HB1	1.75	0.68
55:XY:101:LEU:H	55:XY:103:LYS:HE3	1.57	0.68
35:QD:173:TRP:CD2	35:QD:189:PRO:HG3	2.28	0.68
33:XB:91:PRO:HG3	33:XB:155:LEU:HD23	1.76	0.68
40:XI:46:ALA:HB2	40:XI:74:ILE:HG23	1.76	0.68
47:QP:13:HIS:O	47:QP:42:ARG:NH1	2.27	0.68
1:RA:1817:G:OP1	3:RD:88:ARG:NH2	2.26	0.68
32:XA:1412:C:H2'	32:XA:1413:A:C8	2.29	0.68
6:YG:41:GLN:HB3	6:YG:43:LEU:HD13	1.74	0.68
33:QB:195:ASP:O	39:QH:68:ARG:NH2	2.27	0.68
33:QB:185:ILE:HG22	33:QB:199:TYR:HB2	1.75	0.68
38:QG:113:GLU:HG2	38:QG:119:ARG:HG2	1.76	0.68
46:QO:7:GLU:OE2	46:QO:38:ARG:NH2	2.26	0.68
32:XA:1278:U:H5''	32:XA:1279:A:H5'	1.74	0.68
4:YE:52:LEU:HB3	4:YE:53:PRO:HD2	1.74	0.68
5:RF:18:ARG:HG2	5:RF:19:GLU:H	1.58	0.67
1:YA:2206:G:H5''	1:YA:2207:G:C8	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:XC:152:ILE:HG12	34:XC:199:LYS:HB2	1.76	0.67
33:QB:19:HIS:NE2	33:QB:189:ASP:OD2	2.27	0.67
33:XB:187:LEU:HA	33:XB:201:ILE:HB	1.75	0.67
9:RN:46:VAL:HG23	9:RN:48:MET:HG2	1.77	0.67
1:YA:11:G:H2'	1:YA:12:U:H5'	1.76	0.67
1:YA:2206:G:H3'	1:YA:2207:G:H8	1.58	0.67
41:XJ:61:GLU:OE1	45:XN:58:LYS:NZ	2.27	0.67
32:QA:664:G:H22	32:QA:741:G:H1	1.42	0.67
5:RF:51:THR:HB	5:RF:88:VAL:HG11	1.77	0.67
15:RT:55:ASN:N	15:RT:59:THR:HG22	2.06	0.67
32:XA:978:A:O2'	32:XA:1322:C:N3	2.27	0.67
22:Y0:10:THR:HG22	22:Y0:12:ASN:H	1.60	0.67
6:YG:143:GLU:OE2	26:Y4:26:SER:OG	2.10	0.67
35:QD:23:GLY:N	35:QD:26:CYS:SG	2.68	0.67
6:RG:143:GLU:OE2	26:R4:26:SER:OG	2.12	0.67
8:RI:109:ILE:HG13	8:RI:130:TYR:CZ	2.30	0.67
32:XA:1223:C:OP1	50:XS:78:ARG:NH2	2.27	0.67
1:YA:1639:U:H2'	1:YA:1640:C:H5''	1.76	0.67
1:RA:956:G:OP2	12:RQ:14:ARG:NH2	2.27	0.67
26:R4:50:VAL:HG11	44:QM:65:LYS:HA	1.76	0.66
37:QF:15:ASP:OD1	37:QF:18:GLN:N	2.25	0.66
27:R5:40:LYS:HD3	27:R5:46:CYS:HA	1.77	0.66
1:RA:2206:G:H3'	1:RA:2207:G:H8	1.60	0.66
32:XA:559:A:H4'	32:XA:560:U:H3'	1.78	0.66
1:YA:517:C:OP1	27:Y5:16:ARG:NH2	2.28	0.66
1:YA:987:G:O2'	1:YA:1000:A:N3	2.29	0.66
32:XA:64:G:H4'	32:XA:65:U:H3'	1.77	0.66
34:XC:152:ILE:HD11	34:XC:199:LYS:HD2	1.78	0.66
28:Y6:35:GLU:OE2	28:Y6:50:ARG:NH1	2.28	0.66
3:RD:71:ASP:HB3	3:RD:103:ARG:HH22	1.61	0.66
21:RZ:144:LEU:HD21	21:RZ:150:LEU:HD13	1.76	0.66
23:R1:3:LYS:HG3	23:R1:4:VAL:H	1.60	0.66
1:RA:1063:G:N2	1:RA:1075:C:N3	2.43	0.66
1:RA:2576:G:O2'	1:RA:2579:C:OP2	2.11	0.66
6:RG:18:GLU:OE1	6:RG:21:ARG:NH1	2.28	0.66
1:YA:714:U:N3	1:YA:717:G:OP2	2.27	0.66
1:YA:2753:A:N3	31:Y9:15:LYS:NZ	2.37	0.66
34:QC:114:PRO:O	34:QC:118:GLN:HG3	1.96	0.66
1:RA:2355:C:H1'	22:R0:39:ARG:HH21	1.61	0.66
27:Y5:16:ARG:NH1	27:Y5:17:ASP:OD1	2.29	0.66
6:YG:21:ARG:HD3	6:YG:22:ARG:N	2.11	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:2469:A:O2'	12:RQ:56:ARG:NH1	2.29	0.66
5:RF:165:ARG:HA	5:RF:168:ARG:HD2	1.78	0.66
43:QL:70:ILE:HG12	43:QL:100:ILE:HD12	1.77	0.66
32:XA:976:G:H5'	32:XA:1358:U:O2'	1.96	0.66
35:XD:23:GLY:N	35:XD:26:CYS:SG	2.68	0.66
3:YD:147:LEU:HD11	3:YD:183:ARG:HE	1.60	0.66
32:XA:954:G:H21	32:XA:1227:A:H62	1.44	0.65
32:XA:9:G:O5'	36:XE:126:ARG:NH1	2.29	0.65
1:YA:2469:A:HO2'	12:YQ:56:ARG:HH11	1.44	0.65
29:Y7:9:ARG:HH21	29:Y7:47:ARG:HD2	1.61	0.65
1:YA:637:A:H5''	11:YP:117:GLU:HG2	1.79	0.65
38:QG:27:ILE:HD12	38:QG:40:ALA:HA	1.77	0.65
1:RA:2134:A:N6	1:RA:2156:G:O2'	2.29	0.65
32:XA:1128:C:H1'	32:XA:1147:C:H42	1.60	0.65
32:QA:532:A:H61	34:QC:193:TYR:HA	1.61	0.65
32:XA:1518:MA6:H93	32:XA:1519:MA6:C10	2.27	0.65
27:Y5:40:LYS:NZ	27:Y5:44:THR:O	2.28	0.65
16:YU:89:GLU:OE1	17:YV:50:PRO:HB3	1.97	0.65
1:RA:2781:A:H5''	1:RA:2782:G:H5'	1.78	0.65
32:XA:1510:U:H2'	32:XA:1511:G:C8	2.31	0.65
39:XH:64:LYS:HG2	39:XH:79:VAL:HG21	1.78	0.65
1:RA:1667:G:O2'	1:RA:1991:U:O4	2.10	0.65
32:XA:1005:A:OP2	32:XA:1024:G:N2	2.30	0.65
55:XY:292:SER:O	55:XY:296:ASN:ND2	2.30	0.65
6:YG:136:ARG:HG2	6:YG:137:GLU:HG3	1.78	0.65
32:XA:552:U:O3'	43:XL:87:GLY:HA2	1.96	0.65
1:YA:334:C:OP1	1:YA:335:C:N4	2.30	0.65
32:XA:1073:U:O2'	33:XB:104:ASN:OD1	2.13	0.65
26:Y4:61:ARG:HH22	50:XS:9:VAL:HG21	1.62	0.65
5:YF:51:THR:HB	5:YF:88:VAL:HG11	1.79	0.65
32:QA:922:G:H4'	36:QE:20:GLN:HA	1.78	0.65
34:QC:58:GLU:HB3	41:QJ:92:THR:HG21	1.77	0.65
41:QJ:52:GLY:O	45:QN:41:ARG:NH2	2.28	0.65
50:QS:41:VAL:HG12	50:QS:44:MET:HG3	1.78	0.65
1:RA:2357:U:OP1	22:R0:20:ARG:NH1	2.29	0.65
26:Y4:59:PHE:HE1	50:XS:64:GLU:HB2	1.58	0.65
55:QY:332:VAL:HG13	55:QY:337:LEU:HD22	1.79	0.64
11:RP:63:PRO:HD3	30:R8:27:THR:HG22	1.78	0.64
32:XA:955:U:OP1	55:XY:137:ARG:NH2	2.30	0.64
32:QA:1030(A):C:N4	32:QA:1032:G:O6	2.30	0.64
1:RA:1069:A:H5'	1:RA:1096:A:H5'	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:YD:242:ARG:HD3	3:YD:242:ARG:H	1.62	0.64
32:QA:142:G:O2'	32:QA:196:A:N1	2.29	0.64
34:QC:40:ARG:O	34:QC:44:GLU:HB2	1.96	0.64
1:RA:26:G:H1'	1:RA:515:A:H61	1.61	0.64
1:RA:309:G:N3	1:RA:329:G:O2'	2.29	0.64
32:XA:406:G:O2'	35:XD:3:ARG:NH2	2.31	0.64
1:YA:307:G:N1	1:YA:310:A:OP2	2.31	0.64
41:QJ:61:GLU:OE2	45:QN:49:HIS:NE2	2.25	0.64
4:YE:11:MET:HG2	4:YE:24:THR:HG22	1.78	0.64
1:RA:1045:A:O2'	1:RA:1046:A:OP2	2.15	0.64
40:X1:32:ASP:HB3	40:X1:35:GLU:HB3	1.79	0.64
32:XA:1070:U:OP1	36:XE:20:GLN:NE2	2.26	0.64
9:YN:15:LEU:HB2	9:YN:135:PRO:HB2	1.79	0.64
1:YA:143(A):G:H4'	19:YX:35:THR:HG21	1.80	0.64
32:QA:560:U:O2'	32:QA:561:U:OP2	2.14	0.64
1:RA:582:G:H2'	1:RA:583:G:C8	2.33	0.64
32:XA:974:A:OP2	45:XN:29:ARG:NH2	2.31	0.64
1:YA:1786:A:H1'	1:YA:1938:A:N6	2.12	0.64
55:QY:245:ARG:HG3	55:QY:256:GLU:CD	2.17	0.64
44:XM:96:LEU:O	44:XM:110:ARG:NH1	2.31	0.64
32:QA:707:C:OP1	42:QK:85:ARG:NH1	2.30	0.63
15:RT:56:GLY:O	15:RT:59:THR:HG23	1.98	0.63
35:XD:18:LYS:NZ	35:XD:31:CYS:SG	2.71	0.63
44:XM:17:VAL:O	44:XM:20:THR:OG1	2.11	0.63
51:XT:56:MET:CE	51:XT:85:MET:HG2	2.27	0.63
1:YA:2206:G:H3'	1:YA:2207:G:C8	2.33	0.63
1:YA:997:G:OP1	16:YU:92:ARG:HG2	1.98	0.63
32:QA:159:G:N2	32:QA:162:A:OP2	2.19	0.63
32:QA:316:G:OP2	32:QA:351:G:O2'	2.16	0.63
1:RA:102:G:OP1	24:R2:7:ARG:NH2	2.31	0.63
1:RA:1786:A:H1'	1:RA:1938:A:N6	2.13	0.63
39:XH:10:LEU:HD22	39:XH:83:ILE:HD11	1.79	0.63
1:YA:2478:A:OP2	31:Y9:2:LYS:NZ	2.27	0.63
1:YA:2572:A:C8	4:YE:144:ARG:HD3	2.32	0.63
24:R2:16:LEU:O	24:R2:67:LYS:NZ	2.31	0.63
1:RA:321:G:OP1	5:RF:135:LYS:NZ	2.27	0.63
35:XD:175:SER:HB3	35:XD:186:LEU:HD11	1.80	0.63
1:YA:1721:G:H8	1:YA:1741:A:H62	1.44	0.63
1:YA:652(C):A:H61	1:YA:655:A:H1'	1.64	0.63
1:YA:1500:G:O2'	3:YD:100:GLY:O	2.14	0.63
35:QD:108:LEU:HD21	35:QD:183:GLY:HA3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:QJ:49:VAL:HG23	45:QN:41:ARG:HB2	1.79	0.63
32:XA:687:A:O2'	32:XA:701:C:N4	2.30	0.63
36:QE:8:GLU:HG2	36:QE:34:VAL:HG22	1.80	0.63
31:R9:16:VAL:HG22	31:R9:25:VAL:HG22	1.79	0.63
1:RA:2223:G:OP1	3:RD:172:TYR:OH	2.16	0.63
18:RW:14:PRO:HG2	18:RW:78:GLU:HG3	1.81	0.63
32:XA:316:G:OP2	32:XA:351:G:O2'	2.15	0.63
6:YG:16:ARG:HE	6:YG:31:VAL:HG21	1.64	0.63
11:YP:138:LEU:HD23	11:YP:145:PRO:HB3	1.80	0.63
32:QA:673:G:H2'	32:QA:674:G:C8	2.34	0.63
32:XA:501:C:OP1	43:XL:117:ARG:NH2	2.32	0.63
1:YA:851:U:O2'	25:Y3:42:ALA:O	2.14	0.63
1:YA:956:G:OP2	12:YQ:14:ARG:NH2	2.32	0.63
32:QA:791:G:N2	32:QA:1497:G:O3'	2.31	0.63
15:RT:24:PRO:HA	15:RT:49:VAL:HG23	1.80	0.63
1:RA:1064:C:H3'	1:RA:1065:U:H5'	1.80	0.63
1:RA:336:C:O2'	20:RY:35:TYR:OH	2.16	0.63
55:XY:108:GLU:HA	55:XY:170:GLY:HA2	1.81	0.63
55:XY:136:SER:HA	55:XY:146:VAL:HG21	1.81	0.63
1:YA:2156:G:N7	1:YA:2157:G:N2	2.47	0.63
1:RA:1087:G:N2	1:RA:1102:C:N3	2.37	0.62
11:YP:63:PRO:HG2	30:Y8:25:MET:HB2	1.81	0.62
1:YA:1491:G:O2'	3:YD:101:GLU:HB2	1.99	0.62
32:QA:1310:G:OP2	44:QM:88:ARG:NH1	2.31	0.62
33:QB:118:LEU:HB3	33:QB:142:LEU:HD13	1.81	0.62
36:QE:69:VAL:HG11	36:QE:113:ALA:HB1	1.80	0.62
55:QY:296:ASN:O	55:QY:306:ARG:NH1	2.32	0.62
1:YA:1823:G:OP1	3:YD:54:ARG:NH1	2.32	0.62
1:YA:637:A:H8	11:YP:117:GLU:HG3	1.64	0.62
1:RA:1064:C:H3'	1:RA:1065:U:C5'	2.30	0.62
1:RA:2285:C:OP2	28:R6:26:ASN:ND2	2.31	0.62
1:YA:1063:G:N2	1:YA:1075:C:N3	2.48	0.62
4:YE:12:THR:HG22	4:YE:13:ARG:H	1.63	0.62
32:QA:78:G:H1	32:QA:91:C:N4	1.96	0.62
1:RA:1019:U:OP1	1:RA:1035:U:O2'	2.17	0.62
1:YA:2619:C:OP1	4:YE:152:LYS:NZ	2.28	0.62
7:YH:7:LEU:O	7:YH:69:ARG:NH1	2.33	0.62
32:QA:1239:A:O2'	38:QG:114:ARG:O	2.13	0.62
55:QY:138:TYR:CE1	55:QY:338:ASP:HB3	2.35	0.62
1:RA:2424:C:O2	1:RA:2429:G:O2'	2.13	0.62
1:YA:1113:U:O2'	1:YA:1114:G:H8	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:974:A:OP2	45:QN:29:ARG:NH2	2.33	0.62
43:QL:117:ARG:HG2	43:QL:122:THR:HB	1.81	0.62
32:XA:1492:A:H5'	43:XL:47:LYS:HE2	1.81	0.62
32:XA:552:U:H4'	43:XL:86:ARG:HD3	1.81	0.62
33:QB:16:HIS:HB2	33:QB:204:ASN:HB3	1.81	0.62
1:RA:2390:U:P	30:R8:35:GLN:HE22	2.22	0.62
1:RA:2572:A:N7	4:RE:144:ARG:HD2	2.15	0.62
12:RQ:32:TYR:OH	12:RQ:111:GLU:OE1	2.17	0.62
40:XI:50:LEU:HD23	40:XI:85:LEU:HD11	1.80	0.62
4:YE:119:ARG:HG3	4:YE:160:TYR:HB2	1.82	0.62
32:QA:1097:C:O2'	32:QA:1169:A:N3	2.27	0.61
46:QO:16:ALA:HB1	46:QO:21:ASP:HB3	1.81	0.61
1:RA:1971:A:OP2	3:RD:242:ARG:NH2	2.32	0.61
1:RA:307:G:N1	1:RA:310:A:OP2	2.32	0.61
10:RO:64:ARG:NE	10:RO:101:PRO:O	2.31	0.61
18:RW:4:LYS:HB2	18:RW:106:ILE:HG12	1.82	0.61
35:QD:55:ALA:O	35:QD:59:ARG:HG2	2.00	0.61
1:RA:1568:G:H5''	3:RD:61:LEU:HD13	1.81	0.61
32:XA:1103:C:OP1	33:XB:96:ARG:NH2	2.33	0.61
32:XA:662:G:H2'	32:XA:663:A:C8	2.36	0.61
33:XB:101:MET:HA	33:XB:108:ILE:HG13	1.81	0.61
33:XB:118:LEU:HB3	33:XB:142:LEU:HD12	1.81	0.61
42:QK:99:GLN:HG2	42:QK:105:VAL:HG21	1.83	0.61
2:RB:66:A:H61	2:RB:109:C:H5''	1.65	0.61
35:XD:12:CYS:SG	35:XD:19:LEU:HB2	2.40	0.61
32:QA:1020:U:H2'	32:QA:1021:G:C8	2.36	0.61
26:R4:59:PHE:HZ	50:QS:45:VAL:HG21	1.64	0.61
1:RA:1639:U:H2'	1:RA:1640:C:H5''	1.82	0.61
53:XV:4:G:HO2'	53:XV:5:G:H8	1.48	0.61
11:YP:59:LEU:HD21	30:Y8:10:ALA:HA	1.82	0.61
1:YA:1049:C:H42	1:YA:2751:G:N2	1.98	0.61
1:RA:764:A:H5'	3:RD:210:GLY:HA2	1.81	0.61
1:YA:1038:C:H42	1:YA:1117:G:H1	1.47	0.61
1:YA:1086:A:OP1	1:YA:1104:C:O2'	2.18	0.61
1:YA:1641:A:H2'	1:YA:1642:G:O4'	2.00	0.61
6:YG:80:PHE:O	6:YG:82:LEU:N	2.33	0.61
46:QO:25:THR:HG21	46:QO:70:LEU:HB2	1.82	0.61
32:XA:1221:G:OP1	32:XA:1320:C:N4	2.31	0.61
33:XB:78:GLN:O	33:XB:94:ASN:ND2	2.30	0.61
40:XI:42:ARG:NH1	40:XI:71:SER:O	2.33	0.61
55:XY:340:LEU:O	55:XY:343:PRO:HD2	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:RP:99:LEU:HD23	11:RP:102:ARG:HH21	1.65	0.61
32:XA:1189:C:OP1	41:XJ:51:ARG:NH2	2.32	0.61
1:YA:1593:G:H2'	1:YA:1594:G:H8	1.66	0.61
1:YA:1889:A:N1	1:YA:2234:G:H1'	2.16	0.61
32:QA:126:G:OP1	32:QA:605:U:O2'	2.14	0.61
6:RG:101:ILE:HD13	26:R4:25:TYR:HB2	1.83	0.61
5:YF:164:ARG:HD2	5:YF:175:THR:HG23	1.83	0.61
44:QM:81:LEU:HD13	44:QM:88:ARG:HD2	1.82	0.61
24:R2:31:GLU:HB3	24:R2:53:LEU:HD11	1.82	0.61
33:XB:98:LEU:O	33:XB:101:MET:HG3	2.01	0.61
35:XD:65:ARG:NH2	35:XD:72:GLU:HB2	2.16	0.61
55:XY:123:GLU:HG2	55:XY:188:PRO:HB3	1.83	0.61
1:YA:1266:G:O5'	18:YW:15:ARG:NH2	2.34	0.61
1:YA:265:A:N1	1:YA:427:U:O2'	2.28	0.61
50:QS:12:ASP:HB3	50:QS:14:HIS:CE1	2.36	0.61
1:RA:2126:A:H4'	1:RA:2127:G:O5'	2.01	0.61
1:RA:212:G:H2'	1:RA:213:A:O4'	2.00	0.61
1:RA:2206:G:H5''	1:RA:2207:G:N7	2.16	0.61
44:XM:3:ARG:HG3	44:XM:8:GLU:HG3	1.83	0.61
49:XR:32:ARG:HA	49:XR:69:THR:HG21	1.83	0.61
3:YD:108:PRO:HB3	3:YD:143:HIS:CE1	2.35	0.61
18:YW:14:PRO:HG2	18:YW:78:GLU:CG	2.31	0.61
13:RR:67:LEU:HD13	13:RR:76:VAL:HG21	1.83	0.60
32:XA:992:U:H4'	32:XA:993:G:O5'	2.00	0.60
51:XT:50:GLU:HG3	51:XT:100:ILE:HD11	1.83	0.60
1:YA:2130:U:H2'	1:YA:2158:A:H61	1.66	0.60
1:YA:2327:A:H2'	1:YA:2328:A:C8	2.35	0.60
12:YQ:34:LEU:HB2	12:YQ:118:LEU:HD22	1.83	0.60
1:RA:577:G:O2'	1:RA:1254:A:OP1	2.19	0.60
38:XG:15:ASP:OD1	38:XG:20:ASP:N	2.29	0.60
30:Y8:6:THR:HG22	30:Y8:63:PRO:HD2	1.84	0.60
1:YA:1651:G:H5'	13:YR:39:PRO:HG2	1.82	0.60
55:QY:247:THR:HA	55:QY:254:VAL:HG12	1.83	0.60
7:YH:27:LYS:HD3	7:YH:32:GLU:HB2	1.82	0.60
1:RA:1053:C:H2'	1:RA:1054:A:H8	1.66	0.60
8:RI:54:GLN:HG3	8:RI:57:ARG:HH11	1.67	0.60
9:RN:67:LEU:HD12	9:RN:87:LEU:HD13	1.83	0.60
34:XC:57:ILE:HG12	34:XC:66:VAL:HG22	1.84	0.60
4:RE:78:LEU:O	4:RE:79:ARG:NH1	2.30	0.60
1:YA:1507:A:O2'	1:YA:1508:A:O5'	2.18	0.60
1:YA:1657:C:H2'	1:YA:1658:C:C6	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:YF:184:TYR:CE2	5:YF:188:ARG:HD2	2.37	0.60
11:YP:50:ARG:HD3	30:Y8:7:HIS:CD2	2.37	0.60
16:YU:89:GLU:O	17:YV:11:GLN:NE2	2.34	0.60
35:QD:162:LEU:HD13	35:QD:181:MET:HG2	1.82	0.60
23:R1:50:ARG:HG2	23:R1:59:THR:HG22	1.83	0.60
32:XA:359:U:H2'	32:XA:360:A:C8	2.37	0.60
36:XE:102:ALA:HB1	36:XE:106:PRO:HG2	1.82	0.60
1:YA:83:G:N2	1:YA:103:A:OP2	2.35	0.60
13:YR:36:THR:HG22	13:YR:37:THR:H	1.65	0.60
37:QF:23:LYS:HG2	37:QF:61:LEU:HD21	1.84	0.60
23:Y1:53:VAL:HG22	23:Y1:74:VAL:HG13	1.83	0.60
1:YA:2218:U:O2	23:Y1:52:ARG:NH2	2.35	0.60
5:RF:157:VAL:HB	5:RF:194:MET:HG2	1.82	0.60
55:XY:245:ARG:HG3	55:XY:256:GLU:CG	2.32	0.60
25:Y3:10:LYS:NZ	25:Y3:15:TYR:OH	2.30	0.60
32:QA:269:C:H2'	32:QA:270:A:C8	2.37	0.60
32:XA:1316:G:N1	32:XA:1319:A:OP2	2.33	0.60
33:XB:229:VAL:HG12	33:XB:230:VAL:H	1.67	0.60
34:XC:8:ILE:HG23	34:XC:16:ARG:HD3	1.82	0.60
20:RY:92:ASN:N	20:RY:93:GLY:HA2	2.16	0.59
32:XA:537:G:H5''	43:XL:113:ARG:NH1	2.17	0.59
33:XB:18:GLY:HA2	33:XB:42:ILE:HD12	1.84	0.59
7:YH:87:LEU:HD23	7:YH:164:TYR:HA	1.83	0.59
44:QM:15:VAL:HG11	44:QM:48:LEU:HD21	1.84	0.59
28:R6:9:LEU:HD13	28:R6:51:GLU:HG3	1.83	0.59
7:RH:3:ARG:HD3	7:RH:54:ARG:HH12	1.66	0.59
21:RZ:19:ARG:NH1	21:RZ:84:GLU:O	2.35	0.59
32:XA:17:U:H2'	32:XA:18:C:C6	2.36	0.59
33:XB:73:THR:OG1	33:XB:170:GLU:OE1	2.19	0.59
1:YA:1935:G:H3'	1:YA:1962:5MC:HN41	1.66	0.59
39:QH:86:ILE:HG13	39:QH:133:LEU:HD22	1.84	0.59
33:XB:185:ILE:HG13	33:XB:199:TYR:HB2	1.85	0.59
32:XA:790:A:OP1	53:XV:38:A:O2'	2.18	0.59
1:YA:1073:A:H2'	1:YA:1074:G:C8	2.36	0.59
1:YA:2552:2MU:H6	1:YA:2552:2MU:O5'	2.02	0.59
2:YB:14:U:OP2	2:YB:70:C:O2'	2.19	0.59
35:XD:122:ARG:NH1	35:XD:134:ASP:O	2.36	0.59
1:YA:1803:A:O2'	3:YD:259:THR:HG21	2.02	0.59
32:QA:1030(D):G:N7	32:QA:1031:G:N2	2.50	0.59
53:QV:15:G:N2	53:QV:21:A:N3	2.50	0.59
33:XB:47:THR:HA	33:XB:202:PRO:HG2	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:QC:8:ILE:HG23	34:QC:16:ARG:HD3	1.83	0.59
55:XY:151:ALA:HB2	55:XY:162:ILE:HD12	1.85	0.59
1:YA:2122:U:H3	1:YA:2176:A:H61	1.51	0.59
1:YA:2787:C:H1'	4:YE:62:PRO:HG3	1.85	0.59
21:YZ:198:LYS:NZ	53:XV:53:G:O4'	2.34	0.59
1:RA:2755:C:O2	31:R9:20:HIS:NE2	2.35	0.59
5:RF:167:ALA:HB1	5:RF:173:VAL:HG11	1.84	0.59
41:XJ:5:ARG:N	41:XJ:99:LYS:O	2.36	0.59
14:YS:27:SER:HA	14:YS:88:ASP:HB3	1.83	0.59
1:RA:1075:C:H2'	1:RA:1076:C:H5'	1.85	0.59
36:XE:20:GLN:NE2	36:XE:25:ARG:HD2	2.17	0.59
23:Y1:76:ARG:HH22	23:Y1:97:LEU:HB3	1.66	0.59
1:YA:1688:U:O2	1:YA:1700:A:H5'	2.03	0.59
32:QA:45:U:H2'	32:QA:46:G:C8	2.38	0.59
32:QA:524:G:H2'	32:QA:525:C:C6	2.37	0.59
43:QL:33:ARG:HH11	43:QL:62:SER:HB3	1.66	0.59
46:QO:39:LEU:HD13	46:QO:56:LEU:HB2	1.83	0.59
8:RI:54:GLN:HG3	8:RI:57:ARG:NH1	2.18	0.59
3:YD:71:ASP:HB3	3:YD:103:ARG:HH22	1.67	0.59
35:QD:12:CYS:SG	35:QD:19:LEU:HB2	2.43	0.59
40:QI:16:ARG:HB2	40:QI:64:THR:HG22	1.83	0.59
1:RA:2537:U:H2'	1:RA:2538:C:C6	2.38	0.59
33:XB:166:ASP:HB3	33:XB:169:LYS:HB3	1.83	0.59
1:YA:2279:G:N7	22:Y0:14:ARG:NH1	2.51	0.59
26:Y4:16:CYS:SG	26:Y4:17:GLY:N	2.76	0.59
1:YA:1794:U:H2'	1:YA:1795:C:H6	1.68	0.59
29:R7:12:ARG:NH2	29:R7:44:PRO:HB3	2.18	0.58
1:RA:994:C:OP1	16:RU:53:ARG:NH2	2.36	0.58
24:Y2:31:GLU:HB3	24:Y2:53:LEU:HD11	1.85	0.58
9:YN:96:GLU:HB2	9:YN:122:VAL:HG12	1.84	0.58
11:YP:100:LEU:HD12	11:YP:112:LEU:HD11	1.84	0.58
39:QH:64:LYS:HG2	39:QH:79:VAL:HG21	1.84	0.58
32:XA:1182:G:H4'	32:XA:1183:A:H3'	1.85	0.58
32:XA:1314:C:OP2	50:XS:4:SER:OG	2.12	0.58
38:XG:113:GLU:HG2	38:XG:119:ARG:HG2	1.85	0.58
1:YA:616:G:H5'	5:YF:205:ARG:HD3	1.84	0.58
1:YA:796:C:H2'	1:YA:797:C:C6	2.39	0.58
7:YH:55:PRO:HG2	7:YH:61:HIS:CE1	2.37	0.58
9:YN:67:LEU:O	9:YN:88:GLU:HG3	2.03	0.58
32:QA:692:U:O2'	32:QA:694:A:N7	2.32	0.58
35:QD:85:LYS:HD3	35:QD:86:LYS:H	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:2619:C:OP1	4:RE:152:LYS:NZ	2.33	0.58
1:RA:192:C:O2'	1:RA:802:A:N3	2.30	0.58
1:RA:2312:U:H5'	6:RG:88:ILE:HD11	1.85	0.58
18:RW:14:PRO:HG2	18:RW:78:GLU:CG	2.32	0.58
32:XA:1244:C:H2'	32:XA:1245:A:C8	2.39	0.58
1:YA:286:C:H2'	1:YA:287:C:C6	2.38	0.58
1:YA:601:C:O2'	1:YA:605:C:OP1	2.20	0.58
5:YF:167:ALA:HB1	5:YF:173:VAL:HG11	1.85	0.58
20:RY:102:CYS:SG	20:RY:104:GLY:N	2.67	0.58
32:XA:539:A:H2'	32:XA:540:G:C8	2.38	0.58
1:YA:1073:A:H2'	1:YA:1074:G:H8	1.68	0.58
1:RA:1073:A:H2'	1:RA:1074:G:C8	2.38	0.58
1:RA:1798:U:H5'	3:RD:259:THR:HG22	1.86	0.58
32:XA:890:G:O2'	32:XA:906:G:O6	2.17	0.58
32:XA:1047:G:H5''	45:XN:4:LYS:HD3	1.83	0.58
55:XY:330:ASP:O	55:XY:334:GLU:HB3	2.02	0.58
18:YW:14:PRO:HG2	18:YW:78:GLU:HG2	1.85	0.58
35:QD:15:GLU:OE2	35:QD:59:ARG:NH2	2.20	0.58
11:RP:63:PRO:HG2	30:R8:25:MET:HB2	1.84	0.58
10:RO:64:ARG:NH2	10:RO:99:PHE:O	2.37	0.58
15:RT:60:THR:HG22	15:RT:77:PRO:HA	1.86	0.58
32:XA:1116:C:H2'	32:XA:1117:G:H5''	1.86	0.58
32:XA:1318:A:H5''	50:XS:3:ARG:HH22	1.66	0.58
13:YR:29:LEU:HB3	13:YR:75:LEU:HD21	1.86	0.58
32:QA:1309:G:N7	44:QM:99:ARG:NH2	2.50	0.58
32:QA:1391:U:H2'	32:QA:1392:G:C8	2.39	0.58
21:RZ:203:GLU:CD	53:QV:54:U:H5''	2.24	0.58
26:R4:59:PHE:CZ	50:QS:45:VAL:HG21	2.38	0.58
1:RA:1165:U:H2'	1:RA:1166:C:C6	2.38	0.58
5:RF:24:LEU:HD23	5:RF:115:ALA:HA	1.85	0.58
1:RA:1266:G:O4'	18:RW:15:ARG:NH2	2.34	0.58
33:XB:114:ARG:NH1	33:XB:141:GLU:OE1	2.37	0.58
32:QA:1402:4OC:HM22	32:QA:1403:C:H5'	1.84	0.58
55:QY:346:GLN:O	55:QY:349:GLN:HG2	2.03	0.58
42:XK:117:ASN:N	42:XK:117:ASN:OD1	2.36	0.58
1:YA:2115:G:N1	1:YA:2119:A:OP2	2.37	0.58
1:YA:572:A:OP2	17:YV:78:LYS:NZ	2.34	0.58
1:YA:78:A:H2'	1:YA:79:G:H8	1.68	0.58
2:YB:14:U:O3'	2:YB:108:U:O2'	2.22	0.58
6:YG:15:VAL:HG21	6:YG:176:LEU:HD23	1.86	0.58
1:RA:674:G:H1'	5:RF:74:ARG:HD3	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:RX:60:ARG:NH2	29:R7:47:ARG:HH22	2.01	0.58
42:XK:62:GLN:HB2	42:XK:93:GLN:HG3	1.86	0.58
5:YF:185:ASP:HA	5:YF:188:ARG:HD3	1.86	0.58
6:YG:77:ILE:HG21	6:YG:80:PHE:CD2	2.39	0.58
35:QD:167:GLY:H	35:QD:168:ARG:NH2	2.02	0.58
32:XA:1031:G:H2'	32:XA:1032:G:C8	2.39	0.58
44:QM:3:ARG:HG3	44:QM:4:ILE:H	1.69	0.57
1:RA:198:C:H5'	1:RA:2244:U:OP1	2.04	0.57
15:RT:39:ARG:HH12	15:RT:41:ARG:HD3	1.67	0.57
32:XA:1343:G:H4'	40:XI:122:ALA:HB3	1.86	0.57
1:YA:2115:G:H21	1:YA:2171:A:H61	1.53	0.57
20:YY:15:VAL:O	20:YY:22:GLY:N	2.26	0.57
32:QA:103:C:O2'	32:QA:172:A:N1	2.31	0.57
37:QF:36:ARG:NH2	37:QF:66:GLU:OE1	2.36	0.57
32:QA:1298:C:C4	38:QG:114:ARG:HD2	2.39	0.57
55:QY:204:ALA:HB2	55:QY:298:LEU:HD21	1.86	0.57
1:RA:1289:C:H2'	1:RA:1290:C:C6	2.39	0.57
41:XJ:35:SER:HB3	41:XJ:73:ASP:H	1.68	0.57
55:XY:226:THR:HG22	55:XY:244:ILE:HD12	1.86	0.57
1:YA:1470:G:N2	1:YA:1520:G:OP2	2.32	0.57
1:RA:1936:A:OP2	1:RA:1962:5MC:N4	2.28	0.57
32:XA:452:A:N3	47:XP:72:ARG:NH1	2.52	0.57
55:XY:214:LEU:HB2	55:XY:215:PRO:CA	2.35	0.57
1:YA:36:G:N3	1:YA:450:G:O2'	2.35	0.57
1:YA:300:A:OP1	20:YY:86:ARG:NH2	2.36	0.57
49:QR:32:ARG:HA	49:QR:69:THR:HG21	1.86	0.57
1:RA:1507:A:O2'	1:RA:1508:A:O5'	2.19	0.57
1:RA:1800:C:OP1	3:RD:260:ARG:NH2	2.36	0.57
39:XH:14:ARG:O	39:XH:18:ARG:HG2	2.05	0.57
41:XJ:11:PHE:HE1	41:XJ:67:THR:HG22	1.69	0.57
1:YA:2711:A:H5''	1:YA:2712(A):U:H5''	1.86	0.57
49:QR:29:PHE:HE1	49:QR:31:LEU:HD13	1.70	0.57
1:RA:1289:C:H2'	1:RA:1290:C:H6	1.68	0.57
33:XB:77:ALA:HB2	33:XB:211:ILE:HD13	1.86	0.57
32:QA:1435:G:H2'	32:QA:1436:U:C6	2.40	0.57
53:XV:51:C:H2'	53:XV:52:G:O4'	2.04	0.57
1:RA:1062:G:H5'	1:RA:1070:A:H5''	1.85	0.57
1:YA:784:A:C6	3:YD:229:VAL:HG11	2.40	0.57
6:YG:11:TYR:HA	6:YG:15:VAL:HB	1.87	0.57
32:QA:1519:MA6:O5'	32:QA:1519:MA6:H8	2.04	0.57
1:RA:482:A:O2'	1:RA:497:A:N1	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:RD:10:THR:OG1	3:RD:13:ARG:HG2	2.05	0.57
1:RA:1252:G:N1	16:RU:37:GLU:OE1	2.37	0.57
32:XA:501:C:H2'	32:XA:502:G:C8	2.39	0.57
44:QM:32:GLU:HG2	44:QM:64:TRP:CZ2	2.40	0.57
44:QM:32:GLU:HG2	44:QM:64:TRP:HZ2	1.70	0.57
32:XA:201:C:H42	32:XA:216:G:H1	1.51	0.57
32:QA:642:A:N3	39:QH:113:SER:OG	2.33	0.57
39:QH:6:ILE:HB	39:QH:85:ARG:NH1	2.20	0.57
7:RH:11:VAL:HG21	7:RH:50:VAL:HG23	1.86	0.57
1:RA:2820:A:OP2	13:RR:2:ARG:NH2	2.38	0.57
32:XA:380:G:N2	32:XA:383:A:OP2	2.37	0.57
55:XY:145:ARG:HB2	55:XY:167:SER:OG	2.05	0.57
1:YA:2233:U:H2'	1:YA:2234:G:C8	2.39	0.57
1:YA:2312:U:H5'	6:YG:88:ILE:HD11	1.86	0.57
32:QA:403:C:O2'	35:QD:122:ARG:NH1	2.38	0.56
32:QA:814:A:H2'	32:QA:816:A:H5''	1.86	0.56
1:RA:958:U:OP2	12:RQ:14:ARG:NH1	2.37	0.56
26:Y4:18:CYS:SG	26:Y4:39:CYS:HB3	2.45	0.56
1:YA:1064:C:H5''	1:YA:1065:U:H3'	1.87	0.56
3:YD:242:ARG:HD3	3:YD:242:ARG:N	2.20	0.56
5:YF:53:THR:HG22	5:YF:56:GLU:HG3	1.87	0.56
7:YH:86:GLU:OE2	7:YH:132:ARG:NH2	2.38	0.56
36:QE:33:VAL:HG21	36:QE:109:ILE:HA	1.86	0.56
1:RA:1796:U:H2'	1:RA:1797:C:C6	2.40	0.56
34:XC:109:PRO:HB3	34:XC:115:LEU:HD23	1.87	0.56
55:XY:115:VAL:HG22	55:XY:203:VAL:HG22	1.87	0.56
12:YQ:80:GLU:OE2	55:XY:264:HIS:CD2	2.58	0.56
1:YA:2150:U:H2'	1:YA:2151:G:C8	2.40	0.56
4:YE:34:VAL:HG12	4:YE:72:VAL:HG21	1.87	0.56
32:QA:1013:G:N2	32:QA:1016:A:OP2	2.37	0.56
35:QD:168:ARG:HH21	3:YD:135:PHE:HE1	1.52	0.56
1:RA:2115:G:H21	1:RA:2171:A:H61	1.54	0.56
1:RA:729:G:C8	3:RD:208:LYS:HD2	2.40	0.56
13:RR:28:LEU:HD12	13:RR:44:LEU:HD13	1.86	0.56
1:YA:1359:A:N6	1:YA:1372:U:H3	2.01	0.56
1:RA:2452:C:H4'	55:QY:239:THR:HG21	1.86	0.56
8:RI:92:VAL:HG13	8:RI:120:ILE:HB	1.87	0.56
44:XM:19:LEU:HD21	44:XM:56:LEU:HD21	1.87	0.56
1:YA:1794:U:H2'	1:YA:1795:C:C6	2.40	0.56
1:YA:1856:G:N2	1:YA:1886:C:O2	2.34	0.56
1:YA:566:U:H5''	11:YP:29:LYS:HE3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:YD:10:THR:OG1	3:YD:13:ARG:HG2	2.05	0.56
39:QH:10:LEU:HD22	39:QH:83:ILE:HD11	1.88	0.56
47:QP:75:ARG:HG3	47:QP:80:PHE:HD2	1.70	0.56
6:RG:108:ASN:O	26:R4:37:SER:N	2.38	0.56
1:RA:1569:A:H5'	3:RD:61:LEU:HD11	1.86	0.56
6:RG:59:GLU:OE2	6:RG:153:ARG:NH2	2.38	0.56
1:YA:1124:C:O2'	31:Y9:36:GLN:HG2	2.05	0.56
1:YA:749:C:O2	1:YA:1618:A:H2'	2.06	0.56
32:QA:194:C:H2'	32:QA:195:A:H5''	1.87	0.56
22:R0:11:ARG:O	22:R0:14:ARG:NH2	2.38	0.56
1:YA:2206:G:H5''	1:YA:2207:G:N7	2.21	0.56
1:YA:2243:U:H2'	1:YA:2244:U:C6	2.41	0.56
1:RA:530:G:N1	1:RA:2023:G:OP1	2.30	0.56
34:XC:179:ARG:NH1	34:XC:206:GLU:OE1	2.38	0.56
40:XI:50:LEU:HB2	40:XI:56:LEU:HD23	1.87	0.56
1:YA:740:U:H2'	1:YA:741:G:C8	2.41	0.56
32:QA:109:A:C6	32:QA:326:G:C6	2.94	0.56
33:QB:229:VAL:HG12	33:QB:230:VAL:H	1.70	0.56
48:QQ:66:SER:O	48:QQ:70:ARG:NH1	2.39	0.56
1:RA:2115:G:N1	1:RA:2119:A:OP2	2.39	0.56
1:RA:83:G:OP1	20:RY:95:LYS:NZ	2.30	0.56
55:XY:224:ILE:HD13	55:XY:267:LYS:HE3	1.86	0.56
1:YA:644:A:H4'	1:YA:645:C:H5	1.70	0.56
7:YH:89:ILE:O	7:YH:129:THR:HG23	2.06	0.56
14:YS:14:VAL:O	14:YS:18:ILE:HG12	2.06	0.56
15:YT:60:THR:HG22	15:YT:77:PRO:HA	1.88	0.56
1:RA:1065:U:H4'	1:RA:1066:U:H5'	1.87	0.56
1:RA:2698:U:H2'	1:RA:2699:C:C6	2.41	0.56
1:RA:539:G:H2'	1:RA:540:C:C6	2.40	0.56
1:RA:272(M):G:H21	8:RI:50:ARG:HD3	1.70	0.56
35:XD:153:ARG:HH12	35:XD:181:MET:HB2	1.71	0.56
32:XA:35:G:O2'	43:XL:118:SER:O	2.21	0.56
1:YA:184:C:H2'	1:YA:185:U:C6	2.40	0.56
1:YA:2785:C:O2'	4:YE:66:HIS:ND1	2.36	0.56
1:YA:1143:A:OP1	9:YN:25:ARG:NH2	2.39	0.56
1:YA:1649:G:O2'	13:YR:107:ASP:OD2	2.16	0.56
1:RA:2889:C:H3'	1:RA:2891:G:C8	2.41	0.56
7:RH:86:GLU:OE2	7:RH:132:ARG:NH2	2.39	0.56
23:Y1:3:LYS:HB2	23:Y1:61:ARG:NH1	2.21	0.56
1:YA:1050:A:H2'	1:YA:1051:G:H8	1.71	0.56
1:YA:1076:C:H4'	1:YA:1077:A:OP1	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2889:C:H3'	1:YA:2891:G:C8	2.40	0.56
32:QA:1427:U:H2'	32:QA:1428:A:C8	2.41	0.56
37:QF:89:MET:HE1	49:QR:72:ARG:HB3	1.88	0.56
8:RI:38:LEU:HD12	8:RI:38:LEU:H	1.71	0.56
39:XH:6:ILE:HB	39:XH:85:ARG:NH1	2.21	0.56
41:XJ:37:PRO:HA	41:XJ:72:VAL:HG12	1.86	0.56
10:YO:23:ARG:HD3	10:YO:24:VAL:N	2.21	0.56
32:QA:1003:G:H2'	32:QA:1004:A:H4'	1.87	0.55
1:RA:1062:G:N7	1:RA:1070:A:H1'	2.21	0.55
32:XA:1075:C:OP1	33:XB:179:LYS:NZ	2.24	0.55
55:XY:110:ASN:OD1	55:XY:167:SER:HA	2.06	0.55
6:YG:46:ALA:HB2	6:YG:53:LEU:HG	1.87	0.55
34:QC:155:GLY:HA3	34:QC:196:LEU:HD22	1.88	0.55
55:QY:312:PHE:N	55:QY:313:PRO:HD2	2.20	0.55
36:XE:10:MET:HB3	36:XE:13:ILE:HD11	1.88	0.55
55:XY:147:GLU:HB3	55:XY:165:LYS:HB3	1.88	0.55
32:QA:38:G:N2	32:QA:397:A:H5'	2.20	0.55
26:R4:59:PHE:HE1	50:QS:64:GLU:HA	1.71	0.55
1:RA:1057:A:N7	1:RA:1086:A:H2'	2.21	0.55
43:XL:33:ARG:HD3	43:XL:62:SER:HB3	1.88	0.55
1:YA:1308:A:H2'	1:YA:1309:G:O4'	2.06	0.55
1:YA:2355:C:H1'	22:Y0:39:ARG:HH21	1.71	0.55
1:YA:588:U:H2'	1:YA:589:C:C6	2.41	0.55
32:QA:406:G:H5'	35:QD:5:ILE:HD11	1.89	0.55
15:YT:54:ARG:HA	15:YT:59:THR:HG23	1.88	0.55
16:YU:76:TYR:OH	16:YU:92:ARG:NH1	2.39	0.55
34:QC:8:ILE:HD12	34:QC:16:ARG:HD3	1.88	0.55
38:QG:48:LYS:O	38:QG:52:GLU:HG2	2.06	0.55
55:QY:263:GLN:O	55:QY:267:LYS:N	2.40	0.55
55:QY:330:ASP:O	55:QY:334:GLU:HB3	2.05	0.55
1:RA:1053:C:H2'	1:RA:1054:A:C8	2.42	0.55
1:RA:1935:G:H1'	1:RA:1964:G:N2	2.22	0.55
1:RA:574:C:N3	4:RE:145:LYS:NZ	2.55	0.55
5:RF:185:ASP:HA	5:RF:188:ARG:HD3	1.88	0.55
26:Y4:53:GLU:CD	26:Y4:53:GLU:H	2.09	0.55
1:YA:833:U:O2	11:YP:55:ARG:NH2	2.40	0.55
1:RA:2094:G:P	8:RI:22:LYS:HD2	2.47	0.55
10:RO:2:ILE:HB	10:RO:33:ALA:HB3	1.88	0.55
35:QD:3:ARG:HD3	35:QD:118:ARG:NE	2.14	0.55
1:RA:1292:U:H2'	1:RA:1293:C:C6	2.42	0.55
34:XC:6:HIS:CE1	34:XC:8:ILE:HB	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:YG:5:VAL:HG12	26:Y4:25:TYR:CE1	2.42	0.55
32:QA:1503:A:OP1	32:QA:1531:A:O2'	2.25	0.55
41:QJ:38:ILE:HD11	41:QJ:71:LEU:HD23	1.88	0.55
44:QM:40:ASN:HB3	44:QM:43:THR:HG23	1.89	0.55
1:RA:2816:C:O3'	13:RR:99:LYS:NZ	2.39	0.55
43:XL:32:PHE:CD2	43:XL:86:ARG:HB3	2.41	0.55
44:XM:6:GLY:HA3	44:XM:67:GLU:HG3	1.89	0.55
46:XO:4:THR:HG23	46:XO:7:GLU:H	1.72	0.55
10:YO:115:VAL:HG13	10:YO:121:VAL:HG21	1.89	0.55
1:RA:1076:C:H4'	1:RA:1077:A:OP1	2.07	0.55
1:RA:2156:G:N7	1:RA:2157:G:N2	2.54	0.55
15:RT:39:ARG:NH1	15:RT:41:ARG:HD3	2.22	0.55
12:YQ:16:ARG:HG3	12:YQ:17:LEU:H	1.72	0.55
1:RA:2171:A:H4'	1:RA:2172:U:OP1	2.07	0.55
1:RA:2648:C:H2'	1:RA:2649:U:C6	2.42	0.55
1:RA:299:A:N1	1:RA:322:A:O2'	2.31	0.55
33:XB:88:ALA:HB2	33:XB:219:VAL:HG13	1.89	0.55
40:XI:51:ARG:HG2	40:XI:56:LEU:HD21	1.89	0.55
24:Y2:35:LEU:HD12	24:Y2:53:LEU:HD12	1.89	0.55
1:YA:212:G:H2'	1:YA:213:A:O4'	2.07	0.55
1:YA:2646:C:OP2	1:YA:2732:G:O2'	2.18	0.55
1:YA:192:C:O2'	1:YA:802:A:N3	2.31	0.55
32:QA:1441:G:H5''	32:QA:1442(A):G:H5'	1.88	0.54
55:QY:135:TYR:HE1	55:QY:178:GLU:HG3	1.72	0.54
30:R8:52:LYS:O	30:R8:56:GLU:HG3	2.07	0.54
1:RA:2023:G:H5'	1:RA:2617:C:H4'	1.89	0.54
1:RA:2683:C:OP1	15:RT:53:ARG:NH2	2.40	0.54
13:RR:36:THR:HG22	13:RR:37:THR:H	1.72	0.54
14:RS:14:VAL:O	14:RS:18:ILE:HG12	2.07	0.54
32:XA:266:G:H3'	48:XQ:67:LYS:HB2	1.88	0.54
1:YA:1657:C:H2'	1:YA:1658:C:H6	1.71	0.54
1:YA:641:C:O2'	1:YA:2350:C:OP1	2.22	0.54
1:YA:458:G:O2'	1:YA:469:G:O6	2.18	0.54
32:QA:1020:U:H2'	32:QA:1021:G:H8	1.72	0.54
33:QB:21:ARG:H	33:QB:21:ARG:HD3	1.70	0.54
35:QD:98:GLU:OE1	35:QD:103:ASN:ND2	2.38	0.54
39:QH:51:VAL:HG12	39:QH:52:ASP:H	1.72	0.54
1:RA:372:G:H5'	23:R1:66:HIS:NE2	2.22	0.54
1:RA:2206:G:H5''	1:RA:2207:G:C8	2.42	0.54
1:RA:2646:C:OP2	1:RA:2732:G:O2'	2.22	0.54
1:RA:2744:G:N2	7:RH:143:GLN:OE1	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:589:C:H2'	1:RA:590:A:C8	2.42	0.54
1:RA:2839:G:H5'	13:RR:46:GLY:HA2	1.89	0.54
15:RT:24:PRO:HD3	15:RT:52:ILE:HD12	1.89	0.54
55:XY:133:ARG:HG3	55:XY:134:MET:HE2	1.87	0.54
1:YA:829:A:N7	1:YA:2247:A:O2'	2.39	0.54
40:QI:77:ILE:O	40:QI:81:ILE:HG23	2.07	0.54
26:R4:16:CYS:SG	26:R4:17:GLY:N	2.80	0.54
3:RD:183:ARG:HG3	3:RD:183:ARG:HH11	1.72	0.54
5:RF:184:TYR:CE2	5:RF:188:ARG:HD2	2.43	0.54
12:RQ:16:ARG:HG2	12:RQ:18:LYS:HG3	1.89	0.54
32:XA:1118:C:H1'	32:XA:1179:A:C4	2.42	0.54
32:XA:474:G:H2'	32:XA:475:G:C8	2.41	0.54
42:XK:116:HIS:N	42:XK:117:ASN:HA	2.22	0.54
55:XY:127:PHE:HA	55:XY:130:ASP:HB2	1.89	0.54
1:YA:1796:U:H2'	1:YA:1797:C:C6	2.42	0.54
4:YE:24:THR:HG23	4:YE:186:GLY:O	2.05	0.54
32:QA:341:C:H2'	32:QA:342:C:C6	2.43	0.54
40:QI:46:ALA:HB2	40:QI:74:ILE:HG23	1.89	0.54
37:QF:100:ASN:ND2	49:QR:26:LEU:O	2.40	0.54
27:R5:49:CYS:HA	27:R5:60:VAL:HG11	1.90	0.54
1:RA:1530:C:H42	1:RA:1539:G:H1	1.54	0.54
36:XE:33:VAL:HG21	36:XE:109:ILE:HA	1.89	0.54
55:XY:229:SER:HA	55:XY:258:GLN:OE1	2.08	0.54
1:YA:250:G:P	30:Y8:13:ARG:HH22	2.30	0.54
1:YA:1087:G:N2	1:YA:1102:C:N3	2.41	0.54
1:YA:1364:G:OP2	23:Y1:3:LYS:HG3	2.08	0.54
32:QA:976:G:H5'	32:QA:1358:U:O2'	2.08	0.54
44:QM:80:ARG:O	44:QM:84:ILE:HG23	2.08	0.54
1:RA:1011:G:H1'	1:RA:1013:C:O4'	2.06	0.54
1:RA:1073:A:H2'	1:RA:1074:G:H8	1.71	0.54
1:RA:1903:G:OP1	3:RD:241:PRO:HB2	2.07	0.54
3:RD:69:ARG:NH1	3:RD:69:ARG:HG2	2.21	0.54
32:XA:1146:A:H3'	32:XA:1147:C:H5''	1.89	0.54
34:XC:150:LYS:HG3	34:XC:169:ALA:HB2	1.90	0.54
33:XB:178:ARG:NH2	39:XH:74:PRO:HB3	2.23	0.54
1:RA:2611:U:C4	27:R5:3:LYS:HG2	2.43	0.54
32:XA:975:A:N1	41:XJ:48:THR:HB	2.23	0.54
35:XD:70:ILE:HD11	35:XD:74:GLN:HB3	1.90	0.54
1:YA:1378:A:OP1	29:Y7:10:ARG:NH2	2.40	0.54
1:YA:1530:C:H42	1:YA:1539:G:H1	1.56	0.54
1:YA:2081:C:H2'	1:YA:2082:A:H8	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2206:G:H8	1:YA:2207:G:N7	2.05	0.54
1:YA:2336:A:H61	22:Y0:43:THR:CG2	2.21	0.54
7:YH:11:VAL:HG21	7:YH:50:VAL:HG23	1.90	0.54
1:RA:2111:C:H42	1:RA:2147:G:H22	1.54	0.54
1:RA:270:A:OP2	1:RA:272(X):G:N1	2.33	0.54
1:YA:1075:C:H2'	1:YA:1076:C:H5'	1.88	0.54
1:YA:2757:A:P	31:Y9:20:HIS:H	2.30	0.54
1:RA:1385:G:O2'	1:RA:1396:U:O2	2.25	0.54
32:XA:1305:G:N2	32:XA:1331:G:H1'	2.23	0.54
32:XA:1391:U:H2'	32:XA:1392:G:C8	2.43	0.54
33:XB:16:HIS:CG	33:XB:210:SER:HB3	2.42	0.54
1:YA:2031:A:C6	1:YA:2498:C:H1'	2.43	0.54
32:QA:1414:U:H3	32:QA:1486:G:H1	1.56	0.54
1:RA:607:U:OP1	5:RF:102:PRO:HA	2.08	0.54
11:RP:52:GLU:OE1	11:RP:55:ARG:NH1	2.40	0.54
13:RR:83:ILE:O	13:RR:86:ARG:HG2	2.08	0.54
19:RX:11:PRO:HB3	19:RX:92:LEU:HD11	1.88	0.54
33:XB:84:GLU:HB3	33:XB:219:VAL:HG21	1.90	0.54
1:YA:1117:G:H2'	1:YA:1118:C:C6	2.42	0.54
32:QA:1492:A:H4'	43:QL:47:LYS:NZ	2.22	0.54
34:QC:6:HIS:CE1	34:QC:8:ILE:HB	2.43	0.54
1:RA:2577:A:OP2	27:R5:3:LYS:NZ	2.29	0.54
42:XK:115:PRO:C	42:XK:117:ASN:HA	2.27	0.54
1:YA:2345:G:N3	1:YA:2381:C:H2'	2.23	0.54
1:YA:889:C:O2'	1:YA:890:A:O5'	2.24	0.54
7:YH:46:GLU:HB2	7:YH:49:VAL:HG12	1.89	0.54
33:QB:54:THR:HG21	33:QB:201:ILE:HD11	1.89	0.53
1:RA:1686:C:H2'	1:RA:1687:G:O4'	2.07	0.53
1:RA:1847:A:H3'	1:RA:1848:A:H5'	1.90	0.53
4:RE:119:ARG:HD2	4:RE:120:TRP:CE2	2.43	0.53
6:RG:179:PRO:HB2	26:R4:42:PHE:CE2	2.37	0.53
7:RH:8:PRO:C	7:RH:69:ARG:HH12	2.11	0.53
32:XA:1286:A:H2'	32:XA:1287:A:H4'	1.90	0.53
32:XA:486:U:H2'	32:XA:487:A:C8	2.40	0.53
32:XA:501:C:H2'	32:XA:502:G:H8	1.71	0.53
30:Y8:23:VAL:HG11	30:Y8:47:LYS:HD3	1.89	0.53
1:YA:1084:A:H3'	1:YA:1085:A:H4'	1.88	0.53
1:YA:1432:C:H2'	1:YA:1433:U:O4'	2.08	0.53
1:YA:634:C:H2'	1:YA:635:C:C6	2.43	0.53
4:YE:14:ILE:HG13	4:YE:21:VAL:HG13	1.90	0.53
32:QA:1187:G:H4'	40:QI:111:ARG:HH11	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1028:A:N3	1:RA:2486:G:O2'	2.33	0.53
15:RT:53:ARG:HH11	15:RT:53:ARG:HB3	1.73	0.53
32:XA:859:A:H2'	32:XA:860:A:O4'	2.09	0.53
38:XG:132:GLY:O	38:XG:136:LYS:HG2	2.07	0.53
46:XO:25:THR:HG21	46:XO:70:LEU:HB2	1.91	0.53
47:XP:19:ILE:HG22	47:XP:36:ILE:HG13	1.90	0.53
6:YG:113:ARG:HD2	6:YG:140:ILE:O	2.08	0.53
7:YH:115:VAL:HG11	7:YH:148:ILE:HD11	1.90	0.53
32:QA:1260:C:H4'	32:QA:1284:C:H5'	1.89	0.53
1:RA:1057:A:O2'	1:RA:1058:G:OP1	2.25	0.53
1:RA:2122:U:H3	1:RA:2176:A:H61	1.55	0.53
17:RV:72:VAL:HG13	17:RV:85:LYS:HB3	1.90	0.53
32:XA:148:G:H2'	32:XA:149:A:H8	1.73	0.53
40:XI:16:ARG:HH11	40:XI:64:THR:HG21	1.73	0.53
32:QA:1003:G:N2	32:QA:1004:A:H1'	2.24	0.53
55:QY:177:PHE:O	55:QY:321:ARG:NH2	2.41	0.53
4:RE:143:ASN:HD22	4:RE:147:PRO:HD3	1.72	0.53
17:RV:76:LYS:HB2	17:RV:81:TYR:HB3	1.90	0.53
1:YA:1064:C:H3'	1:YA:1065:U:C5'	2.38	0.53
5:YF:24:LEU:HD23	5:YF:115:ALA:HA	1.89	0.53
7:YH:154:PRO:HB3	7:YH:163:TYR:CE2	2.43	0.53
43:QL:71:PRO:O	43:QL:102:ARG:NH1	2.41	0.53
1:RA:2031:A:N3	1:RA:2455:G:O2'	2.30	0.53
1:RA:642:G:N2	1:RA:645:C:OP2	2.41	0.53
12:RQ:16:ARG:HG3	12:RQ:17:LEU:H	1.73	0.53
32:XA:600:C:H2'	32:XA:601:C:C6	2.44	0.53
43:XL:28:LYS:N	43:XL:29:GLY:HA2	2.24	0.53
1:YA:2119:A:H61	1:YA:2168:G:H21	1.56	0.53
1:YA:309:G:N3	1:YA:329:G:O2'	2.38	0.53
35:QD:61:LYS:NZ	35:QD:72:GLU:OE2	2.41	0.53
5:RF:197:ASP:N	5:RF:197:ASP:OD1	2.42	0.53
32:XA:359:U:H2'	32:XA:360:A:H8	1.73	0.53
1:YA:1184:G:OP1	25:Y3:30:ARG:HD2	2.08	0.53
1:YA:1062:G:N7	1:YA:1070:A:H1'	2.24	0.53
1:YA:2144:U:O2'	1:YA:2147:G:N1	2.40	0.53
32:XA:437:U:H5'	35:XD:155:LEU:HD21	1.90	0.53
35:XD:173:TRP:CD1	35:XD:174:LEU:HG	2.44	0.53
1:YA:2171:A:H4'	1:YA:2172:U:OP1	2.07	0.53
1:YA:2698:U:H2'	1:YA:2699:C:C6	2.44	0.53
32:QA:1034:G:H3'	32:QA:1035:A:C8	2.43	0.53
32:QA:1516:G:N1	32:QA:1519:MA6:OP2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:QB:69:LEU:HB3	33:QB:162:ILE:HG22	1.91	0.53
41:QJ:37:PRO:HA	41:QJ:72:VAL:HG12	1.90	0.53
1:RA:1049:C:H42	1:RA:2751:G:H1	1.56	0.53
1:RA:1268:A:H2'	1:RA:1269:A:O4'	2.08	0.53
1:RA:2074:U:H2'	1:RA:2075:U:C6	2.44	0.53
1:RA:1971:A:C4	3:RD:241:PRO:HD3	2.44	0.53
3:RD:71:ASP:HB3	3:RD:103:ARG:NH2	2.22	0.53
38:XG:27:ILE:HD12	38:XG:40:ALA:HA	1.89	0.53
49:XR:31:LEU:HD21	49:XR:62:GLU:HB2	1.91	0.53
1:YA:1296:G:OP1	1:YA:2709:G:O2'	2.20	0.53
1:YA:1514:U:H2'	1:YA:1515:G:C8	2.43	0.53
15:YT:24:PRO:HD3	15:YT:52:ILE:HD12	1.91	0.53
1:RA:1769:G:O2'	1:RA:1958:C:OP1	2.19	0.53
32:XA:1347:G:N2	32:XA:1373:G:H2'	2.24	0.53
32:XA:142:G:H2'	32:XA:143:A:H8	1.74	0.53
1:YA:2336:A:H61	22:Y0:43:THR:HG22	1.74	0.53
1:YA:1416:G:O2'	1:YA:1417:C:OP2	2.23	0.53
7:YH:137:ASP:HB3	7:YH:140:LYS:HB3	1.91	0.53
21:YZ:125:LEU:HB3	21:YZ:165:VAL:HG13	1.91	0.53
32:QA:1492:A:H8	55:QY:119:THR:HG21	1.74	0.53
32:QA:581:G:OP1	46:QO:61:GLY:HA3	2.09	0.53
55:QY:257:CYS:O	55:QY:266:ASN:ND2	2.35	0.53
1:RA:11:G:H2'	1:RA:12:U:H5'	1.91	0.53
1:RA:876:C:H2'	1:RA:877:U:O4'	2.10	0.53
16:RU:108:GLU:HG2	17:RV:45:THR:HG21	1.90	0.53
37:XF:37:VAL:HA	37:XF:65:VAL:HG12	1.91	0.53
43:XL:83:VAL:HG13	43:XL:100:ILE:HG23	1.91	0.53
1:YA:78:A:H2'	1:YA:79:G:C8	2.43	0.53
6:YG:55:LYS:HA	6:YG:58:GLN:HB3	1.90	0.53
32:QA:159:G:N2	32:QA:161:A:H3'	2.24	0.52
32:QA:921:U:O2'	36:QE:19:MET:O	2.18	0.52
38:QG:45:ASP:O	38:QG:49:ILE:HG13	2.08	0.52
54:QX:21:A:H62	55:QY:198:THR:HG1	1.54	0.52
1:RA:1991:U:H2'	1:RA:1992:G:H5''	1.92	0.52
1:RA:362:U:O2'	1:RA:363(A):G:H5'	2.09	0.52
32:XA:769:G:H4'	32:XA:1513:A:H4'	1.90	0.52
35:XD:173:TRP:CD1	35:XD:189:PRO:HG3	2.44	0.52
43:XL:70:ILE:HG12	43:XL:100:ILE:HD12	1.90	0.52
1:YA:2189:U:H2'	1:YA:2190:G:C8	2.44	0.52
17:YV:29:PRO:HA	17:YV:61:VAL:HG23	1.89	0.52
21:YZ:33:LEU:HD11	21:YZ:90:VAL:HG21	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:17:U:H2'	32:QA:18:C:C6	2.44	0.52
32:QA:188:C:O4'	51:QT:89:ARG:NH2	2.42	0.52
1:RA:2232:U:OP1	23:R1:40:ARG:NH1	2.39	0.52
1:RA:247:G:H4'	1:RA:386:G:C5	2.44	0.52
6:RG:50:ALA:C	6:RG:52:ILE:H	2.13	0.52
32:XA:1004:A:H5'	32:XA:1025:U:H5	1.73	0.52
35:XD:79:PHE:HE1	35:XD:204:ILE:HD13	1.74	0.52
40:XI:9:ARG:HG2	40:XI:14:VAL:HG12	1.91	0.52
10:YO:80:ASP:OD1	15:YT:64:ARG:NH2	2.42	0.52
41:QJ:11:PHE:HE1	41:QJ:67:THR:HG22	1.74	0.52
38:QG:150:ALA:HA	42:QK:59:TYR:HB3	1.92	0.52
4:RE:105:THR:OG1	4:RE:199:ARG:NH2	2.43	0.52
40:XI:53:VAL:C	40:XI:55:ALA:H	2.11	0.52
47:XP:23:ASP:OD1	47:XP:25:ARG:HD3	2.10	0.52
55:XY:212:ALA:CB	55:XY:214:LEU:HG	2.37	0.52
55:XY:312:PHE:N	55:XY:313:PRO:HD2	2.24	0.52
5:YF:178:PRO:HB2	5:YF:201:VAL:CG2	2.37	0.52
8:YI:14:ASP:OD1	8:YI:15:VAL:N	2.41	0.52
12:YQ:30:GLY:HA2	12:YQ:107:ALA:HB2	1.89	0.52
32:QA:539:A:OP2	43:QL:115:LYS:NZ	2.43	0.52
38:QG:79:ARG:HA	38:QG:84:ASN:HA	1.91	0.52
1:RA:1101:U:H2'	1:RA:1102:C:H6	1.75	0.52
1:RA:1139:G:O2'	1:RA:1143:A:N1	2.31	0.52
1:RA:1756:G:H4'	1:RA:1758:G:O4'	2.10	0.52
9:RN:120:LEU:HD22	9:RN:122:VAL:HG23	1.91	0.52
32:XA:1117:G:H4'	40:XI:104:ARG:NH1	2.24	0.52
24:Y2:17:SER:OG	24:Y2:20:GLU:HG3	2.09	0.52
1:YA:2438:U:O2'	1:YA:2440:C:OP1	2.23	0.52
36:QE:102:ALA:HB1	36:QE:106:PRO:HG2	1.91	0.52
32:QA:1292:U:OP2	38:QG:41:ARG:NH2	2.43	0.52
44:QM:34:LEU:HD13	44:QM:41:PRO:HA	1.90	0.52
55:QY:98:VAL:C	55:QY:100:LEU:H	2.13	0.52
1:RA:1081:U:H3'	1:RA:1085:A:H61	1.74	0.52
1:RA:1068:G:H3'	1:RA:1096:A:OP2	2.10	0.52
1:RA:2567:G:H2'	1:RA:2568:C:C6	2.45	0.52
7:RH:59:ARG:HH11	7:RH:59:ARG:HG2	1.75	0.52
1:YA:1057:A:N7	1:YA:1086:A:H2'	2.24	0.52
1:YA:1239:G:H2'	1:YA:1240:U:O4'	2.10	0.52
1:YA:1530:C:HO2'	1:YA:1531:C:P	2.30	0.52
1:YA:2128:C:N4	1:YA:2160:G:H1	2.04	0.52
1:YA:277:C:O2'	1:YA:278:A:OP1	2.19	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:1004:A:O2'	32:QA:1038:C:O2	2.16	0.52
33:QB:16:HIS:HB3	33:QB:210:SER:HB2	1.92	0.52
44:QM:13:LYS:HA	44:QM:44:ARG:HH11	1.73	0.52
1:RA:2110:G:H5''	1:RA:2111:C:H5	1.75	0.52
1:RA:2032:G:H1'	4:RE:145:LYS:HD3	1.92	0.52
1:YA:1102:C:H2'	1:YA:1103:A:C8	2.45	0.52
6:YG:11:TYR:CZ	6:YG:16:ARG:HD2	2.45	0.52
20:YY:23:ARG:HG3	20:YY:42:VAL:HG22	1.92	0.52
32:QA:519:C:OP1	55:QY:183:ARG:NH1	2.43	0.52
35:QD:116:GLN:NE2	35:QD:157:LEU:HD11	2.24	0.52
48:QQ:67:LYS:HA	48:QQ:70:ARG:HH12	1.74	0.52
1:RA:2130:U:H2'	1:RA:2158:A:H61	1.75	0.52
1:YA:1068:G:H3'	1:YA:1096:A:OP2	2.10	0.52
1:YA:2065:C:H2'	1:YA:2066:C:C6	2.45	0.52
1:YA:2334:G:H5'	14:YS:9:ARG:HG2	1.91	0.52
1:YA:644:A:H4'	1:YA:645:C:C5	2.44	0.52
5:YF:165:ARG:HG2	5:YF:168:ARG:NH2	2.25	0.52
44:QM:76:ALA:HA	44:QM:79:LYS:HB3	1.91	0.52
1:RA:1259:G:H2'	1:RA:1260:G:C8	2.45	0.52
1:RA:922:U:H2'	1:RA:923:C:C6	2.45	0.52
32:XA:123:C:OP1	32:XA:311:C:O2'	2.25	0.52
32:XA:660:G:H1	32:XA:745:C:H42	1.58	0.52
39:XH:51:VAL:HG11	39:XH:60:ARG:HH11	1.75	0.52
42:XK:82:VAL:HB	42:XK:108:ILE:HG12	1.91	0.52
44:XM:20:THR:HG21	44:XM:27:LYS:HD2	1.90	0.52
44:XM:81:LEU:HD13	44:XM:88:ARG:HD2	1.92	0.52
28:Y6:6:ARG:NE	28:Y6:24:GLU:OE1	2.35	0.52
1:YA:336:C:O2'	20:YY:35:TYR:OH	2.23	0.52
11:RP:50:ARG:HD3	30:R8:7:HIS:CD2	2.45	0.52
1:RA:2119:A:H61	1:RA:2168:G:H21	1.58	0.52
1:RA:2390:U:OP2	30:R8:35:GLN:NE2	2.34	0.52
8:RI:130:TYR:CE2	8:RI:132:PRO:HB3	2.45	0.52
32:XA:1223:C:P	50:XS:78:ARG:HH22	2.32	0.52
33:XB:115:LEU:O	33:XB:119:GLU:HG2	2.10	0.52
36:XE:12:LEU:HD12	36:XE:128:PRO:HB2	1.92	0.52
23:Y1:54:ALA:HB1	23:Y1:83:GLU:HG3	1.92	0.52
1:YA:2127:G:H2'	1:YA:2128:C:O4'	2.09	0.52
12:YQ:32:TYR:OH	12:YQ:111:GLU:OE1	2.24	0.52
10:RO:97:ARG:NH1	32:QA:339:C:OP2	2.43	0.52
39:QH:6:ILE:O	39:QH:10:LEU:HG	2.10	0.52
23:R1:51:VAL:HG11	23:R1:74:VAL:HG21	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:2152:G:H2'	1:RA:2153:G:C8	2.44	0.52
1:RA:2165:G:H2'	1:RA:2166:G:O4'	2.10	0.52
2:RB:89:G:OP2	2:RB:89:G:H8	1.93	0.52
1:RA:2018:G:O2'	16:RU:34:LYS:HE3	2.10	0.52
20:RY:90:LEU:HD21	20:RY:96:ILE:HG12	1.90	0.52
32:XA:390:C:H2'	32:XA:391:G:C8	2.45	0.52
35:XD:162:LEU:HD13	35:XD:181:MET:HG2	1.92	0.52
40:XI:4:TYR:HB2	40:XI:19:LEU:HB2	1.92	0.52
28:Y6:13:CYS:SG	28:Y6:47:THR:HG21	2.49	0.52
1:YA:1514:U:H2'	1:YA:1515:G:H8	1.75	0.52
1:YA:2065:C:H2'	1:YA:2066:C:H6	1.75	0.52
1:YA:2111:C:H42	1:YA:2147:G:H22	1.57	0.52
1:YA:2280:G:O2'	1:YA:2388:A:N1	2.35	0.52
32:QA:1086:U:H3	32:QA:1099:G:H22	1.58	0.51
32:QA:337:C:H2'	32:QA:338:A:C8	2.45	0.51
40:QI:16:ARG:HD3	40:QI:64:THR:HG21	1.92	0.51
55:QY:221:ASP:HB3	55:QY:250:PRO:HD3	1.91	0.51
55:QY:338:ASP:N	55:QY:338:ASP:OD1	2.44	0.51
5:RF:20:LEU:HD23	5:RF:21:ALA:H	1.75	0.51
32:XA:1127:G:H5'	32:XA:1280:A:O2'	2.10	0.51
32:XA:1201:A:H4'	32:XA:1202:G:H5''	1.92	0.51
32:XA:438:G:O2'	32:XA:494:U:O4	2.24	0.51
1:YA:455:C:N3	1:YA:472:A:H2'	2.25	0.51
1:YA:483:A:H5''	20:YY:50:ARG:HD3	1.92	0.51
33:QB:73:THR:OG1	33:QB:170:GLU:OE1	2.27	0.51
34:QC:47:LEU:HD13	34:QC:68:VAL:HG11	1.92	0.51
35:QD:76:ARG:HD3	35:QD:207:TYR:CE1	2.45	0.51
32:QA:1279:A:H5''	41:QJ:7:LYS:NZ	2.26	0.51
55:QY:115:VAL:HG22	55:QY:203:VAL:HG22	1.92	0.51
32:XA:1015:A:H2'	32:XA:1016:A:C8	2.45	0.51
17:YV:35:LEU:HB2	17:YV:57:VAL:HG22	1.93	0.51
19:YX:57:LEU:HD11	19:YX:78:LYS:HE3	1.92	0.51
32:QA:833:U:H2'	32:QA:834:C:H6	1.74	0.51
35:QD:170:VAL:HG12	35:QD:174:LEU:HB2	1.91	0.51
37:QF:69:GLU:O	37:QF:72:VAL:HG12	2.10	0.51
1:RA:1739:U:HO2'	1:RA:1740:G:H8	1.58	0.51
21:RZ:92:SER:O	21:RZ:130:PRO:HG2	2.11	0.51
32:XA:1002:G:H2'	32:XA:1003:G:C8	2.45	0.51
55:XY:342:GLU:O	55:XY:346:GLN:N	2.36	0.51
1:YA:1067:A:H4'	1:YA:1068:G:OP2	2.09	0.51
1:YA:322:A:OP1	5:YF:168:ARG:HD2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:952:G:P	12:YQ:16:ARG:HH22	2.33	0.51
21:YZ:19:ARG:NH1	21:YZ:84:GLU:O	2.44	0.51
32:QA:614:A:OP1	35:QD:85:LYS:NZ	2.43	0.51
1:RA:2128:C:N4	1:RA:2160:G:H1	2.06	0.51
1:RA:272(E):U:H2'	1:RA:272(F):C:C6	2.45	0.51
6:RG:9:ARG:O	6:RG:13:GLU:HG3	2.09	0.51
32:XA:1158:C:H2'	32:XA:1158:C:O2	2.09	0.51
32:XA:767:A:H2'	32:XA:768:A:O4'	2.09	0.51
33:XB:179:LYS:HG2	39:XH:72:PRO:HG3	1.92	0.51
35:XD:8:VAL:HG22	35:XD:21:LEU:HD13	1.92	0.51
39:XH:41:ARG:NH2	39:XH:123:GLU:OE2	2.43	0.51
51:XT:37:SER:O	51:XT:41:ILE:HG12	2.10	0.51
1:YA:811:U:H2'	11:YP:21:ARG:HA	1.91	0.51
1:YA:958:U:O2'	1:YA:959:A:OP2	2.24	0.51
4:YE:111:ARG:HG2	4:YE:160:TYR:O	2.11	0.51
32:QA:102:G:O2'	32:QA:151:A:N3	2.36	0.51
1:RA:2321:G:O2'	1:RA:2322:A:OP1	2.23	0.51
1:RA:581:C:H2'	1:RA:582:G:C8	2.45	0.51
1:RA:944:G:H5''	1:RA:945:A:O5'	2.11	0.51
4:RE:36:ARG:HG2	4:RE:47:VAL:HG22	1.92	0.51
32:XA:407:G:O2'	35:XD:116:GLN:HG3	2.10	0.51
35:XD:111:ALA:HB2	35:XD:120:LEU:HD12	1.92	0.51
55:XY:138:TYR:HD2	55:XY:337:LEU:H	1.59	0.51
1:YA:1866:C:H2'	1:YA:1876:A:O4'	2.10	0.51
1:YA:2033:A:O2'	1:YA:2035:G:OP2	2.24	0.51
1:YA:2430:A:H2'	1:YA:2430:A:N3	2.25	0.51
5:YF:21:ALA:HB3	5:YF:22:ALA:HA	1.91	0.51
32:QA:769:G:H4'	32:QA:1513:A:H4'	1.91	0.51
32:QA:537:G:H5''	43:QL:113:ARG:NH1	2.26	0.51
32:QA:1216:G:H5''	45:QN:5:ALA:HB2	1.91	0.51
1:RA:1530:C:HO2'	1:RA:1531:C:P	2.34	0.51
1:RA:1791:A:N6	1:RA:1828:G:O2'	2.43	0.51
1:RA:2140:C:H2'	1:RA:2141:G:C8	2.37	0.51
1:RA:582:G:H2'	1:RA:583:G:H8	1.75	0.51
11:RP:113:LYS:HA	11:RP:129:ALA:O	2.11	0.51
46:XO:39:LEU:HD13	46:XO:56:LEU:HB2	1.92	0.51
3:YD:16:MET:HG3	3:YD:206:LEU:O	2.11	0.51
32:QA:1278:U:H5'	32:QA:1279:A:O4'	2.10	0.51
32:QA:410:G:OP1	35:QD:30:LYS:NZ	2.29	0.51
55:QY:332:VAL:HG22	55:QY:337:LEU:HB3	1.92	0.51
1:RA:1086:A:OP1	1:RA:1104:C:O2'	2.29	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:851:U:O2'	25:R3:42:ALA:O	2.29	0.51
6:RG:62:LEU:O	6:RG:143:GLU:HG2	2.11	0.51
1:RA:1187:G:H5'	17:RV:81:TYR:CE1	2.46	0.51
47:XP:1:MET:SD	47:XP:65:GLN:HG3	2.51	0.51
24:Y2:16:LEU:O	24:Y2:67:LYS:NZ	2.44	0.51
1:YA:1032:A:OP1	31:Y9:8:LYS:HE3	2.11	0.51
1:YA:1108:U:H3'	1:YA:1109:C:C6	2.45	0.51
32:QA:67:C:H2'	32:QA:68:G:C8	2.46	0.51
55:QY:342:GLU:O	55:QY:346:GLN:N	2.37	0.51
1:RA:861:A:N3	2:RB:79:C:O2'	2.39	0.51
32:XA:736:C:H2'	32:XA:737:A:C8	2.46	0.51
33:XB:124:SER:HB2	33:XB:125:PRO:HD3	1.91	0.51
38:XG:26:PHE:O	38:XG:30:ILE:HG13	2.11	0.51
55:XY:133:ARG:NH2	55:XY:334:GLU:OE1	2.44	0.51
55:XY:202:THR:HB	55:XY:298:LEU:HD22	1.93	0.51
1:YA:2183:C:H2'	1:YA:2184:G:C8	2.45	0.51
1:YA:729:G:C8	3:YD:208:LYS:HD2	2.46	0.51
33:QB:109:SER:O	33:QB:112:VAL:HG22	2.11	0.51
33:QB:231:GLU:HB3	33:QB:232:PRO:CD	2.35	0.51
32:QA:1079:G:O3'	36:QE:14:ARG:NH2	2.44	0.51
1:RA:9:U:O2'	1:RA:10:G:OP1	2.26	0.51
1:RA:1593:G:H2'	1:RA:1594:G:C8	2.46	0.51
1:RA:263:C:H2'	1:RA:264:C:O4'	2.11	0.51
9:RN:15:LEU:HB2	9:RN:135:PRO:HB2	1.93	0.51
49:XR:59:SER:OG	49:XR:62:GLU:HG2	2.11	0.51
1:RA:2689:U:OP2	1:RA:2719:G:N2	2.40	0.51
1:RA:276:A:H5''	1:RA:277:C:H5'	1.92	0.51
6:RG:116:ASP:OD1	44:QM:68:GLY:HA3	2.11	0.51
9:RN:67:LEU:O	9:RN:88:GLU:HG3	2.11	0.51
10:RO:23:ARG:HD3	10:RO:24:VAL:N	2.25	0.51
14:RS:25:ARG:HD3	14:RS:42:ASP:OD2	2.10	0.51
1:YA:1057:A:HO2'	1:YA:1058:G:P	2.34	0.51
1:YA:2627:G:O2'	1:YA:2781:A:N1	2.38	0.51
10:YO:64:ARG:HB2	10:YO:83:ALA:HB3	1.93	0.51
32:QA:1103:C:H2'	32:QA:1104:G:O4'	2.10	0.50
32:QA:1442(A):G:H1'	32:QA:1442(B):G:OP1	2.12	0.50
32:QA:262:A:H2'	32:QA:263:A:C8	2.46	0.50
1:RA:1108:U:H3'	1:RA:1109:C:C6	2.46	0.50
1:RA:873:G:H1	1:RA:904:C:H42	1.57	0.50
6:RG:55:LYS:O	6:RG:59:GLU:HG3	2.11	0.50
32:XA:396:G:O2'	32:XA:398:C:OP1	2.20	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:XO:7:GLU:OE2	46:XO:38:ARG:NH2	2.44	0.50
3:YD:142:VAL:HG23	3:YD:193:VAL:HA	1.92	0.50
13:YR:87:TYR:OH	13:YR:117:VAL:O	2.20	0.50
3:RD:242:ARG:HD3	3:RD:242:ARG:H	1.76	0.50
1:RA:583:G:OP2	16:RU:10:ARG:HD2	2.12	0.50
32:XA:1512:U:H2'	32:XA:1513:A:C8	2.46	0.50
35:XD:61:LYS:HD2	35:XD:207:TYR:OH	2.11	0.50
1:YA:1385:G:O2'	1:YA:1396:U:O2	2.25	0.50
1:YA:1693:U:O2'	3:YD:14:ARG:NH2	2.44	0.50
1:YA:276:A:H5''	1:YA:277:C:H4'	1.93	0.50
1:YA:2820:A:O2'	1:YA:2821:A:OP1	2.29	0.50
3:YD:183:ARG:HG3	3:YD:183:ARG:HH11	1.75	0.50
1:YA:764:A:H5'	3:YD:210:GLY:HA2	1.94	0.50
32:QA:1074:G:O2'	32:QA:1101:A:N1	2.39	0.50
32:QA:1124:G:N2	32:QA:1125:U:O4	2.45	0.50
32:QA:73:G:H1	32:QA:96:U:H3	1.57	0.50
29:R7:30:VAL:O	29:R7:34:ARG:HG3	2.11	0.50
11:RP:8:PRO:HB2	11:RP:12:ALA:HB3	1.94	0.50
13:RR:56:LYS:NZ	13:RR:90:ARG:O	2.43	0.50
32:XA:576:G:O6	32:XA:880:C:O2'	2.27	0.50
32:XA:748:C:H4'	32:XA:749:C:O5'	2.10	0.50
1:YA:1639:U:C2'	1:YA:1640:C:H5''	2.40	0.50
1:YA:2074:U:H2'	1:YA:2075:U:C6	2.46	0.50
1:YA:2168:G:H22	1:YA:2171:A:H2'	1.75	0.50
1:YA:2572:A:C4	4:YE:144:ARG:NH1	2.79	0.50
1:YA:686:G:N2	1:YA:788:A:H61	2.09	0.50
6:YG:16:ARG:O	6:YG:20:ILE:HG13	2.12	0.50
34:QC:70:VAL:HG22	34:QC:72:LYS:H	1.76	0.50
32:QA:1343:G:H4'	40:QI:122:ALA:HB3	1.94	0.50
1:RA:1035:U:O5'	7:RH:59:ARG:NH1	2.44	0.50
6:RG:50:ALA:O	6:RG:52:ILE:N	2.45	0.50
9:RN:15:LEU:HD12	9:RN:137:LYS:HD3	1.92	0.50
1:RA:1278:A:OP1	13:RR:36:THR:HG23	2.11	0.50
32:XA:1327:C:H2'	32:XA:1328:C:C6	2.47	0.50
15:YT:108:ARG:NH1	32:XA:1464:G:OP1	2.45	0.50
32:XA:36:C:H5''	43:XL:123:LYS:HD3	1.92	0.50
40:XI:21:PRO:HA	40:XI:59:PHE:HA	1.92	0.50
1:YA:2317:C:H2'	1:YA:2318:G:H5'	1.93	0.50
1:YA:384:U:H2'	1:YA:385:C:H6	1.76	0.50
1:YA:727:A:C6	1:YA:728:G:C6	3.00	0.50
1:YA:746:A:H2'	1:YA:2612:C:H5''	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:YG:3:LEU:H	6:YG:3:LEU:HD23	1.76	0.50
1:RA:1094:U:OP1	1:RA:1096:A:N6	2.45	0.50
1:RA:900:A:H2'	1:RA:901:A:O4'	2.11	0.50
10:RO:115:VAL:HG13	10:RO:121:VAL:HG21	1.93	0.50
19:RX:35:THR:HG22	19:RX:37:THR:H	1.76	0.50
19:RX:29:TRP:CE3	19:RX:78:LYS:HB3	2.47	0.50
32:XA:1005:A:H5''	32:XA:1006:C:C5	2.47	0.50
32:XA:1015:A:N3	32:XA:1218:C:O2'	2.43	0.50
32:XA:719:C:O2'	49:XR:49:LYS:HB3	2.11	0.50
1:YA:453:C:O2	1:YA:457:A:O2'	2.29	0.50
14:YS:25:ARG:HD3	14:YS:42:ASP:OD2	2.12	0.50
32:QA:1002:G:C6	32:QA:1003:G:C2	2.99	0.50
32:QA:328:C:H4'	32:QA:329:A:H5'	1.94	0.50
51:QT:89:ARG:O	51:QT:93:GLU:HG2	2.11	0.50
55:QY:255:VAL:HG12	55:QY:274:LEU:HG	1.93	0.50
1:RA:740:U:H2'	1:RA:741:G:C8	2.47	0.50
1:RA:729:G:C6	3:RD:208:LYS:HB2	2.47	0.50
3:RD:17:THR:O	3:RD:211:ARG:NH2	2.44	0.50
1:RA:2820:A:P	13:RR:2:ARG:HH22	2.35	0.50
32:XA:411:A:OP2	35:XD:25:ARG:NH2	2.44	0.50
33:XB:71:VAL:HG23	33:XB:164:VAL:HA	1.94	0.50
51:XT:18:GLN:O	51:XT:22:ARG:HG3	2.11	0.50
52:XU:5:ASP:O	52:XU:11:GLY:HA3	2.11	0.50
1:YA:1341:U:OP1	1:YA:1397:U:N3	2.40	0.50
1:YA:2115:G:N1	1:YA:2117:A:N7	2.59	0.50
1:YA:2267:A:H5''	1:YA:2268:A:H5'	1.93	0.50
1:YA:438:G:H2'	1:YA:440:G:H8	1.77	0.50
6:YG:114:ILE:HG23	6:YG:136:ARG:NH2	2.27	0.50
11:YP:52:GLU:OE1	11:YP:55:ARG:NH1	2.43	0.50
32:QA:56:U:H2'	32:QA:57:G:C8	2.46	0.50
35:QD:172:PRO:HB2	35:QD:187:ARG:HH21	1.76	0.50
46:QO:29:VAL:HG11	46:QO:67:LEU:HD21	1.94	0.50
54:QX:21:A:N6	55:QY:198:THR:OG1	2.36	0.50
25:R3:3:ARG:NH1	25:R3:60:GLU:OE2	2.42	0.50
26:R4:51:ASP:CB	44:QM:65:LYS:HD2	2.41	0.50
28:R6:13:CYS:SG	28:R6:47:THR:HG21	2.51	0.50
11:RP:60:MET:SD	30:R8:13:ARG:NH2	2.84	0.50
1:RA:1224:C:O2'	17:RV:85:LYS:HA	2.11	0.50
1:RA:2820:A:O2'	1:RA:2821:A:OP1	2.29	0.50
1:RA:1750:G:O2'	1:RA:2860:A:N1	2.41	0.50
1:RA:848:G:H2'	1:RA:849:A:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:RH:20:ALA:HB3	7:RH:23:ARG:HG2	1.93	0.50
50:XS:12:ASP:OD2	50:XS:35:SER:HB3	2.11	0.50
1:YA:2152:G:H2'	1:YA:2153:G:C8	2.47	0.50
1:YA:2134:A:H8	1:YA:2156:G:H21	1.60	0.50
1:YA:2839:G:H5'	13:YR:46:GLY:HA2	1.94	0.50
8:YI:130:TYR:HB3	8:YI:138:ILE:HB	1.94	0.50
36:QE:78:HIS:ND1	39:QH:104:ARG:HD2	2.26	0.50
55:QY:182:HIS:HB3	55:QY:310:TYR:HE2	1.77	0.50
1:RA:2327:A:H2'	1:RA:2328:A:C8	2.46	0.50
1:RA:26:G:H1'	1:RA:515:A:N6	2.27	0.50
1:RA:517:C:OP1	27:R5:16:ARG:NH2	2.45	0.50
1:RA:581:C:H2'	1:RA:582:G:H8	1.75	0.50
5:RF:18:ARG:HG2	5:RF:19:GLU:N	2.26	0.50
7:RH:3:ARG:HB3	7:RH:6:ARG:HG2	1.94	0.50
32:XA:600:C:H2'	32:XA:601:C:H6	1.76	0.50
32:XA:673:G:H2'	32:XA:674:G:C8	2.47	0.50
30:Y8:6:THR:HG23	30:Y8:64:TYR:HD2	1.77	0.50
1:YA:1608:A:H1'	1:YA:1610:A:OP2	2.12	0.50
1:YA:2114:A:H3'	1:YA:2115:G:H8	1.77	0.50
20:YY:102:CYS:SG	20:YY:104:GLY:N	2.75	0.50
51:QT:43:LEU:HD13	51:QT:51:GLU:HB3	1.93	0.50
1:RA:1023:U:OP2	1:RA:1025:G:O2'	2.29	0.50
1:RA:1101:U:H2'	1:RA:1102:C:C6	2.46	0.50
1:RA:2189:U:H2'	1:RA:2190:G:C8	2.46	0.50
4:RE:12:THR:HG22	15:RT:58:ASN:HD21	1.77	0.50
32:XA:1002:G:N3	32:XA:1003:G:H8	2.10	0.50
32:XA:1129:C:N4	32:XA:1143:G:H1	2.09	0.50
32:XA:662:G:H2'	32:XA:663:A:H8	1.76	0.50
40:XI:24:GLY:HA2	40:XI:59:PHE:O	2.12	0.50
44:XM:34:LEU:HD13	44:XM:41:PRO:HA	1.93	0.50
1:YA:1301:A:C8	1:YA:1303:G:C8	3.00	0.50
1:YA:2304:G:H22	1:YA:2312:U:H3	1.58	0.50
1:YA:2636:U:OP1	4:YE:80:GLU:HB2	2.11	0.50
32:QA:839:U:H1'	32:QA:840:C:OP1	2.12	0.49
32:QA:78:G:N2	32:QA:91:C:N3	2.55	0.49
39:QH:51:VAL:HG11	39:QH:60:ARG:HH12	1.77	0.49
47:QP:74:LEU:HD23	47:QP:79:VAL:HG21	1.93	0.49
26:R4:54:GLY:O	26:R4:56:VAL:HA	2.12	0.49
1:RA:479:A:N3	1:RA:481:G:H5''	2.27	0.49
5:RF:103:LYS:HA	5:RF:106:ARG:HD3	1.93	0.49
32:XA:222:U:H2'	32:XA:223:U:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:343:U:H2'	32:XA:345:C:C5	2.47	0.49
1:YA:2140:C:H2'	1:YA:2141:G:C8	2.41	0.49
1:YA:858:U:O2	1:YA:2268:A:H2'	2.12	0.49
1:YA:881:G:H2'	1:YA:882:G:C8	2.47	0.49
32:QA:833:U:H2'	32:QA:834:C:C6	2.47	0.49
33:QB:8:LYS:HZ1	33:QB:52:GLU:HG3	1.76	0.49
35:QD:85:LYS:HD3	35:QD:86:LYS:N	2.27	0.49
49:QR:31:LEU:HD21	49:QR:62:GLU:HB3	1.93	0.49
53:QV:1:C:H42	53:QV:72:A:H61	1.60	0.49
32:XA:1040:U:H2'	32:XA:1041:A:O4'	2.12	0.49
32:XA:524:G:H2'	32:XA:525:C:C6	2.47	0.49
33:XB:127:ILE:HG12	33:XB:128:GLU:H	1.76	0.49
51:XT:89:ARG:O	51:XT:93:GLU:HG2	2.12	0.49
55:XY:227:PHE:HE2	55:XY:245:ARG:HD3	1.76	0.49
5:YF:132:VAL:HA	5:YF:138:GLU:HB3	1.94	0.49
7:YH:9:ILE:O	7:YH:49:VAL:HA	2.12	0.49
12:YQ:38:GLU:HG3	12:YQ:127:ILE:HB	1.94	0.49
39:QH:18:ARG:N	39:QH:18:ARG:HD2	2.26	0.49
42:QK:85:ARG:HD3	42:QK:113:PRO:HD3	1.93	0.49
55:QY:173:GLY:HA2	55:QY:176:LYS:HE3	1.94	0.49
1:RA:2526:G:H5'	1:RA:2742:C:O2'	2.11	0.49
8:RI:72:LEU:HD12	8:RI:138:ILE:HG21	1.93	0.49
13:RR:24:GLN:HE21	13:RR:44:LEU:HG	1.77	0.49
32:XA:102:G:O2'	32:XA:151:A:N3	2.35	0.49
33:XB:45:GLN:O	33:XB:49:GLU:HG2	2.12	0.49
47:XP:53:VAL:HG13	47:XP:79:VAL:HG22	1.94	0.49
1:YA:1266:G:O2'	1:YA:2012:G:O6	2.22	0.49
1:YA:848:G:H2'	1:YA:849:A:C8	2.46	0.49
2:YB:28:C:OP1	14:YS:36:TYR:OH	2.23	0.49
32:QA:110:C:O2'	47:QP:25:ARG:O	2.26	0.49
50:QS:63:THR:OG1	50:QS:65:ASN:ND2	2.45	0.49
1:RA:2271:G:OP1	22:R0:18:ALA:HB1	2.12	0.49
1:RA:2001:A:H2'	1:RA:2002:G:C8	2.48	0.49
1:RA:919:G:N2	1:RA:2269:A:OP2	2.45	0.49
1:RA:414:C:H2'	1:RA:415:A:C8	2.48	0.49
1:RA:754:C:H2'	1:RA:755:C:C6	2.47	0.49
6:RG:106:LEU:HA	6:RG:110:ALA:HB3	1.93	0.49
11:RP:2:LYS:HE2	11:RP:4:SER:OG	2.12	0.49
32:XA:1305:G:H22	32:XA:1331:G:H1'	1.77	0.49
32:XA:858:G:O6	32:XA:869:G:H3'	2.12	0.49
1:YA:2889:C:H3'	1:YA:2891:G:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:322:A:OP2	5:YF:169:ASN:HB2	2.12	0.49
1:YA:589:C:H2'	1:YA:590:A:C8	2.47	0.49
5:YF:18:ARG:HG2	5:YF:19:GLU:N	2.26	0.49
19:YX:53:LYS:HB3	19:YX:82:GLN:HB3	1.93	0.49
32:QA:171:A:H2'	32:QA:172:A:C8	2.47	0.49
33:QB:187:LEU:HA	33:QB:201:ILE:HB	1.93	0.49
40:QI:108:VAL:HG12	40:QI:109:VAL:H	1.76	0.49
50:QS:3:ARG:NH1	50:QS:10:PHE:HB2	2.26	0.49
27:R5:48:GLU:O	27:R5:60:VAL:HG21	2.12	0.49
1:RA:2243:U:H2'	1:RA:2244:U:C6	2.48	0.49
3:RD:106:ILE:HD11	3:RD:144:ALA:HB2	1.94	0.49
4:RE:170:LEU:HB3	4:RE:184:VAL:HG22	1.93	0.49
6:RG:5:VAL:HG12	26:R4:25:TYR:CE1	2.48	0.49
32:XA:1028:C:H2'	32:XA:1033:G:H22	1.78	0.49
43:XL:86:ARG:HH11	43:XL:99:HIS:HB2	1.77	0.49
49:XR:52:PRO:HB2	49:XR:54:ARG:HG2	1.93	0.49
1:YA:1357:U:H2'	1:YA:1358:G:O4'	2.11	0.49
1:YA:484:C:H2'	1:YA:485:C:C6	2.47	0.49
17:YV:6:LYS:HB2	17:YV:38:LEU:HD21	1.94	0.49
32:QA:1065:U:H4'	32:QA:1066:C:O5'	2.11	0.49
32:QA:1148:U:H2'	32:QA:1149:C:O4'	2.11	0.49
32:QA:452:A:H4'	47:QP:72:ARG:NH1	2.28	0.49
1:RA:2836:U:H2'	1:RA:2837:G:C8	2.48	0.49
32:XA:841:U:C5	32:XA:848:C:H1'	2.48	0.49
32:XA:973:G:H3'	32:XA:974:A:H5''	1.94	0.49
1:YA:1055:G:H21	1:YA:1084:A:N6	2.11	0.49
1:YA:2126:A:H4'	1:YA:2127:G:O5'	2.13	0.49
32:QA:1239:A:C4	32:QA:1298:C:N4	2.81	0.49
1:RA:1689:A:H4'	32:QA:1475:G:H4'	1.94	0.49
1:RA:2889:C:H3'	1:RA:2891:G:H8	1.77	0.49
1:RA:706:A:H2'	1:RA:707:G:O4'	2.13	0.49
1:RA:774:A:H2'	1:RA:774:A:N3	2.27	0.49
2:RB:96:U:OP2	21:RZ:14:LYS:NZ	2.46	0.49
7:RH:137:ASP:HB3	7:RH:140:LYS:HB3	1.94	0.49
16:RU:49:HIS:HA	16:RU:52:ARG:HB3	1.95	0.49
32:XA:1035:A:H2'	32:XA:1036:G:C8	2.47	0.49
44:XM:96:LEU:C	44:XM:110:ARG:HG2	2.33	0.49
1:YA:607:U:OP1	5:YF:102:PRO:HA	2.13	0.49
32:QA:542:G:H5'	35:QD:41:GLY:HA3	1.94	0.49
41:QJ:40:LEU:HB2	41:QJ:69:ASN:HB2	1.95	0.49
41:QJ:30:SER:OG	41:QJ:81:THR:HG22	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1266:G:O5'	18:RW:15:ARG:NH2	2.45	0.49
1:RA:154(B):C:H42	1:RA:171:G:H1	1.61	0.49
1:RA:2206:G:H8	1:RA:2207:G:N7	2.11	0.49
19:RX:53:LYS:HB3	19:RX:82:GLN:HB3	1.93	0.49
32:XA:995:C:H1'	45:XN:4:LYS:HE2	1.94	0.49
23:Y1:64:ALA:HA	23:Y1:67:ILE:HG13	1.94	0.49
26:Y4:59:PHE:CA	26:Y4:61:ARG:H	2.12	0.49
1:YA:1069:A:O2'	1:YA:1072:C:OP1	2.27	0.49
1:YA:2119:A:N6	1:YA:2168:G:H21	2.10	0.49
1:YA:2162:G:O3'	1:YA:2172:U:O2'	2.28	0.49
1:YA:2864:G:OP1	15:YT:119:LYS:HE3	2.13	0.49
32:QA:1441:G:O2'	32:QA:1460:A:N6	2.46	0.49
33:QB:162:ILE:O	33:QB:185:ILE:HG12	2.13	0.49
40:QI:24:GLY:HA2	40:QI:59:PHE:O	2.13	0.49
1:RA:1889:A:O2'	1:RA:2087:G:H5'	2.12	0.49
1:RA:721:C:H2'	1:RA:722:A:C8	2.48	0.49
1:RA:1693:U:O2'	3:RD:14:ARG:NH2	2.46	0.49
12:RQ:55:VAL:HG12	12:RQ:64:ILE:HD12	1.95	0.49
20:RY:6:HIS:HE1	20:RY:72:VAL:O	1.95	0.49
32:XA:1435:G:H2'	32:XA:1436:U:C6	2.48	0.49
32:XA:512:U:H2'	32:XA:513:C:C6	2.48	0.49
35:XD:25:ARG:NH1	35:XD:30:LYS:O	2.45	0.49
36:XE:6:PHE:HB2	36:XE:34:VAL:HG13	1.94	0.49
55:XY:107:ASP:O	55:XY:173:GLY:N	2.35	0.49
55:XY:228:ARG:HD3	55:XY:238:ASN:O	2.12	0.49
1:YA:300:A:H2'	1:YA:334:C:H1'	1.93	0.49
8:YI:114:LEU:HD12	8:YI:116:LEU:HB2	1.95	0.49
32:QA:1305:G:N2	32:QA:1331:G:H1'	2.28	0.49
32:QA:426:G:OP1	35:QD:38:TYR:OH	2.24	0.49
36:QE:8:GLU:OE2	36:QE:63:ARG:NH2	2.46	0.49
1:RA:1569:A:H2'	1:RA:1570:A:C8	2.48	0.49
1:RA:2343:C:O2'	1:RA:2373:G:O2'	2.14	0.49
32:XA:1403:C:H1'	32:XA:1500:A:N1	2.28	0.49
32:XA:189(M):G:H2'	32:XA:190:U:C6	2.48	0.49
32:XA:457:C:H2'	32:XA:458:C:H6	1.78	0.49
35:XD:116:GLN:NE2	35:XD:157:LEU:HD11	2.27	0.49
40:XI:31:GLN:HG3	40:XI:36:TYR:HB2	1.95	0.49
32:XA:36:C:OP1	43:XL:123:LYS:HE2	2.13	0.49
1:YA:2836:U:H2'	1:YA:2837:G:C8	2.48	0.49
1:YA:922:U:H2'	1:YA:923:C:C6	2.48	0.49
16:YU:92:ARG:HA	16:YU:95:LEU:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:890:G:O2'	32:QA:906:G:O6	2.28	0.48
33:QB:115:LEU:HD12	33:QB:142:LEU:HD12	1.94	0.48
35:QD:106:TYR:HE2	35:QD:107:ARG:HH11	1.61	0.48
36:QE:74:GLY:HA3	36:QE:116:THR:HG22	1.95	0.48
1:RA:1045:A:H4'	1:RA:1046:A:C5'	2.44	0.48
1:RA:826:U:H2'	1:RA:828:U:O4'	2.13	0.48
14:RS:48:LEU:HD23	14:RS:82:ILE:HD11	1.95	0.48
19:RX:5:TYR:O	24:R2:36:ARG:NH2	2.42	0.48
32:XA:1129:C:H2'	32:XA:1139:G:N7	2.28	0.48
32:XA:1346:A:OP1	40:XI:120:ARG:NH1	2.34	0.48
55:XY:123:GLU:CG	55:XY:188:PRO:HB3	2.43	0.48
26:Y4:40:HIS:HB3	26:Y4:43:TYR:CD1	2.48	0.48
1:YA:1525:G:H2'	1:YA:1526:G:C8	2.48	0.48
1:YA:2389:G:H5''	1:YA:2390:U:O4'	2.13	0.48
1:YA:1971:A:C4	3:YD:241:PRO:HD3	2.48	0.48
4:YE:119:ARG:HD3	4:YE:120:TRP:NE1	2.28	0.48
6:YG:115:ARG:HG3	6:YG:136:ARG:HH21	1.78	0.48
9:YN:108:PRO:O	9:YN:113:GLY:HA3	2.13	0.48
1:RA:214:G:H1'	1:RA:216:A:O2'	2.13	0.48
4:RE:178:GLU:H	4:RE:178:GLU:CD	2.15	0.48
32:XA:149:A:H2'	32:XA:150:C:C6	2.48	0.48
34:XC:125:GLU:OE1	34:XC:190:ARG:NH1	2.46	0.48
26:Y4:48:ARG:HG3	26:Y4:52:THR:HG23	1.93	0.48
1:YA:272(E):U:H2'	1:YA:272(F):C:C6	2.48	0.48
1:YA:438:G:H2'	1:YA:440:G:C8	2.48	0.48
1:YA:1826:G:H4'	3:YD:242:ARG:CZ	2.43	0.48
32:QA:184:G:H2'	32:QA:185:A:H8	1.78	0.48
51:QT:63:ILE:HG21	51:QT:81:LYS:HG3	1.96	0.48
1:RA:2704:C:H2'	1:RA:2705:A:O4'	2.13	0.48
1:RA:539:G:H2'	1:RA:540:C:H6	1.78	0.48
15:RT:35:LYS:HD3	15:RT:40:THR:HG22	1.94	0.48
40:XI:31:GLN:HB2	40:XI:35:GLU:HG2	1.95	0.48
43:XL:117:ARG:HG2	43:XL:122:THR:HB	1.96	0.48
1:YA:1053:C:H2'	1:YA:1054:A:C8	2.49	0.48
1:YA:2321:G:O2'	1:YA:2322:A:OP1	2.23	0.48
5:YF:185:ASP:OD1	5:YF:188:ARG:NH1	2.46	0.48
10:YO:38:VAL:HG13	10:YO:87:ILE:HD11	1.94	0.48
32:QA:115:G:H4'	32:QA:116:A:O5'	2.13	0.48
32:QA:184:G:H2'	32:QA:185:A:C8	2.49	0.48
35:QD:25:ARG:NH1	35:QD:30:LYS:O	2.47	0.48
51:QT:42:GLN:NE2	51:QT:46:GLU:OE2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:R2:65:ASN:OD1	24:R2:69:ARG:NH1	2.40	0.48
1:RA:2466:C:OP1	31:R9:4:ARG:HB2	2.13	0.48
1:RA:1259:G:H2'	1:RA:1260:G:H8	1.78	0.48
1:RA:2142:C:H2'	1:RA:2143:C:C6	2.48	0.48
1:RA:856:C:H2'	1:RA:857:C:C6	2.49	0.48
4:RE:119:ARG:HH21	4:RE:158:GLY:N	2.11	0.48
11:RP:100:LEU:HD12	11:RP:112:LEU:HD11	1.95	0.48
14:RS:20:ARG:HD3	14:RS:20:ARG:O	2.12	0.48
21:RZ:198:LYS:HB2	21:RZ:203:GLU:HA	1.96	0.48
32:XA:715:A:H2'	32:XA:716:A:C8	2.48	0.48
33:XB:145:LEU:HD12	33:XB:149:LEU:HD12	1.95	0.48
1:YA:1404:C:H2'	1:YA:1405:U:H6	1.78	0.48
7:YH:56:SER:OG	7:YH:58:GLU:HG2	2.13	0.48
11:YP:98:GLU:N	11:YP:98:GLU:OE1	2.40	0.48
20:YY:99:CYS:SG	20:YY:100:ALA:N	2.87	0.48
21:YZ:10:ARG:NH2	21:YZ:26:GLY:O	2.43	0.48
32:QA:1003:G:C2'	32:QA:1004:A:H4'	2.44	0.48
32:QA:1068:G:H8	32:QA:1068:G:OP2	1.96	0.48
32:QA:1359:C:H4'	32:QA:1362:C:H41	1.79	0.48
32:QA:49:U:C2	32:QA:361:G:N2	2.82	0.48
47:QP:17:TYR:HE2	47:QP:41:PRO:HG3	1.78	0.48
53:QV:16:C:O2'	53:QV:61:C:OP1	2.27	0.48
1:RA:1250:G:N7	11:RP:18:ARG:NH2	2.61	0.48
1:RA:2023:G:H4'	1:RA:2617:C:O3'	2.14	0.48
1:RA:764:A:O4'	3:RD:213:ARG:HG3	2.13	0.48
9:RN:58:ASP:N	9:RN:58:ASP:OD1	2.47	0.48
35:XD:64:LEU:HB2	35:XD:198:VAL:HG11	1.95	0.48
7:YH:159:GLU:HG3	7:YH:169:VAL:HG11	1.95	0.48
18:YW:29:LEU:HD22	18:YW:69:LEU:HD12	1.96	0.48
32:QA:1187:G:H4'	40:QI:111:ARG:NH1	2.28	0.48
40:QI:3:GLN:OE1	40:QI:20:ARG:NH2	2.29	0.48
37:QF:97:PHE:HB2	49:QR:32:ARG:HH11	1.79	0.48
49:QR:33:ASP:OD2	49:QR:36:ASN:HB2	2.13	0.48
1:RA:1021:A:O2'	1:RA:1123:C:OP1	2.20	0.48
1:RA:1721:G:N1	1:RA:1739:U:OP2	2.46	0.48
4:RE:119:ARG:HG3	4:RE:160:TYR:HB2	1.94	0.48
11:RP:86:LYS:HB3	11:RP:118:GLY:HA3	1.95	0.48
14:RS:27:SER:HA	14:RS:88:ASP:HB3	1.94	0.48
32:XA:1003:G:H3'	32:XA:1003:G:N3	2.29	0.48
32:XA:1258:G:H2'	32:XA:1259:C:C6	2.48	0.48
32:XA:1442(A):G:H2'	32:XA:1442(A):G:N3	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:473:G:OP2	47:XP:75:ARG:HD3	2.14	0.48
32:XA:444:C:H42	32:XA:490:G:H1	1.61	0.48
53:XV:17:C:H5	53:XV:17(A):U:C5	2.32	0.48
53:XV:20:U:H2'	53:XV:21:A:H5'	1.95	0.48
21:YZ:198:LYS:CE	53:XV:52:G:H2'	2.37	0.48
1:YA:626:U:O4	11:YP:107:LYS:HE2	2.13	0.48
8:YI:72:LEU:HD21	8:YI:107:VAL:HG11	1.95	0.48
18:YW:14:PRO:HG2	18:YW:78:GLU:HG3	1.95	0.48
32:QA:1183:A:O2'	32:QA:1184:G:OP1	2.28	0.48
32:QA:1291:G:OP1	38:QG:37:ASN:ND2	2.47	0.48
32:QA:750:G:O2'	46:QO:22:THR:O	2.21	0.48
1:RA:464:U:H2'	1:RA:465:G:O4'	2.14	0.48
1:RA:796:C:H2'	1:RA:797:C:C6	2.48	0.48
42:XK:27:ASN:OD1	42:XK:28:THR:N	2.46	0.48
1:YA:1364:G:N7	23:Y1:3:LYS:HD2	2.29	0.48
1:YA:1091:G:N3	1:YA:1091:G:H2'	2.28	0.48
1:YA:1636:C:H2'	1:YA:1637:A:C8	2.48	0.48
1:YA:1669:A:O2'	1:YA:2549:G:H5'	2.12	0.48
1:YA:572:A:H2'	1:YA:573:G:O4'	2.14	0.48
1:YA:652(U):C:H2'	1:YA:652(V):G:C8	2.49	0.48
32:QA:1179:A:OP2	40:QI:93:ARG:NH2	2.47	0.48
32:QA:186:C:H2'	32:QA:187:C:C6	2.49	0.48
32:QA:266:G:H2'	32:QA:266:G:N3	2.29	0.48
55:QY:172:TYR:CE1	55:QY:207:PRO:HD3	2.49	0.48
1:RA:2602:A:C5	55:QY:237:VAL:HG23	2.49	0.48
1:RA:93:G:H2'	1:RA:94(A):C:C6	2.48	0.48
18:RW:4:LYS:HG2	18:RW:5:ALA:N	2.29	0.48
32:XA:407:G:OP1	35:XD:115:ARG:NH2	2.37	0.48
1:YA:1645:G:H5''	1:YA:1646:C:H5'	1.94	0.48
1:YA:1991:U:H2'	1:YA:1992:G:H5''	1.95	0.48
32:QA:1479:C:H2'	32:QA:1480:G:H8	1.79	0.48
32:QA:176:C:H2'	32:QA:177:C:C6	2.49	0.48
32:QA:520:A:N1	32:QA:536:C:H1'	2.29	0.48
33:QB:96:ARG:HG2	33:QB:98:LEU:HD23	1.96	0.48
1:RA:1022:G:C5	1:RA:1140:C:C4	3.01	0.48
1:RA:1639:U:C2'	1:RA:1640:C:H5''	2.43	0.48
1:RA:2296:U:OP2	14:RS:9:ARG:NH2	2.42	0.48
3:RD:2:ALA:N	3:RD:200:ASP:OD2	2.47	0.48
34:XC:22:TRP:CD1	34:XC:59:ARG:HD2	2.49	0.48
1:YA:1411:C:H2'	1:YA:1412:A:C8	2.49	0.48
1:YA:751:A:H5'	18:YW:90:ARG:HA	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:YH:55:PRO:HG2	7:YH:61:HIS:ND1	2.29	0.48
1:YA:272(P):C:H5''	8:YI:45:LYS:HD2	1.95	0.48
13:YR:63:ARG:O	13:YR:67:LEU:HB2	2.13	0.48
55:QY:191:GLU:OE2	55:QY:193:GLN:HB2	2.14	0.48
1:RA:265:A:N1	1:RA:427:U:O2'	2.39	0.48
1:RA:721:C:H2'	1:RA:722:A:H8	1.79	0.48
1:RA:754:C:H2'	1:RA:755:C:H6	1.79	0.48
32:XA:1250:A:H2	32:XA:1353:G:H21	1.62	0.48
32:XA:804:U:H5''	32:XA:805:C:OP2	2.13	0.48
46:XO:17:ARG:HD3	46:XO:26:GLU:OE2	2.14	0.48
29:Y7:10:ARG:HG2	29:Y7:14:LYS:HD3	1.96	0.48
1:YA:1493:C:C5	1:YA:2206:G:H2'	2.49	0.48
1:YA:2591:C:H2'	1:YA:2592:G:C8	2.48	0.48
1:YA:614(A):U:H5'	1:YA:614(D):A:N6	2.28	0.48
1:YA:998:C:OP2	16:YU:92:ARG:NH2	2.46	0.48
4:YE:170:LEU:HD23	4:YE:184:VAL:HG11	1.96	0.48
9:YN:4:TYR:CD2	16:YU:100:VAL:HG11	2.48	0.48
12:YQ:68:ILE:HD13	12:YQ:103:MET:HE3	1.96	0.48
32:QA:107:G:H2'	32:QA:108:G:O4'	2.14	0.47
32:QA:486:U:H2'	32:QA:487:A:H8	1.79	0.47
32:QA:744:C:O2'	32:QA:851:G:N2	2.47	0.47
26:R4:41:PRO:HG3	26:R4:49:PHE:CE1	2.49	0.47
1:RA:2572:A:C8	4:RE:144:ARG:HD2	2.49	0.47
10:RO:8:LEU:HD22	10:RO:82:ASN:HB3	1.96	0.47
34:XC:137:ALA:HA	34:XC:140:ARG:HH11	1.79	0.47
40:XI:23:ASN:H	40:XI:23:ASN:HD22	1.62	0.47
40:XI:23:ASN:OD1	40:XI:25:LYS:HE2	2.14	0.47
1:YA:1405:U:H2'	1:YA:1406:U:C6	2.49	0.47
1:YA:459:U:H2'	1:YA:460:A:H8	1.79	0.47
32:QA:973:G:H3'	32:QA:974:A:H5''	1.95	0.47
32:QA:992:U:H4'	32:QA:993:G:H5'	1.95	0.47
39:QH:73:ASP:OD1	39:QH:75:ARG:HG3	2.15	0.47
31:R9:27:CYS:SG	31:R9:28:GLU:N	2.87	0.47
1:RA:1084:A:H3'	1:RA:1085:A:H4'	1.96	0.47
1:RA:2150:U:H2'	1:RA:2151:G:C8	2.49	0.47
2:RB:66:A:N6	2:RB:109:C:H5''	2.27	0.47
21:RZ:129:SER:HB3	21:RZ:132:ASN:HB2	1.95	0.47
32:XA:1179:A:H2'	32:XA:1180:A:O4'	2.14	0.47
32:XA:148:G:H2'	32:XA:149:A:C8	2.49	0.47
32:XA:741:G:H2'	32:XA:742:G:O4'	2.14	0.47
55:XY:258:GLN:HG3	55:XY:258:GLN:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:YP:62:LEU:O	30:Y8:13:ARG:HD3	2.14	0.47
1:YA:1028:A:N3	1:YA:2486:G:O2'	2.39	0.47
1:YA:1053:C:H2'	1:YA:1054:A:H8	1.79	0.47
1:YA:154(B):C:H42	1:YA:171:G:H1	1.62	0.47
1:YA:1798:U:H5'	3:YD:259:THR:CG2	2.39	0.47
1:YA:276:A:H5''	1:YA:277:C:H5'	1.96	0.47
3:YD:177:LEU:HD11	3:YD:183:ARG:HD3	1.96	0.47
1:YA:2032:G:H1'	4:YE:145:LYS:HD3	1.97	0.47
5:YF:53:THR:HG22	5:YF:56:GLU:OE2	2.13	0.47
32:QA:1329:A:N7	52:QU:7:ARG:NH2	2.61	0.47
32:QA:1492:A:H8	55:QY:119:THR:CG2	2.27	0.47
32:QA:262:A:C6	32:QA:263:A:C6	3.02	0.47
33:QB:78:GLN:OE1	33:QB:95:GLN:NE2	2.47	0.47
35:QD:60:GLU:HG3	35:QD:202:LEU:HD12	1.96	0.47
42:QK:62:GLN:HB2	42:QK:93:GLN:HG3	1.96	0.47
50:QS:41:VAL:HG22	50:QS:42:PRO:HD2	1.96	0.47
55:QY:244:ILE:HD12	55:QY:267:LYS:HB2	1.96	0.47
1:RA:1313:U:H2'	1:RA:1610:A:C2	2.49	0.47
1:RA:273(A):G:N7	1:RA:421:U:H2'	2.29	0.47
1:RA:747:U:O2	1:RA:2014:A:H1'	2.14	0.47
5:RF:184:TYR:O	5:RF:188:ARG:HG3	2.14	0.47
9:RN:96:GLU:HB2	9:RN:122:VAL:HG12	1.97	0.47
1:YA:1165:U:H2'	1:YA:1166:C:C6	2.48	0.47
1:YA:1812:A:O2'	3:YD:45:ASN:N	2.44	0.47
20:YY:6:HIS:HE1	20:YY:72:VAL:O	1.97	0.47
32:QA:1062:U:H2'	32:QA:1063:C:C6	2.49	0.47
34:QC:124:ILE:HD12	34:QC:196:LEU:HD12	1.96	0.47
32:QA:1232:U:H5''	40:QI:124:GLN:O	2.13	0.47
40:QI:25:LYS:HA	40:QI:25:LYS:HD3	1.59	0.47
1:RA:1091:G:H2'	1:RA:1091:G:N3	2.30	0.47
1:RA:251:A:C5	1:RA:252:G:H1'	2.50	0.47
1:RA:2646:C:H2'	1:RA:2647:U:O4'	2.14	0.47
34:XC:19:GLU:HB3	34:XC:40:ARG:NH2	2.29	0.47
38:XG:45:ASP:O	38:XG:49:ILE:HG13	2.14	0.47
32:XA:750:G:N3	46:XO:23:GLY:HA3	2.29	0.47
32:XA:108:G:C6	51:XT:15:ARG:HG2	2.49	0.47
26:Y4:15:ILE:HD12	26:Y4:21:VAL:HG22	1.97	0.47
1:YA:1055:G:H2'	1:YA:1056:G:O4'	2.15	0.47
1:YA:1164:G:H2'	1:YA:1165:U:C6	2.50	0.47
1:YA:11:G:C2'	1:YA:12:U:H5'	2.44	0.47
5:YF:157:VAL:HB	5:YF:194:MET:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:838:G:H5'	32:QA:839:U:OP2	2.14	0.47
37:QF:11:ASN:HB3	37:QF:14:LEU:HG	1.95	0.47
32:QA:1347:G:O6	40:QI:10:ARG:NH2	2.47	0.47
30:R8:23:VAL:HG13	30:R8:47:LYS:HB3	1.96	0.47
1:RA:1002:G:H2'	1:RA:1003:G:O4'	2.15	0.47
1:RA:2180:U:H2'	1:RA:2181:G:C8	2.50	0.47
1:RA:2648:C:H2'	1:RA:2649:U:H6	1.78	0.47
1:RA:725:G:C6	1:RA:726:G:N1	2.83	0.47
1:RA:2751:G:C8	7:RH:2:SER:HA	2.50	0.47
15:RT:108:ARG:HA	15:RT:111:ARG:NH1	2.29	0.47
32:XA:1151:A:O2'	32:XA:1152:A:O5'	2.28	0.47
32:XA:1239:A:H62	32:XA:1299:A:H62	1.61	0.47
34:XC:6:HIS:HE1	34:XC:8:ILE:HB	1.79	0.47
35:XD:148:VAL:HG11	35:XD:158:ILE:HG21	1.96	0.47
36:XE:74:GLY:HA3	36:XE:116:THR:HG22	1.96	0.47
11:YP:63:PRO:HD3	30:Y8:27:THR:HG22	1.96	0.47
1:YA:1065:U:H4'	1:YA:1066:U:C5'	2.45	0.47
1:YA:1101:U:H2'	1:YA:1102:C:C6	2.49	0.47
1:YA:774:A:N3	1:YA:774:A:H2'	2.30	0.47
16:YU:46:ALA:O	16:YU:50:ARG:HG3	2.14	0.47
17:YV:52:VAL:HG23	17:YV:55:ALA:HB3	1.97	0.47
32:QA:737:A:H2'	32:QA:738:C:C6	2.50	0.47
32:QA:974:A:OP1	32:QA:974:A:H8	1.97	0.47
33:QB:167:PRO:HG3	33:QB:186:ALA:HB1	1.96	0.47
36:QE:110:LEU:HD13	36:QE:118:ILE:HG21	1.97	0.47
1:RA:1721:G:H8	1:RA:1741:A:H62	1.62	0.47
1:RA:2128:C:H5'	1:RA:2129:C:OP2	2.15	0.47
1:RA:2512:C:H2'	1:RA:2513:G:O4'	2.14	0.47
1:RA:2805:G:H2'	1:RA:2807:G:C8	2.49	0.47
1:RA:330:A:N7	1:RA:1210:A:O2'	2.33	0.47
32:XA:164:U:H2'	32:XA:165:C:C6	2.50	0.47
32:XA:49:U:C2	32:XA:361:G:N2	2.83	0.47
32:XA:784:C:H2'	32:XA:785:G:O4'	2.15	0.47
34:XC:137:ALA:HA	34:XC:140:ARG:NH1	2.30	0.47
55:XY:108:GLU:HA	55:XY:170:GLY:CA	2.44	0.47
55:XY:269:LYS:O	55:XY:273:VAL:HG23	2.15	0.47
1:YA:1899:G:N3	1:YA:1899:G:H2'	2.30	0.47
1:YA:2342:C:O2'	1:YA:2374:C:H5''	2.14	0.47
1:YA:2687:U:H2'	1:YA:2688:U:O4'	2.13	0.47
1:YA:2716:U:H2'	1:YA:2717:G:H8	1.80	0.47
1:YA:2735:G:N2	1:YA:2769:C:O2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:QY:228:ARG:HD3	55:QY:238:ASN:O	2.15	0.47
1:RA:2051:A:H5'	1:RA:2578:G:O4'	2.14	0.47
4:RE:101:ARG:HD2	4:RE:169:ASN:O	2.14	0.47
32:XA:1512:U:H2'	32:XA:1513:A:H8	1.80	0.47
27:Y5:48:GLU:O	27:Y5:60:VAL:HG11	2.15	0.47
1:YA:1070:A:H2'	1:YA:1071:G:C8	2.50	0.47
1:YA:1084:A:H3'	1:YA:1085:A:C4'	2.45	0.47
1:YA:662:G:H5'	11:YP:14:LYS:O	2.15	0.47
3:YD:108:PRO:HD2	3:YD:111:LEU:HD12	1.96	0.47
32:QA:1333:A:H2'	32:QA:1334:G:O4'	2.15	0.47
32:QA:418:C:H2'	32:QA:419:C:C6	2.50	0.47
32:QA:555:C:H2'	32:QA:556:C:C6	2.50	0.47
32:QA:562:C:H1'	43:QL:15:ARG:HD2	1.96	0.47
44:QM:15:VAL:HG12	44:QM:45:VAL:HG22	1.96	0.47
44:QM:4:ILE:HD12	44:QM:57:ARG:HA	1.96	0.47
1:RA:2153:G:H2'	1:RA:2154:G:C8	2.49	0.47
1:RA:588:U:H2'	1:RA:589:C:C6	2.50	0.47
1:RA:8:A:H2'	1:RA:9:U:C6	2.49	0.47
3:RD:61:LEU:O	3:RD:63:ARG:NH1	2.48	0.47
13:RR:95:THR:HG22	13:RR:116:LEU:HD23	1.97	0.47
32:XA:1036:G:H2'	32:XA:1037:C:O4'	2.14	0.47
15:YT:39:ARG:NH2	32:XA:345:C:OP2	2.29	0.47
32:XA:691:G:H1'	32:XA:696:A:N6	2.30	0.47
32:XA:902:G:H2'	32:XA:903:G:H8	1.79	0.47
32:XA:1366:C:HO2'	41:XJ:60:ARG:HH22	1.56	0.47
47:XP:59:TRP:HA	47:XP:62:VAL:HG12	1.97	0.47
55:XY:287:GLN:HA	55:XY:290:GLU:HB2	1.95	0.47
29:Y7:12:ARG:NH2	29:Y7:44:PRO:HB3	2.30	0.47
1:YA:1271:G:C2	1:YA:1617:C:H4'	2.50	0.47
1:YA:2298:A:H62	1:YA:2318:G:H8	1.57	0.47
1:YA:975(B):G:H1'	1:YA:990:A:C2	2.50	0.47
3:YD:108:PRO:HG2	3:YD:111:LEU:HG	1.95	0.47
32:QA:1151:A:O2'	32:QA:1152:A:H8	1.98	0.47
23:R1:53:VAL:HG22	23:R1:74:VAL:HG13	1.97	0.47
1:RA:1796:U:H2'	1:RA:1797:C:H6	1.79	0.47
1:RA:2022:U:O2'	1:RA:2617:C:H5'	2.14	0.47
9:RN:97:ARG:HA	9:RN:100:GLU:HB2	1.97	0.47
35:XD:79:PHE:CE1	35:XD:204:ILE:HD13	2.50	0.47
32:XA:922:G:H4'	36:XE:20:GLN:HA	1.96	0.47
33:XB:178:ARG:HH22	39:XH:74:PRO:HB3	1.79	0.47
26:Y4:48:ARG:HB3	26:Y4:52:THR:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:248:G:H5'	1:YA:250:G:N7	2.29	0.47
4:YE:143:ASN:HD22	4:YE:147:PRO:HD3	1.80	0.47
6:YG:7:LEU:HD23	6:YG:100:TRP:HE3	1.78	0.47
8:YI:4:ILE:HD11	8:YI:44:LEU:HD12	1.97	0.47
32:QA:632:A:H5'	32:QA:633:G:OP2	2.14	0.47
44:QM:80:ARG:HG2	44:QM:80:ARG:HH11	1.80	0.47
47:QP:50:LYS:HD3	47:QP:50:LYS:HA	1.64	0.47
1:RA:2742:C:OP1	31:R9:35:ARG:HD3	2.15	0.47
11:RP:138:LEU:HD23	11:RP:145:PRO:HB3	1.95	0.47
12:RQ:38:GLU:HG3	12:RQ:127:ILE:HB	1.96	0.47
14:RS:66:ALA:O	14:RS:69:VAL:HG22	2.15	0.47
15:RT:37:GLY:HA2	15:RT:38:ASN:HA	1.67	0.47
21:RZ:203:GLU:C	53:QV:53:G:H4'	2.36	0.47
32:XA:583:A:H2'	32:XA:584:G:O4'	2.15	0.47
21:YZ:198:LYS:HE2	53:XV:52:G:C2	2.50	0.47
1:YA:1364:G:C8	23:Y1:3:LYS:HD2	2.49	0.47
1:YA:2109:U:H2'	1:YA:2110:G:C8	2.50	0.47
1:YA:2119:A:H61	1:YA:2168:G:N2	2.12	0.47
1:YA:2272:U:H5''	1:YA:2273:A:OP1	2.14	0.47
1:YA:723:G:H2'	1:YA:724:U:O4'	2.15	0.47
1:YA:1814:G:H4'	3:YD:51:VAL:HG21	1.96	0.47
1:YA:443:A:N7	5:YF:45:ARG:HG2	2.30	0.47
6:YG:120:LEU:HB3	6:YG:131:TYR:OH	2.15	0.47
17:YV:14:VAL:HB	17:YV:96:ILE:HG13	1.96	0.47
32:QA:1255:G:P	41:QJ:45:ARG:HH22	2.38	0.47
32:QA:164:U:H2'	32:QA:165:C:C6	2.50	0.47
32:QA:77:G:H2'	32:QA:78:G:H5'	1.96	0.47
41:QJ:57:LYS:HE2	41:QJ:60:ARG:NH2	2.29	0.47
55:QY:120:GLY:HA3	55:QY:124:ALA:HB2	1.97	0.47
1:RA:2128:C:N3	1:RA:2160:G:N2	2.59	0.47
1:RA:2712(A):U:H1'	1:RA:2712(B):A:C8	2.50	0.47
8:RI:38:LEU:HB2	8:RI:40:THR:HG23	1.96	0.47
15:RT:16:ARG:HD3	15:RT:19:LEU:HG	1.96	0.47
33:XB:17:PHE:HD1	33:XB:18:GLY:N	2.07	0.47
33:XB:201:ILE:HG21	33:XB:214:ILE:HG21	1.97	0.47
36:XE:78:HIS:HA	39:XH:105:ARG:HG3	1.96	0.47
1:YA:1316:U:H2'	1:YA:1317:A:C8	2.50	0.47
1:YA:1379:A:H4'	1:YA:1380:G:OP2	2.13	0.47
1:YA:1479:G:H1'	1:YA:1558:A:OP1	2.14	0.47
1:YA:2641:G:P	9:YN:74:ARG:HH12	2.38	0.47
32:QA:1218:C:H2'	32:QA:1219:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:QB:55:PHE:HD1	33:QB:58:ILE:HD12	1.80	0.46
37:QF:97:PHE:HB2	49:QR:32:ARG:NH1	2.31	0.46
1:RA:1504:C:H2'	1:RA:1505:C:C6	2.50	0.46
1:RA:36:G:N3	1:RA:450:G:O2'	2.46	0.46
20:RY:13:VAL:HG12	20:RY:74:PRO:HA	1.97	0.46
32:XA:110:C:H2'	32:XA:111:G:O4'	2.15	0.46
33:XB:9:GLU:HG3	33:XB:10:LEU:H	1.81	0.46
33:XB:16:HIS:O	33:XB:18:GLY:N	2.48	0.46
40:X1:8:GLY:HA3	40:X1:76:ALA:O	2.15	0.46
1:YA:2884:U:H2'	1:YA:2885:C:O4'	2.15	0.46
10:YO:63:VAL:HG12	10:YO:106:LEU:HD11	1.97	0.46
33:QB:115:LEU:O	33:QB:119:GLU:HG2	2.15	0.46
33:QB:163:PHE:CD1	33:QB:185:ILE:HG13	2.50	0.46
24:R2:35:LEU:HD12	24:R2:53:LEU:HD12	1.97	0.46
1:RA:1913:A:N7	32:QA:1493:A:O2'	2.45	0.46
1:RA:956:G:H2'	1:RA:957:A:H2'	1.97	0.46
32:XA:1101:A:H4'	32:XA:1102:A:O5'	2.15	0.46
46:XO:5:LYS:O	46:XO:9:GLN:HG2	2.15	0.46
1:YA:1021:A:H3'	1:YA:1021:A:N3	2.30	0.46
1:YA:1292:U:H2'	1:YA:1293:C:C6	2.50	0.46
1:YA:1423:G:OP1	1:YA:1492:G:O2'	2.31	0.46
1:YA:1637:A:H4'	1:YA:2711:A:O2'	2.16	0.46
1:YA:2849:U:H4'	1:YA:2868:A:C2	2.51	0.46
32:QA:1101:A:H4'	32:QA:1102:A:O5'	2.15	0.46
32:QA:1286:A:H2'	32:QA:1287:A:H4'	1.96	0.46
34:QC:188:LEU:HD23	34:QC:190:ARG:HH11	1.81	0.46
39:QH:82:HIS:NE2	39:QH:84:ARG:HG2	2.30	0.46
42:QK:20:TYR:HB2	42:QK:31:THR:HG23	1.97	0.46
43:QL:83:VAL:HG13	43:QL:100:ILE:HG23	1.97	0.46
1:RA:1388:G:H4'	1:RA:1525:G:O2'	2.14	0.46
1:RA:2134:A:C5	1:RA:2157:G:H5'	2.51	0.46
1:RA:26:G:C6	1:RA:27:G:N1	2.83	0.46
1:RA:686:G:N2	1:RA:788:A:H61	2.14	0.46
3:RD:132:PRO:HG3	3:RD:190:TYR:CE1	2.51	0.46
8:RI:130:TYR:HB3	8:RI:138:ILE:HB	1.96	0.46
12:RQ:75:THR:HG21	12:RQ:87:LYS:NZ	2.31	0.46
32:XA:1342:C:H2'	32:XA:1343:G:H8	1.80	0.46
32:XA:1504:G:OP1	32:XA:1507:A:H4'	2.15	0.46
33:XB:163:PHE:CE1	33:XB:185:ILE:HG22	2.51	0.46
1:YA:1048:A:N6	1:YA:2751:G:H1	2.14	0.46
1:YA:1359:A:N1	1:YA:1372:U:O4	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1598:C:H2'	1:YA:1599:C:H6	1.81	0.46
1:YA:2142:C:H2'	1:YA:2143:C:C6	2.51	0.46
1:YA:919:G:N2	1:YA:2269:A:OP2	2.48	0.46
1:YA:2629:A:H1'	1:YA:2630:G:H5''	1.98	0.46
1:YA:2683:C:OP1	15:YT:53:ARG:NH2	2.47	0.46
1:YA:857:C:OP1	22:Y0:77:ARG:NH2	2.38	0.46
4:YE:94:GLU:OE2	4:YE:177:PRO:HB3	2.16	0.46
32:QA:1239:A:H62	32:QA:1299:A:N6	2.13	0.46
35:QD:190:ASP:HB2	35:QD:193:ASP:OD2	2.15	0.46
53:QV:51:C:H2'	53:QV:52:G:O4'	2.16	0.46
1:RA:1430:C:H2'	1:RA:1431:U:C6	2.51	0.46
1:RA:143(B):C:H2'	1:RA:144:C:H6	1.81	0.46
1:RA:1916:A:H2'	1:RA:1917:PSU:O4'	2.15	0.46
32:XA:1030(D):G:H2'	32:XA:1030(E):A:C8	2.51	0.46
32:XA:1499:A:H1'	32:XA:1520:G:H5'	1.98	0.46
32:XA:1518:MA6:H8	32:XA:1518:MA6:O5'	2.14	0.46
32:XA:257:G:H2'	32:XA:258:G:O4'	2.16	0.46
41:XJ:25:GLU:O	41:XJ:29:ARG:HG2	2.15	0.46
55:XY:242:SER:CA	55:XY:263:GLN:HB3	2.36	0.46
1:YA:273(A):G:N7	1:YA:421:U:H2'	2.29	0.46
32:QA:486:U:H2'	32:QA:487:A:C8	2.50	0.46
32:QA:501:C:H2'	32:QA:502:G:C8	2.50	0.46
32:QA:657:G:O2'	46:QO:23:GLY:HA2	2.15	0.46
33:QB:69:LEU:HD13	33:QB:91:PRO:HB2	1.97	0.46
24:R2:64:LEU:HD21	24:R2:68:ARG:HE	1.80	0.46
1:RA:1379:A:H4'	1:RA:1380:G:OP2	2.16	0.46
1:RA:1625:C:H2'	1:RA:1626:G:O4'	2.15	0.46
32:XA:727:G:N2	32:XA:730:G:OP2	2.47	0.46
44:XM:80:ARG:NH2	50:XS:65:ASN:O	2.49	0.46
1:YA:2593:U:H2'	1:YA:2594:C:C6	2.51	0.46
1:YA:813:U:H2'	1:YA:814:C:C6	2.50	0.46
32:QA:976:G:N2	32:QA:1363(A):C:OP2	2.38	0.46
35:QD:148:VAL:HG11	35:QD:158:ILE:HD12	1.97	0.46
36:QE:33:VAL:HG13	36:QE:112:LEU:HD12	1.98	0.46
39:QH:51:VAL:HG21	39:QH:60:ARG:HH11	1.81	0.46
50:QS:27:GLU:CB	50:QS:28:LYS:HG3	2.46	0.46
53:QV:76:A:H3'	55:QY:234:GLY:HA3	1.96	0.46
26:R4:46:GLN:O	26:R4:48:ARG:N	2.48	0.46
1:RA:2420:C:OP1	30:R8:34:TRP:HB3	2.16	0.46
1:RA:1263:U:C4	1:RA:1264:G:C6	3.03	0.46
1:RA:2304:G:H22	1:RA:2312:U:H3	1.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:RG:5:VAL:HG12	26:R4:25:TYR:HE1	1.81	0.46
8:RI:90:GLY:O	8:RI:121:LYS:HE2	2.15	0.46
13:RR:29:LEU:HB3	13:RR:75:LEU:HD21	1.96	0.46
21:RZ:198:LYS:HE2	53:QV:53:G:O4'	2.16	0.46
32:XA:1002:G:N3	32:XA:1003:G:C8	2.84	0.46
32:XA:1030(A):C:N3	32:XA:1031:G:N2	2.63	0.46
33:XB:7:VAL:O	33:XB:217:ARG:NE	2.39	0.46
34:XC:8:ILE:HD12	34:XC:16:ARG:HD3	1.98	0.46
55:XY:175:LEU:O	55:XY:205:VAL:HG21	2.15	0.46
1:YA:1803:A:H4'	3:YD:259:THR:HG23	1.98	0.46
1:YA:1188:U:H4'	17:YV:79:VAL:HG22	1.97	0.46
33:QB:124:SER:HA	33:QB:125:PRO:HA	1.68	0.46
37:QF:37:VAL:HA	37:QF:65:VAL:HG12	1.97	0.46
32:QA:1492:A:H4'	43:QL:47:LYS:HZ1	1.80	0.46
1:RA:2397:G:H5''	23:R1:28:GLY:HA2	1.98	0.46
28:R6:35:GLU:HG2	28:R6:50:ARG:HD3	1.98	0.46
31:R9:24:TYR:CE2	31:R9:35:ARG:HG3	2.50	0.46
1:RA:1038:C:N4	1:RA:1117:G:H1	2.06	0.46
1:RA:1127:A:N7	1:RA:2488:A:O2'	2.43	0.46
1:RA:1530:C:H1'	1:RA:1531:C:OP1	2.16	0.46
1:RA:2119:A:N6	1:RA:2168:G:H21	2.13	0.46
1:RA:2802:G:H2'	1:RA:2803:C:O4'	2.16	0.46
9:RN:4:TYR:CD2	16:RU:100:VAL:HG11	2.50	0.46
32:XA:1376:U:H2'	32:XA:1377:A:H8	1.80	0.46
32:XA:540:G:H2'	32:XA:541:G:O4'	2.16	0.46
34:XC:114:PRO:O	34:XC:118:GLN:HG3	2.16	0.46
48:XQ:41:LYS:HZ3	48:XQ:92:ARG:HH21	1.64	0.46
55:XY:176:LYS:HE3	55:XY:177:PHE:CZ	2.50	0.46
1:YA:1065:U:H4'	1:YA:1066:U:H5'	1.97	0.46
1:YA:1525:G:H2'	1:YA:1526:G:H8	1.80	0.46
1:YA:2347:C:OP1	28:Y6:38:LYS:NZ	2.26	0.46
9:YN:58:ASP:N	9:YN:58:ASP:OD1	2.49	0.46
33:QB:114:ARG:HD2	33:QB:114:ARG:HA	1.84	0.46
32:QA:1492:A:H1'	54:QX:20:A:O2'	2.15	0.46
55:QY:244:ILE:H	55:QY:266:ASN:ND2	2.14	0.46
30:R8:62:LEU:HB3	30:R8:65:GLU:HG2	1.96	0.46
1:RA:1036:G:H1	1:RA:1119:C:H42	1.64	0.46
1:RA:1087:G:H2'	1:RA:1088:A:H5'	1.96	0.46
1:RA:1155:A:H5''	16:RU:55:ARG:HD3	1.98	0.46
1:RA:2291:U:O2'	1:RA:2374:C:O2	2.34	0.46
1:RA:2376:A:H2'	1:RA:2377:A:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:239:U:H2'	1:RA:240:G:O4'	2.16	0.46
1:RA:2507:C:H5''	1:RA:2573:C:N4	2.30	0.46
1:RA:2774:C:H2'	1:RA:2775:A:O4'	2.15	0.46
1:RA:878:A:H3'	1:RA:879:G:H8	1.78	0.46
32:XA:114:U:H1'	32:XA:353:A:H1'	1.97	0.46
32:XA:1218:C:H2'	32:XA:1219:U:C6	2.51	0.46
32:XA:1309:G:OP1	44:XM:88:ARG:HD3	2.15	0.46
32:XA:265:G:H2'	32:XA:267:C:H5	1.80	0.46
1:YA:1056:G:H5''	1:YA:1057:A:H5'	1.97	0.46
1:YA:183:C:N4	1:YA:213:A:H61	2.13	0.46
1:YA:2079:U:H2'	1:YA:2080:G:O4'	2.15	0.46
1:YA:876:C:H2'	1:YA:877:U:O4'	2.16	0.46
7:YH:28:GLY:HA3	7:YH:79:VAL:HB	1.98	0.46
11:YP:100:LEU:HD22	11:YP:105:LEU:HD12	1.97	0.46
32:QA:1054:C:O2	32:QA:1196:U:O2'	2.33	0.46
32:QA:992:U:H2'	32:QA:1043:C:H41	1.79	0.46
46:QO:82:ILE:O	46:QO:86:GLY:N	2.48	0.46
32:QA:187:C:H5''	51:QT:86:ARG:HG3	1.98	0.46
53:QV:43:A:H2'	53:QV:44:A:C8	2.51	0.46
30:R8:23:VAL:HG11	30:R8:47:LYS:HD3	1.97	0.46
30:R8:50:LEU:HD23	30:R8:50:LEU:HA	1.79	0.46
1:RA:2477:C:N4	31:R9:10:ILE:HG12	2.31	0.46
1:RA:1104:C:H2'	1:RA:1105:U:C6	2.51	0.46
1:RA:2690:C:N4	1:RA:2713:A:H1'	2.31	0.46
1:RA:2680:C:H5'	4:RE:189:PRO:HA	1.98	0.46
20:RY:99:CYS:SG	20:RY:100:ALA:N	2.89	0.46
32:XA:632:A:H5'	32:XA:633:G:OP2	2.16	0.46
34:XC:130:VAL:HG21	34:XC:157:ILE:HG23	1.97	0.46
30:Y8:63:PRO:HG2	30:Y8:64:TYR:CE2	2.51	0.46
1:YA:2262:U:H4'	1:YA:2328:A:C2	2.51	0.46
1:YA:2704:C:H2'	1:YA:2705:A:O4'	2.16	0.46
1:YA:456:C:O2'	19:YX:68:ARG:NH1	2.44	0.46
1:YA:740:U:H2'	1:YA:741:G:H8	1.81	0.46
1:YA:752:A:OP1	29:Y7:3:ARG:NH2	2.42	0.46
1:YA:960:A:C8	1:YA:962:G:C8	3.04	0.46
18:YW:97:LYS:HE2	18:YW:99:ARG:NH2	2.31	0.46
32:QA:1143:G:H2'	32:QA:1144:G:C8	2.51	0.46
32:QA:946:A:O2'	32:QA:1333:A:N3	2.41	0.46
32:QA:222:U:H2'	32:QA:223:U:C6	2.51	0.46
33:QB:98:LEU:O	33:QB:101:MET:HG3	2.16	0.46
42:QK:84:VAL:HG11	42:QK:91:ARG:HD2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1067:A:H4'	1:RA:1068:G:OP2	2.11	0.46
1:RA:1073:A:O2'	1:RA:1074:G:O5'	2.34	0.46
1:RA:1097:U:H2'	1:RA:1097:U:O2	2.15	0.46
1:RA:1341:U:OP2	1:RA:1394:U:O2'	2.21	0.46
1:RA:1495:A:H2'	1:RA:1496:A:C8	2.50	0.46
1:RA:1588:C:H2'	1:RA:1589:C:C6	2.51	0.46
3:RD:206:LEU:HD22	3:RD:211:ARG:HD2	1.98	0.46
12:RQ:30:GLY:HA2	12:RQ:107:ALA:HB2	1.98	0.46
32:XA:266:G:O2'	32:XA:267:C:OP2	2.30	0.46
1:YA:1587:A:H2'	1:YA:1588:C:C6	2.51	0.46
1:YA:2321:G:HO2'	1:YA:2322:A:P	2.35	0.46
1:YA:2390:U:P	30:Y8:35:GLN:HE22	2.39	0.46
1:YA:2805:G:H2'	1:YA:2807:G:C8	2.51	0.46
32:QA:1036:G:H5''	32:QA:1037:C:C5	2.52	0.45
32:QA:431:A:H2'	32:QA:432:A:O4'	2.17	0.45
33:QB:160:ASP:OD1	33:QB:160:ASP:N	2.49	0.45
32:QA:1106:G:H5''	34:QC:172:ARG:HG2	1.97	0.45
50:QS:12:ASP:O	50:QS:14:HIS:N	2.42	0.45
55:QY:222:LEU:HD23	55:QY:248:HIS:HA	1.98	0.45
31:R9:2:LYS:NZ	31:R9:31:LYS:O	2.37	0.45
1:RA:1657:C:H2'	1:RA:1658:C:C6	2.51	0.45
1:RA:573:G:O2'	1:RA:574:C:H3'	2.15	0.45
1:RA:634:C:H2'	1:RA:635:C:C6	2.51	0.45
1:RA:78:A:H2'	1:RA:79:G:C8	2.51	0.45
1:RA:9:U:HO2'	1:RA:10:G:P	2.39	0.45
21:RZ:109:ALA:HB3	21:RZ:145:GLU:OE1	2.16	0.45
55:XY:227:PHE:CE2	55:XY:245:ARG:HD3	2.51	0.45
1:YA:2611:U:C4	27:Y5:3:LYS:HG2	2.50	0.45
5:YF:20:LEU:CD2	5:YF:21:ALA:H	2.28	0.45
7:YH:8:PRO:C	7:YH:69:ARG:HH12	2.19	0.45
32:QA:580:U:H2'	32:QA:581:G:O4'	2.16	0.45
32:QA:786:G:H2'	32:QA:787:A:O4'	2.16	0.45
34:QC:88:ARG:NH2	34:QC:101:LEU:O	2.50	0.45
28:R6:6:ARG:NH1	28:R6:26:ASN:HB2	2.30	0.45
1:RA:1179:C:H2'	1:RA:1180:C:C6	2.51	0.45
1:RA:768:G:O2'	1:RA:1379:A:N1	2.37	0.45
1:RA:1930:G:N2	1:RA:1968:G:H2'	2.32	0.45
1:RA:1942:5MC:H4'	55:QY:257:CYS:SG	2.55	0.45
1:RA:827:U:O2	1:RA:2246:G:H4'	2.16	0.45
19:RX:2:LYS:NZ	19:RX:38:GLU:OE2	2.38	0.45
32:XA:31:G:O2'	32:XA:48:C:N4	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:XB:16:HIS:HB2	33:XB:204:ASN:HB3	1.97	0.45
35:XD:163:GLU:O	35:XD:166:LYS:HG2	2.16	0.45
47:XP:17:TYR:HE1	47:XP:41:PRO:HG3	1.82	0.45
1:YA:195:A:OP1	11:YP:46:LYS:NZ	2.40	0.45
1:YA:2689:U:H4'	1:YA:2690:C:H5'	1.97	0.45
1:YA:2756:U:OP2	31:Y9:19:ARG:NH2	2.48	0.45
1:YA:277:C:H1'	1:YA:278:A:P	2.56	0.45
4:YE:51:PHE:O	4:YE:77:ILE:N	2.45	0.45
28:R6:6:ARG:NE	28:R6:24:GLU:OE1	2.43	0.45
1:RA:2224:G:H4'	1:RA:2226:C:C2	2.50	0.45
1:RA:2390:U:O2'	1:RA:2391:G:H5'	2.16	0.45
1:RA:2629:A:H1'	1:RA:2630:G:H5''	1.98	0.45
3:RD:148:GLU:HB2	3:RD:151:LYS:HD2	1.99	0.45
4:RE:7:VAL:HG13	4:RE:27:LEU:HB3	1.98	0.45
8:RI:133:HIS:ND1	8:RI:134:PRO:O	2.49	0.45
15:RT:11:GLU:O	15:RT:15:VAL:HG23	2.16	0.45
17:RV:40:LEU:HB2	17:RV:46:VAL:HG12	1.98	0.45
1:RA:751:A:H5'	18:RW:90:ARG:HA	1.98	0.45
32:XA:1029:C:N4	32:XA:1030(A):C:H41	2.14	0.45
44:XM:97:PRO:N	44:XM:110:ARG:HG2	2.31	0.45
34:XC:12:LEU:HD11	45:XN:51:GLY:HA2	1.98	0.45
26:Y4:15:ILE:HB	26:Y4:32:TYR:CD1	2.52	0.45
1:YA:2832:U:O4	1:YA:2883:A:H5''	2.16	0.45
1:YA:857:C:N4	1:YA:858:U:O4	2.49	0.45
32:QA:1297:C:O2'	38:QG:114:ARG:NH2	2.50	0.45
33:QB:16:HIS:CG	33:QB:17:PHE:N	2.84	0.45
37:QF:61:LEU:HD23	37:QF:63:TYR:OH	2.17	0.45
1:RA:2357:U:P	22:R0:20:ARG:HH11	2.40	0.45
26:R4:34:GLU:H	26:R4:34:GLU:HG2	1.41	0.45
1:RA:1557:C:H5''	1:RA:1558:A:OP2	2.17	0.45
1:RA:1907:G:C6	1:RA:1908:C:C4	3.04	0.45
1:RA:2552:2MU:C2	1:RA:2554:U:H5'	2.46	0.45
5:RF:110:LEU:HD23	5:RF:110:LEU:HA	1.77	0.45
5:RF:178:PRO:HB2	5:RF:201:VAL:CG2	2.47	0.45
32:XA:1237:C:O3'	32:XA:1300:G:N2	2.45	0.45
32:XA:142:G:H2'	32:XA:143:A:C8	2.50	0.45
32:XA:187:C:H2'	32:XA:188:C:H6	1.82	0.45
1:YA:1092:C:H6	1:YA:1092:C:OP2	1.99	0.45
1:YA:1041:C:N4	1:YA:1114:G:H1	2.10	0.45
1:YA:70:G:H5''	1:YA:112:U:O2	2.17	0.45
1:YA:2261:C:OP1	22:Y0:19:LYS:NZ	2.36	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:492:A:H2'	1:YA:493:G:O4'	2.15	0.45
1:YA:779:U:OP1	3:YD:49:ILE:HG13	2.16	0.45
32:QA:629:G:H2'	32:QA:630:G:O4'	2.17	0.45
34:QC:148:GLY:HA3	34:QC:172:ARG:O	2.16	0.45
32:QA:1316:G:H5''	45:QN:17:LYS:NZ	2.32	0.45
31:R9:25:VAL:O	31:R9:33:LYS:HA	2.17	0.45
1:RA:1223:G:N2	1:RA:1226:A:OP2	2.44	0.45
1:RA:1418:G:H8	1:RA:1418:G:O5'	1.99	0.45
1:RA:1490:A:O2'	3:RD:99:ASP:OD1	2.34	0.45
1:RA:184:C:H2'	1:RA:185:U:C6	2.51	0.45
1:RA:2133:G:N2	1:RA:2157:G:H2'	2.31	0.45
1:RA:2810:A:N6	1:RA:2891:G:O2'	2.39	0.45
1:RA:27:G:O2'	1:RA:28:A:OP2	2.30	0.45
1:RA:1826:G:H4'	3:RD:242:ARG:CZ	2.46	0.45
3:RD:242:ARG:HD3	3:RD:242:ARG:N	2.31	0.45
3:RD:72:LYS:HG3	3:RD:103:ARG:HH22	1.81	0.45
18:RW:18:ARG:NH1	18:RW:76:VAL:O	2.49	0.45
35:XD:10:ARG:HB2	35:XD:40:PRO:HG3	1.99	0.45
26:Y4:61:ARG:NH2	50:XS:9:VAL:HG11	2.32	0.45
1:YA:1112:G:H2'	1:YA:1112:G:N3	2.31	0.45
1:YA:1493:C:N4	1:YA:2206:G:O2'	2.49	0.45
1:YA:1638:C:H2'	1:YA:1639:U:O4'	2.16	0.45
5:YF:150:GLY:HA2	5:YF:172:TRP:CD2	2.52	0.45
8:YI:50:ARG:O	8:YI:54:GLN:HG2	2.17	0.45
32:QA:1060:C:C5	34:QC:2:GLY:HA3	2.52	0.45
33:QB:178:ARG:NH2	33:QB:198:ASP:OD1	2.49	0.45
37:QF:19:LEU:HD11	37:QF:59:TYR:CE2	2.52	0.45
42:QK:27:ASN:OD1	42:QK:28:THR:N	2.49	0.45
1:RA:2643:G:H2'	1:RA:2644:G:O4'	2.17	0.45
5:RF:10:PRO:HB3	5:RF:17:ARG:HE	1.80	0.45
2:RB:41:U:H5	6:RG:70:VAL:O	1.99	0.45
16:RU:92:ARG:HA	16:RU:95:LEU:HB2	1.99	0.45
32:XA:625:G:H4'	47:XP:16:HIS:CD2	2.52	0.45
36:XE:110:LEU:HD13	36:XE:118:ILE:HG21	1.98	0.45
40:XI:6:GLY:HA3	40:XI:83:ARG:HB2	1.97	0.45
41:XJ:57:LYS:HE3	41:XJ:60:ARG:NH2	2.31	0.45
43:XL:57:LYS:HD3	43:XL:65:GLU:OE2	2.15	0.45
51:XT:57:ARG:HH12	51:XT:100:ILE:HB	1.81	0.45
1:YA:1050:A:H2'	1:YA:1051:G:C8	2.50	0.45
1:YA:2306:C:C4	1:YA:2307:G:C6	3.05	0.45
1:YA:2808:U:H5''	1:YA:2891:G:O6	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:YD:19:ALA:HB2	3:YD:204:ILE:HD11	1.99	0.45
4:YE:120:TRP:CD1	4:YE:155:LYS:HB3	2.51	0.45
4:YE:35:GLN:OE1	4:YE:66:HIS:HE1	1.99	0.45
1:YA:674:G:H1'	5:YF:74:ARG:HD3	1.99	0.45
32:QA:1201:A:H1'	32:QA:1202:G:OP2	2.16	0.45
32:QA:411:A:OP2	35:QD:25:ARG:NH2	2.50	0.45
46:QO:21:ASP:OD1	46:QO:24:SER:HB3	2.17	0.45
1:RA:1030:G:OP2	12:RQ:128:LYS:NZ	2.38	0.45
1:RA:1889:A:N1	1:RA:2234:G:H1'	2.32	0.45
1:RA:2695:C:H2'	1:RA:2696:U:C6	2.52	0.45
1:RA:329:G:OP1	1:RA:329:G:H8	2.00	0.45
8:RI:72:LEU:C	8:RI:74:ASN:H	2.20	0.45
10:RO:10:VAL:HG21	10:RO:16:ALA:HB3	1.99	0.45
12:RQ:34:LEU:HB2	12:RQ:118:LEU:HD22	1.99	0.45
13:RR:44:LEU:HD22	13:RR:48:VAL:HG23	1.99	0.45
32:XA:1270:C:O2'	32:XA:1314:C:H5'	2.16	0.45
36:XE:78:HIS:ND1	39:XH:104:ARG:HD2	2.31	0.45
1:YA:530:G:N1	1:YA:2023:G:OP1	2.35	0.45
1:YA:2128:C:H5'	1:YA:2129:C:OP2	2.16	0.45
1:YA:2716:U:H2'	1:YA:2717:G:C8	2.52	0.45
3:YD:12:SER:HB3	3:YD:208:LYS:HB3	1.99	0.45
1:YA:2572:A:N7	4:YE:144:ARG:HD3	2.30	0.45
6:YG:170:ARG:NH2	6:YG:182:LYS:O	2.49	0.45
12:YQ:109:VAL:HG13	12:YQ:113:GLN:HB2	1.98	0.45
41:QJ:44:VAL:HG13	41:QJ:66:ARG:HD2	1.99	0.45
47:QP:59:TRP:HA	47:QP:62:VAL:HG12	1.98	0.45
55:QY:308:ARG:HD2	55:QY:310:TYR:OH	2.17	0.45
27:R5:8:LYS:O	27:R5:9:LYS:HD2	2.16	0.45
1:RA:676:A:H1'	1:RA:2443:C:H1'	1.99	0.45
20:RY:9:LYS:HA	20:RY:10:GLY:HA2	1.67	0.45
32:XA:1023:G:H3'	32:XA:1024:G:H8	1.81	0.45
32:XA:1227:A:N3	50:XS:83:HIS:HB3	2.32	0.45
32:XA:1366:C:O2'	41:XJ:60:ARG:NH2	2.33	0.45
32:XA:814:A:H2'	32:XA:816:A:H5''	1.99	0.45
32:XA:958:A:N3	32:XA:985:C:O2'	2.44	0.45
38:XG:12:LEU:HD12	38:XG:12:LEU:H	1.82	0.45
53:XV:40:C:H2'	53:XV:41:C:H6	1.81	0.45
55:XY:133:ARG:HG3	55:XY:134:MET:CE	2.47	0.45
55:XY:230:SER:OG	55:XY:258:GLN:NE2	2.49	0.45
55:XY:322:ILE:HG21	55:XY:347:GLU:CD	2.36	0.45
1:YA:2331:G:O2'	22:Y0:43:THR:HG22	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1411:C:H2'	1:YA:1412:A:H8	1.82	0.45
1:YA:1581:G:H2'	1:YA:1582:C:O4'	2.17	0.45
1:YA:2137:C:H1'	1:YA:2154:G:H22	1.82	0.45
1:YA:392:C:H5''	1:YA:409:C:H5''	1.98	0.45
1:YA:428:A:OP2	1:YA:428:A:H8	2.00	0.45
1:YA:478:A:C6	1:YA:480:A:C6	3.05	0.45
16:YU:108:GLU:O	16:YU:112:ARG:HG2	2.17	0.45
32:QA:1146:A:H5'	32:QA:1147:C:OP2	2.17	0.45
32:QA:438:G:N1	32:QA:495:A:OP2	2.35	0.45
32:QA:946:A:H2'	32:QA:947:G:C8	2.52	0.45
37:QF:23:LYS:NZ	37:QF:42:GLU:OE2	2.36	0.45
38:QG:70:LYS:O	38:QG:138:LYS:HE2	2.16	0.45
55:QY:214:LEU:H	55:QY:215:PRO:CD	2.30	0.45
1:RA:1378:A:P	29:R7:10:ARG:HH22	2.40	0.45
1:RA:2321:G:HO2'	1:RA:2322:A:P	2.39	0.45
1:RA:568:U:H5'	1:RA:945:A:N6	2.31	0.45
5:RF:150:GLY:HA2	5:RF:172:TRP:CD2	2.51	0.45
10:RO:26:LYS:O	10:RO:30:ALA:HB2	2.17	0.45
34:XC:8:ILE:HD12	34:XC:16:ARG:CD	2.47	0.45
39:XH:42:GLU:HG3	39:XH:109:ILE:HD13	1.98	0.45
45:XN:3:ARG:HG2	45:XN:3:ARG:HH21	1.82	0.45
47:XP:4:ILE:O	47:XP:66:PRO:HA	2.17	0.45
55:XY:112:PHE:O	55:XY:205:VAL:HA	2.17	0.45
55:XY:183:ARG:CZ	55:XY:309:THR:HG21	2.46	0.45
1:YA:1166:C:H2'	1:YA:1167:U:C6	2.52	0.45
1:YA:142(B):C:H2'	1:YA:143(A):G:O4'	2.16	0.45
1:YA:827:U:O2'	1:YA:2068:U:C2	2.67	0.45
1:YA:615:G:OP1	5:YF:40:GLN:NE2	2.36	0.45
1:YA:818:G:H4'	1:YA:838:C:O3'	2.17	0.45
2:YB:73:A:C4	2:YB:105:A:C2	3.05	0.45
7:YH:4:ILE:O	7:YH:69:ARG:HG2	2.17	0.45
18:YW:79:GLY:HA3	18:YW:100:THR:HG22	1.98	0.45
42:QK:79:SER:HA	42:QK:104:GLN:HB2	1.99	0.45
1:RA:2127:G:H2'	1:RA:2128:C:O4'	2.17	0.45
1:RA:856:C:O2'	1:RA:857:C:OP1	2.26	0.45
3:RD:142:VAL:HG23	3:RD:193:VAL:HA	1.99	0.45
1:RA:2786:U:O2'	4:RE:62:PRO:O	2.29	0.45
8:RI:140:LEU:HD22	8:RI:142:VAL:HG22	1.99	0.45
32:XA:1519:MA6:O5'	32:XA:1519:MA6:H8	2.16	0.45
32:XA:397:A:H3'	32:XA:397:A:N3	2.32	0.45
32:XA:730:G:C5	32:XA:731:G:H1'	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:XB:189:ASP:HB3	33:XB:205:ASP:H	1.81	0.45
33:XB:224:GLN:HA	33:XB:228:GLY:O	2.17	0.45
32:XA:1349:A:H5''	40:XI:121:ARG:HB2	1.99	0.45
1:YA:2557:G:H4'	55:XY:245:ARG:NH2	2.32	0.45
1:YA:1028:A:N6	1:YA:1125:G:H2'	2.32	0.45
1:YA:1063:G:N3	1:YA:1063:G:H2'	2.32	0.45
1:YA:1557:C:H5''	1:YA:1558:A:OP2	2.17	0.45
1:YA:190:A:N3	1:YA:679:C:O2'	2.47	0.45
1:YA:320:A:H4'	1:YA:322:A:N7	2.31	0.45
1:YA:738:G:C2	1:YA:759:G:C5	3.05	0.45
5:YF:10:PRO:HB3	5:YF:17:ARG:NE	2.23	0.45
21:YZ:91:LEU:HG	21:YZ:130:PRO:HG3	1.99	0.45
21:YZ:33:LEU:HD21	21:YZ:90:VAL:HG11	1.98	0.45
32:QA:179:A:H2'	32:QA:180:U:C6	2.52	0.44
32:QA:339:C:H2'	32:QA:340:U:C6	2.52	0.44
32:QA:433:C:H2'	32:QA:434:U:H6	1.82	0.44
35:QD:178:VAL:HG12	35:QD:179:GLU:H	1.82	0.44
51:QT:18:GLN:O	51:QT:22:ARG:HG3	2.17	0.44
55:QY:319:ASP:OD2	55:QY:344:ILE:HG12	2.16	0.44
1:RA:1075:C:C2'	1:RA:1076:C:H5'	2.48	0.44
1:RA:1790:C:H2'	1:RA:1791:A:C5	2.52	0.44
1:RA:2336:A:H61	22:R0:43:THR:HG22	1.81	0.44
1:RA:2355:C:H1'	22:R0:39:ARG:NH2	2.29	0.44
32:XA:1469:G:H2'	32:XA:1470:G:H8	1.82	0.44
41:XJ:11:PHE:CE1	41:XJ:67:THR:HG22	2.51	0.44
1:YA:184:C:H2'	1:YA:185:U:H6	1.82	0.44
1:YA:330:A:HO2'	1:YA:331:A:H8	1.65	0.44
11:YP:70:GLN:N	11:YP:70:GLN:OE1	2.50	0.44
21:YZ:118:GLN:N	21:YZ:173:ALA:O	2.49	0.44
32:QA:1223:C:H5''	32:QA:1224:G:H5''	2.00	0.44
32:QA:159:G:H2'	32:QA:161:A:OP2	2.17	0.44
34:QC:9:GLY:HA2	34:QC:12:LEU:HG	1.98	0.44
55:QY:227:PHE:CE2	55:QY:245:ARG:HD2	2.52	0.44
1:RA:1607:C:H4'	1:RA:1608:A:O5'	2.18	0.44
1:RA:228:A:H8	1:RA:229:A:H5'	1.81	0.44
1:RA:2298:A:H62	1:RA:2318:G:H8	1.63	0.44
10:RO:7:TYR:O	10:RO:8:LEU:HD23	2.17	0.44
16:RU:46:ALA:O	16:RU:50:ARG:HG3	2.16	0.44
32:XA:189(L):U:H2'	32:XA:189(M):G:C8	2.52	0.44
32:XA:688:G:H2'	32:XA:689:C:H6	1.82	0.44
32:XA:921:U:O2'	36:XE:19:MET:O	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:XK:84:VAL:HG11	42:XK:91:ARG:HD2	1.98	0.44
1:YA:2364:C:OP1	22:Y0:55:ARG:NH1	2.50	0.44
1:YA:2119:A:O2'	1:YA:2120:G:H5'	2.17	0.44
1:YA:236:C:H2'	1:YA:237:C:C6	2.53	0.44
1:YA:2630:G:H2'	1:YA:2631:G:C8	2.52	0.44
1:YA:518:G:H2'	1:YA:519:U:C6	2.52	0.44
6:YG:11:TYR:OH	6:YG:33:ARG:HG2	2.17	0.44
11:YP:101:VAL:HA	11:YP:106:LEU:O	2.18	0.44
17:YV:72:VAL:HG13	17:YV:85:LYS:HB3	2.00	0.44
20:YY:37:VAL:HG21	20:YY:72:VAL:HG21	1.99	0.44
32:QA:551:U:H2'	32:QA:552:U:C6	2.52	0.44
32:QA:786:G:C2	32:QA:797:C:C2	3.05	0.44
32:QA:1060:C:C4	34:QC:2:GLY:HA3	2.51	0.44
35:QD:155:LEU:O	35:QD:159:ARG:HG3	2.17	0.44
35:QD:79:PHE:HE1	35:QD:204:ILE:HD13	1.82	0.44
36:QE:137:GLU:OE1	36:QE:140:ARG:HD2	2.18	0.44
40:QI:22:GLY:HA3	40:QI:60:ASP:OD1	2.17	0.44
32:QA:186:C:O2'	51:QT:85:MET:SD	2.66	0.44
25:R3:3:ARG:HH11	25:R3:60:GLU:CD	2.20	0.44
25:R3:59:VAL:O	25:R3:60:GLU:HG2	2.17	0.44
8:RI:9:LEU:HA	8:RI:9:LEU:HD13	1.86	0.44
32:XA:1004:A:H5'	32:XA:1025:U:C5	2.51	0.44
32:XA:1164:G:H1	32:XA:1172:C:H42	1.63	0.44
32:XA:1315:U:H2'	32:XA:1316:G:O4'	2.17	0.44
32:XA:1372:U:H2'	32:XA:1373:G:O4'	2.18	0.44
32:XA:1513:A:H2'	32:XA:1514:C:C6	2.52	0.44
43:XL:32:PHE:HD2	43:XL:86:ARG:HB3	1.82	0.44
54:XX:20:A:N6	55:XY:190:THR:O	2.50	0.44
1:YA:1057:A:O2'	1:YA:1058:G:OP1	2.27	0.44
1:YA:1036:G:H1	1:YA:1119:C:H42	1.66	0.44
1:YA:1268:A:H2'	1:YA:1269:A:O4'	2.18	0.44
1:YA:1278:A:OP1	13:YR:36:THR:HG23	2.17	0.44
1:YA:2165:G:H2'	1:YA:2166:G:O4'	2.16	0.44
1:YA:460:A:H2'	1:YA:461:C:O4'	2.17	0.44
1:YA:910:A:C6	1:YA:911:A:C6	3.05	0.44
6:YG:36:LYS:HD3	6:YG:95:ARG:NH1	2.32	0.44
7:YH:20:ALA:HB1	7:YH:21:PRO:HD2	2.00	0.44
32:QA:1225:A:H2'	32:QA:1226:C:C5	2.53	0.44
32:QA:627:G:H2'	32:QA:628:G:H8	1.81	0.44
33:QB:166:ASP:HB3	33:QB:169:LYS:HB3	2.00	0.44
33:QB:80:ILE:HD11	33:QB:212:GLN:HB2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:QC:181:ASN:HB3	34:QC:205:GLY:O	2.17	0.44
36:QE:50:GLU:HB2	36:QE:53:LEU:HD13	1.98	0.44
47:QP:19:ILE:HD11	47:QP:74:LEU:HD11	1.99	0.44
50:QS:20:LEU:HD23	50:QS:23:ASN:HD22	1.82	0.44
1:RA:459:U:H4'	29:R7:40:TRP:CZ3	2.52	0.44
1:RA:2134:A:H8	1:RA:2156:G:H21	1.64	0.44
1:RA:68:G:H2'	1:RA:69:C:O4'	2.18	0.44
1:RA:760:G:H2'	1:RA:761:A:O4'	2.18	0.44
2:RB:66:A:H61	2:RB:108:U:H2'	1.81	0.44
6:RG:115:ARG:HB3	6:RG:136:ARG:HH22	1.82	0.44
33:XB:28:PHE:O	33:XB:32:ILE:HG13	2.18	0.44
39:XH:46:LYS:HG3	39:XH:64:LYS:HB2	1.98	0.44
55:XY:349:GLN:O	55:XY:353:LEU:N	2.41	0.44
1:YA:1053:C:O2'	1:YA:1054:A:OP1	2.29	0.44
1:YA:323:G:C8	5:YF:171:PRO:HG3	2.52	0.44
5:YF:101:LEU:HD12	5:YF:102:PRO:HD2	1.99	0.44
1:YA:272(P):C:HO2'	8:YI:42:SER:HG	1.39	0.44
26:R4:58:ARG:HD2	50:QS:68:GLY:H	1.83	0.44
54:QX:14:A:N3	54:QX:14:A:H2'	2.31	0.44
55:QY:349:GLN:O	55:QY:353:LEU:HG	2.17	0.44
1:RA:1178:C:P	1:RA:1178:C:H6	2.41	0.44
1:RA:1866:C:H2'	1:RA:1876:A:O4'	2.18	0.44
1:RA:2029:G:H2'	1:RA:2031:A:OP1	2.16	0.44
1:RA:2516:G:C6	1:RA:2517:C:N4	2.86	0.44
1:RA:78:A:H2'	1:RA:79:G:H8	1.82	0.44
1:RA:1803:A:O2'	3:RD:259:THR:HG21	2.17	0.44
19:RX:35:THR:HB	19:RX:38:GLU:HB2	2.00	0.44
1:RA:84:A:H5''	20:RY:8:LYS:HE2	1.98	0.44
32:XA:828:A:H2'	32:XA:829:G:O4'	2.17	0.44
36:XE:137:GLU:OE1	36:XE:141:GLN:NE2	2.50	0.44
40:XI:53:VAL:HG11	40:XI:92:TYR:CE1	2.52	0.44
26:Y4:58:ARG:HD3	50:XS:65:ASN:O	2.18	0.44
1:YA:1496:A:N3	1:YA:1577:C:O2'	2.41	0.44
1:YA:2180:U:H2'	1:YA:2181:G:C8	2.51	0.44
11:YP:97:PRO:HD3	11:YP:126:VAL:O	2.17	0.44
12:YQ:11:LYS:HE2	12:YQ:88:GLY:O	2.18	0.44
13:YR:95:THR:HG22	13:YR:116:LEU:HD23	2.00	0.44
32:QA:1442(A):G:N3	32:QA:1442(A):G:H2'	2.32	0.44
32:QA:363:A:OP1	43:QL:33:ARG:HD3	2.18	0.44
32:QA:501:C:H2'	32:QA:502:G:H8	1.81	0.44
34:QC:50:ALA:HB1	34:QC:70:VAL:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:QD:156:GLU:O	35:QD:160:GLN:HG2	2.17	0.44
51:QT:101:GLY:HA2	51:QT:102:GLY:HA2	1.66	0.44
53:QV:15:G:H21	53:QV:21:A:H1'	1.82	0.44
24:R2:65:ASN:O	24:R2:69:ARG:HG3	2.17	0.44
1:RA:1045:A:H4'	1:RA:1046:A:H5'	1.99	0.44
1:RA:2342:C:O2'	1:RA:2374:C:H5''	2.18	0.44
1:RA:620:G:N3	1:RA:620:G:H5'	2.32	0.44
1:RA:807:U:OP2	11:RP:41:ARG:NH2	2.51	0.44
5:RF:12:LEU:HD13	5:RF:124:LEU:HD11	1.99	0.44
12:RQ:59:ARG:HG2	12:RQ:59:ARG:HH11	1.83	0.44
16:RU:76:TYR:CZ	16:RU:80:ILE:HG13	2.53	0.44
21:RZ:125:LEU:HB3	21:RZ:165:VAL:HG13	1.99	0.44
21:RZ:91:LEU:HD12	21:RZ:91:LEU:HA	1.84	0.44
32:XA:1151:A:O2'	32:XA:1152:A:H8	2.01	0.44
32:XA:933:G:O6	38:XG:3:ARG:NH2	2.49	0.44
44:XM:4:ILE:HD11	44:XM:60:VAL:HG11	1.99	0.44
22:Y0:23:VAL:HG22	22:Y0:38:VAL:HG22	1.99	0.44
6:YG:113:ARG:NH2	26:Y4:33:VAL:HG12	2.24	0.44
26:Y4:59:PHE:HA	26:Y4:60:GLN:C	2.38	0.44
30:Y8:52:LYS:O	30:Y8:56:GLU:HG3	2.17	0.44
1:YA:1025:G:C4	1:YA:1135:C:H1'	2.53	0.44
1:YA:2070:G:H2'	1:YA:2071:A:C8	2.53	0.44
1:YA:2115:G:N2	1:YA:2171:A:H61	2.14	0.44
1:YA:2712(A):U:O2'	1:YA:2712(B):A:P	2.76	0.44
10:YO:68:GLU:HB3	10:YO:78:ARG:HB2	2.00	0.44
32:QA:297:G:N2	32:QA:300:A:OP2	2.43	0.44
32:QA:7:G:H5''	32:QA:298:A:O4'	2.18	0.44
34:QC:32:LEU:HD22	34:QC:59:ARG:NH1	2.32	0.44
38:QG:113:GLU:HG3	38:QG:118:VAL:HG12	2.00	0.44
39:QH:121:ASP:N	39:QH:121:ASP:OD1	2.51	0.44
1:RA:2573:C:N4	55:QY:238:ASN:O	2.50	0.44
1:RA:2507:C:H5''	1:RA:2573:C:H41	1.83	0.44
4:RE:116:VAL:HG13	4:RE:122:PHE:HB2	2.00	0.44
15:RT:28:VAL:HG13	15:RT:86:ILE:HG23	1.99	0.44
21:RZ:5:LEU:HD11	21:RZ:44:PHE:HD1	1.83	0.44
32:XA:865:A:H2	32:XA:918:A:H4'	1.82	0.44
33:XB:174:VAL:O	33:XB:178:ARG:HG2	2.18	0.44
34:XC:148:GLY:HA3	34:XC:172:ARG:O	2.18	0.44
32:XA:410:G:P	35:XD:30:LYS:HZ1	2.40	0.44
40:XI:26:VAL:HA	40:XI:61:ALA:O	2.18	0.44
42:XK:48:ILE:HD13	42:XK:48:ILE:HA	1.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:XS:62:ILE:HA	50:XS:66:MET:SD	2.57	0.44
55:XY:114:GLU:HG2	55:XY:163:ILE:HG23	2.00	0.44
22:Y0:26:TYR:O	22:Y0:29:GLN:HB2	2.18	0.44
26:Y4:61:ARG:NH2	50:XS:9:VAL:HG21	2.30	0.44
1:YA:247:G:H4'	1:YA:386:G:C5	2.53	0.44
1:YA:632:A:H2'	1:YA:633:A:C8	2.53	0.44
4:YE:112:GLY:O	4:YE:159:HIS:HA	2.17	0.44
7:YH:12:PRO:O	7:YH:15:VAL:HG22	2.17	0.44
1:YA:2467:C:H4'	12:YQ:123:HIS:CG	2.53	0.44
33:QB:82:ARG:HH11	33:QB:82:ARG:HG3	1.82	0.44
40:QI:16:ARG:HH11	40:QI:64:THR:HG21	1.82	0.44
1:RA:1688:U:O2	1:RA:1700:A:H5'	2.18	0.44
1:RA:1721:G:H2'	1:RA:1740:G:O6	2.18	0.44
1:RA:1918:A:O2'	1:RA:1920:4OC:N4	2.51	0.44
1:RA:522:G:H2'	1:RA:523:C:C6	2.53	0.44
3:RD:108:PRO:HD2	3:RD:111:LEU:HG	1.99	0.44
8:RI:62:LYS:O	8:RI:66:GLU:HG2	2.18	0.44
1:RA:1141:U:P	9:RN:25:ARG:HH12	2.40	0.44
18:RW:84:ARG:O	18:RW:96:ILE:N	2.44	0.44
32:XA:41:G:H2'	32:XA:42:G:C8	2.52	0.44
33:XB:69:LEU:HB3	33:XB:162:ILE:HG22	1.99	0.44
32:XA:581:G:OP1	46:XO:61:GLY:HA3	2.18	0.44
6:YG:101:ILE:HD13	26:Y4:25:TYR:HB2	2.00	0.44
1:YA:82:G:N2	1:YA:103:A:OP2	2.51	0.44
1:YA:1429:G:H2'	1:YA:1430:C:C6	2.53	0.44
1:YA:2136:C:O2	1:YA:2156:G:O2'	2.27	0.44
1:YA:2314:C:H2'	1:YA:2315:G:C8	2.53	0.44
1:YA:250:G:C6	1:YA:251:A:C6	3.06	0.44
1:YA:729:G:C6	3:YD:208:LYS:HB2	2.53	0.44
5:YF:29:ASN:HB3	5:YF:112:MET:HE1	1.99	0.44
5:YF:150:GLY:HA2	5:YF:172:TRP:CE3	2.53	0.44
6:YG:36:LYS:HB3	6:YG:95:ARG:HG2	2.00	0.44
32:QA:1024:G:N3	32:QA:1024:G:H2'	2.32	0.44
32:QA:1031:G:C2'	32:QA:1032:G:H5'	2.48	0.44
32:QA:571:U:O2	32:QA:918:A:H5'	2.17	0.44
35:QD:173:TRP:CE3	35:QD:174:LEU:HG	2.52	0.44
35:QD:57:ARG:NH2	36:QE:107:ARG:HD3	2.33	0.44
36:QE:57:LYS:HG2	36:QE:61:TYR:CE2	2.52	0.44
36:QE:90:VAL:O	36:QE:120:THR:HA	2.18	0.44
39:QH:46:LYS:HG3	39:QH:64:LYS:HB2	2.00	0.44
55:QY:191:GLU:HG2	55:QY:195:ARG:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:R4:59:PHE:CE1	50:QS:64:GLU:HG3	2.53	0.44
11:RP:63:PRO:HB2	30:R8:30:ARG:NH2	2.32	0.44
1:RA:2345:G:H1'	1:RA:2382:G:H5'	2.00	0.44
1:RA:286:C:H2'	1:RA:287:C:C6	2.52	0.44
1:RA:652(C):A:N6	1:RA:655:A:H1'	2.29	0.44
6:RG:15:VAL:HG13	6:RG:175:LEU:HB3	2.00	0.44
7:RH:3:ARG:HH12	7:RH:65:HIS:HB3	1.83	0.44
10:RO:36:GLY:HA3	10:RO:109:LYS:HD2	1.98	0.44
32:XA:1100:C:H2'	32:XA:1102:A:O5'	2.17	0.44
32:XA:131:C:H2'	32:XA:132:C:C6	2.52	0.44
32:XA:1333:A:H2'	32:XA:1334:G:O4'	2.17	0.44
32:XA:560:U:H4'	32:XA:561:U:O5'	2.18	0.44
32:XA:688:G:H2'	32:XA:689:C:C6	2.53	0.44
33:XB:218:ALA:O	33:XB:222:ILE:HG23	2.18	0.44
38:XG:16:LEU:HD11	40:XI:45:ALA:HB2	1.99	0.44
55:XY:101:LEU:N	55:XY:103:LYS:HE3	2.28	0.44
23:Y1:23:LYS:HB3	23:Y1:29:GLY:HA3	2.00	0.44
25:Y3:7:LYS:HG3	25:Y3:34:GLU:HG3	2.00	0.44
1:YA:1097:U:H2'	1:YA:1097:U:O2	2.17	0.44
1:YA:1721:G:H5''	1:YA:1721:G:N3	2.33	0.44
1:YA:699:A:H2'	1:YA:700:G:O4'	2.18	0.44
1:YA:747:U:O2	1:YA:2014:A:H1'	2.17	0.44
1:YA:7:G:H2'	1:YA:8:A:C8	2.53	0.44
5:YF:24:LEU:HD21	5:YF:114:VAL:HG12	2.00	0.44
14:YS:71:ARG:O	14:YS:75:GLU:HG2	2.18	0.44
18:YW:10:VAL:HG12	18:YW:12:ILE:HG22	2.00	0.44
32:QA:1030(D):G:H2'	32:QA:1030(E):A:C8	2.53	0.43
32:QA:1158:C:H5	32:QA:1181:G:H1	1.64	0.43
32:QA:1438:G:H2'	32:QA:1439:C:C6	2.52	0.43
32:QA:532:A:N6	34:QC:193:TYR:HA	2.32	0.43
32:QA:881:G:P	43:QL:12:ARG:HH22	2.41	0.43
44:QM:3:ARG:HG3	44:QM:4:ILE:N	2.32	0.43
1:RA:1171:G:N2	1:RA:1178:C:O2	2.51	0.43
1:RA:1916:A:O5'	1:RA:1916:A:H8	2.02	0.43
1:RA:207:A:H2'	1:RA:208:C:O4'	2.18	0.43
1:RA:2149:G:C2	1:RA:2150:U:H1'	2.53	0.43
1:RA:2262:U:H4'	1:RA:2328:A:C2	2.53	0.43
1:RA:375:C:H2'	1:RA:376:C:C6	2.53	0.43
1:RA:27:G:C4	1:RA:512:G:N2	2.86	0.43
3:RD:182:LEU:HB2	3:RD:272:ALA:HB3	2.00	0.43
1:RA:1815:A:OP2	3:RD:54:ARG:NH2	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:RZ:198:LYS:HE3	53:QV:52:G:N2	2.33	0.43
32:XA:1181:G:O2'	32:XA:1182:G:N7	2.47	0.43
32:XA:1191:A:OP2	34:XC:3:ASN:ND2	2.51	0.43
32:XA:376:G:H5''	47:XP:5:ARG:HB2	2.00	0.43
33:XB:19:HIS:CG	33:XB:20:GLU:H	2.37	0.43
55:XY:225:ASP:O	55:XY:245:ARG:HB3	2.18	0.43
1:YA:1141:U:OP2	9:YN:63:THR:OG1	2.33	0.43
1:YA:2109:U:H1'	1:YA:2181:G:N2	2.32	0.43
1:YA:2313:C:H2'	1:YA:2314:C:C6	2.52	0.43
1:YA:824:A:H1'	1:YA:2358:G:N7	2.34	0.43
1:YA:2749:A:O3'	7:YH:62:LYS:HE3	2.18	0.43
1:YA:1050:A:O2'	1:YA:2752:C:H4'	2.18	0.43
1:YA:2893:G:H5''	1:YA:2894:G:O4'	2.18	0.43
2:YB:78:A:C2	2:YB:100:A:C4	3.06	0.43
3:YD:147:LEU:HD11	3:YD:183:ARG:NE	2.31	0.43
3:YD:51:VAL:CG1	3:YD:54:ARG:HD2	2.48	0.43
6:YG:12:TYR:HA	6:YG:16:ARG:HG2	2.00	0.43
8:YI:114:LEU:HD11	8:YI:128:LEU:HD13	2.00	0.43
9:YN:97:ARG:HA	9:YN:100:GLU:HB2	2.00	0.43
21:YZ:91:LEU:HA	21:YZ:91:LEU:HD12	1.83	0.43
32:QA:401:C:OP2	35:QD:73:ARG:NH2	2.48	0.43
32:QA:460:G:H1'	32:QA:472:A:H61	1.83	0.43
32:QA:677:U:H2'	32:QA:678:U:C6	2.53	0.43
35:QD:194:LEU:HD12	35:QD:195:ALA:H	1.83	0.43
36:QE:92:LYS:HB3	36:QE:119:LEU:HB2	2.00	0.43
1:RA:1358:G:O2'	1:RA:1359:A:H5'	2.18	0.43
1:RA:2784:C:O2'	4:RE:37:ARG:NH1	2.51	0.43
11:RP:94:GLU:HG3	11:RP:124:LYS:HD3	2.00	0.43
21:RZ:158:PRO:O	21:RZ:161:VAL:HG13	2.18	0.43
32:XA:302:G:N3	32:XA:556:C:H4'	2.33	0.43
33:XB:16:HIS:CD2	33:XB:210:SER:HB3	2.53	0.43
33:XB:71:VAL:HG12	33:XB:93:VAL:HG22	2.00	0.43
43:XL:28:LYS:HD2	43:XL:62:SER:HB2	2.00	0.43
32:XA:186:C:O2'	51:XT:85:MET:SD	2.71	0.43
1:YA:1112:G:C6	1:YA:1113:U:H1'	2.54	0.43
1:YA:971:C:H2'	1:YA:972:G:O4'	2.19	0.43
5:YF:64:ILE:HD12	5:YF:65:TRP:CZ3	2.53	0.43
32:QA:1030(A):C:N3	32:QA:1031:G:N2	2.66	0.43
32:QA:1031:G:H2'	32:QA:1032:G:H5'	1.99	0.43
32:QA:1068:G:N2	32:QA:1191:A:N3	2.53	0.43
41:QJ:62:HIS:HB3	45:QN:59:ALA:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:QP:20:VAL:HG21	47:QP:32:TYR:CG	2.53	0.43
48:QQ:10:VAL:HG13	48:QQ:19:VAL:HB	2.00	0.43
1:RA:1107:G:C2	1:RA:1108:U:H1'	2.53	0.43
1:RA:2114:A:H3'	1:RA:2115:G:H8	1.83	0.43
1:RA:1999:C:H5''	1:RA:2723:C:O2'	2.18	0.43
1:RA:839:U:H2'	1:RA:840:C:C6	2.53	0.43
13:RR:63:ARG:O	13:RR:67:LEU:HB2	2.18	0.43
15:RT:65:LYS:HE2	15:RT:67:SER:HB2	2.00	0.43
32:XA:1004:A:N7	32:XA:1037:C:H2'	2.32	0.43
32:XA:1030(B):G:H2'	32:XA:1030(C):C:H5''	1.99	0.43
32:XA:1327:C:H2'	32:XA:1328:C:H6	1.82	0.43
32:XA:485:G:O2'	32:XA:486:U:OP2	2.34	0.43
32:XA:1187:G:H4'	40:XI:111:ARG:HH11	1.83	0.43
44:XM:22:ILE:HG21	44:XM:66:LEU:HD13	2.01	0.43
48:XQ:41:LYS:NZ	48:XQ:88:TYR:OH	2.44	0.43
29:Y7:33:ARG:HD2	29:Y7:33:ARG:HH11	1.69	0.43
1:YA:1714:G:N2	1:YA:1745(B):C:O2	2.51	0.43
1:YA:2659:G:O2'	7:YH:175:LYS:HE2	2.17	0.43
1:YA:579:G:H2'	1:YA:580:C:C6	2.53	0.43
3:YD:111:LEU:HA	3:YD:111:LEU:HD23	1.74	0.43
1:YA:784:A:N6	3:YD:229:VAL:HG11	2.33	0.43
32:QA:620:C:H2'	32:QA:621:A:O4'	2.19	0.43
32:QA:778:G:H2'	32:QA:779:C:O4'	2.19	0.43
43:QL:113:ARG:HH21	43:QL:116:SER:HB2	1.83	0.43
47:QP:75:ARG:HG3	47:QP:80:PHE:CD2	2.52	0.43
26:R4:61:ARG:HG3	26:R4:62:ARG:H	1.83	0.43
1:RA:108:U:H2'	1:RA:109:G:C8	2.54	0.43
1:RA:1449:A:N3	1:RA:1529:G:H1'	2.33	0.43
1:RA:2119:A:H61	1:RA:2168:G:N2	2.15	0.43
1:RA:38:A:H2'	1:RA:39:C:C6	2.54	0.43
1:RA:18:C:O2'	1:RA:554:U:OP1	2.34	0.43
1:RA:858:U:O2	1:RA:2268:A:H2'	2.19	0.43
4:RE:73:GLU:CD	4:RE:73:GLU:H	2.21	0.43
14:RS:99:LYS:HE2	14:RS:103:GLU:OE2	2.18	0.43
12:RQ:61:GLY:HA2	21:RZ:177:PRO:HB2	2.00	0.43
32:XA:1252:A:H2'	32:XA:1253:G:O4'	2.19	0.43
32:XA:790:A:C6	32:XA:791:G:C6	3.06	0.43
32:XA:404:U:C5'	35:XD:122:ARG:HD3	2.48	0.43
37:XF:33:TYR:HB2	37:XF:75:LEU:HD23	2.00	0.43
32:XA:1151:A:O4'	41:XJ:39:PRO:HB2	2.17	0.43
42:XK:16:SER:OG	42:XK:106:LYS:NZ	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:273:A:H1'	48:XQ:16:GLN:OE1	2.19	0.43
55:XY:144:TRP:CH2	55:XY:171:VAL:HA	2.52	0.43
1:YA:2218:U:C2	23:Y1:52:ARG:NH2	2.86	0.43
30:Y8:23:VAL:CG1	30:Y8:47:LYS:HD3	2.48	0.43
1:YA:64:A:O3'	19:YX:71:GLY:HA3	2.18	0.43
1:YA:785:G:C6	1:YA:786:C:C4	3.06	0.43
17:YV:25:LEU:HD12	17:YV:94:LEU:HD21	2.00	0.43
32:QA:1027:C:H2'	32:QA:1028:C:C5	2.54	0.43
32:QA:1315:U:H2'	32:QA:1316:G:O4'	2.18	0.43
35:QD:107:ARG:HD2	35:QD:107:ARG:HA	1.78	0.43
35:QD:13:ARG:NH2	35:QD:40:PRO:HA	2.34	0.43
43:QL:33:ARG:NH1	43:QL:62:SER:HB3	2.31	0.43
32:QA:1312:G:H5'	50:QS:5:LEU:HD12	2.01	0.43
53:QV:76:A:H5''	55:QY:233:GLY:O	2.19	0.43
55:QY:114:GLU:OE1	55:QY:294:ARG:NE	2.51	0.43
1:RA:1864:U:OP1	1:RA:2410:G:O2'	2.21	0.43
1:RA:2245:U:H5''	1:RA:2246:G:H5'	2.01	0.43
1:RA:2869:G:H2'	1:RA:2870:C:O4'	2.18	0.43
1:RA:300:A:H2'	1:RA:334:C:H1'	1.99	0.43
32:XA:1342:C:H2'	32:XA:1343:G:C8	2.53	0.43
32:XA:1431:C:H2'	32:XA:1432:G:O4'	2.18	0.43
32:XA:269:C:H2'	32:XA:270:A:C8	2.54	0.43
15:YT:41:ARG:NH2	32:XA:345:C:H3'	2.33	0.43
32:XA:770:C:O2'	32:XA:771:G:H5'	2.18	0.43
40:XI:25:LYS:HD3	40:XI:25:LYS:HA	1.77	0.43
47:XP:13:HIS:O	47:XP:42:ARG:NH1	2.52	0.43
50:XS:41:VAL:HG22	50:XS:42:PRO:HD2	1.99	0.43
23:Y1:3:LYS:HB2	23:Y1:61:ARG:HH11	1.84	0.43
29:Y7:24:THR:O	29:Y7:28:ARG:HG3	2.19	0.43
1:YA:1364:G:P	23:Y1:3:LYS:HG3	2.58	0.43
1:YA:1815:A:C5	1:YA:1817:G:C6	3.05	0.43
1:YA:1936:A:OP2	1:YA:1962:5MC:N4	2.50	0.43
1:YA:2296:U:OP2	14:YS:9:ARG:NH2	2.48	0.43
1:YA:2747:G:O6	1:YA:2755:C:H5''	2.17	0.43
1:YA:445:C:C4	1:YA:446:G:C6	3.07	0.43
6:YG:165:THR:OG1	6:YG:168:GLU:HG3	2.18	0.43
7:YH:154:PRO:HB3	7:YH:163:TYR:CZ	2.53	0.43
32:QA:1003:G:C2	32:QA:1004:A:N3	2.86	0.43
32:QA:18:C:H4'	32:QA:1078:U:O2	2.19	0.43
32:QA:840:C:H4'	32:QA:841:U:OP1	2.18	0.43
33:QB:115:LEU:HD13	33:QB:145:LEU:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:QJ:4:ILE:N	41:QJ:100:THR:HG22	2.33	0.43
51:QT:24:LEU:HD12	51:QT:24:LEU:HA	1.91	0.43
51:QT:9:ASN:OD1	51:QT:9:ASN:N	2.50	0.43
55:QY:170:GLY:O	55:QY:174:ARG:HG2	2.18	0.43
1:RA:2320:A:N3	1:RA:2320:A:H2'	2.33	0.43
1:RA:2724:C:OP1	4:RE:111:ARG:NH1	2.49	0.43
1:RA:2846:G:H2'	1:RA:2847:U:O4'	2.19	0.43
1:RA:2872:G:C2	1:RA:2873:A:N6	2.87	0.43
1:RA:586:A:N1	1:RA:809:G:O2'	2.45	0.43
1:RA:998:C:P	16:RU:92:ARG:HH22	2.42	0.43
7:RH:88:LEU:HD23	7:RH:130:ARG:HG3	2.01	0.43
10:RO:3:GLN:HB2	10:RO:4:PRO:HD2	2.01	0.43
32:XA:1025:U:H3	32:XA:1036:G:H1	1.67	0.43
32:XA:736:C:H2'	32:XA:737:A:H8	1.82	0.43
32:XA:881:G:P	43:XL:12:ARG:HH22	2.41	0.43
33:XB:8:LYS:CD	33:XB:51:LEU:HB3	2.48	0.43
43:XL:77:LEU:HD21	43:XL:107:ALA:HA	2.00	0.43
55:XY:114:GLU:HB2	55:XY:204:ALA:HB3	1.99	0.43
55:XY:114:GLU:HG2	55:XY:163:ILE:HG12	2.01	0.43
1:YA:117:G:C6	1:YA:119:A:C6	3.07	0.43
1:YA:1570:A:H2'	1:YA:1571:A:C8	2.53	0.43
1:YA:1802:A:C6	1:YA:1803:A:C6	3.07	0.43
1:YA:2113:U:H2'	1:YA:2114:A:O4'	2.18	0.43
8:YI:12:LEU:HD11	8:YI:25:TYR:HE2	1.84	0.43
32:QA:1356:G:H2'	32:QA:1357:A:C8	2.54	0.43
32:QA:383:A:C5	32:QA:384:G:H1'	2.54	0.43
38:QG:68:ASN:O	38:QG:138:LYS:HD2	2.18	0.43
47:QP:1:MET:SD	47:QP:65:GLN:HG3	2.59	0.43
55:QY:255:VAL:HG21	55:QY:273:VAL:CG1	2.49	0.43
27:R5:35:GLU:HG2	27:R5:51:TYR:CG	2.54	0.43
1:RA:2756:U:H5''	31:R9:19:ARG:HA	2.01	0.43
1:RA:1404:C:H2'	1:RA:1405:U:H6	1.84	0.43
1:RA:2077:A:H2'	1:RA:2078:C:H6	1.83	0.43
1:RA:2352:A:N6	1:RA:2365:G:O2'	2.51	0.43
1:RA:2465:C:O2	1:RA:2486:G:C2	2.72	0.43
1:RA:527:C:N4	1:RA:2777:G:O2'	2.46	0.43
1:RA:524:U:H4'	1:RA:555:U:H4'	2.00	0.43
1:RA:974:G:OP1	1:RA:1187:G:O2'	2.26	0.43
19:RX:12:VAL:HG21	19:RX:27:THR:HG22	2.01	0.43
32:XA:1005:A:C5	32:XA:1006:C:H1'	2.54	0.43
32:XA:952:U:H2'	32:XA:953:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:XB:71:VAL:HG12	33:XB:93:VAL:CG2	2.49	0.43
35:XD:13:ARG:NH2	35:XD:40:PRO:HA	2.34	0.43
35:QD:195:ALA:O	37:XF:16:GLN:HB3	2.18	0.43
39:XH:84:ARG:HG3	39:XH:84:ARG:O	2.19	0.43
45:XN:27:CYS:SG	45:XN:29:ARG:HB2	2.59	0.43
24:Y2:32:LEU:HD22	24:Y2:36:ARG:HH11	1.84	0.43
1:YA:1260:G:C6	1:YA:1261:C:C4	3.07	0.43
1:YA:185:U:H4'	1:YA:218:A:H4'	2.01	0.43
3:YD:275:LYS:HA	3:YD:275:LYS:HD2	1.86	0.43
4:YE:111:ARG:HG3	4:YE:160:TYR:CD2	2.54	0.43
1:YA:411:G:C5	11:YP:72:PRO:HB3	2.53	0.43
1:YA:1287:A:O4'	13:YR:104:ARG:HD3	2.18	0.43
20:YY:86:ARG:HB2	20:YY:98:VAL:HG23	2.00	0.43
32:QA:1308:U:OP1	44:QM:98:VAL:N	2.39	0.43
35:QD:57:ARG:HD3	35:QD:205:GLU:HB3	1.99	0.43
38:QG:136:LYS:HE3	38:QG:136:LYS:HB2	1.86	0.43
47:QP:74:LEU:HB3	47:QP:79:VAL:HG21	1.99	0.43
1:RA:1084:A:H3'	1:RA:1085:A:C4'	2.48	0.43
1:RA:2115:G:N2	1:RA:2171:A:H61	2.15	0.43
1:RA:2251:OMG:H1'	1:RA:2251:OMG:HM23	1.76	0.43
1:RA:2563:U:H2'	1:RA:2565:A:OP2	2.18	0.43
1:RA:875:G:H2'	1:RA:876:C:O4'	2.18	0.43
3:RD:72:LYS:HG3	3:RD:103:ARG:NH2	2.33	0.43
1:RA:1188:U:H4'	17:RV:79:VAL:HG22	2.01	0.43
19:RX:88:LYS:HB2	19:RX:88:LYS:HE3	1.84	0.43
32:XA:176:C:H2'	32:XA:177:C:C6	2.54	0.43
32:XA:922:G:C6	32:XA:923:A:C6	3.07	0.43
34:XC:19:GLU:HB3	34:XC:40:ARG:HH22	1.84	0.43
32:XA:537:G:H5''	43:XL:113:ARG:HH12	1.82	0.43
1:YA:1486:A:H2'	1:YA:1487:G:C8	2.54	0.43
1:YA:1696:G:C6	1:YA:1697:G:C4	3.07	0.43
1:YA:2413:G:H2'	1:YA:2414:G:O4'	2.19	0.43
1:YA:2455:G:H2'	1:YA:2456:C:C6	2.53	0.43
3:YD:69:ARG:HG3	3:YD:119:ALA:HB2	2.01	0.43
1:YA:560:C:H5'	16:YU:52:ARG:HH21	1.84	0.43
32:QA:447:G:H2'	32:QA:485:G:N2	2.34	0.43
33:QB:211:ILE:HG13	33:QB:211:ILE:H	1.65	0.43
33:QB:8:LYS:NZ	33:QB:52:GLU:HG3	2.33	0.43
35:QD:88:VAL:HG22	36:QE:96:PRO:HB2	2.00	0.43
35:QD:88:VAL:HG13	36:QE:97:GLY:HA2	1.99	0.43
39:QH:95:VAL:HB	39:QH:99:GLU:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:QJ:5:ARG:O	41:QJ:98:ILE:HA	2.19	0.43
1:RA:388:G:OP2	23:R1:32:LYS:HG2	2.19	0.43
1:RA:1210:A:H5''	1:RA:1212:G:O4'	2.18	0.43
1:RA:2098:U:H2'	1:RA:2099:U:O4'	2.19	0.43
1:RA:470:A:H2'	1:RA:471:A:O4'	2.19	0.43
17:RV:5:VAL:HG21	17:RV:35:LEU:HD23	2.00	0.43
32:XA:126:G:OP1	32:XA:605:U:O2'	2.26	0.43
32:XA:791:G:N2	32:XA:1497:G:O3'	2.51	0.43
32:XA:501:C:H1'	32:XA:549:C:H1'	2.01	0.43
32:XA:972:C:H4'	41:XJ:57:LYS:HB2	2.01	0.43
33:XB:28:PHE:CE1	33:XB:31:TYR:HB2	2.54	0.43
35:XD:61:LYS:NZ	35:XD:72:GLU:OE2	2.52	0.43
32:XA:598:U:H4'	39:XH:94:TYR:CG	2.54	0.43
44:XM:54:VAL:HA	44:XM:57:ARG:HB3	2.01	0.43
55:XY:215:PRO:O	55:XY:216:ASP:C	2.57	0.43
1:YA:2106:G:C4	1:YA:2107:C:H1'	2.54	0.43
1:YA:2188:C:H2'	1:YA:2189:U:O4'	2.19	0.43
1:YA:2572:A:OP1	1:YA:2574:G:O2'	2.33	0.43
1:YA:2522:U:O2'	1:YA:2647:U:OP1	2.23	0.43
1:YA:2756:U:OP2	31:Y9:19:ARG:NE	2.49	0.43
1:YA:796:C:H2'	1:YA:797:C:H6	1.82	0.43
5:YF:164:ARG:O	5:YF:168:ARG:HB2	2.19	0.43
7:YH:105:LEU:HD12	7:YH:105:LEU:HA	1.86	0.43
1:YA:1036:G:OP1	7:YH:59:ARG:HG2	2.18	0.43
1:YA:1040:C:H4'	21:YZ:46:LYS:HE3	2.00	0.43
32:QA:743:U:H2'	32:QA:744:C:C6	2.54	0.43
32:QA:943:U:H1'	40:QI:124:GLN:HE22	1.84	0.43
36:QE:145:LYS:O	36:QE:149:GLU:HG2	2.19	0.43
38:QG:104:LEU:HD12	38:QG:104:LEU:HA	1.84	0.43
38:QG:26:PHE:O	38:QG:30:ILE:HG13	2.19	0.43
47:QP:20:VAL:HG23	47:QP:35:LYS:HA	2.01	0.43
24:R2:32:LEU:HD22	24:R2:36:ARG:NH1	2.34	0.43
1:RA:2762:G:H2'	1:RA:2763:G:O4'	2.19	0.43
1:RA:27:G:HO2'	1:RA:28:A:P	2.40	0.43
1:RA:284:U:H2'	1:RA:285:C:C6	2.54	0.43
1:RA:886:C:O2'	1:RA:889:C:N4	2.49	0.43
6:RG:181:ARG:HG3	6:RG:182:LYS:N	2.34	0.43
21:RZ:102:LEU:HD11	21:RZ:124:ILE:HB	2.00	0.43
32:XA:1320:C:H2'	32:XA:1321:C:O4'	2.19	0.43
32:XA:314:C:O2'	32:XA:315:A:H5'	2.19	0.43
32:XA:828:A:N6	32:XA:858:G:O2'	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:XC:9:GLY:HA3	45:XN:49:HIS:HA	2.01	0.43
37:XF:45:LEU:HD12	37:XF:59:TYR:CD2	2.54	0.43
38:XG:111:ARG:HD3	38:XG:113:GLU:OE2	2.19	0.43
25:Y3:43:ILE:O	25:Y3:47:VAL:HG23	2.19	0.43
1:YA:183:C:H42	1:YA:213:A:N6	2.16	0.43
1:YA:2564:A:OP1	1:YA:2648:C:H4'	2.18	0.43
1:YA:618:C:H2'	1:YA:619:G:O4'	2.19	0.43
5:YF:63:LYS:HA	5:YF:76:GLY:O	2.18	0.43
20:YY:56:PRO:C	20:YY:58:GLY:H	2.22	0.43
54:QX:21:A:C2	55:QY:196:ILE:HG23	2.54	0.42
1:RA:2282:G:H4'	1:RA:2389:G:O2'	2.19	0.42
1:RA:2466:C:C2	1:RA:2485:G:C2	3.07	0.42
5:RF:29:ASN:HB3	5:RF:112:MET:HE1	2.00	0.42
6:RG:108:ASN:HA	26:R4:37:SER:HB3	2.00	0.42
8:RI:109:ILE:HA	8:RI:109:ILE:HD12	1.67	0.42
9:RN:24:GLY:O	9:RN:28:THR:HG23	2.19	0.42
17:RV:81:TYR:C	17:RV:82:ARG:HD2	2.39	0.42
21:RZ:144:LEU:HD11	21:RZ:150:LEU:HD22	2.00	0.42
35:XD:107:ARG:HD2	35:XD:107:ARG:HA	1.90	0.42
35:XD:200:GLU:O	35:XD:204:ILE:HG12	2.18	0.42
40:X1:22:GLY:HA3	40:X1:60:ASP:OD1	2.19	0.42
1:YA:1073:A:H4'	1:YA:1074:G:OP1	2.19	0.42
1:YA:1312:U:H4'	1:YA:1313:U:O5'	2.18	0.42
1:YA:1408:C:C2	1:YA:1595:G:N2	2.87	0.42
1:YA:1889:A:H2'	1:YA:1890:A:C8	2.54	0.42
1:YA:2086:U:H2'	1:YA:2087:G:C8	2.54	0.42
1:YA:875:G:H2'	1:YA:876:C:O4'	2.18	0.42
5:YF:140:LEU:HD13	5:YF:170:LEU:HD21	2.00	0.42
15:YT:4:GLY:O	15:YT:8:LYS:HG2	2.19	0.42
32:QA:1003:G:C2	32:QA:1004:A:H1'	2.54	0.42
32:QA:612:C:O2	32:QA:629:G:N2	2.52	0.42
32:QA:1055:A:O2'	34:QC:161:GLU:O	2.30	0.42
40:QI:106:ALA:O	40:QI:108:VAL:HG23	2.19	0.42
40:QI:110:GLU:OE2	40:QI:113:LYS:NZ	2.51	0.42
23:R1:64:ALA:HA	23:R1:67:ILE:HG13	1.99	0.42
1:RA:942:G:H1'	1:RA:1189:A:C2	2.54	0.42
1:RA:1351:C:H2'	1:RA:1352:U:C6	2.54	0.42
1:RA:1422:G:C6	1:RA:1423:G:C5	3.07	0.42
1:RA:1784:A:H4'	1:RA:1785:A:O5'	2.19	0.42
1:RA:2242:G:H2'	1:RA:2243:U:O4'	2.20	0.42
3:RD:29:PRO:HB2	3:RD:34:VAL:HG11	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:1376:U:H2'	32:XA:1377:A:C8	2.54	0.42
32:XA:409:G:H2'	32:XA:410:G:O4'	2.20	0.42
32:XA:737:A:H2'	32:XA:738:C:C6	2.54	0.42
23:Y1:73:LEU:HA	23:Y1:73:LEU:HD23	1.88	0.42
1:YA:2106:G:C6	1:YA:2107:C:C2	3.06	0.42
1:YA:245:G:O5'	11:YP:73:GLY:HA2	2.19	0.42
1:YA:2461:C:H2'	1:YA:2462:U:C6	2.54	0.42
1:YA:26:G:C6	1:YA:27:G:N1	2.87	0.42
1:YA:45:C:OP2	1:YA:215:G:H2'	2.18	0.42
1:YA:484:C:H2'	1:YA:485:C:H6	1.83	0.42
5:YF:21:ALA:CB	5:YF:22:ALA:HA	2.49	0.42
6:YG:72:ARG:HG2	6:YG:87:PRO:HA	2.01	0.42
32:QA:1263:C:H2'	32:QA:1264:C:C6	2.54	0.42
32:QA:130:A:OP2	48:QQ:63:ARG:NE	2.47	0.42
33:QB:9:GLU:OE1	33:QB:217:ARG:NH2	2.45	0.42
34:QC:180:ALA:HB1	34:QC:203:PHE:CE1	2.53	0.42
34:QC:43:LEU:O	34:QC:47:LEU:HB2	2.19	0.42
36:QE:6:PHE:HD1	36:QE:36:ASP:HB3	1.83	0.42
55:QY:105:PRO:O	55:QY:107:ASP:N	2.51	0.42
55:QY:106:ASP:OD1	55:QY:109:ARG:HD2	2.19	0.42
26:R4:18:CYS:SG	26:R4:20:ASN:HB2	2.59	0.42
1:RA:108:U:H2'	1:RA:109:G:H8	1.84	0.42
1:RA:2267:A:H5''	1:RA:2268:A:H5'	2.02	0.42
1:RA:2438:U:O2'	1:RA:2440:C:OP1	2.26	0.42
1:RA:2462:U:H2'	1:RA:2463:C:C6	2.55	0.42
4:RE:12:THR:HG21	15:RT:11:GLU:OE2	2.19	0.42
19:RX:44:GLU:HG3	19:RX:51:VAL:HG23	2.01	0.42
32:XA:1039:C:C4	32:XA:1040:U:C4	3.06	0.42
32:XA:116:A:H61	32:XA:313:A:H1'	1.83	0.42
33:XB:8:LYS:HD2	33:XB:51:LEU:HD13	2.00	0.42
36:XE:100:VAL:O	36:XE:107:ARG:NH2	2.49	0.42
51:XT:43:LEU:HD13	51:XT:51:GLU:HB3	2.01	0.42
1:YA:1914:C:O2	55:XY:295:ARG:HD3	2.19	0.42
1:YA:2064:C:H2'	1:YA:2065:C:C6	2.55	0.42
1:YA:2583:G:N2	55:XY:238:ASN:OD1	2.52	0.42
1:YA:2762:G:H2'	1:YA:2763:G:O4'	2.19	0.42
1:YA:553:G:H2'	1:YA:554:U:O4'	2.20	0.42
1:YA:560:C:C5'	16:YU:52:ARG:HH21	2.31	0.42
1:YA:571:A:O2'	17:YV:78:LYS:HE2	2.18	0.42
3:YD:5:LYS:HB3	3:YD:5:LYS:HE3	1.84	0.42
16:YU:86:ALA:O	17:YV:49:THR:HG23	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:1074:G:C6	32:QA:1075:C:C4	3.07	0.42
32:QA:399:G:H2'	32:QA:400:C:C6	2.54	0.42
32:QA:45:U:H2'	32:QA:46:G:H8	1.80	0.42
32:QA:519:C:H2'	32:QA:520:A:O4'	2.20	0.42
32:QA:713:G:H2'	32:QA:714:G:C8	2.55	0.42
34:QC:127:ARG:HB3	34:QC:127:ARG:CZ	2.48	0.42
37:QF:23:LYS:HB3	37:QF:23:LYS:HE2	1.84	0.42
48:QQ:81:ARG:HA	48:QQ:81:ARG:HD2	1.76	0.42
55:QY:258:GLN:HG3	55:QY:258:GLN:O	2.19	0.42
1:RA:771:G:OP1	29:R7:14:LYS:HE2	2.19	0.42
1:RA:10:G:H1'	1:RA:2801(B):A:N1	2.35	0.42
1:RA:742:G:O2'	1:RA:1676:A:H4'	2.19	0.42
1:RA:2152:G:H2'	1:RA:2153:G:H8	1.82	0.42
1:RA:2636:U:H1'	1:RA:2783:G:N2	2.34	0.42
1:RA:2712(A):U:OP1	1:RA:2714:G:H4'	2.20	0.42
1:RA:2849:U:O4	15:RT:23:ARG:NH2	2.53	0.42
1:RA:569:U:C4	1:RA:570:G:C6	3.07	0.42
1:RA:631:A:H2'	1:RA:632:A:O4'	2.18	0.42
3:RD:16:MET:HG3	3:RD:206:LEU:O	2.19	0.42
8:RI:4:ILE:HG12	8:RI:18:VAL:HG22	2.01	0.42
1:RA:996:A:H4'	16:RU:91:ASP:OD2	2.19	0.42
21:RZ:108:PRO:HA	21:RZ:142:SER:HA	1.99	0.42
32:XA:346:G:H2'	32:XA:347:G:O4'	2.19	0.42
32:XA:504:C:H1'	32:XA:510:A:C4	2.54	0.42
34:XC:180:ALA:HB1	34:XC:203:PHE:HE1	1.84	0.42
45:XN:4:LYS:HG3	45:XN:7:ILE:HD11	2.00	0.42
55:XY:317:VAL:HG23	55:XY:329:LEU:HD12	2.01	0.42
1:YA:82:G:N1	1:YA:103:A:OP2	2.48	0.42
1:YA:1153:C:H2'	1:YA:1154:G:O4'	2.19	0.42
1:YA:1697:G:OP2	1:YA:1698:A:O2'	2.31	0.42
1:YA:1939:5MU:O2	1:YA:1967:C:H4'	2.19	0.42
1:YA:2114:A:H3'	1:YA:2115:G:C8	2.55	0.42
1:YA:2128:C:N3	1:YA:2160:G:N2	2.63	0.42
1:YA:2193:G:H2'	1:YA:2194:G:C8	2.54	0.42
1:YA:2564:A:C2	1:YA:2647:U:H4'	2.55	0.42
1:YA:2641:G:OP1	9:YN:74:ARG:NH1	2.53	0.42
1:YA:671:C:H2'	1:YA:672:C:H6	1.84	0.42
1:YA:817:C:O2'	1:YA:839:U:H5''	2.19	0.42
6:YG:55:LYS:HD3	6:YG:150:ASP:OD2	2.19	0.42
18:YW:86:LEU:HD22	18:YW:96:ILE:HD11	2.01	0.42
19:YX:65:ARG:HB3	19:YX:70:LEU:HD23	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:YB:106:G:H5'	21:YZ:31:ARG:HB3	2.01	0.42
32:QA:1015:A:H2'	32:QA:1016:A:C8	2.54	0.42
32:QA:1058:G:OP1	34:QC:199:LYS:HE3	2.20	0.42
32:QA:1075:C:OP1	33:QB:179:LYS:NZ	2.52	0.42
32:QA:687:A:N3	32:QA:688:G:H1'	2.34	0.42
37:QF:6:VAL:HG22	37:QF:90:VAL:HG22	2.01	0.42
42:QK:84:VAL:CG1	42:QK:91:ARG:HD2	2.49	0.42
48:QQ:58:GLU:OE2	48:QQ:75:ARG:NH2	2.52	0.42
51:QT:63:ILE:HD13	51:QT:80:ARG:HB3	2.00	0.42
55:QY:222:LEU:HD21	55:QY:248:HIS:HD2	1.85	0.42
55:QY:97:GLN:O	55:QY:99:LEU:N	2.53	0.42
1:RA:1104:C:H2'	1:RA:1105:U:H6	1.84	0.42
1:RA:2418:A:H2'	1:RA:2419:U:C6	2.55	0.42
1:RA:200:U:O2	1:RA:386:G:N2	2.52	0.42
4:RE:98:PRO:HD3	4:RE:175:VAL:HG12	2.02	0.42
5:RF:165:ARG:HA	5:RF:168:ARG:CD	2.45	0.42
5:RF:178:PRO:HB2	5:RF:201:VAL:HG21	2.02	0.42
5:RF:7:TYR:O	5:RF:21:ALA:HA	2.19	0.42
11:RP:84:ASN:HB3	11:RP:117:GLU:O	2.19	0.42
12:RQ:18:LYS:HB2	12:RQ:18:LYS:HE2	1.74	0.42
32:XA:1062:U:H2'	32:XA:1063:C:C6	2.54	0.42
32:XA:1063:C:H2'	32:XA:1064:G:C8	2.54	0.42
32:XA:1469:G:H2'	32:XA:1470:G:C8	2.54	0.42
32:XA:57:G:H2'	32:XA:58:C:C6	2.54	0.42
32:XA:692:U:O2'	32:XA:694:A:N7	2.41	0.42
32:XA:950:U:H2'	32:XA:951:G:C8	2.55	0.42
33:XB:230:VAL:HG22	33:XB:231:GLU:H	1.84	0.42
40:XI:28:VAL:N	40:XI:31:GLN:O	2.45	0.42
55:XY:217:ILE:HD13	55:XY:278:ILE:CD1	2.50	0.42
23:Y1:83:GLU:HA	23:Y1:84:GLY:HA2	1.72	0.42
1:YA:1069:A:H2'	1:YA:1073:A:N7	2.34	0.42
1:YA:1080:C:H2'	1:YA:1081:U:C6	2.55	0.42
1:YA:1283:G:H2'	1:YA:1285:G:OP2	2.19	0.42
1:YA:2391:G:O6	1:YA:2425:A:H8	2.02	0.42
1:YA:2660:A:H2'	1:YA:2661:G:O4'	2.19	0.42
3:YD:61:LEU:O	3:YD:63:ARG:NH1	2.52	0.42
32:QA:1033:G:H2'	32:QA:1034:G:H8	1.85	0.42
32:QA:110:C:H2'	32:QA:111:G:O4'	2.20	0.42
32:QA:1425:U:H2'	32:QA:1426:C:C6	2.54	0.42
33:QB:141:GLU:HG2	33:QB:145:LEU:HD23	2.02	0.42
37:QF:45:LEU:HD12	37:QF:59:TYR:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:QI:65:VAL:HG21	40:QI:73:GLN:HB3	2.01	0.42
1:RA:1264:G:N2	1:RA:2015:A:OP2	2.53	0.42
1:RA:2336:A:H61	22:R0:43:THR:CG2	2.33	0.42
1:RA:2695:C:H2'	1:RA:2696:U:H6	1.84	0.42
1:RA:898:C:H2'	1:RA:899:A:O4'	2.20	0.42
6:RG:114:ILE:HG12	6:RG:140:ILE:HG12	2.00	0.42
13:RR:55:ALA:HB2	13:RR:79:LEU:HD13	2.01	0.42
38:XG:65:ALA:HB1	38:XG:127:ALA:HB3	2.00	0.42
43:XL:89:ARG:HB3	43:XL:97:ARG:HA	2.00	0.42
55:XY:218:ASN:HA	55:XY:219:PRO:HD3	1.89	0.42
1:YA:2586:C:C5	1:YA:2608:G:N2	2.88	0.42
1:YA:305:U:H2'	1:YA:306:U:C6	2.55	0.42
1:YA:49:A:H4'	1:YA:50:U:H5''	2.00	0.42
1:YA:795:C:H2'	1:YA:796:C:C6	2.55	0.42
1:YA:978:G:C2	1:YA:986:C:C2	3.08	0.42
6:YG:114:ILE:HG23	6:YG:136:ARG:HH22	1.84	0.42
18:YW:48:ALA:O	18:YW:52:GLU:HG2	2.20	0.42
32:QA:376:G:H5''	47:QP:5:ARG:HD3	2.01	0.42
32:QA:624:C:H2'	32:QA:625:G:H8	1.85	0.42
35:QD:76:ARG:HD2	35:QD:76:ARG:HA	1.84	0.42
39:QH:38:ILE:HD13	39:QH:41:ARG:NH2	2.35	0.42
1:RA:1654:A:H1'	1:RA:2823:A:H5'	2.02	0.42
1:RA:2028:U:H2'	1:RA:2029:G:O4'	2.20	0.42
1:RA:2574:G:H2'	1:RA:2575:C:O4'	2.19	0.42
1:RA:821:A:H2'	1:RA:946:G:H5''	2.00	0.42
1:RA:962:G:H2'	1:RA:963:U:C6	2.55	0.42
5:RF:17:ARG:NH2	5:RF:19:GLU:OE2	2.53	0.42
32:XA:1104:G:H4'	33:XB:111:ARG:NH1	2.34	0.42
32:XA:114:U:H2'	32:XA:115:G:C8	2.54	0.42
32:XA:279:A:OP2	48:XQ:95:TYR:OH	2.23	0.42
32:XA:435:C:H2'	32:XA:436:C:H6	1.84	0.42
1:YA:1019:U:OP1	1:YA:1035:U:O2'	2.25	0.42
1:YA:2193:G:H2'	1:YA:2194:G:H8	1.84	0.42
1:YA:226:G:C2	1:YA:227:A:C6	3.07	0.42
1:YA:649:G:H2'	1:YA:650:C:C6	2.55	0.42
1:YA:886:C:O2'	1:YA:889:C:N4	2.52	0.42
1:YA:952:G:C6	1:YA:953:A:N7	2.88	0.42
3:YD:182:LEU:HB2	3:YD:272:ALA:HB3	2.02	0.42
5:YF:184:TYR:O	5:YF:188:ARG:HG3	2.19	0.42
7:YH:8:PRO:HB2	7:YH:49:VAL:CG2	2.49	0.42
1:YA:2406:U:N3	11:YP:73:GLY:O	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:YT:53:ARG:NH1	15:YT:53:ARG:HB3	2.34	0.42
1:YA:483:A:H1'	20:YY:59:GLY:O	2.20	0.42
21:YZ:5:LEU:HD11	21:YZ:39:VAL:HB	2.01	0.42
32:QA:108:G:N1	51:QT:15:ARG:HG2	2.34	0.42
32:QA:1316:G:N2	32:QA:1318:A:H3'	2.34	0.42
32:QA:441:A:H3'	32:QA:442:C:C6	2.55	0.42
32:QA:77:G:C2'	32:QA:78:G:H5'	2.49	0.42
35:QD:196:LEU:HD12	35:QD:196:LEU:H	1.85	0.42
35:QD:53:ASP:HB3	35:QD:57:ARG:NH1	2.28	0.42
37:QF:45:LEU:HD23	37:QF:57:GLN:OE1	2.20	0.42
40:QI:4:TYR:HB2	40:QI:19:LEU:HB2	2.01	0.42
40:QI:97:LYS:HB3	40:QI:98:PRO:HD3	2.02	0.42
32:QA:1125:U:H4'	41:QJ:5:ARG:NH2	2.35	0.42
51:QT:10:LEU:HD23	51:QT:11:SER:H	1.84	0.42
25:R3:3:ARG:HD3	25:R3:60:GLU:CD	2.40	0.42
1:RA:2006:C:H6	1:RA:2006:C:O5'	2.02	0.42
1:RA:2630:G:H2'	1:RA:2631:G:C8	2.54	0.42
1:RA:458:G:O2'	1:RA:469:G:O6	2.25	0.42
1:RA:492:A:H2'	1:RA:493:G:O4'	2.20	0.42
1:RA:652(U):C:H2'	1:RA:652(V):G:C8	2.55	0.42
1:RA:984:A:H5''	1:RA:985:C:H5	1.84	0.42
1:RA:2334:G:H5'	14:RS:9:ARG:HG2	2.01	0.42
32:XA:1009:G:H1	32:XA:1020:U:H3	1.68	0.42
32:XA:919:A:O2'	32:XA:1080:A:N1	2.38	0.42
32:XA:559:A:H5''	32:XA:560:U:H3'	2.01	0.42
32:XA:601:C:H2'	32:XA:602:A:C8	2.55	0.42
32:XA:407:G:H5''	35:XD:115:ARG:HG2	2.00	0.42
38:XG:69:VAL:HG21	38:XG:104:LEU:HD11	2.02	0.42
46:XO:54:ARG:HD2	46:XO:58:MET:HE2	2.02	0.42
47:XP:60:LEU:HA	47:XP:60:LEU:HD12	1.86	0.42
32:XA:266:G:C3'	48:XQ:67:LYS:HB2	2.49	0.42
53:XV:40:C:H2'	53:XV:41:C:C6	2.54	0.42
30:Y8:23:VAL:HG13	30:Y8:47:LYS:HB3	2.02	0.42
1:YA:1040:C:H4'	21:YZ:46:LYS:CE	2.49	0.42
1:YA:1270:C:H5''	1:YA:1271:G:O5'	2.20	0.42
1:YA:1719:G:C6	1:YA:1720:U:C4	3.07	0.42
1:YA:2028:U:H2'	1:YA:2029:G:O4'	2.19	0.42
1:YA:2320:A:N3	1:YA:2320:A:H2'	2.34	0.42
32:QA:1427:U:H2'	32:QA:1428:A:H8	1.85	0.42
32:QA:1517:G:C6	32:QA:1518:MA6:C6	3.03	0.42
39:QH:51:VAL:HG11	39:QH:60:ARG:NH1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:QN:27:CYS:SG	45:QN:29:ARG:HB2	2.59	0.42
50:QS:22:LEU:HD12	50:QS:31:ILE:HD11	2.02	0.42
52:QU:5:ASP:O	52:QU:11:GLY:HA3	2.20	0.42
26:R4:24:THR:OG1	26:R4:25:TYR:N	2.53	0.42
1:RA:2001:A:OP1	13:RR:9:LYS:NZ	2.43	0.42
1:RA:297:C:H2'	1:RA:298:G:O4'	2.20	0.42
1:RA:579:G:H2'	1:RA:580:C:C6	2.54	0.42
5:RF:148:LEU:CD2	5:RF:191:ARG:HE	2.33	0.42
20:RY:5:MET:HE2	20:RY:35:TYR:CD1	2.55	0.42
32:XA:1129:C:H4'	32:XA:1130:A:OP1	2.20	0.42
32:XA:7:G:H5'	32:XA:298:A:O4'	2.20	0.42
55:XY:108:GLU:HB3	55:XY:170:GLY:H	1.85	0.42
26:Y4:61:ARG:HH21	50:XS:9:VAL:HG11	1.85	0.42
1:YA:2081:C:H2'	1:YA:2082:A:C8	2.52	0.42
1:YA:183:C:H42	1:YA:213:A:H61	1.68	0.42
7:YH:16:SER:O	7:YH:26:VAL:HA	2.20	0.42
8:YI:65:ALA:O	8:YI:69:LYS:N	2.53	0.42
32:QA:1479:C:H2'	32:QA:1480:G:C8	2.55	0.42
33:QB:185:ILE:HG22	33:QB:199:TYR:CD2	2.55	0.42
33:QB:212:GLN:O	33:QB:216:SER:OG	2.37	0.42
33:QB:45:GLN:O	33:QB:49:GLU:HG2	2.19	0.42
33:QB:8:LYS:H	33:QB:8:LYS:HG3	1.60	0.42
34:QC:179:ARG:NH1	34:QC:206:GLU:OE1	2.53	0.42
37:QF:76:ALA:O	37:QF:80:ARG:HG3	2.20	0.42
43:QL:109:GLY:HA3	43:QL:121:GLY:O	2.20	0.42
26:R4:59:PHE:CD1	50:QS:64:GLU:HG3	2.54	0.42
1:RA:1087:G:H1	1:RA:1102:C:H42	1.68	0.42
1:RA:117:G:C6	1:RA:119:A:C6	3.08	0.42
1:RA:2119:A:O2'	1:RA:2120:G:H5'	2.20	0.42
1:RA:185:U:H4'	1:RA:218:A:H4'	2.02	0.42
1:RA:2393:A:H2'	1:RA:2394:C:O4'	2.20	0.42
1:RA:2693:A:H2'	1:RA:2694:G:H8	1.85	0.42
1:RA:323:G:H1'	1:RA:1205:U:O2	2.20	0.42
1:RA:792:G:H5''	1:RA:793:A:H5'	2.01	0.42
7:RH:12:PRO:O	7:RH:15:VAL:HG22	2.19	0.42
15:RT:51:ARG:HG3	15:RT:98:LYS:HE3	2.01	0.42
32:XA:371:G:O2'	32:XA:373:A:N7	2.51	0.42
32:XA:781:A:H4'	32:XA:1522:U:O2'	2.19	0.42
32:XA:865:A:H5'	32:XA:1078:U:C5	2.55	0.42
33:XB:57:PHE:CE2	33:XB:185:ILE:HD11	2.54	0.42
55:XY:310:TYR:HB3	55:XY:329:LEU:HD11	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Y9:27:CYS:SG	31:Y9:28:GLU:N	2.93	0.42
1:YA:1709:U:H2'	1:YA:1710:C:C6	2.55	0.42
3:YD:69:ARG:HG2	3:YD:130:ALA:HB3	2.02	0.42
6:YG:139:LEU:HA	6:YG:144:ILE:HB	2.02	0.42
7:YH:144:VAL:O	7:YH:148:ILE:HG12	2.20	0.42
10:YO:9:GLU:O	10:YO:83:ALA:HA	2.20	0.42
12:YQ:41:TRP:CD1	12:YQ:96:VAL:HG22	2.55	0.42
13:YR:96:ARG:HG2	13:YR:115:GLU:HG3	2.01	0.42
14:YS:83:LYS:HB3	14:YS:111:GLU:OE1	2.19	0.42
15:YT:16:ARG:HG2	15:YT:18:ASP:OD1	2.20	0.42
32:QA:1323:G:H2'	32:QA:1324:A:C8	2.55	0.41
32:QA:1327:C:H2'	32:QA:1328:C:C6	2.55	0.41
32:QA:821:G:H2'	32:QA:822:C:C6	2.55	0.41
32:QA:757:U:O2'	32:QA:879:C:O2	2.32	0.41
32:QA:921:U:O2	36:QE:19:MET:HB2	2.19	0.41
39:QH:119:LEU:HB3	39:QH:123:GLU:HB2	2.01	0.41
41:QJ:35:SER:N	41:QJ:73:ASP:O	2.44	0.41
55:QY:248:HIS:CE1	55:QY:250:PRO:HG2	2.55	0.41
1:RA:1058:G:N2	1:RA:1080:C:N3	2.61	0.41
1:RA:1356:G:N2	1:RA:1376:C:C2	2.88	0.41
1:RA:1412:A:H2'	1:RA:1413:G:O4'	2.20	0.41
1:RA:1812:A:O2'	3:RD:45:ASN:N	2.52	0.41
1:RA:2061:G:C2	1:RA:2063:C:C4	3.08	0.41
1:RA:42:G:H1'	1:RA:437:G:N2	2.35	0.41
1:RA:468:G:H5''	5:RF:60:SER:HB2	2.01	0.41
4:RE:94:GLU:OE2	4:RE:177:PRO:HB3	2.20	0.41
18:RW:46:PHE:O	18:RW:50:VAL:HG23	2.20	0.41
19:RX:41:ASN:O	19:RX:45:THR:HG23	2.20	0.41
32:XA:1070:U:H2'	32:XA:1071:C:C6	2.55	0.41
32:XA:921:U:H2'	32:XA:922:G:O4'	2.20	0.41
42:XK:84:VAL:HG21	42:XK:95:ILE:HD11	2.01	0.41
45:XN:58:LYS:HE3	45:XN:58:LYS:HB3	1.82	0.41
1:YA:1913:A:OP1	55:XY:160:LYS:HE2	2.20	0.41
1:YA:2286:A:OP1	28:Y6:29:ASN:HB3	2.20	0.41
1:YA:272(O):C:H2'	1:YA:272(P):C:C6	2.55	0.41
1:YA:674:G:O2'	5:YF:74:ARG:HD3	2.19	0.41
2:YB:13:A:O2'	2:YB:14:U:H3'	2.19	0.41
5:YF:89:VAL:HG12	5:YF:90:PHE:CD2	2.55	0.41
7:YH:98:LEU:HD12	7:YH:98:LEU:HA	1.86	0.41
1:YA:2319:G:H22	14:YS:3:ARG:CZ	2.33	0.41
38:QG:12:LEU:HD12	38:QG:12:LEU:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:QY:317:VAL:HG23	55:QY:329:LEU:HB2	2.03	0.41
1:RA:1070:A:H2'	1:RA:1071:G:C8	2.55	0.41
1:RA:1080:C:H2'	1:RA:1081:U:C6	2.54	0.41
1:RA:738:G:C6	1:RA:739:G:C2	3.08	0.41
1:RA:911:A:H2'	12:RQ:9:TYR:OH	2.20	0.41
32:XA:1286:A:C8	32:XA:1287:A:H4'	2.55	0.41
32:XA:1346:A:N1	32:XA:1374:A:H5''	2.34	0.41
32:XA:1516:G:H2'	32:XA:1518:MA6:OP2	2.20	0.41
32:XA:176:C:H2'	32:XA:177:C:H6	1.85	0.41
32:XA:324:G:N1	32:XA:327:A:OP2	2.52	0.41
33:XB:19:HIS:CG	33:XB:20:GLU:N	2.88	0.41
40:XI:100:GLY:O	40:XI:103:THR:HG22	2.20	0.41
40:XI:5:TYR:HE1	40:XI:16:ARG:HB3	1.85	0.41
41:XJ:9:ARG:NH2	41:XJ:95:GLU:OE1	2.45	0.41
28:Y6:6:ARG:NH1	28:Y6:26:ASN:HB2	2.35	0.41
1:YA:2493:U:HO2'	55:XY:264:HIS:CD2	2.38	0.41
1:YA:434:U:H1'	1:YA:435:C:H5	1.85	0.41
1:YA:671:C:H2'	1:YA:672:C:C6	2.55	0.41
1:YA:272(P):C:O2'	8:YI:42:SER:OG	2.17	0.41
32:QA:1179:A:H2'	32:QA:1180:A:O4'	2.20	0.41
32:QA:1182:G:H5'	32:QA:1184:G:H5'	2.03	0.41
33:QB:146:GLN:O	33:QB:150:SER:HB3	2.20	0.41
33:QB:15:VAL:O	33:QB:15:VAL:HG22	2.20	0.41
36:QE:31:LEU:HD11	36:QE:129:ILE:HA	2.02	0.41
47:QP:34:GLU:OE2	47:QP:55:ARG:NH2	2.54	0.41
47:QP:74:LEU:HB3	47:QP:79:VAL:CG2	2.51	0.41
22:R0:27:GLU:HB2	22:R0:69:PHE:HD1	1.85	0.41
24:R2:3:LEU:HD23	24:R2:3:LEU:HA	1.90	0.41
1:RA:1213:A:N3	1:RA:1238:G:H1'	2.34	0.41
1:RA:1803:A:H4'	3:RD:259:THR:HG23	2.01	0.41
1:RA:908:C:OP1	12:RQ:22:LYS:HB3	2.20	0.41
4:RE:144:ARG:HB3	4:RE:145:LYS:H	1.66	0.41
6:RG:45:GLU:HG2	6:RG:45:GLU:H	1.53	0.41
17:RV:40:LEU:HB2	17:RV:46:VAL:CG1	2.51	0.41
17:RV:14:VAL:HB	17:RV:96:ILE:HG13	2.02	0.41
18:RW:23:LEU:HD11	27:R5:25:LEU:HB2	2.02	0.41
32:XA:1521:G:H2'	32:XA:1522:U:C6	2.54	0.41
32:XA:841:U:H6	32:XA:841:U:OP1	2.03	0.41
32:XA:913:A:H4'	32:XA:914:A:O5'	2.21	0.41
38:XG:113:GLU:HG3	38:XG:118:VAL:HG12	2.03	0.41
40:XI:5:TYR:OH	40:XI:16:ARG:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:YN:23:ARG:NH1	45:YN:28:GLY:O	2.50	0.41
48:XQ:4:LYS:H	48:XQ:61:GLU:HG2	1.84	0.41
55:XY:259:ASP:N	55:XY:259:ASP:OD1	2.51	0.41
23:Y1:82:LEU:O	23:Y1:85:LEU:HD13	2.20	0.41
31:Y9:22:ARG:HB2	31:Y9:24:TYR:CE1	2.55	0.41
1:YA:1721:G:H2'	1:YA:1740:G:O6	2.20	0.41
1:YA:1932:A:H2'	1:YA:1933:G:O4'	2.18	0.41
1:YA:981:A:HO2'	1:YA:2036:C:HO2'	1.69	0.41
1:YA:2251:OMG:HM23	1:YA:2251:OMG:H1'	1.85	0.41
1:YA:2262:U:OP1	1:YA:2387:U:O2'	2.28	0.41
1:YA:459:U:H2'	1:YA:460:A:C8	2.55	0.41
1:YA:601:C:O2'	1:YA:605:C:H5''	2.21	0.41
1:YA:738:G:C6	1:YA:739:G:C2	3.09	0.41
1:YA:960:A:H2'	1:YA:962:G:H5'	2.02	0.41
12:YQ:31:ASP:OD1	12:YQ:134:ARG:NH1	2.44	0.41
32:QA:1398:A:H5'	32:QA:1401:G:H4'	2.03	0.41
32:QA:1513:A:H2'	32:QA:1514:C:C6	2.55	0.41
32:QA:159:G:O2'	32:QA:161:A:N7	2.50	0.41
35:QD:18:LYS:NZ	35:QD:31:CYS:SG	2.91	0.41
26:R4:50:VAL:HG21	44:QM:64:TRP:C	2.41	0.41
49:QR:65:ILE:O	49:QR:69:THR:HG23	2.21	0.41
26:R4:10:VAL:HG21	26:R4:29:PRO:HG3	2.01	0.41
1:RA:1778:U:H2'	1:RA:1784:A:N6	2.35	0.41
1:RA:1794:U:H2'	1:RA:1795:C:C6	2.56	0.41
1:RA:2679:A:C2	1:RA:2729:G:C2	3.08	0.41
3:RD:69:ARG:HE	3:RD:130:ALA:HB2	1.86	0.41
1:RA:2730:C:O2'	4:RE:168:MET:O	2.28	0.41
5:RF:22:ALA:HB1	5:RF:203:GLN:HE22	1.85	0.41
1:RA:1006:C:O2'	9:RN:106:MET:HB3	2.20	0.41
9:RN:108:PRO:O	9:RN:113:GLY:HA3	2.20	0.41
32:XA:321:A:H2	32:XA:332:G:H22	1.69	0.41
39:XH:121:ASP:N	39:XH:121:ASP:OD1	2.51	0.41
39:XH:73:ASP:OD1	39:XH:75:ARG:HG3	2.21	0.41
39:XH:85:ARG:NH2	39:XH:87:SER:O	2.53	0.41
44:XM:108:ARG:HD3	44:XM:108:ARG:HA	1.90	0.41
49:XR:41:LYS:HG2	49:XR:41:LYS:O	2.20	0.41
51:XT:42:GLN:NE2	51:XT:46:GLU:OE2	2.53	0.41
1:YA:1912:A:H4'	55:XY:160:LYS:HZ3	1.85	0.41
31:Y9:22:ARG:HB2	31:Y9:24:TYR:HE1	1.84	0.41
1:YA:1683:C:H2'	1:YA:1684:C:C6	2.56	0.41
1:YA:242:G:O2'	1:YA:254:G:O6	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:YD:38:LYS:HD2	3:YD:38:LYS:HA	1.88	0.41
1:YA:1654:A:O2'	4:YE:113:PHE:O	2.26	0.41
11:YP:126:VAL:HG22	11:YP:146:VAL:HB	2.03	0.41
32:QA:1010:G:N2	32:QA:1020:U:H1'	2.35	0.41
32:QA:782:A:O3'	32:QA:1515:C:H4'	2.20	0.41
32:QA:345:C:H4'	32:QA:346:G:C4	2.56	0.41
32:QA:437:U:H5'	35:QD:155:LEU:HD21	2.02	0.41
32:QA:689:C:OP1	42:QK:44:SER:OG	2.23	0.41
33:QB:91:PRO:HG2	33:QB:155:LEU:HD23	2.02	0.41
34:QC:125:GLU:HG3	34:QC:189:ALA:HB1	2.03	0.41
47:QP:79:VAL:HG23	47:QP:80:PHE:CD1	2.55	0.41
1:RA:1789:A:H5'	3:RD:221:VAL:HG12	2.01	0.41
1:RA:2699:C:H2'	1:RA:2700:C:O4'	2.19	0.41
1:RA:304:G:C2	1:RA:305:U:C2	3.09	0.41
1:RA:300:A:H1'	1:RA:319:C:H1'	2.03	0.41
3:RD:106:ILE:O	3:RD:108:PRO:HD3	2.20	0.41
4:RE:47:VAL:HG23	4:RE:84:PHE:O	2.20	0.41
1:RA:674:G:C1'	5:RF:74:ARG:HD3	2.50	0.41
1:RA:272(M):G:N2	8:RI:50:ARG:HD3	2.35	0.41
10:RO:22:ILE:HG12	10:RO:40:VAL:O	2.20	0.41
10:RO:73:ASP:HB2	15:RT:82:LEU:HD13	2.03	0.41
17:RV:71:LEU:HD23	17:RV:71:LEU:HA	1.91	0.41
19:RX:56:THR:HB	19:RX:77:LYS:HE3	2.02	0.41
34:XC:28:GLN:HB3	34:XC:32:LEU:HD23	2.02	0.41
35:XD:76:ARG:HD3	35:XD:207:TYR:CE1	2.55	0.41
46:XO:4:THR:CG2	46:XO:7:GLU:H	2.33	0.41
53:XV:47:U:H3'	53:XV:48:C:C5'	2.50	0.41
1:YA:1900:A:N1	1:YA:1970:A:C6	2.88	0.41
1:YA:859:G:O2'	1:YA:916:G:O6	2.35	0.41
10:YO:4:PRO:HA	10:YO:21:CYS:O	2.20	0.41
11:YP:39:LYS:HD2	11:YP:45:LEU:HD11	2.01	0.41
15:YT:91:ARG:HD2	15:YT:120:ARG:NH1	2.35	0.41
32:QA:266:G:O3'	48:QQ:67:LYS:HB2	2.19	0.41
32:QA:627:G:H2'	32:QA:628:G:C8	2.55	0.41
32:QA:736:C:H2'	32:QA:737:A:C8	2.56	0.41
35:QD:111:ALA:HB2	35:QD:120:LEU:HD12	2.02	0.41
55:QY:221:ASP:HB3	55:QY:250:PRO:CD	2.50	0.41
55:QY:99:LEU:HD12	55:QY:349:GLN:HE22	1.86	0.41
24:R2:63:VAL:HA	24:R2:66:GLU:HB2	2.02	0.41
1:RA:242:G:C8	30:R8:5:LYS:HG2	2.56	0.41
1:RA:675:A:C6	1:RA:676:A:C6	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:RF:153:SER:OG	5:RF:190:GLU:HG3	2.20	0.41
14:RS:59:LYS:CD	14:RS:60:GLY:H	2.21	0.41
15:RT:16:ARG:HG2	15:RT:18:ASP:OD1	2.19	0.41
32:XA:1323:G:H2'	32:XA:1324:A:C8	2.56	0.41
32:XA:881:G:OP2	43:XL:12:ARG:NH2	2.51	0.41
34:XC:180:ALA:HB1	34:XC:203:PHE:CE1	2.55	0.41
41:XJ:7:LYS:HB2	41:XJ:97:GLU:HB2	2.03	0.41
23:Y1:77:ALA:O	23:Y1:80:LEU:HB2	2.20	0.41
1:YA:1069:A:H5'	1:YA:1096:A:C5'	2.51	0.41
1:YA:1069:A:H5'	1:YA:1096:A:H5'	2.03	0.41
1:YA:1316:U:H2'	1:YA:1317:A:H8	1.86	0.41
1:YA:1430:C:H2'	1:YA:1431:U:C6	2.55	0.41
1:YA:2361:A:H5'	30:Y8:26:LYS:HZ1	1.84	0.41
1:YA:581:C:H2'	1:YA:582:G:C8	2.55	0.41
1:YA:582:G:H2'	1:YA:583:G:C8	2.56	0.41
2:YB:105:A:H2'	2:YB:106:G:O4'	2.21	0.41
4:YE:116:VAL:HG13	4:YE:122:PHE:HB2	2.02	0.41
1:YA:1130:U:C2	4:YE:147:PRO:HB3	2.54	0.41
32:QA:1143:G:H2'	32:QA:1144:G:H8	1.85	0.41
32:QA:499:A:H4'	32:QA:500:G:H5'	2.03	0.41
32:QA:619:U:N3	35:QD:134:ASP:OD1	2.38	0.41
35:QD:188:LEU:HD23	35:QD:188:LEU:H	1.85	0.41
35:QD:173:TRP:CG	35:QD:189:PRO:HG3	2.55	0.41
37:QF:91:VAL:HG11	49:QR:72:ARG:NH1	2.36	0.41
40:QI:17:VAL:HG23	40:QI:63:ILE:HG12	2.01	0.41
41:QJ:19:SER:O	41:QJ:23:ILE:HG12	2.21	0.41
41:QJ:49:VAL:HG21	45:QN:41:ARG:O	2.21	0.41
45:QN:41:ARG:HG3	45:QN:42:ILE:HG13	2.03	0.41
53:QV:10:G:N2	53:QV:26:G:H1'	2.36	0.41
55:QY:244:ILE:H	55:QY:266:ASN:HD22	1.68	0.41
1:RA:1899:G:N3	1:RA:1899:G:H2'	2.35	0.41
1:RA:1133:U:O4	1:RA:2026:C:H1'	2.21	0.41
1:RA:2445:G:OP1	5:RF:74:ARG:NH2	2.53	0.41
1:RA:321:G:H5'	5:RF:134:GLY:O	2.19	0.41
1:RA:309:G:C5	1:RA:330:A:C6	3.09	0.41
4:RE:119:ARG:HG3	4:RE:160:TYR:CG	2.55	0.41
5:RF:110:LEU:HA	5:RF:183:VAL:HG12	2.03	0.41
13:RR:54:LEU:HD12	13:RR:54:LEU:HA	1.97	0.41
21:RZ:103:ARG:HD2	21:RZ:136:PHE:CG	2.56	0.41
32:XA:255:G:H2'	32:XA:256:U:C6	2.56	0.41
32:XA:292:G:C5	32:XA:293:G:H1'	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:407:G:OP1	35:XD:115:ARG:HD3	2.20	0.41
32:XA:8:A:H5'	36:XE:101:ILE:HG22	2.01	0.41
33:XB:24:TRP:CZ3	33:XB:26:PRO:HA	2.55	0.41
35:XD:88:VAL:HG22	36:XE:96:PRO:HB2	2.02	0.41
32:XA:1329:A:P	44:XM:28:ALA:HB3	2.60	0.41
55:XY:255:VAL:CG1	55:XY:274:LEU:HG	2.45	0.41
1:YA:2137:C:C2	1:YA:2154:G:N1	2.89	0.41
1:YA:2264:C:H2'	1:YA:2265:U:C6	2.55	0.41
1:YA:57:C:H2'	1:YA:58:G:O4'	2.21	0.41
1:YA:635:C:O2'	1:YA:639:U:OP1	2.30	0.41
1:YA:687:C:H2'	1:YA:688:U:O4'	2.19	0.41
1:YA:910:A:N1	1:YA:2277:G:H1'	2.36	0.41
4:YE:12:THR:HG22	4:YE:13:ARG:N	2.32	0.41
4:YE:174:ASP:OD1	4:YE:175:VAL:N	2.54	0.41
9:YN:62:VAL:CG1	9:YN:66:LYS:HB2	2.50	0.41
16:YU:27:LEU:HB3	16:YU:31:SER:HB3	2.03	0.41
18:YW:8:ARG:HG2	18:YW:102:HIS:ND1	2.36	0.41
32:QA:1418:A:N6	32:QA:1482:G:O2'	2.47	0.41
32:QA:408:A:H2'	32:QA:409:G:O4'	2.21	0.41
33:QB:77:ALA:HB2	33:QB:211:ILE:HD13	2.03	0.41
35:QD:108:LEU:HB3	35:QD:110:PHE:CD1	2.56	0.41
31:R9:32:HIS:O	31:R9:34:GLN:HG3	2.21	0.41
1:RA:1073:A:H4'	1:RA:1074:G:OP1	2.21	0.41
1:RA:1092:C:H6	1:RA:1092:C:OP2	2.04	0.41
1:RA:1359:A:H61	1:RA:1372:U:H3	1.69	0.41
1:RA:1421:G:C2	1:RA:1422:G:C8	3.09	0.41
1:RA:2228:G:OP1	3:RD:261:LYS:NZ	2.36	0.41
1:RA:329:G:P	1:RA:329:G:H8	2.43	0.41
1:RA:523:C:O2	1:RA:554:U:O2'	2.35	0.41
1:RA:777:A:H2'	1:RA:778:G:C8	2.56	0.41
2:RB:13:A:N1	2:RB:69:G:O2'	2.39	0.41
1:RA:559:G:H22	16:RU:49:HIS:CE1	2.39	0.41
32:XA:1366:C:H2'	32:XA:1367:C:C6	2.55	0.41
32:XA:189(M):G:H2'	32:XA:190:U:H6	1.86	0.41
32:XA:738:C:OP1	37:XF:2:ARG:NH1	2.51	0.41
32:XA:575:G:O2'	32:XA:821:G:H5'	2.20	0.41
32:XA:979:C:H42	45:YN:18:VAL:HG12	1.84	0.41
35:XD:190:ASP:O	35:XD:193:ASP:HB2	2.20	0.41
36:XE:141:GLN:HA	36:XE:143:ARG:HH21	1.86	0.41
41:XJ:70:ARG:HD3	41:XJ:70:ARG:HA	1.92	0.41
37:XF:100:ASN:HB2	49:XR:27:GLY:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:XY:129:GLY:HA2	55:XY:159:TYR:HD2	1.86	0.41
1:YA:560:C:H4'	16:YU:52:ARG:HE	1.86	0.41
1:YA:839:U:H2'	1:YA:840:C:C6	2.56	0.41
7:YH:171:LEU:H	7:YH:171:LEU:HD23	1.85	0.41
10:YO:8:LEU:HD12	10:YO:84:ALA:HB2	2.02	0.41
1:YA:2318:G:N2	14:YS:3:ARG:HH11	2.18	0.41
14:YS:43:GLU:OE1	22:Y0:49:LYS:HE3	2.21	0.41
32:QA:1441:G:H4'	32:QA:1442(A):G:C4	2.56	0.41
32:QA:58:C:O2'	32:QA:388:G:N7	2.50	0.41
32:QA:7:G:O2'	36:QE:120:THR:O	2.39	0.41
34:QC:6:HIS:HE1	34:QC:8:ILE:HB	1.83	0.41
35:QD:8:VAL:HG22	35:QD:21:LEU:HD13	2.03	0.41
37:QF:41:GLU:HG2	37:QF:43:LEU:HD12	2.02	0.41
41:QJ:78:ASN:O	41:QJ:80:LYS:N	2.54	0.41
41:QJ:84:GLN:HE21	41:QJ:84:GLN:HB3	1.61	0.41
55:QY:214:LEU:HD12	55:QY:215:PRO:CD	2.50	0.41
1:RA:1071:G:OP1	1:RA:1073:A:N6	2.53	0.41
1:RA:1055:G:H21	1:RA:1084:A:N6	2.19	0.41
1:RA:1482:G:C6	1:RA:1507:A:C6	3.08	0.41
1:RA:2070:G:H2'	1:RA:2071:A:O4'	2.21	0.41
1:RA:2158:A:H1'	1:RA:2159:G:C8	2.56	0.41
1:RA:2306:C:C4	1:RA:2307:G:C6	3.08	0.41
4:RE:143:ASN:HD22	4:RE:147:PRO:CD	2.34	0.41
6:RG:53:LEU:HD23	6:RG:53:LEU:H	1.86	0.41
12:RQ:35:VAL:HG13	12:RQ:130:LYS:HB3	2.03	0.41
1:RA:1649:G:O2'	13:RR:107:ASP:OD2	2.33	0.41
16:RU:28:ARG:NH1	16:RU:38:THR:OG1	2.47	0.41
32:XA:1070:U:H2'	32:XA:1071:C:H6	1.85	0.41
32:XA:1099:G:OP2	33:XB:144:ARG:NH2	2.54	0.41
32:XA:1225:A:H2'	32:XA:1226:C:C5	2.56	0.41
32:XA:449:C:O2	47:XP:42:ARG:HD2	2.21	0.41
36:XE:78:HIS:CG	39:XH:104:ARG:HD2	2.56	0.41
44:XM:22:ILE:HB	44:XM:25:ILE:HD12	2.03	0.41
32:XA:728:A:C8	46:XO:54:ARG:NH2	2.88	0.41
32:XA:663:A:H5''	49:XR:61:LYS:NZ	2.36	0.41
55:XY:183:ARG:O	55:XY:309:THR:HA	2.20	0.41
1:YA:1420:U:O2'	1:YA:1421:G:OP1	2.31	0.41
1:YA:2287:A:C8	1:YA:2289:G:C8	3.08	0.41
1:YA:646:A:H2'	1:YA:647:G:O4'	2.21	0.41
9:YN:35:ARG:HH21	9:YN:42:TRP:HZ2	1.68	0.41
12:YQ:137:TYR:O	12:YQ:141:GLN:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:YU:36:ARG:HD3	16:YU:40:PHE:CZ	2.56	0.41
32:QA:1005:A:OP1	32:QA:1006:C:N4	2.53	0.41
32:QA:1466:C:H2'	32:QA:1467:G:O4'	2.21	0.41
32:QA:266:G:H5''	32:QA:267:C:C5	2.56	0.41
32:QA:540:G:H2'	32:QA:541:G:O4'	2.21	0.41
35:QD:188:LEU:HA	35:QD:189:PRO:HD3	1.91	0.41
32:QA:193:C:H4'	51:QT:60:GLU:HG2	2.03	0.41
1:RA:116:C:H2'	1:RA:117:G:O4'	2.21	0.41
1:RA:2046:G:H5'	27:R5:19:ARG:HB2	2.03	0.41
1:RA:2122:U:H2'	1:RA:2123:G:C8	2.56	0.41
1:RA:337:C:H2'	1:RA:338:G:O4'	2.21	0.41
1:RA:812:C:HO2'	1:RA:1226:A:HO2'	1.62	0.41
7:RH:98:LEU:HA	7:RH:98:LEU:HD12	1.97	0.41
10:RO:80:ASP:OD1	15:RT:64:ARG:NH2	2.54	0.41
21:RZ:198:LYS:HE2	53:QV:52:G:H2'	2.02	0.41
32:XA:1518:MA6:H93	32:XA:1519:MA6:N6	2.36	0.41
32:XA:20:U:H2'	32:XA:21:G:O4'	2.20	0.41
32:XA:796:C:O5'	32:XA:796:C:H6	2.03	0.41
32:XA:952:U:H2'	32:XA:953:G:C8	2.56	0.41
34:XC:50:ALA:HB1	34:XC:70:VAL:HG21	2.03	0.41
39:XH:96:GLY:N	39:XH:99:GLU:HG3	2.36	0.41
47:XP:20:VAL:HG23	47:XP:35:LYS:HA	2.03	0.41
47:XP:4:ILE:HG23	47:XP:36:ILE:HD11	2.03	0.41
1:YA:1472:A:H2'	1:YA:1473:G:O4'	2.21	0.41
1:YA:2031:A:N3	1:YA:2455:G:O2'	2.49	0.41
1:YA:2405:G:H5'	11:YP:75:ILE:HD13	2.03	0.41
2:YB:12:C:H2'	22:Y0:73:GLY:HA3	2.03	0.41
5:YF:11:VAL:HG22	5:YF:125:LEU:HB2	2.03	0.41
14:YS:11:LYS:HG3	14:YS:91:PRO:HD3	2.02	0.41
4:YE:179:GLU:HG3	15:YT:9:LEU:CD2	2.51	0.41
20:YY:13:VAL:O	20:YY:24:VAL:HA	2.21	0.41
32:QA:1492:A:O2'	55:QY:119:THR:HG23	2.20	0.41
32:QA:255:G:C2	32:QA:272:C:C2	3.09	0.41
32:QA:36:C:OP1	43:QL:123:LYS:HE2	2.21	0.41
32:QA:441:A:H3'	32:QA:442:C:H6	1.86	0.41
32:QA:757:U:H2'	32:QA:758:G:O4'	2.21	0.41
32:QA:772:U:C4	32:QA:773:G:N7	2.89	0.41
40:QI:8:GLY:HA3	40:QI:76:ALA:O	2.21	0.41
41:QJ:21:GLN:O	41:QJ:25:GLU:HG3	2.20	0.41
34:QC:5:ILE:HD13	41:QJ:51:ARG:HH12	1.86	0.41
34:QC:58:GLU:CB	41:QJ:92:THR:HG21	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:QV:19:G:H5'	53:QV:20:U:H5	1.86	0.41
1:RA:1053:C:H4'	1:RA:1054:A:OP1	2.21	0.41
1:RA:2075:U:C4	1:RA:2238:G:C6	3.08	0.41
1:RA:2391:G:O6	1:RA:2425:A:H8	2.03	0.41
1:RA:2502:G:H5''	1:RA:2503:2MA:H5''	2.03	0.41
1:RA:2503:2MA:H4'	1:RA:2504:U:OP1	2.21	0.41
1:RA:2507:C:C2	1:RA:2508:G:C8	3.09	0.41
1:RA:2578:G:OP1	1:RA:2614:A:N6	2.51	0.41
1:RA:2717:G:H1'	15:RT:96:ARG:HH21	1.86	0.41
1:RA:2849:U:H4'	1:RA:2868:A:C2	2.56	0.41
1:RA:392:C:H5''	1:RA:409:C:H5''	2.02	0.41
1:RA:411:G:C5	11:RP:72:PRO:HB3	2.56	0.41
1:RA:500:G:N1	1:RA:503:A:OP2	2.54	0.41
1:RA:859:G:O2'	1:RA:916:G:O6	2.35	0.41
7:RH:69:ARG:HH11	7:RH:69:ARG:HD3	1.62	0.41
11:RP:88:LEU:HD11	11:RP:114:ILE:HD12	2.02	0.41
32:XA:25:C:H2'	32:XA:26:A:C8	2.55	0.41
32:XA:539:A:H2'	32:XA:540:G:H8	1.84	0.41
32:XA:946:A:H2'	32:XA:947:G:C8	2.55	0.41
36:XE:69:VAL:HA	36:XE:70:PRO:HD3	1.84	0.41
40:XI:121:ARG:NH1	40:XI:122:ALA:O	2.53	0.41
32:XA:530:G:C6	54:XX:21:A:C4	3.08	0.41
55:XY:328:ARG:NH1	55:XY:331:GLU:OE1	2.42	0.41
24:Y2:12:GLU:HA	24:Y2:15:LYS:NZ	2.36	0.41
25:Y3:26:LEU:O	25:Y3:35:ARG:NE	2.48	0.41
26:Y4:61:ARG:HG2	50:XS:42:PRO:CG	2.51	0.41
1:YA:1317:A:H2'	1:YA:1318:C:C6	2.56	0.41
1:YA:2077:A:H2'	1:YA:2078:C:H6	1.86	0.41
1:YA:2330:G:H2'	1:YA:2331:G:O4'	2.21	0.41
1:YA:2359:C:H2'	1:YA:2360:A:O4'	2.20	0.41
1:YA:2887:U:H2'	1:YA:2888:C:C6	2.55	0.41
1:YA:613:G:O2'	1:YA:614(D):A:N1	2.40	0.41
1:YA:775:G:C4	1:YA:794:G:C8	3.09	0.41
1:YA:2680:C:H5'	4:YE:189:PRO:HA	2.02	0.41
7:YH:140:LYS:HB2	7:YH:140:LYS:HE3	1.89	0.41
9:YN:120:LEU:HD22	9:YN:122:VAL:HG23	2.03	0.41
10:YO:105:GLU:N	10:YO:105:GLU:OE1	2.49	0.41
12:YQ:29:PHE:O	21:YZ:122:ARG:NH2	2.52	0.41
20:YY:35:TYR:CE2	20:YY:69:ALA:HB3	2.56	0.41
21:YZ:72:ARG:HD2	21:YZ:72:ARG:HH11	1.75	0.41
32:QA:1005:A:O5'	32:QA:1005:A:H8	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:31:G:N7	32:QA:306:G:H1'	2.36	0.40
32:QA:652:U:O4	32:QA:752:G:O2'	2.29	0.40
34:QC:181:ASN:OD1	34:QC:204:LEU:HD12	2.20	0.40
35:QD:111:ALA:HB1	35:QD:116:GLN:HB3	2.03	0.40
42:QK:78:GLN:O	42:QK:103:LEU:HD23	2.22	0.40
49:QR:28:GLU:HG2	49:QR:28:GLU:H	1.63	0.40
55:QY:322:ILE:HD11	55:QY:344:ILE:HA	2.03	0.40
19:RX:60:ARG:NH1	29:R7:47:ARG:HH12	2.19	0.40
1:RA:241:A:H8	1:RA:241:A:OP1	2.04	0.40
1:RA:2577:A:H2'	1:RA:2614:A:N6	2.36	0.40
1:RA:674:G:O2'	5:RF:74:ARG:HD3	2.20	0.40
16:RU:86:ALA:O	17:RV:49:THR:HG23	2.21	0.40
20:RY:56:PRO:C	20:RY:58:GLY:H	2.25	0.40
21:RZ:28:MET:HG3	21:RZ:90:VAL:CG2	2.51	0.40
32:XA:1289:A:N1	32:XA:1371:G:O2'	2.40	0.40
32:XA:217:C:H2'	32:XA:218:C:C6	2.56	0.40
32:XA:411:A:OP1	35:XD:30:LYS:NZ	2.37	0.40
32:XA:657:G:C2	32:XA:658:G:C8	3.09	0.40
32:XA:687:A:H4'	32:XA:688:G:OP1	2.21	0.40
36:XE:92:LYS:HB3	36:XE:119:LEU:HB2	2.03	0.40
32:XA:539:A:OP2	43:XL:115:LYS:NZ	2.54	0.40
44:XM:13:LYS:HA	44:XM:44:ARG:HH11	1.86	0.40
44:XM:57:ARG:O	44:XM:61:GLU:HG3	2.21	0.40
32:XA:1458:G:H5''	51:XT:31:SER:HB2	2.02	0.40
24:Y2:65:ASN:OD1	24:Y2:69:ARG:NH1	2.53	0.40
1:YA:1427:A:H4'	1:YA:1428:C:O4'	2.21	0.40
1:YA:2001:A:H2'	1:YA:2002:G:C8	2.56	0.40
1:YA:2181:G:H2'	1:YA:2182:G:O4'	2.21	0.40
1:YA:2818:G:O2'	1:YA:2819:G:H5'	2.21	0.40
1:YA:588:U:H1'	5:YF:90:PHE:HB3	2.02	0.40
1:YA:753:C:H2'	1:YA:754:C:H6	1.86	0.40
1:YA:947:G:H2'	1:YA:948:G:C8	2.56	0.40
1:YA:2823:A:OP1	4:YE:113:PHE:HB2	2.20	0.40
4:YE:18:ASP:HB3	15:YT:82:LEU:HD21	2.03	0.40
5:YF:53:THR:CG2	5:YF:56:GLU:HG3	2.52	0.40
15:YT:39:ARG:NH1	15:YT:41:ARG:HD3	2.36	0.40
32:QA:1277:C:O2'	32:QA:1279:A:H1'	2.20	0.40
32:QA:1280:A:O2'	32:QA:1281:U:H5'	2.21	0.40
32:QA:35:G:O2'	43:QL:118:SER:O	2.28	0.40
23:R1:23:LYS:HB3	23:R1:29:GLY:HA3	2.03	0.40
27:R5:35:GLU:HG2	27:R5:51:TYR:CD2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1583:A:H5''	1:RA:1584:C:OP1	2.21	0.40
1:RA:2033:A:O2'	1:RA:2035:G:OP2	2.29	0.40
1:RA:2315:G:H2'	1:RA:2316:C:C6	2.56	0.40
1:RA:2519:U:C4	1:RA:2542:A:C5	3.10	0.40
1:RA:2870:C:H5''	13:RR:65:LEU:HD21	2.03	0.40
1:RA:37:C:H2'	1:RA:38:A:C8	2.55	0.40
2:RB:33:G:C6	2:RB:34:U:C4	3.09	0.40
2:RB:7:G:H5''	2:RB:7:G:H8	1.86	0.40
20:RY:5:MET:HE3	20:RY:32:PRO:HA	2.03	0.40
32:XA:18:C:H4'	32:XA:1078:U:O2	2.21	0.40
32:XA:163:C:H2'	32:XA:164:U:O4'	2.21	0.40
32:XA:581:G:OP1	46:XO:65:ARG:NH2	2.48	0.40
33:XB:101:MET:HG2	33:XB:108:ILE:HG21	2.02	0.40
49:XR:76:LEU:HA	49:XR:76:LEU:HD12	1.89	0.40
1:YA:1064:C:H5	1:YA:1065:U:C6	2.38	0.40
1:YA:225:A:O2'	1:YA:257:A:H4'	2.20	0.40
1:YA:2667:C:H2'	1:YA:2668:G:O4'	2.21	0.40
1:YA:272(F):C:H2'	1:YA:272(G):C:C6	2.56	0.40
1:YA:2732:G:H3'	1:YA:2733:A:O4'	2.20	0.40
3:YD:18:VAL:HG12	3:YD:211:ARG:NH1	2.37	0.40
5:YF:192:LEU:HD22	5:YF:194:MET:HG3	2.03	0.40
7:YH:113:VAL:HG11	7:YH:151:ILE:HD13	2.02	0.40
9:YN:99:LEU:HD23	9:YN:99:LEU:HA	1.81	0.40
10:YO:70:LYS:HE2	10:YO:70:LYS:HB3	1.91	0.40
12:YQ:35:VAL:HG12	12:YQ:130:LYS:O	2.21	0.40
1:YA:2018:G:O2'	16:YU:34:LYS:HE3	2.21	0.40
2:YB:77:U:OP1	21:YZ:19:ARG:NH2	2.53	0.40
32:QA:637:G:H2'	32:QA:638:G:C8	2.56	0.40
33:QB:169:LYS:HG3	33:QB:170:GLU:OE1	2.22	0.40
48:QQ:62:SER:OG	48:QQ:72:ARG:HG3	2.21	0.40
55:QY:105:PRO:C	55:QY:107:ASP:H	2.24	0.40
1:RA:1425:G:H2'	1:RA:1426:G:O4'	2.21	0.40
1:RA:2553:G:C2	1:RA:2583:G:H1'	2.56	0.40
1:RA:321:G:O2'	1:RA:340:A:N3	2.52	0.40
1:RA:820:A:H2'	1:RA:821:A:O4'	2.22	0.40
2:RB:105:A:H2'	2:RB:106:G:O4'	2.22	0.40
4:RE:2:LYS:HB2	4:RE:95:ILE:HD12	2.02	0.40
6:RG:50:ALA:C	6:RG:52:ILE:N	2.74	0.40
6:RG:64:THR:HB	6:RG:94:LEU:HD21	2.03	0.40
12:RQ:35:VAL:HG12	12:RQ:130:LYS:O	2.21	0.40
18:RW:14:PRO:HG2	18:RW:78:GLU:HG2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:RZ:35:ARG:HD2	21:RZ:35:ARG:HA	1.93	0.40
32:XA:1133:G:H2'	32:XA:1134:G:C8	2.57	0.40
32:XA:986:A:H2'	32:XA:987:G:O4'	2.21	0.40
33:XB:41:ILE:HD13	33:XB:41:ILE:HA	1.78	0.40
34:XC:43:LEU:HB3	34:XC:47:LEU:HD12	2.03	0.40
38:XG:114:ARG:HB2	38:XG:115:ARG:HH21	1.86	0.40
47:XP:14:ASN:HD22	47:XP:42:ARG:NH2	2.19	0.40
47:XP:75:ARG:HG3	47:XP:80:PHE:CD2	2.56	0.40
53:XV:52:G:C2	53:XV:63:G:C2	3.10	0.40
53:XV:76:A:H3'	55:XY:234:GLY:HA3	2.03	0.40
55:XY:183:ARG:NH2	55:XY:309:THR:HG21	2.36	0.40
1:YA:1359:A:N3	1:YA:1359:A:H5'	2.36	0.40
1:YA:1417:C:H2'	1:YA:1418:G:O4'	2.21	0.40
1:YA:1598:C:H2'	1:YA:1599:C:C6	2.56	0.40
1:YA:1668:A:C8	1:YA:1674:G:C6	3.09	0.40
1:YA:249:C:O2	30:Y8:12:LYS:NZ	2.31	0.40
1:YA:2679:A:H4'	4:YE:165:VAL:HG11	2.02	0.40
1:YA:612:C:H2'	1:YA:613:G:O4'	2.20	0.40
1:YA:724:U:H2'	1:YA:725:G:O4'	2.21	0.40
2:YB:17:C:H2'	2:YB:18:G:O4'	2.21	0.40
2:YB:75:G:H4'	21:YZ:36:LYS:HG2	2.02	0.40
3:YD:102:LYS:O	3:YD:103:ARG:HG2	2.21	0.40
6:YG:16:ARG:NE	6:YG:31:VAL:HG21	2.34	0.40
12:YQ:75:THR:HA	12:YQ:89:ASN:O	2.21	0.40
16:YU:112:ARG:H	16:YU:112:ARG:HG2	1.73	0.40
21:YZ:92:SER:O	21:YZ:130:PRO:HG2	2.22	0.40
32:QA:790:A:C6	32:QA:791:G:C6	3.09	0.40
46:QO:8:LYS:O	46:QO:12:ILE:HG13	2.21	0.40
32:QA:582:U:OP1	46:QO:64:ARG:NH1	2.55	0.40
22:R0:22:GLY:N	22:R0:39:ARG:O	2.43	0.40
31:R9:10:ILE:HD12	31:R9:32:HIS:HA	2.02	0.40
1:RA:523:C:H4'	1:RA:540:C:O2	2.20	0.40
5:RF:29:ASN:H	5:RF:112:MET:HE3	1.86	0.40
7:RH:4:ILE:O	7:RH:69:ARG:HG2	2.21	0.40
1:RA:272(K):U:H1'	8:RI:50:ARG:NH2	2.36	0.40
13:RR:96:ARG:NH1	13:RR:115:GLU:OE1	2.52	0.40
32:XA:101:A:H5''	51:XT:10:LEU:HD21	2.03	0.40
32:XA:1492:A:O4'	43:XL:47:LYS:HD3	2.22	0.40
32:XA:403:C:OP1	35:XD:137:SER:OG	2.32	0.40
34:XC:140:ARG:HB2	34:XC:140:ARG:NH1	2.36	0.40
34:XC:8:ILE:HG12	34:XC:184:TYR:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:542:G:H5'	35:XD:41:GLY:HA3	2.03	0.40
37:XF:82:ARG:HB2	37:XF:85:VAL:HG23	2.03	0.40
42:XK:65:ALA:HB3	42:XK:97:ALA:HB3	2.03	0.40
44:XM:16:ASP:OD1	44:XM:16:ASP:N	2.53	0.40
22:Y0:19:LYS:HA	22:Y0:19:LYS:HD3	1.86	0.40
1:YA:1093:G:H2'	1:YA:1094:U:O4'	2.21	0.40
1:YA:1486:A:H2'	1:YA:1487:G:H8	1.86	0.40
1:YA:300:A:H1'	1:YA:319:C:H1'	2.04	0.40
1:YA:329:G:P	1:YA:329:G:H8	2.44	0.40
1:YA:2314:C:H5'	6:YG:38:VAL:HG11	2.04	0.40
6:YG:43:LEU:HB3	6:YG:44:GLY:H	1.70	0.40
32:QA:1279:A:O2'	32:QA:1281:U:OP2	2.22	0.40
32:QA:427:U:OP1	35:QD:13:ARG:NH2	2.55	0.40
32:QA:947:G:H2'	32:QA:948:C:O4'	2.21	0.40
36:QE:126:ARG:HG3	36:QE:126:ARG:NH1	2.30	0.40
40:QI:4:TYR:O	40:QI:19:LEU:N	2.40	0.40
55:QY:101:LEU:H	55:QY:102:PRO:HD2	1.87	0.40
55:QY:214:LEU:H	55:QY:215:PRO:HD3	1.85	0.40
30:R8:23:VAL:CG1	30:R8:47:LYS:HB3	2.51	0.40
1:RA:1817:G:C6	1:RA:1818:U:C4	3.10	0.40
1:RA:1907:G:C2	1:RA:1908:C:C2	3.10	0.40
1:RA:2106:G:C6	1:RA:2107:C:C2	3.10	0.40
1:RA:2540:C:H2'	1:RA:2541:A:O4'	2.21	0.40
1:RA:536:A:H2'	1:RA:537:C:C6	2.56	0.40
1:RA:643:A:N1	1:RA:2369:A:O2'	2.44	0.40
1:RA:1789:A:OP1	3:RD:221:VAL:HA	2.21	0.40
3:RD:5:LYS:HE3	3:RD:5:LYS:HB3	1.85	0.40
8:RI:61:ARG:HD3	8:RI:61:ARG:HA	1.74	0.40
14:RS:39:ILE:HB	14:RS:49:VAL:HG12	2.03	0.40
32:XA:1273:G:H3'	32:XA:1274:G:H8	1.86	0.40
32:XA:266:G:O3'	48:XQ:67:LYS:HB2	2.22	0.40
32:XA:404:U:H5''	35:XD:122:ARG:HD3	2.03	0.40
32:XA:936:C:H2'	32:XA:937:A:O4'	2.21	0.40
33:XB:9:GLU:O	33:XB:11:LEU:N	2.55	0.40
37:XF:45:LEU:HD23	37:XF:57:GLN:OE1	2.21	0.40
42:XK:92:GLU:O	42:XK:96:ARG:HD2	2.22	0.40
43:XL:8:ASN:O	43:XL:12:ARG:HG3	2.21	0.40
55:XY:119:THR:O	55:XY:199:SER:HB2	2.21	0.40
26:Y4:64:GLY:C	26:Y4:66:SER:N	2.75	0.40
1:YA:242:G:C8	30:Y8:3:LYS:HG3	2.56	0.40
1:YA:307:G:N2	1:YA:309:G:H3'	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YE:52:LEU:O	4:YE:76:ARG:N	2.49	0.40
5:YF:130:ALA:HB3	5:YF:142:TRP:HD1	1.87	0.40
14:YS:20:ARG:O	14:YS:20:ARG:HD3	2.21	0.40
16:YU:65:ILE:CD1	16:YU:95:LEU:HB3	2.51	0.40
20:YY:38:ILE:HD11	20:YY:66:PRO:HG3	2.03	0.40
21:YZ:183:LEU:HA	21:YZ:183:LEU:HD23	1.95	0.40
21:YZ:35:ARG:HD2	21:YZ:35:ARG:HA	1.94	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)
24:R2:46:GLN:OE1	1:YA:277:C:O2'[3_555]	2.02	0.18

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	RD	273/276 (99%)	263 (96%)	10 (4%)	0	100	100
3	YD	273/276 (99%)	262 (96%)	11 (4%)	0	100	100
4	RE	202/206 (98%)	195 (96%)	6 (3%)	1 (0%)	34	74
4	YE	202/206 (98%)	194 (96%)	8 (4%)	0	100	100
5	RF	201/210 (96%)	196 (98%)	5 (2%)	0	100	100
5	YF	201/210 (96%)	194 (96%)	6 (3%)	1 (0%)	34	74
6	RG	179/182 (98%)	168 (94%)	9 (5%)	2 (1%)	17	56
6	YG	179/182 (98%)	169 (94%)	9 (5%)	1 (1%)	30	70
7	RH	172/180 (96%)	164 (95%)	8 (5%)	0	100	100
7	YH	171/180 (95%)	163 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	RI	145/148 (98%)	134 (92%)	10 (7%)	1 (1%)	26	67
8	YI	144/148 (97%)	136 (94%)	8 (6%)	0	100	100
9	RN	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
9	YN	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
10	RO	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
10	YO	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
11	RP	147/150 (98%)	141 (96%)	5 (3%)	1 (1%)	26	67
11	YP	147/150 (98%)	141 (96%)	5 (3%)	1 (1%)	26	67
12	RQ	139/141 (99%)	136 (98%)	3 (2%)	0	100	100
12	YQ	139/141 (99%)	136 (98%)	3 (2%)	0	100	100
13	RR	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
13	YR	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
14	RS	108/112 (96%)	104 (96%)	3 (3%)	1 (1%)	21	61
14	YS	108/112 (96%)	105 (97%)	3 (3%)	0	100	100
15	RT	129/146 (88%)	124 (96%)	5 (4%)	0	100	100
15	YT	129/146 (88%)	125 (97%)	4 (3%)	0	100	100
16	RU	114/118 (97%)	114 (100%)	0	0	100	100
16	YU	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
17	RV	99/101 (98%)	95 (96%)	4 (4%)	0	100	100
17	YV	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	19	58
18	RW	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
18	YW	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
19	RX	93/96 (97%)	92 (99%)	1 (1%)	0	100	100
19	YX	93/96 (97%)	92 (99%)	0	1 (1%)	17	56
20	RY	105/110 (96%)	98 (93%)	7 (7%)	0	100	100
20	YY	105/110 (96%)	101 (96%)	4 (4%)	0	100	100
21	RZ	201/206 (98%)	196 (98%)	5 (2%)	0	100	100
21	YZ	199/206 (97%)	194 (98%)	5 (2%)	0	100	100
22	R0	75/85 (88%)	73 (97%)	2 (3%)	0	100	100
22	Y0	75/85 (88%)	72 (96%)	3 (4%)	0	100	100
23	R1	95/98 (97%)	94 (99%)	0	1 (1%)	17	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	Y1	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	17	56
24	R2	68/72 (94%)	68 (100%)	0	0	100	100
24	Y2	68/72 (94%)	68 (100%)	0	0	100	100
25	R3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
25	Y3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
26	R4	67/71 (94%)	55 (82%)	7 (10%)	5 (8%)	1	6
26	Y4	67/71 (94%)	56 (84%)	9 (13%)	2 (3%)	5	27
27	R5	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
27	Y5	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
28	R6	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
28	Y6	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
29	R7	46/49 (94%)	46 (100%)	0	0	100	100
29	Y7	46/49 (94%)	46 (100%)	0	0	100	100
30	R8	62/65 (95%)	62 (100%)	0	0	100	100
30	Y8	62/65 (95%)	62 (100%)	0	0	100	100
31	R9	35/37 (95%)	35 (100%)	0	0	100	100
31	Y9	35/37 (95%)	35 (100%)	0	0	100	100
33	QB	229/256 (90%)	204 (89%)	17 (7%)	8 (4%)	4	23
33	XB	229/256 (90%)	203 (89%)	21 (9%)	5 (2%)	8	35
34	QC	204/239 (85%)	191 (94%)	13 (6%)	0	100	100
34	XC	204/239 (85%)	189 (93%)	14 (7%)	1 (0%)	34	74
35	QD	206/209 (99%)	196 (95%)	10 (5%)	0	100	100
35	XD	206/209 (99%)	199 (97%)	7 (3%)	0	100	100
36	QE	146/162 (90%)	145 (99%)	1 (1%)	0	100	100
36	XE	146/162 (90%)	145 (99%)	1 (1%)	0	100	100
37	QF	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
37	XF	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
38	QG	153/156 (98%)	150 (98%)	3 (2%)	0	100	100
38	XG	153/156 (98%)	150 (98%)	3 (2%)	0	100	100
39	QH	135/138 (98%)	133 (98%)	2 (2%)	0	100	100
39	XH	135/138 (98%)	133 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	QI	125/128 (98%)	116 (93%)	9 (7%)	0	100	100
40	XI	124/128 (97%)	113 (91%)	9 (7%)	2 (2%)	12	45
41	QJ	95/105 (90%)	81 (85%)	11 (12%)	3 (3%)	5	25
41	XJ	94/105 (90%)	83 (88%)	10 (11%)	1 (1%)	17	56
42	QK	112/129 (87%)	105 (94%)	7 (6%)	0	100	100
42	XK	112/129 (87%)	106 (95%)	5 (4%)	1 (1%)	21	61
43	QL	119/132 (90%)	118 (99%)	1 (1%)	0	100	100
43	XL	119/132 (90%)	117 (98%)	2 (2%)	0	100	100
44	QM	114/126 (90%)	105 (92%)	8 (7%)	1 (1%)	21	61
44	XM	112/126 (89%)	104 (93%)	7 (6%)	1 (1%)	21	61
45	QN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
45	XN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
46	QO	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
46	XO	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
47	QP	80/88 (91%)	77 (96%)	3 (4%)	0	100	100
47	XP	80/88 (91%)	77 (96%)	3 (4%)	0	100	100
48	QQ	97/105 (92%)	94 (97%)	3 (3%)	0	100	100
48	XQ	97/105 (92%)	95 (98%)	2 (2%)	0	100	100
49	QR	66/88 (75%)	66 (100%)	0	0	100	100
49	XR	66/88 (75%)	66 (100%)	0	0	100	100
50	QS	81/93 (87%)	77 (95%)	4 (5%)	0	100	100
50	XS	81/93 (87%)	77 (95%)	4 (5%)	0	100	100
51	QT	94/106 (89%)	90 (96%)	3 (3%)	1 (1%)	17	56
51	XT	96/106 (91%)	90 (94%)	4 (4%)	2 (2%)	9	37
52	QU	21/27 (78%)	19 (90%)	2 (10%)	0	100	100
52	XU	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
55	QY	257/360 (71%)	218 (85%)	21 (8%)	18 (7%)	1	7
55	XY	258/360 (72%)	215 (83%)	30 (12%)	13 (5%)	3	14
All	All	11955/12848 (93%)	11397 (95%)	481 (4%)	77 (1%)	30	70

All (77) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	R4	47	GLN
26	R4	49	PHE
33	QB	16	HIS
55	QY	98	VAL
55	QY	210	PRO
55	QY	241	ASP
55	QY	304	SER
5	YF	21	ALA
23	Y1	3	LYS
26	Y4	60	GLN
33	XB	17	PHE
40	XI	44	VAL
40	XI	54	ASP
44	XM	67	GLU
51	XT	95	ALA
55	XY	216	ASP
55	XY	241	ASP
6	RG	51	ARG
26	R4	45	GLY
26	R4	55	ARG
33	QB	17	PHE
41	QJ	31	GLY
41	QJ	78	ASN
51	QT	95	ALA
55	QY	211	ASP
55	QY	214	LEU
55	QY	299	GLY
55	QY	324	LEU
55	QY	337	LEU
6	YG	81	LYS
33	XB	20	GLU
33	XB	124	SER
55	XY	106	ASP
55	XY	217	ILE
55	XY	306	ARG
26	R4	57	GLU
55	QY	101	LEU
33	XB	10	LEU
33	XB	125	PRO
41	XJ	78	ASN
55	XY	101	LEU
55	XY	102	PRO
55	XY	324	LEU

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Mol	Chain	Res	Type
4	RE	52	LEU
6	RG	49	ASP
33	QB	21	ARG
55	QY	99	LEU
55	QY	109	ARG
55	QY	213	GLU
33	QB	20	GLU
44	QM	12	ASN
55	QY	143	ARG
55	QY	305	ASP
55	QY	322	ILE
55	XY	305	ASP
55	XY	323	ASN
55	XY	337	LEU
8	RI	73	GLU
23	R1	3	LYS
33	QB	127	ILE
55	QY	217	ILE
26	Y4	55	ARG
34	XC	108	ASN
55	QY	313	PRO
51	XT	100	ILE
33	QB	124	SER
41	QJ	77	PRO
11	YP	122	PRO
17	YV	79	VAL
11	RP	122	PRO
14	RS	60	GLY
33	QB	231	GLU
42	XK	118	GLY
55	XY	301	GLY
19	YX	94	GLY
55	XY	299	GLY
33	QB	125	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	RD	214/218 (98%)	210 (98%)	4 (2%)	65	89
3	YD	215/218 (99%)	209 (97%)	6 (3%)	51	83
4	RE	164/166 (99%)	157 (96%)	7 (4%)	35	73
4	YE	164/166 (99%)	157 (96%)	7 (4%)	35	73
5	RF	160/166 (96%)	151 (94%)	9 (6%)	26	63
5	YF	159/166 (96%)	153 (96%)	6 (4%)	40	77
6	RG	144/156 (92%)	139 (96%)	5 (4%)	43	79
6	YG	142/156 (91%)	134 (94%)	8 (6%)	26	63
7	RH	144/148 (97%)	141 (98%)	3 (2%)	61	88
7	YH	143/148 (97%)	138 (96%)	5 (4%)	43	79
8	RI	111/124 (90%)	106 (96%)	5 (4%)	34	72
8	YI	108/124 (87%)	99 (92%)	9 (8%)	14	44
9	RN	119/119 (100%)	113 (95%)	6 (5%)	30	68
9	YN	118/119 (99%)	111 (94%)	7 (6%)	24	61
10	RO	100/100 (100%)	99 (99%)	1 (1%)	82	94
10	YO	100/100 (100%)	100 (100%)	0	100	100
11	RP	115/116 (99%)	110 (96%)	5 (4%)	35	73
11	YP	115/116 (99%)	109 (95%)	6 (5%)	29	66
12	RQ	111/111 (100%)	108 (97%)	3 (3%)	52	84
12	YQ	111/111 (100%)	107 (96%)	4 (4%)	42	78
13	RR	101/101 (100%)	95 (94%)	6 (6%)	24	61
13	YR	101/101 (100%)	95 (94%)	6 (6%)	24	61
14	RS	87/88 (99%)	84 (97%)	3 (3%)	44	80
14	YS	85/88 (97%)	82 (96%)	3 (4%)	43	79
15	RT	115/127 (91%)	110 (96%)	5 (4%)	35	73
15	YT	113/127 (89%)	109 (96%)	4 (4%)	43	79
16	RU	93/94 (99%)	91 (98%)	2 (2%)	60	87
16	YU	93/94 (99%)	92 (99%)	1 (1%)	80	94
17	RV	81/82 (99%)	77 (95%)	4 (5%)	31	69
17	YV	80/82 (98%)	76 (95%)	4 (5%)	30	68
18	RW	90/92 (98%)	86 (96%)	4 (4%)	35	73
18	YW	90/92 (98%)	86 (96%)	4 (4%)	35	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	RX	77/78 (99%)	76 (99%)	1 (1%)	76	93
19	YX	77/78 (99%)	76 (99%)	1 (1%)	76	93
20	RY	86/91 (94%)	85 (99%)	1 (1%)	78	93
20	YY	86/91 (94%)	84 (98%)	2 (2%)	58	86
21	RZ	169/179 (94%)	165 (98%)	4 (2%)	57	86
21	YZ	165/179 (92%)	163 (99%)	2 (1%)	78	93
22	R0	61/67 (91%)	59 (97%)	2 (3%)	45	81
22	Y0	61/67 (91%)	61 (100%)	0	100	100
23	R1	79/83 (95%)	76 (96%)	3 (4%)	40	77
23	Y1	81/83 (98%)	77 (95%)	4 (5%)	31	69
24	R2	65/67 (97%)	65 (100%)	0	100	100
24	Y2	66/67 (98%)	66 (100%)	0	100	100
25	R3	51/52 (98%)	48 (94%)	3 (6%)	24	61
25	Y3	50/52 (96%)	47 (94%)	3 (6%)	24	60
26	R4	58/63 (92%)	56 (97%)	2 (3%)	44	80
26	Y4	54/63 (86%)	50 (93%)	4 (7%)	17	50
27	R5	51/52 (98%)	48 (94%)	3 (6%)	24	61
27	Y5	50/52 (96%)	47 (94%)	3 (6%)	24	60
28	R6	51/52 (98%)	49 (96%)	2 (4%)	39	76
28	Y6	50/52 (96%)	49 (98%)	1 (2%)	63	88
29	R7	41/42 (98%)	39 (95%)	2 (5%)	31	69
29	Y7	41/42 (98%)	39 (95%)	2 (5%)	31	69
30	R8	54/55 (98%)	51 (94%)	3 (6%)	26	63
30	Y8	54/55 (98%)	51 (94%)	3 (6%)	26	63
31	R9	34/34 (100%)	34 (100%)	0	100	100
31	Y9	34/34 (100%)	34 (100%)	0	100	100
33	QB	191/220 (87%)	177 (93%)	14 (7%)	17	51
33	XB	187/220 (85%)	173 (92%)	14 (8%)	17	49
34	QC	144/188 (77%)	138 (96%)	6 (4%)	36	74
34	XC	140/188 (74%)	133 (95%)	7 (5%)	30	68
35	QD	171/181 (94%)	166 (97%)	5 (3%)	50	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	XD	172/181 (95%)	163 (95%)	9 (5%)	29	66
36	QE	114/123 (93%)	112 (98%)	2 (2%)	66	90
36	XE	114/123 (93%)	110 (96%)	4 (4%)	43	79
37	QF	85/90 (94%)	85 (100%)	0	100	100
37	XF	85/90 (94%)	84 (99%)	1 (1%)	78	93
38	QG	120/127 (94%)	115 (96%)	5 (4%)	36	74
38	XG	119/127 (94%)	116 (98%)	3 (2%)	55	85
39	QH	116/119 (98%)	112 (97%)	4 (3%)	44	80
39	XH	114/119 (96%)	111 (97%)	3 (3%)	54	84
40	QI	91/99 (92%)	85 (93%)	6 (7%)	21	56
40	XI	88/99 (89%)	83 (94%)	5 (6%)	25	62
41	QJ	68/92 (74%)	67 (98%)	1 (2%)	72	91
41	XJ	68/92 (74%)	68 (100%)	0	100	100
42	QK	83/99 (84%)	80 (96%)	3 (4%)	42	78
42	XK	83/99 (84%)	80 (96%)	3 (4%)	42	78
43	QL	96/108 (89%)	96 (100%)	0	100	100
43	XL	96/108 (89%)	92 (96%)	4 (4%)	36	74
44	QM	90/101 (89%)	88 (98%)	2 (2%)	60	87
44	XM	87/101 (86%)	84 (97%)	3 (3%)	44	80
45	QN	49/50 (98%)	45 (92%)	4 (8%)	14	45
45	XN	49/50 (98%)	48 (98%)	1 (2%)	63	88
46	QO	78/80 (98%)	77 (99%)	1 (1%)	76	93
46	XO	78/80 (98%)	76 (97%)	2 (3%)	54	84
47	QP	69/74 (93%)	66 (96%)	3 (4%)	35	73
47	XP	68/74 (92%)	64 (94%)	4 (6%)	24	61
48	QQ	94/97 (97%)	93 (99%)	1 (1%)	80	94
48	XQ	94/97 (97%)	92 (98%)	2 (2%)	61	88
49	QR	59/77 (77%)	57 (97%)	2 (3%)	44	80
49	XR	59/77 (77%)	58 (98%)	1 (2%)	68	90
50	QS	68/80 (85%)	65 (96%)	3 (4%)	35	73
50	XS	67/80 (84%)	67 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	QT	71/82 (87%)	67 (94%)	4 (6%)	26	63
51	XT	70/82 (85%)	67 (96%)	3 (4%)	35	73
52	QU	18/22 (82%)	18 (100%)	0	100	100
52	XU	18/22 (82%)	17 (94%)	1 (6%)	26	63
55	QY	210/300 (70%)	206 (98%)	4 (2%)	65	89
55	XY	211/300 (70%)	202 (96%)	9 (4%)	35	73
All	All	9784/10664 (92%)	9432 (96%)	352 (4%)	42	78

All (352) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	RD	52	ARG
3	RD	142	VAL
3	RD	211	ARG
3	RD	257	LEU
4	RE	9	VAL
4	RE	21	VAL
4	RE	75	VAL
4	RE	111	ARG
4	RE	113	PHE
4	RE	116	VAL
4	RE	184	VAL
5	RF	20	LEU
5	RF	33	LEU
5	RF	53	THR
5	RF	57	VAL
5	RF	110	LEU
5	RF	125	LEU
5	RF	168	ARG
5	RF	192	LEU
5	RF	197	ASP
6	RG	7	LEU
6	RG	60	LEU
6	RG	82	LEU
6	RG	146	TYR
6	RG	170	ARG
7	RH	23	ARG
7	RH	62	LYS
7	RH	105	LEU
8	RI	12	LEU

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Mol	Chain	Res	Type
8	RI	57	ARG
8	RI	75	LEU
8	RI	109	ILE
8	RI	121	LYS
9	RN	12	ARG
9	RN	48	MET
9	RN	61	ARG
9	RN	99	LEU
9	RN	120	LEU
9	RN	121	LYS
10	RO	69	ILE
11	RP	55	ARG
11	RP	59	LEU
11	RP	65	ARG
11	RP	106	LEU
11	RP	112	LEU
12	RQ	16	ARG
12	RQ	75	THR
12	RQ	109	VAL
13	RR	18	LEU
13	RR	28	LEU
13	RR	44	LEU
13	RR	60	LEU
13	RR	79	LEU
13	RR	86	ARG
14	RS	23	ARG
14	RS	25	ARG
14	RS	59	LYS
15	RT	16	ARG
15	RT	53	ARG
15	RT	64	ARG
15	RT	78	LEU
15	RT	96	ARG
16	RU	74	LEU
16	RU	92	ARG
17	RV	18	LEU
17	RV	61	VAL
17	RV	79	VAL
17	RV	82	ARG
18	RW	4	LYS
18	RW	11	ARG
18	RW	51	LEU

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Mol	Chain	Res	Type
18	RW	67	ASP
19	RX	76	ARG
20	RY	90	LEU
21	RZ	28	MET
21	RZ	150	LEU
21	RZ	161	VAL
21	RZ	185	GLU
22	R0	39	ARG
22	R0	59	LEU
23	R1	21	ARG
23	R1	52	ARG
23	R1	95	LEU
25	R3	8	LEU
25	R3	44	ARG
25	R3	54	VAL
26	R4	49	PHE
26	R4	61	ARG
27	R5	29	THR
27	R5	35	GLU
27	R5	60	VAL
28	R6	19	ARG
28	R6	28	ARG
29	R7	23	ARG
29	R7	43	THR
30	R8	30	ARG
30	R8	31	HIS
30	R8	34	TRP
33	QB	15	VAL
33	QB	16	HIS
33	QB	21	ARG
33	QB	24	TRP
33	QB	44	LEU
33	QB	76	GLN
33	QB	106	LYS
33	QB	122	PHE
33	QB	135	GLN
33	QB	144	ARG
33	QB	157	ARG
33	QB	160	ASP
33	QB	163	PHE
33	QB	195	ASP
34	QC	29	TYR

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Mol	Chain	Res	Type
34	QC	36	ASP
34	QC	127	ARG
34	QC	150	LYS
34	QC	178	LEU
34	QC	196	LEU
35	QD	8	VAL
35	QD	31	CYS
35	QD	49	ARG
35	QD	115	ARG
35	QD	135	LEU
36	QE	12	LEU
36	QE	41	VAL
38	QG	56	GLN
38	QG	73	MET
38	QG	104	LEU
38	QG	114	ARG
38	QG	143	ARG
39	QH	18	ARG
39	QH	25	ASP
39	QH	56	LYS
39	QH	112	LEU
40	QI	42	ARG
40	QI	66	ARG
40	QI	81	ILE
40	QI	83	ARG
40	QI	92	TYR
40	QI	93	ARG
41	QJ	84	GLN
42	QK	96	ARG
42	QK	116	HIS
42	QK	117	ASN
44	QM	3	ARG
44	QM	65	LYS
45	QN	3	ARG
45	QN	18	VAL
45	QN	33	VAL
45	QN	41	ARG
46	QO	39	LEU
47	QP	19	ILE
47	QP	20	VAL
47	QP	50	LYS
48	QQ	72	ARG

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Mol	Chain	Res	Type
49	QR	31	LEU
49	QR	76	LEU
50	QS	5	LEU
50	QS	41	VAL
50	QS	65	ASN
51	QT	9	ASN
51	QT	10	LEU
51	QT	84	LEU
51	QT	100	ILE
55	QY	184	VAL
55	QY	244	ILE
55	QY	305	ASP
55	QY	311	ASN
3	YD	69	ARG
3	YD	94	LEU
3	YD	142	VAL
3	YD	211	ARG
3	YD	257	LEU
3	YD	275	LYS
4	YE	9	VAL
4	YE	21	VAL
4	YE	52	LEU
4	YE	75	VAL
4	YE	111	ARG
4	YE	113	PHE
4	YE	116	VAL
5	YF	20	LEU
5	YF	33	LEU
5	YF	57	VAL
5	YF	110	LEU
5	YF	183	VAL
5	YF	197	ASP
6	YG	3	LEU
6	YG	21	ARG
6	YG	49	ASP
6	YG	113	ARG
6	YG	115	ARG
6	YG	136	ARG
6	YG	146	TYR
6	YG	170	ARG
7	YH	23	ARG
7	YH	30	LYS

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Mol	Chain	Res	Type
7	YH	33	LEU
7	YH	71	LEU
7	YH	88	LEU
8	YI	9	LEU
8	YI	50	ARG
8	YI	61	ARG
8	YI	68	LEU
8	YI	75	LEU
8	YI	77	LEU
8	YI	92	VAL
8	YI	116	LEU
8	YI	123	LEU
9	YN	12	ARG
9	YN	28	THR
9	YN	67	LEU
9	YN	87	LEU
9	YN	96	GLU
9	YN	99	LEU
9	YN	120	LEU
11	YP	55	ARG
11	YP	59	LEU
11	YP	65	ARG
11	YP	106	LEU
11	YP	112	LEU
11	YP	148	LEU
12	YQ	16	ARG
12	YQ	21	THR
12	YQ	75	THR
12	YQ	109	VAL
13	YR	18	LEU
13	YR	28	LEU
13	YR	44	LEU
13	YR	60	LEU
13	YR	79	LEU
13	YR	111	LEU
14	YS	23	ARG
14	YS	25	ARG
14	YS	67	ARG
15	YT	16	ARG
15	YT	64	ARG
15	YT	95	ARG
15	YT	96	ARG

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Mol	Chain	Res	Type
16	YU	74	LEU
17	YV	38	LEU
17	YV	53	GLU
17	YV	79	VAL
17	YV	82	ARG
18	YW	11	ARG
18	YW	15	ARG
18	YW	23	LEU
18	YW	51	LEU
19	YX	88	LYS
20	YY	23	ARG
20	YY	72	VAL
21	YZ	94	GLU
21	YZ	150	LEU
23	Y1	21	ARG
23	Y1	26	ARG
23	Y1	52	ARG
23	Y1	96	LYS
25	Y3	8	LEU
25	Y3	30	ARG
25	Y3	54	VAL
26	Y4	8	LYS
26	Y4	48	ARG
26	Y4	58	ARG
26	Y4	62	ARG
27	Y5	29	THR
27	Y5	35	GLU
27	Y5	40	LYS
28	Y6	19	ARG
29	Y7	23	ARG
29	Y7	43	THR
30	Y8	30	ARG
30	Y8	31	HIS
30	Y8	34	TRP
33	XB	16	HIS
33	XB	17	PHE
33	XB	24	TRP
33	XB	44	LEU
33	XB	114	ARG
33	XB	122	PHE
33	XB	127	ILE
33	XB	154	LEU

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Mol	Chain	Res	Type
33	XB	157	ARG
33	XB	160	ASP
33	XB	163	PHE
33	XB	217	ARG
33	XB	224	GLN
33	XB	226	ARG
34	XC	29	TYR
34	XC	30	ARG
34	XC	45	LYS
34	XC	85	ARG
34	XC	140	ARG
34	XC	178	LEU
34	XC	190	ARG
35	XD	8	VAL
35	XD	28	SER
35	XD	31	CYS
35	XD	65	ARG
35	XD	108	LEU
35	XD	115	ARG
35	XD	118	ARG
35	XD	135	LEU
35	XD	150	GLU
36	XE	41	VAL
36	XE	68	GLU
36	XE	72	GLN
36	XE	143	ARG
37	XF	72	VAL
38	XG	90	GLU
38	XG	104	LEU
38	XG	115	ARG
39	XH	14	ARG
39	XH	69	ARG
39	XH	112	LEU
40	XI	23	ASN
40	XI	35	GLU
40	XI	83	ARG
40	XI	92	TYR
40	XI	102	LEU
42	XK	96	ARG
42	XK	116	HIS
42	XK	117	ASN
43	XL	41	ARG

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Mol	Chain	Res	Type
43	XL	52	LEU
43	XL	86	ARG
43	XL	117	ARG
44	XM	63	THR
44	XM	69	GLU
44	XM	110	ARG
45	XN	18	VAL
46	XO	54	ARG
46	XO	83	GLU
47	XP	20	VAL
47	XP	28	ARG
47	XP	54	GLU
47	XP	60	LEU
48	XQ	72	ARG
48	XQ	74	LEU
49	XR	41	LYS
51	XT	84	LEU
51	XT	89	ARG
51	XT	100	ILE
52	XU	15	ARG
55	XY	99	LEU
55	XY	100	LEU
55	XY	101	LEU
55	XY	103	LYS
55	XY	104	ASP
55	XY	249	LEU
55	XY	259	ASP
55	XY	318	THR
55	XY	340	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
18	RW	60	ASN
20	RY	6	HIS
33	QB	78	GLN
33	QB	95	GLN
50	QS	65	ASN
6	YG	79	ASN
15	YT	58	ASN
20	YY	6	HIS
33	XB	78	GLN

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Mol	Chain	Res	Type
47	XP	14	ASN
47	XP	16	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	RA	2855/2915 (97%)	494 (17%)	22 (0%)
1	YA	2855/2915 (97%)	484 (16%)	24 (0%)
2	RB	119/122 (97%)	14 (11%)	0
2	YB	119/122 (97%)	13 (10%)	0
32	QA	1494/1521 (98%)	257 (17%)	15 (1%)
32	XA	1498/1521 (98%)	234 (15%)	16 (1%)
53	QV	76/77 (98%)	16 (21%)	0
53	XV	76/77 (98%)	16 (21%)	1 (1%)
54	QX	8/25 (32%)	4 (50%)	0
54	XX	9/25 (36%)	4 (44%)	0
All	All	9109/9320 (97%)	1536 (16%)	78 (0%)

All (1536) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	RA	10	G
1	RA	12	U
1	RA	36	G
1	RA	45	C
1	RA	59	U
1	RA	61	G
1	RA	71	A
1	RA	74	A
1	RA	75	G
1	RA	83	G
1	RA	84	A
1	RA	92	A
1	RA	95	G
1	RA	102	G
1	RA	118	A
1	RA	119	A
1	RA	120	U
1	RA	125	G
1	RA	128	C
1	RA	141	A

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Mol	Chain	Res	Type
1	RA	157	U
1	RA	181	A
1	RA	182	A
1	RA	196	A
1	RA	199	A
1	RA	201	C
1	RA	205	G
1	RA	214	G
1	RA	215	G
1	RA	216	A
1	RA	221	A
1	RA	222	A
1	RA	225	A
1	RA	229	A
1	RA	230	U
1	RA	232	G
1	RA	248	G
1	RA	250	G
1	RA	272(K)	U
1	RA	272(L)	U
1	RA	272(M)	G
1	RA	272(N)	U
1	RA	272(O)	C
1	RA	273(B)	U
1	RA	273(C)	G
1	RA	273(K)	C
1	RA	277	C
1	RA	278	A
1	RA	311	A
1	RA	317	G
1	RA	324	A
1	RA	327	G
1	RA	329	G
1	RA	330	A
1	RA	352	G
1	RA	363(A)	G
1	RA	372	G
1	RA	386	G
1	RA	396	G
1	RA	405	U
1	RA	407	G
1	RA	411	G

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Mol	Chain	Res	Type
1	RA	428	A
1	RA	444	C
1	RA	456	C
1	RA	457	A
1	RA	470	A
1	RA	481	G
1	RA	482	A
1	RA	494	G
1	RA	496	G
1	RA	504	U
1	RA	505	A
1	RA	508	G
1	RA	509	C
1	RA	530	G
1	RA	531	C
1	RA	532	A
1	RA	533	G
1	RA	545	G
1	RA	556	G
1	RA	563	G
1	RA	567	A
1	RA	568	U
1	RA	573	G
1	RA	575	A
1	RA	586	A
1	RA	587	C
1	RA	595	C
1	RA	603	A
1	RA	604	G
1	RA	607	U
1	RA	614(C)	G
1	RA	615	G
1	RA	627	A
1	RA	637	A
1	RA	645	C
1	RA	646	A
1	RA	652(C)	A
1	RA	652(D)	G
1	RA	652(V)	G
1	RA	653	A
1	RA	669	G
1	RA	686	G

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Mol	Chain	Res	Type
1	RA	715	G
1	RA	729	G
1	RA	730	C
1	RA	753	C
1	RA	764	A
1	RA	775	G
1	RA	776	G
1	RA	782	A
1	RA	784	A
1	RA	785	G
1	RA	792	G
1	RA	805	G
1	RA	812	C
1	RA	827	U
1	RA	828	U
1	RA	857	C
1	RA	859	G
1	RA	869	G
1	RA	877	U
1	RA	880	G
1	RA	886	C
1	RA	887	A
1	RA	888	C
1	RA	889	C
1	RA	890	A
1	RA	893	C
1	RA	896	A
1	RA	897	C
1	RA	900	A
1	RA	907	U
1	RA	910	A
1	RA	914	C
1	RA	915	C
1	RA	917	A
1	RA	926	A
1	RA	932	G
1	RA	936	C
1	RA	941	A
1	RA	945	A
1	RA	946	G
1	RA	953	A
1	RA	959	A

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Mol	Chain	Res	Type
1	RA	961	C
1	RA	974	G
1	RA	975(A)	C
1	RA	983	A
1	RA	996	A
1	RA	1008	C
1	RA	1012	U
1	RA	1013	C
1	RA	1017	G
1	RA	1025	G
1	RA	1026	U
1	RA	1033	U
1	RA	1034	G
1	RA	1038	C
1	RA	1039	G
1	RA	1043	C
1	RA	1044	G
1	RA	1045	A
1	RA	1046	A
1	RA	1047	G
1	RA	1048	A
1	RA	1049	C
1	RA	1053	C
1	RA	1054	A
1	RA	1055	G
1	RA	1058	G
1	RA	1060	U
1	RA	1063	G
1	RA	1064	C
1	RA	1065	U
1	RA	1066	U
1	RA	1067	A
1	RA	1068	G
1	RA	1069	A
1	RA	1070	A
1	RA	1071	G
1	RA	1073	A
1	RA	1074	G
1	RA	1076	C
1	RA	1078	U
1	RA	1079	C
1	RA	1082	U

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Mol	Chain	Res	Type
1	RA	1083	U
1	RA	1084	A
1	RA	1085	A
1	RA	1086	A
1	RA	1087	G
1	RA	1088	A
1	RA	1090	U
1	RA	1091	G
1	RA	1092	C
1	RA	1094	U
1	RA	1096	A
1	RA	1097	U
1	RA	1098	A
1	RA	1100	C
1	RA	1109	C
1	RA	1110	G
1	RA	1111	A
1	RA	1112	G
1	RA	1129	A
1	RA	1130	U
1	RA	1135	C
1	RA	1136	G
1	RA	1138	G
1	RA	1142(B)	A
1	RA	1170	G
1	RA	1171	G
1	RA	1211	U
1	RA	1219	G
1	RA	1236	G
1	RA	1241	A
1	RA	1248	G
1	RA	1250	G
1	RA	1253	A
1	RA	1256	G
1	RA	1271	G
1	RA	1272	A
1	RA	1300	U
1	RA	1301	A
1	RA	1306	C
1	RA	1309	G
1	RA	1314	C
1	RA	1320	C

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Mol	Chain	Res	Type
1	RA	1321	A
1	RA	1352	U
1	RA	1359	A
1	RA	1360	A
1	RA	1365	A
1	RA	1368	G
1	RA	1378	A
1	RA	1384	A
1	RA	1385	G
1	RA	1395	A
1	RA	1416	G
1	RA	1417	C
1	RA	1420	U
1	RA	1421	G
1	RA	1427	A
1	RA	1428	C
1	RA	1445(A)	A
1	RA	1450(A)	G
1	RA	1455	G
1	RA	1459	G
1	RA	1460	A
1	RA	1467	C
1	RA	1471	A
1	RA	1482	G
1	RA	1493	C
1	RA	1497	U
1	RA	1508	A
1	RA	1509(A)	C
1	RA	1509(B)	A
1	RA	1509(C)	A
1	RA	1531	C
1	RA	1542	A
1	RA	1543	C
1	RA	1554	A
1	RA	1558	A
1	RA	1566	A
1	RA	1569	A
1	RA	1578	U
1	RA	1580	A
1	RA	1584	C
1	RA	1586	A
1	RA	1608	A

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Mol	Chain	Res	Type
1	RA	1609	A
1	RA	1618	A
1	RA	1640	C
1	RA	1648	C
1	RA	1654	A
1	RA	1674	G
1	RA	1675	C
1	RA	1696	G
1	RA	1698	A
1	RA	1700	A
1	RA	1701	A
1	RA	1703	G
1	RA	1721	G
1	RA	1722	A
1	RA	1746	G
1	RA	1756	G
1	RA	1762	A
1	RA	1763	G
1	RA	1764	G
1	RA	1773	A
1	RA	1776	G
1	RA	1780	A
1	RA	1782	C
1	RA	1784	A
1	RA	1791	A
1	RA	1800	C
1	RA	1801	G
1	RA	1812	A
1	RA	1816	G
1	RA	1833	U
1	RA	1835	G
1	RA	1847	A
1	RA	1848	A
1	RA	1877	A
1	RA	1878	G
1	RA	1889	A
1	RA	1895	C
1	RA	1900	A
1	RA	1906	G
1	RA	1913	A
1	RA	1914	C
1	RA	1929	G

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Mol	Chain	Res	Type
1	RA	1930	G
1	RA	1936	A
1	RA	1937	A
1	RA	1938	A
1	RA	1939	5MU
1	RA	1955	U
1	RA	1960	A
1	RA	1963	U
1	RA	1967	C
1	RA	1970	A
1	RA	1971	A
1	RA	1972	A
1	RA	1975	G
1	RA	1993	U
1	RA	1997	G
1	RA	2023	G
1	RA	2031	A
1	RA	2032	G
1	RA	2033	A
1	RA	2037	G
1	RA	2043	C
1	RA	2055	C
1	RA	2056	G
1	RA	2060	A
1	RA	2061	G
1	RA	2062	A
1	RA	2063	C
1	RA	2069	G
1	RA	2096	U
1	RA	2099	U
1	RA	2103	C
1	RA	2104	G
1	RA	2105	C
1	RA	2107	C
1	RA	2108	C
1	RA	2109	U
1	RA	2112	G
1	RA	2114	A
1	RA	2116	G
1	RA	2117	A
1	RA	2119	A
1	RA	2121	G

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Mol	Chain	Res	Type
1	RA	2123	G
1	RA	2126	A
1	RA	2127	G
1	RA	2129	C
1	RA	2131	G
1	RA	2132	U
1	RA	2133	G
1	RA	2134	A
1	RA	2135	A
1	RA	2136	C
1	RA	2138	C
1	RA	2145	C
1	RA	2146	C
1	RA	2147	G
1	RA	2148	G
1	RA	2151	G
1	RA	2157	G
1	RA	2158	A
1	RA	2159	G
1	RA	2161	C
1	RA	2165	G
1	RA	2172	U
1	RA	2173	A
1	RA	2174	C
1	RA	2180	U
1	RA	2186	G
1	RA	2189	U
1	RA	2192	G
1	RA	2198	A
1	RA	2206	G
1	RA	2207	G
1	RA	2208	A
1	RA	2218	U
1	RA	2219	G
1	RA	2225	A
1	RA	2238	G
1	RA	2239	G
1	RA	2243	U
1	RA	2269	A
1	RA	2275	C
1	RA	2278	A
1	RA	2283	C

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Mol	Chain	Res	Type
1	RA	2287	A
1	RA	2291	U
1	RA	2292	C
1	RA	2305	A
1	RA	2308	G
1	RA	2309	A
1	RA	2311	A
1	RA	2312	U
1	RA	2319	G
1	RA	2320	A
1	RA	2321	G
1	RA	2322	A
1	RA	2325	G
1	RA	2334	G
1	RA	2335	A
1	RA	2336	A
1	RA	2343	C
1	RA	2347	C
1	RA	2350	C
1	RA	2372	G
1	RA	2379	G
1	RA	2383	G
1	RA	2385	C
1	RA	2400	G
1	RA	2406	U
1	RA	2410	G
1	RA	2414	G
1	RA	2422	A
1	RA	2424	C
1	RA	2425	A
1	RA	2429	G
1	RA	2430	A
1	RA	2434	A
1	RA	2435	A
1	RA	2439	A
1	RA	2441	C
1	RA	2448	A
1	RA	2474	C
1	RA	2475	C
1	RA	2476	A
1	RA	2478	A
1	RA	2498	C

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Mol	Chain	Res	Type
1	RA	2502	G
1	RA	2504	U
1	RA	2505	G
1	RA	2518	A
1	RA	2520	C
1	RA	2529	G
1	RA	2549	G
1	RA	2554	U
1	RA	2555	U
1	RA	2566	A
1	RA	2567	G
1	RA	2601	C
1	RA	2602	A
1	RA	2609	U
1	RA	2611	U
1	RA	2612	C
1	RA	2615	U
1	RA	2629	A
1	RA	2630	G
1	RA	2632	A
1	RA	2654	A
1	RA	2689	U
1	RA	2690	C
1	RA	2691	C
1	RA	2700	C
1	RA	2702	U
1	RA	2703	C
1	RA	2712(B)	A
1	RA	2713	A
1	RA	2714	G
1	RA	2726	U
1	RA	2733	A
1	RA	2744	G
1	RA	2751	G
1	RA	2758	A
1	RA	2759	G
1	RA	2764	A
1	RA	2765	A
1	RA	2766	G
1	RA	2778	A
1	RA	2789	C
1	RA	2794(A)	C

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Mol	Chain	Res	Type
1	RA	2818	G
1	RA	2820	A
1	RA	2821	A
1	RA	2833	G
1	RA	2872	G
1	RA	2873	A
1	RA	2879	C
1	RA	2880	C
1	RA	2886	G
1	RA	2892	A
1	RA	2894	G
1	RA	2897	U
2	RB	2	C
2	RB	7	G
2	RB	8	U
2	RB	13	A
2	RB	24	G
2	RB	30	C
2	RB	34	U
2	RB	45	A
2	RB	53	A
2	RB	56	G
2	RB	73	A
2	RB	85	G
2	RB	106	G
2	RB	110	G
32	QA	5	U
32	QA	7	G
32	QA	9	G
32	QA	32	A
32	QA	39	G
32	QA	41	G
32	QA	42	G
32	QA	48	C
32	QA	50	A
32	QA	51	A
32	QA	53	A
32	QA	61	G
32	QA	78	G
32	QA	79	G
32	QA	101	A
32	QA	116	A

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Mol	Chain	Res	Type
32	QA	121	C
32	QA	127	G
32	QA	131	C
32	QA	137	C
32	QA	163	C
32	QA	169	C
32	QA	174	C
32	QA	182	U
32	QA	189(F)	U
32	QA	195	A
32	QA	201	C
32	QA	203	U
32	QA	204	U
32	QA	216	G
32	QA	231	G
32	QA	247	G
32	QA	251	G
32	QA	266	G
32	QA	267	C
32	QA	289	G
32	QA	298	A
32	QA	306	G
32	QA	321	A
32	QA	328	C
32	QA	332	G
32	QA	343	U
32	QA	345	C
32	QA	347	G
32	QA	348	G
32	QA	352	C
32	QA	353	A
32	QA	354	G
32	QA	367	U
32	QA	372	C
32	QA	373	A
32	QA	384	G
32	QA	397	A
32	QA	406	G
32	QA	412	A
32	QA	413	G
32	QA	423	G
32	QA	424	G

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Mol	Chain	Res	Type
32	QA	429	U
32	QA	439	A
32	QA	442	C
32	QA	446	G
32	QA	452	A
32	QA	454	C
32	QA	458	C
32	QA	461	A
32	QA	470	C
32	QA	477	A
32	QA	485	G
32	QA	496	A
32	QA	498	U
32	QA	505	G
32	QA	509	A
32	QA	510	A
32	QA	511	C
32	QA	513	C
32	QA	517	G
32	QA	518	C
32	QA	521	G
32	QA	524	G
32	QA	527	7MG
32	QA	532	A
32	QA	547	A
32	QA	550	G
32	QA	559	A
32	QA	561	U
32	QA	564	C
32	QA	572	A
32	QA	573	A
32	QA	574	A
32	QA	575	G
32	QA	576	G
32	QA	577	G
32	QA	596	C
32	QA	607	A
32	QA	619	U
32	QA	630	G
32	QA	631	G
32	QA	632	A
32	QA	653	A

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Mol	Chain	Res	Type
32	QA	661	G
32	QA	665	A
32	QA	687	A
32	QA	688	G
32	QA	721	G
32	QA	723	U
32	QA	731	G
32	QA	755	G
32	QA	760	G
32	QA	774	G
32	QA	777	A
32	QA	787	A
32	QA	792	A
32	QA	793	U
32	QA	794	A
32	QA	796	C
32	QA	798	G
32	QA	816	A
32	QA	817	C
32	QA	821	G
32	QA	828	A
32	QA	829	G
32	QA	839	U
32	QA	840	C
32	QA	841	U
32	QA	848	C
32	QA	851	G
32	QA	902	G
32	QA	914	A
32	QA	916	G
32	QA	917	G
32	QA	926	G
32	QA	927	G
32	QA	934	C
32	QA	935	A
32	QA	939	G
32	QA	942	G
32	QA	944	G
32	QA	960	U
32	QA	961	U
32	QA	968	A
32	QA	969	A

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Mol	Chain	Res	Type
32	QA	971	G
32	QA	974	A
32	QA	975	A
32	QA	976	G
32	QA	977	A
32	QA	992	U
32	QA	993	G
32	QA	994	A
32	QA	998	G
32	QA	1003	G
32	QA	1006	C
32	QA	1009	G
32	QA	1022	G
32	QA	1023	G
32	QA	1024	G
32	QA	1025	U
32	QA	1026	G
32	QA	1027	C
32	QA	1028	C
32	QA	1029	C
32	QA	1030(A)	C
32	QA	1030(B)	G
32	QA	1030(C)	C
32	QA	1030(E)	A
32	QA	1032	G
32	QA	1034	G
32	QA	1037	C
32	QA	1044	A
32	QA	1053	G
32	QA	1065	U
32	QA	1066	C
32	QA	1068	G
32	QA	1070	U
32	QA	1081	G
32	QA	1087	G
32	QA	1094	G
32	QA	1095	U
32	QA	1101	A
32	QA	1108	G
32	QA	1113	C
32	QA	1125	U
32	QA	1126	U

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Mol	Chain	Res	Type
32	QA	1130	A
32	QA	1134	G
32	QA	1136	U
32	QA	1138	G
32	QA	1139	G
32	QA	1146	A
32	QA	1152	A
32	QA	1159	U
32	QA	1168	A
32	QA	1183	A
32	QA	1184	G
32	QA	1193	G
32	QA	1196	U
32	QA	1197	G
32	QA	1202	G
32	QA	1204	A
32	QA	1208	C
32	QA	1212	U
32	QA	1213	A
32	QA	1225	A
32	QA	1227	A
32	QA	1238	A
32	QA	1256	A
32	QA	1257	U
32	QA	1258	G
32	QA	1278	U
32	QA	1280	A
32	QA	1286	A
32	QA	1287	A
32	QA	1299	A
32	QA	1300	G
32	QA	1302	U
32	QA	1305	G
32	QA	1311	G
32	QA	1319	A
32	QA	1320	C
32	QA	1338	G
32	QA	1340	A
32	QA	1347	G
32	QA	1353	G
32	QA	1359	C
32	QA	1363(A)	C

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Mol	Chain	Res	Type
32	QA	1363(B)	A
32	QA	1364	U
32	QA	1370	G
32	QA	1379	G
32	QA	1381	U
32	QA	1397	C
32	QA	1398	A
32	QA	1401	G
32	QA	1419	G
32	QA	1442(A)	G
32	QA	1442(B)	G
32	QA	1442(C)	A
32	QA	1446	U
32	QA	1447	A
32	QA	1452	C
32	QA	1456	G
32	QA	1487	G
32	QA	1491	G
32	QA	1492	A
32	QA	1493	A
32	QA	1497	G
32	QA	1499	A
32	QA	1503	A
32	QA	1504	G
32	QA	1505	G
32	QA	1506	U
32	QA	1507	A
32	QA	1517	G
32	QA	1520	G
32	QA	1529	G
32	QA	1530	G
53	QV	4	G
53	QV	5	G
53	QV	8	U
53	QV	9	G
53	QV	17(A)	U
53	QV	18	G
53	QV	19	G
53	QV	21	A
53	QV	22	G
53	QV	31	G
53	QV	47	U

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Mol	Chain	Res	Type
53	QV	48	C
53	QV	54	U
53	QV	68	C
53	QV	75	C
53	QV	76	A
54	QX	15	A
54	QX	17	U
54	QX	21	A
54	QX	22	C
1	YA	9	U
1	YA	10	G
1	YA	12	U
1	YA	15	G
1	YA	34	C
1	YA	45	C
1	YA	55	G
1	YA	71	A
1	YA	74	A
1	YA	75	G
1	YA	84	A
1	YA	92	A
1	YA	95	G
1	YA	118	A
1	YA	119	A
1	YA	120	U
1	YA	154(A)	G
1	YA	154(B)	C
1	YA	157	U
1	YA	181	A
1	YA	182	A
1	YA	188	G
1	YA	196	A
1	YA	199	A
1	YA	205	G
1	YA	214	G
1	YA	215	G
1	YA	216	A
1	YA	221	A
1	YA	222	A
1	YA	229	A
1	YA	230	U
1	YA	233	A

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Mol	Chain	Res	Type
1	YA	248	G
1	YA	266	G
1	YA	272(K)	U
1	YA	272(L)	U
1	YA	272(M)	G
1	YA	272(N)	U
1	YA	272(O)	C
1	YA	273(B)	U
1	YA	273(C)	G
1	YA	273(K)	C
1	YA	277	C
1	YA	278	A
1	YA	311	A
1	YA	317	G
1	YA	324	A
1	YA	327	G
1	YA	329	G
1	YA	330	A
1	YA	342	G
1	YA	346	A
1	YA	352	G
1	YA	362	U
1	YA	363(A)	G
1	YA	372	G
1	YA	386	G
1	YA	389	G
1	YA	407	G
1	YA	411	G
1	YA	428	A
1	YA	444	C
1	YA	455	C
1	YA	463	G
1	YA	464	U
1	YA	470	A
1	YA	481	G
1	YA	505	A
1	YA	508	G
1	YA	509	C
1	YA	530	G
1	YA	531	C
1	YA	532	A
1	YA	533	G

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Mol	Chain	Res	Type
1	YA	545	G
1	YA	563	G
1	YA	567	A
1	YA	573	G
1	YA	575	A
1	YA	586	A
1	YA	595	C
1	YA	603	A
1	YA	604	G
1	YA	607	U
1	YA	615	G
1	YA	616	G
1	YA	620	G
1	YA	627	A
1	YA	637	A
1	YA	644	A
1	YA	645	C
1	YA	646	A
1	YA	652(C)	A
1	YA	652(D)	G
1	YA	652(V)	G
1	YA	653	A
1	YA	669	G
1	YA	686	G
1	YA	715	G
1	YA	730	C
1	YA	747	U
1	YA	752	A
1	YA	753	C
1	YA	762	U
1	YA	775	G
1	YA	776	G
1	YA	782	A
1	YA	784	A
1	YA	785	G
1	YA	792	G
1	YA	805	G
1	YA	811	U
1	YA	812	C
1	YA	827	U
1	YA	828	U
1	YA	833	U

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Mol	Chain	Res	Type
1	YA	859	G
1	YA	866	A
1	YA	878	A
1	YA	880	G
1	YA	886	C
1	YA	887	A
1	YA	888	C
1	YA	889	C
1	YA	890	A
1	YA	893	C
1	YA	896	A
1	YA	897	C
1	YA	899	A
1	YA	907	U
1	YA	910	A
1	YA	914	C
1	YA	917	A
1	YA	932	G
1	YA	941	A
1	YA	945	A
1	YA	946	G
1	YA	958	U
1	YA	959	A
1	YA	961	C
1	YA	962	G
1	YA	974	G
1	YA	975(A)	C
1	YA	983	A
1	YA	989	G
1	YA	996	A
1	YA	999	U
1	YA	1008	C
1	YA	1012	U
1	YA	1013	C
1	YA	1015	G
1	YA	1017	G
1	YA	1025	G
1	YA	1026	U
1	YA	1033	U
1	YA	1041	C
1	YA	1044	G
1	YA	1045	A

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Mol	Chain	Res	Type
1	YA	1046	A
1	YA	1047	G
1	YA	1048	A
1	YA	1049	C
1	YA	1050	A
1	YA	1052	C
1	YA	1053	C
1	YA	1054	A
1	YA	1058	G
1	YA	1060	U
1	YA	1064	C
1	YA	1065	U
1	YA	1066	U
1	YA	1067	A
1	YA	1068	G
1	YA	1069	A
1	YA	1070	A
1	YA	1071	G
1	YA	1073	A
1	YA	1074	G
1	YA	1076	C
1	YA	1077	A
1	YA	1078	U
1	YA	1079	C
1	YA	1082	U
1	YA	1083	U
1	YA	1084	A
1	YA	1085	A
1	YA	1086	A
1	YA	1088	A
1	YA	1090	U
1	YA	1091	G
1	YA	1092	C
1	YA	1094	U
1	YA	1096	A
1	YA	1097	U
1	YA	1098	A
1	YA	1100	C
1	YA	1108	U
1	YA	1109	C
1	YA	1110	G
1	YA	1112	G

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Mol	Chain	Res	Type
1	YA	1113	U
1	YA	1114	G
1	YA	1117	G
1	YA	1118	C
1	YA	1119	C
1	YA	1126	A
1	YA	1129	A
1	YA	1130	U
1	YA	1135	C
1	YA	1136	G
1	YA	1142(B)	A
1	YA	1151	G
1	YA	1155	A
1	YA	1157	G
1	YA	1171	G
1	YA	1211	U
1	YA	1212	G
1	YA	1220	A
1	YA	1236	G
1	YA	1250	G
1	YA	1253	A
1	YA	1256	G
1	YA	1271	G
1	YA	1272	A
1	YA	1273	U
1	YA	1300	U
1	YA	1301	A
1	YA	1313	U
1	YA	1314	C
1	YA	1352	U
1	YA	1359	A
1	YA	1365	A
1	YA	1368	G
1	YA	1378	A
1	YA	1380	G
1	YA	1384	A
1	YA	1385	G
1	YA	1386	C
1	YA	1416	G
1	YA	1417	C
1	YA	1420	U
1	YA	1421	G

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Mol	Chain	Res	Type
1	YA	1428	C
1	YA	1445(A)	A
1	YA	1450(A)	G
1	YA	1451	C
1	YA	1455	G
1	YA	1459	G
1	YA	1467	C
1	YA	1471	A
1	YA	1478	G
1	YA	1482	G
1	YA	1490	A
1	YA	1493	C
1	YA	1497	U
1	YA	1508	A
1	YA	1509(A)	C
1	YA	1509(B)	A
1	YA	1531	C
1	YA	1542	A
1	YA	1543	C
1	YA	1547	C
1	YA	1554	A
1	YA	1558	A
1	YA	1559	G
1	YA	1566	A
1	YA	1569	A
1	YA	1578	U
1	YA	1580	A
1	YA	1584	C
1	YA	1586	A
1	YA	1608	A
1	YA	1609	A
1	YA	1610	A
1	YA	1640	C
1	YA	1648	C
1	YA	1651	G
1	YA	1664	A
1	YA	1674	G
1	YA	1675	C
1	YA	1696	G
1	YA	1700	A
1	YA	1701	A
1	YA	1703	G

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Mol	Chain	Res	Type
1	YA	1721	G
1	YA	1722	A
1	YA	1756	G
1	YA	1762	A
1	YA	1763	G
1	YA	1764	G
1	YA	1773	A
1	YA	1776	G
1	YA	1780	A
1	YA	1782	C
1	YA	1786	A
1	YA	1791	A
1	YA	1800	C
1	YA	1801	G
1	YA	1812	A
1	YA	1816	G
1	YA	1829	A
1	YA	1834	U
1	YA	1835	G
1	YA	1847	A
1	YA	1848	A
1	YA	1877	A
1	YA	1878	G
1	YA	1890	A
1	YA	1900	A
1	YA	1906	G
1	YA	1914	C
1	YA	1929	G
1	YA	1930	G
1	YA	1937	A
1	YA	1938	A
1	YA	1955	U
1	YA	1963	U
1	YA	1965	C
1	YA	1967	C
1	YA	1970	A
1	YA	1971	A
1	YA	1972	A
1	YA	1993	U
1	YA	1997	G
1	YA	2020	A
1	YA	2023	G

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Mol	Chain	Res	Type
1	YA	2031	A
1	YA	2032	G
1	YA	2033	A
1	YA	2043	C
1	YA	2055	C
1	YA	2056	G
1	YA	2060	A
1	YA	2061	G
1	YA	2062	A
1	YA	2069	G
1	YA	2096	U
1	YA	2099	U
1	YA	2103	C
1	YA	2105	C
1	YA	2107	C
1	YA	2108	C
1	YA	2109	U
1	YA	2112	G
1	YA	2116	G
1	YA	2117	A
1	YA	2118	U
1	YA	2119	A
1	YA	2121	G
1	YA	2123	G
1	YA	2126	A
1	YA	2127	G
1	YA	2128	C
1	YA	2129	C
1	YA	2131	G
1	YA	2132	U
1	YA	2133	G
1	YA	2134	A
1	YA	2136	C
1	YA	2138	C
1	YA	2145	C
1	YA	2146	C
1	YA	2147	G
1	YA	2151	G
1	YA	2158	A
1	YA	2159	G
1	YA	2161	C
1	YA	2165	G

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Mol	Chain	Res	Type
1	YA	2172	U
1	YA	2173	A
1	YA	2180	U
1	YA	2186	G
1	YA	2189	U
1	YA	2192	G
1	YA	2198	A
1	YA	2206	G
1	YA	2207	G
1	YA	2208	A
1	YA	2218	U
1	YA	2225	A
1	YA	2238	G
1	YA	2239	G
1	YA	2269	A
1	YA	2275	C
1	YA	2279	G
1	YA	2283	C
1	YA	2287	A
1	YA	2305	A
1	YA	2308	G
1	YA	2312	U
1	YA	2320	A
1	YA	2321	G
1	YA	2322	A
1	YA	2325	G
1	YA	2334	G
1	YA	2335	A
1	YA	2336	A
1	YA	2343	C
1	YA	2347	C
1	YA	2350	C
1	YA	2372	G
1	YA	2383	G
1	YA	2384	G
1	YA	2385	C
1	YA	2389	G
1	YA	2400	G
1	YA	2406	U
1	YA	2410	G
1	YA	2414	G
1	YA	2422	A

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Mol	Chain	Res	Type
1	YA	2425	A
1	YA	2429	G
1	YA	2430	A
1	YA	2431	U
1	YA	2435	A
1	YA	2439	A
1	YA	2441	C
1	YA	2448	A
1	YA	2468	G
1	YA	2474	C
1	YA	2476	A
1	YA	2487	G
1	YA	2502	G
1	YA	2504	U
1	YA	2505	G
1	YA	2518	A
1	YA	2520	C
1	YA	2525	G
1	YA	2529	G
1	YA	2530	A
1	YA	2549	G
1	YA	2554	U
1	YA	2566	A
1	YA	2567	G
1	YA	2578	G
1	YA	2582	G
1	YA	2602	A
1	YA	2609	U
1	YA	2611	U
1	YA	2612	C
1	YA	2629	A
1	YA	2630	G
1	YA	2636	U
1	YA	2654	A
1	YA	2663	G
1	YA	2682	U
1	YA	2689	U
1	YA	2690	C
1	YA	2691	C
1	YA	2702	U
1	YA	2703	C
1	YA	2712(B)	A

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Mol	Chain	Res	Type
1	YA	2713	A
1	YA	2714	G
1	YA	2726	U
1	YA	2733	A
1	YA	2744	G
1	YA	2751	G
1	YA	2758	A
1	YA	2759	G
1	YA	2764	A
1	YA	2765	A
1	YA	2769	C
1	YA	2778	A
1	YA	2780	G
1	YA	2802	G
1	YA	2811	G
1	YA	2818	G
1	YA	2820	A
1	YA	2821	A
1	YA	2833	G
1	YA	2835	A
1	YA	2849	U
1	YA	2866	U
1	YA	2872	G
1	YA	2873	A
1	YA	2879	C
1	YA	2880	C
1	YA	2886	G
1	YA	2891	G
1	YA	2892	A
1	YA	2894	G
1	YA	2897	U
2	YB	8	U
2	YB	9	G
2	YB	12	C
2	YB	25	A
2	YB	30	C
2	YB	51	G
2	YB	56	G
2	YB	63	G
2	YB	73	A
2	YB	84	C
2	YB	106	G

Continued on next page...

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Mol	Chain	Res	Type
2	YB	109	C
2	YB	110	G
32	XA	5	U
32	XA	7	G
32	XA	9	G
32	XA	32	A
32	XA	39	G
32	XA	47	C
32	XA	48	C
32	XA	50	A
32	XA	51	A
32	XA	61	G
32	XA	65	U
32	XA	66	G
32	XA	69	G
32	XA	78	G
32	XA	88	A
32	XA	89	C
32	XA	101	A
32	XA	116	A
32	XA	121	C
32	XA	131	C
32	XA	151	A
32	XA	163	C
32	XA	174	C
32	XA	182	U
32	XA	189(F)	U
32	XA	195	A
32	XA	197	A
32	XA	202	U
32	XA	203	U
32	XA	204	U
32	XA	216	G
32	XA	247	G
32	XA	251	G
32	XA	262	A
32	XA	266	G
32	XA	267	C
32	XA	281	G
32	XA	289	G
32	XA	321	A
32	XA	328	C

Continued on next page...

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Mol	Chain	Res	Type
32	XA	332	G
32	XA	340	U
32	XA	351	G
32	XA	352	C
32	XA	353	A
32	XA	354	G
32	XA	356	A
32	XA	367	U
32	XA	372	C
32	XA	373	A
32	XA	384	G
32	XA	397	A
32	XA	398	C
32	XA	406	G
32	XA	412	A
32	XA	413	G
32	XA	424	G
32	XA	429	U
32	XA	439	A
32	XA	442	C
32	XA	452	A
32	XA	458	C
32	XA	470	C
32	XA	482	A
32	XA	484	G
32	XA	485	G
32	XA	496	A
32	XA	498	U
32	XA	505	G
32	XA	509	A
32	XA	510	A
32	XA	511	C
32	XA	518	C
32	XA	527	7MG
32	XA	532	A
32	XA	533	A
32	XA	536	C
32	XA	547	A
32	XA	559	A
32	XA	561	U
32	XA	564	C
32	XA	572	A

Continued on next page...

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Mol	Chain	Res	Type
32	XA	573	A
32	XA	574	A
32	XA	575	G
32	XA	576	G
32	XA	577	G
32	XA	596	C
32	XA	630	G
32	XA	631	G
32	XA	632	A
32	XA	646	U
32	XA	653	A
32	XA	661	G
32	XA	665	A
32	XA	688	G
32	XA	695	A
32	XA	701	C
32	XA	721	G
32	XA	723	U
32	XA	724	G
32	XA	731	G
32	XA	749	C
32	XA	753	A
32	XA	755	G
32	XA	766	A
32	XA	774	G
32	XA	776	G
32	XA	777	A
32	XA	792	A
32	XA	793	U
32	XA	794	A
32	XA	816	A
32	XA	817	C
32	XA	818	G
32	XA	821	G
32	XA	828	A
32	XA	829	G
32	XA	836	G
32	XA	840	C
32	XA	841	U
32	XA	848	C
32	XA	851	G
32	XA	902	G

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Mol	Chain	Res	Type
32	XA	914	A
32	XA	926	G
32	XA	927	G
32	XA	931	C
32	XA	934	C
32	XA	935	A
32	XA	960	U
32	XA	961	U
32	XA	965	A
32	XA	968	A
32	XA	969	A
32	XA	971	G
32	XA	974	A
32	XA	975	A
32	XA	976	G
32	XA	977	A
32	XA	992	U
32	XA	993	G
32	XA	994	A
32	XA	1003	G
32	XA	1004	A
32	XA	1005	A
32	XA	1006	C
32	XA	1009	G
32	XA	1016	A
32	XA	1020	U
32	XA	1022	G
32	XA	1023	G
32	XA	1025	U
32	XA	1026	G
32	XA	1027	C
32	XA	1028	C
32	XA	1030(B)	G
32	XA	1030(C)	C
32	XA	1038	C
32	XA	1041	A
32	XA	1043	C
32	XA	1044	A
32	XA	1045	C
32	XA	1065	U
32	XA	1066	C
32	XA	1068	G

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Mol	Chain	Res	Type
32	XA	1081	G
32	XA	1094	G
32	XA	1095	U
32	XA	1101	A
32	XA	1117	G
32	XA	1125	U
32	XA	1129	C
32	XA	1130	A
32	XA	1136	U
32	XA	1137	C
32	XA	1139	G
32	XA	1147	C
32	XA	1152	A
32	XA	1159	U
32	XA	1160	G
32	XA	1183	A
32	XA	1184	G
32	XA	1196	U
32	XA	1197	G
32	XA	1211	U
32	XA	1213	A
32	XA	1227	A
32	XA	1236	A
32	XA	1238	A
32	XA	1250	A
32	XA	1256	A
32	XA	1257	U
32	XA	1258	G
32	XA	1270	C
32	XA	1278	U
32	XA	1279	A
32	XA	1280	A
32	XA	1281	U
32	XA	1282	C
32	XA	1286	A
32	XA	1287	A
32	XA	1300	G
32	XA	1302	U
32	XA	1305	G
32	XA	1320	C
32	XA	1329	A
32	XA	1340	A

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Mol	Chain	Res	Type
32	XA	1346	A
32	XA	1347	G
32	XA	1353	G
32	XA	1363(A)	C
32	XA	1363(B)	A
32	XA	1364	U
32	XA	1397	C
32	XA	1401	G
32	XA	1419	G
32	XA	1442(A)	G
32	XA	1442(B)	G
32	XA	1447	A
32	XA	1456	G
32	XA	1457	G
32	XA	1487	G
32	XA	1491	G
32	XA	1493	A
32	XA	1497	G
32	XA	1503	A
32	XA	1504	G
32	XA	1507	A
32	XA	1517	G
32	XA	1520	G
32	XA	1525	G
32	XA	1529	G
32	XA	1530	G
53	XV	2	G
53	XV	4	G
53	XV	5	G
53	XV	8	U
53	XV	9	G
53	XV	17(A)	U
53	XV	18	G
53	XV	19	G
53	XV	21	A
53	XV	22	G
53	XV	31	G
53	XV	47	U
53	XV	48	C
53	XV	54	U
53	XV	68	C
53	XV	76	A

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Mol	Chain	Res	Type
54	XX	15	A
54	XX	17	U
54	XX	21	A
54	XX	22	C

All (78) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	RA	9	U
1	RA	214	G
1	RA	272(M)	G
1	RA	277	C
1	RA	752	A
1	RA	856	C
1	RA	1045	A
1	RA	1053	C
1	RA	1057	A
1	RA	1065	U
1	RA	1067	A
1	RA	1073	A
1	RA	1210	A
1	RA	1240	U
1	RA	1420	U
1	RA	1530	C
1	RA	1992	G
1	RA	2126	A
1	RA	2171	A
1	RA	2172	U
1	RA	2321	G
1	RA	2689	U
32	QA	115	G
32	QA	266	G
32	QA	509	A
32	QA	560	U
32	QA	687	A
32	QA	839	U
32	QA	913	A
32	QA	943	U
32	QA	991	U
32	QA	1065	U
32	QA	1067	A
32	QA	1201	A

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Mol	Chain	Res	Type
32	QA	1207	2MG
32	QA	1285	A
32	QA	1442(A)	G
1	YA	9	U
1	YA	272(M)	G
1	YA	277	C
1	YA	752	A
1	YA	764	A
1	YA	774	A
1	YA	827	U
1	YA	832	G
1	YA	958	U
1	YA	1053	C
1	YA	1057	A
1	YA	1065	U
1	YA	1067	A
1	YA	1073	A
1	YA	1420	U
1	YA	1530	C
1	YA	1608	A
1	YA	1992	G
1	YA	2126	A
1	YA	2171	A
1	YA	2172	U
1	YA	2321	G
1	YA	2430	A
1	YA	2689	U
32	XA	60	A
32	XA	115	G
32	XA	266	G
32	XA	509	A
32	XA	560	U
32	XA	687	A
32	XA	748	C
32	XA	840	C
32	XA	913	A
32	XA	991	U
32	XA	992	U
32	XA	1065	U
32	XA	1067	A
32	XA	1183	A
32	XA	1256	A

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Mol	Chain	Res	Type
32	XA	1442(A)	G
53	XV	53	G

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

48 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$
32	2MG	QA	1207	32	18,26,27	4.28	6 (33%)	21,38,41	3.87	7 (33%)
32	5MC	QA	1400	32	14,22,23	3.59	6 (42%)	17,32,35	1.25	2 (11%)
32	4OC	QA	1402	32	15,23,24	3.42	5 (33%)	21,32,35	2.13	4 (19%)
32	5MC	QA	1404	32	14,22,23	3.62	5 (35%)	17,32,35	1.24	2 (11%)
32	5MC	QA	1407	32	14,22,23	3.48	5 (35%)	17,32,35	1.23	2 (11%)
32	UR3	QA	1498	32	13,22,23	3.18	3 (23%)	18,32,35	0.94	2 (11%)
32	MA6	QA	1518	32	18,26,27	1.17	2 (11%)	15,38,41	3.52	3 (20%)
32	MA6	QA	1519	32	18,26,27	1.25	2 (11%)	15,38,41	3.38	2 (13%)
32	PSU	QA	516	32,56	15,21,22	1.07	1 (6%)	16,30,33	2.07	2 (12%)
32	7MG	QA	527	32,56	20,26,27	5.47	11 (55%)	23,39,42	3.32	9 (39%)
32	M2G	QA	966	32	18,27,28	3.78	5 (27%)	22,40,43	3.65	5 (22%)
32	5MC	QA	967	32	14,22,23	3.62	5 (35%)	17,32,35	1.36	2 (11%)
43	0TD	QL	92	43	4,9,10	1.22	0	4,11,13	3.60	2 (50%)
1	PSU	RA	1911	1	15,21,22	0.92	1 (6%)	16,30,33	1.99	4 (25%)
1	5MU	RA	1915	1	13,22,23	1.62	3 (23%)	16,32,35	2.64	2 (12%)
1	PSU	RA	1917	1	15,21,22	1.08	2 (13%)	16,30,33	2.25	3 (18%)
1	4OC	RA	1920	1	15,22,24	3.69	6 (40%)	20,31,35	1.88	4 (20%)
1	5MU	RA	1939	1	13,22,23	1.61	3 (23%)	16,32,35	2.52	2 (12%)
1	5MC	RA	1942	1,56	14,22,23	3.45	5 (35%)	17,32,35	1.37	2 (11%)
1	5MC	RA	1962	1,56	14,22,23	3.43	5 (35%)	17,32,35	1.31	1 (5%)
1	OMG	RA	2251	1,56,53	18,26,27	3.49	7 (38%)	21,38,41	3.32	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	2MA	RA	2503	1,56	17,25,26	3.95	6 (35%)	18,37,40	6.61	5 (27%)
1	2MU	RA	2552	1,56	14,22,24	7.42	8 (57%)	19,31,36	1.69	3 (15%)
1	PSU	RA	2605	1	15,21,22	0.96	1 (6%)	16,30,33	2.20	4 (25%)
32	2MG	XA	1207	32	18,26,27	4.13	6 (33%)	21,38,41	3.68	6 (28%)
32	5MC	XA	1400	32	14,22,23	3.64	6 (42%)	17,32,35	1.50	2 (11%)
32	4OC	XA	1402	32	15,23,24	3.33	5 (33%)	21,32,35	2.87	4 (19%)
32	5MC	XA	1404	32	14,22,23	3.55	5 (35%)	17,32,35	1.16	2 (11%)
32	5MC	XA	1407	32	14,22,23	3.52	5 (35%)	17,32,35	1.69	2 (11%)
32	UR3	XA	1498	32,56	13,22,23	3.08	3 (23%)	18,32,35	0.87	1 (5%)
32	MA6	XA	1518	32	18,26,27	1.07	2 (11%)	15,38,41	3.26	2 (13%)
32	MA6	XA	1519	32	18,26,27	1.36	2 (11%)	15,38,41	2.42	4 (26%)
32	PSU	XA	516	32	15,21,22	1.08	1 (6%)	16,30,33	1.94	3 (18%)
32	7MG	XA	527	32,56	20,26,27	5.39	11 (55%)	23,39,42	3.21	7 (30%)
32	M2G	XA	966	32	18,27,28	3.59	5 (27%)	22,40,43	3.59	5 (22%)
32	5MC	XA	967	32	14,22,23	3.56	5 (35%)	17,32,35	1.47	2 (11%)
43	0TD	XL	92	43	4,9,10	1.05	0	4,11,13	2.98	2 (50%)
1	PSU	YA	1911	1	15,21,22	1.04	1 (6%)	16,30,33	2.12	3 (18%)
1	5MU	YA	1915	1	13,22,23	1.61	3 (23%)	16,32,35	2.69	2 (12%)
1	PSU	YA	1917	1	15,21,22	0.99	1 (6%)	16,30,33	1.98	4 (25%)
1	4OC	YA	1920	1	15,22,24	3.51	6 (40%)	20,31,35	1.72	4 (20%)
1	5MU	YA	1939	1,56	13,22,23	1.63	3 (23%)	16,32,35	2.42	3 (18%)
1	5MC	YA	1942	1	14,22,23	3.39	5 (35%)	17,32,35	1.32	2 (11%)
1	5MC	YA	1962	1,56	14,22,23	3.40	5 (35%)	17,32,35	1.43	1 (5%)
1	OMG	YA	2251	1,56,53	18,26,27	3.50	7 (38%)	21,38,41	3.40	5 (23%)
1	2MA	YA	2503	1,56	17,25,26	3.76	5 (29%)	18,37,40	6.40	4 (22%)
1	2MU	YA	2552	1,56	14,22,24	7.60	7 (50%)	19,31,36	1.81	4 (21%)
1	PSU	YA	2605	1	15,21,22	1.01	1 (6%)	16,30,33	2.09	4 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	2MG	QA	1207	32	-	0/5/27/28	0/3/3/3
32	5MC	QA	1400	32	-	0/3/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	4OC	QA	1402	32	-	0/7/29/30	0/2/2/2
32	5MC	QA	1404	32	-	0/3/25/26	0/2/2/2
32	5MC	QA	1407	32	-	0/3/25/26	0/2/2/2
32	UR3	QA	1498	32	-	0/3/25/26	0/2/2/2
32	MA6	QA	1518	32	-	0/7/29/30	0/3/3/3
32	MA6	QA	1519	32	-	0/7/29/30	0/3/3/3
32	PSU	QA	516	32,56	-	0/7/25/26	0/2/2/2
32	7MG	QA	527	32,56	-	0/7/37/38	0/3/3/3
32	M2G	QA	966	32	-	0/7/29/30	0/3/3/3
32	5MC	QA	967	32	-	0/3/25/26	0/2/2/2
43	0TD	QL	92	43	-	0/2/12/14	0/0/0/0
1	PSU	RA	1911	1	-	0/7/25/26	0/2/2/2
1	5MU	RA	1915	1	-	0/3/25/26	0/2/2/2
1	PSU	RA	1917	1	-	0/7/25/26	0/2/2/2
1	4OC	RA	1920	1	-	0/5/27/30	0/2/2/2
1	5MU	RA	1939	1	-	0/3/25/26	0/2/2/2
1	5MC	RA	1942	1,56	-	0/3/25/26	0/2/2/2
1	5MC	RA	1962	1,56	-	0/3/25/26	0/2/2/2
1	OMG	RA	2251	1,56,53	-	0/5/27/28	0/3/3/3
1	2MA	RA	2503	1,56	-	0/3/25/26	0/3/3/3
1	2MU	RA	2552	1,56	-	0/5/27/28	0/2/2/2
1	PSU	RA	2605	1	-	0/7/25/26	0/2/2/2
32	2MG	XA	1207	32	-	0/5/27/28	0/3/3/3
32	5MC	XA	1400	32	-	0/3/25/26	0/2/2/2
32	4OC	XA	1402	32	-	0/7/29/30	0/2/2/2
32	5MC	XA	1404	32	-	0/3/25/26	0/2/2/2
32	5MC	XA	1407	32	-	0/3/25/26	0/2/2/2
32	UR3	XA	1498	32,56	-	0/3/25/26	0/2/2/2
32	MA6	XA	1518	32	-	0/7/29/30	0/3/3/3
32	MA6	XA	1519	32	-	0/7/29/30	0/3/3/3
32	PSU	XA	516	32	-	0/7/25/26	0/2/2/2
32	7MG	XA	527	32,56	-	0/7/37/38	0/3/3/3
32	M2G	XA	966	32	-	0/7/29/30	0/3/3/3
32	5MC	XA	967	32	-	0/3/25/26	0/2/2/2
43	0TD	XL	92	43	-	0/2/12/14	0/0/0/0
1	PSU	YA	1911	1	-	0/7/25/26	0/2/2/2
1	5MU	YA	1915	1	-	0/3/25/26	0/2/2/2
1	PSU	YA	1917	1	-	0/7/25/26	0/2/2/2
1	4OC	YA	1920	1	-	0/5/27/30	0/2/2/2
1	5MU	YA	1939	1,56	-	0/3/25/26	0/2/2/2
1	5MC	YA	1942	1	-	0/3/25/26	0/2/2/2
1	5MC	YA	1962	1,56	-	0/3/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	YA	2251	1,56,53	-	0/5/27/28	0/3/3/3
1	2MA	YA	2503	1,56	-	0/3/25/26	0/3/3/3
1	2MU	YA	2552	1,56	-	0/5/27/28	0/2/2/2
1	PSU	YA	2605	1	-	0/7/25/26	0/2/2/2

All (203) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	RA	2552	2MU	C3'-C2'	-8.46	1.34	1.53
1	YA	2552	2MU	C3'-C2'	-8.33	1.34	1.53
1	RA	2552	2MU	C6-C5	-8.26	1.20	1.38
1	YA	2552	2MU	C6-C5	-8.16	1.20	1.38
1	YA	2552	2MU	C4-N3	-7.89	1.18	1.33
1	RA	2552	2MU	C4-N3	-7.57	1.19	1.33
1	RA	2552	2MU	O4'-C4'	-5.92	1.31	1.45
1	YA	2552	2MU	O4'-C4'	-5.59	1.32	1.45
1	YA	1939	5MU	C4-N3	-4.53	1.24	1.33
1	RA	1939	5MU	C4-N3	-4.45	1.25	1.33
1	RA	1915	5MU	C4-N3	-3.99	1.25	1.33
1	YA	1915	5MU	C4-N3	-3.97	1.25	1.33
1	YA	2251	OMG	O6-C6	-3.28	1.16	1.24
1	RA	2251	OMG	O6-C6	-3.22	1.16	1.24
1	RA	2605	PSU	C5-C1'	-2.49	1.50	1.52
32	QA	1519	MA6	C5-C4	-2.21	1.35	1.40
1	RA	1917	PSU	C5-C1'	-2.06	1.50	1.52
1	YA	1939	5MU	C5M-C5	2.00	1.54	1.51
32	XA	1518	MA6	C2-N1	2.00	1.37	1.33
32	QA	1400	5MC	CM5-C5	2.05	1.55	1.51
32	QA	527	7MG	C8-N7	2.07	1.53	1.43
1	RA	2251	OMG	C2-N3	2.08	1.46	1.35
32	XA	1400	5MC	CM5-C5	2.09	1.55	1.51
32	XA	527	7MG	C8-N7	2.10	1.53	1.43
1	RA	2503	2MA	CM2-C2	2.14	1.56	1.49
1	YA	2251	OMG	C2-N3	2.16	1.46	1.35
1	RA	2552	2MU	O2'-C2'	2.16	1.48	1.42
32	XA	527	7MG	C1'-N9	2.17	1.49	1.44
1	RA	1939	5MU	C5M-C5	2.18	1.55	1.51
32	QA	1518	MA6	C2-N3	2.29	1.36	1.32
1	YA	1939	5MU	C6-C5	2.30	1.46	1.40
32	QA	1518	MA6	C2-N1	2.33	1.38	1.33
1	RA	1939	5MU	C6-C5	2.39	1.46	1.40
32	QA	527	7MG	C1'-N9	2.39	1.49	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	RA	1915	5MU	C5M-C5	2.41	1.55	1.51
32	XA	1519	MA6	C2-N3	2.46	1.36	1.32
32	XA	1518	MA6	C2-N3	2.47	1.36	1.32
1	YA	1962	5MC	C6-C5	2.58	1.46	1.40
1	RA	1911	PSU	C4-N3	2.58	1.37	1.33
1	YA	1915	5MU	C5M-C5	2.59	1.55	1.51
1	YA	2605	PSU	C4-N3	2.67	1.37	1.33
1	YA	1917	PSU	C4-N3	2.70	1.37	1.33
1	RA	1917	PSU	C4-N3	2.73	1.38	1.33
1	YA	1915	5MU	C6-C5	2.85	1.47	1.40
1	YA	1911	PSU	C4-N3	2.95	1.38	1.33
1	RA	1915	5MU	C6-C5	2.95	1.47	1.40
1	RA	1962	5MC	C6-C5	2.98	1.47	1.40
32	QA	1519	MA6	C2-N3	2.98	1.37	1.32
32	QA	527	7MG	C5-C4	3.04	1.47	1.39
1	RA	1942	5MC	C6-C5	3.04	1.48	1.40
1	YA	1942	5MC	C6-C5	3.06	1.48	1.40
32	XA	1400	5MC	C6-C5	3.08	1.48	1.40
32	XA	527	7MG	CM7-N7	3.10	1.51	1.46
32	XA	1404	5MC	C6-C5	3.12	1.48	1.40
32	XA	527	7MG	C5-C4	3.13	1.47	1.39
32	XA	967	5MC	C6-C5	3.15	1.48	1.40
32	XA	1519	MA6	C10-N6	3.15	1.53	1.45
32	QA	1404	5MC	C6-C5	3.18	1.48	1.40
32	XA	1407	5MC	C6-C5	3.19	1.48	1.40
32	QA	967	5MC	C6-C5	3.19	1.48	1.40
32	QA	516	PSU	C4-N3	3.19	1.38	1.33
32	QA	1400	5MC	C6-C5	3.23	1.48	1.40
32	QA	527	7MG	CM7-N7	3.24	1.51	1.46
32	XA	516	PSU	C4-N3	3.27	1.38	1.33
32	QA	1407	5MC	C6-C5	3.30	1.48	1.40
1	YA	1920	4OC	C5-C4	3.50	1.49	1.41
32	QA	1207	2MG	C2-N1	3.51	1.46	1.34
32	XA	1207	2MG	C2-N1	3.53	1.46	1.34
1	YA	2552	2MU	C3'-C4'	3.61	1.62	1.53
32	XA	1207	2MG	C2-N3	3.65	1.47	1.34
32	QA	1207	2MG	C2-N3	3.78	1.47	1.34
1	RA	1920	4OC	C5-C4	3.79	1.49	1.41
1	RA	2552	2MU	C3'-C4'	3.82	1.63	1.53
1	YA	1920	4OC	C4-N4	3.91	1.46	1.35
1	RA	1920	4OC	C4-N4	4.25	1.47	1.35
32	XA	1402	4OC	C2-N3	4.31	1.47	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	YA	1962	5MC	C4-N4	4.36	1.45	1.34
32	XA	1402	4OC	C5-C4	4.41	1.49	1.39
1	RA	1962	5MC	C4-N4	4.42	1.46	1.34
32	QA	1402	4OC	C5-C4	4.45	1.49	1.39
32	QA	1400	5MC	C4-N4	4.53	1.46	1.34
32	XA	1400	5MC	C4-N4	4.63	1.46	1.34
1	RA	2251	OMG	C6-C5	4.68	1.50	1.41
32	XA	1407	5MC	C5-C4	4.72	1.48	1.41
32	XA	1407	5MC	C4-N4	4.75	1.46	1.34
32	QA	1407	5MC	C4-N4	4.76	1.46	1.34
1	YA	1942	5MC	C4-N4	4.77	1.46	1.34
1	RA	1942	5MC	C4-N4	4.78	1.46	1.34
1	YA	1962	5MC	C5-C4	4.80	1.48	1.41
32	XA	1498	UR3	C6-C5	4.82	1.48	1.38
32	QA	1498	UR3	C6-C5	4.84	1.48	1.38
32	QA	1402	4OC	C2-N3	4.86	1.48	1.38
32	XA	967	5MC	C4-N4	4.89	1.47	1.34
32	QA	1404	5MC	C4-N4	4.92	1.47	1.34
32	QA	967	5MC	C4-N4	4.95	1.47	1.34
1	YA	1920	4OC	C2-N3	4.97	1.48	1.38
32	XA	1404	5MC	C4-N4	4.98	1.47	1.34
1	YA	2503	2MA	C2-N1	5.02	1.43	1.34
32	QA	966	M2G	C6-C5	5.13	1.51	1.41
32	XA	966	M2G	C6-C5	5.15	1.51	1.41
32	QA	1207	2MG	C6-C5	5.18	1.51	1.41
1	YA	2503	2MA	C6-N1	5.19	1.45	1.34
32	XA	967	5MC	C5-C4	5.24	1.49	1.41
32	XA	1207	2MG	C6-C5	5.28	1.52	1.41
1	RA	1920	4OC	C2-N3	5.29	1.49	1.38
32	XA	1400	5MC	C5-C4	5.36	1.49	1.41
1	RA	1942	5MC	C5-C4	5.39	1.49	1.41
1	RA	2503	2MA	C6-N1	5.41	1.46	1.34
32	QA	1402	4OC	C6-C5	5.43	1.49	1.38
1	RA	1962	5MC	C5-C4	5.46	1.49	1.41
32	XA	1402	4OC	C6-C5	5.46	1.50	1.38
1	YA	1942	5MC	C2-N3	5.47	1.49	1.38
1	YA	2251	OMG	C6-C5	5.47	1.52	1.41
1	RA	2503	2MA	C2-N1	5.51	1.44	1.34
1	RA	1942	5MC	C2-N3	5.54	1.49	1.38
1	YA	2503	2MA	C6-C5	5.54	1.51	1.40
32	QA	967	5MC	C5-C4	5.56	1.50	1.41
1	YA	1962	5MC	C2-N3	5.57	1.49	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	YA	1942	5MC	C5-C4	5.59	1.50	1.41
32	QA	1407	5MC	C5-C4	5.61	1.50	1.41
32	XA	1404	5MC	C2-N3	5.64	1.49	1.38
32	XA	1402	4OC	C4-N3	5.69	1.44	1.34
32	QA	1400	5MC	C5-C4	5.69	1.50	1.41
1	RA	1962	5MC	C2-N3	5.72	1.50	1.38
1	YA	1920	4OC	C6-C5	5.73	1.50	1.38
32	QA	1404	5MC	C5-C4	5.77	1.50	1.41
32	QA	1407	5MC	C2-N3	5.77	1.50	1.38
32	XA	966	M2G	C2-N1	5.77	1.44	1.34
32	QA	967	5MC	C2-N3	5.82	1.50	1.38
32	QA	1400	5MC	C2-N3	5.86	1.50	1.38
32	XA	967	5MC	C2-N3	5.88	1.50	1.38
1	RA	1920	4OC	C6-C5	5.90	1.51	1.38
1	YA	1920	4OC	C4-N3	5.92	1.46	1.35
1	YA	2251	OMG	C6-N1	5.94	1.43	1.33
32	QA	1404	5MC	C2-N3	5.94	1.50	1.38
1	RA	2251	OMG	C2-N2	5.96	1.46	1.34
32	XA	966	M2G	C6-N1	6.03	1.43	1.33
32	XA	1407	5MC	C2-N3	6.04	1.50	1.38
32	QA	966	M2G	C2-N1	6.12	1.45	1.34
32	XA	1400	5MC	C2-N3	6.13	1.50	1.38
1	YA	2251	OMG	C2-N1	6.16	1.47	1.35
32	XA	1404	5MC	C5-C4	6.18	1.51	1.41
32	XA	1498	UR3	C4-N3	6.18	1.47	1.38
1	YA	2251	OMG	C2-N2	6.29	1.47	1.34
1	RA	1920	4OC	C4-N3	6.33	1.47	1.35
32	QA	966	M2G	C6-N1	6.34	1.44	1.33
1	RA	2251	OMG	C2-N1	6.34	1.47	1.35
1	RA	2503	2MA	C6-C5	6.54	1.52	1.40
32	QA	1402	4OC	C4-N3	6.66	1.46	1.34
1	RA	2251	OMG	C6-N1	6.67	1.45	1.33
32	QA	1498	UR3	C4-N3	6.68	1.48	1.38
32	XA	527	7MG	C2-N2	6.77	1.48	1.34
32	QA	527	7MG	C2-N2	6.90	1.48	1.34
1	YA	2503	2MA	C2-N3	6.92	1.46	1.34
32	XA	1207	2MG	C6-N1	7.03	1.45	1.33
32	QA	1207	2MG	C6-N1	7.12	1.45	1.33
32	QA	1402	4OC	C6-N1	7.54	1.45	1.35
1	RA	2503	2MA	C2-N3	7.55	1.48	1.34
32	XA	1498	UR3	C6-N1	7.59	1.45	1.35
32	XA	527	7MG	C2-N3	7.67	1.49	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	YA	2251	OMG	C4-N3	7.69	1.47	1.35
32	QA	1498	UR3	C6-N1	7.70	1.45	1.35
32	XA	527	7MG	C8-N9	7.71	1.56	1.45
1	RA	2251	OMG	C4-N3	7.75	1.48	1.35
32	QA	527	7MG	C2-N1	7.82	1.50	1.35
32	XA	527	7MG	C2-N1	7.89	1.50	1.35
32	XA	1402	4OC	C6-N1	7.90	1.46	1.35
32	QA	527	7MG	C2-N3	7.91	1.50	1.35
1	YA	1920	4OC	C6-N1	7.93	1.46	1.35
32	XA	966	M2G	C2-N2	7.98	1.48	1.34
1	YA	1942	5MC	C4-N3	8.01	1.46	1.35
32	QA	527	7MG	C8-N9	8.04	1.56	1.45
32	XA	966	M2G	C4-N3	8.14	1.48	1.35
32	QA	1407	5MC	C4-N3	8.17	1.47	1.35
1	RA	1920	4OC	C6-N1	8.19	1.46	1.35
32	XA	1404	5MC	C4-N3	8.24	1.47	1.35
1	RA	1962	5MC	C4-N3	8.31	1.47	1.35
1	RA	1942	5MC	C4-N3	8.35	1.47	1.35
32	QA	966	M2G	C4-N3	8.49	1.49	1.35
32	QA	966	M2G	C2-N2	8.66	1.49	1.34
32	XA	1207	2MG	C4-N3	8.67	1.49	1.35
32	QA	527	7MG	C6-C5	8.71	1.53	1.41
32	QA	1404	5MC	C4-N3	8.72	1.48	1.35
32	XA	1407	5MC	C4-N3	8.76	1.48	1.35
32	QA	1400	5MC	C4-N3	8.77	1.48	1.35
32	XA	967	5MC	C4-N3	8.80	1.48	1.35
1	YA	1962	5MC	C4-N3	8.85	1.48	1.35
32	QA	527	7MG	C6-N1	8.85	1.49	1.33
32	XA	527	7MG	C6-N1	8.90	1.49	1.33
32	QA	967	5MC	C4-N3	8.92	1.48	1.35
32	QA	1207	2MG	C4-N3	9.01	1.50	1.35
32	XA	1400	5MC	C4-N3	9.05	1.48	1.35
32	XA	527	7MG	C6-C5	9.15	1.54	1.41
1	RA	2503	2MA	C4-N3	9.93	1.51	1.35
1	YA	2503	2MA	C4-N3	10.06	1.51	1.35
32	XA	1207	2MG	C2-N2	11.07	1.47	1.34
32	QA	1207	2MG	C2-N2	11.71	1.47	1.34
1	RA	2552	2MU	O4'-C1'	11.98	1.58	1.41
1	YA	2552	2MU	O4'-C1'	12.29	1.58	1.41
32	XA	527	7MG	C4-N3	12.64	1.50	1.34
32	QA	527	7MG	C4-N3	13.17	1.51	1.34
1	RA	2552	2MU	C6-N1	19.23	1.60	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	YA	2552	2MU	C6-N1	20.18	1.61	1.35

All (157) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	2503	2MA	C1'-N9-C4	-13.50	111.73	126.81
32	XA	966	M2G	C1'-N9-C4	-12.88	112.43	126.81
32	QA	966	M2G	C1'-N9-C4	-12.52	112.83	126.81
32	QA	1518	MA6	N3-C2-N1	-12.29	119.22	128.87
32	QA	1519	MA6	N3-C2-N1	-12.26	119.24	128.87
32	XA	1518	MA6	N3-C2-N1	-11.55	119.80	128.87
1	RA	2503	2MA	C1'-N9-C4	-11.00	114.53	126.81
32	XA	1402	4OC	CM4-N4-C4	-10.44	114.07	122.87
1	YA	2251	OMG	N3-C2-N1	-10.23	113.63	127.56
1	RA	2251	OMG	N3-C2-N1	-10.19	113.69	127.56
32	QA	527	7MG	N1-C2-N3	-8.49	111.63	125.51
32	QA	1207	2MG	N3-C2-N1	-8.49	113.50	126.19
32	XA	527	7MG	N1-C2-N3	-8.21	112.10	125.51
32	QA	527	7MG	C5-C4-N3	-8.15	118.43	126.74
32	XA	527	7MG	C5-C4-N3	-7.90	118.70	126.74
32	XA	1207	2MG	N3-C2-N1	-7.77	114.56	126.19
32	XA	1519	MA6	N3-C2-N1	-7.69	122.83	128.87
1	RA	2251	OMG	C6-C5-C4	-5.71	114.33	120.86
32	QA	966	M2G	N3-C2-N1	-5.70	116.66	126.35
1	YA	2251	OMG	C6-C5-C4	-5.56	114.50	120.86
43	QL	92	0TD	CB-CA-N	-4.91	100.00	109.83
1	RA	2503	2MA	N3-C2-N1	-4.82	116.14	125.60
32	XA	966	M2G	N3-C2-N1	-4.81	118.17	126.35
1	YA	2503	2MA	N3-C2-N1	-4.69	116.40	125.60
32	QA	1207	2MG	C6-C5-C4	-4.29	115.96	120.86
1	RA	2605	PSU	C5-C1'-C2'	-4.28	108.16	115.44
1	RA	1920	4OC	C5-C4-N3	-4.22	116.44	121.79
32	QA	1402	4OC	CM4-N4-C4	-4.07	119.44	122.87
32	XA	1207	2MG	C6-C5-C4	-3.93	116.37	120.86
1	YA	1920	4OC	C5-C4-N3	-3.80	116.97	121.79
1	RA	1917	PSU	C5-C1'-C2'	-3.70	109.15	115.44
1	RA	2552	2MU	C4'-O4'-C1'	-3.50	105.93	109.64
1	YA	1917	PSU	C5-C1'-C2'	-3.40	109.67	115.44
32	XA	1207	2MG	CM2-N2-C2	-3.19	119.44	123.03
32	QA	1402	4OC	C5-C4-N3	-3.17	117.50	123.22
32	XA	1404	5MC	C5-C4-N3	-3.09	116.00	121.26
1	YA	1942	5MC	C5-C4-N3	-2.84	116.43	121.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	XL	92	0TD	CB-CA-N	-2.78	104.28	109.83
32	XA	1519	MA6	C2'-C1'-N9	-2.75	106.09	113.47
1	YA	2605	PSU	C5-C1'-C2'	-2.74	110.78	115.44
1	YA	2552	2MU	C4'-O4'-C1'	-2.68	106.80	109.64
1	RA	2605	PSU	C5-C6-N1	-2.67	120.65	124.38
32	QA	1404	5MC	C5-C4-N3	-2.58	116.88	121.26
32	XA	1407	5MC	C5-C4-N3	-2.54	116.95	121.26
1	YA	1911	PSU	C5-C1'-C2'	-2.53	111.14	115.44
32	XA	1400	5MC	C5-C4-N3	-2.51	116.99	121.26
32	QA	1407	5MC	C5-C4-N3	-2.46	117.08	121.26
32	XA	967	5MC	C5-C4-N3	-2.43	117.12	121.26
32	QA	967	5MC	C5-C4-N3	-2.40	117.18	121.26
1	RA	1911	PSU	C5-C1'-C2'	-2.38	111.39	115.44
1	YA	2605	PSU	C5-C6-N1	-2.37	121.08	124.38
32	QA	1518	MA6	C1'-N9-C4	-2.37	124.16	126.81
1	YA	1917	PSU	C5-C6-N1	-2.34	121.12	124.38
32	XA	516	PSU	C5-C6-N1	-2.23	121.28	124.38
32	QA	1400	5MC	C5-C4-N3	-2.21	117.50	121.26
32	XA	1402	4OC	C5-C4-N3	-2.19	119.27	123.22
1	RA	1920	4OC	C6-N1-C2	-2.11	117.89	121.33
1	RA	1911	PSU	C5-C6-N1	-2.10	121.45	124.38
1	YA	1920	4OC	C6-N1-C2	-2.07	117.95	121.33
1	RA	1942	5MC	C5-C4-N3	-2.06	117.76	121.26
32	XA	1519	MA6	C1'-N9-C4	-2.04	124.53	126.81
32	QA	527	7MG	C8-N9-C1'	2.00	128.43	122.43
1	YA	2552	2MU	C3'-C2'-C1'	2.02	106.49	102.63
32	QA	1207	2MG	O3'-C3'-C2'	2.09	118.60	111.86
1	YA	2605	PSU	O4'-C1'-C2'	2.18	107.04	104.69
32	QA	527	7MG	C5-C6-N1	2.19	126.65	123.39
32	QA	1207	2MG	N2-C2-N3	2.20	119.50	116.94
1	RA	2552	2MU	C5-C4-N3	2.23	128.75	123.28
32	QA	1498	UR3	C6-C5-C4	2.26	121.48	117.30
32	XA	1207	2MG	C6-N1-C2	2.29	118.52	115.24
32	XA	1498	UR3	C6-C5-C4	2.32	121.59	117.30
1	YA	2552	2MU	C5-C4-N3	2.35	129.05	123.28
1	RA	1939	5MU	C5M-C5-C4	2.36	122.58	119.97
32	XA	527	7MG	N2-C2-N3	2.36	121.09	117.20
1	RA	2503	2MA	CM2-C2-N3	2.40	121.30	117.22
32	QA	1498	UR3	C3U-N3-C4	2.42	121.59	118.21
1	RA	2605	PSU	O4'-C1'-C2'	2.50	107.40	104.69
1	YA	1917	PSU	O4'-C1'-C2'	2.53	107.42	104.69
32	QA	1207	2MG	C6-N1-C2	2.66	119.06	115.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	QA	527	7MG	N2-C2-N3	2.72	121.69	117.20
1	YA	1911	PSU	O4'-C1'-C2'	2.74	107.66	104.69
1	RA	1917	PSU	O4'-C1'-C2'	2.76	107.67	104.69
1	RA	1911	PSU	O4'-C1'-C2'	2.80	107.72	104.69
1	YA	1939	5MU	C5-C4-N3	2.89	127.77	125.35
1	YA	1939	5MU	C5M-C5-C4	2.92	123.20	119.97
32	QA	516	PSU	O4'-C1'-C2'	2.97	107.90	104.69
32	XA	516	PSU	O4'-C1'-C2'	2.99	107.93	104.69
32	XA	966	M2G	N3-C2-N2	3.09	120.55	117.14
1	RA	2503	2MA	CM2-C2-N1	3.14	122.56	117.20
32	XA	1404	5MC	N4-C4-N3	3.18	121.58	116.92
1	YA	1915	5MU	C5M-C5-C4	3.24	123.56	119.97
1	RA	2251	OMG	C6-N1-C2	3.48	119.97	115.88
1	RA	1920	4OC	N4-C4-N3	3.49	122.59	116.50
1	YA	1920	4OC	N4-C4-N3	3.50	122.62	116.50
32	QA	1407	5MC	N4-C4-N3	3.52	122.08	116.92
1	YA	2503	2MA	CM2-C2-N1	3.55	123.27	117.20
1	RA	2552	2MU	C4-N3-C2	3.55	117.95	114.21
32	XA	1519	MA6	C2-N1-C6	3.56	120.03	111.64
32	QA	1519	MA6	C2-N1-C6	3.57	120.05	111.64
1	RA	1915	5MU	C5M-C5-C4	3.59	123.94	119.97
1	YA	2251	OMG	C6-N1-C2	3.75	120.27	115.88
32	QA	527	7MG	C6-N1-C2	3.78	120.31	115.88
32	XA	966	M2G	N1-C2-N2	3.80	121.28	117.14
32	XA	527	7MG	C6-N1-C2	3.87	120.42	115.88
32	QA	1404	5MC	N4-C4-N3	3.90	122.63	116.92
32	QA	966	M2G	N3-C2-N2	3.94	121.48	117.14
32	QA	1400	5MC	N4-C4-N3	4.00	122.78	116.92
32	XA	527	7MG	N3-C4-N9	4.00	132.16	126.98
32	XA	1518	MA6	C2-N1-C6	4.07	121.25	111.64
1	RA	1942	5MC	N4-C4-N3	4.11	122.94	116.92
1	YA	1942	5MC	N4-C4-N3	4.12	122.95	116.92
1	RA	1962	5MC	N4-C4-N3	4.29	123.20	116.92
32	QA	1402	4OC	C6-C5-C4	4.33	119.12	117.42
32	QA	966	M2G	N1-C2-N2	4.33	121.86	117.14
32	QA	527	7MG	N3-C4-N9	4.36	132.62	126.98
1	YA	2552	2MU	C4-N3-C2	4.40	118.85	114.21
1	YA	1920	4OC	C6-C5-C4	4.45	119.18	117.44
32	QA	967	5MC	N4-C4-N3	4.51	123.53	116.92
32	QA	1518	MA6	C2-N1-C6	4.59	122.46	111.64
1	YA	2251	OMG	N2-C2-N1	4.74	125.02	117.20
32	XA	967	5MC	N4-C4-N3	4.88	124.07	116.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	XA	1402	4OC	C2-N3-C4	4.90	121.67	115.43
43	XL	92	0TD	CSB-SB-CB	4.94	110.67	101.44
32	XA	1400	5MC	N4-C4-N3	4.98	124.22	116.92
43	QL	92	0TD	CSB-SB-CB	5.04	110.86	101.44
32	XA	527	7MG	C2-N3-C4	5.10	129.00	114.50
1	YA	1962	5MC	N4-C4-N3	5.14	124.45	116.92
32	QA	527	7MG	C2-N3-C4	5.20	129.31	114.50
1	RA	1920	4OC	C6-C5-C4	5.30	119.51	117.44
32	XA	1402	4OC	C6-C5-C4	5.35	119.52	117.42
32	XA	1407	5MC	N4-C4-N3	5.48	124.96	116.92
1	RA	2251	OMG	N2-C2-N1	5.70	126.60	117.20
32	QA	527	7MG	N2-C2-N1	5.75	126.68	117.20
1	YA	1917	PSU	C4-N3-C2	5.77	119.97	115.16
32	XA	527	7MG	N2-C2-N1	5.83	126.81	117.20
1	RA	2605	PSU	C4-N3-C2	6.07	120.22	115.16
32	XA	516	PSU	C4-N3-C2	6.38	120.48	115.16
1	RA	1911	PSU	C4-N3-C2	6.48	120.56	115.16
1	RA	2251	OMG	C1'-N9-C4	6.61	134.18	126.81
32	QA	1402	4OC	C2-N3-C4	6.69	123.94	115.43
1	YA	2605	PSU	C4-N3-C2	6.72	120.77	115.16
1	YA	1911	PSU	C4-N3-C2	7.05	121.04	115.16
32	QA	516	PSU	C4-N3-C2	7.21	121.17	115.16
1	RA	1917	PSU	C4-N3-C2	7.24	121.20	115.16
32	XA	966	M2G	C2-N3-C4	7.76	123.50	114.99
1	YA	2251	OMG	C1'-N9-C4	7.84	135.55	126.81
32	QA	966	M2G	C2-N3-C4	7.85	123.60	114.99
1	YA	1939	5MU	C4-N3-C2	8.50	122.25	115.16
32	QA	1207	2MG	N2-C2-N1	8.67	127.01	116.94
32	XA	1207	2MG	N2-C2-N1	8.73	127.08	116.94
1	RA	1939	5MU	C4-N3-C2	9.33	122.94	115.16
1	RA	1915	5MU	C4-N3-C2	9.52	123.10	115.16
1	YA	1915	5MU	C4-N3-C2	9.94	123.45	115.16
32	XA	1207	2MG	C2-N3-C4	10.34	126.33	114.99
32	QA	1207	2MG	C2-N3-C4	10.95	127.00	114.99
1	YA	2503	2MA	C2-N3-C4	22.59	126.17	115.29
1	RA	2503	2MA	C2-N3-C4	24.90	127.28	115.29

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

16 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	QA	1402	4OC	1	0
32	QA	1518	MA6	1	0
32	QA	1519	MA6	2	0
1	RA	1917	PSU	1	0
1	RA	1920	4OC	1	0
1	RA	1942	5MC	1	0
1	RA	1962	5MC	1	0
1	RA	2251	OMG	1	0
1	RA	2503	2MA	2	0
1	RA	2552	2MU	3	0
32	XA	1518	MA6	5	0
32	XA	1519	MA6	4	0
1	YA	1939	5MU	1	0
1	YA	1962	5MC	2	0
1	YA	2251	OMG	1	0
1	YA	2552	2MU	3	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2450 ligands modelled in this entry, 2448 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	$\# Z > 2$
58	SF4	QD	302	35	0,12,12	0.00	-	0,24,24	0.00	-
58	SF4	XD	301	35	0,12,12	0.00	-	0,24,24	0.00	-

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
58	SF4	QD	302	35	-	0/0/48/48	0/6/5/5
58	SF4	XD	301	35	-	0/0/48/48	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS failed to run properly - this section will therefore be empty.

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

EDS failed to run properly - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS failed to run properly - this section will therefore be empty.

6.4 Ligands [i](#)

EDS failed to run properly - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS failed to run properly - this section will therefore be empty.