



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 14, 2017 – 02:50 PM EDT

PDB ID : 5J30  
Title : Thermus thermophilus 70S termination complex containing E. coli RF1  
Authors : Hoffer, E.D.; Dunham, C.M.  
Deposited on : unknown  
Resolution : 3.20 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : **FAILED**  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029824

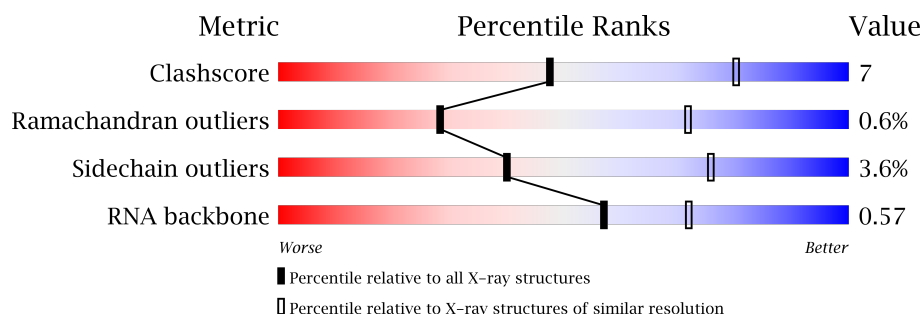
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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	112137	1009 (3.20-3.20)
Ramachandran outliers	110173	1118 (3.22-3.18)
Sidechain outliers	110143	1117 (3.22-3.18)
RNA backbone	2435	1045 (3.60-2.80)


























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  $\geq 3$ , 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	 81% 16% ..
4	YE	206	 78% 19% ..
5	RF	210	 75% 20% ..
5	YF	210	 71% 20% 5% .
6	RG	182	 74% 23% ..
6	YG	182	 63% 32% ..
7	RH	180	 79% 17% ..
7	YH	180	 66% 26% . .
8	RI	148	 78% 20% ..
8	YI	148	 78% 17% ..
9	RN	140	 81% 16% .
9	YN	140	 81% 17% .
10	RO	122	 89% 11%
10	YO	122	 86% 14%
11	RP	150	 79% 19% ..
11	YP	150	 77% 21% ..
12	RQ	141	 79% 20% .
12	YQ	141	 79% 18% .
13	RR	118	 81% 17% .
13	YR	118	 81% 19%
14	RS	112	 85% 12% ..
14	YS	112	 78% 20% ..
15	RT	146	 68% 21% . 10%
15	YT	146	 75% 14% . 10%
16	RU	118	 83% 14% ..


























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Mol	Chain	Length	Quality of chain
16	YU	118	 84% 14% ..
17	RV	101	 89% 10% .
17	YV	101	 75% 22% .
18	RW	113	 82% 13% ..
18	YW	113	 89% 8% ..
19	RX	96	 79% 20% .
19	YX	96	 78% 21% .
20	RY	110	 77% 18% ..
20	YY	110	 72% 24% ..
21	RZ	206	 76% 15% . 8%
21	YZ	206	 73% 17% . 8%
22	R0	85	 76% 12% . 9%
22	Y0	85	 72% 19% 9%
23	R1	98	 84% 13% ..
23	Y1	98	 74% 20% . ..
24	R2	72	 88% 8% ..
24	Y2	72	 81% 15% ..
25	R3	60	 92% 7% .
25	Y3	60	 77% 18% ..
26	R4	71	 56% 37% . ..
26	Y4	71	 55% 37% 6% .
27	R5	60	 75% 22% ..
27	Y5	60	 85% 12% ..
28	R6	54	 76% 20% ..
28	Y6	54	 87% 11% .


























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Mol	Chain	Length	Quality of chain
29	R7	49	
29	Y7	49	
30	R8	65	
30	Y8	65	
31	R9	37	
31	Y9	37	
32	QA	1521	
32	XA	1521	
33	QB	256	
33	XB	256	
34	QC	239	
34	XC	239	
35	QD	209	
35	XD	209	
36	QE	162	
36	XE	162	
37	QF	101	
37	XF	101	
38	QG	156	
38	XG	156	
39	QH	138	
39	XH	138	
40	QI	128	
40	XI	128	
41	QJ	105	




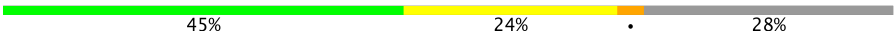
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Mol	Chain	Length	Quality of chain
41	XJ	105	
42	QK	129	
42	XK	129	
43	QL	132	
43	XL	132	
44	QM	126	
44	XM	126	
45	QN	61	
45	XN	61	
46	QO	89	
46	XO	89	
47	QP	88	
47	XP	88	
48	QQ	105	
48	XQ	105	
49	QR	88	
49	XR	88	
50	QS	93	
50	XS	93	
51	QT	106	
51	XT	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 294739 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	189	Total	C	N	O	S	0	0	0
			1485	946	265	272	2			
21	YZ	189	Total	C	N	O	S	0	0	0
			1469	938	259	270	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 P-site tRNA fMet.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	QV	77	Total	C	N	O	P	0	0	0
			1644	732	297	538	77			
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	10	Total	C	N	O	P	0	0	0
			215	97	42	66	10			
54	XX	9	Total	C	N	O	P	0	0	0
			193	87	37	60	9			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	QY	258	Total	C	N	O	S	0	0	0
			2014	1235	382	389	8			
55	XY	259	Total	C	N	O	S	0	0	0
			2023	1240	384	391	8			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	QA	256	Total	Mg	0	0
			256	256		
56	YV	1	Total	Mg	0	0
			1	1		
56	RP	1	Total	Mg	0	0
			1	1		
56	R7	2	Total	Mg	0	0
			2	2		
56	YA	744	Total	Mg	0	0
			744	744		
56	QM	1	Total	Mg	0	0
			1	1		
56	YR	1	Total	Mg	0	0
			1	1		
56	RT	2	Total	Mg	0	0
			2	2		
56	QD	3	Total	Mg	0	0
			3	3		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	RN	2	Total 2	Mg 2	0	0
56	XE	1	Total 1	Mg 1	0	0
56	RG	4	Total 4	Mg 4	0	0
56	QI	1	Total 1	Mg 1	0	0
56	YD	9	Total 9	Mg 9	0	0
56	XX	1	Total 1	Mg 1	0	0
56	QV	6	Total 6	Mg 6	0	0
56	RX	1	Total 1	Mg 1	0	0
56	Y8	2	Total 2	Mg 2	0	0
56	YO	2	Total 2	Mg 2	0	0
56	XA	183	Total 183	Mg 183	0	0
56	Y1	1	Total 1	Mg 1	0	0
56	RQ	6	Total 6	Mg 6	0	0
56	R0	4	Total 4	Mg 4	0	0
56	XT	1	Total 1	Mg 1	0	0
56	QR	1	Total 1	Mg 1	0	0
56	QL	2	Total 2	Mg 2	0	0
56	RU	2	Total 2	Mg 2	0	0
56	QG	2	Total 2	Mg 2	0	0
56	RO	1	Total 1	Mg 1	0	0
56	XJ	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	Y7	2	Total 2	Mg 2	0	0
56	QH	1	Total 1	Mg 1	0	0
56	YG	2	Total 2	Mg 2	0	0
56	YQ	2	Total 2	Mg 2	0	0
56	RY	1	Total 1	Mg 1	0	0
56	YN	1	Total 1	Mg 1	0	0
56	R8	1	Total 1	Mg 1	0	0
56	YX	1	Total 1	Mg 1	0	0
56	RR	3	Total 3	Mg 3	0	0
56	RD	15	Total 15	Mg 15	0	0
56	R1	4	Total 4	Mg 4	0	0
56	XL	1	Total 1	Mg 1	0	0
56	QO	1	Total 1	Mg 1	0	0
56	YT	4	Total 4	Mg 4	0	0
56	RV	4	Total 4	Mg 4	0	0
56	QF	1	Total 1	Mg 1	0	0
56	RH	1	Total 1	Mg 1	0	0
56	R5	3	Total 3	Mg 3	0	0
56	Y0	1	Total 1	Mg 1	0	0
56	QQ	1	Total 1	Mg 1	0	0
56	RA	1039	Total 1039	Mg 1039	0	0

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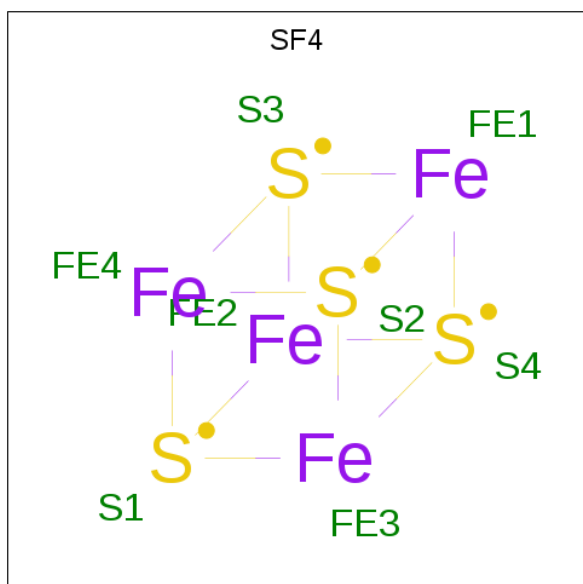
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	YF	3	Total 3	Mg 3	0	0
56	YP	1	Total 1	Mg 1	0	0
56	RZ	1	Total 1	Mg 1	0	0
56	QB	1	Total 1	Mg 1	0	0
56	Y5	1	Total 1	Mg 1	0	0
56	RE	8	Total 8	Mg 8	0	0
56	XK	1	Total 1	Mg 1	0	0
56	YB	18	Total 18	Mg 18	0	0
56	XR	1	Total 1	Mg 1	0	0
56	QT	2	Total 2	Mg 2	0	0
56	QN	2	Total 2	Mg 2	0	0
56	YW	2	Total 2	Mg 2	0	0
56	RW	2	Total 2	Mg 2	0	0
56	XV	4	Total 4	Mg 4	0	0
56	RB	27	Total 27	Mg 27	0	0
56	YI	1	Total 1	Mg 1	0	0
56	QE	2	Total 2	Mg 2	0	0
56	XF	2	Total 2	Mg 2	0	0
56	RF	12	Total 12	Mg 12	0	0
56	R3	2	Total 2	Mg 2	0	0
56	YE	5	Total 5	Mg 5	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	Y9	1	Total	Zn	0	0
			1	1		
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: Fe<sub>4</sub>S<sub>4</sub>).



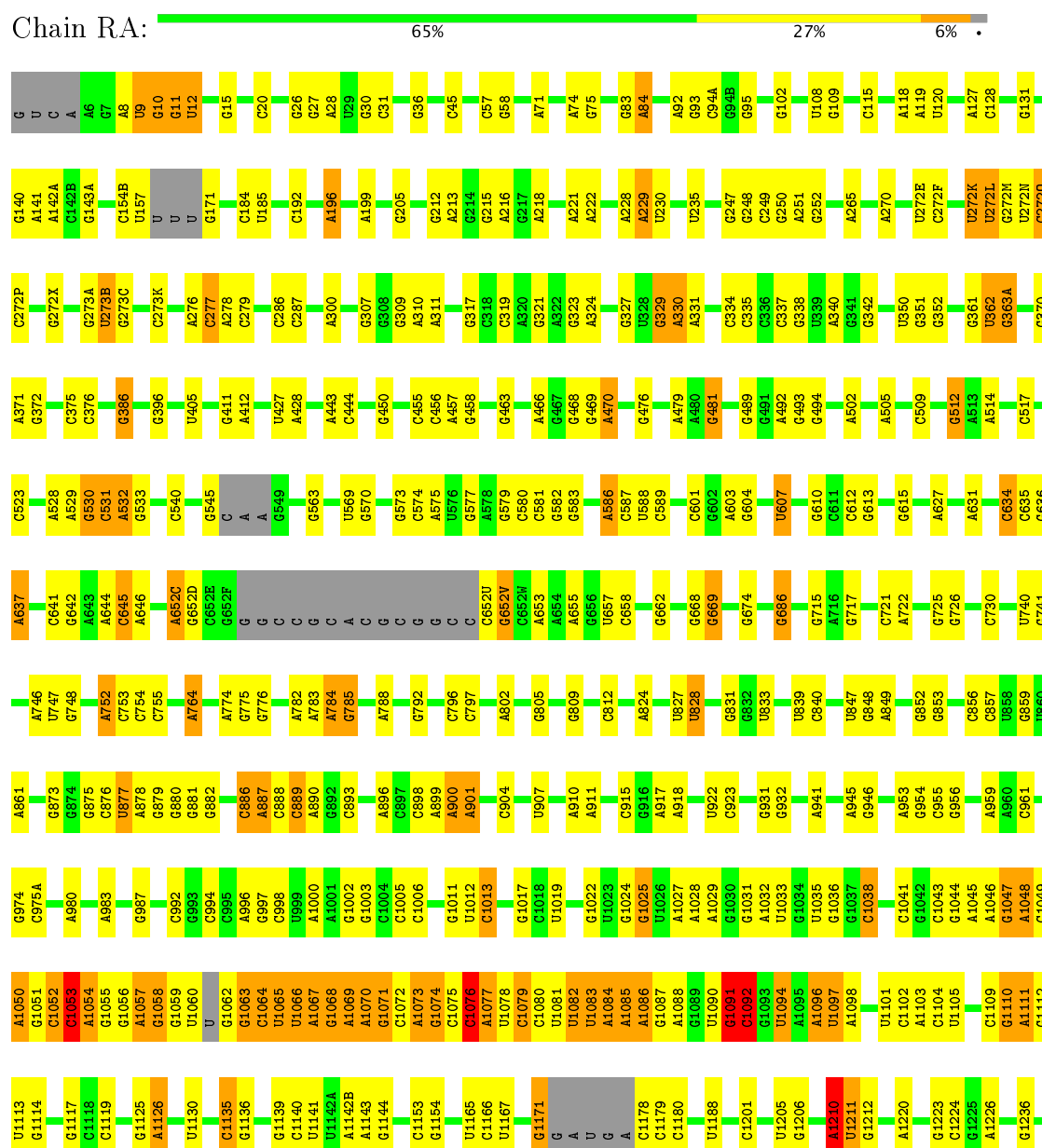
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
58	QD	1	Total 8	Fe 4	S 4	0	0
58	XD	1	Total 8	Fe 4	S 4	0	0

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

Note EDS failed to run properly.

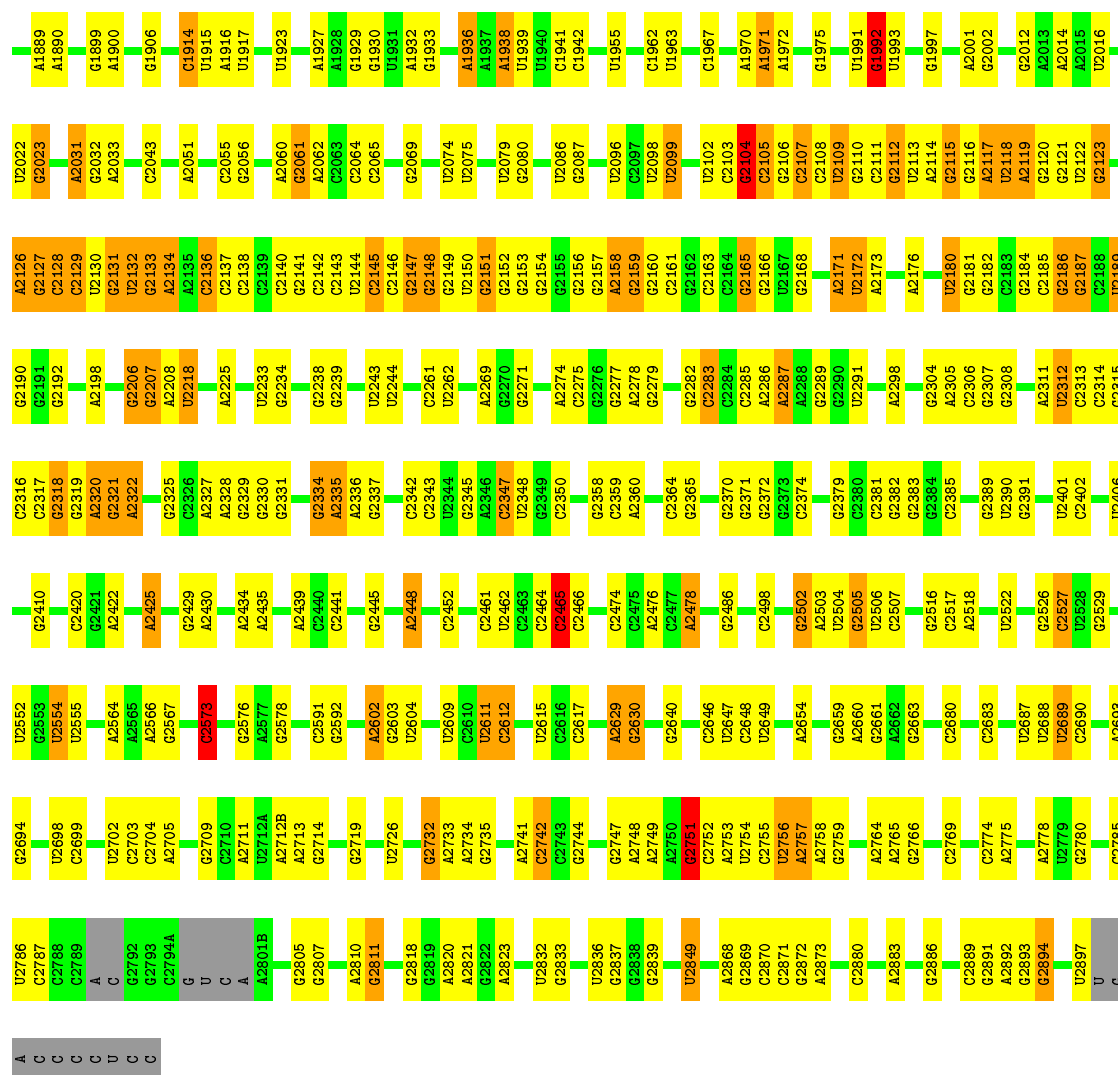
#### • Molecule 1: 23S rRNA







A1741	A1579	A1365	U1205	U1097	G1034	G982	A824	G700	G610	A505	C334	G250	U120	G
G1750	A1580	G1368	G1206	A1098	U1035	A941	U827	A706	U614A	C509	C336	G252	G125	U
G1753	C1584	G1492	G1212	U1101	G1036	A945	U828	G707	G615	C512	G342	A265	A126	A
G1756	U1371	U1372	A1220	C1104	G1038	G946	U833	U714	G616	G512	G342	A270	G131	G7
U1757	A1378	A1379	G1236	U1105	A1045	A953	U847	G715	A627	A514	U850	U272E	G141	A8
A1759	G1380	G1385	U1239	U1108	A1046	C955	G848	G716	A631	C517	G352	C272F	A141	U9
G1762	A1384	U1385	U1240	U1110	G1047	G956	A849	G717	A631	C523	U362	U272K	G143A	G10
G1763	U1386	U1388	U1250	G1112	A1049	A957	G855	A721	G634	C523	G363A	U272L	C143B	G11
G1764	C1506	U1396	G1251	U1113	A1050	A958	C857	G723	G636	A528	G370	G272M	C144	G15
A1773	A1507	U1397	G1252	U1114	G1051	A960	U858	U724	A637	A529	A371	U272N	C154B	G24
U1778	A1508	G1400	A1253	C1053	C1052	C961	U859	G725	U639	C531	G372	U272O	U157	U25
U1779	A1509A	G1401	A1254	C1054	C1053	U969	U860	C730	U640	A532	C385	C272P	U	G26
A1780	A1509B	G1401	U1255	C1118	G1055	C970	G862	G747	C641	G533	G386	G272X	U	G27
A1784	U1510	C1404	G1266	C1119	A1057	C971	A863	G748	G642	C540	A394	G273A	G171	G30
A1785	C1511	U1405	U1267	C1124	G1058	A973	G873	G741	A644	C540	A394	G273B	G180	C31
A1786	U1514	U1406	U1267	G1125	G1059	G974	G874	A746	C645	G545	G396	G273C	G184	G36
C1640	G1515	C1407	A1268	A1126	U1060	C975A	C876	U747	A646	C	U405	C273K	U185	C45
A1841	C1408	C1408	A1269	U1130	U	A880	C877	G748	A652C	A	G411	G273K	A195	G55
G1642	C1409	G1410	G1270	U1130	G1062	A880	U877	A752	G652D	G549	A412	A276	A195	A56
C1632	G1410	C1411	G1271	C1135	G1063	A983	A878	C753	C852E	G563	U421	C277	A197	C57
C1638	U1405	U1406	U1272	G1136	C1064	A1272	G879	C754	G652F	U566	U427	A278	C198	G58
U1639	U1514	U1407	U1273	G1139	U1065	G987	G880	C755	G	U566	U427	C279	A199	G61
A1841	G1408	C1408	A1269	G1139	U1066	G987	G881	C755	G	U566	U427	C279	A199	G61
G1642	C1409	G1410	G1270	U1130	U1067	C994	G882	G760	A652C	U566	U427	C279	A199	G61
C1648	C1411	C1411	G1271	C1135	G1068	C995	C886	A761	G652D	U566	U427	C279	A199	G61
C1657	U1416	U1417	A1278	G1140	A1069	C996	A887	A764	G652D	U566	U427	C279	A199	G61
C1658	C1417	C1417	A1287	C1140	A1070	C997	C888	A764	G652D	U566	U427	C279	A199	G61
A1665	U1419	U1420	C1291	A1142B	G1071	C998	C889	A764	G652D	U566	U427	C279	A199	G61
C1800	C1531	G1421	U1292	A1143	C1072	U999	A890	A774	G652D	U566	U427	C279	A199	G61
A1668	G1532	G1422	C1293	C1153	C1073	U999	G892	G775	G652D	U566	U427	C279	A199	G61
A1669	U	G1423	C1293	G1154	G1074	A1000	C893	G776	G652D	U566	U427	C279	A199	G61
C1803	C1533	U	U1300	G1154	C1075	C1005	C896	G776	G652D	U566	U427	C279	A199	G61
G1674	A	U	A1301	G1163	C1076	C1006	A896	A782	G652D	U566	U427	C279	A199	G61
C1804	C1536	U	A1302	U1164	C1077	C1006	A896	A782	G652D	U566	U427	C279	A199	G61
C1883	G1303	U	G1303	U1165	U1077	C1006	A896	A782	G652D	U566	U427	C279	A199	G61
C1884	G1303	U	G1303	U1165	U1077	C1006	A896	A782	G652D	U566	U427	C279	A199	G61
U1810	U1340	U	G1340	U1167	C1078	U1012	A900	A785	G652D	U566	U427	C279	A199	G61
A1812	A1454A	U	G1340	U1167	C1079	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
G1813	U1454A	U	G1340	U1167	C1080	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
G1814	U1454A	U	G1340	U1167	C1081	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
A1815	U1454A	U	G1340	U1167	C1082	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
G1816	U1454A	U	G1340	U1167	C1083	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
G1822	U1454A	U	G1340	U1167	C1084	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
A1700	U1454A	U	G1340	U1167	C1085	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
A1701	U1454A	U	G1340	U1167	C1086	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
G1826	U1454A	U	G1340	U1167	C1087	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
G1835	U1454A	U	G1340	U1167	C1088	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
U1709	U1454A	U	G1340	U1167	C1089	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
C1710	U1454A	U	G1340	U1167	C1090	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
A1847	U1454A	U	G1340	U1167	C1091	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
A1848	U1454A	U	G1340	U1167	C1092	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
A1721	U1454A	U	G1340	U1167	C1093	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
A1722	U1454A	U	G1340	U1167	C1094	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
U1739	U1454A	U	G1340	U1167	C1095	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
A1877	U1454A	U	G1340	U1167	C1096	U1013	A901	G785	G652D	U566	U427	C279	A199	G61
G1878	U1454A	U	G1340	U1167	C1097	U1013	A901	G785	G652D	U566	U427	C279	A199	G61



- Molecule 2: 5S rRNA

Chain RB: 82% 16%



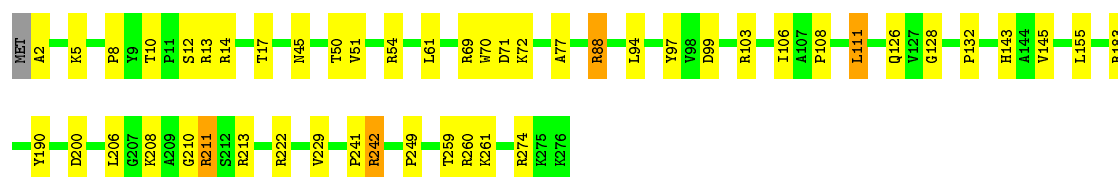
- Molecule 2: 5S rRNA

Chain YB: 68% 26%



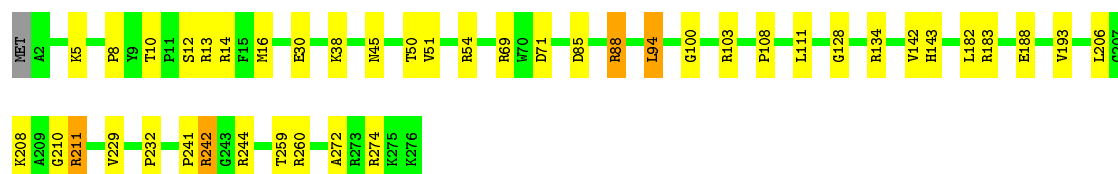
- Molecule 3: 50S ribosomal protein L2

Chain RD: 82% 16%



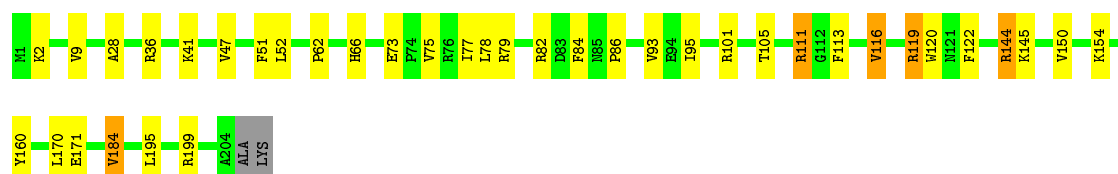
- Molecule 3: 50S ribosomal protein L2

Chain YD: 84% 14% .



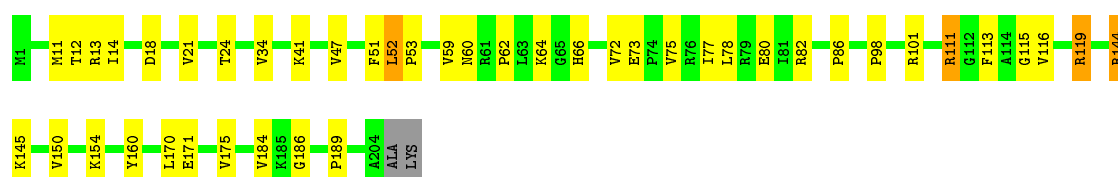
- Molecule 4: 50S ribosomal protein L3

Chain RE: 81% 16% ..



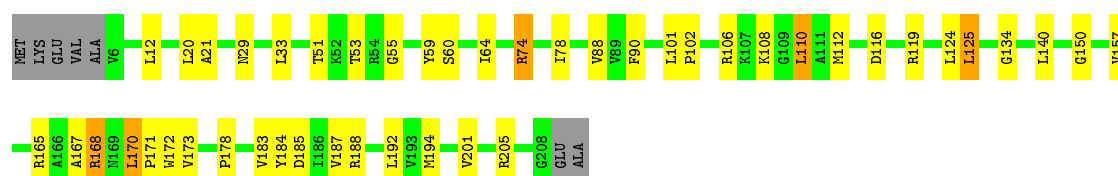
- Molecule 4: 50S ribosomal protein L3

Chain YE: 78% 19% ..



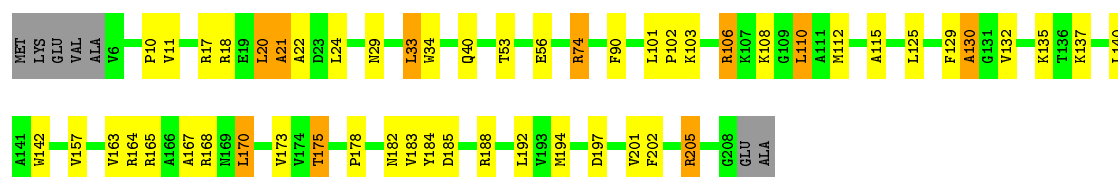
- Molecule 5: 50S ribosomal protein L4

Chain RF: 75% 20% ..



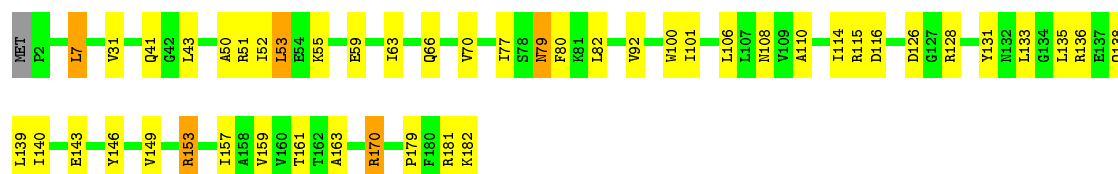
- Molecule 5: 50S ribosomal protein L4

Chain YF: 71% 20% 5% .



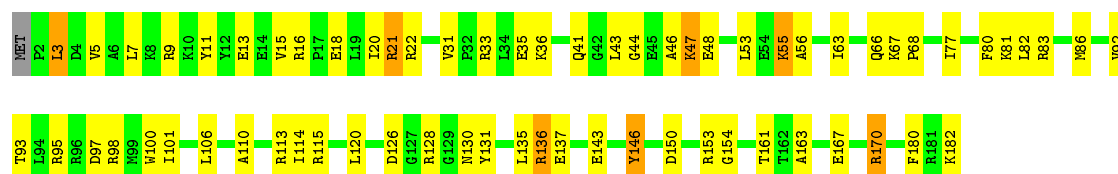
- Molecule 6: 50S ribosomal protein L5

Chain RG: 74% 23% ..



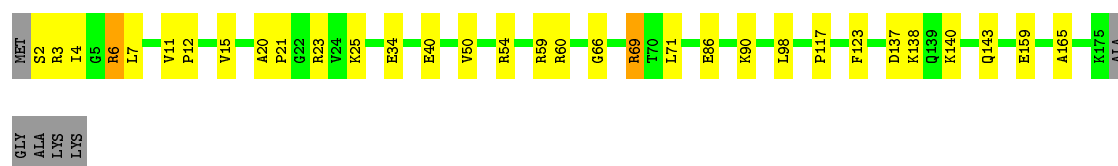
- Molecule 6: 50S ribosomal protein L5

Chain YG: 63% 32% ..



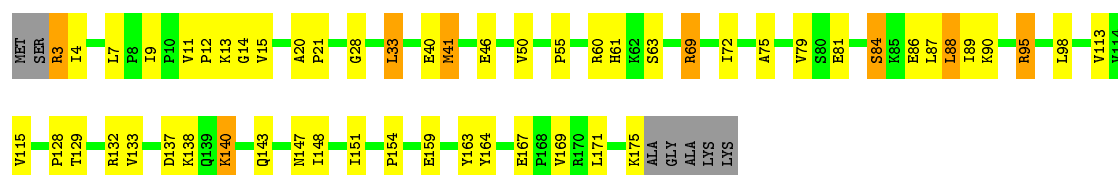
- Molecule 7: 50S ribosomal protein L6

Chain RH: 79% 17% ..



- Molecule 7: 50S ribosomal protein L6

Chain YH: 66% 26% ..




- Molecule 8: 50S ribosomal protein L9

Chain RI: 78% 20% ..




- Molecule 8: 50S ribosomal protein L9

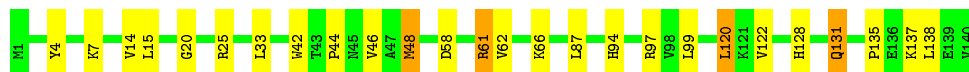
Chain YI:  78% 17%




GLU  
GLU

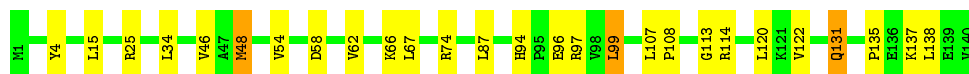
- Molecule 9: 50S ribosomal protein L13

Chain RN:  81% 16%



- Molecule 9: 50S ribosomal protein L13

Chain YN:  81% 17%




- Molecule 10: 50S ribosomal protein L14

Chain RO:  89% 11%




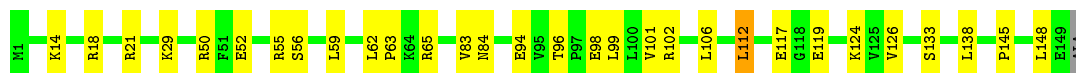
- Molecule 10: 50S ribosomal protein L14

Chain YO:  86% 14%




- Molecule 11: 50S ribosomal protein L15

Chain RP:  79% 19%

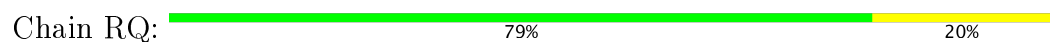


- Molecule 11: 50S ribosomal protein L15

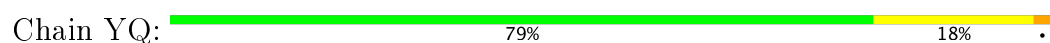
Chain YP:  77% 21%



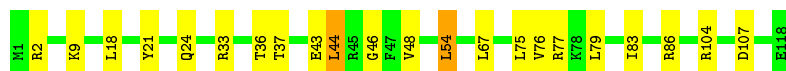
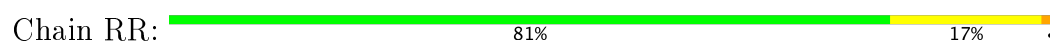
- Molecule 12: 50S ribosomal protein L16



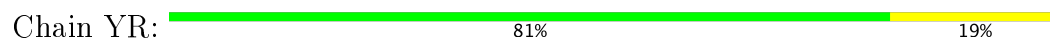
- Molecule 12: 50S ribosomal protein L16



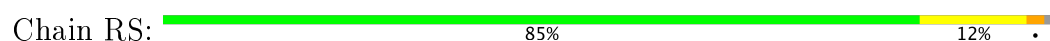
- Molecule 13: 50S ribosomal protein L17



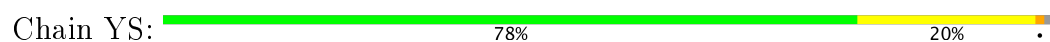
- Molecule 13: 50S ribosomal protein L17



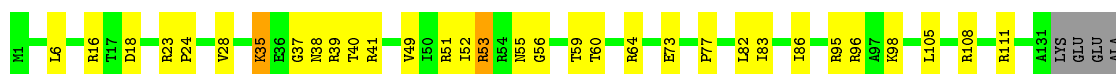
- Molecule 14: 50S ribosomal protein L18



- Molecule 14: 50S ribosomal protein L18




- Molecule 15: 50S ribosomal protein L19




GLN  
LYS  
ALA  
GLN  
GLU  
PRO  
LYS  
ALA  
SER  
GLN  
GLU

- Molecule 15: 50S ribosomal protein L19

Chain YT:  75% 14% 10%




- Molecule 16: 50S ribosomal protein L20

Chain RU:  83% 14% ..



- Molecule 16: 50S ribosomal protein L20

Chain YU:  84% 14% ..





- Molecule 17: 50S ribosomal protein L21

Chain RV:  89% 10% .




- Molecule 17: 50S ribosomal protein L21

Chain YV:  75% 22% .



- Molecule 18: 50S ribosomal protein L22

Chain RW:  82% 13% ..




- Molecule 18: 50S ribosomal protein L22

Chain YW:  89% 8% ..






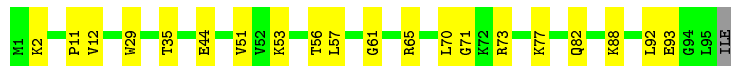
- Molecule 19: 50S ribosomal protein L23

Chain RX:  79% 20%




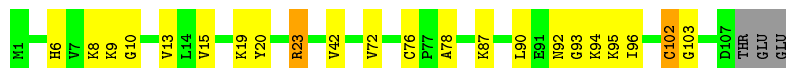
- Molecule 19: 50S ribosomal protein L23

Chain YX:  78% 21%



- Molecule 20: 50S ribosomal protein L24

Chain RY:  77% 18%




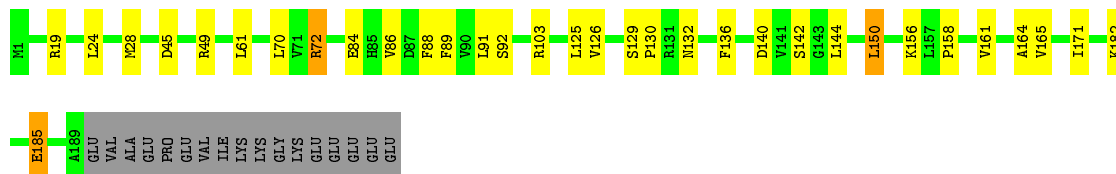
- Molecule 20: 50S ribosomal protein L24

Chain YY:  72% 24%



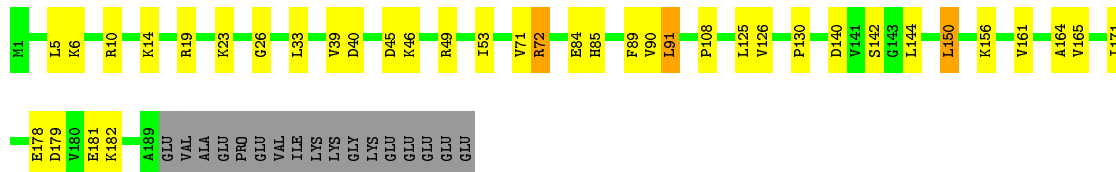
- Molecule 21: 50S ribosomal protein L25

Chain RZ:  76% 15% 8%




- Molecule 21: 50S ribosomal protein L25

Chain YZ:  73% 17% 8%



- Molecule 22: 50S ribosomal protein L27

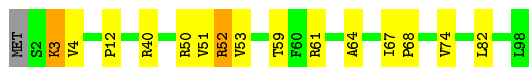
Chain R0:  76% 12% 9%



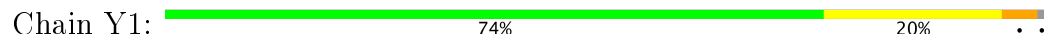
- Molecule 22: 50S ribosomal protein L27



- Molecule 23: 50S ribosomal protein L28



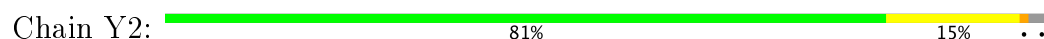
- Molecule 23: 50S ribosomal protein L28



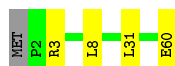
- Molecule 24: 50S ribosomal protein L29



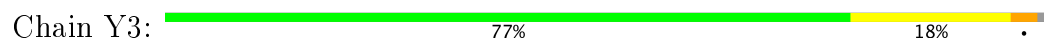
- Molecule 24: 50S ribosomal protein L29



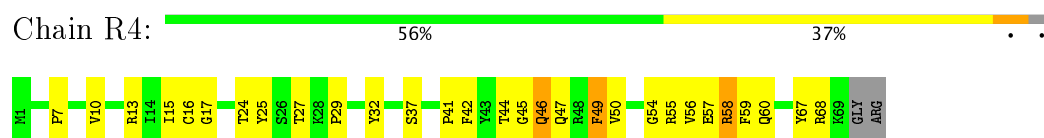
- Molecule 25: 50S ribosomal protein L30



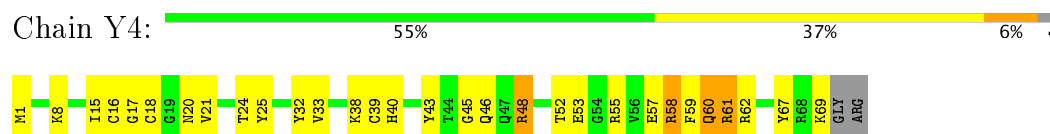
- Molecule 25: 50S ribosomal protein L30



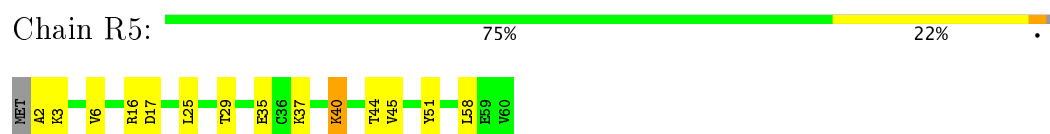
- Molecule 26: 50S ribosomal protein L31



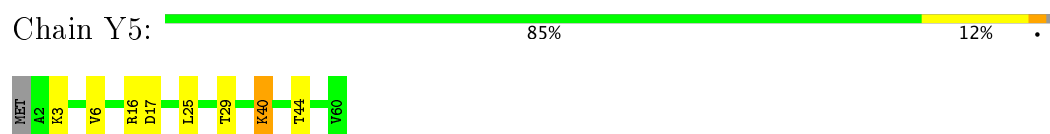
- Molecule 26: 50S ribosomal protein L31



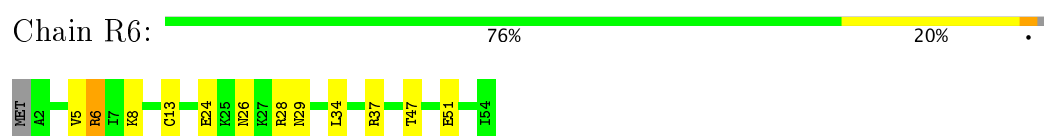
- Molecule 27: 50S ribosomal protein L32



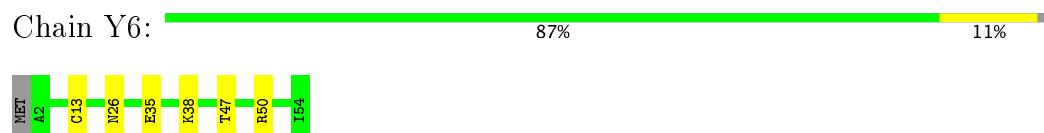
- Molecule 27: 50S ribosomal protein L32



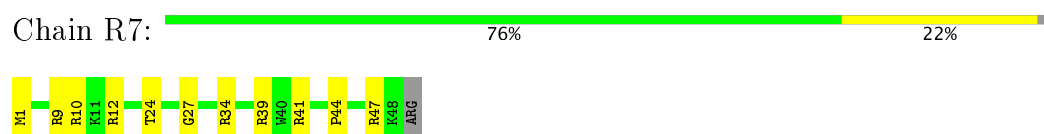
- Molecule 28: 50S ribosomal protein L33



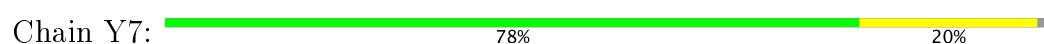
- Molecule 28: 50S ribosomal protein L33



- Molecule 29: 50S ribosomal protein L34



- Molecule 29: 50S ribosomal protein L34





- Molecule 30: 50S ribosomal protein L35

Chain R8: 69% 28% ..



- Molecule 30: 50S ribosomal protein L35

Chain Y8: 78% 18% ..



- Molecule 31: 50S ribosomal protein L36

Chain R9: 81% 19%



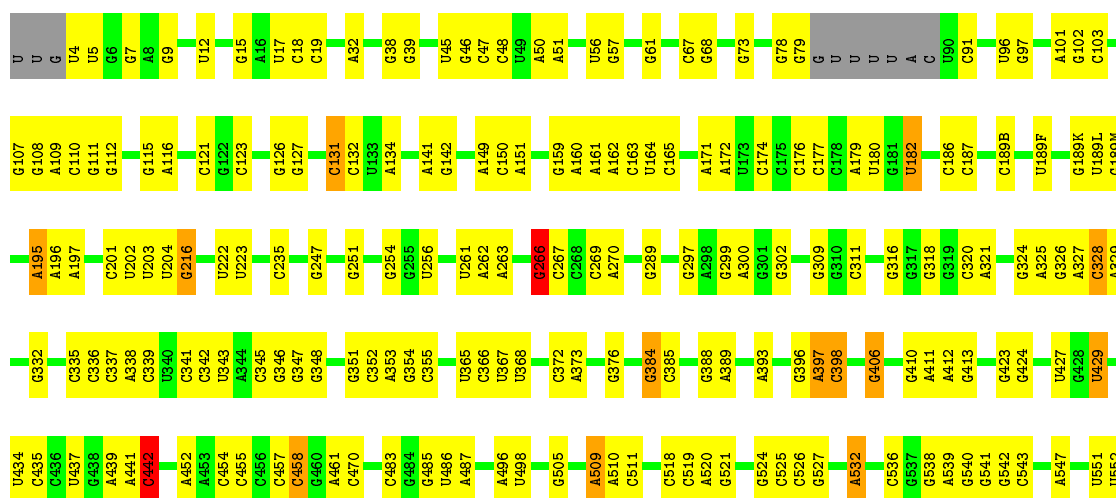
- Molecule 31: 50S ribosomal protein L36

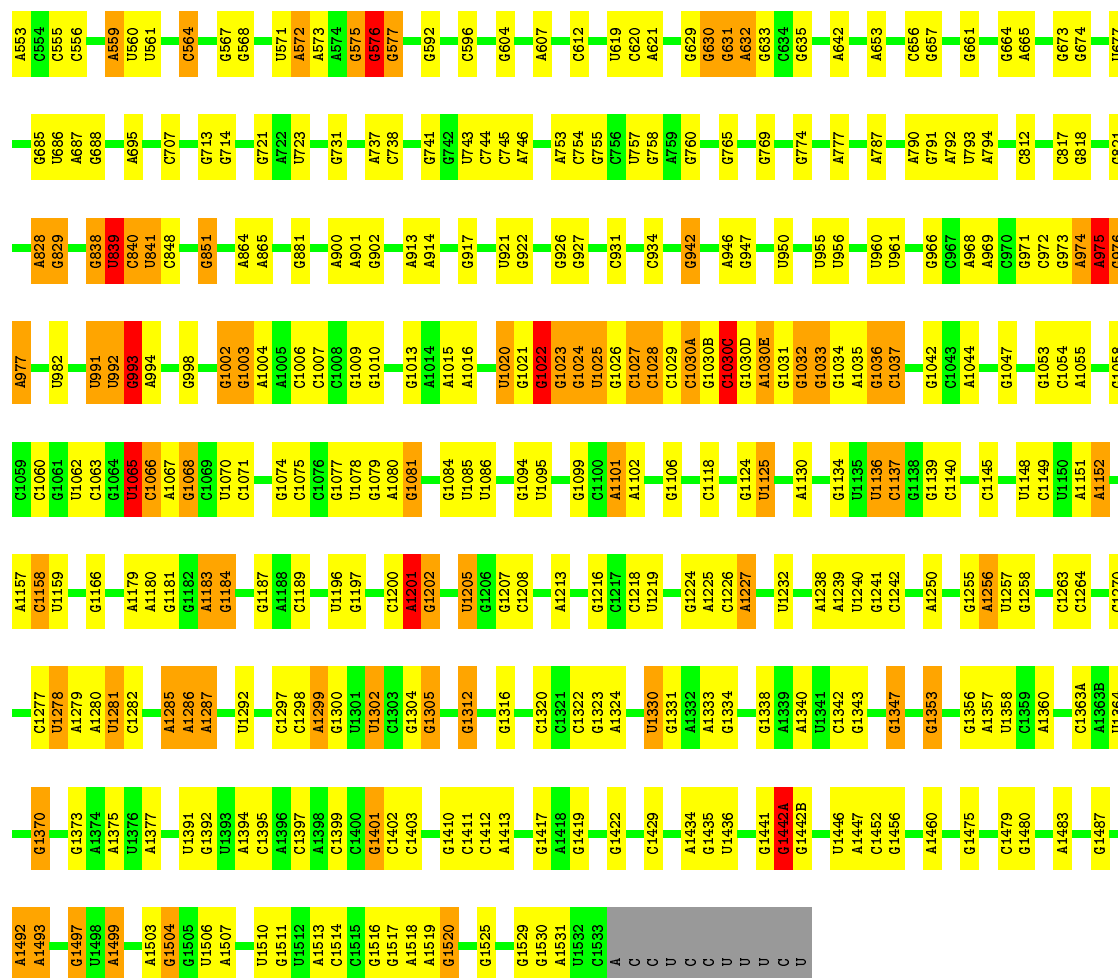
Chain Y9: 70% 30%



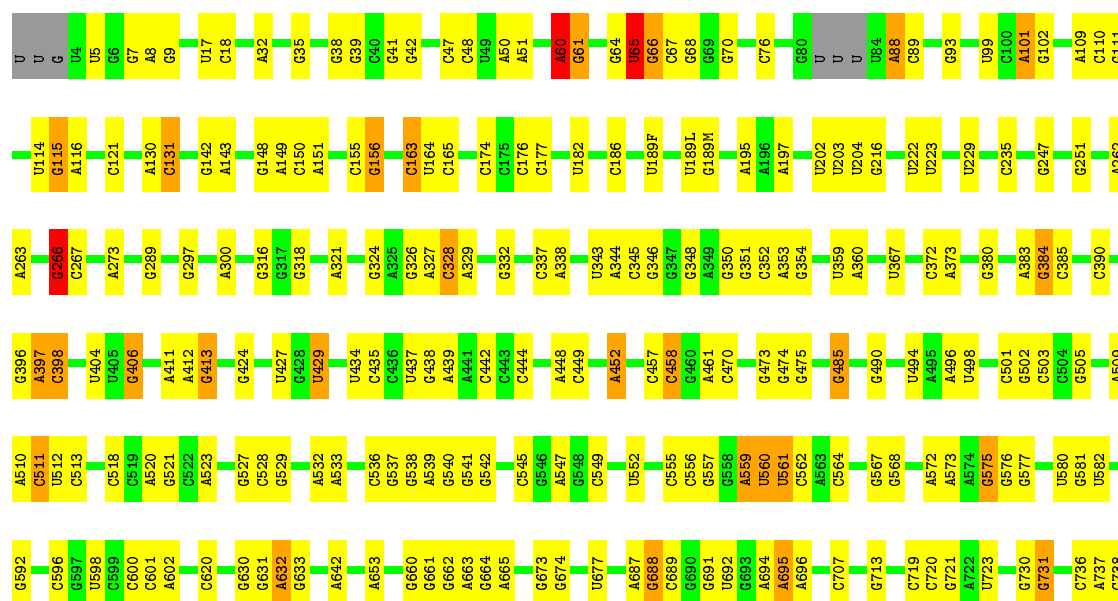
- Molecule 32: 16S rRNA

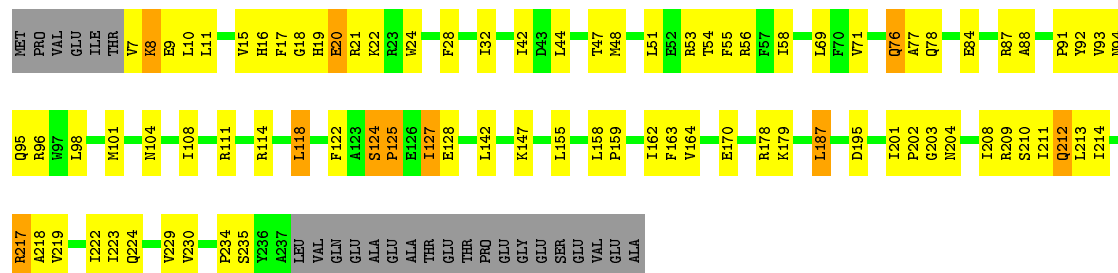
Chain QA: 63% 29% 5% ..





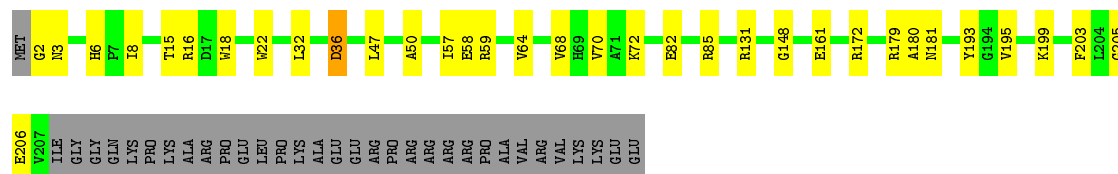
Chain XA: 63% 30% 6% ..





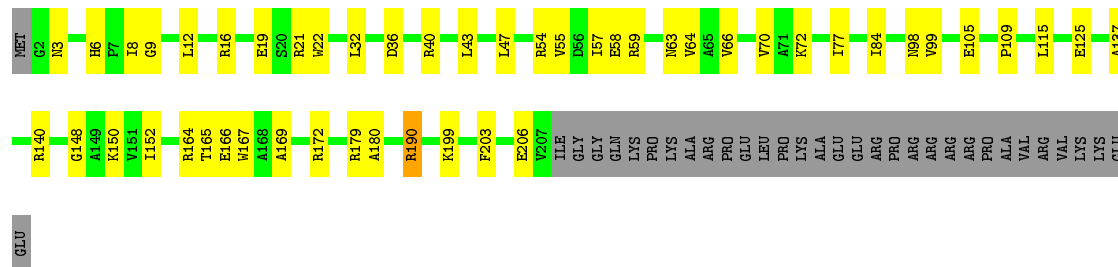
- Molecule 34: 30S ribosomal protein S3

Chain QC:  72% 14% 14%




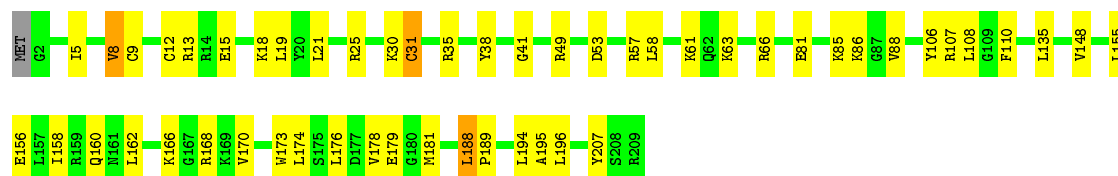
- Molecule 34: 30S ribosomal protein S3

Chain XC:  66% 20% 14%




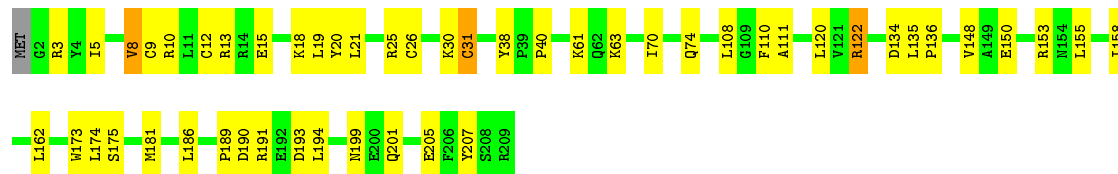
- Molecule 35: 30S ribosomal protein S4

Chain QD:  75% 23% .



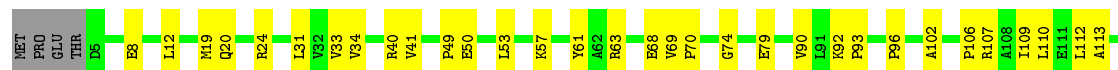
- Molecule 35: 30S ribosomal protein S4

Chain XD:  76% 22% .



- Molecule 36: 30S ribosomal protein S5

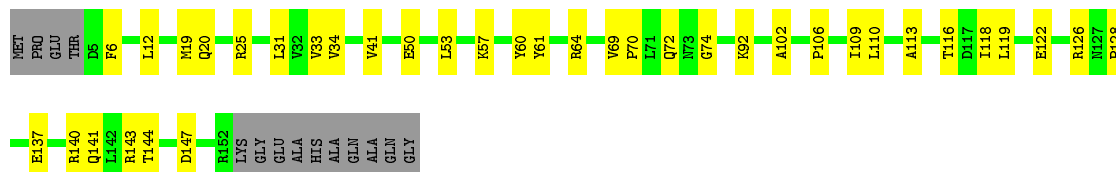
Chain QE:  65% 26% 9%





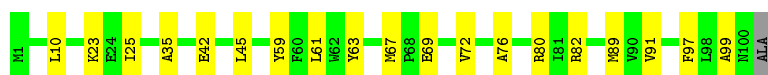
- Molecule 36: 30S ribosomal protein S5

Chain XE: 69% 23% 9%



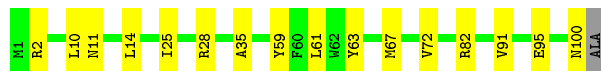
- Molecule 37: 30S ribosomal protein S6

Chain QF: 80% 19%



- Molecule 37: 30S ribosomal protein S6

Chain XF: 83% 16%



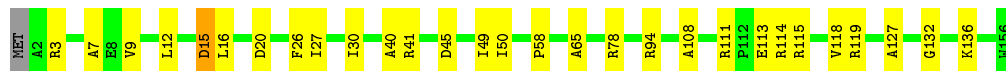
- Molecule 38: 30S ribosomal protein S7

Chain QG: 80% 19%



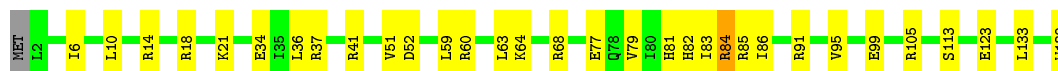
- Molecule 38: 30S ribosomal protein S7

Chain XG: 81% 18%




- Molecule 39: 30S ribosomal protein S8

Chain QH: 76% 22%



- Molecule 39: 30S ribosomal protein S8

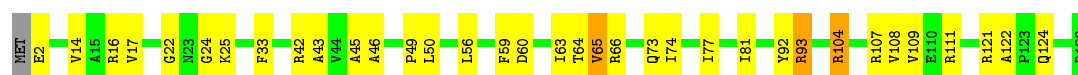


Chain XH:  82% 16% ..



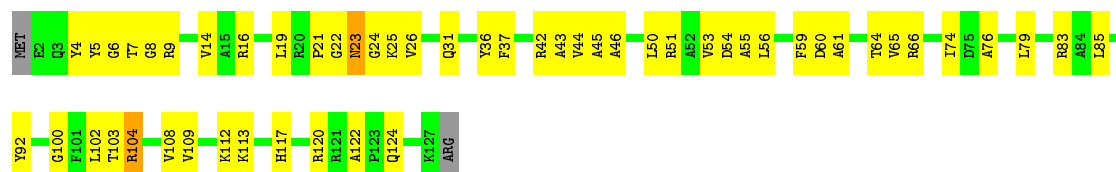
- Molecule 40: 30S ribosomal protein S9

Chain QI:  72% 25% ..



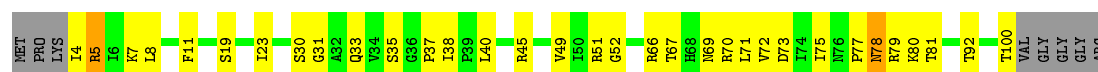
- Molecule 40: 30S ribosomal protein S9

Chain XI:  57% 40% ..



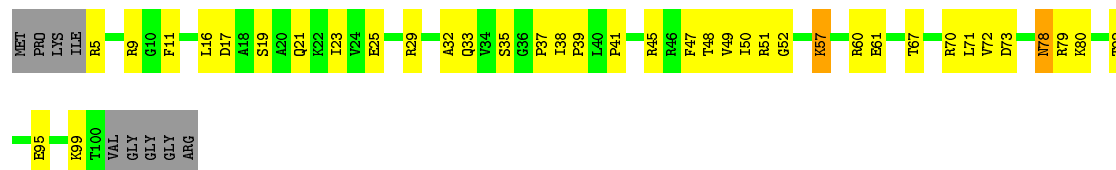
- Molecule 41: 30S ribosomal protein S10

Chain QJ:  61% 30% 8%



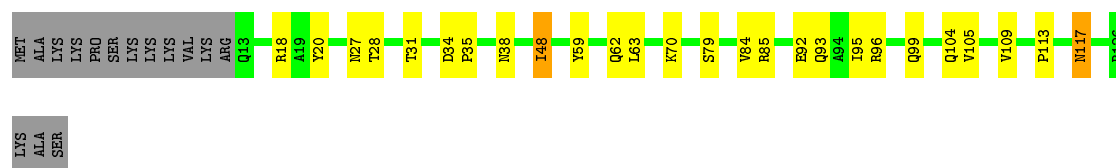
- Molecule 41: 30S ribosomal protein S10

Chain XJ:  55% 34% 9%




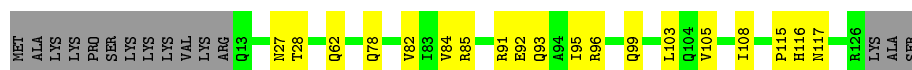
- Molecule 42: 30S ribosomal protein S11

Chain QK:  68% 19% 12%



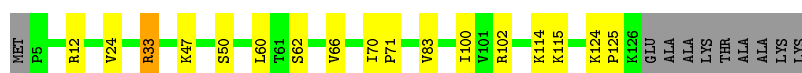
- Molecule 42: 30S ribosomal protein S11

Chain XK: 



- Molecule 43: 30S ribosomal protein S12

Chain QL: 



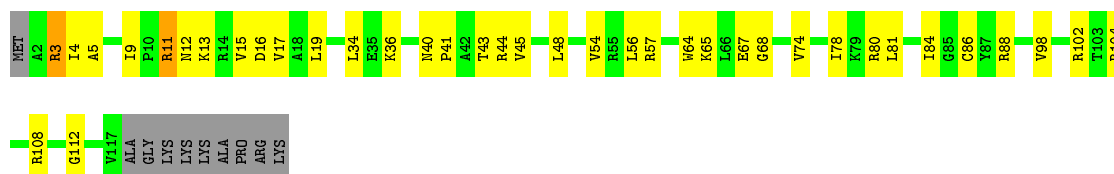
- Molecule 43: 30S ribosomal protein S12

Chain XL: 



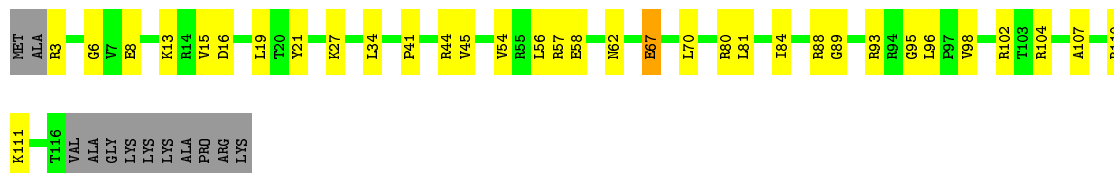
- Molecule 44: 30S ribosomal protein S13

Chain QM: 



- Molecule 44: 30S ribosomal protein S13

Chain XM: 



- Molecule 45: 30S ribosomal protein S14 type Z

Chain QN: 

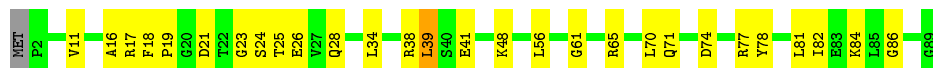


- Molecule 45: 30S ribosomal protein S14 type Z

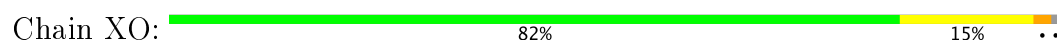
Chain XN: 



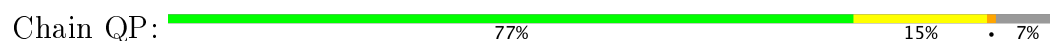
- Molecule 46: 30S ribosomal protein S15



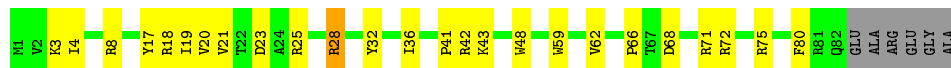
- Molecule 46: 30S ribosomal protein S15



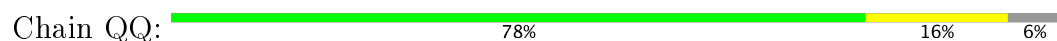
- Molecule 47: 30S ribosomal protein S16



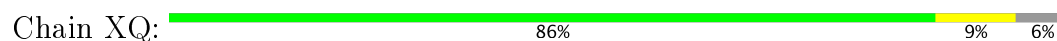
- Molecule 47: 30S ribosomal protein S16



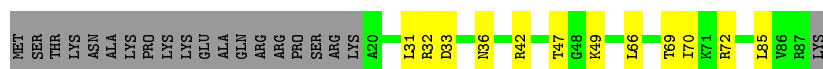
- Molecule 48: 30S ribosomal protein S17



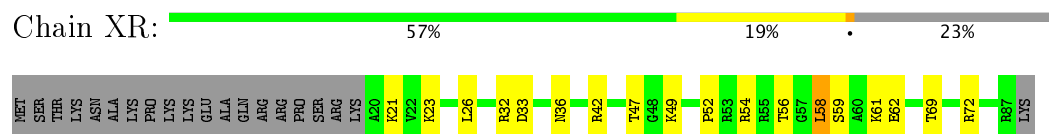
- Molecule 48: 30S ribosomal protein S17



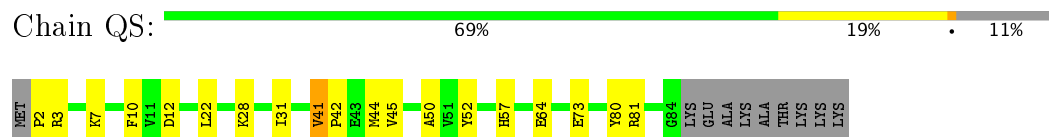
- Molecule 49: 30S ribosomal protein S18



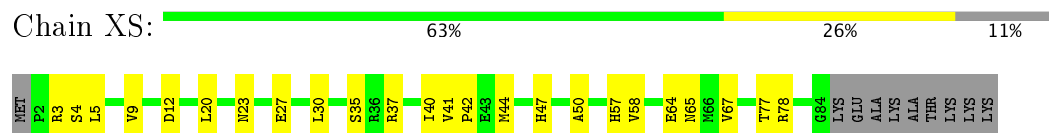
- Molecule 49: 30S ribosomal protein S18



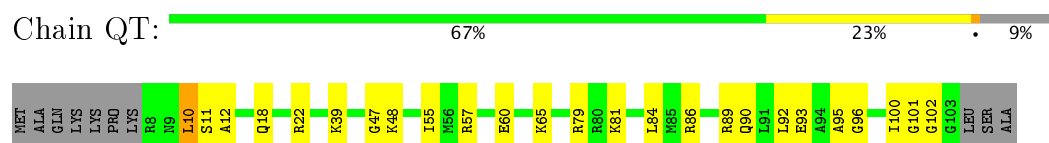
- Molecule 50: 30S ribosomal protein S19



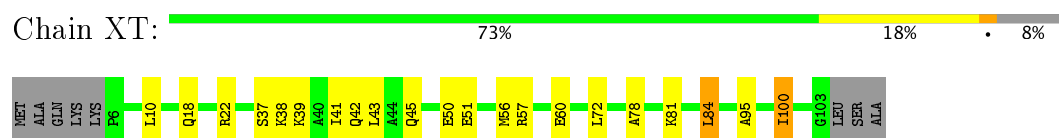
- Molecule 50: 30S ribosomal protein S19



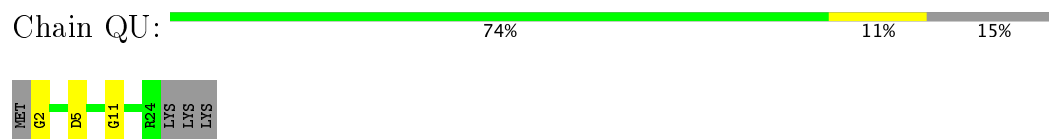
- Molecule 51: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S20



- Molecule 52: 30S ribosomal protein Thx



- Molecule 52: 30S ribosomal protein Thx



- Molecule 53: P-site tRNA fMet

C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15	C16	C17	C18	C19	C20	C21	C22	C23	C24	C25	C26	C27	C28	C29	C30	C31	C32	C33	C34	C35	C36	C37	C38	C39	C40	C41	C42	C43	C44	C45	C46	C47	C48	C49	C50	C51	C52	C53	C54	C55	C56	C57	C58	C59	C60	C61	C62	C63	C64	C65	C66	C67	C68	C69	C70	C71	C72	C73	C74	C75	C76	C77	C78	C79	C80	C81	C82	C83	C84	C85	C86	C87	C88	C89	C90	C91	C92	C93	C94	C95	C96	C97	C98	C99	C100
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|----|----|----|----|----|----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| C1 | C2 | C3 | C4 | C5 | G9 | G10 | C16 | C17 | U17A | C18 | C19 | U20 | A21 | U24 | C25 | C26 | G31 | C32 | A43 | A44 | G45 | G46 | U47 | C48 | G49 | U50 | G51 | G52 | G53 | U54 | C61 | G64 | C75 | A76 | C77 |
|----|----|----|----|----|----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- G G C A A G G A G G U A A A14 A20 A21 C22 A23 G A

- |   |   |   |   |   |   |   |   |   |   |   |   |   |   |     |     |     |     |     |     |     |     |     |   |   |   |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|---|---|
| G | G | C | A | A | G | G | A | G | G | G | U | A | A | A14 | A15 | A16 | U17 | G18 | U19 | A20 | A21 | C22 | A | G | A |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|---|---|

- |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | LYS | PRO | SER | ILE | VAL | ALA | LYS | LEU | GLU | LEU | ALA | LEU | HIS | GLU | ARG | GLY | HIS | GLU | GLU | VAL | GLN | ALA | ALA | LEU | GLY | ASP | ASP | GLN | THR | THR | ILE | ALA | ASP | GLN | GLU | ARG | PHE | ARG | ALA | LEU | SER | SER | CYS | PHE | THR | ASP | TRP | GLN | VAL | GLN | GLN |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

[illegible]

I162	I163	Y172	F177		H182	H183	H184	I185	R186	H187	P188		Q193	G194	R195		T198		A204		I209		L214	P215	D216	I217	I218	P219	A220	A221	D221	L222		G233	G234	Q235	H236	V237	I238	I239	T240	D241	S242		R245	L246	T247	H248	L249	P250		V254	V255	E256	C257		S262
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Q263	H264	K265	N266	K267	L274	R294	L298	G299	R303	R306	T309	Y310	N311	F312	P313	Q314	G315	R316	V317	T318	R321	I322	N323	T325	T326	Y327	R328	L329	V332	R333	G334	G335	R336	L337	D338	M339	L340	I341	T345	G351	L351	ALA	ALA	ALA	LEU	LEU	SER	GLU	GLN
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GLU

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | LYS | PRO | SER | ILE | VAL | ALA | ALA | LYS | LEU | GLU | ALA | ALA | LEU | HIS | ARG | HIS | GLU | GLU | VAL | GLN | ALA | LEU | LEU | LEU | GLY | ASP | ASP | GLN | GLU | GLU | GLN | THR | THR | ILE | ALA | ALA | ASP | GLN | GLN | GLU | ARG | ARG | PHE | ARG | ALA | ALA | LEU | LEU | SER | SER | ASP | VAL | ARG | CYS | PHE | THR | THR | ASP | TRP | GLN | GLN | GLN | VAL | GLN | GLU |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|



## 4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	210.03Å 449.71Å 620.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.81 – 3.20	Depositor
% Data completeness (in resolution range)	99.9 (49.81-3.20)	Depositor
$R_{merge}$	0.28	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.39 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, $R_{free}$	0.214 , 0.244	Depositor
Wilson B-factor (Å <sup>2</sup> )	93.8	Xtriage
Anisotropy	0.251	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	294739	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	117.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.59% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, MEQ, 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	0.26	0/68901	0.85	52/107544 (0.0%)
1	YA	0.30	4/68901 (0.0%)	0.87	72/107544 (0.1%)
2	RB	0.25	0/2876	0.83	0/4486
2	YB	0.27	0/2878	0.84	0/4490
3	RD	0.30	0/2181	0.54	0/2940
3	YD	0.30	0/2186	0.56	0/2944
4	RE	0.29	0/1592	0.53	0/2149
4	YE	0.31	0/1592	0.57	1/2149 (0.0%)
5	RF	0.28	0/1619	0.52	0/2193
5	YF	0.30	0/1615	0.53	0/2188
6	RG	0.28	0/1451	0.53	0/1961
6	YG	0.29	0/1449	0.52	0/1957
7	RH	0.28	0/1356	0.50	0/1834
7	YH	0.29	0/1350	0.56	2/1826 (0.1%)
8	RI	0.27	0/1109	0.54	0/1512
8	YI	0.27	0/1091	0.55	1/1490 (0.1%)
9	RN	0.28	0/1148	0.51	0/1547
9	YN	0.28	0/1144	0.50	0/1543
10	RO	0.29	0/943	0.55	0/1269
10	YO	0.29	0/943	0.55	0/1269
11	RP	0.28	0/1152	0.56	0/1533
11	YP	0.28	0/1152	0.56	0/1533
12	RQ	0.30	0/1143	0.52	0/1527
12	YQ	0.29	0/1143	0.51	0/1527
13	RR	0.27	0/982	0.54	0/1312
13	YR	0.27	0/982	0.53	0/1312
14	RS	0.27	0/887	0.52	0/1180
14	YS	0.29	0/880	0.52	0/1172
15	RT	0.29	0/1105	0.58	0/1477
15	YT	0.28	0/1097	0.55	0/1468
16	RU	0.29	0/977	0.45	0/1301



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
16	YU	0.30	0/977	0.46	0/1301
17	RV	0.28	0/786	0.52	0/1053
17	YV	0.32	0/782	0.57	0/1049
18	RW	0.27	0/897	0.48	0/1205
18	YW	0.28	0/897	0.50	0/1205
19	RX	0.30	0/764	0.53	0/1025
19	YX	0.30	0/764	0.53	0/1025
20	RY	0.29	0/823	0.55	0/1099
20	YY	0.33	0/823	0.55	0/1100
21	RZ	0.31	0/1517	0.53	0/2062
21	YZ	0.28	0/1501	0.52	0/2043
22	R0	0.28	0/616	0.53	0/821
22	Y0	0.27	0/616	0.55	0/821
23	R1	0.27	0/761	0.53	0/1013
23	Y1	0.28	0/766	0.56	0/1018
24	R2	0.29	0/590	0.51	0/781
24	Y2	0.26	0/594	0.46	0/785
25	R3	0.28	0/474	0.51	0/635
25	Y3	0.29	0/469	0.54	0/630
26	R4	0.32	0/559	0.66	0/754
26	Y4	0.37	0/549	0.63	0/741
27	R5	0.33	0/473	0.54	0/639
27	Y5	0.32	0/469	0.54	0/635
28	R6	0.28	0/460	0.53	0/613
28	Y6	0.23	0/456	0.46	0/608
29	R7	0.26	0/426	0.49	0/561
29	Y7	0.26	0/426	0.45	0/561
30	R8	0.29	0/525	0.52	0/691
30	Y8	0.28	0/525	0.51	0/691
31	R9	0.23	0/310	0.47	0/407
31	Y9	0.26	0/310	0.51	0/407
32	QA	0.26	0/35795	0.86	38/55864 (0.1%)
32	XA	0.26	0/35890	0.85	30/56012 (0.1%)
33	QB	0.28	0/1876	0.54	0/2533
33	XB	0.30	0/1860	0.57	0/2518
34	QC	0.27	0/1582	0.52	0/2137
34	XC	0.28	0/1566	0.52	0/2119
35	QD	0.28	0/1695	0.50	0/2274
35	XD	0.27	0/1698	0.47	0/2277
36	QE	0.30	0/1149	0.52	0/1548
36	XE	0.28	0/1149	0.51	0/1548
37	QF	0.26	0/827	0.51	0/1120
37	XF	0.26	0/829	0.52	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
38	QG	0.27	0/1254	0.43	0/1683
38	XG	0.27	0/1248	0.45	0/1676
39	QH	0.27	0/1118	0.50	0/1506
39	XH	0.28	0/1108	0.51	0/1494
40	QI	0.28	0/1005	0.53	0/1351
40	XI	0.28	0/985	0.52	0/1329
41	QJ	0.26	0/732	0.51	0/993
41	XJ	0.26	0/723	0.51	0/984
42	QK	0.26	0/849	0.48	0/1150
42	XK	0.26	0/848	0.53	0/1149
43	QL	0.28	0/937	0.54	0/1260
43	XL	0.29	0/937	0.59	0/1260
44	QM	0.26	0/924	0.52	0/1242
44	XM	0.26	0/905	0.50	0/1217
45	QN	0.28	0/501	0.44	0/664
45	XN	0.29	0/501	0.46	0/664
46	QO	0.26	0/739	0.48	0/985
46	XO	0.26	0/739	0.49	0/985
47	QP	0.28	0/697	0.51	0/939
47	XP	0.28	0/693	0.50	0/935
48	QQ	0.26	0/836	0.50	0/1117
48	XQ	0.26	0/836	0.50	0/1117
49	QR	0.26	0/560	0.51	0/746
49	XR	0.26	0/560	0.51	0/746
50	QS	0.27	0/663	0.57	0/895
50	XS	0.27	0/660	0.55	0/893
51	QT	0.27	0/734	0.48	0/969
51	XT	0.27	0/736	0.42	0/976
52	QU	0.25	0/203	0.52	0/266
52	XU	0.30	0/203	0.52	0/266
53	QV	0.33	1/1836 (0.1%)	0.82	0/2859
53	XV	0.34	1/1836 (0.1%)	0.82	0/2859
54	QX	0.33	0/241	0.95	0/373
54	XX	0.27	0/216	0.89	0/334
55	QY	0.31	0/2035	0.51	0/2742
55	XY	0.29	0/2044	0.51	0/2754
All	All	0.28	6/316288 (0.0%)	0.78	196/472607 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
14	RS	0	1
26	R4	0	1
33	QB	0	1
43	XL	0	1
All	All	0	4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	XV	1	C	OP3-P	-10.46	1.48	1.61
53	QV	1	C	OP3-P	-10.44	1.48	1.61
1	YA	2751	G	N1-C2	-8.70	1.30	1.37
1	YA	2751	G	C2-N3	-6.96	1.27	1.32
1	YA	1029	A	N3-C4	-5.78	1.31	1.34
1	YA	1050	A	C2-N3	-5.73	1.28	1.33

All (196) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	1029	A	N1-C2-N3	12.53	135.56	129.30
32	QA	576	G	OP1-P-O3'	-11.19	80.59	105.20
1	RA	2602	A	OP2-P-O3'	-11.18	80.60	105.20
32	QA	576	G	OP2-P-O3'	-10.40	82.31	105.20
1	RA	1050	A	N1-C2-N3	10.32	134.46	129.30
1	YA	277	C	C5-C4-N4	-10.13	113.11	120.20
1	YA	2187	G	C5-C6-O6	-9.72	122.77	128.60
1	RA	2187	G	C5-C6-O6	-9.53	122.88	128.60
1	RA	1050	A	C2-N3-C4	-9.28	105.96	110.60
32	XA	1158	C	C2-N1-C1'	8.99	128.69	118.80
1	YA	277	C	C6-N1-C1'	-8.50	110.60	120.80
1	YA	1050	A	C5-N7-C8	-8.46	99.67	103.90
1	RA	1050	A	C5-C6-N1	-8.28	113.56	117.70
1	YA	1050	A	N7-C8-N9	8.24	117.92	113.80
1	YA	2751	G	C2-N3-C4	8.14	115.97	111.90
1	RA	1050	A	C4-C5-C6	8.10	121.05	117.00
1	YA	1029	A	C6-N1-C2	-8.05	113.77	118.60
1	YA	2465	C	N1-C2-O2	7.72	123.53	118.90
1	RA	1092	C	N1-C2-O2	7.72	123.53	118.90
32	XA	1158	C	N1-C2-O2	7.70	123.52	118.90
1	YA	2187	G	N1-C6-O6	7.68	124.51	119.90
32	QA	1036	G	C5-C6-O6	-7.61	124.03	128.60
1	RA	2187	G	N1-C6-O6	7.60	124.46	119.90
1	YA	1092	C	N1-C2-O2	7.53	123.42	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	2187	G	C6-C5-N7	-7.43	125.94	130.40
32	QA	1030(C)	C	C2-N1-C1'	7.36	126.90	118.80
1	RA	1097	U	C2-N1-C1'	7.34	126.51	117.70
32	QA	1030(C)	C	N1-C2-O2	7.28	123.27	118.90
1	YA	2187	G	C4-C5-N7	7.26	113.70	110.80
32	QA	577	G	OP1-P-OP2	7.24	130.47	119.60
1	YA	2742	C	O5'-P-OP1	-7.13	99.28	105.70
1	YA	277	C	C2-N1-C1'	7.07	126.57	118.80
32	XA	1158	C	C6-N1-C2	-7.03	117.49	120.30
1	RA	2603	G	OP1-P-OP2	7.00	130.10	119.60
32	QA	1022	G	C5-C6-O6	-6.99	124.41	128.60
1	RA	1092	C	C2-N1-C1'	6.99	126.48	118.80
1	RA	2602	A	OP1-P-O3'	-6.94	89.93	105.20
1	RA	2102	U	N1-C2-O2	-6.86	118.00	122.80
1	YA	1092	C	C2-N1-C1'	6.85	126.33	118.80
32	XA	1003	G	C4-N9-C1'	6.85	135.40	126.50
1	YA	1028	A	N9-C4-C5	-6.83	103.07	105.80
32	XA	266	G	P-O3'-C3'	6.82	127.89	119.70
1	YA	277	C	N3-C4-N4	6.78	122.74	118.00
32	XA	754	C	N1-C2-O2	6.75	122.95	118.90
1	YA	2102	U	N1-C2-O2	-6.74	118.08	122.80
1	YA	1097	U	C2-N1-C1'	6.72	125.77	117.70
1	YA	2187	G	N3-C4-N9	6.71	130.03	126.00
1	YA	512	G	O4'-C1'-N9	6.62	113.50	108.20
1	YA	1029	A	C2-N3-C4	-6.61	107.30	110.60
32	QA	1036	G	C4-C5-N7	6.59	113.44	110.80
1	YA	1030	G	N1-C6-O6	6.58	123.85	119.90
32	XA	1183	A	P-O3'-C3'	6.57	127.58	119.70
1	YA	2573	C	N3-C4-C5	6.57	124.53	121.90
1	RA	2104	G	N3-C4-N9	6.55	129.93	126.00
32	XA	1054	C	N1-C2-O2	6.54	122.83	118.90
32	QA	1322	C	N1-C2-O2	-6.53	114.98	118.90
1	YA	1030	G	C4-C5-N7	6.51	113.41	110.80
1	YA	1125	G	N3-C4-C5	-6.45	125.37	128.60
32	XA	1158	C	N3-C2-O2	-6.44	117.39	121.90
8	YI	75	LEU	CA-CB-CG	6.41	130.04	115.30
1	YA	1097	U	N3-C2-O2	-6.40	117.72	122.20
1	YA	1028	A	N3-C4-N9	6.35	132.48	127.40
32	QA	1030(C)	C	N3-C2-O2	-6.35	117.46	121.90
32	XA	754	C	C2-N1-C1'	6.35	125.78	118.80
1	YA	2104	G	N3-C4-N9	6.34	129.81	126.00
1	RA	2187	G	C4-C5-N7	6.34	113.33	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	1313	U	C2-N1-C1'	6.32	125.29	117.70
1	YA	1028	A	C5-C6-N1	6.29	120.84	117.70
1	YA	1097	U	N1-C2-O2	6.29	127.20	122.80
1	YA	1125	G	N3-C4-N9	6.27	129.76	126.00
1	YA	1092	C	C5-C6-N1	6.27	124.13	121.00
1	RA	2187	G	C6-C5-N7	-6.25	126.65	130.40
32	XA	1003	G	N7-C8-N9	6.23	116.21	113.10
1	YA	2187	G	N9-C4-C5	-6.19	102.93	105.40
1	RA	2573	C	N3-C4-C5	6.18	124.37	121.90
1	RA	1097	U	N3-C2-O2	-6.18	117.88	122.20
1	RA	1092	C	C5-C6-N1	6.17	124.08	121.00
32	QA	1036	G	N3-C4-N9	6.16	129.70	126.00
32	XA	1003	G	N3-C4-C5	-6.16	125.52	128.60
1	RA	1097	U	N1-C2-O2	6.15	127.11	122.80
1	YA	1030	G	C6-C5-N7	-6.14	126.72	130.40
1	RA	1082	U	C2-N1-C1'	6.09	125.00	117.70
1	RA	512	G	O4'-C1'-N9	6.07	113.05	108.20
32	XA	88	A	C5-C6-N6	-6.03	118.88	123.70
32	XA	1003	G	C8-N9-C4	-6.01	104.00	106.40
1	RA	1092	C	C6-N1-C2	-5.97	117.91	120.30
32	QA	1322	C	N1-C2-N3	5.96	123.37	119.20
32	XA	1158	C	C6-N1-C1'	-5.95	113.66	120.80
1	RA	1092	C	N3-C2-O2	-5.95	117.74	121.90
1	YA	226	G	O4'-C1'-N9	5.93	112.94	108.20
1	YA	1082	U	C2-N1-C1'	5.90	124.78	117.70
32	QA	754	C	N1-C2-O2	5.88	122.43	118.90
32	QA	1030(C)	C	C6-N1-C2	-5.87	117.95	120.30
1	YA	847	U	N1-C2-O2	5.87	126.91	122.80
32	XA	65	U	P-O3'-C3'	5.85	126.72	119.70
32	XA	88	A	N1-C6-N6	5.83	122.10	118.60
1	YA	1092	C	C6-N1-C2	-5.81	117.98	120.30
32	XA	1004	A	O4'-C1'-N9	5.77	112.81	108.20
32	QA	1285	A	P-O3'-C3'	5.76	126.61	119.70
1	YA	1092	C	N3-C2-O2	-5.75	117.87	121.90
1	YA	1372	U	N1-C2-O2	5.74	126.81	122.80
1	YA	1030	G	N9-C4-C5	-5.72	103.11	105.40
32	XA	88	A	N9-C4-C5	-5.72	103.51	105.80
4	YE	52	LEU	CA-CB-CG	5.71	128.44	115.30
32	QA	1137	C	C6-N1-C2	-5.69	118.03	120.30
1	RA	847	U	C2-N1-C1'	5.67	124.50	117.70
1	YA	887	A	O4'-C1'-N9	5.67	112.73	108.20
32	XA	1158	C	C5-C6-N1	5.67	123.83	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	1530	C	P-O3'-C3'	5.65	126.48	119.70
1	YA	847	U	C2-N1-C1'	5.64	124.47	117.70
1	RA	1530	C	P-O3'-C3'	5.61	126.43	119.70
32	QA	1036	G	C6-C5-N7	-5.61	127.03	130.40
1	RA	1050	A	C5-C6-N6	5.58	128.16	123.70
7	YH	69	ARG	NE-CZ-NH1	-5.58	117.51	120.30
1	YA	1091	G	N3-C4-C5	-5.55	125.83	128.60
32	XA	1054	C	N3-C2-O2	-5.55	118.02	121.90
1	RA	1091	G	N3-C4-C5	-5.54	125.83	128.60
32	XA	1256	A	O4'-C1'-N9	-5.54	103.77	108.20
1	YA	1052	C	C2-N1-C1'	5.53	124.89	118.80
1	RA	1992	G	P-O3'-C3'	5.53	126.34	119.70
32	QA	1205	U	N3-C4-O4	-5.52	115.54	119.40
1	RA	2187	G	N3-C4-N9	5.52	129.31	126.00
1	RA	1313	U	C2-N1-C1'	5.51	124.31	117.70
1	RA	1076	C	OP1-P-O3'	5.50	117.29	105.20
1	RA	1210	A	P-O3'-C3'	5.49	126.29	119.70
32	QA	993	G	C4-N9-C1'	5.49	133.64	126.50
1	YA	277	C	N3-C4-C5	5.47	124.09	121.90
32	QA	1330	U	O5'-P-OP1	5.46	117.25	110.70
1	RA	2573	C	C5-C4-N4	-5.45	116.38	120.20
1	YA	2573	C	C4-C5-C6	-5.43	114.69	117.40
1	YA	1028	A	C5-C6-N6	-5.42	119.36	123.70
32	QA	993	G	N3-C4-C5	-5.41	125.90	128.60
32	QA	1201	A	P-O3'-C3'	5.41	126.19	119.70
32	QA	839	U	P-O3'-C3'	5.40	126.18	119.70
1	YA	1050	A	C4-C5-N7	5.40	113.40	110.70
32	QA	266	G	P-O3'-C3'	5.39	126.17	119.70
32	XA	60	A	P-O3'-C3'	5.38	126.16	119.70
1	RA	847	U	N1-C2-O2	5.37	126.56	122.80
1	RA	2187	G	N9-C4-C5	-5.37	103.25	105.40
1	RA	2218	U	N3-C2-O2	-5.36	118.45	122.20
1	YA	277	C	P-O3'-C3'	5.35	126.12	119.70
7	YH	88	LEU	CA-CB-CG	5.34	127.59	115.30
1	YA	1992	G	P-O3'-C3'	5.34	126.11	119.70
1	YA	1052	C	N1-C2-O2	5.34	122.10	118.90
1	RA	2573	C	C6-N1-C2	5.33	122.43	120.30
1	YA	614(A)	U	N3-C2-O2	-5.33	118.47	122.20
32	QA	991	U	P-O3'-C3'	5.33	126.10	119.70
32	XA	88	A	C4-C5-N7	5.32	113.36	110.70
1	RA	748	G	C8-N9-C1'	5.31	133.90	127.00
32	QA	1022	G	N3-C4-N9	5.31	129.19	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	XA	748	C	P-O3'-C3'	5.30	126.06	119.70
1	RA	2465	C	C2-N1-C1'	5.30	124.63	118.80
32	XA	1025	U	C5-C6-N1	-5.29	120.06	122.70
32	QA	975	A	O4'-C1'-N9	-5.25	104.00	108.20
32	QA	1022	G	N1-C6-O6	5.23	123.04	119.90
1	RA	2603	G	C4-N9-C1'	-5.22	119.71	126.50
32	QA	754	C	C2-N1-C1'	5.22	124.54	118.80
32	QA	1442(A)	G	P-O3'-C3'	5.22	125.96	119.70
1	YA	2603	G	N3-C4-C5	5.22	131.21	128.60
1	RA	1914	C	C2-N1-C1'	5.21	124.53	118.80
1	RA	1053	C	P-O3'-C3'	5.21	125.95	119.70
32	QA	365	U	C2-N1-C1'	5.21	123.95	117.70
1	YA	847	U	N3-C2-O2	-5.19	118.56	122.20
1	RA	1052	C	N1-C2-O2	5.19	122.01	118.90
1	YA	614(A)	U	N1-C2-O2	5.18	126.43	122.80
1	YA	2318	G	C4-N9-C1'	5.18	133.24	126.50
32	QA	442	C	C2-N1-C1'	5.18	124.50	118.80
32	QA	254	G	O5'-P-OP1	-5.18	101.04	105.70
1	RA	2603	G	C8-N9-C1'	5.17	133.72	127.00
1	RA	887	A	O4'-C1'-N9	5.17	112.33	108.20
1	YA	1126	A	C5-N7-C8	5.16	106.48	103.90
1	YA	2318	G	N3-C4-C5	-5.15	126.02	128.60
32	QA	266	G	O4'-C1'-N9	-5.15	104.08	108.20
1	YA	859	G	N3-C4-C5	5.15	131.17	128.60
32	QA	365	U	O4'-C1'-N1	5.14	112.31	108.20
1	YA	1028	A	C6-N1-C2	-5.14	115.52	118.60
1	YA	1053	C	P-O3'-C3'	5.12	125.84	119.70
32	QA	1137	C	C5-C6-N1	5.11	123.55	121.00
1	RA	748	G	C4-N9-C1'	-5.10	119.87	126.50
1	YA	2318	G	C8-N9-C4	-5.10	104.36	106.40
1	RA	1313	U	N1-C2-O2	5.10	126.37	122.80
1	RA	1372	U	N1-C2-O2	5.08	126.36	122.80
32	XA	1067	A	P-O3'-C3'	5.08	125.80	119.70
1	RA	1076	C	P-O3'-C3'	5.08	125.79	119.70
32	XA	1442(A)	G	P-O3'-C3'	5.06	125.78	119.70
1	YA	1029	A	N9-C4-C5	5.06	107.82	105.80
1	YA	2751	G	C5-N7-C8	-5.06	101.77	104.30
1	YA	301	G	N3-C4-C5	5.05	131.13	128.60
32	XA	1442(A)	G	C4-N9-C1'	5.05	133.06	126.50
1	YA	1125	G	C4-N9-C1'	5.04	133.05	126.50
32	QA	1065	U	P-O3'-C3'	5.04	125.75	119.70
1	YA	2465	C	N3-C2-O2	-5.04	118.37	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	RA	2104	G	N3-C4-C5	-5.03	126.08	128.60
32	QA	1030(A)	C	C5-C4-N4	-5.03	116.68	120.20
32	XA	1003	G	N3-C4-N9	5.02	129.01	126.00
1	RA	2186	G	C8-N9-C1'	5.00	133.50	127.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	QB	231	GLU	Peptide
26	R4	67	TYR	Peptide
14	RS	58	LEU	Peptide
43	XL	86	ARG	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	RA	61758	0	31145	564	0
1	YA	61758	0	31148	595	1
2	RB	2572	0	1305	8	0
2	YB	2573	0	1306	23	0
3	RD	2131	0	2207	42	0
3	YD	2136	0	2218	37	0
4	RE	1559	0	1618	27	0
4	YE	1559	0	1618	30	0
5	RF	1584	0	1625	31	0
5	YF	1580	0	1619	42	0
6	RG	1426	0	1445	34	0
6	YG	1424	0	1441	45	0
7	RH	1330	0	1407	24	0
7	YH	1324	0	1402	36	0
8	RI	1094	0	1127	23	0
8	YI	1076	0	1094	21	0
9	RN	1121	0	1195	14	0
9	YN	1117	0	1184	21	0
10	RO	933	0	996	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	YO	933	0	996	10	0
11	RP	1135	0	1212	25	0
11	YP	1135	0	1212	32	0
12	RQ	1122	0	1179	22	0
12	YQ	1122	0	1179	20	0
13	RR	968	0	1033	15	0
13	YR	968	0	1033	11	0
14	RS	877	0	938	9	0
14	YS	870	0	923	14	0
15	RT	1091	0	1151	21	0
15	YT	1083	0	1136	19	0
16	RU	959	0	1019	12	0
16	YU	959	0	1019	13	0
17	RV	775	0	841	7	0
17	YV	771	0	830	15	0
18	RW	886	0	940	13	0
18	YW	886	0	940	8	0
19	RX	750	0	814	17	0
19	YX	750	0	814	12	0
20	RY	810	0	892	14	0
20	YY	810	0	888	18	0
21	RZ	1485	0	1493	19	0
21	YZ	1469	0	1467	26	0
22	R0	608	0	622	10	0
22	Y0	608	0	622	14	0
23	R1	754	0	823	10	0
23	Y1	759	0	837	20	0
24	R2	588	0	643	5	1
24	Y2	592	0	654	7	0
25	R3	469	0	518	4	0
25	Y3	464	0	514	7	0
26	R4	546	0	522	26	0
26	Y4	536	0	514	28	0
27	R5	459	0	476	11	0
27	Y5	455	0	465	7	0
28	R6	453	0	473	14	0
28	Y6	449	0	469	4	0
29	R7	418	0	467	13	0
29	Y7	418	0	467	8	0
30	R8	517	0	582	21	0
30	Y8	517	0	582	17	0
31	R9	307	0	335	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	Y9	307	0	335	15	0
32	QA	32246	0	16294	310	0
32	XA	32331	0	16338	344	0
33	QB	1842	0	1862	55	0
33	XB	1825	0	1828	57	0
34	QC	1558	0	1557	30	0
34	XC	1542	0	1517	38	0
35	QD	1665	0	1688	42	0
35	XD	1668	0	1704	39	0
36	QE	1133	0	1191	31	0
36	XE	1133	0	1191	24	0
37	QF	814	0	808	14	0
37	XF	816	0	808	11	0
38	QG	1235	0	1249	20	0
38	XG	1229	0	1238	16	0
39	QH	1098	0	1143	26	0
39	XH	1088	0	1126	14	0
40	QI	986	0	990	28	0
40	XI	966	0	953	37	0
41	QJ	719	0	672	22	0
41	XJ	710	0	661	30	0
42	QK	834	0	838	15	0
42	XK	833	0	836	12	0
43	QL	932	0	980	14	0
43	XL	932	0	981	20	0
44	QM	914	0	954	30	0
44	XM	895	0	920	24	0
45	QN	492	0	529	19	0
45	XN	492	0	529	19	0
46	QO	728	0	760	17	0
46	XO	728	0	760	9	0
47	QP	681	0	697	11	0
47	XP	677	0	686	19	0
48	QQ	823	0	891	12	0
48	XQ	823	0	891	7	0
49	QR	555	0	618	11	0
49	XR	555	0	618	14	0
50	QS	648	0	658	16	0
50	XS	645	0	635	27	0
51	QT	732	0	809	16	0
51	XT	733	0	795	15	0
52	QU	199	0	208	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	XU	199	0	208	7	0
53	QV	1644	0	835	23	0
53	XV	1644	0	836	15	0
54	QX	215	0	109	1	0
54	XX	193	0	97	5	0
55	QY	2014	0	1981	60	0
55	XY	2023	0	1988	78	0
56	QA	256	0	0	0	0
56	QB	1	0	0	0	0
56	QD	3	0	0	0	0
56	QE	2	0	0	0	0
56	QF	1	0	0	0	0
56	QG	2	0	0	0	0
56	QH	1	0	0	0	0
56	QI	1	0	0	0	0
56	QL	2	0	0	0	0
56	QM	1	0	0	0	0
56	QN	2	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	2	0	0	0	0
56	QV	6	0	0	0	0
56	R0	4	0	0	0	0
56	R1	4	0	0	0	0
56	R3	2	0	0	0	0
56	R5	3	0	0	0	0
56	R7	2	0	0	0	0
56	R8	1	0	0	0	0
56	RA	1039	0	0	0	0
56	RB	27	0	0	0	0
56	RD	15	0	0	0	0
56	RE	8	0	0	0	0
56	RF	12	0	0	0	0
56	RG	4	0	0	0	0
56	RH	1	0	0	0	0
56	RN	2	0	0	0	0
56	RO	1	0	0	0	0
56	RP	1	0	0	0	0
56	RQ	6	0	0	0	0
56	RR	3	0	0	0	0
56	RT	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	RU	2	0	0	0	0
56	RV	4	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	RZ	1	0	0	0	0
56	XA	183	0	0	0	0
56	XE	1	0	0	0	0
56	XF	2	0	0	0	0
56	XJ	1	0	0	0	0
56	XK	1	0	0	0	0
56	XL	1	0	0	0	0
56	XR	1	0	0	0	0
56	XT	1	0	0	0	0
56	XV	4	0	0	0	0
56	XX	1	0	0	0	0
56	Y0	1	0	0	0	0
56	Y1	1	0	0	0	0
56	Y5	1	0	0	0	0
56	Y7	2	0	0	0	0
56	Y8	2	0	0	0	0
56	YA	744	0	0	0	0
56	YB	18	0	0	0	0
56	YD	9	0	0	0	0
56	YE	5	0	0	0	0
56	YF	3	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	2	0	0	0	0
56	YP	1	0	0	0	0
56	YQ	2	0	0	0	0
56	YR	1	0	0	0	0
56	YT	4	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	294739	0	198434	3343	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 (3343) 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:YA:2552:2MU:C5	1:YA:2552:2MU:C4	1.80	1.59
1:RA:2552:2MU:C4	1:RA:2552:2MU:C5	1.80	1.58
32:XA:1003:G:H2'	32:XA:1004:A:H4'	1.32	1.08
1:YA:1029:A:N6	1:YA:1125:G:O2'	1.87	1.06
26:Y4:59:PHE:HA	26:Y4:61:ARG:N	1.76	1.00
26:Y4:59:PHE:HA	26:Y4:61:ARG:H	1.28	0.99
1:YA:2131:G:H5''	1:YA:2132:U:H5'	1.45	0.98
10:RO:48:PRO:HB3	32:QA:1422:G:H5''	1.46	0.97
1:RA:2131:G:H5''	1:RA:2132:U:H5'	1.45	0.97
1:RA:2285:C:OP2	28:R6:29:ASN:ND2	1.99	0.94
15:RT:55:ASN:H	15:RT:59:THR:HG22	1.31	0.92
14:RS:59:LYS:HD2	14:RS:60:GLY:H	1.30	0.92
1:YA:2128:C:H42	1:YA:2160:G:H1	1.17	0.91
40:QI:17:VAL:HG21	40:QI:81:ILE:HG22	1.53	0.90
1:RA:2128:C:H42	1:RA:2160:G:H1	1.15	0.90
10:YO:48:PRO:HB3	32:XA:1422:G:H5''	1.52	0.90
1:RA:2573:C:N4	55:QY:241:ASP:OD1	2.05	0.89
1:YA:1041:C:H42	1:YA:1114:G:H1	1.19	0.89
6:RG:179:PRO:HB2	26:R4:42:PHE:HE2	1.37	0.89
1:RA:250:G:OP2	30:R8:13:ARG:NH2	2.06	0.89
33:XB:15:VAL:HB	33:XB:209:ARG:HB3	1.53	0.88
32:QA:78:G:H1	32:QA:91:C:H42	1.22	0.87
32:XA:1493:A:H4'	55:XY:121:GLY:H	1.39	0.87
32:QA:975:A:H4'	32:QA:976:G:H5''	1.58	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1041:C:H42	1:RA:1114:G:H1	1.24	0.85
50:XS:50:ALA:HB1	50:XS:57:HIS:HB3	1.57	0.85
8:YI:92:VAL:HG23	8:YI:120:ILE:HB	1.58	0.85
32:XA:390:C:O3'	47:XP:28:ARG:NH2	2.11	0.83
1:YA:1028:A:HO2'	1:YA:2486:G:HO2'	1.18	0.83
35:XD:18:LYS:NZ	35:XD:31:CYS:SG	2.51	0.83
5:YF:178:PRO:HB2	5:YF:201:VAL:HG21	1.60	0.83
55:XY:200:ALA:HB3	55:XY:302:ASP:HB3	1.60	0.83
1:YA:250:G:OP2	30:Y8:13:ARG:NH2	2.11	0.83
4:RE:47:VAL:HG21	4:RE:86:PRO:HD2	1.60	0.82
44:XM:107:ALA:HB3	44:XM:111:LYS:HD2	1.61	0.82
6:YG:136:ARG:HG2	6:YG:137:GLU:HG3	1.60	0.82
1:YA:2452:C:H4'	55:XY:239:THR:HG21	1.61	0.82
4:YE:47:VAL:HG11	4:YE:86:PRO:HD2	1.60	0.82
29:R7:34:ARG:NH1	29:R7:41:ARG:O	2.13	0.81
1:RA:2552:2MU:C4	1:RA:2552:2MU:C6	2.54	0.81
1:YA:2753:A:N3	31:Y9:15:LYS:NZ	2.28	0.81
10:RO:35:VAL:HG11	10:RO:103:ALA:HB3	1.62	0.81
32:XA:975:A:H4'	32:XA:976:G:H5''	1.60	0.81
41:XJ:49:VAL:HG23	45:YN:41:ARG:HB2	1.62	0.81
40:XI:53:VAL:O	40:XI:55:ALA:N	2.13	0.81
1:YA:1038:C:H42	1:YA:1117:G:H1	1.28	0.81
1:YA:833:U:O2	11:YP:55:ARG:NH2	2.14	0.81
1:YA:1028:A:O2'	1:YA:2486:G:O2'	1.98	0.80
1:RA:1798:U:H5'	3:RD:259:THR:HG22	1.63	0.80
15:YT:16:ARG:NH2	15:YT:83:ILE:O	2.14	0.80
32:QA:664:G:H22	32:QA:741:G:H1	1.30	0.80
32:QA:538:G:H5''	43:QL:114:LYS:HB2	1.64	0.79
1:RA:83:G:OP1	20:RY:95:LYS:NZ	2.15	0.79
27:Y5:16:ARG:NH1	27:Y5:17:ASP:OD1	2.16	0.79
1:YA:2748:A:H5'	7:YH:4:ILE:HD12	1.63	0.79
4:YE:12:THR:HG23	15:YT:58:ASN:HD21	1.48	0.79
1:RA:956:G:OP2	12:RQ:14:ARG:NH2	2.16	0.79
32:QA:1189:C:OP1	41:QJ:51:ARG:NH2	2.15	0.78
32:QA:532:A:H61	34:QC:193:TYR:HA	1.49	0.78
42:QK:48:ILE:HD12	42:QK:63:LEU:HB2	1.65	0.78
1:YA:2756:U:H5''	31:Y9:19:ARG:HA	1.65	0.78
1:YA:1798:U:OP2	3:YD:274:ARG:NH2	2.16	0.78
10:YO:35:VAL:HG11	10:YO:103:ALA:HB3	1.66	0.78
50:XS:20:LEU:HD23	50:XS:23:ASN:HD22	1.47	0.78
1:RA:272(K):U:H1'	8:RI:50:ARG:HH21	1.46	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:QB:21:ARG:HH22	33:QB:23:ARG:HH21	1.32	0.78
1:RA:2343:C:HO2'	1:RA:2373:G:HO2'	1.32	0.78
33:XB:88:ALA:HB1	33:XB:222:ILE:HD11	1.65	0.77
1:YA:530:G:N1	1:YA:2023:G:OP1	2.16	0.77
48:XQ:66:SER:O	48:XQ:70:ARG:NH1	2.18	0.77
1:RA:1250:G:N7	11:RP:18:ARG:NH2	2.32	0.77
14:YS:50:SER:O	14:YS:76:LYS:NZ	2.14	0.77
32:XA:1314:C:OP2	50:XS:4:SER:OG	2.03	0.76
32:QA:1183:A:O2'	32:QA:1184:G:OP1	2.03	0.76
18:RW:14:PRO:HG2	18:RW:78:GLU:HG2	1.67	0.76
21:YZ:45:ASP:OD1	21:YZ:49:ARG:NH1	2.18	0.76
1:RA:1036:G:OP2	7:RH:59:ARG:NH1	2.19	0.76
1:RA:2140:C:H2'	1:RA:2141:G:H8	1.51	0.76
40:QI:50:LEU:HD13	40:QI:56:LEU:HA	1.66	0.75
32:QA:189(B):C:H42	32:QA:189(K):G:H1	1.33	0.75
6:RG:161:THR:HG22	6:RG:163:ALA:H	1.51	0.75
41:QJ:49:VAL:HG23	45:QN:41:ARG:HB2	1.67	0.75
55:QY:242:SER:HA	55:QY:263:GLN:HB3	1.68	0.75
32:QA:38:G:H22	32:QA:397:A:H5'	1.52	0.75
41:XJ:17:ASP:OD1	41:XJ:70:ARG:NH1	2.19	0.75
1:YA:1051:G:H4'	1:YA:2752:C:H4'	1.68	0.75
27:R5:40:LYS:NZ	27:R5:44:THR:O	2.18	0.75
51:QT:86:ARG:O	51:QT:90:GLN:NE2	2.20	0.74
53:XV:75:C:OP2	55:XY:261:ARG:NH2	2.18	0.74
1:YA:958:U:OP2	12:YQ:14:ARG:NH1	2.19	0.74
26:R4:59:PHE:HZ	50:QS:45:VAL:HG21	1.50	0.74
1:YA:1815:A:OP2	3:YD:54:ARG:NH2	2.20	0.74
19:YX:88:LYS:HE2	19:YX:93:GLU:HG3	1.69	0.74
55:QY:217:ILE:HD11	55:QY:222:LEU:HD21	1.69	0.74
32:QA:159:G:N2	32:QA:162:A:OP2	2.15	0.74
1:RA:631:A:OP1	11:RP:65:ARG:NH1	2.19	0.74
1:YA:1062:G:H5'	1:YA:1070:A:H5''	1.67	0.74
28:R6:24:GLU:OE2	30:R8:34:TRP:NE1	2.19	0.74
1:RA:1049:C:N4	1:RA:2751:G:O6	2.19	0.74
55:QY:315:GLY:HA2	55:QY:329:LEU:HD12	1.70	0.74
32:XA:642:A:N3	39:XH:113:SER:OG	2.20	0.73
35:QD:18:LYS:NZ	35:QD:31:CYS:SG	2.61	0.73
44:XM:58:GLU:O	44:XM:62:ASN:ND2	2.21	0.73
55:XY:183:ARG:HB3	55:XY:309:THR:HG22	1.68	0.73
20:RY:92:ASN:HB2	20:RY:94:LYS:H	1.51	0.73
1:RA:1038:C:H42	1:RA:1117:G:H1	1.35	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:1047:G:H5''	45:XN:4:LYS:HD3	1.68	0.73
6:YG:161:THR:HG22	6:YG:163:ALA:H	1.53	0.73
32:QA:201:C:H42	32:QA:216:G:H1	1.35	0.73
22:R0:10:THR:HG22	22:R0:12:ASN:H	1.53	0.73
32:QA:1279:A:O2'	32:QA:1281:U:OP2	2.07	0.73
3:RD:69:ARG:NH2	3:RD:128:GLY:O	2.22	0.73
15:RT:35:LYS:HG2	15:RT:40:THR:HG22	1.71	0.73
34:XC:109:PRO:HB3	34:XC:115:LEU:HD23	1.71	0.73
1:YA:2140:C:H2'	1:YA:2141:G:H8	1.52	0.72
1:RA:1062:G:H5'	1:RA:1070:A:H5''	1.70	0.72
1:YA:1071:G:N2	1:YA:1089:G:O6	2.15	0.72
1:RA:2384:G:OP2	22:R0:55:ARG:NH1	2.22	0.72
44:XM:98:VAL:HG23	44:XM:110:ARG:HH12	1.55	0.72
55:QY:177:PHE:O	55:QY:321:ARG:NH1	2.20	0.72
1:RA:1971:A:OP2	3:RD:242:ARG:NH2	2.20	0.72
1:RA:994:C:OP1	16:RU:53:ARG:NH2	2.23	0.72
32:XA:1189:C:OP1	41:XJ:51:ARG:NH2	2.22	0.72
22:Y0:11:ARG:O	22:Y0:14:ARG:NH2	2.22	0.72
32:XA:955:U:OP1	55:XY:137:ARG:NH1	2.22	0.72
2:YB:105:A:OP1	21:YZ:72:ARG:NH1	2.21	0.72
35:QD:148:VAL:HG11	35:QD:158:ILE:HD12	1.70	0.71
41:QJ:35:SER:HB3	41:QJ:73:ASP:HB2	1.70	0.71
47:QP:53:VAL:HG13	47:QP:79:VAL:HG12	1.72	0.71
55:QY:248:HIS:HB2	55:QY:274:LEU:HD11	1.70	0.71
22:R0:11:ARG:O	22:R0:14:ARG:NH2	2.19	0.71
21:RZ:72:ARG:HG2	21:RZ:89:PHE:HB2	1.72	0.71
3:RD:71:ASP:HB3	3:RD:103:ARG:HH22	1.55	0.71
15:RT:16:ARG:NH2	15:RT:83:ILE:O	2.23	0.71
55:XY:208:GLU:HG2	55:XY:210:PRO:HD3	1.72	0.71
1:YA:2134:A:N6	1:YA:2156:G:O2'	2.23	0.71
11:YP:59:LEU:HD11	30:Y8:10:ALA:HB2	1.69	0.71
7:YH:7:LEU:O	7:YH:69:ARG:NH1	2.23	0.71
17:YV:6:LYS:HB2	17:YV:38:LEU:HD21	1.69	0.71
32:QA:316:G:OP2	32:QA:351:G:O2'	2.09	0.71
10:RO:97:ARG:NH1	32:QA:339:C:OP2	2.23	0.71
50:QS:41:VAL:HG12	50:QS:44:MET:HG3	1.72	0.71
6:YG:66:GLN:HG3	26:Y4:1:MET:HE3	1.72	0.71
6:RG:41:GLN:HB3	6:RG:43:LEU:HD13	1.72	0.71
34:XC:58:GLU:HB3	41:XJ:92:THR:HG21	1.72	0.71
1:YA:2573:C:N4	55:XY:239:THR:HA	2.04	0.71
1:YA:1530:C:O2'	1:YA:1531:C:O5'	2.07	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:538:G:H5''	43:XL:114:LYS:HB2	1.73	0.71
1:YA:1028:A:N6	1:YA:1126:A:OP1	2.19	0.71
1:YA:272(P):C:O2'	8:YI:42:SER:OG	2.07	0.71
33:QB:82:ARG:NH1	33:QB:86:GLU:OE2	2.23	0.71
32:XA:1292:U:OP2	38:XG:41:ARG:NH2	2.23	0.71
5:YF:24:LEU:HD23	5:YF:115:ALA:HA	1.73	0.71
6:YG:136:ARG:HD3	6:YG:136:ARG:H	1.56	0.70
4:RE:77:ILE:HD13	4:RE:195:LEU:HD13	1.72	0.70
42:XK:99:GLN:HG2	42:XK:105:VAL:HG21	1.72	0.70
1:RA:1073:A:H2'	1:RA:1074:G:H8	1.57	0.70
32:XA:992:U:H4'	32:XA:993:G:O5'	1.91	0.70
32:XA:1031:G:H2'	32:XA:1032:G:C8	2.26	0.70
26:R4:59:PHE:CZ	50:QS:45:VAL:HG21	2.27	0.70
6:YG:63:ILE:HA	6:YG:143:GLU:HG3	1.74	0.70
1:RA:1141:U:OP1	9:RN:25:ARG:NH1	2.25	0.70
21:RZ:144:LEU:HD21	21:RZ:150:LEU:HD13	1.73	0.70
15:RT:56:GLY:O	15:RT:59:THR:HG23	1.92	0.70
11:RP:59:LEU:HD11	30:R8:10:ALA:HB2	1.72	0.69
55:XY:217:ILE:HD11	55:XY:222:LEU:HD21	1.73	0.69
1:YA:309:G:N3	1:YA:329:G:O2'	2.24	0.69
32:QA:1003:G:N2	32:QA:1004:A:N3	2.40	0.69
1:RA:1087:G:H1	1:RA:1102:C:H42	1.38	0.69
1:YA:1971:A:OP2	3:YD:242:ARG:NH2	2.24	0.69
1:RA:2128:C:N4	1:RA:2160:G:H1	1.89	0.69
33:XB:78:GLN:O	33:XB:94:ASN:ND2	2.25	0.69
1:RA:530:G:N1	1:RA:2023:G:OP1	2.24	0.69
1:RA:20:C:OP1	16:RU:22:LYS:NZ	2.25	0.69
22:Y0:10:THR:HG22	22:Y0:12:ASN:H	1.58	0.69
1:YA:1419:A:N6	1:YA:1578:U:O2	2.20	0.69
32:QA:1492:A:HO2'	54:QX:20:A:HO2'	1.35	0.69
1:RA:1024:G:HO2'	1:RA:1144:G:HO2'	1.35	0.69
1:YA:2640:G:O3'	9:YN:74:ARG:NH2	2.16	0.69
1:YA:2304:G:H22	1:YA:2312:U:H3	1.41	0.69
1:RA:1094:U:OP1	1:RA:1096:A:N6	2.26	0.69
32:XA:664:G:H22	32:XA:741:G:H1	1.40	0.69
32:QA:1297:C:O2'	38:QG:114:ARG:NH2	2.26	0.69
1:RA:1073:A:H2'	1:RA:1074:G:C8	2.26	0.69
1:RA:143(A):G:H4'	19:RX:35:THR:HG21	1.74	0.69
32:XA:582:U:OP1	46:XO:68:ARG:NH2	2.22	0.69
55:QY:255:VAL:HG12	55:QY:274:LEU:HD23	1.75	0.69
40:XI:16:ARG:HB2	40:XI:64:THR:HG22	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y4:59:PHE:CZ	50:XS:64:GLU:HB2	2.28	0.69
1:YA:1057:A:N7	1:YA:1086:A:H2'	2.08	0.69
33:XB:47:THR:HA	33:XB:202:PRO:HG2	1.73	0.69
1:RA:1815:A:OP2	3:RD:54:ARG:NH2	2.27	0.68
32:XA:677:U:H3	32:XA:713:G:H22	1.38	0.68
5:YF:185:ASP:HA	5:YF:188:ARG:HD3	1.75	0.68
55:QY:328:ARG:HH22	55:QY:339:MET:C	1.96	0.68
6:RG:63:ILE:HA	6:RG:143:GLU:HG3	1.74	0.68
41:XJ:52:GLY:O	45:XN:41:ARG:NH2	2.26	0.68
1:RA:587:C:OP2	11:RP:21:ARG:NH2	2.25	0.68
1:YA:270:A:OP2	1:YA:272(X):G:N1	2.18	0.68
1:RA:1024:G:O2'	1:RA:1144:G:O2'	2.11	0.68
1:YA:2646:C:OP2	1:YA:2732:G:O2'	2.10	0.68
9:YN:94:HIS:HB3	9:YN:97:ARG:HD3	1.74	0.68
32:XA:1005:A:OP2	32:XA:1024:G:N2	2.27	0.68
55:XY:145:ARG:HB3	55:XY:167:SER:HB2	1.75	0.68
26:R4:50:VAL:HG11	44:QM:65:LYS:HA	1.75	0.68
1:YA:855:G:O2'	22:Y0:27:GLU:OE2	2.09	0.68
32:QA:1492:A:O4'	43:QL:47:LYS:NZ	2.26	0.68
32:XA:64:G:H4'	32:XA:65:U:H3'	1.76	0.68
26:Y4:59:PHE:CE1	50:XS:64:GLU:HB2	2.28	0.68
1:YA:1073:A:H2'	1:YA:1074:G:H8	1.59	0.68
1:RA:2749:A:H5'	7:RH:3:ARG:HH21	1.58	0.68
6:RG:179:PRO:HB2	26:R4:42:PHE:CE2	2.25	0.68
1:YA:1028:A:N6	1:YA:1125:G:H2'	2.09	0.68
1:YA:2785:C:OP1	4:YE:41:LYS:NZ	2.25	0.68
32:XA:1285:A:H4'	32:XA:1286:A:H5'	1.76	0.68
41:XJ:35:SER:HB3	41:XJ:73:ASP:H	1.59	0.68
1:YA:1073:A:H2'	1:YA:1074:G:C8	2.28	0.68
55:XY:134:MET:HB2	55:XY:333:MET:HA	1.76	0.67
32:QA:559:A:OP1	36:QE:126:ARG:NH2	2.26	0.67
44:XM:3:ARG:HG3	44:XM:8:GLU:HG3	1.76	0.67
1:YA:1798:U:H5'	3:YD:259:THR:HG22	1.76	0.67
8:YI:50:ARG:O	8:YI:54:GLN:NE2	2.27	0.67
33:QB:19:HIS:NE2	33:QB:189:ASP:OD2	2.27	0.67
21:RZ:45:ASP:OD1	21:RZ:49:ARG:NH1	2.27	0.67
1:YA:1087:G:H1	1:YA:1102:C:H42	1.41	0.67
37:QF:97:PHE:HB2	49:QR:32:ARG:HH11	1.60	0.67
32:XA:1183:A:O2'	32:XA:1184:G:OP1	2.09	0.67
32:XA:474:G:H2'	32:XA:475:G:H8	1.59	0.67
1:YA:1094:U:OP1	1:YA:1096:A:N6	2.26	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:YG:41:GLN:HB3	6:YG:43:LEU:HD13	1.77	0.67
1:RA:1530:C:O2'	1:RA:1531:C:O5'	2.07	0.67
32:XA:316:G:OP2	32:XA:351:G:O2'	2.13	0.67
1:RA:1310:G:OP2	29:R7:9:ARG:NH1	2.28	0.67
8:RI:109:ILE:HG13	8:RI:130:TYR:CZ	2.30	0.67
32:XA:427:U:OP1	35:XD:13:ARG:NH2	2.28	0.67
36:XE:69:VAL:HG11	36:XE:113:ALA:HB1	1.74	0.67
6:YG:44:GLY:O	6:YG:47:LYS:HD2	1.95	0.67
51:QT:57:ARG:HH12	51:QT:100:ILE:HD12	1.60	0.67
11:YP:59:LEU:HD21	30:Y8:10:ALA:HA	1.77	0.67
33:XB:91:PRO:HG3	33:XB:155:LEU:HD23	1.77	0.66
1:YA:1266:G:O5'	18:YW:15:ARG:NH2	2.28	0.66
20:YY:23:ARG:HG2	20:YY:42:VAL:HG22	1.77	0.66
6:RG:139:LEU:HD21	6:RG:149:VAL:HG11	1.75	0.66
55:XY:119:THR:N	55:XY:302:ASP:OD2	2.28	0.66
1:YA:1049:C:H2'	1:YA:1050:A:H8	1.60	0.66
1:YA:307:G:N1	1:YA:310:A:OP2	2.28	0.66
11:YP:2:LYS:NZ	11:YP:4:SER:OG	2.27	0.66
32:QA:78:G:H1	32:QA:91:C:N4	1.92	0.66
5:RF:165:ARG:HA	5:RF:168:ARG:HD2	1.77	0.66
32:XA:1164:G:H1	32:XA:1172:C:H42	1.43	0.66
32:XA:976:G:H5'	32:XA:1358:U:O2'	1.95	0.66
34:XC:6:HIS:HD2	34:XC:9:GLY:H	1.41	0.66
55:XY:186:ARG:HB3	55:XY:312:PHE:HD2	1.60	0.66
36:QE:79:GLU:HG3	36:QE:93:PRO:HD2	1.77	0.66
11:RP:52:GLU:OE1	11:RP:55:ARG:NH1	2.28	0.66
1:YA:2445:G:OP1	5:YF:74:ARG:NH2	2.22	0.66
1:RA:2751:G:C8	7:RH:2:SER:HA	2.31	0.66
50:XS:41:VAL:HG12	50:XS:44:MET:HG3	1.76	0.66
32:QA:922:G:H4'	36:QE:20:GLN:HA	1.78	0.66
1:YA:1064:C:H3'	1:YA:1065:U:H5'	1.77	0.66
1:YA:987:G:O2'	1:YA:1000:A:N3	2.29	0.66
43:XL:70:ILE:HG12	43:XL:100:ILE:HD12	1.78	0.66
4:YE:52:LEU:HB3	4:YE:53:PRO:HD2	1.76	0.66
1:RA:1923:U:OP1	53:QV:24:U:O2'	2.14	0.66
1:RA:1064:C:H3'	1:RA:1065:U:C5'	2.26	0.66
32:XA:1318:A:H5"	50:XS:3:ARG:HH22	1.61	0.66
1:YA:637:A:H8	11:YP:117:GLU:HG3	1.60	0.66
21:YZ:10:ARG:NH2	21:YZ:26:GLY:O	2.28	0.66
27:R5:16:ARG:NH1	27:R5:17:ASP:OD1	2.29	0.65
32:QA:78:G:N2	32:QA:91:C:N3	2.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:QQ:66:SER:O	48:QQ:70:ARG:NH1	2.29	0.65
1:RA:2218:U:O2	23:R1:52:ARG:NH2	2.29	0.65
32:XA:1136:U:OP2	32:XA:1137:C:N4	2.29	0.65
1:YA:2206:G:H5''	1:YA:2207:G:C8	2.30	0.65
4:YE:11:MET:HG2	4:YE:24:THR:HG22	1.77	0.65
35:QD:53:ASP:HB3	35:QD:57:ARG:HH12	1.60	0.65
1:RA:2785:C:OP1	4:RE:41:LYS:NZ	2.30	0.65
12:RQ:21:THR:HG21	12:RQ:101:ARG:HB2	1.79	0.65
35:QD:173:TRP:CD2	35:QD:189:PRO:HG3	2.31	0.65
1:RA:2134:A:N6	1:RA:2156:G:O2'	2.30	0.65
1:YA:857:C:OP2	22:Y0:77:ARG:NH2	2.30	0.65
23:Y1:75:GLU:HA	23:Y1:78:LYS:HE2	1.78	0.65
1:YA:1064:C:H3'	1:YA:1065:U:C5'	2.25	0.65
51:QT:89:ARG:O	51:QT:93:GLU:HG2	1.96	0.65
4:RE:111:ARG:HG3	4:RE:160:TYR:CD2	2.32	0.65
15:RT:55:ASN:N	15:RT:59:THR:HG22	2.08	0.65
35:XD:175:SER:HB3	35:XD:186:LEU:HD11	1.78	0.65
1:YA:1031:G:O2'	31:Y9:7:VAL:O	2.12	0.65
42:XK:62:GLN:HB2	42:XK:93:GLN:HG3	1.79	0.65
1:YA:1693:U:O2'	3:YD:14:ARG:NH2	2.30	0.65
32:QA:1030(D):G:N7	32:QA:1031:G:N2	2.44	0.65
32:XA:559:A:OP1	36:XE:126:ARG:NH2	2.29	0.65
1:YA:1028:A:H61	1:YA:1126:A:P	2.19	0.65
1:YA:2128:C:N4	1:YA:2160:G:H1	1.90	0.65
12:YQ:34:LEU:HB2	12:YQ:118:LEU:HD22	1.77	0.65
35:QD:12:CYS:SG	35:QD:19:LEU:HB2	2.37	0.65
35:XD:122:ARG:NH1	35:XD:134:ASP:O	2.29	0.65
1:YA:2334:G:H5'	14:YS:9:ARG:HG2	1.79	0.65
18:YW:14:PRO:HG2	18:YW:78:GLU:HG2	1.78	0.64
38:XG:113:GLU:HG2	38:XG:119:ARG:HG2	1.78	0.64
44:QM:3:ARG:HG3	44:QM:4:ILE:H	1.63	0.64
32:XA:673:G:H2'	32:XA:674:G:C8	2.32	0.64
1:RA:1064:C:H3'	1:RA:1065:U:H5'	1.78	0.64
36:XE:50:GLU:HB2	36:XE:53:LEU:HD13	1.80	0.64
1:YA:1049:C:H2'	1:YA:1050:A:C8	2.33	0.64
1:YA:1786:A:H1'	1:YA:1938:A:N6	2.12	0.64
32:QA:1086:U:H3	32:QA:1099:G:H22	1.45	0.64
40:X1:46:ALA:HB2	40:X1:74:ILE:HG23	1.79	0.64
1:YA:1029:A:C2	1:YA:2465:C:H2'	2.32	0.64
1:YA:1385:G:O2'	1:YA:1396:U:O2	2.15	0.64
1:YA:2128:C:N3	1:YA:2160:G:N2	2.45	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:861:A:N3	2:RB:79:C:O2'	2.30	0.64
23:Y1:76:ARG:HH22	23:Y1:97:LEU:HB3	1.62	0.64
26:Y4:58:ARG:NH1	50:XS:65:ASN:O	2.30	0.64
21:YZ:19:ARG:NH1	21:YZ:84:GLU:O	2.31	0.64
21:RZ:158:PRO:HG2	21:RZ:161:VAL:HG11	1.80	0.64
30:Y8:6:THR:HG22	30:Y8:63:PRO:HD2	1.78	0.64
32:QA:974:A:OP2	45:QN:29:ARG:NH2	2.30	0.64
1:RA:637:A:H8	11:RP:117:GLU:HG3	1.62	0.64
5:RF:157:VAL:HB	5:RF:194:MET:HG2	1.79	0.64
32:XA:1004:A:H5'	32:XA:1025:U:H5	1.63	0.64
1:YA:1065:U:H4'	1:YA:1066:U:H5'	1.80	0.64
1:YA:2156:G:N7	1:YA:2157:G:N2	2.46	0.64
8:YI:86:THR:HA	8:YI:123:LEU:HD23	1.79	0.64
20:YY:102:CYS:SG	20:YY:103:GLY:N	2.71	0.64
1:RA:1053:C:H2'	1:RA:1054:A:H8	1.62	0.64
1:RA:307:G:N1	1:RA:310:A:OP2	2.31	0.64
1:YA:2742:C:OP1	31:Y9:35:ARG:HD3	1.98	0.64
1:RA:1266:G:O5'	18:RW:15:ARG:NH2	2.31	0.64
1:RA:309:G:N3	1:RA:329:G:O2'	2.30	0.64
1:YA:143(A):G:H4'	19:YX:35:THR:HG21	1.80	0.64
55:QY:183:ARG:HB3	55:QY:309:THR:HG22	1.80	0.63
1:RA:987:G:O2'	1:RA:1000:A:N3	2.26	0.63
21:YZ:72:ARG:HG2	21:YZ:89:PHE:HB2	1.79	0.63
32:QA:269:C:H2'	32:QA:270:A:C8	2.34	0.63
33:QB:96:ARG:HD2	33:QB:98:LEU:HD23	1.80	0.63
1:RA:11:G:H2'	1:RA:12:U:H5'	1.79	0.63
1:RA:2156:G:N7	1:RA:2157:G:N2	2.46	0.63
32:XA:1221:G:OP1	32:XA:1320:C:N4	2.28	0.63
1:YA:2464:C:H2'	1:YA:2465:C:O4'	1.98	0.63
6:YG:21:ARG:HE	6:YG:22:ARG:HG2	1.63	0.63
1:RA:1028:A:N6	1:RA:1125:G:H2'	2.13	0.63
1:YA:631:A:OP1	11:YP:65:ARG:NH1	2.30	0.63
1:RA:2327:A:H2'	1:RA:2328:A:C8	2.34	0.63
1:RA:652(C):A:H61	1:RA:655:A:H1'	1.64	0.63
40:XI:50:LEU:HD23	40:XI:85:LEU:HD11	1.80	0.63
26:Y4:48:ARG:HG3	26:Y4:52:THR:HG23	1.81	0.63
2:YB:24:G:N7	2:YB:56:G:H2'	2.13	0.63
1:RA:1076:C:H4'	1:RA:1077:A:OP1	1.97	0.63
10:RO:80:ASP:OD1	15:RT:64:ARG:NH2	2.32	0.63
1:YA:2206:G:H3'	1:YA:2207:G:H8	1.63	0.63
32:XA:1288:A:O3'	52:XU:10:ARG:NH2	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:QF:25:ILE:HG13	37:QF:82:ARG:NH1	2.14	0.63
26:Y4:18:CYS:SG	26:Y4:39:CYS:HB3	2.39	0.63
11:YP:126:VAL:HG12	11:YP:148:LEU:HD22	1.79	0.63
44:QM:15:VAL:HG11	44:QM:48:LEU:HD21	1.81	0.63
1:RA:2206:G:H3'	1:RA:2207:G:C8	2.34	0.63
32:XA:1343:G:H4'	40:XI:122:ALA:HB3	1.81	0.63
32:XA:581:G:OP1	46:XO:65:ARG:NH2	2.31	0.63
54:XX:19:U:N3	55:XY:121:GLY:O	2.31	0.63
32:QA:73:G:H1	32:QA:96:U:H3	1.46	0.63
1:RA:1057:A:N7	1:RA:1086:A:H2'	2.14	0.63
32:XA:1302:U:OP1	44:XM:13:LYS:NZ	2.28	0.63
38:XG:15:ASP:OD1	38:XG:20:ASP:N	2.31	0.63
1:YA:2126:A:H4'	1:YA:2127:G:O5'	1.98	0.62
32:QA:1519:MA6:O5'	32:QA:1519:MA6:H8	1.99	0.62
38:QG:113:GLU:HG2	38:QG:119:ARG:HG2	1.80	0.62
1:RA:2744:G:N2	7:RH:143:GLN:OE1	2.30	0.62
32:QA:142:G:O2'	32:QA:196:A:N1	2.33	0.62
1:RA:997:G:H5''	16:RU:92:ARG:HH21	1.63	0.62
55:XY:328:ARG:HH22	55:XY:339:MET:C	2.02	0.62
1:YA:2552:2MU:C6	1:YA:2552:2MU:C4	2.55	0.62
14:YS:15:ARG:O	14:YS:19:LYS:HG2	1.98	0.62
32:QA:1075:C:OP1	33:QB:179:LYS:NZ	2.31	0.62
32:XA:1187:G:OP1	40:XI:113:LYS:NZ	2.32	0.62
1:YA:2206:G:H3'	1:YA:2207:G:C8	2.33	0.62
36:QE:143:ARG:NH1	39:QH:77:GLU:OE2	2.32	0.62
23:R1:50:ARG:HG2	23:R1:59:THR:HG22	1.81	0.62
1:RA:1063:G:N2	1:RA:1075:C:N3	2.48	0.62
1:RA:2646:C:OP2	1:RA:2732:G:O2'	2.17	0.62
32:XA:1128:C:H1'	32:XA:1147:C:H42	1.65	0.62
35:QD:108:LEU:HD22	35:QD:174:LEU:HD13	1.82	0.62
55:QY:219:PRO:O	55:QY:222:LEU:N	2.30	0.62
36:QE:8:GLU:OE2	36:QE:63:ARG:NH2	2.32	0.62
1:YA:1379:A:H4'	1:YA:1380:G:OP2	2.00	0.62
1:YA:483:A:O2'	20:YY:49:VAL:O	2.15	0.62
41:QJ:52:GLY:O	45:QN:41:ARG:NH2	2.33	0.62
51:QT:60:GLU:HG3	51:QT:81:LYS:HD2	1.81	0.62
33:XB:77:ALA:HB2	33:XB:211:ILE:HD13	1.82	0.62
36:XE:102:ALA:HB1	36:XE:106:PRO:HG2	1.81	0.62
3:YD:108:PRO:HB3	3:YD:143:HIS:CE1	2.35	0.62
17:YV:62:LEU:HD21	17:YV:95:LEU:HB2	1.81	0.62
32:QA:976:G:H5'	32:QA:1358:U:O2'	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:RP:63:PRO:HG2	30:R8:25:MET:HB2	1.80	0.61
32:XA:1494:G:O3'	55:XY:160:LYS:NZ	2.26	0.61
32:QA:1020:U:H2'	32:QA:1021:G:C8	2.35	0.61
53:QV:1:C:H42	53:QV:72:A:H61	1.48	0.61
6:RG:108:ASN:O	26:R4:37:SER:N	2.33	0.61
1:RA:2839:G:H5'	13:RR:46:GLY:HA2	1.81	0.61
53:XV:4:G:HO2'	53:XV:5:G:H8	1.48	0.61
36:QE:8:GLU:HG2	36:QE:34:VAL:HG22	1.80	0.61
55:QY:316:ARG:NE	55:QY:327:TYR:OH	2.33	0.61
1:RA:1530:C:H42	1:RA:1539:G:H1	1.47	0.61
32:XA:865:A:H5'	32:XA:1078:U:C5	2.35	0.61
32:XA:437:U:H5'	35:XD:155:LEU:HD21	1.82	0.61
32:QA:1003:G:H2'	32:QA:1004:A:H4'	1.81	0.61
33:QB:21:ARG:O	33:QB:23:ARG:N	2.29	0.61
40:XI:50:LEU:HB2	40:XI:56:LEU:HD23	1.82	0.61
37:QF:10:LEU:HD21	37:QF:61:LEU:HD22	1.81	0.61
1:RA:2126:A:H4'	1:RA:2127:G:O5'	2.01	0.61
44:XM:96:LEU:O	44:XM:110:ARG:NH1	2.34	0.61
1:YA:2122:U:H3	1:YA:2176:A:H61	1.48	0.61
44:QM:13:LYS:HA	44:QM:44:ARG:HH11	1.64	0.61
1:RA:1057:A:O2'	1:RA:1058:G:OP1	2.18	0.61
1:RA:2206:G:H5''	1:RA:2207:G:C8	2.36	0.61
1:RA:272(L):U:H5'	8:RI:50:ARG:HH12	1.64	0.61
32:XA:1025:U:H3	32:XA:1036:G:H1	1.48	0.61
26:Y4:59:PHE:CA	26:Y4:61:ARG:H	2.10	0.61
39:QH:64:LYS:HG2	39:QH:79:VAL:HG21	1.83	0.61
1:RA:998:C:P	16:RU:92:ARG:HH22	2.23	0.61
33:XB:76:GLN:HB2	33:XB:208:ILE:HG12	1.83	0.61
1:YA:1063:G:N2	1:YA:1075:C:N3	2.48	0.61
1:YA:2839:G:H5'	13:YR:46:GLY:HA2	1.83	0.61
32:QA:297:G:N2	32:QA:300:A:OP2	2.30	0.61
1:RA:1067:A:H4'	1:RA:1068:G:OP2	2.01	0.61
32:XA:1073:U:O2'	33:XB:104:ASN:OD1	2.19	0.61
33:XB:101:MET:HA	33:XB:108:ILE:HG13	1.83	0.61
1:YA:11:G:H2'	1:YA:12:U:H5'	1.83	0.61
1:YA:652(U):C:H2'	1:YA:652(V):G:C8	2.36	0.61
33:QB:69:LEU:HD13	33:QB:91:PRO:HB2	1.83	0.61
1:RA:2128:C:N3	1:RA:2160:G:N2	2.42	0.61
32:XA:102:G:O2'	32:XA:151:A:N3	2.30	0.61
1:YA:1423:G:OP1	1:YA:1492:G:O2'	2.19	0.61
33:QB:195:ASP:O	39:QH:68:ARG:NH2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1379:A:H4'	1:RA:1380:G:OP2	2.00	0.60
1:RA:2612:C:OP2	27:R5:2:ALA:N	2.34	0.60
34:XC:152:ILE:HG13	34:XC:199:LYS:HB2	1.81	0.60
25:Y3:8:LEU:HD12	25:Y3:31:LEU:HA	1.83	0.60
26:Y4:16:CYS:SG	26:Y4:17:GLY:N	2.74	0.60
1:YA:1639:U:H2'	1:YA:1640:C:H5''	1.83	0.60
32:QA:791:G:N2	32:QA:1497:G:O3'	2.34	0.60
34:QC:6:HIS:CE1	34:QC:8:ILE:HB	2.35	0.60
35:QD:88:VAL:HG22	36:QE:96:PRO:HB2	1.83	0.60
1:RA:2206:G:H3'	1:RA:2207:G:H8	1.65	0.60
1:RA:2286:A:C8	28:R6:34:LEU:HD21	2.36	0.60
5:RF:185:ASP:HA	5:RF:188:ARG:HD3	1.84	0.60
32:XA:266:G:O3'	48:XQ:67:LYS:HB2	2.00	0.60
1:YA:1050:A:C2	1:YA:2751:G:C2	2.89	0.60
1:YA:334:C:OP1	1:YA:335:C:N4	2.34	0.60
1:YA:2306:C:N4	6:YG:43:LEU:O	2.33	0.60
36:QE:33:VAL:HG21	36:QE:109:ILE:HA	1.82	0.60
41:QJ:11:PHE:HE1	41:QJ:67:THR:HG22	1.65	0.60
55:QY:263:GLN:O	55:QY:267:LYS:N	2.33	0.60
21:YZ:144:LEU:HD21	21:YZ:150:LEU:HD13	1.83	0.60
15:RT:95:ARG:HG2	15:RT:95:ARG:HH11	1.65	0.60
20:RY:102:CYS:SG	20:RY:103:GLY:N	2.74	0.60
32:XA:1002:G:H2'	32:XA:1003:G:C8	2.36	0.60
32:XA:1319:A:OP2	50:XS:3:ARG:NH2	2.32	0.60
26:Y4:61:ARG:NH2	50:XS:9:VAL:HG11	2.16	0.60
1:YA:784:A:C6	3:YD:229:VAL:HG11	2.36	0.60
32:QA:921:U:O2	36:QE:19:MET:HB2	2.01	0.60
23:R1:51:VAL:HG11	23:R1:74:VAL:HG21	1.84	0.60
1:RA:2122:U:H3	1:RA:2176:A:H61	1.50	0.60
28:Y6:13:CYS:SG	28:Y6:47:THR:HG21	2.42	0.60
32:QA:612:C:O2	32:QA:629:G:N2	2.35	0.60
46:QO:39:LEU:HD13	46:QO:56:LEU:HB2	1.82	0.60
15:RT:24:PRO:HA	15:RT:49:VAL:HG23	1.84	0.60
1:YA:1038:C:N4	1:YA:1117:G:H1	1.98	0.60
38:QG:27:ILE:HD12	38:QG:40:ALA:HA	1.82	0.60
1:RA:1507:A:O2'	1:RA:1508:A:O5'	2.18	0.60
33:XB:16:HIS:CG	33:XB:210:SER:HB3	2.37	0.60
1:YA:2261:C:OP1	22:Y0:19:LYS:NZ	2.29	0.60
2:YB:13:A:N1	2:YB:69:G:O2'	2.28	0.60
32:QA:1070:U:OP1	36:QE:20:GLN:NE2	2.24	0.60
32:QA:901:A:O2'	32:QA:1513:A:OP1	2.11	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:RP:59:LEU:HD21	30:R8:10:ALA:HA	1.83	0.60
9:RN:15:LEU:HB2	9:RN:135:PRO:HB2	1.83	0.60
41:XJ:11:PHE:HE1	41:XJ:67:THR:HG22	1.65	0.60
35:QD:162:LEU:HD13	35:QD:181:MET:HG2	1.84	0.60
32:XA:769:G:H4'	32:XA:1513:A:H4'	1.84	0.60
33:XB:187:LEU:HA	33:XB:201:ILE:HB	1.83	0.60
1:RA:1798:U:OP2	3:RD:274:ARG:NH2	2.31	0.59
32:XA:696:A:N1	32:XA:797:C:O2'	2.30	0.59
1:YA:2527:C:O4'	31:Y9:1:MET:N	2.35	0.59
4:YE:12:THR:HG22	4:YE:13:ARG:H	1.66	0.59
32:QA:335:C:H1'	32:QA:1434:A:H1'	1.84	0.59
32:QA:955:U:OP1	55:QY:137:ARG:NH1	2.34	0.59
32:QA:1298:C:C4	38:QG:114:ARG:HD2	2.37	0.59
39:QH:51:VAL:HG12	39:QH:52:ASP:H	1.67	0.59
32:XA:1360:A:OP2	45:XN:35:ARG:NH2	2.36	0.59
55:XY:326:LEU:HD21	55:XY:328:ARG:HH21	1.66	0.59
22:Y0:27:GLU:HG3	22:Y0:68:GLU:HA	1.84	0.59
1:YA:674:G:H1'	5:YF:74:ARG:HD3	1.84	0.59
32:QA:1010:G:N2	32:QA:1020:U:H1'	2.17	0.59
32:QA:642:A:N3	39:QH:113:SER:OG	2.33	0.59
55:QY:263:GLN:HA	55:QY:266:ASN:HB2	1.83	0.59
8:RI:69:LYS:NZ	8:RI:137:PRO:O	2.27	0.59
33:XB:118:LEU:HD13	33:XB:142:LEU:HB2	1.84	0.59
9:YN:15:LEU:HB2	9:YN:135:PRO:HB2	1.84	0.59
32:QA:1435:G:H2'	32:QA:1436:U:C6	2.36	0.59
36:QE:57:LYS:HG2	36:QE:61:TYR:CE2	2.37	0.59
1:RA:2749:A:H5'	7:RH:3:ARG:NH2	2.17	0.59
1:RA:2748:A:H5'	7:RH:4:ILE:HD12	1.84	0.59
33:XB:8:LYS:HG2	33:XB:9:GLU:H	1.68	0.59
1:YA:1800:C:OP2	3:YD:183:ARG:NH2	2.35	0.59
3:YD:71:ASP:HB3	3:YD:103:ARG:HH22	1.67	0.59
6:YG:80:PHE:O	6:YG:82:LEU:N	2.35	0.59
1:RA:674:G:H1'	5:RF:74:ARG:HD3	1.83	0.59
1:YA:1530:C:H42	1:YA:1539:G:H1	1.50	0.59
1:YA:2787:C:H1'	4:YE:62:PRO:HG3	1.84	0.59
6:YG:77:ILE:HG21	6:YG:80:PHE:CD2	2.36	0.59
32:QA:17:U:H2'	32:QA:18:C:C6	2.37	0.59
32:QA:256:U:OP1	48:QQ:17:LYS:NZ	2.30	0.59
1:RA:1639:U:H2'	1:RA:1640:C:H5''	1.83	0.59
1:RA:270:A:OP2	1:RA:272(X):G:N1	2.29	0.59
51:XT:50:GLU:HG3	51:XT:100:ILE:HD11	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2279:G:N7	22:Y0:14:ARG:NH1	2.50	0.59
37:QF:99:ALA:HB2	49:QR:31:LEU:HD21	1.83	0.59
55:QY:217:ILE:HD12	55:QY:274:LEU:HD12	1.84	0.59
1:RA:2150:U:H2'	1:RA:2151:G:C8	2.37	0.59
7:RH:11:VAL:HG21	7:RH:50:VAL:HG23	1.85	0.59
23:Y1:50:ARG:HG2	23:Y1:59:THR:HG22	1.84	0.59
32:QA:673:G:H2'	32:QA:674:G:C8	2.38	0.59
36:QE:137:GLU:OE1	36:QE:141:GLN:NE2	2.29	0.59
1:YA:1076:C:H4'	1:YA:1077:A:OP1	2.02	0.59
34:QC:8:ILE:HG23	34:QC:16:ARG:HG2	1.84	0.59
36:QE:74:GLY:HA3	36:QE:116:THR:HG22	1.85	0.59
23:R1:3:LYS:HG3	23:R1:4:VAL:H	1.68	0.59
1:RA:2001:A:H2'	1:RA:2002:G:C8	2.38	0.59
32:XA:1376:U:H2'	32:XA:1377:A:H8	1.67	0.59
32:XA:17:U:H2'	32:XA:18:C:C6	2.38	0.59
36:XE:12:LEU:HD12	36:XE:128:PRO:HB2	1.85	0.59
32:QA:1256:A:OP2	32:QA:1279:A:N6	2.36	0.59
1:RA:2304:G:H22	1:RA:2312:U:H3	1.48	0.59
39:XH:10:LEU:HD22	39:XH:83:ILE:HD11	1.84	0.59
1:YA:1507:A:O2'	1:YA:1508:A:O5'	2.19	0.59
1:YA:588:U:H2'	1:YA:589:C:C6	2.38	0.59
3:YD:206:LEU:HD22	3:YD:211:ARG:HG2	1.85	0.59
35:QD:106:TYR:HE2	35:QD:107:ARG:HH11	1.50	0.58
17:RV:72:VAL:HG13	17:RV:85:LYS:HB3	1.84	0.58
32:XA:1129:C:H2'	32:XA:1139:G:N7	2.17	0.58
37:XF:10:LEU:HD21	37:XF:61:LEU:HD22	1.84	0.58
2:YB:91:C:OP2	12:YQ:16:ARG:NH1	2.36	0.58
33:QB:167:PRO:HG3	33:QB:186:ALA:HB1	1.85	0.58
33:QB:54:THR:HG21	33:QB:201:ILE:HD11	1.85	0.58
14:RS:59:LYS:HD2	14:RS:60:GLY:N	2.12	0.58
32:XA:890:G:O2'	32:XA:906:G:O6	2.18	0.58
1:YA:652(C):A:H61	1:YA:655:A:H1'	1.68	0.58
5:YF:178:PRO:HB2	5:YF:201:VAL:CG2	2.31	0.58
7:YH:113:VAL:HG11	7:YH:151:ILE:HD13	1.84	0.58
11:YP:86:LYS:HB3	11:YP:118:GLY:HA3	1.85	0.58
34:QC:6:HIS:HE1	34:QC:8:ILE:HB	1.69	0.58
35:QD:170:VAL:HG12	35:QD:174:LEU:HB2	1.84	0.58
36:XE:74:GLY:HA3	36:XE:116:THR:HG22	1.85	0.58
31:Y9:25:VAL:HB	31:Y9:34:GLN:HB2	1.85	0.58
1:YA:878:A:H3'	1:YA:879:G:H8	1.68	0.58
4:YE:24:THR:HG23	4:YE:186:GLY:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:YF:11:VAL:HB	5:YF:18:ARG:HB3	1.85	0.58
21:YZ:5:LEU:HD11	21:YZ:39:VAL:HB	1.84	0.58
32:QA:677:U:H3	32:QA:713:G:H22	1.52	0.58
43:QL:70:ILE:HG12	43:QL:100:ILE:HD12	1.86	0.58
4:RE:119:ARG:HD3	4:RE:160:TYR:HB2	1.85	0.58
32:QA:441:A:H3'	32:QA:442:C:H6	1.69	0.58
1:RA:652(U):C:H2'	1:RA:652(V):G:C8	2.37	0.58
1:RA:2747:G:OP1	7:RH:138:LYS:NZ	2.34	0.58
1:YA:1721:G:H2'	1:YA:1740:G:O6	2.04	0.58
1:YA:2218:U:O2	23:Y1:52:ARG:NH2	2.36	0.58
1:YA:2347:C:OP1	28:Y6:38:LYS:NZ	2.25	0.58
1:YA:301:G:OP2	20:YY:84:ARG:NH2	2.37	0.58
36:QE:92:LYS:HB3	36:QE:119:LEU:HB2	1.86	0.58
53:QV:28:C:H2'	53:QV:29:G:C8	2.39	0.58
7:YH:11:VAL:HG21	7:YH:50:VAL:HG23	1.85	0.58
32:QA:1292:U:OP2	38:QG:41:ARG:NH2	2.37	0.58
55:QY:262:SER:HB3	55:QY:265:LYS:HG2	1.84	0.58
32:XA:164:U:H2'	32:XA:165:C:C6	2.39	0.58
1:YA:2502:G:H5''	1:YA:2503:2MA:H5''	1.84	0.58
10:YO:115:VAL:HG13	10:YO:121:VAL:HG21	1.85	0.58
19:YX:11:PRO:HB3	19:YX:92:LEU:HD11	1.86	0.58
32:QA:1375:A:H4'	38:QG:29:LYS:HE2	1.85	0.58
3:YD:182:LEU:HB2	3:YD:272:ALA:HB3	1.85	0.58
32:QA:45:U:H2'	32:QA:46:G:C8	2.38	0.58
55:QY:182:HIS:HB3	55:QY:310:TYR:HE1	1.69	0.58
6:RG:115:ARG:HB3	6:RG:136:ARG:HH22	1.69	0.58
34:XC:6:HIS:CD2	34:XC:9:GLY:H	2.22	0.58
1:YA:2573:C:N4	55:XY:228:ARG:HE	2.02	0.58
1:YA:2110:G:H5''	1:YA:2111:C:H5	1.69	0.58
1:YA:2150:U:H2'	1:YA:2151:G:C8	2.38	0.58
32:QA:1441:G:O2'	32:QA:1460:A:N6	2.36	0.57
32:QA:992:U:H4'	32:QA:993:G:H5'	1.86	0.57
37:QF:69:GLU:O	37:QF:72:VAL:HG12	2.04	0.57
7:RH:40:GLU:OE1	7:RH:60:ARG:NH1	2.36	0.57
32:XA:1004:A:N7	32:XA:1037:C:H2'	2.18	0.57
32:XA:473:G:OP2	47:XP:75:ARG:HD3	2.04	0.57
32:XA:933:G:O6	38:XG:3:ARG:NH2	2.35	0.57
1:YA:1056:G:N1	1:YA:1102:C:OP2	2.37	0.57
32:QA:222:U:H2'	32:QA:223:U:C6	2.39	0.57
49:QR:32:ARG:HA	49:QR:69:THR:HG21	1.86	0.57
40:XI:9:ARG:HG2	40:XI:14:VAL:HG12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:XY:263:GLN:HA	55:XY:266:ASN:HB2	1.86	0.57
1:YA:1053:C:H2'	1:YA:1054:A:H8	1.68	0.57
1:YA:1087:G:N2	1:YA:1102:C:N3	2.43	0.57
33:QB:115:LEU:O	33:QB:119:GLU:HG2	2.03	0.57
1:RA:2529:G:O6	31:R9:31:LYS:NZ	2.37	0.57
32:XA:1412:C:H2'	32:XA:1413:A:C8	2.39	0.57
34:XC:179:ARG:NH1	34:XC:206:GLU:OE1	2.35	0.57
46:XO:25:THR:HG21	46:XO:70:LEU:HB2	1.86	0.57
55:XY:200:ALA:HB3	55:XY:302:ASP:CB	2.32	0.57
1:YA:2115:G:N1	1:YA:2119:A:OP2	2.38	0.57
1:YA:2152:G:H2'	1:YA:2153:G:C8	2.40	0.57
1:YA:1049:C:N4	1:YA:2751:G:O6	2.33	0.57
32:QA:737:A:H2'	32:QA:738:C:C6	2.39	0.57
1:RA:1087:G:H1	1:RA:1102:C:N4	2.02	0.57
1:RA:247:G:H4'	1:RA:386:G:C5	2.40	0.57
5:RF:184:TYR:CE2	5:RF:188:ARG:HD2	2.40	0.57
32:QA:1013:G:N2	32:QA:1016:A:OP2	2.35	0.57
32:QA:159:G:N2	32:QA:161:A:H3'	2.20	0.57
33:QB:178:ARG:HH22	39:QH:68:ARG:HH12	1.53	0.57
1:RA:1889:A:N1	1:RA:2234:G:H1'	2.19	0.57
7:RH:3:ARG:HD3	7:RH:54:ARG:HH12	1.70	0.57
32:XA:1191:A:OP2	34:XC:3:ASN:ND2	2.37	0.57
32:XA:662:G:H2'	32:XA:663:A:C8	2.40	0.57
33:QB:229:VAL:HG12	33:QB:230:VAL:H	1.68	0.57
35:QD:166:LYS:N	35:QD:168:ARG:HH21	2.02	0.57
1:RA:2127:G:H2'	1:RA:2128:C:O4'	2.04	0.57
7:RH:3:ARG:HB3	7:RH:6:ARG:HG2	1.87	0.57
32:XA:1023:G:H3'	32:XA:1024:G:H8	1.70	0.57
34:XC:40:ARG:NH2	34:XC:55:VAL:O	2.38	0.57
1:YA:2115:G:H21	1:YA:2171:A:H61	1.53	0.57
32:QA:1286:A:H2'	32:QA:1287:A:H4'	1.87	0.57
33:QB:16:HIS:HB2	33:QB:204:ASN:HB3	1.87	0.57
38:QG:89:MET:HE1	38:QG:155:ARG:HB2	1.87	0.57
1:RA:1786:A:H1'	1:RA:1938:A:N6	2.19	0.57
32:XA:1435:G:H2'	32:XA:1436:U:C6	2.40	0.57
32:XA:474:G:H2'	32:XA:475:G:C8	2.40	0.57
1:YA:1371:G:HO2'	1:YA:1372:U:H5	1.53	0.57
32:QA:1179:A:OP2	40:QI:93:ARG:NH2	2.38	0.57
32:QA:539:A:OP2	43:QL:115:LYS:NZ	2.38	0.57
1:RA:2115:G:N1	1:RA:2119:A:OP2	2.38	0.57
1:RA:992:C:OP1	16:RU:47:TYR:OH	2.14	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:RD:71:ASP:HB3	3:RD:103:ARG:NH2	2.19	0.57
4:RE:2:LYS:HB2	4:RE:95:ILE:HD12	1.86	0.57
5:RF:51:THR:HB	5:RF:88:VAL:HG11	1.86	0.57
33:XB:7:VAL:O	33:XB:217:ARG:NE	2.32	0.57
32:XA:953:G:N7	44:XM:104:ARG:NH2	2.52	0.57
1:YA:1688:U:O2	1:YA:1700:A:H5'	2.05	0.57
32:QA:1216:G:H5''	45:QN:5:ALA:HB2	1.84	0.56
5:RF:64:ILE:HG21	5:RF:78:ILE:HG23	1.87	0.56
13:RR:83:ILE:O	13:RR:86:ARG:HG2	2.04	0.56
33:XB:229:VAL:HG12	33:XB:230:VAL:H	1.68	0.56
36:XE:137:GLU:HG2	36:XE:140:ARG:HH11	1.69	0.56
32:XA:921:U:O2	36:XE:19:MET:HB2	2.05	0.56
43:XL:60:LEU:HD21	43:XL:66:VAL:HG22	1.87	0.56
1:RA:1049:C:H2'	1:RA:1050:A:H8	1.70	0.56
7:RH:90:LYS:HD3	7:RH:159:GLU:HG2	1.87	0.56
32:XA:35:G:O2'	43:XL:118:SER:O	2.21	0.56
1:YA:1057:A:O2'	1:YA:1058:G:OP1	2.19	0.56
1:YA:1086:A:OP1	1:YA:1104:C:O2'	2.23	0.56
7:YH:40:GLU:OE1	7:YH:60:ARG:NH1	2.38	0.56
33:QB:185:ILE:HG22	33:QB:199:TYR:HB2	1.86	0.56
1:RA:876:C:H2'	1:RA:877:U:O4'	2.05	0.56
1:YA:2321:G:O2'	1:YA:2322:A:OP1	2.21	0.56
1:YA:637:A:H5''	11:YP:117:GLU:HG2	1.87	0.56
55:QY:332:VAL:HG13	55:QY:337:LEU:HB3	1.88	0.56
1:YA:796:C:H2'	1:YA:797:C:C6	2.40	0.56
1:YA:2012:G:OP1	18:YW:11:ARG:NH2	2.38	0.56
19:RX:35:THR:HG22	19:RX:37:THR:H	1.70	0.56
21:RZ:19:ARG:NH1	21:RZ:84:GLU:O	2.38	0.56
32:XA:919:A:O2'	32:XA:1080:A:N1	2.26	0.56
32:XA:38:G:H22	32:XA:397:A:H5''	1.69	0.56
34:XC:57:ILE:HG12	34:XC:66:VAL:HG22	1.88	0.56
1:YA:714:U:N3	1:YA:717:G:OP2	2.24	0.56
32:QA:1030(A):C:N4	32:QA:1032:G:O6	2.38	0.56
32:QA:966:M2G:HM12	53:QV:34:C:H5'	1.86	0.56
33:QB:27:LYS:HD2	33:QB:193:ASP:OD1	2.06	0.56
24:R2:23:LYS:O	24:R2:27:GLU:HG3	2.05	0.56
32:XA:1305:G:N2	32:XA:1331:G:H1'	2.20	0.56
32:XA:539:A:H2'	32:XA:540:G:C8	2.41	0.56
33:XB:88:ALA:HB2	33:XB:219:VAL:HG13	1.87	0.56
55:XY:228:ARG:HA	55:XY:241:ASP:HA	1.86	0.56
1:YA:300:A:O2'	1:YA:318:C:O2	2.22	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:YR:18:LEU:HD11	13:YR:22:ARG:CZ	2.35	0.56
17:YV:35:LEU:HB2	17:YV:57:VAL:HG22	1.88	0.56
33:QB:16:HIS:HB3	33:QB:210:SER:HB2	1.87	0.56
53:QV:52:G:N3	53:QV:52:G:H2'	2.21	0.56
1:RA:517:C:OP1	27:R5:16:ARG:NH2	2.39	0.56
9:RN:120:LEU:HD22	9:RN:122:VAL:HG23	1.88	0.56
15:RT:64:ARG:HB2	15:RT:73:GLU:HG2	1.87	0.56
35:XD:12:CYS:SG	35:XD:19:LEU:HB2	2.46	0.56
1:YA:876:C:H2'	1:YA:877:U:O4'	2.06	0.56
5:RF:29:ASN:HB3	5:RF:112:MET:HE1	1.87	0.56
32:XA:1353:G:OP1	52:XU:10:ARG:NH1	2.39	0.56
55:XY:114:GLU:HB3	55:XY:163:ILE:HB	1.87	0.56
46:QO:11:VAL:HG21	46:QO:34:LEU:HD22	1.88	0.56
8:RI:92:VAL:HG13	8:RI:120:ILE:HB	1.86	0.56
32:XA:719:C:O2'	49:XR:49:LYS:HB3	2.05	0.56
5:YF:164:ARG:HD2	5:YF:175:THR:HG23	1.88	0.56
32:QA:187:C:O2'	51:QT:89:ARG:NH2	2.34	0.56
32:QA:343:U:O2'	32:QA:346:G:O6	2.15	0.56
32:QA:1239:A:O2'	38:QG:114:ARG:O	2.21	0.56
40:QI:108:VAL:HG12	40:QI:109:VAL:H	1.71	0.56
1:RA:1076:C:H1'	1:RA:1077:A:H5'	1.86	0.56
1:RA:1798:U:H5'	3:RD:259:THR:CG2	2.36	0.56
20:RY:92:ASN:N	20:RY:93:GLY:HA2	2.21	0.56
32:XA:1053:G:N7	32:XA:1200:C:H5''	2.21	0.56
1:YA:1062:G:O2'	1:YA:1063:G:H5'	2.06	0.56
1:YA:1124:C:H2'	1:YA:1125:G:O4'	2.06	0.56
1:YA:1028:A:H62	1:YA:1126:A:H8	1.53	0.56
21:YZ:91:LEU:HG	21:YZ:130:PRO:HG3	1.87	0.56
48:QQ:78:GLU:HG2	48:QQ:79:SER:H	1.71	0.56
1:RA:2464:C:H2'	1:RA:2465:C:O4'	2.05	0.56
21:RZ:72:ARG:CG	21:RZ:89:PHE:HB2	2.35	0.56
1:YA:323:G:H1'	1:YA:1205:U:O2	2.06	0.56
1:RA:2094:G:P	8:RI:22:LYS:HD2	2.46	0.55
1:RA:2171:A:H4'	1:RA:2172:U:OP1	2.06	0.55
1:YA:1889:A:N1	1:YA:2234:G:H1'	2.21	0.55
32:QA:110:C:O2'	47:QP:25:ARG:O	2.22	0.55
53:QV:4:G:HO2'	53:QV:5:G:H8	1.53	0.55
1:RA:2321:G:O2'	1:RA:2322:A:OP1	2.23	0.55
4:RE:51:PHE:H	4:RE:75:VAL:CG1	2.19	0.55
32:XA:142:G:H2'	32:XA:143:A:H8	1.72	0.55
32:XA:411:A:OP2	35:XD:25:ARG:NH2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:444:C:H42	32:XA:490:G:H1	1.54	0.55
49:XR:56:THR:HB	49:XR:58:LEU:HD23	1.87	0.55
1:YA:1364:G:P	23:Y1:3:LYS:HG3	2.46	0.55
1:YA:2659:G:O2'	7:YH:175:LYS:HE2	2.06	0.55
1:RA:212:G:H2'	1:RA:213:A:O4'	2.07	0.55
49:XR:59:SER:OG	49:XR:62:GLU:HG2	2.06	0.55
1:YA:300:A:H2'	1:YA:334:C:H1'	1.87	0.55
16:YU:108:GLU:O	16:YU:112:ARG:HG2	2.06	0.55
19:RX:53:LYS:HB3	19:RX:82:GLN:HB3	1.87	0.55
32:XA:1030(A):C:N3	32:XA:1031:G:N2	2.54	0.55
32:XA:1047:G:OP1	45:YN:4:LYS:NZ	2.34	0.55
55:XY:108:GLU:HA	55:XY:170:GLY:HA2	1.89	0.55
1:YA:528:A:OP2	9:YN:114:ARG:NH1	2.39	0.55
33:QB:21:ARG:H	33:QB:21:ARG:CD	2.20	0.55
1:RA:2810:A:N6	1:RA:2891:G:O2'	2.34	0.55
1:RA:1800:C:OP2	3:RD:183:ARG:NH2	2.40	0.55
4:RE:170:LEU:HB3	4:RE:184:VAL:HG22	1.89	0.55
26:Y4:61:ARG:HH22	50:XS:9:VAL:HG21	1.71	0.55
5:YF:132:VAL:HG21	5:YF:163:VAL:HG22	1.89	0.55
7:YH:89:ILE:O	7:YH:129:THR:HG23	2.06	0.55
35:QD:13:ARG:NH1	35:QD:38:TYR:O	2.40	0.55
1:RA:1050:A:C2	1:RA:2751:G:C2	2.95	0.55
1:RA:588:U:H2'	1:RA:589:C:C6	2.41	0.55
6:RG:50:ALA:C	6:RG:52:ILE:H	2.10	0.55
12:YQ:45:GLN:N	12:YQ:45:GLN:OE1	2.37	0.55
32:QA:1187:G:H4'	40:QI:111:ARG:HH11	1.71	0.55
46:QO:74:ASP:OD2	46:QO:77:ARG:HG3	2.07	0.55
1:RA:250:G:P	30:R8:13:ARG:HH22	2.30	0.55
1:RA:1049:C:H2'	1:RA:1050:A:C8	2.42	0.55
1:RA:1688:U:O2	1:RA:1700:A:H5'	2.06	0.55
40:XI:53:VAL:C	40:XI:55:ALA:H	2.07	0.55
46:XO:74:ASP:OD2	46:XO:77:ARG:HG3	2.06	0.55
3:YD:69:ARG:NH2	3:YD:128:GLY:O	2.32	0.55
8:YI:130:TYR:HB3	8:YI:138:ILE:HB	1.88	0.55
19:YX:53:LYS:HB3	19:YX:82:GLN:HB3	1.88	0.55
8:RI:38:LEU:HD12	8:RI:38:LEU:H	1.72	0.55
11:RP:98:GLU:OE1	11:RP:102:ARG:NH1	2.30	0.55
53:XV:9:G:O2'	53:XV:10:G:N7	2.37	0.55
1:YA:2128:C:H5'	1:YA:2129:C:OP2	2.07	0.55
6:YG:11:TYR:HA	6:YG:15:VAL:HB	1.88	0.55
21:YZ:125:LEU:HB3	21:YZ:165:VAL:HG13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:QB:158:LEU:HG	33:QB:182:ILE:HD11	1.89	0.55
44:QM:3:ARG:HD2	44:QM:9:ILE:HG12	1.88	0.55
23:R1:64:ALA:HA	23:R1:67:ILE:HG13	1.89	0.55
1:RA:2142:C:H2'	1:RA:2143:C:C6	2.42	0.55
1:RA:84:A:H5''	20:RY:8:LYS:HE2	1.88	0.55
21:RZ:126:VAL:CG1	21:RZ:161:VAL:HG23	2.37	0.55
35:XD:150:GLU:HA	35:XD:153:ARG:HE	1.72	0.55
1:YA:1087:G:H1	1:YA:1102:C:N4	2.04	0.55
1:YA:607:U:OP1	5:YF:102:PRO:HA	2.07	0.55
32:XA:438:G:O2'	32:XA:494:U:O4	2.23	0.55
35:XD:13:ARG:NH1	35:XD:38:TYR:O	2.40	0.55
9:RN:94:HIS:HB3	9:RN:97:ARG:HD3	1.89	0.54
13:RR:67:LEU:HD13	13:RR:76:VAL:HG21	1.89	0.54
33:XB:84:GLU:HB3	33:XB:219:VAL:HG21	1.89	0.54
32:XA:922:G:H4'	36:XE:20:GLN:HA	1.89	0.54
39:XH:64:LYS:HG2	39:XH:79:VAL:HG21	1.88	0.54
34:XC:12:LEU:HD11	45:XN:51:GLY:HA2	1.89	0.54
23:Y1:64:ALA:HA	23:Y1:67:ILE:HG13	1.89	0.54
1:YA:82:G:N1	1:YA:103:A:OP2	2.35	0.54
1:YA:1075:C:H2'	1:YA:1076:C:H5'	1.90	0.54
1:YA:2189:U:H2'	1:YA:2190:G:C8	2.42	0.54
1:YA:276:A:H5''	1:YA:277:C:H5'	1.89	0.54
1:YA:747:U:O2	1:YA:2014:A:H1'	2.08	0.54
32:QA:1391:U:H2'	32:QA:1392:G:C8	2.42	0.54
46:QO:84:LYS:O	46:QO:84:LYS:HD3	2.06	0.54
1:RA:1721:G:H2'	1:RA:1740:G:O6	2.07	0.54
1:RA:764:A:H5'	3:RD:210:GLY:HA2	1.88	0.54
5:RF:140:LEU:HD21	5:RF:170:LEU:HD11	1.88	0.54
9:RN:4:TYR:CD2	16:RU:100:VAL:HG11	2.42	0.54
20:RY:87:LYS:HB3	20:RY:95:LYS:HD3	1.90	0.54
33:XB:44:LEU:H	33:XB:44:LEU:HD22	1.73	0.54
1:YA:2127:G:H2'	1:YA:2128:C:O4'	2.07	0.54
1:YA:2142:C:H2'	1:YA:2143:C:C6	2.41	0.54
39:QH:10:LEU:HD22	39:QH:83:ILE:HD11	1.89	0.54
50:QS:22:LEU:HD22	50:QS:28:LYS:HA	1.89	0.54
1:RA:1086:A:OP1	1:RA:1104:C:O2'	2.24	0.54
1:RA:2110:G:H5''	1:RA:2111:C:H5	1.73	0.54
1:RA:2128:C:H5'	1:RA:2129:C:OP2	2.07	0.54
32:XA:406:G:H5'	35:XD:5:ILE:HD11	1.88	0.54
32:XA:503:C:OP2	43:XL:116:SER:HB3	2.07	0.54
32:XA:632:A:H5'	32:XA:633:G:OP2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:XH:12:ARG:HD2	39:XH:26:VAL:HG12	1.89	0.54
1:YA:1359:A:H61	1:YA:1372:U:H3	1.54	0.54
15:YT:65:LYS:HE3	15:YT:67:SER:HB2	1.90	0.54
32:QA:324:G:N1	32:QA:327:A:OP2	2.40	0.54
32:QA:38:G:N2	32:QA:397:A:H5'	2.21	0.54
32:QA:396:G:O2'	32:QA:398:C:OP1	2.15	0.54
32:QA:261:U:OP2	51:QT:79:ARG:NH2	2.40	0.54
1:RA:2189:U:H2'	1:RA:2190:G:C8	2.42	0.54
1:RA:2445:G:OP1	5:RF:74:ARG:NH2	2.38	0.54
1:RA:1803:A:O2'	3:RD:259:THR:HG21	2.07	0.54
1:YA:1032:A:H4'	31:Y9:16:VAL:HG11	1.88	0.54
1:YA:2099:U:H3	1:YA:2190:G:H1	1.54	0.54
1:YA:2327:A:H2'	1:YA:2328:A:C8	2.42	0.54
1:YA:265:A:N1	1:YA:427:U:O2'	2.33	0.54
3:YD:30:GLU:HG3	3:YD:94:LEU:HD21	1.90	0.54
15:YT:95:ARG:HG2	15:YT:95:ARG:HH11	1.73	0.54
32:QA:921:U:O2'	36:QE:19:MET:O	2.12	0.54
19:RX:5:TYR:O	24:R2:36:ARG:NH2	2.39	0.54
1:RA:747:U:O2	1:RA:2014:A:H1'	2.08	0.54
32:XA:1510:U:H2'	32:XA:1511:G:C8	2.43	0.54
1:YA:1184:G:OP1	25:Y3:30:ARG:HD2	2.07	0.54
6:YG:113:ARG:HH21	26:Y4:33:VAL:HG12	1.71	0.54
1:YA:1341:U:OP1	1:YA:1397:U:N3	2.33	0.54
3:YD:10:THR:OG1	3:YD:13:ARG:HG2	2.08	0.54
1:YA:601:C:OP1	5:YF:108:LYS:HE3	2.07	0.54
13:RR:36:THR:HG22	13:RR:37:THR:H	1.73	0.54
32:XA:1157:A:H5'	32:XA:1158:C:C6	2.43	0.54
41:XJ:37:PRO:HA	41:XJ:72:VAL:HG12	1.89	0.54
41:XJ:57:LYS:HE2	41:XJ:60:ARG:NH2	2.23	0.54
1:YA:1250:G:N7	11:YP:18:ARG:NH2	2.55	0.54
32:QA:1003:G:N2	32:QA:1004:A:H1'	2.23	0.54
32:QA:1442(A):G:N3	32:QA:1442(A):G:H2'	2.23	0.54
32:QA:1055:A:O2'	34:QC:161:GLU:O	2.18	0.54
35:QD:81:GLU:O	35:QD:85:LYS:HB2	2.08	0.54
32:QA:1279:A:H5''	41:QJ:7:LYS:NZ	2.23	0.54
37:QF:97:PHE:HB2	49:QR:32:ARG:HD2	1.90	0.54
25:R3:8:LEU:HD12	25:R3:31:LEU:HA	1.89	0.54
26:R4:41:PRO:HG3	26:R4:49:PHE:CE1	2.42	0.54
1:RA:1036:G:H1	1:RA:1119:C:H42	1.55	0.54
1:RA:2336:A:H61	22:R0:43:THR:HG22	1.73	0.54
32:XA:1030(B):G:H2'	32:XA:1030(C):C:H5''	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:1131:G:H2'	32:XA:1132:C:C6	2.43	0.54
1:YA:1049:C:O2	1:YA:1113:U:H4'	2.07	0.54
1:YA:1101:U:H2'	1:YA:1102:C:C6	2.43	0.54
1:YA:2461:C:H2'	1:YA:2462:U:C6	2.43	0.54
17:YV:43:GLU:N	17:YV:43:GLU:OE2	2.41	0.54
40:QI:49:PRO:HD2	40:QI:81:ILE:HD11	1.89	0.54
1:RA:2354:G:H21	22:R0:36:ILE:HD11	1.73	0.54
25:R3:3:ARG:NH1	25:R3:60:GLU:OE2	2.36	0.54
1:RA:2152:G:H2'	1:RA:2153:G:C8	2.42	0.54
1:RA:2507:C:O4'	55:QY:238:ASN:HB3	2.08	0.54
3:RD:108:PRO:HD2	3:RD:111:LEU:HG	1.88	0.54
4:RE:73:GLU:CD	4:RE:73:GLU:H	2.10	0.54
9:RN:128:HIS:O	9:RN:131:GLN:NE2	2.40	0.54
32:XA:1239:A:H62	32:XA:1299:A:H62	1.56	0.54
32:XA:692:U:O2'	32:XA:694:A:N7	2.27	0.54
35:XD:173:TRP:CD1	35:XD:189:PRO:HG3	2.42	0.54
45:XN:4:LYS:HG3	45:XN:7:ILE:HD11	1.90	0.54
51:XT:60:GLU:HG3	51:XT:81:LYS:HD2	1.89	0.54
1:YA:2262:U:H4'	1:YA:2328:A:C2	2.42	0.54
5:YF:167:ALA:HB1	5:YF:173:VAL:HG11	1.88	0.54
5:YF:184:TYR:O	5:YF:188:ARG:HG3	2.07	0.54
40:QI:16:ARG:HD3	40:QI:64:THR:HG21	1.89	0.54
55:QY:106:ASP:HA	55:QY:109:ARG:HD3	1.90	0.54
4:RE:78:LEU:O	4:RE:79:ARG:NH1	2.36	0.54
6:RG:116:ASP:OD1	44:QM:68:GLY:HA3	2.07	0.54
9:RN:46:VAL:HG23	9:RN:48:MET:HG2	1.90	0.54
32:XA:1151:A:O2'	32:XA:1152:A:H8	1.90	0.54
34:XC:150:LYS:HG3	34:XC:169:ALA:HB2	1.90	0.54
32:XA:1106:G:H5'	34:XC:172:ARG:HG2	1.89	0.54
38:XG:132:GLY:O	38:XG:136:LYS:HG2	2.06	0.54
32:XA:452:A:N3	47:XP:72:ARG:NH1	2.56	0.54
1:YA:517:C:OP1	27:Y5:16:ARG:NH2	2.41	0.54
30:Y8:63:PRO:HG2	30:Y8:64:TYR:CE2	2.42	0.54
6:YG:18:GLU:OE1	6:YG:21:ARG:NH2	2.40	0.54
51:QT:47:GLY:HA2	51:QT:48:LYS:HB2	1.88	0.54
1:RA:2115:G:H21	1:RA:2171:A:H61	1.55	0.54
32:XA:1015:A:H2'	32:XA:1016:A:C8	2.43	0.54
32:XA:979:C:H42	45:XN:18:VAL:HG12	1.73	0.54
33:XB:54:THR:HG21	33:XB:201:ILE:HD11	1.89	0.54
44:XM:95:GLY:O	44:XM:110:ARG:HG3	2.08	0.54
1:YA:774:A:N3	1:YA:774:A:H2'	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:YG:11:TYR:OH	6:YG:33:ARG:HG3	2.08	0.54
55:QY:245:ARG:HB2	55:QY:256:GLU:HB3	1.90	0.53
5:RF:178:PRO:HB2	5:RF:201:VAL:CG2	2.38	0.53
8:RI:130:TYR:HB3	8:RI:138:ILE:HB	1.89	0.53
35:XD:173:TRP:CD1	35:XD:174:LEU:HG	2.43	0.53
55:XY:119:THR:H	55:XY:302:ASP:CG	2.11	0.53
55:XY:177:PHE:HB3	55:XY:321:ARG:HH22	1.74	0.53
32:QA:411:A:OP2	35:QD:25:ARG:NH2	2.41	0.53
33:QB:15:VAL:HG23	33:QB:209:ARG:HB3	1.89	0.53
42:QK:99:GLN:HG2	42:QK:105:VAL:HG21	1.90	0.53
1:RA:1029:A:OP1	12:RQ:128:LYS:NZ	2.40	0.53
1:RA:2502:G:H5''	1:RA:2503:2MA:H5''	1.89	0.53
5:RF:53:THR:HG22	5:RF:55:GLY:H	1.74	0.53
13:RR:24:GLN:HB3	13:RR:44:LEU:HD11	1.90	0.53
32:XA:324:G:N1	32:XA:327:A:OP2	2.40	0.53
36:XE:57:LYS:HG2	36:XE:61:TYR:HE2	1.72	0.53
41:XJ:5:ARG:N	41:XJ:99:LYS:O	2.40	0.53
32:XA:1492:A:OP2	43:XL:47:LYS:HG3	2.09	0.53
30:Y8:6:THR:HG23	30:Y8:64:TYR:HD2	1.73	0.53
1:YA:2022:U:O2'	1:YA:2617:C:H5'	2.08	0.53
1:YA:998:C:OP2	16:YU:92:ARG:NH2	2.41	0.53
19:YX:65:ARG:HB3	19:YX:70:LEU:HD23	1.89	0.53
33:QB:76:GLN:NE2	33:QB:206:ASP:OD1	2.42	0.53
35:QD:15:GLU:HG3	35:QD:63:LYS:HD3	1.91	0.53
36:QE:110:LEU:HD13	36:QE:118:ILE:HG21	1.89	0.53
39:QH:86:ILE:HG13	39:QH:133:LEU:HD22	1.90	0.53
1:RA:185:U:H4'	1:RA:218:A:H4'	1.91	0.53
32:XA:404:U:C5'	35:XD:122:ARG:HD3	2.38	0.53
1:YA:299:A:N1	1:YA:322:A:O2'	2.37	0.53
32:QA:1068:G:H8	32:QA:1068:G:OP2	1.91	0.53
32:QA:355:C:O2'	32:QA:388:G:N3	2.29	0.53
46:QO:17:ARG:HD3	46:QO:26:GLU:OE1	2.09	0.53
1:RA:2022:U:O2'	1:RA:2617:C:H5'	2.08	0.53
32:XA:1402:4OC:HM22	32:XA:1403:C:H5'	1.90	0.53
32:XA:975:A:N1	41:XJ:48:THR:HB	2.24	0.53
40:XI:4:TYR:HB2	40:XI:19:LEU:HB2	1.91	0.53
40:XI:22:GLY:HA3	40:XI:60:ASP:OD1	2.07	0.53
32:XA:707:C:OP1	42:XK:85:ARG:NH1	2.41	0.53
52:XU:5:ASP:O	52:XU:11:GLY:HA3	2.09	0.53
1:YA:2313:C:H2'	1:YA:2314:C:C6	2.43	0.53
8:YI:114:LEU:HD12	8:YI:116:LEU:HB2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:YT:39:ARG:HH22	32:XA:344:A:H4'	1.73	0.53
32:QA:1030(A):C:N3	32:QA:1031:G:N2	2.56	0.53
1:RA:1031:G:O2'	31:R9:7:VAL:O	2.24	0.53
6:RG:77:ILE:HG21	6:RG:80:PHE:CD2	2.43	0.53
32:XA:17:U:O2'	32:XA:1079:G:H1'	2.07	0.53
33:XB:69:LEU:HB3	33:XB:162:ILE:HG22	1.90	0.53
32:XA:942:G:H21	40:XI:124:GLN:NE2	2.05	0.53
1:YA:1048:A:N1	1:YA:1112:G:O2'	2.30	0.53
1:YA:1471:A:OP2	1:YA:1519:G:N2	2.38	0.53
1:YA:2478:A:OP2	31:Y9:2:LYS:NZ	2.22	0.53
1:RA:1075:C:H2'	1:RA:1076:C:H5'	1.89	0.53
1:RA:1087:G:N2	1:RA:1102:C:N3	2.44	0.53
1:RA:1824:G:O3'	3:RD:249:PRO:HD3	2.09	0.53
1:RA:2526:G:H5'	1:RA:2742:C:O2'	2.09	0.53
32:XA:1006:C:H2'	32:XA:1007:C:C6	2.43	0.53
41:XJ:61:GLU:OE1	45:XN:58:LYS:NZ	2.38	0.53
55:XY:184:VAL:HG23	55:XY:200:ALA:HA	1.90	0.53
1:YA:1991:U:H2'	1:YA:1992:G:H5''	1.91	0.53
32:QA:1158:C:H5	32:QA:1181:G:H1	1.55	0.53
44:QM:34:LEU:HD13	44:QM:41:PRO:HA	1.89	0.53
1:RA:2756:U:H5''	31:R9:19:ARG:HA	1.91	0.53
1:RA:1171:G:N2	1:RA:1178:C:O2	2.42	0.53
1:RA:1889:A:H2'	1:RA:1890:A:C8	2.44	0.53
1:RA:2311:A:C6	6:RG:80:PHE:HB3	2.44	0.53
32:XA:1029:C:N4	32:XA:1030(A):C:H41	2.07	0.53
1:YA:1101:U:H2'	1:YA:1102:C:H6	1.73	0.53
15:YT:108:ARG:NH1	32:XA:1464:G:OP1	2.41	0.53
53:QV:19:G:H5'	53:QV:20:U:C5	2.44	0.53
55:QY:328:ARG:HH22	55:QY:340:LEU:N	2.06	0.53
1:RA:1062:G:N7	1:RA:1070:A:H1'	2.24	0.53
32:XA:1157:A:H4'	32:XA:1158:C:O5'	2.09	0.53
38:XG:113:GLU:HG3	38:XG:118:VAL:HG12	1.91	0.53
1:YA:2171:A:H4'	1:YA:2172:U:OP1	2.07	0.53
1:YA:2805:G:H2'	1:YA:2807:G:C8	2.43	0.53
13:YR:36:THR:HG22	13:YR:37:THR:H	1.73	0.53
32:QA:1412:C:H2'	32:QA:1413:A:C8	2.44	0.53
32:XA:737:A:H2'	32:XA:738:C:C6	2.44	0.53
33:XB:71:VAL:HG12	33:XB:93:VAL:HG22	1.91	0.53
40:XI:26:VAL:HA	40:XI:61:ALA:O	2.09	0.53
1:YA:2345:G:H1'	1:YA:2382:G:H5'	1.90	0.53
4:YE:111:ARG:HG3	4:YE:160:TYR:CD2	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:YF:184:TYR:CE2	5:YF:188:ARG:HD2	2.43	0.53
32:QA:1033:G:H2'	32:QA:1034:G:H8	1.74	0.53
39:QH:86:ILE:HG21	39:QH:133:LEU:HD13	1.91	0.53
22:R0:27:GLU:HG3	22:R0:68:GLU:HA	1.91	0.53
32:XA:1347:G:N2	32:XA:1373:G:H2'	2.24	0.53
24:Y2:16:LEU:O	24:Y2:67:LYS:NZ	2.41	0.53
1:YA:1062:G:N7	1:YA:1070:A:H1'	2.24	0.53
12:YQ:7:MET:HG3	12:YQ:9:TYR:O	2.09	0.53
17:YV:29:PRO:HA	17:YV:61:VAL:HG23	1.91	0.53
40:QI:33:PHE:HE1	40:QI:43:ALA:HB1	1.74	0.52
1:RA:273(A):G:H4'	1:RA:273(B):U:H5''	1.90	0.52
1:RA:300:A:H2'	1:RA:334:C:H1'	1.90	0.52
44:XM:54:VAL:HA	44:XM:57:ARG:HB3	1.91	0.52
26:Y4:53:GLU:CD	26:Y4:53:GLU:H	2.13	0.52
1:YA:1378:A:OP1	29:Y7:10:ARG:NH2	2.42	0.52
1:YA:1406:U:H2'	1:YA:1407:C:C6	2.44	0.52
1:YA:2893:G:H5''	1:YA:2894:G:O4'	2.09	0.52
1:YA:321:G:OP2	5:YF:135:LYS:HD3	2.09	0.52
11:YP:100:LEU:HD12	11:YP:112:LEU:HD11	1.90	0.52
20:YY:82:PRO:O	20:YY:101:LYS:NZ	2.27	0.52
44:QM:3:ARG:HG3	44:QM:4:ILE:N	2.23	0.52
1:RA:2836:U:H2'	1:RA:2837:G:C8	2.44	0.52
1:RA:922:U:H2'	1:RA:923:C:C6	2.44	0.52
19:RX:11:PRO:HB3	19:RX:92:LEU:HD11	1.91	0.52
36:XE:12:LEU:HB3	36:XE:31:LEU:HB2	1.91	0.52
41:XJ:9:ARG:NH2	41:XJ:95:GLU:OE1	2.42	0.52
1:YA:2659:G:H4'	7:YH:175:LYS:HD3	1.91	0.52
17:YV:52:VAL:HG23	17:YV:55:ALA:HB3	1.90	0.52
32:QA:376:G:H5''	47:QP:5:ARG:HD3	1.91	0.52
49:QR:33:ASP:OD2	49:QR:36:ASN:HB2	2.10	0.52
34:XC:164:ARG:NH1	34:XC:166:GLU:OE1	2.42	0.52
32:XA:1129:C:OP1	40:XI:16:ARG:NH1	2.43	0.52
1:YA:1110:G:H1'	1:YA:1111:A:C8	2.44	0.52
1:YA:2206:G:H5''	1:YA:2207:G:N7	2.24	0.52
5:YF:103:LYS:O	5:YF:106:ARG:HG2	2.10	0.52
7:YH:143:GLN:NE2	7:YH:147:ASN:OD1	2.42	0.52
17:YV:72:VAL:HG13	17:YV:85:LYS:HB3	1.90	0.52
32:QA:176:C:H2'	32:QA:177:C:C6	2.44	0.52
26:R4:59:PHE:HE1	50:QS:64:GLU:HA	1.75	0.52
51:QT:10:LEU:HB3	51:QT:12:ALA:H	1.74	0.52
1:RA:1084:A:H3'	1:RA:1085:A:C4'	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:RX:2:LYS:NZ	19:RX:38:GLU:OE2	2.23	0.52
32:XA:977:A:N6	32:XA:1224:G:OP1	2.38	0.52
33:XB:16:HIS:HB2	33:XB:204:ASN:HB3	1.90	0.52
40:XI:24:GLY:HA2	40:XI:59:PHE:O	2.10	0.52
55:XY:174:ARG:NH1	55:XY:338:ASP:OD1	2.43	0.52
1:YA:1300:U:H4'	1:YA:1301:A:H5'	1.92	0.52
1:YA:2104:G:N2	1:YA:2105:C:C4	2.77	0.52
1:YA:922:U:H2'	1:YA:923:C:C6	2.44	0.52
10:YO:80:ASP:OD1	15:YT:64:ARG:NH2	2.40	0.52
32:QA:410:G:OP1	35:QD:30:LYS:NZ	2.32	0.52
34:QC:148:GLY:HA3	34:QC:172:ARG:O	2.09	0.52
1:RA:2206:G:H8	1:RA:2207:G:N7	2.08	0.52
1:RA:272(E):U:H2'	1:RA:272(F):C:C6	2.44	0.52
1:RA:514:A:N3	1:RA:581:C:O2'	2.40	0.52
32:XA:457:C:H2'	32:XA:458:C:H6	1.75	0.52
35:XD:15:GLU:HG3	35:XD:63:LYS:HD3	1.91	0.52
1:YA:1067:A:H4'	1:YA:1068:G:OP2	2.09	0.52
6:YG:36:LYS:HE2	6:YG:95:ARG:NH1	2.24	0.52
1:YA:2752:C:OP2	7:YH:4:ILE:HD11	2.09	0.52
9:YN:62:VAL:CG1	9:YN:66:LYS:HB2	2.40	0.52
13:YR:67:LEU:HD13	13:YR:76:VAL:HG21	1.92	0.52
21:YZ:72:ARG:CG	21:YZ:89:PHE:HB2	2.39	0.52
32:QA:328:C:H4'	32:QA:329:A:H5'	1.92	0.52
33:QB:82:ARG:HG3	33:QB:92:TYR:CZ	2.43	0.52
34:QC:22:TRP:CZ2	45:QN:54:PRO:HG2	2.44	0.52
11:RP:63:PRO:HD3	30:R8:27:THR:HG22	1.91	0.52
1:RA:1038:C:N4	1:RA:1117:G:H1	2.06	0.52
1:RA:1165:U:H2'	1:RA:1166:C:C6	2.45	0.52
14:RS:14:VAL:O	14:RS:18:ILE:HG12	2.10	0.52
14:RS:15:ARG:O	14:RS:19:LYS:HG2	2.08	0.52
32:XA:1002:G:N3	32:XA:1003:G:H8	2.07	0.52
32:XA:841:U:OP1	32:XA:841:U:H6	1.92	0.52
40:XI:8:GLY:HA3	40:XI:76:ALA:O	2.09	0.52
44:XM:6:GLY:HA3	44:XM:67:GLU:HG3	1.92	0.52
46:XO:17:ARG:HD3	46:XO:26:GLU:OE1	2.10	0.52
49:XR:32:ARG:HA	49:XR:69:THR:HG21	1.92	0.52
1:YA:154(B):C:H42	1:YA:171:G:H1	1.57	0.52
1:YA:212:G:H2'	1:YA:213:A:O4'	2.10	0.52
2:YB:14:U:OP2	2:YB:70:C:O2'	2.21	0.52
32:QA:457:C:H2'	32:QA:458:C:H6	1.74	0.52
41:QJ:8:LEU:HB2	41:QJ:70:ARG:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:QO:25:THR:HG21	46:QO:70:LEU:HB2	1.91	0.52
1:RA:2023:G:H5'	1:RA:2617:C:H4'	1.91	0.52
1:RA:586:A:N1	1:RA:809:G:O2'	2.38	0.52
18:RW:23:LEU:HD11	27:R5:25:LEU:HB2	1.92	0.52
32:XA:1456:G:O3'	51:XT:39:LYS:NZ	2.43	0.52
1:YA:2756:U:OP2	31:Y9:19:ARG:NE	2.30	0.52
1:YA:637:A:OP1	11:YP:133:SER:OG	2.24	0.52
32:QA:1360:A:OP2	45:QN:35:ARG:NH2	2.42	0.52
32:QA:1479:C:H2'	32:QA:1480:G:H8	1.75	0.52
36:QE:12:LEU:HB3	36:QE:31:LEU:HB2	1.92	0.52
1:RA:1796:U:H2'	1:RA:1797:C:C6	2.45	0.52
1:YA:1310:G:OP2	29:Y7:9:ARG:HD2	2.09	0.52
30:Y8:23:VAL:HG13	30:Y8:47:LYS:HB3	1.92	0.52
1:YA:1019:U:OP1	1:YA:1035:U:O2'	2.23	0.52
32:QA:1479:C:H2'	32:QA:1480:G:C8	2.45	0.52
32:QA:56:U:H2'	32:QA:57:G:C8	2.44	0.52
40:QI:121:ARG:NH1	40:QI:122:ALA:O	2.43	0.52
43:QL:60:LEU:HD21	43:QL:66:VAL:HG22	1.91	0.52
55:QY:326:LEU:CD1	55:QY:328:ARG:HH21	2.22	0.52
1:RA:1530:C:HO2'	1:RA:1531:C:P	2.32	0.52
1:RA:8:A:H2'	1:RA:9:U:C6	2.44	0.52
13:RR:21:TYR:OH	13:RR:43:GLU:HG2	2.09	0.52
32:XA:539:A:OP2	43:XL:115:LYS:NZ	2.43	0.52
44:XM:19:LEU:HD21	44:XM:56:LEU:HD21	1.91	0.52
1:YA:1411:C:H2'	1:YA:1412:A:C8	2.45	0.52
1:YA:2602:A:N1	55:XY:242:SER:OG	2.42	0.52
5:YF:157:VAL:HB	5:YF:194:MET:HG2	1.92	0.52
7:YH:115:VAL:HG11	7:YH:148:ILE:HD11	1.91	0.52
32:QA:1216:G:OP1	45:QN:2:ALA:HA	2.10	0.52
53:QV:9:G:O2'	53:QV:10:G:N7	2.41	0.52
1:RA:2165:G:H2'	1:RA:2166:G:O4'	2.09	0.52
18:RW:4:LYS:HG2	18:RW:5:ALA:N	2.24	0.52
32:XA:1391:U:H2'	32:XA:1392:G:C8	2.45	0.52
51:XT:57:ARG:HH12	51:XT:100:ILE:HB	1.75	0.52
1:YA:2165:G:H2'	1:YA:2166:G:O4'	2.10	0.52
1:YA:2319:G:H22	14:YS:3:ARG:CZ	2.23	0.52
16:YU:86:ALA:O	17:YV:49:THR:HG23	2.10	0.52
32:QA:1060:C:C5	34:QC:2:GLY:HA3	2.45	0.51
32:QA:1240:U:C2	38:QG:32:ARG:HD3	2.45	0.51
35:QD:196:LEU:HD12	35:QD:196:LEU:H	1.76	0.51
1:RA:2284:C:OP1	28:R6:5:VAL:HG13	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1101:U:H2'	1:RA:1102:C:H6	1.75	0.51
1:RA:1991:U:H2'	1:RA:1992:G:H5''	1.91	0.51
1:RA:2099:U:H3	1:RA:2190:G:H1	1.57	0.51
1:RA:2758:A:C2	7:RH:71:LEU:HD21	2.45	0.51
21:RZ:129:SER:HB3	21:RZ:132:ASN:HB2	1.91	0.51
21:RZ:126:VAL:HG11	21:RZ:161:VAL:HG23	1.92	0.51
32:XA:1218:C:H2'	32:XA:1219:U:C6	2.45	0.51
55:XY:229:SER:OG	55:XY:242:SER:OG	2.27	0.51
27:Y5:40:LYS:NZ	27:Y5:44:THR:O	2.25	0.51
32:QA:109:A:C6	32:QA:326:G:C6	2.99	0.51
33:QB:84:GLU:HB3	33:QB:219:VAL:HG21	1.92	0.51
34:QC:58:GLU:HB3	41:QJ:92:THR:HG21	1.92	0.51
1:RA:2105:C:N4	1:RA:2106:G:O6	2.42	0.51
3:RD:106:ILE:O	3:RD:108:PRO:HD3	2.11	0.51
5:RF:101:LEU:O	5:RF:106:ARG:NH1	2.42	0.51
32:XA:1513:A:H2'	32:XA:1514:C:C6	2.45	0.51
55:XY:116:ARG:HH11	55:XY:161:GLU:HG3	1.75	0.51
22:Y0:8:GLY:N	53:XV:2:G:H5'	2.25	0.51
6:YG:56:ALA:HA	6:YG:153:ARG:NH2	2.25	0.51
18:YW:23:LEU:O	18:YW:27:LYS:NZ	2.44	0.51
32:QA:164:U:H2'	32:QA:165:C:C6	2.45	0.51
1:RA:833:U:O2	11:RP:55:ARG:NH2	2.38	0.51
1:RA:878:A:H3'	1:RA:879:G:H8	1.74	0.51
9:RN:62:VAL:CG1	9:RN:66:LYS:HB2	2.40	0.51
1:RA:956:G:P	12:RQ:14:ARG:HH22	2.33	0.51
19:RX:5:TYR:HB3	24:R2:33:MET:HB2	1.93	0.51
37:XF:95:GLU:O	49:XR:32:ARG:NH2	2.43	0.51
43:XL:28:LYS:N	43:XL:29:GLY:HA2	2.24	0.51
1:YA:1029:A:H2	1:YA:2465:C:H2'	1.74	0.51
1:YA:218:A:C2	1:YA:235:U:H4'	2.45	0.51
10:YO:2:ILE:HB	10:YO:33:ALA:HB3	1.91	0.51
34:QC:32:LEU:HD22	34:QC:59:ARG:NH1	2.26	0.51
32:XA:404:U:H5''	35:XD:122:ARG:HD3	1.90	0.51
32:XA:660:G:H1	32:XA:745:C:H42	1.58	0.51
33:XB:96:ARG:HD2	33:XB:98:LEU:HD23	1.91	0.51
34:XC:8:ILE:HD12	34:XC:16:ARG:HD3	1.93	0.51
32:XA:545:C:OP1	35:XD:61:LYS:NZ	2.44	0.51
44:XM:81:LEU:HD13	44:XM:88:ARG:HG2	1.92	0.51
47:XP:23:ASP:OD1	47:XP:25:ARG:HD3	2.10	0.51
1:YA:1721:G:H8	1:YA:1741:A:H62	1.58	0.51
1:YA:1796:U:H2'	1:YA:1797:C:C6	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:YF:103:LYS:HA	5:YF:106:ARG:HD3	1.91	0.51
6:YG:97:ASP:HA	6:YG:100:TRP:HD1	1.75	0.51
28:R6:6:ARG:NH1	28:R6:26:ASN:HB2	2.26	0.51
1:RA:1084:A:H3'	1:RA:1085:A:H4'	1.92	0.51
1:RA:1453:U:OP1	13:RR:77:ARG:NH1	2.39	0.51
1:RA:774:A:H2'	1:RA:774:A:N3	2.26	0.51
21:RZ:92:SER:O	21:RZ:130:PRO:HG2	2.10	0.51
32:XA:1309:G:OP1	44:XM:88:ARG:HD2	2.09	0.51
32:XA:501:C:H2'	32:XA:502:G:C8	2.45	0.51
35:XD:70:ILE:HD11	35:XD:74:GLN:HB3	1.93	0.51
36:XE:57:LYS:HG2	36:XE:61:TYR:CE2	2.44	0.51
46:XO:39:LEU:HD13	46:XO:56:LEU:HB2	1.92	0.51
1:YA:2573:C:H41	55:XY:239:THR:HA	1.72	0.51
23:Y1:3:LYS:HB2	23:Y1:61:ARG:NH1	2.26	0.51
1:YA:250:G:P	30:Y8:13:ARG:HH22	2.33	0.51
1:YA:2168:G:H22	1:YA:2171:A:H2'	1.75	0.51
32:QA:1402:4OC:HM22	32:QA:1403:C:H5'	1.92	0.51
34:QC:179:ARG:NH1	34:QC:206:GLU:OE1	2.44	0.51
41:QJ:38:ILE:HG12	41:QJ:71:LEU:HB3	1.91	0.51
1:RA:1756:G:H4'	1:RA:1758:G:O4'	2.11	0.51
1:RA:587:C:P	11:RP:21:ARG:HH22	2.34	0.51
4:RE:105:THR:OG1	4:RE:199:ARG:NH2	2.44	0.51
20:RY:13:VAL:HB	20:RY:72:VAL:HG13	1.93	0.51
32:XA:1346:A:OP1	40:XI:120:ARG:NH1	2.38	0.51
32:XA:841:U:C5	32:XA:848:C:H1'	2.46	0.51
32:XA:858:G:O6	32:XA:869:G:H3'	2.11	0.51
36:XE:6:PHE:HB2	36:XE:34:VAL:HG13	1.91	0.51
1:YA:1069:A:H5'	1:YA:1096:A:H5'	1.93	0.51
1:YA:273(A):G:H4'	1:YA:273(B):U:H5''	1.91	0.51
6:YG:5:VAL:HG12	26:Y4:25:TYR:CE1	2.45	0.51
32:QA:1101:A:H4'	32:QA:1102:A:O5'	2.10	0.51
32:QA:1278:U:H5''	32:QA:1279:A:H5'	1.92	0.51
32:QA:946:A:H2'	32:QA:947:G:C8	2.46	0.51
35:QD:108:LEU:HB3	35:QD:110:PHE:CE1	2.46	0.51
50:QS:41:VAL:HG22	50:QS:42:PRO:HD2	1.93	0.51
28:R6:13:CYS:SG	28:R6:47:THR:HG21	2.51	0.51
1:RA:1019:U:OP1	1:RA:1035:U:O2'	2.23	0.51
1:RA:2698:U:H2'	1:RA:2699:C:C6	2.46	0.51
36:XE:144:THR:H	36:XE:147:ASP:HB2	1.76	0.51
32:XA:229:U:O2'	47:XP:23:ASP:OD2	2.28	0.51
1:YA:2134:A:H8	1:YA:2156:G:H21	1.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2683:C:OP1	15:YT:53:ARG:NH2	2.44	0.51
7:YH:55:PRO:HG2	7:YH:61:HIS:CE1	2.45	0.51
20:YY:38:ILE:HD11	20:YY:66:PRO:HG3	1.92	0.51
38:QG:111:ARG:NH1	38:QG:113:GLU:OE1	2.43	0.51
32:XA:1304:G:OP1	52:XU:2:GLY:N	2.43	0.51
32:XA:926:G:H22	54:XX:16:A:P	2.33	0.51
55:XY:316:ARG:NH2	55:XY:327:TYR:OH	2.43	0.51
26:Y4:15:ILE:HD12	26:Y4:21:VAL:HG22	1.93	0.51
1:YA:2206:G:H8	1:YA:2207:G:N7	2.09	0.51
1:YA:2698:U:H2'	1:YA:2699:C:C6	2.45	0.51
32:QA:1227:A:OP1	50:QS:80:TYR:OH	2.24	0.51
32:QA:189(L):U:H2'	32:QA:189(M):G:H8	1.76	0.51
32:QA:189(L):U:H2'	32:QA:189(M):G:C8	2.46	0.51
30:R8:62:LEU:HB3	30:R8:65:GLU:HG2	1.92	0.51
1:RA:1053:C:O2'	1:RA:1054:A:O4'	2.27	0.51
8:RI:133:HIS:ND1	8:RI:134:PRO:O	2.44	0.51
1:YA:61:G:H5'	24:Y2:50:ILE:HG21	1.93	0.51
1:YA:1778:U:H2'	1:YA:1784:A:N6	2.26	0.51
1:YA:2023:G:H5'	1:YA:2617:C:H4'	1.93	0.51
32:QA:186:C:H2'	32:QA:187:C:C6	2.45	0.51
41:QJ:37:PRO:HA	41:QJ:72:VAL:HG12	1.92	0.51
1:RA:954:G:O2'	1:RA:2274:A:N1	2.40	0.51
1:RA:2334:G:H5'	14:RS:9:ARG:HG2	1.93	0.51
6:RG:50:ALA:O	6:RG:52:ILE:N	2.44	0.51
12:RQ:14:ARG:HG2	12:RQ:41:TRP:HH2	1.76	0.51
19:RX:60:ARG:HH22	29:R7:47:ARG:HH22	1.57	0.51
32:XA:1118:C:H1'	32:XA:1179:A:C4	2.46	0.51
1:YA:1593:G:H2'	1:YA:1594:G:C8	2.46	0.51
1:YA:489:G:N7	18:YW:49:LYS:NZ	2.58	0.51
7:YH:28:GLY:HA3	7:YH:79:VAL:HB	1.92	0.51
32:QA:368:U:O4	8:YI:82:ARG:HD2	2.11	0.51
1:YA:300:A:OP1	20:YY:86:ARG:NH2	2.44	0.51
32:QA:1347:G:H5'	40:QI:107:ARG:HB3	1.93	0.50
32:QA:1510:U:H2'	32:QA:1511:G:C8	2.45	0.50
32:QA:881:G:P	43:QL:12:ARG:HH22	2.33	0.50
53:QV:51:C:H2'	53:QV:52:G:O4'	2.11	0.50
1:RA:321:G:H5'	5:RF:134:GLY:O	2.10	0.50
1:RA:784:A:C6	3:RD:229:VAL:HG11	2.45	0.50
5:RF:12:LEU:HD13	5:RF:124:LEU:HD11	1.93	0.50
32:XA:921:U:O2'	36:XE:19:MET:O	2.19	0.50
1:YA:1932:A:H2'	1:YA:1933:G:O4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:YG:66:GLN:HB3	6:YG:92:VAL:HG21	1.91	0.50
32:QA:441:A:H3'	32:QA:442:C:C6	2.45	0.50
32:QA:973:G:H3'	32:QA:974:A:H5''	1.93	0.50
1:RA:1667:G:O2'	1:RA:1991:U:O4	2.23	0.50
32:XA:689:C:OP1	42:XK:27:ASN:ND2	2.38	0.50
47:XP:20:VAL:HG21	47:XP:32:TYR:CG	2.46	0.50
30:Y8:23:VAL:HG11	30:Y8:47:LYS:HD3	1.93	0.50
1:YA:616:G:H5'	5:YF:205:ARG:HD2	1.93	0.50
11:YP:100:LEU:HD22	11:YP:105:LEU:HD12	1.91	0.50
32:QA:171:A:H2'	32:QA:172:A:C8	2.47	0.50
32:QA:454:C:OP2	32:QA:455:C:N4	2.39	0.50
32:QA:629:G:H2'	32:QA:630:G:O4'	2.11	0.50
44:QM:19:LEU:HD21	44:QM:56:LEU:HD21	1.93	0.50
30:R8:23:VAL:HG11	30:R8:47:LYS:HD3	1.92	0.50
1:RA:272(L):U:H5'	8:RI:50:ARG:NH1	2.26	0.50
11:RP:99:LEU:HD23	11:RP:102:ARG:HH21	1.77	0.50
32:XA:1146:A:H3'	32:XA:1147:C:H5''	1.92	0.50
32:XA:380:G:N2	32:XA:383:A:OP2	2.44	0.50
33:XB:95:GLN:HG3	33:XB:147:LYS:O	2.11	0.50
12:YQ:80:GLU:CD	55:XY:264:HIS:HB2	2.32	0.50
6:YG:120:LEU:HB3	6:YG:131:TYR:OH	2.11	0.50
32:QA:1305:G:N2	32:QA:1331:G:H1'	2.26	0.50
32:QA:67:C:H2'	32:QA:68:G:C8	2.47	0.50
32:QA:96:U:H2'	32:QA:97:G:C8	2.45	0.50
33:QB:178:ARG:NH2	39:QH:68:ARG:HH12	2.09	0.50
27:R5:16:ARG:HH11	27:R5:16:ARG:HG2	1.76	0.50
1:RA:2206:G:H5''	1:RA:2207:G:N7	2.25	0.50
1:RA:2345:G:H1'	1:RA:2382:G:H5'	1.93	0.50
32:XA:1005:A:H5''	32:XA:1006:C:C5	2.46	0.50
35:XD:162:LEU:HD13	35:XD:181:MET:HG2	1.93	0.50
42:XK:115:PRO:C	42:XK:117:ASN:HA	2.31	0.50
51:XT:18:GLN:O	51:XT:22:ARG:HG3	2.10	0.50
1:YA:2115:G:N1	1:YA:2117:A:N7	2.58	0.50
1:YA:2180:U:H2'	1:YA:2181:G:C8	2.45	0.50
2:YB:66:A:H61	2:YB:109:C:H5'	1.76	0.50
1:YA:997:G:OP1	16:YU:92:ARG:HG2	2.11	0.50
38:QG:48:LYS:O	38:QG:52:GLU:HG2	2.12	0.50
1:RA:1794:U:H2'	1:RA:1795:C:C6	2.47	0.50
1:RA:2104:G:N2	1:RA:2105:C:C4	2.80	0.50
32:XA:1100:C:H2'	32:XA:1102:A:O5'	2.11	0.50
45:YN:32:SER:OG	45:YN:41:ARG:HG2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1058:G:H1	1:YA:1080:C:H42	1.60	0.50
1:YA:1063:G:H2'	1:YA:1065:U:H6	1.76	0.50
32:QA:838:G:H2'	32:QA:839:U:H2'	1.93	0.50
40:QI:16:ARG:HB2	40:QI:64:THR:HG22	1.94	0.50
55:QY:328:ARG:HD2	55:QY:332:VAL:HG23	1.93	0.50
1:RA:1068:G:H3'	1:RA:1096:A:OP2	2.12	0.50
1:RA:2785:C:O2'	4:RE:66:HIS:ND1	2.38	0.50
33:XB:201:ILE:HG21	33:XB:214:ILE:HG21	1.93	0.50
47:XP:59:TRP:HA	47:XP:62:VAL:HG12	1.94	0.50
32:XA:1313:U:P	50:XS:5:LEU:HG	2.51	0.50
25:Y3:23:LEU:HD22	25:Y3:50:VAL:HG11	1.93	0.50
1:YA:1364:G:OP2	23:Y1:3:LYS:HG3	2.11	0.50
6:YG:3:LEU:H	6:YG:3:LEU:HD23	1.76	0.50
7:YH:87:LEU:HD23	7:YH:164:TYR:HA	1.93	0.50
9:YN:96:GLU:HB2	9:YN:122:VAL:HG12	1.93	0.50
1:RA:1223:G:N2	1:RA:1226:A:OP2	2.39	0.50
16:RU:76:TYR:CZ	16:RU:80:ILE:HG13	2.46	0.50
32:XA:1302:U:OP2	44:XM:21:TYR:OH	2.22	0.50
32:XA:429:U:H3'	35:XD:9:CYS:SG	2.52	0.50
32:XA:1456:G:N1	51:XT:51:GLU:OE1	2.44	0.50
5:YF:21:ALA:HB3	5:YF:22:ALA:HA	1.94	0.50
1:RA:2168:G:H22	1:RA:2171:A:H2'	1.77	0.50
26:Y4:20:ASN:HD21	26:Y4:38:LYS:HG3	1.76	0.50
27:Y5:16:ARG:HH11	27:Y5:16:ARG:HG2	1.77	0.50
1:YA:26:G:C6	1:YA:27:G:N1	2.79	0.50
14:YS:67:ARG:HG3	14:YS:71:ARG:NH1	2.27	0.50
1:YA:583:G:OP2	16:YU:10:ARG:HD2	2.12	0.50
16:YU:76:TYR:OH	16:YU:92:ARG:NH1	2.44	0.50
33:QB:115:LEU:HD13	33:QB:145:LEU:HB3	1.93	0.50
50:QS:50:ALA:HB1	50:QS:57:HIS:HB3	1.93	0.50
51:QT:10:LEU:HD23	51:QT:11:SER:H	1.77	0.50
1:RA:2704:C:H2'	1:RA:2705:A:O4'	2.11	0.50
1:RA:642:G:N2	1:RA:645:C:OP2	2.45	0.50
1:RA:796:C:H2'	1:RA:797:C:C6	2.47	0.50
8:RI:140:LEU:HD12	8:RI:142:VAL:HG22	1.93	0.50
32:XA:1376:U:H2'	32:XA:1377:A:C8	2.47	0.50
32:XA:881:G:P	43:XL:12:ARG:HH22	2.35	0.50
34:XC:152:ILE:HG22	34:XC:167:TRP:HB2	1.94	0.50
1:YA:1739:U:HO2'	1:YA:1740:G:H8	1.58	0.50
1:YA:514:A:N3	1:YA:581:C:O2'	2.43	0.50
1:YA:642:G:N2	1:YA:645:C:OP2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1812:A:O2'	3:YD:45:ASN:N	2.45	0.50
4:YE:51:PHE:O	4:YE:77:ILE:N	2.44	0.50
32:QA:1030(D):G:H2'	32:QA:1030(E):A:C8	2.46	0.49
32:QA:1157:A:H4'	32:QA:1158:C:O5'	2.12	0.49
32:QA:509:A:N3	32:QA:543:C:O2'	2.39	0.49
34:QC:70:VAL:HG22	34:QC:72:LYS:H	1.77	0.49
26:R4:16:CYS:SG	26:R4:17:GLY:N	2.85	0.49
1:RA:2420:C:H5''	28:R6:8:LYS:HD2	1.94	0.49
1:RA:265:A:N1	1:RA:427:U:O2'	2.38	0.49
1:RA:479:A:N3	1:RA:481:G:H5''	2.27	0.49
6:RG:77:ILE:HG13	6:RG:82:LEU:HD12	1.94	0.49
26:Y4:15:ILE:HB	26:Y4:32:TYR:CD1	2.47	0.49
1:YA:1794:U:H2'	1:YA:1795:C:C6	2.47	0.49
1:YA:2805:G:H2'	1:YA:2807:G:H8	1.77	0.49
6:YG:7:LEU:HD23	6:YG:100:TRP:HE3	1.76	0.49
9:YN:54:VAL:HB	9:YN:122:VAL:HG22	1.94	0.49
14:YS:14:VAL:O	14:YS:18:ILE:HG12	2.11	0.49
32:QA:1356:G:H2'	32:QA:1357:A:C8	2.47	0.49
55:QY:138:TYR:HD1	55:QY:336:LYS:HB2	1.77	0.49
32:XA:1179:A:H2'	32:XA:1180:A:O4'	2.12	0.49
33:XB:16:HIS:CD2	33:XB:210:SER:HB3	2.48	0.49
34:XC:22:TRP:CD1	34:XC:59:ARG:HD2	2.48	0.49
55:XY:138:TYR:HD1	55:XY:336:LYS:HB2	1.77	0.49
1:YA:2233:U:H2'	1:YA:2234:G:C8	2.47	0.49
1:YA:572:A:OP2	17:YV:78:LYS:NZ	2.39	0.49
32:QA:1255:G:OP1	41:QJ:45:ARG:NH2	2.43	0.49
1:RA:9:U:O2'	1:RA:10:G:OP1	2.30	0.49
9:RN:94:HIS:CB	9:RN:97:ARG:HD3	2.42	0.49
32:XA:1030(A):C:H42	32:XA:1031:G:H1	1.58	0.49
32:XA:1270:C:O2'	32:XA:1314:C:H5'	2.11	0.49
40:XI:5:TYR:HE1	40:XI:16:ARG:HB3	1.77	0.49
42:XK:84:VAL:HG21	42:XK:95:ILE:HD11	1.94	0.49
32:XA:1340:A:O2'	53:XV:32:C:H5'	2.12	0.49
1:YA:272(E):U:H2'	1:YA:272(F):C:C6	2.47	0.49
1:YA:910:A:N1	1:YA:2277:G:H1'	2.28	0.49
32:QA:1003:G:C2'	32:QA:1004:A:H4'	2.42	0.49
32:QA:1118:C:H1'	32:QA:1179:A:C4	2.47	0.49
33:QB:178:ARG:HH22	39:QH:68:ARG:NH1	2.10	0.49
39:QH:14:ARG:O	39:QH:18:ARG:HG2	2.12	0.49
26:R4:57:GLU:HB2	26:R4:58:ARG:HA	1.93	0.49
1:RA:26:G:C6	1:RA:27:G:N1	2.80	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:RH:4:ILE:O	7:RH:69:ARG:HG2	2.12	0.49
15:RT:28:VAL:HG13	15:RT:86:ILE:HG23	1.94	0.49
16:RU:61:TRP:CH2	16:RU:93:LYS:HB2	2.48	0.49
40:XI:5:TYR:OH	40:XI:16:ARG:HG2	2.12	0.49
1:YA:824:A:H1'	1:YA:2358:G:N7	2.28	0.49
1:YA:300:A:H1'	1:YA:319:C:H1'	1.94	0.49
6:YG:146:TYR:HD2	44:XM:8:GLU:CD	2.14	0.49
55:QY:101:LEU:H	55:QY:102:PRO:HD2	1.76	0.49
26:R4:44:THR:O	26:R4:46:GLN:N	2.46	0.49
1:RA:2285:C:H5''	28:R6:29:ASN:ND2	2.27	0.49
1:RA:2031:A:C6	1:RA:2498:C:H1'	2.48	0.49
5:RF:184:TYR:O	5:RF:188:ARG:HG3	2.12	0.49
7:RH:25:LYS:HG3	7:RH:34:GLU:HG2	1.93	0.49
32:XA:1002:G:N3	32:XA:1003:G:C8	2.81	0.49
36:XE:33:VAL:HG21	36:XE:109:ILE:HA	1.95	0.49
1:YA:2130:U:H2'	1:YA:2158:A:H61	1.77	0.49
1:YA:8:A:H2'	1:YA:9:U:C6	2.48	0.49
1:YA:764:A:H5'	3:YD:210:GLY:HA2	1.95	0.49
14:YS:93:LYS:HD2	14:YS:95:HIS:HB2	1.93	0.49
32:QA:555:C:H2'	32:QA:556:C:C6	2.48	0.49
26:R4:54:GLY:O	26:R4:56:VAL:HA	2.12	0.49
33:XB:9:GLU:C	33:XB:11:LEU:H	2.15	0.49
33:XB:124:SER:HB2	33:XB:125:PRO:HD3	1.94	0.49
36:XE:143:ARG:NH1	39:XH:77:GLU:OE2	2.42	0.49
1:YA:1028:A:O2'	1:YA:1029:A:O4'	2.30	0.49
1:YA:1057:A:HO2'	1:YA:1058:G:P	2.34	0.49
1:YA:1063:G:H2'	1:YA:1065:U:C6	2.47	0.49
1:YA:1411:C:H2'	1:YA:1412:A:H8	1.77	0.49
1:YA:1889:A:H2'	1:YA:1890:A:C8	2.48	0.49
1:YA:2389:G:H5''	1:YA:2390:U:O4'	2.12	0.49
7:YH:90:LYS:HD2	7:YH:163:TYR:CD1	2.48	0.49
11:YP:50:ARG:HD3	30:Y8:7:HIS:CD2	2.47	0.49
32:QA:1060:C:C4	34:QC:2:GLY:HA3	2.47	0.49
32:QA:950:U:OP2	44:QM:102:ARG:HD2	2.13	0.49
49:QR:47:THR:HG23	49:QR:49:LYS:HG3	1.94	0.49
55:QY:204:ALA:HB2	55:QY:298:LEU:HD21	1.94	0.49
23:R1:51:VAL:HG12	23:R1:53:VAL:HG23	1.95	0.49
1:RA:1101:U:H2'	1:RA:1102:C:C6	2.48	0.49
1:RA:2074:U:H2'	1:RA:2075:U:C6	2.47	0.49
1:RA:272(K):U:H1'	8:RI:50:ARG:NH2	2.22	0.49
1:RA:2805:G:H2'	1:RA:2807:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:978:A:O2'	32:XA:1322:C:N3	2.37	0.49
38:XG:45:ASP:O	38:XG:49:ILE:HG13	2.11	0.49
1:YA:1923:U:OP1	53:XV:24:U:O2'	2.29	0.49
11:YP:63:PRO:HD3	30:Y8:27:THR:HG22	1.94	0.49
1:YA:1607:C:N4	1:YA:1622:G:OP2	2.31	0.49
5:YF:110:LEU:HA	5:YF:183:VAL:HG12	1.95	0.49
15:YT:64:ARG:HB2	15:YT:73:GLU:HG2	1.95	0.49
32:QA:1513:A:H2'	32:QA:1514:C:C6	2.48	0.49
32:QA:235:C:H5'	48:QQ:70:ARG:HG2	1.93	0.49
32:QA:1106:G:H5'	34:QC:172:ARG:HG2	1.94	0.49
34:QC:47:LEU:HD13	34:QC:68:VAL:HG11	1.93	0.49
48:QQ:6:LEU:HG	48:QQ:23:VAL:HG11	1.94	0.49
1:RA:1065:U:H4'	1:RA:1066:U:H5'	1.94	0.49
1:RA:1224:C:O2'	17:RV:85:LYS:HA	2.13	0.49
1:RA:1721:G:H8	1:RA:1741:A:H62	1.60	0.49
1:RA:323:G:C8	5:RF:171:PRO:HG3	2.47	0.49
1:RA:468:G:N7	29:R7:39:ARG:NH2	2.53	0.49
7:RH:3:ARG:HH22	7:RH:66:GLY:HA3	1.77	0.49
32:XA:512:U:H2'	32:XA:513:C:C6	2.48	0.49
32:XA:70:G:H1	32:XA:99:U:H3	1.61	0.49
34:XC:152:ILE:CG1	34:XC:199:LYS:HB2	2.43	0.49
34:XC:32:LEU:HD12	34:XC:59:ARG:NH1	2.28	0.49
32:XA:406:G:O2'	35:XD:3:ARG:NH2	2.46	0.49
37:XF:67:MET:SD	37:XF:72:VAL:HG12	2.53	0.49
49:XR:47:THR:HG23	49:XR:49:LYS:HG3	1.93	0.49
50:XS:20:LEU:HD23	50:XS:23:ASN:ND2	2.24	0.49
26:Y4:57:GLU:CB	26:Y4:58:ARG:HD2	2.42	0.49
1:YA:2105:C:N4	1:YA:2106:G:O6	2.46	0.49
1:YA:2298:A:H62	1:YA:2318:G:H8	1.60	0.49
9:YN:46:VAL:HG23	9:YN:48:MET:HG2	1.94	0.49
51:QT:57:ARG:HH22	51:QT:100:ILE:HD12	1.78	0.49
28:R6:6:ARG:NE	28:R6:24:GLU:OE1	2.32	0.49
30:R8:23:VAL:HG13	30:R8:47:LYS:HB3	1.94	0.49
1:RA:1032:A:H1'	31:R9:23:VAL:HG21	1.94	0.49
1:RA:362:U:O2'	1:RA:363(A):G:H5'	2.12	0.49
4:RE:51:PHE:H	4:RE:75:VAL:HG11	1.77	0.49
1:RA:1188:U:H4'	17:RV:79:VAL:HG22	1.95	0.49
32:XA:1135:U:H2'	32:XA:1137:C:N3	2.28	0.49
32:XA:1223:C:P	50:XS:78:ARG:HH22	2.36	0.49
32:XA:1366:C:O2'	41:XJ:60:ARG:NH2	2.31	0.49
32:XA:328:C:H4'	32:XA:329:A:H5'	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:XE:137:GLU:OE1	36:XE:141:GLN:NE2	2.40	0.49
1:YA:2243:U:H2'	1:YA:2244:U:C6	2.47	0.49
6:YG:41:GLN:NE2	6:YG:154:GLY:O	2.40	0.49
32:QA:1010:G:H22	32:QA:1020:U:H1'	1.78	0.49
32:QA:1062:U:H2'	32:QA:1063:C:C6	2.47	0.49
34:QC:58:GLU:O	34:QC:64:VAL:HG23	2.13	0.49
27:R5:45:VAL:HG11	27:R5:58:LEU:HD12	1.93	0.49
1:RA:1059:G:N1	1:RA:1079:C:N4	2.61	0.49
1:RA:2115:G:N1	1:RA:2117:A:N7	2.61	0.49
3:RD:108:PRO:HG3	3:RD:143:HIS:CE1	2.48	0.49
21:RZ:182:LYS:O	21:RZ:185:GLU:HG3	2.13	0.49
36:XE:92:LYS:HB3	36:XE:119:LEU:HB2	1.95	0.49
40:XI:23:ASN:H	40:XI:23:ASN:HD22	1.60	0.49
1:YA:881:G:H2'	1:YA:882:G:C8	2.47	0.49
32:QA:1151:A:O2'	32:QA:1152:A:H8	1.96	0.48
32:QA:632:A:H5'	32:QA:633:G:OP2	2.12	0.48
45:QN:48:ALA:HB2	45:QN:53:LEU:HD12	1.95	0.48
46:QO:16:ALA:HB1	46:QO:21:ASP:HB3	1.95	0.48
30:R8:14:VAL:HG13	30:R8:22:VAL:HG13	1.95	0.48
1:RA:1084:A:C8	1:RA:1085:A:H4'	2.48	0.48
1:RA:1803:A:H4'	3:RD:259:THR:HG23	1.95	0.48
6:RG:77:ILE:N	6:RG:82:LEU:O	2.37	0.48
32:XA:1030(D):G:H2'	32:XA:1030(E):A:C8	2.48	0.48
47:XP:68:ASP:O	47:XP:71:ARG:HG2	2.13	0.48
1:YA:1104:C:H2'	1:YA:1105:U:C6	2.48	0.48
1:YA:2137:C:C2	1:YA:2154:G:N1	2.81	0.48
1:YA:2391:G:O6	1:YA:2425:A:H8	1.96	0.48
1:YA:994:C:OP1	16:YU:53:ARG:NH2	2.46	0.48
32:QA:103:C:O2'	32:QA:172:A:N1	2.32	0.48
32:QA:341:C:H2'	32:QA:342:C:C6	2.48	0.48
33:QB:166:ASP:OD2	33:QB:169:LYS:HB2	2.13	0.48
32:QA:532:A:N6	34:QC:193:TYR:HA	2.23	0.48
41:QJ:78:ASN:O	41:QJ:80:LYS:N	2.46	0.48
1:RA:2689:U:P	1:RA:2719:G:H22	2.36	0.48
33:XB:16:HIS:O	33:XB:18:GLY:N	2.46	0.48
34:XC:36:ASP:O	34:XC:40:ARG:HG3	2.13	0.48
35:XD:108:LEU:HB3	35:XD:110:PHE:CE1	2.48	0.48
40:XI:16:ARG:HD3	40:XI:64:THR:HG21	1.93	0.48
30:Y8:46:ARG:HB2	30:Y8:46:ARG:HH21	1.78	0.48
1:YA:1059:G:N1	1:YA:1079:C:N4	2.61	0.48
1:YA:2104:G:O6	1:YA:2186:G:C4	2.66	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:YP:101:VAL:HA	11:YP:106:LEU:O	2.14	0.48
32:QA:1070:U:H2'	32:QA:1071:C:C6	2.47	0.48
32:QA:524:G:H2'	32:QA:525:C:C6	2.48	0.48
32:QA:542:G:H5'	35:QD:41:GLY:HA3	1.94	0.48
50:QS:3:ARG:HH21	50:QS:7:LYS:HE2	1.77	0.48
1:RA:2343:C:O2'	1:RA:2373:G:O2'	2.10	0.48
1:RA:2390:U:P	30:R8:35:GLN:HE22	2.36	0.48
33:XB:155:LEU:HD21	33:XB:159:PRO:HG3	1.95	0.48
36:XE:122:GLU:O	36:XE:126:ARG:NH1	2.46	0.48
43:XL:77:LEU:HD21	43:XL:107:ALA:HA	1.96	0.48
49:XR:52:PRO:HB2	49:XR:54:ARG:HG2	1.95	0.48
53:XV:50:U:H3	53:XV:64:G:H1	1.61	0.48
1:YA:1084:A:H3'	1:YA:1085:A:C4'	2.44	0.48
1:YA:1525:G:H2'	1:YA:1526:G:C8	2.47	0.48
5:YF:165:ARG:HG2	5:YF:168:ARG:NH2	2.28	0.48
9:YN:94:HIS:CB	9:YN:97:ARG:HD3	2.42	0.48
32:QA:1023:G:H2'	32:QA:1024:G:C8	2.48	0.48
6:RG:101:ILE:HD13	26:R4:25:TYR:HB2	1.94	0.48
1:RA:1341:U:OP1	1:RA:1397:U:N3	2.37	0.48
1:RA:2537:U:H2'	1:RA:2538:C:C6	2.49	0.48
1:RA:330:A:N7	1:RA:1210:A:O2'	2.33	0.48
8:RI:130:TYR:CE2	8:RI:132:PRO:HB3	2.49	0.48
32:XA:222:U:H2'	32:XA:223:U:C6	2.48	0.48
32:XA:973:G:H3'	32:XA:974:A:H5''	1.94	0.48
11:YP:62:LEU:O	30:Y8:13:ARG:HD3	2.13	0.48
6:YG:67:LYS:HE3	6:YG:68:PRO:O	2.13	0.48
32:QA:1202:G:N1	45:QN:46:GLU:OE1	2.46	0.48
32:QA:1377:A:HO2'	38:QG:2:ALA:N	2.11	0.48
32:QA:769:G:H4'	32:QA:1513:A:H4'	1.96	0.48
33:QB:15:VAL:O	33:QB:15:VAL:HG22	2.14	0.48
35:QD:108:LEU:HD21	35:QD:174:LEU:HD22	1.95	0.48
41:QJ:40:LEU:HB2	41:QJ:69:ASN:HB2	1.95	0.48
44:QM:3:ARG:O	44:QM:57:ARG:NH2	2.43	0.48
55:QY:186:ARG:HB3	55:QY:312:PHE:HD2	1.79	0.48
1:RA:1005:C:H2'	1:RA:1006:C:C6	2.49	0.48
1:RA:848:G:H2'	1:RA:849:A:C8	2.48	0.48
12:RQ:109:VAL:HG13	12:RQ:113:GLN:HB2	1.96	0.48
33:XB:218:ALA:O	33:XB:222:ILE:HG23	2.13	0.48
25:Y3:29:ARG:HB2	25:Y3:30:ARG:HD3	1.95	0.48
1:YA:1165:U:H2'	1:YA:1166:C:C6	2.48	0.48
11:YP:97:PRO:HD3	11:YP:126:VAL:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:QB:231:GLU:HB3	33:QB:232:PRO:HD3	1.96	0.48
35:QD:166:LYS:HB2	35:QD:168:ARG:NH2	2.28	0.48
1:RA:1104:C:H2'	1:RA:1105:U:C6	2.48	0.48
1:RA:218:A:C2	1:RA:235:U:H4'	2.48	0.48
32:XA:1158:C:O2	32:XA:1158:C:H2'	2.12	0.48
40:XI:31:GLN:HG3	40:XI:36:TYR:HB2	1.95	0.48
1:YA:569:U:C4	1:YA:570:G:C6	3.02	0.48
1:YA:587:C:OP2	11:YP:21:ARG:NH2	2.46	0.48
4:YE:18:ASP:HB3	15:YT:82:LEU:HD21	1.95	0.48
5:YF:130:ALA:HB3	5:YF:142:TRP:HD1	1.79	0.48
9:YN:4:TYR:CD2	16:YU:100:VAL:HG11	2.48	0.48
32:QA:1002:G:C6	32:QA:1003:G:C2	3.02	0.48
32:QA:337:C:H2'	32:QA:338:A:C8	2.48	0.48
1:RA:1739:U:HO2'	1:RA:1740:G:H8	1.59	0.48
1:RA:721:C:H2'	1:RA:722:A:C8	2.49	0.48
8:RI:81:VAL:O	8:RI:146:ALA:HA	2.14	0.48
32:XA:511:C:HO2'	32:XA:512:U:H6	1.59	0.48
34:XC:9:GLY:HA3	45:XN:49:HIS:HA	1.95	0.48
1:YA:2079:U:OP1	23:Y1:21:ARG:NH2	2.47	0.48
1:YA:2755:C:C2	31:Y9:19:ARG:HD3	2.49	0.48
32:QA:457:C:H2'	32:QA:458:C:C6	2.49	0.48
47:QP:20:VAL:HG21	47:QP:32:TYR:CG	2.49	0.48
55:QY:219:PRO:O	55:QY:221:ASP:N	2.46	0.48
1:RA:2010:G:H5''	18:RW:42:ARG:HB2	1.96	0.48
1:RA:2849:U:O4	15:RT:23:ARG:NH2	2.46	0.48
1:RA:637:A:OP1	11:RP:133:SER:OG	2.23	0.48
1:RA:873:G:H1	1:RA:904:C:H42	1.60	0.48
12:RQ:21:THR:CG2	12:RQ:101:ARG:HB2	2.43	0.48
32:XA:1036:G:H3'	32:XA:1037:C:C6	2.49	0.48
41:XJ:78:ASN:O	41:XJ:80:LYS:N	2.46	0.48
1:YA:1570:A:H2'	1:YA:1571:A:C8	2.49	0.48
1:YA:273(A):G:N7	1:YA:421:U:H2'	2.29	0.48
1:YA:1826:G:H4'	3:YD:242:ARG:CZ	2.44	0.48
5:YF:140:LEU:HD21	5:YF:170:LEU:HD11	1.95	0.48
8:YI:110:ASP:N	8:YI:130:TYR:OH	2.37	0.48
32:QA:974:A:OP1	32:QA:974:A:H8	1.96	0.48
38:QG:26:PHE:O	38:QG:30:ILE:HG13	2.14	0.48
26:R4:68:ARG:HA	26:R4:68:ARG:NH2	2.29	0.48
1:RA:2286:A:H4'	1:RA:2287:A:O4'	2.14	0.48
1:RA:2478:A:H5'	31:R9:31:LYS:HE2	1.96	0.48
32:XA:109:A:C6	32:XA:326:G:C6	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y4:20:ASN:ND2	26:Y4:38:LYS:HG3	2.28	0.48
1:YA:2115:G:N2	1:YA:2171:A:H61	2.12	0.48
1:YA:2507:C:O4'	55:XY:238:ASN:HB3	2.13	0.48
1:YA:1803:A:O2'	3:YD:259:THR:HG21	2.13	0.48
6:YG:35:GLU:HG3	6:YG:36:LYS:HE3	1.95	0.48
21:YZ:179:ASP:O	21:YZ:182:LYS:HG2	2.14	0.48
34:QC:50:ALA:HB1	34:QC:70:VAL:HG21	1.96	0.48
47:QP:75:ARG:HG3	47:QP:80:PHE:HD2	1.78	0.48
51:QT:18:GLN:O	51:QT:22:ARG:HG3	2.13	0.48
1:RA:2611:U:C4	27:R5:3:LYS:HG2	2.48	0.48
1:RA:1410:G:H2'	1:RA:1411:C:C6	2.48	0.48
5:RF:165:ARG:HA	5:RF:168:ARG:CD	2.44	0.48
5:RF:167:ALA:HB1	5:RF:173:VAL:HG11	1.96	0.48
32:XA:396:G:O2'	32:XA:398:C:OP1	2.21	0.48
32:XA:972:C:H4'	41:XJ:57:LYS:HB2	1.96	0.48
33:XB:222:ILE:HG13	33:XB:223:ILE:N	2.29	0.48
55:XY:177:PHE:O	55:XY:321:ARG:NH1	2.47	0.48
12:YQ:77:LYS:NZ	12:YQ:86:GLY:O	2.47	0.48
32:QA:1516:G:N1	32:QA:1519:MA6:OP2	2.46	0.47
33:QB:21:ARG:H	33:QB:21:ARG:HD3	1.78	0.47
32:QA:1316:G:H5'	45:QN:17:LYS:NZ	2.29	0.47
1:RA:1814:G:H4'	3:RD:51:VAL:HG21	1.95	0.47
1:RA:2262:U:H4'	1:RA:2328:A:C2	2.49	0.47
18:RW:46:PHE:O	18:RW:50:VAL:HG23	2.14	0.47
33:XB:9:GLU:O	33:XB:11:LEU:N	2.47	0.47
28:Y6:35:GLU:OE2	28:Y6:50:ARG:NH1	2.46	0.47
1:YA:2152:G:H2'	1:YA:2153:G:H8	1.78	0.47
17:YV:52:VAL:CG2	17:YV:55:ALA:HB3	2.44	0.47
21:YZ:126:VAL:HG11	21:YZ:161:VAL:HG13	1.96	0.47
32:QA:384:G:H2'	32:QA:385:C:C6	2.48	0.47
35:QD:178:VAL:HG12	35:QD:179:GLU:H	1.79	0.47
40:QI:16:ARG:H	40:QI:64:THR:HG22	1.78	0.47
44:QM:11:ARG:HA	44:QM:45:VAL:HB	1.96	0.47
55:QY:114:GLU:OE2	55:QY:294:ARG:HD3	2.13	0.47
1:RA:1070:A:H2'	1:RA:1071:G:C8	2.48	0.47
1:RA:2137:C:C2	1:RA:2154:G:N1	2.82	0.47
1:RA:2683:C:OP1	15:RT:53:ARG:NH2	2.47	0.47
1:RA:57:C:H2'	1:RA:58:G:O4'	2.14	0.47
3:RD:72:LYS:HG3	3:RD:103:ARG:NH2	2.29	0.47
5:RF:178:PRO:HB2	5:RF:201:VAL:HG21	1.95	0.47
10:RO:73:ASP:HB2	15:RT:82:LEU:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:972:C:O5'	41:XJ:57:LYS:HG2	2.14	0.47
33:XB:28:PHE:O	33:XB:32:ILE:HG13	2.14	0.47
34:XC:8:ILE:HG23	34:XC:16:ARG:HG2	1.95	0.47
39:XH:86:ILE:HG12	39:XH:135:CYS:HA	1.96	0.47
40:XI:21:PRO:HA	40:XI:59:PHE:HA	1.96	0.47
26:Y4:24:THR:OG1	26:Y4:25:TYR:N	2.47	0.47
1:YA:2420:C:OP1	30:Y8:34:TRP:HB3	2.14	0.47
1:YA:1278:A:OP1	13:YR:36:THR:HG23	2.14	0.47
1:YA:2086:U:H2'	1:YA:2087:G:C8	2.49	0.47
32:QA:1402:4OC:H6	32:QA:1402:4OC:O5'	2.13	0.47
28:R6:34:LEU:HB2	28:R6:51:GLU:HB2	1.95	0.47
11:RP:50:ARG:HD3	30:R8:7:HIS:CD2	2.50	0.47
1:RA:1300:U:H4'	1:RA:1301:A:H5'	1.95	0.47
1:RA:2098:U:H2'	1:RA:2099:U:O4'	2.14	0.47
1:RA:2567:G:H2'	1:RA:2568:C:C6	2.49	0.47
1:RA:2889:C:H3'	1:RA:2891:G:C8	2.49	0.47
20:RY:76:CYS:SG	20:RY:78:ALA:HB3	2.54	0.47
21:RZ:103:ARG:HD2	21:RZ:136:PHE:CD2	2.49	0.47
32:XA:1518:MA6:H93	32:XA:1519:MA6:H102	1.96	0.47
40:XI:100:GLY:O	40:XI:103:THR:HG22	2.14	0.47
1:YA:1405:U:H2'	1:YA:1406:U:C6	2.49	0.47
1:YA:2342:C:O2'	1:YA:2374:C:H5''	2.13	0.47
1:YA:2401:U:H3'	1:YA:2402:C:C6	2.48	0.47
1:YA:1805:U:O2	3:YD:50:THR:HB	2.15	0.47
7:YH:20:ALA:HB1	7:YH:21:PRO:HD2	1.96	0.47
32:QA:266:G:H2'	32:QA:266:G:N3	2.29	0.47
33:QB:95:GLN:HB3	33:QB:96:ARG:H	1.58	0.47
32:QA:1316:G:O2'	45:QN:18:VAL:HG11	2.14	0.47
44:QM:86:CYS:HB2	50:QS:73:GLU:HB3	1.96	0.47
1:RA:579:G:H2'	1:RA:580:C:C6	2.49	0.47
9:RN:15:LEU:HD12	9:RN:137:LYS:HG2	1.96	0.47
32:XA:1333:A:H2'	32:XA:1334:G:O4'	2.13	0.47
33:XB:71:VAL:HG23	33:XB:164:VAL:HA	1.96	0.47
38:XG:65:ALA:HB1	38:XG:127:ALA:HB3	1.96	0.47
38:XG:26:PHE:O	38:XG:30:ILE:HG13	2.15	0.47
50:XS:77:THR:HG23	50:XS:78:ARG:HG3	1.97	0.47
1:YA:1171:G:N2	1:YA:1178:C:O2	2.47	0.47
1:YA:2359:C:H2'	1:YA:2360:A:O4'	2.13	0.47
5:YF:10:PRO:HB3	5:YF:17:ARG:HE	1.80	0.47
1:YA:1665:A:H4'	10:YO:67:LYS:HB2	1.96	0.47
1:RA:11:G:C2'	1:RA:12:U:H5'	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:2391:G:O6	1:RA:2425:A:H8	1.97	0.47
1:RA:918:A:H5''	2:RB:98:G:O2'	2.14	0.47
3:RD:2:ALA:N	3:RD:200:ASP:OD2	2.47	0.47
32:XA:1040:U:H2'	32:XA:1041:A:H5''	1.96	0.47
55:XY:341:ILE:HA	55:XY:344:ILE:HD12	1.96	0.47
1:YA:2031:A:C6	1:YA:2498:C:H1'	2.49	0.47
6:YG:55:LYS:HD3	6:YG:150:ASP:OD2	2.14	0.47
21:YZ:10:ARG:HH21	21:YZ:26:GLY:H	1.61	0.47
21:YZ:150:LEU:HB3	21:YZ:171:ILE:HD11	1.96	0.47
32:QA:630:G:O2'	32:QA:631:G:H5'	2.14	0.47
33:QB:115:LEU:HD12	33:QB:142:LEU:HD12	1.95	0.47
33:QB:16:HIS:CG	33:QB:17:PHE:N	2.82	0.47
35:QD:166:LYS:H	35:QD:168:ARG:HH21	1.62	0.47
48:QQ:78:GLU:HG2	48:QQ:79:SER:N	2.28	0.47
1:RA:1058:G:H1	1:RA:1080:C:H42	1.62	0.47
1:RA:523:C:H4'	1:RA:540:C:O2	2.14	0.47
1:RA:574:C:N3	4:RE:145:LYS:NZ	2.42	0.47
1:RA:2820:A:OP2	13:RR:2:ARG:NH2	2.47	0.47
32:XA:1032:G:C2'	32:XA:1033:G:H5'	2.44	0.47
32:XA:1286:A:H2'	32:XA:1287:A:H4'	1.97	0.47
38:XG:111:ARG:HD3	38:XG:113:GLU:OE2	2.15	0.47
4:YE:98:PRO:HD3	4:YE:175:VAL:HG12	1.97	0.47
14:YS:27:SER:HA	14:YS:88:ASP:HB3	1.96	0.47
32:QA:1003:G:C2	32:QA:1004:A:H1'	2.50	0.47
36:QE:90:VAL:O	36:QE:120:THR:HA	2.14	0.47
26:R4:50:VAL:HG21	44:QM:64:TRP:C	2.35	0.47
1:RA:1899:G:N3	1:RA:1899:G:H2'	2.30	0.47
1:RA:2111:C:H42	1:RA:2147:G:H22	1.62	0.47
1:RA:2122:U:H2'	1:RA:2123:G:C8	2.50	0.47
1:RA:752:A:H3'	29:R7:1:MET:HE2	1.95	0.47
11:RP:94:GLU:HG3	11:RP:124:LYS:HD3	1.97	0.47
19:RX:44:GLU:HG3	19:RX:51:VAL:HG23	1.97	0.47
32:XA:1036:G:H3'	32:XA:1037:C:H6	1.79	0.47
32:XA:1118:C:P	40:XI:104:ARG:HH11	2.37	0.47
32:XA:542:G:OP1	35:XD:10:ARG:NH1	2.43	0.47
35:XD:199:ASN:OD1	35:XD:201:GLN:HB2	2.14	0.47
50:XS:27:GLU:OE1	50:XS:47:HIS:NE2	2.46	0.47
1:YA:1092:C:H6	1:YA:1092:C:OP2	1.98	0.47
3:YD:16:MET:HG3	3:YD:206:LEU:O	2.15	0.47
15:YT:118:ARG:HG2	32:XA:1442(B):G:C8	2.49	0.47
32:QA:1027:C:H2'	32:QA:1028:C:C5	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:QC:8:ILE:HD12	34:QC:16:ARG:HD3	1.97	0.47
1:RA:1359:A:H61	1:RA:1372:U:H3	1.63	0.47
7:RH:7:LEU:O	7:RH:69:ARG:NH1	2.46	0.47
8:RI:72:LEU:HD13	8:RI:140:LEU:HD23	1.95	0.47
32:XA:961:U:OP2	32:XA:1223:C:O2'	2.26	0.47
34:XC:140:ARG:HB2	34:XC:140:ARG:NH1	2.30	0.47
41:XJ:38:ILE:HG12	41:XJ:71:LEU:HB3	1.96	0.47
32:XA:950:U:OP2	44:XM:102:ARG:HD3	2.15	0.47
1:YA:2336:A:H61	22:Y0:43:THR:HG22	1.79	0.47
1:YA:2158:A:H1'	1:YA:2159:G:C8	2.50	0.47
3:YD:12:SER:HB3	3:YD:208:LYS:HB3	1.97	0.47
7:YH:12:PRO:O	7:YH:15:VAL:HG22	2.15	0.47
8:YI:50:ARG:HB3	8:YI:50:ARG:HE	1.40	0.47
17:YV:15:GLU:O	17:YV:18:LEU:HB2	2.15	0.47
20:YY:13:VAL:HB	20:YY:72:VAL:HG13	1.95	0.47
32:QA:1218:C:H2'	32:QA:1219:U:C6	2.50	0.47
32:QA:1279:A:O2'	32:QA:1282:C:N4	2.48	0.47
32:QA:186:C:H2'	32:QA:187:C:H6	1.80	0.47
39:QH:95:VAL:HB	39:QH:99:GLU:HB2	1.97	0.47
43:QL:33:ARG:HD2	43:QL:33:ARG:HA	1.62	0.47
1:RA:1817:G:OP1	3:RD:88:ARG:NH2	2.33	0.47
12:RQ:18:LYS:O	12:RQ:98:LYS:NZ	2.33	0.47
32:XA:130:A:O2'	32:XA:131:C:O5'	2.31	0.47
55:XY:133:ARG:O	55:XY:137:ARG:HG2	2.14	0.47
1:YA:1125:G:C6	1:YA:1126:A:N6	2.83	0.47
1:YA:272(O):C:H2'	1:YA:272(P):C:C6	2.49	0.47
1:YA:2823:A:OP1	4:YE:113:PHE:HB2	2.13	0.47
32:QA:179:A:H2'	32:QA:180:U:C6	2.50	0.47
32:QA:745:C:H2'	32:QA:746:A:C8	2.49	0.47
44:QM:40:ASN:HB3	44:QM:43:THR:HG23	1.96	0.47
46:QO:26:GLU:OE1	46:QO:77:ARG:NE	2.48	0.47
1:RA:2104:G:O6	1:RA:2186:G:C4	2.67	0.47
1:RA:228:A:H8	1:RA:229:A:H5'	1.79	0.47
1:RA:1805:U:O2	3:RD:50:THR:HB	2.14	0.47
14:RS:27:SER:HA	14:RS:88:ASP:HB3	1.96	0.47
55:XY:138:TYR:HD1	55:XY:337:LEU:H	1.63	0.47
1:YA:1608:A:H1'	1:YA:1610:A:OP2	2.15	0.47
1:YA:2122:U:H3	1:YA:2176:A:N6	2.13	0.47
1:YA:2552:2MU:H6	1:YA:2552:2MU:O5'	2.15	0.47
1:YA:2836:U:H2'	1:YA:2837:G:C8	2.49	0.47
1:YA:295:G:OP1	20:YY:1:MET:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:529:A:OP2	9:YN:114:ARG:NH2	2.47	0.47
1:YA:581:C:H2'	1:YA:582:G:C8	2.49	0.47
1:YA:57:C:H2'	1:YA:58:G:O4'	2.14	0.47
1:YA:2811:G:OP1	4:YE:60:ASN:HB2	2.14	0.47
5:YF:29:ASN:HB3	5:YF:112:MET:HE1	1.97	0.47
6:YG:83:ARG:O	6:YG:86:MET:HB2	2.15	0.47
8:YI:72:LEU:O	8:YI:75:LEU:HD22	2.15	0.47
40:QI:33:PHE:CE1	40:QI:43:ALA:HB1	2.50	0.47
53:QV:43:A:H2'	53:QV:44:A:C8	2.49	0.47
53:QV:21:A:H61	53:QV:46:G:H2'	1.80	0.47
1:RA:1053:C:H4'	1:RA:1054:A:OP1	2.15	0.47
1:RA:1139:G:O2'	1:RA:1143:A:N1	2.37	0.47
1:RA:1657:C:H2'	1:RA:1658:C:C6	2.50	0.47
1:RA:1936:A:OP2	1:RA:1962:5MC:N4	2.37	0.47
1:RA:1939:5MU:OP1	1:RA:2604:U:O2'	2.33	0.47
1:RA:2528:U:H2'	1:RA:2530:A:O5'	2.15	0.47
1:RA:668:G:H5'	1:RA:669:G:OP2	2.14	0.47
18:RW:4:LYS:HB2	18:RW:106:ILE:HG12	1.97	0.47
20:RY:6:HIS:HE1	20:RY:72:VAL:O	1.98	0.47
21:RZ:125:LEU:HB3	21:RZ:165:VAL:HG13	1.96	0.47
32:XA:1142:G:H2'	32:XA:1143:G:O4'	2.14	0.47
32:XA:1342:C:H2'	32:XA:1343:G:H8	1.80	0.47
32:XA:662:G:H2'	32:XA:663:A:H8	1.80	0.47
32:XA:828:A:H2'	32:XA:829:G:O4'	2.15	0.47
40:XI:51:ARG:HG2	40:XI:56:LEU:HD21	1.97	0.47
51:XT:56:MET:HE2	51:XT:84:LEU:HD22	1.97	0.47
1:YA:1914:C:OP1	55:XY:116:ARG:NH2	2.48	0.47
1:YA:1028:A:N7	1:YA:1126:A:N7	2.63	0.47
1:YA:1252:G:C2	1:YA:1253:A:C2	3.03	0.47
1:YA:1514:U:H2'	1:YA:1515:G:H8	1.79	0.47
1:YA:1683:C:H2'	1:YA:1684:C:C6	2.50	0.47
1:YA:2111:C:H42	1:YA:2147:G:H22	1.62	0.47
1:YA:859:G:O2'	1:YA:916:G:O6	2.31	0.47
1:YA:1814:G:H4'	3:YD:51:VAL:HG21	1.97	0.47
4:YE:14:ILE:HG13	4:YE:21:VAL:HG13	1.96	0.47
20:YY:37:VAL:HG21	20:YY:72:VAL:HG21	1.96	0.47
32:QA:1074:G:O2'	32:QA:1101:A:N1	2.37	0.46
43:QL:71:PRO:O	43:QL:102:ARG:NH1	2.47	0.46
53:QV:50:U:H3	53:QV:64:G:H1	1.62	0.46
1:RA:2478:A:H5'	31:R9:31:LYS:HG2	1.98	0.46
1:RA:2438:U:O2'	1:RA:2440:C:OP1	2.21	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:2849:U:H4'	1:RA:2868:A:C2	2.50	0.46
1:RA:375:C:H2'	1:RA:376:C:C6	2.50	0.46
32:XA:41:G:H2'	32:XA:42:G:C8	2.50	0.46
32:XA:8:A:N6	35:XD:205:GLU:O	2.46	0.46
41:XJ:11:PHE:CE1	41:XJ:67:THR:HG22	2.48	0.46
1:YA:2611:U:C4	27:Y5:3:LYS:HG2	2.50	0.46
1:YA:746:A:H2'	1:YA:2612:C:H5''	1.97	0.46
1:YA:98:G:H5'	24:Y2:3:LEU:HG	1.97	0.46
6:YG:36:LYS:HE2	6:YG:95:ARG:HH12	1.81	0.46
8:YI:4:ILE:HD11	8:YI:44:LEU:HD13	1.96	0.46
11:YP:97:PRO:HA	11:YP:112:LEU:HD12	1.96	0.46
11:YP:91:PHE:CE2	11:YP:99:LEU:HD21	2.50	0.46
1:YA:954:G:H5''	12:YQ:13:GLN:HB3	1.96	0.46
32:QA:1124:G:N2	32:QA:1125:U:O4	2.47	0.46
32:QA:335:C:H2'	32:QA:336:C:C6	2.50	0.46
55:QY:133:ARG:O	55:QY:137:ARG:HG2	2.15	0.46
1:RA:2850:A:N7	1:RA:2868:A:O2'	2.37	0.46
1:RA:824:A:H1'	1:RA:2358:G:N7	2.31	0.46
37:XF:35:ALA:HA	37:XF:67:MET:HB3	1.97	0.46
49:XR:33:ASP:OD2	49:XR:36:ASN:HB2	2.15	0.46
1:YA:1657:C:H2'	1:YA:1658:C:C6	2.50	0.46
1:YA:1756:G:H4'	1:YA:1758:G:O4'	2.15	0.46
1:YA:2306:C:C4	1:YA:2307:G:C6	3.04	0.46
5:YF:132:VAL:CG2	5:YF:163:VAL:HG22	2.44	0.46
32:QA:18:C:H4'	32:QA:1078:U:O2	2.15	0.46
32:QA:1395:C:O2'	32:QA:1401:G:O2'	2.15	0.46
32:QA:1118:C:P	40:QI:104:ARG:HH11	2.39	0.46
47:QP:43:LYS:HG2	47:QP:48:TRP:CE2	2.50	0.46
55:QY:221:ASP:HB3	55:QY:250:PRO:HD3	1.96	0.46
1:RA:2149:G:C2	1:RA:2150:U:H1'	2.50	0.46
1:RA:272(O):C:H2'	1:RA:272(P):C:C6	2.50	0.46
3:RD:17:THR:O	3:RD:211:ARG:NH2	2.38	0.46
8:RI:72:LEU:C	8:RI:74:ASN:H	2.18	0.46
32:XA:60:A:H4'	32:XA:61:G:O5'	2.16	0.46
32:XA:784:C:H2'	32:XA:785:G:O4'	2.16	0.46
33:XB:19:HIS:CG	33:XB:20:GLU:N	2.83	0.46
42:XK:27:ASN:OD1	42:XK:28:THR:N	2.46	0.46
55:XY:233:GLY:HA3	55:XY:237:VAL:HG23	1.97	0.46
1:YA:1514:U:H2'	1:YA:1515:G:C8	2.51	0.46
1:YA:1557:C:H5''	1:YA:1558:A:OP2	2.15	0.46
1:YA:184:C:H2'	1:YA:185:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:YD:108:PRO:HB3	3:YD:143:HIS:HE1	1.78	0.46
7:YH:41:MET:N	7:YH:41:MET:SD	2.88	0.46
32:QA:840:C:H4'	32:QA:841:U:OP1	2.16	0.46
40:QI:17:VAL:HG23	40:QI:63:ILE:HG12	1.96	0.46
1:RA:1239:G:H2'	1:RA:1240:U:O4'	2.15	0.46
1:RA:1385:G:O2'	1:RA:1396:U:O2	2.31	0.46
1:RA:1404:C:H2'	1:RA:1405:U:H6	1.80	0.46
1:RA:1514:U:H2'	1:RA:1515:G:H8	1.81	0.46
1:RA:1686:C:H2'	1:RA:1687:G:O4'	2.15	0.46
1:RA:2158:A:H1'	1:RA:2159:G:C8	2.50	0.46
1:RA:2180:U:H2'	1:RA:2181:G:C8	2.50	0.46
1:RA:1971:A:C4	3:RD:241:PRO:HD3	2.50	0.46
6:RG:43:LEU:HD23	6:RG:53:LEU:HD12	1.98	0.46
8:RI:117:GLU:HG3	8:RI:118:LYS:N	2.31	0.46
9:RN:20:GLY:HA2	9:RN:61:ARG:HD3	1.97	0.46
32:XA:1305:G:H22	32:XA:1331:G:H1'	1.79	0.46
40:XI:8:GLY:HA2	40:XI:79:LEU:HD23	1.96	0.46
55:XY:114:GLU:OE2	55:XY:294:ARG:HD3	2.15	0.46
23:Y1:51:VAL:HG12	23:Y1:53:VAL:HG23	1.97	0.46
1:YA:1163:G:OP1	17:YV:24:LYS:NZ	2.31	0.46
1:YA:2134:A:C5	1:YA:2157:G:H5'	2.50	0.46
1:YA:286:C:H2'	1:YA:287:C:C6	2.49	0.46
4:YE:170:LEU:HD23	4:YE:184:VAL:HG11	1.96	0.46
15:YT:118:ARG:HG2	32:XA:1442(B):G:N9	2.30	0.46
15:YT:39:ARG:NH2	32:XA:345:C:OP2	2.46	0.46
21:YZ:125:LEU:HG	21:YZ:164:ALA:HB3	1.96	0.46
32:QA:551:U:H2'	32:QA:552:U:C6	2.50	0.46
32:QA:664:G:N2	32:QA:741:G:H1	2.06	0.46
32:QA:765:G:N1	32:QA:812:C:O2'	2.44	0.46
32:QA:881:G:OP2	43:QL:12:ARG:NH2	2.49	0.46
33:QB:69:LEU:HB3	33:QB:162:ILE:HG22	1.97	0.46
33:QB:91:PRO:HG2	33:QB:155:LEU:HD23	1.96	0.46
39:QH:36:LEU:HD12	39:QH:59:LEU:HD13	1.97	0.46
27:R5:35:GLU:HG3	27:R5:51:TYR:CB	2.45	0.46
1:RA:249:C:O2	30:R8:12:LYS:NZ	2.41	0.46
1:RA:300:A:H1'	1:RA:319:C:H1'	1.98	0.46
1:RA:839:U:H2'	1:RA:840:C:C6	2.49	0.46
1:RA:1278:A:OP1	13:RR:36:THR:HG23	2.15	0.46
55:XY:329:LEU:HG	55:XY:330:ASP:N	2.30	0.46
1:YA:1041:C:N4	1:YA:1114:G:H1	2.00	0.46
1:YA:1525:G:H2'	1:YA:1526:G:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2315:G:H2'	1:YA:2316:C:C6	2.51	0.46
1:YA:7:G:H2'	1:YA:8:A:C8	2.50	0.46
2:YB:42:C:O2	6:YG:93:THR:N	2.40	0.46
6:YG:106:LEU:HA	6:YG:110:ALA:HB3	1.96	0.46
9:YN:120:LEU:HD11	9:YN:122:VAL:HG23	1.98	0.46
9:YN:137:LYS:HD3	9:YN:138:LEU:N	2.30	0.46
32:QA:1036:G:H5'	32:QA:1037:C:OP2	2.16	0.46
32:QA:540:G:H2'	32:QA:541:G:O4'	2.16	0.46
32:QA:564:C:O2'	39:QH:91:ARG:NH2	2.45	0.46
32:QA:757:U:H2'	32:QA:758:G:O4'	2.16	0.46
33:QB:146:GLN:O	33:QB:150:SER:HB3	2.15	0.46
32:QA:4:U:O4	39:QH:105:ARG:HA	2.16	0.46
32:QA:1302:U:H5	44:QM:17:VAL:HG21	1.80	0.46
48:QQ:10:VAL:HG13	48:QQ:19:VAL:HB	1.98	0.46
1:RA:1062:G:O2'	1:RA:1063:G:H5'	2.16	0.46
2:RB:41:U:H5	6:RG:70:VAL:O	1.98	0.46
6:RG:7:LEU:HD13	6:RG:100:TRP:CE3	2.50	0.46
18:RW:14:PRO:HG2	18:RW:78:GLU:CG	2.42	0.46
32:XA:555:C:H2'	32:XA:556:C:C6	2.51	0.46
35:XD:61:LYS:HD2	35:XD:207:TYR:OH	2.15	0.46
50:XS:50:ALA:HA	50:XS:58:VAL:O	2.16	0.46
55:XY:109:ARG:CZ	55:XY:209:LEU:HD13	2.46	0.46
55:XY:326:LEU:HD13	55:XY:328:ARG:HB2	1.98	0.46
1:YA:2285:C:OP2	28:Y6:26:ASN:ND2	2.42	0.46
1:YA:579:G:H2'	1:YA:580:C:C6	2.50	0.46
1:YA:886:C:O2'	1:YA:889:C:N4	2.46	0.46
33:QB:76:GLN:HE21	33:QB:206:ASP:HA	1.81	0.46
44:QM:54:VAL:HA	44:QM:57:ARG:HB3	1.98	0.46
53:QV:19:G:H5'	53:QV:20:U:H5	1.81	0.46
22:R0:23:VAL:HG22	22:R0:38:VAL:HG22	1.98	0.46
1:RA:140:G:N3	1:RA:142(A):A:N6	2.57	0.46
1:RA:2023:G:H4'	1:RA:2617:C:O3'	2.16	0.46
13:RR:44:LEU:HD22	13:RR:48:VAL:HG23	1.97	0.46
32:XA:520:A:N1	32:XA:536:C:H1'	2.30	0.46
32:XA:736:C:H2'	32:XA:737:A:C8	2.51	0.46
38:XG:27:ILE:HD12	38:XG:40:ALA:HA	1.97	0.46
55:XY:227:PHE:O	55:XY:243:ALA:HB3	2.16	0.46
1:YA:1053:C:O2'	1:YA:1054:A:O5'	2.34	0.46
1:YA:185:U:H4'	1:YA:218:A:H4'	1.98	0.46
1:YA:740:U:H2'	1:YA:741:G:C8	2.50	0.46
1:YA:84:A:N1	1:YA:98:G:O2'	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:817:C:H4'	1:YA:932:G:C5	2.51	0.46
32:QA:1003:G:C2	32:QA:1004:A:N3	2.84	0.46
52:QU:5:ASP:O	52:QU:11:GLY:HA3	2.16	0.46
1:RA:1063:G:H2'	1:RA:1065:U:H6	1.80	0.46
1:RA:10:G:H1'	1:RA:2801(B):A:N1	2.31	0.46
1:RA:2693:A:H2'	1:RA:2694:G:H8	1.80	0.46
1:RA:192:C:O2'	1:RA:802:A:N3	2.42	0.46
15:RT:108:ARG:HA	15:RT:111:ARG:NH1	2.30	0.46
44:XM:34:LEU:HD13	44:XM:41:PRO:HA	1.98	0.46
1:YA:2564:A:C2	1:YA:2647:U:H4'	2.51	0.46
1:YA:2741:A:OP1	31:Y9:22:ARG:NH2	2.42	0.46
1:YA:2754:U:O2'	31:Y9:17:ILE:HG12	2.16	0.46
1:YA:247:G:H4'	1:YA:386:G:C5	2.50	0.46
1:YA:492:A:H2'	1:YA:493:G:O4'	2.16	0.46
1:YA:668:G:H5'	1:YA:669:G:OP2	2.15	0.46
1:YA:754:C:H2'	1:YA:755:C:C6	2.51	0.46
10:YO:10:VAL:HG21	10:YO:16:ALA:HB3	1.97	0.46
12:YQ:109:VAL:HG13	12:YQ:113:GLN:HB2	1.97	0.46
32:QA:1053:G:N7	32:QA:1200:C:H5''	2.31	0.46
32:QA:828:A:H2'	32:QA:829:G:O4'	2.16	0.46
36:QE:31:LEU:HA	36:QE:31:LEU:HD23	1.82	0.46
42:QK:34:ASP:OD2	42:QK:38:ASN:HB2	2.16	0.46
42:QK:92:GLU:O	42:QK:96:ARG:HG2	2.16	0.46
1:RA:1581:G:H2'	1:RA:1582:C:O4'	2.15	0.46
6:RG:7:LEU:HD13	6:RG:100:TRP:HE3	1.81	0.46
1:RA:2012:G:OP1	18:RW:11:ARG:NH2	2.46	0.46
32:XA:1129:C:N4	32:XA:1143:G:H1	2.14	0.46
32:XA:1164:G:H1	32:XA:1172:C:N4	2.13	0.46
32:XA:1286:A:C8	32:XA:1287:A:H4'	2.51	0.46
32:XA:262:A:H2'	32:XA:263:A:C8	2.51	0.46
1:YA:277:C:H1'	1:YA:278:A:OP1	2.15	0.46
1:YA:455:C:N3	1:YA:472:A:H2'	2.30	0.46
2:YB:84:C:OP1	25:Y3:15:TYR:OH	2.24	0.46
3:YD:5:LYS:HB3	3:YD:5:LYS:HE3	1.67	0.46
32:QA:1015:A:H2'	32:QA:1016:A:C8	2.51	0.46
32:QA:1201:A:H1'	32:QA:1202:G:OP2	2.16	0.46
32:QA:15:G:H1'	36:QE:24:ARG:HE	1.79	0.46
37:QF:76:ALA:O	37:QF:80:ARG:HG3	2.16	0.46
32:QA:1343:G:H4'	40:QI:122:ALA:HB3	1.98	0.46
55:QY:316:ARG:HG2	55:QY:327:TYR:CE2	2.51	0.46
1:RA:1587:A:H2'	1:RA:1588:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1790:C:H5''	1:RA:1791:A:OP1	2.15	0.46
1:RA:1693:U:O2'	3:RD:14:ARG:NH2	2.48	0.46
3:RD:12:SER:HB3	3:RD:208:LYS:HB3	1.98	0.46
6:RG:50:ALA:C	6:RG:52:ILE:N	2.69	0.46
32:XA:1035:A:H2'	32:XA:1036:G:C8	2.51	0.46
32:XA:767:A:H2'	32:XA:768:A:O4'	2.16	0.46
33:XB:48:MET:HA	33:XB:51:LEU:HD12	1.98	0.46
50:XS:41:VAL:HG22	50:XS:42:PRO:HD2	1.97	0.46
55:XY:177:PHE:CA	55:XY:321:ARG:HH22	2.29	0.46
1:YA:1899:G:N3	1:YA:1899:G:H2'	2.31	0.46
1:YA:479:A:N3	1:YA:481:G:H5''	2.31	0.46
33:QB:134:GLU:HG3	33:QB:137:ARG:NH2	2.32	0.45
32:QA:427:U:OP1	35:QD:13:ARG:NH2	2.49	0.45
39:QH:82:HIS:NE2	39:QH:84:ARG:HG2	2.31	0.45
41:QJ:33:GLN:O	41:QJ:75:ILE:N	2.37	0.45
44:QM:81:LEU:HD13	44:QM:88:ARG:HG2	1.98	0.45
55:QY:133:ARG:NH1	55:QY:334:GLU:HG2	2.31	0.45
55:QY:236:HIS:CD2	55:QY:240:THR:HG21	2.51	0.45
55:QY:311:ASN:O	55:QY:329:LEU:HD11	2.16	0.45
1:RA:1341:U:O4'	19:RX:57:LEU:HD23	2.16	0.45
1:RA:2184:G:N1	1:RA:2185:C:O2	2.49	0.45
1:RA:2328:A:H2'	1:RA:2329:G:C8	2.51	0.45
6:RG:181:ARG:HG3	6:RG:182:LYS:N	2.31	0.45
11:RP:126:VAL:CG1	11:RP:148:LEU:HD21	2.46	0.45
32:XA:1028:C:H2'	32:XA:1033:G:H22	1.81	0.45
32:XA:1101:A:H4'	32:XA:1102:A:O5'	2.16	0.45
32:XA:1279:A:O2'	32:XA:1281:U:OP2	2.30	0.45
26:Y4:48:ARG:HB3	26:Y4:52:THR:HA	1.98	0.45
11:YP:63:PRO:HG2	30:Y8:25:MET:HB2	1.98	0.45
1:YA:848:G:H2'	1:YA:849:A:C8	2.51	0.45
6:YG:46:ALA:HB2	6:YG:53:LEU:HG	1.97	0.45
16:YU:103:PRO:HD2	16:YU:104:GLN:NE2	2.30	0.45
17:YV:98:GLU:OE1	17:YV:100:ARG:NH1	2.50	0.45
32:QA:1304:G:OP1	52:QU:2:GLY:N	2.49	0.45
35:QD:53:ASP:HB3	35:QD:57:ARG:NH1	2.30	0.45
40:QI:77:ILE:O	40:QI:81:ILE:HG23	2.17	0.45
50:QS:22:LEU:HD12	50:QS:31:ILE:HD11	1.97	0.45
53:QV:17(A):U:H5''	53:QV:18:G:OP2	2.16	0.45
1:RA:1340:U:OP1	19:RX:16:LYS:NZ	2.46	0.45
1:RA:2134:A:H8	1:RA:2156:G:H21	1.63	0.45
12:RQ:11:LYS:HE2	12:RQ:88:GLY:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:1318:A:H5''	50:XS:3:ARG:NH2	2.30	0.45
33:XB:22:LYS:HE3	33:XB:22:LYS:HB2	1.73	0.45
1:YA:2279:G:O6	22:Y0:14:ARG:HD2	2.15	0.45
23:Y1:51:VAL:HG11	23:Y1:74:VAL:HG21	1.98	0.45
1:YA:1292:U:H2'	1:YA:1293:C:C6	2.50	0.45
1:YA:1341:U:O4'	19:YX:57:LEU:HD23	2.15	0.45
1:YA:1936:A:OP2	1:YA:1962:5MC:N4	2.43	0.45
1:YA:2106:G:C4	1:YA:2107:C:H1'	2.51	0.45
1:YA:662:G:H5'	11:YP:14:LYS:O	2.16	0.45
3:YD:108:PRO:HG2	3:YD:111:LEU:HB2	1.98	0.45
7:YH:3:ARG:NH1	7:YH:3:ARG:HB3	2.31	0.45
20:YY:99:CYS:SG	20:YY:100:ALA:N	2.88	0.45
32:QA:1136:U:H5''	32:QA:1137:C:C2	2.51	0.45
32:QA:620:C:C2	35:QD:135:LEU:HG	2.52	0.45
32:QA:657:G:H4'	46:QO:28:GLN:HG2	1.98	0.45
32:QA:744:C:O2'	32:QA:851:G:N2	2.48	0.45
39:QH:6:ILE:HB	39:QH:85:ARG:NH1	2.30	0.45
32:QA:1226:C:N4	44:QM:104:ARG:HD2	2.31	0.45
25:R3:3:ARG:HH11	25:R3:60:GLU:CD	2.19	0.45
26:R4:10:VAL:HG21	26:R4:29:PRO:HG3	1.99	0.45
1:RA:30:G:H2'	1:RA:31:C:C6	2.50	0.45
5:RF:125:LEU:HD12	5:RF:194:MET:HB2	1.97	0.45
19:RX:60:ARG:NH2	29:R7:47:ARG:HH22	2.14	0.45
32:XA:848:C:H2'	32:XA:849:C:H6	1.82	0.45
32:XA:946:A:H2'	32:XA:947:G:C8	2.51	0.45
34:XC:19:GLU:HB3	34:XC:40:ARG:HH22	1.80	0.45
35:XD:190:ASP:O	35:XD:193:ASP:HB2	2.16	0.45
49:XR:26:LEU:HD11	49:XR:42:ARG:NE	2.31	0.45
24:Y2:21:LEU:HB2	24:Y2:64:LEU:HD23	1.98	0.45
26:Y4:40:HIS:HB3	26:Y4:43:TYR:CD1	2.51	0.45
1:YA:2311:A:H3'	1:YA:2312:U:C6	2.52	0.45
19:YX:61:GLY:HA3	19:YX:73:ARG:O	2.16	0.45
32:QA:1239:A:H62	32:QA:1299:A:N6	2.15	0.45
1:RA:1032:A:H4'	31:R9:16:VAL:HG11	1.98	0.45
1:RA:108:U:H2'	1:RA:109:G:C8	2.51	0.45
1:RA:1102:C:H2'	1:RA:1103:A:C8	2.51	0.45
1:RA:2572:A:C8	4:RE:144:ARG:HG2	2.52	0.45
16:RU:108:GLU:O	16:RU:112:ARG:HG2	2.16	0.45
32:XA:142:G:H2'	32:XA:143:A:C8	2.49	0.45
35:XD:108:LEU:HB3	35:XD:110:PHE:CD1	2.52	0.45
35:XD:148:VAL:HG11	35:XD:158:ILE:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:XI:23:ASN:OD1	40:XI:25:LYS:HE3	2.17	0.45
54:XX:21:A:H62	55:XY:198:THR:HG1	1.64	0.45
1:YA:1051:G:H4'	1:YA:2752:C:C4'	2.44	0.45
1:YA:1070:A:H2'	1:YA:1071:G:C8	2.52	0.45
1:YA:2061:G:H5''	1:YA:2503:2MA:C2	2.46	0.45
1:YA:2064:C:H2'	1:YA:2065:C:C6	2.52	0.45
12:YQ:30:GLY:HA2	12:YQ:107:ALA:HB2	1.98	0.45
13:YR:33:ARG:NH1	13:YR:115:GLU:OE2	2.49	0.45
32:QA:123:C:OP1	32:QA:311:C:O2'	2.27	0.45
33:QB:40:HIS:HB3	33:QB:190:THR:HG21	1.98	0.45
33:QB:44:LEU:HD12	33:QB:44:LEU:HA	1.77	0.45
35:QD:108:LEU:HD12	35:QD:176:LEU:HD13	1.99	0.45
36:QE:102:ALA:HB1	36:QE:106:PRO:HG2	1.97	0.45
55:QY:111:ALA:HB2	55:QY:172:TYR:HB2	1.98	0.45
1:RA:1593:G:H2'	1:RA:1594:G:C8	2.51	0.45
1:RA:2693:A:H2'	1:RA:2694:G:C8	2.52	0.45
1:RA:323:G:H1'	1:RA:1205:U:O2	2.16	0.45
1:RA:36:G:N3	1:RA:450:G:O2'	2.48	0.45
4:RE:36:ARG:HG2	4:RE:47:VAL:HG22	1.98	0.45
6:RG:108:ASN:HA	26:R4:37:SER:HB3	1.97	0.45
7:RH:117:PRO:HG3	7:RH:123:PHE:CD2	2.51	0.45
15:RT:39:ARG:NH1	15:RT:41:ARG:HD3	2.31	0.45
33:XB:87:ARG:HD3	33:XB:234:PRO:HD2	1.97	0.45
32:XA:235:C:H5'	48:XQ:70:ARG:HG2	1.98	0.45
53:XV:43:A:H2'	53:XV:44:A:C8	2.51	0.45
1:YA:2001:A:H2'	1:YA:2002:G:C8	2.51	0.45
1:YA:2051:A:H5'	1:YA:2578:G:O4'	2.16	0.45
1:YA:910:A:C6	1:YA:911:A:C6	3.04	0.45
2:YB:17:C:H2'	2:YB:18:G:O4'	2.16	0.45
7:YH:86:GLU:OE2	7:YH:132:ARG:NH2	2.49	0.45
32:QA:1030(C):C:H2'	32:QA:1030(C):C:O2	2.16	0.45
32:QA:12:U:H4'	32:QA:526:C:H4'	1.99	0.45
42:QK:62:GLN:HB2	42:QK:93:GLN:HG3	1.98	0.45
44:QM:4:ILE:HA	44:QM:5:ALA:HA	1.65	0.45
50:QS:3:ARG:NH1	50:QS:10:PHE:HB2	2.31	0.45
53:QV:76:A:H2'	55:QY:234:GLY:HA3	1.99	0.45
55:QY:222:LEU:HD22	55:QY:246:ILE:HG22	1.98	0.45
1:RA:1053:C:H2'	1:RA:1054:A:C8	2.46	0.45
1:RA:1097:U:H2'	1:RA:1097:U:O2	2.15	0.45
1:RA:1049:C:H1'	1:RA:1113:U:O2'	2.17	0.45
1:RA:2092:U:H4'	1:RA:2093:G:O5'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:2243:U:H2'	1:RA:2244:U:C6	2.51	0.45
1:RA:2364:C:H2'	1:RA:2365:G:O4'	2.16	0.45
1:RA:2466:C:H5''	31:R9:6:SER:HB3	1.99	0.45
15:RT:16:ARG:HD3	15:RT:18:ASP:OD1	2.17	0.45
15:RT:24:PRO:HD3	15:RT:52:ILE:HD12	1.99	0.45
32:XA:1005:A:H1'	32:XA:1025:U:N3	2.32	0.45
32:XA:815:A:N7	32:XA:1509:C:O2'	2.44	0.45
39:XH:19:VAL:HG23	39:XH:21:LYS:HD3	1.97	0.45
55:XY:229:SER:HB2	55:XY:237:VAL:HG13	1.99	0.45
29:Y7:10:ARG:NH1	29:Y7:14:LYS:HE3	2.31	0.45
1:YA:1005:C:H2'	1:YA:1006:C:C6	2.52	0.45
1:YA:1084:A:C8	1:YA:1085:A:H4'	2.52	0.45
1:YA:1050:A:H2	1:YA:2751:G:C2	2.33	0.45
4:YE:115:GLY:O	4:YE:119:ARG:HB2	2.17	0.45
12:YQ:55:VAL:HG23	21:YZ:178:GLU:HB3	1.97	0.45
32:QA:1148:U:H2'	32:QA:1149:C:O4'	2.17	0.45
32:QA:1347:G:N2	32:QA:1373:G:H2'	2.32	0.45
33:QB:7:VAL:HG12	33:QB:217:ARG:HD2	1.99	0.45
45:QN:27:CYS:SG	45:QN:29:ARG:HB2	2.57	0.45
55:QY:236:HIS:NE2	55:QY:240:THR:HG21	2.32	0.45
1:RA:1932:A:H2'	1:RA:1933:G:O4'	2.17	0.45
1:RA:2061:G:H5''	1:RA:2503:2MA:C2	2.46	0.45
1:RA:852:G:H2'	1:RA:853:G:C8	2.51	0.45
4:RE:111:ARG:HG2	4:RE:160:TYR:O	2.17	0.45
15:RT:37:GLY:HA2	15:RT:38:ASN:HA	1.69	0.45
32:XA:1068:G:H8	32:XA:1068:G:OP2	1.99	0.45
32:XA:580:U:H2'	32:XA:581:G:O4'	2.17	0.45
32:XA:67:C:H2'	32:XA:68:G:C8	2.52	0.45
32:XA:814:A:H2'	32:XA:816:A:H5''	1.98	0.45
1:YA:144:C:H5'	19:YX:2:LYS:HE2	1.98	0.45
1:YA:700:G:O2'	1:YA:1632:A:N3	2.44	0.45
1:YA:1916:A:H2'	1:YA:1917:PSU:O4'	2.16	0.45
1:YA:2298:A:N6	1:YA:2318:G:C8	2.83	0.45
1:YA:2298:A:N6	1:YA:2318:G:H8	2.15	0.45
2:YB:8:U:O2'	14:YS:40:ILE:HD13	2.16	0.45
1:YA:1971:A:C4	3:YD:241:PRO:HD3	2.52	0.45
4:YE:101:ARG:CZ	4:YE:171:GLU:HB2	2.47	0.45
8:YI:130:TYR:CE2	8:YI:132:PRO:HB3	2.52	0.45
32:QA:707:C:OP1	42:QK:85:ARG:NH1	2.49	0.45
37:QF:91:VAL:HG11	49:QR:72:ARG:NH1	2.31	0.45
39:QH:6:ILE:O	39:QH:10:LEU:HG	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:QJ:19:SER:O	41:QJ:23:ILE:HG12	2.17	0.45
48:QQ:58:GLU:OE2	48:QQ:75:ARG:NH2	2.50	0.45
30:R8:34:TRP:CE2	30:R8:35:GLN:HB3	2.51	0.45
1:RA:1153:C:H2'	1:RA:1154:G:O4'	2.17	0.45
1:RA:1557:C:H5''	1:RA:1558:A:OP2	2.17	0.45
1:RA:1847:A:H3'	1:RA:1848:A:H5'	1.99	0.45
1:RA:2031:A:N3	1:RA:2455:G:O2'	2.38	0.45
1:RA:2107:C:H42	1:RA:2182:G:H1	1.65	0.45
1:RA:2128:C:H3'	1:RA:2129:C:H5''	1.98	0.45
1:RA:2401:U:H3'	1:RA:2402:C:C6	2.52	0.45
1:RA:2832:U:O4	1:RA:2883:A:H5''	2.17	0.45
11:RP:55:ARG:HG2	11:RP:56:SER:N	2.31	0.45
17:RV:40:LEU:HB2	17:RV:46:VAL:HG12	1.97	0.45
33:XB:42:ILE:HD13	33:XB:203:GLY:HA2	1.98	0.45
51:XT:38:LYS:HE2	51:XT:38:LYS:HB3	1.68	0.45
1:YA:1049:C:H1'	1:YA:1113:U:O2'	2.16	0.45
1:YA:2023:G:H4'	1:YA:2617:C:O3'	2.17	0.45
1:YA:2516:G:C6	1:YA:2517:C:N4	2.85	0.45
1:YA:2849:U:H4'	1:YA:2868:A:C2	2.51	0.45
1:YA:350:U:H2'	1:YA:351:G:O4'	2.17	0.45
1:YA:574:C:N3	4:YE:145:LYS:NZ	2.45	0.45
4:YE:150:VAL:HG13	4:YE:154:LYS:HG3	1.98	0.45
7:YH:164:TYR:HB2	7:YH:167:GLU:HB2	1.98	0.45
32:QA:657:G:O2'	46:QO:23:GLY:HA2	2.17	0.45
1:RA:1055:G:H2'	1:RA:1056:G:O4'	2.17	0.45
1:RA:1166:C:H2'	1:RA:1167:U:C6	2.52	0.45
1:RA:1358:G:O2'	1:RA:1359:A:H5'	2.16	0.45
1:RA:2313:C:H2'	1:RA:2314:C:C6	2.52	0.45
1:RA:2477:C:N4	31:R9:10:ILE:HG23	2.32	0.45
1:RA:1812:A:O2'	3:RD:45:ASN:N	2.49	0.45
32:XA:1154:G:H2'	32:XA:1155:G:H8	1.82	0.45
32:XA:1327:C:H2'	32:XA:1328:C:C6	2.52	0.45
32:XA:189(L):U:H2'	32:XA:189(M):G:C8	2.52	0.45
38:XG:9:VAL:HG11	38:XG:94:ARG:HD3	1.98	0.45
41:XJ:38:ILE:CG1	41:XJ:71:LEU:HB3	2.47	0.45
32:XA:1492:A:C8	43:XL:47:LYS:HG2	2.51	0.45
51:XT:39:LYS:HB2	51:XT:39:LYS:HE3	1.80	0.45
53:XV:21:A:N6	53:XV:46:G:H2'	2.32	0.45
1:YA:1029:A:C2	1:YA:2465:C:C2'	3.00	0.45
1:YA:1097:U:H2'	1:YA:1097:U:O2	2.15	0.45
1:YA:1358:G:O2'	1:YA:1359:A:H5'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2870:C:H2'	1:YA:2871:C:O4'	2.16	0.45
1:YA:458:G:O2'	1:YA:469:G:O6	2.22	0.45
8:YI:4:ILE:HG12	8:YI:18:VAL:HG22	1.99	0.45
12:YQ:137:TYR:O	12:YQ:141:GLN:HG2	2.17	0.45
32:QA:1058:G:OP1	34:QC:199:LYS:HE3	2.17	0.45
32:QA:1124:G:N7	32:QA:1145:C:O2'	2.50	0.45
32:QA:262:A:H2'	32:QA:263:A:C8	2.51	0.45
32:QA:309:G:O2'	32:QA:607:A:N1	2.48	0.45
35:QD:173:TRP:CE3	35:QD:174:LEU:HG	2.52	0.45
35:QD:85:LYS:HD3	35:QD:86:LYS:N	2.31	0.45
38:QG:79:ARG:HA	38:QG:84:ASN:HA	1.98	0.45
1:RA:2317:C:H2'	1:RA:2318:G:H5'	1.99	0.45
32:XA:859:A:OP2	32:XA:869:G:N1	2.45	0.45
37:XF:100:ASN:ND2	49:XR:23:LYS:HE2	2.32	0.45
53:XV:47:U:H3'	53:XV:48:C:C5'	2.46	0.45
29:Y7:34:ARG:NH1	29:Y7:41:ARG:O	2.50	0.45
1:YA:1794:U:H2'	1:YA:1795:C:H6	1.81	0.45
1:YA:1939:5MU:OP1	1:YA:2604:U:O2'	2.33	0.45
1:YA:2074:U:H2'	1:YA:2075:U:C6	2.52	0.45
1:YA:2774:C:H2'	1:YA:2775:A:O4'	2.16	0.45
8:YI:40:THR:O	8:YI:44:LEU:HD22	2.17	0.45
10:YO:120:GLU:HG2	10:YO:122:LEU:HG	1.98	0.45
10:YO:9:GLU:O	10:YO:83:ALA:HA	2.17	0.45
16:YU:36:ARG:HD2	16:YU:40:PHE:CZ	2.52	0.45
32:QA:1034:G:H3'	32:QA:1035:A:C8	2.51	0.44
32:QA:1148:U:O3'	40:QL:14:VAL:HG11	2.17	0.44
1:RA:2629:A:H1'	1:RA:2630:G:H5''	1.99	0.44
1:RA:686:G:N2	1:RA:788:A:H61	2.15	0.44
1:RA:272(K):U:O2	8:RI:50:ARG:HD3	2.16	0.44
19:RX:60:ARG:HH12	29:R7:47:ARG:HH22	1.65	0.44
32:XA:434:U:H2'	32:XA:435:C:C6	2.51	0.44
34:XC:43:LEU:O	34:XC:47:LEU:HB2	2.16	0.44
35:XD:20:TYR:CD2	35:XD:26:CYS:HB3	2.52	0.44
36:XE:20:GLN:OE1	36:XE:25:ARG:HD2	2.17	0.44
37:XF:25:ILE:HD13	37:XF:82:ARG:HE	1.82	0.44
42:XK:78:GLN:O	42:XK:103:LEU:HA	2.17	0.44
47:XP:43:LYS:HA	47:XP:48:TRP:HB3	1.98	0.44
23:Y1:3:LYS:HB2	23:Y1:61:ARG:HH12	1.81	0.44
25:Y3:23:LEU:HD12	25:Y3:28:LEU:HB2	1.99	0.44
1:YA:1084:A:H3'	1:YA:1085:A:H4'	1.99	0.44
1:YA:11:G:C2'	1:YA:12:U:H5'	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2629:A:H1'	1:YA:2630:G:H5''	1.99	0.44
1:YA:523:C:H4'	1:YA:540:C:O2	2.17	0.44
4:YE:11:MET:CG	4:YE:24:THR:HG22	2.43	0.44
8:YI:69:LYS:HB2	8:YI:138:ILE:HG12	1.98	0.44
8:YI:6:LEU:HD11	8:YI:37:VAL:HG23	2.00	0.44
33:QB:41:ILE:HA	33:QB:41:ILE:HD13	1.84	0.44
40:QI:22:GLY:HA3	40:QI:60:ASP:OD1	2.17	0.44
29:R7:24:THR:HG22	29:R7:27:GLY:H	1.82	0.44
1:RA:2115:G:N2	1:RA:2171:A:H61	2.14	0.44
1:RA:2315:G:H2'	1:RA:2316:C:C6	2.52	0.44
1:RA:764:A:O4'	3:RD:213:ARG:HG3	2.17	0.44
4:RE:119:ARG:HG2	4:RE:120:TRP:CD1	2.52	0.44
32:XA:1159:U:O4'	32:XA:1182:G:N2	2.50	0.44
32:XA:692:U:H1'	32:XA:695:A:N7	2.32	0.44
44:XM:16:ASP:OD1	44:XM:16:ASP:N	2.49	0.44
1:YA:1416:G:O2'	1:YA:1417:C:OP2	2.29	0.44
1:YA:1472:A:H2'	1:YA:1473:G:O4'	2.17	0.44
1:YA:2016:U:H1'	27:Y5:6:VAL:HG13	1.98	0.44
1:YA:2317:C:H2'	1:YA:2318:G:H5'	1.98	0.44
1:YA:2839:G:H5'	13:YR:46:GLY:CA	2.46	0.44
11:YP:106:LEU:HD13	11:YP:107:LYS:O	2.17	0.44
1:YA:863:A:P	12:YQ:22:LYS:HG3	2.58	0.44
32:QA:1179:A:H2'	32:QA:1180:A:O4'	2.17	0.44
33:QB:185:ILE:HG22	33:QB:199:TYR:HD2	1.80	0.44
35:QD:108:LEU:HB3	35:QD:110:PHE:CD1	2.53	0.44
36:QE:69:VAL:HG12	36:QE:139:LEU:HB3	1.98	0.44
39:QH:51:VAL:HG21	39:QH:60:ARG:HH11	1.81	0.44
39:QH:51:VAL:HG11	39:QH:60:ARG:HH12	1.83	0.44
45:QN:4:LYS:O	45:QN:7:ILE:HG12	2.18	0.44
46:QO:18:PHE:HB2	46:QO:19:PRO:HD2	1.99	0.44
32:QA:1456:G:C2	51:QT:55:ILE:HD11	2.53	0.44
26:R4:24:THR:OG1	26:R4:25:TYR:N	2.51	0.44
1:RA:1025:G:C4	1:RA:1135:C:H1'	2.52	0.44
1:RA:1092:C:H6	1:RA:1092:C:OP2	2.00	0.44
1:RA:2277:G:OP2	22:R0:10:THR:HG21	2.17	0.44
1:RA:528:A:O2'	1:RA:529:A:H5'	2.17	0.44
1:RA:754:C:H2'	1:RA:755:C:C6	2.52	0.44
1:RA:911:A:H2'	12:RQ:9:TYR:OH	2.17	0.44
1:RA:2786:U:O2'	4:RE:62:PRO:O	2.30	0.44
1:RA:470:A:OP1	5:RF:59:TYR:HE1	2.01	0.44
32:XA:1148:U:O2'	40:XI:66:ARG:NH1	2.44	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:XB:212:GLN:OE1	33:XB:235:SER:OG	2.32	0.44
55:XY:308:ARG:NH2	55:XY:319:ASP:OD2	2.25	0.44
1:YA:1104:C:H2'	1:YA:1105:U:H6	1.81	0.44
1:YA:1408:C:C2	1:YA:1595:G:N2	2.85	0.44
1:YA:2119:A:H61	1:YA:2168:G:H21	1.66	0.44
1:YA:2704:C:H2'	1:YA:2705:A:O4'	2.17	0.44
32:QA:17:U:O2'	32:QA:1079:G:H1'	2.17	0.44
32:QA:393:A:H5'	32:QA:483:C:O2'	2.18	0.44
46:QO:26:GLU:HG3	46:QO:81:LEU:HD22	1.99	0.44
46:QO:82:ILE:O	46:QO:86:GLY:N	2.50	0.44
29:R7:12:ARG:NH2	29:R7:44:PRO:HB3	2.33	0.44
1:RA:2420:C:OP1	30:R8:34:TRP:HB3	2.18	0.44
1:RA:1406:U:H2'	1:RA:1407:C:C6	2.52	0.44
1:RA:1639:U:C2'	1:RA:1640:C:H5''	2.47	0.44
1:RA:2375:G:O2'	1:RA:2377:A:N7	2.46	0.44
1:RA:2805:G:H2'	1:RA:2807:G:H8	1.83	0.44
1:RA:580:C:H2'	1:RA:581:C:C6	2.52	0.44
3:RD:10:THR:OG1	3:RD:13:ARG:HG2	2.16	0.44
32:XA:1403:C:H1'	32:XA:1500:A:N1	2.33	0.44
32:XA:359:U:H2'	32:XA:360:A:C8	2.53	0.44
32:XA:881:G:OP2	43:XL:12:ARG:NH2	2.51	0.44
35:XD:8:VAL:HG22	35:XD:21:LEU:HD13	1.97	0.44
44:XM:15:VAL:HG12	44:XM:45:VAL:HG22	1.99	0.44
53:XV:21:A:H61	53:XV:46:G:H2'	1.82	0.44
55:XY:103:LYS:HG2	55:XY:103:LYS:H	1.60	0.44
1:YA:1239:G:H2'	1:YA:1240:U:O4'	2.17	0.44
1:YA:2648:C:H2'	1:YA:2649:U:C6	2.52	0.44
1:YA:2832:U:O4	1:YA:2883:A:H5''	2.17	0.44
2:YB:96:U:H2'	2:YB:97:G:C8	2.53	0.44
1:YA:2680:C:H5'	4:YE:189:PRO:HA	2.00	0.44
15:YT:91:ARG:HD2	15:YT:120:ARG:NH1	2.32	0.44
19:YX:12:VAL:HG22	19:YX:29:TRP:CE2	2.52	0.44
32:QA:1333:A:H2'	32:QA:1334:G:O4'	2.18	0.44
32:QA:149:A:H2'	32:QA:150:C:C6	2.52	0.44
40:QI:65:VAL:HG21	40:QI:73:GLN:HB3	2.00	0.44
32:QA:656:C:O2'	46:QO:28:GLN:OE1	2.21	0.44
55:QY:318:THR:HG22	55:QY:325:THR:HB	2.00	0.44
1:RA:1794:U:H2'	1:RA:1795:C:H6	1.81	0.44
1:RA:1796:U:H2'	1:RA:1797:C:H6	1.81	0.44
1:RA:1916:A:H2'	1:RA:1917:PSU:O4'	2.17	0.44
1:RA:2512:C:H2'	1:RA:2513:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:875:G:H2'	1:RA:876:C:O4'	2.18	0.44
5:RF:110:LEU:HA	5:RF:183:VAL:HG12	1.99	0.44
20:RY:9:LYS:HA	20:RY:10:GLY:HA2	1.74	0.44
32:XA:1005:A:H1'	32:XA:1025:U:C2	2.52	0.44
32:XA:397:A:H3'	32:XA:397:A:N3	2.32	0.44
35:XD:191:ARG:HA	35:XD:191:ARG:HD2	1.76	0.44
47:XP:18:ARG:NH1	47:XP:32:TYR:OH	2.51	0.44
50:XS:12:ASP:OD2	50:XS:35:SER:HB3	2.17	0.44
55:XY:213:GLU:C	55:XY:215:PRO:HD3	2.38	0.44
1:YA:1069:A:H5'	1:YA:1096:A:C5'	2.48	0.44
1:YA:9:U:O2'	1:YA:10:G:OP1	2.32	0.44
1:YA:1102:C:H2'	1:YA:1103:A:C8	2.52	0.44
1:YA:93:G:H2'	1:YA:94(A):C:C6	2.53	0.44
8:YI:62:LYS:HG2	8:YI:133:HIS:NE2	2.33	0.44
16:YU:92:ARG:HA	16:YU:95:LEU:HB2	1.98	0.44
32:QA:864:A:H2'	32:QA:865:A:C8	2.52	0.44
33:QB:185:ILE:HG22	33:QB:199:TYR:CD2	2.53	0.44
33:QB:8:LYS:HZ3	33:QB:52:GLU:HB2	1.83	0.44
34:QC:22:TRP:CD1	34:QC:59:ARG:HD2	2.52	0.44
35:QD:194:LEU:HD12	35:QD:195:ALA:H	1.82	0.44
32:QA:406:G:H5'	35:QD:5:ILE:HD11	1.99	0.44
40:QI:16:ARG:HH11	40:QI:64:THR:HG21	1.83	0.44
26:R4:15:ILE:HB	26:R4:32:TYR:CD1	2.53	0.44
1:RA:1011:G:H1'	1:RA:1013:C:O4'	2.18	0.44
1:RA:1104:C:H2'	1:RA:1105:U:H6	1.83	0.44
1:RA:2016:U:H1'	27:R5:6:VAL:HG13	1.98	0.44
20:RY:90:LEU:HD21	20:RY:96:ILE:HG12	1.99	0.44
32:XA:266:G:H5''	32:XA:266:G:N3	2.33	0.44
32:XA:992:U:H4'	32:XA:993:G:C5'	2.48	0.44
34:XC:63:ASN:HB2	34:XC:98:ASN:HB2	1.99	0.44
49:XR:21:LYS:HA	49:XR:21:LYS:HD3	1.79	0.44
1:YA:1045:A:N3	1:YA:1045:A:H2'	2.33	0.44
1:YA:1164:G:H2'	1:YA:1165:U:C6	2.52	0.44
1:YA:1400:G:H2'	1:YA:1401:G:C8	2.53	0.44
1:YA:195:A:H61	1:YA:198:C:H3'	1.83	0.44
1:YA:2320:A:N3	1:YA:2320:A:H2'	2.33	0.44
5:YF:20:LEU:HD12	5:YF:125:LEU:HD13	2.00	0.44
13:YR:56:LYS:NZ	13:YR:90:ARG:O	2.51	0.44
32:QA:1070:U:H2'	32:QA:1071:C:H6	1.83	0.44
32:QA:956:U:OP2	55:QY:137:ARG:NH2	2.51	0.44
33:QB:9:GLU:CD	33:QB:217:ARG:HH22	2.20	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:QF:25:ILE:HG13	37:QF:82:ARG:HH12	1.81	0.44
38:QG:111:ARG:HB3	38:QG:113:GLU:OE2	2.17	0.44
38:QG:45:ASP:O	38:QG:49:ILE:HG13	2.18	0.44
42:QK:85:ARG:HD3	42:QK:113:PRO:HD3	2.00	0.44
51:QT:57:ARG:NH1	51:QT:100:ILE:HD12	2.31	0.44
1:RA:1309:G:P	29:R7:9:ARG:HD3	2.58	0.44
1:RA:1041:C:N4	1:RA:1114:G:H1	2.04	0.44
1:RA:1514:U:H2'	1:RA:1515:G:C8	2.53	0.44
1:RA:1827:C:O2'	1:RA:1970:A:N3	2.41	0.44
1:RA:2133:G:N2	1:RA:2157:G:H2'	2.33	0.44
1:RA:2152:G:H2'	1:RA:2153:G:H8	1.81	0.44
1:RA:2228:G:OP1	3:RD:261:LYS:NZ	2.29	0.44
1:RA:2331:G:O2'	1:RA:2336:A:N1	2.41	0.44
32:XA:1239:A:C4	32:XA:1298:C:N4	2.86	0.44
32:XA:1244:C:H2'	32:XA:1245:A:C8	2.53	0.44
32:XA:1266:G:N2	32:XA:1269:A:OP2	2.46	0.44
32:XA:297:G:H4'	32:XA:557:G:H4'	1.99	0.44
33:XB:53:ARG:HG2	33:XB:56:ARG:HH21	1.83	0.44
44:XM:13:LYS:HA	44:XM:44:ARG:HH11	1.82	0.44
48:XQ:81:ARG:HD2	48:XQ:81:ARG:HA	1.81	0.44
32:XA:1492:A:C2'	55:XY:303:ARG:HH12	2.31	0.44
3:YD:71:ASP:HB3	3:YD:103:ARG:NH2	2.32	0.44
3:YD:85:ASP:OD2	3:YD:88:ARG:HD2	2.18	0.44
1:YA:1143:A:OP1	9:YN:25:ARG:NH2	2.51	0.44
32:QA:1158:C:H5	32:QA:1181:G:N1	2.16	0.44
32:QA:179:A:H2'	32:QA:180:U:H6	1.83	0.44
32:QA:520:A:N1	32:QA:536:C:H1'	2.33	0.44
32:QA:1071:C:H5''	36:QE:49:PRO:HG2	1.99	0.44
41:QJ:11:PHE:CE1	41:QJ:67:THR:HG22	2.48	0.44
43:QL:33:ARG:NH1	43:QL:62:SER:HB3	2.33	0.44
44:QM:15:VAL:O	44:QM:19:LEU:HD13	2.18	0.44
1:RA:1027:A:C6	1:RA:1126:A:C4	3.06	0.44
1:RA:2823:A:OP1	4:RE:113:PHE:HB2	2.18	0.44
1:RA:634:C:H2'	1:RA:635:C:C6	2.53	0.44
3:RD:5:LYS:HB3	3:RD:5:LYS:HE3	1.82	0.44
40:XI:26:VAL:HG13	40:XI:61:ALA:HB3	1.99	0.44
55:XY:123:GLU:OE2	55:XY:186:ARG:HD3	2.18	0.44
24:Y2:35:LEU:HD21	24:Y2:49:LYS:HE2	2.00	0.44
1:YA:1410:G:H2'	1:YA:1411:C:C6	2.53	0.44
1:YA:2107:C:H42	1:YA:2182:G:H1	1.66	0.44
1:YA:362:U:O2'	1:YA:363(A):G:H5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:721:C:H2'	1:YA:722:A:C8	2.53	0.44
12:YQ:52:VAL:HA	12:YQ:55:VAL:HG12	1.99	0.44
32:QA:1241:G:H2'	32:QA:1242:C:C6	2.53	0.44
32:QA:131:C:H2'	32:QA:132:C:C6	2.52	0.44
32:QA:134:A:H61	47:QP:25:ARG:NH1	2.16	0.44
32:QA:19:C:O2'	32:QA:572:A:N1	2.42	0.44
33:QB:155:LEU:HD11	33:QB:159:PRO:HD3	2.00	0.44
34:QC:180:ALA:HB1	34:QC:203:PHE:CE1	2.52	0.44
44:QM:16:ASP:N	44:QM:16:ASP:OD1	2.49	0.44
26:R4:7:PRO:HB2	26:R4:27:THR:HG21	1.99	0.44
1:RA:1210:A:H4'	1:RA:1211:U:O5'	2.17	0.44
1:RA:2893:G:H5''	1:RA:2894:G:O4'	2.18	0.44
1:RA:881:G:H2'	1:RA:882:G:C8	2.52	0.44
8:RI:85:GLU:HB3	8:RI:86:THR:H	1.59	0.44
15:RT:51:ARG:HG3	15:RT:98:LYS:HE3	1.99	0.44
32:XA:1414:U:H3	32:XA:1486:G:H1	1.65	0.44
32:XA:738:C:OP1	37:XF:2:ARG:NH1	2.48	0.44
23:Y1:83:GLU:HA	23:Y1:84:GLY:HA2	1.66	0.44
1:YA:1941:C:C5	1:YA:1942:5MC:HM52	2.53	0.44
1:YA:2128:C:H3'	1:YA:2129:C:H5''	2.00	0.44
1:YA:2552:2MU:H2'	1:YA:2554:U:OP2	2.18	0.44
1:YA:2687:U:H2'	1:YA:2688:U:O4'	2.18	0.44
1:YA:2889:C:H3'	1:YA:2891:G:C8	2.53	0.44
2:YB:95:C:H2'	2:YB:96:U:C6	2.53	0.44
7:YH:95:ARG:HB2	7:YH:128:PRO:HB3	1.99	0.44
11:YP:135:LEU:HA	11:YP:135:LEU:HD23	1.72	0.44
14:YS:43:GLU:OE1	22:Y0:49:LYS:HE3	2.17	0.44
32:QA:1024:G:N2	32:QA:1025:U:O4'	2.48	0.43
32:QA:134:A:H1'	32:QA:325:A:C5	2.53	0.43
32:QA:977:A:H1'	32:QA:982:U:O4	2.18	0.43
40:QI:24:GLY:HA2	40:QI:59:PHE:O	2.18	0.43
1:RA:531:C:H4'	1:RA:532:A:H5''	2.00	0.43
32:XA:1030(B):G:O5'	32:XA:1030(B):G:H8	2.01	0.43
32:XA:1347:G:HO2'	32:XA:1373:G:H1	1.64	0.43
32:XA:501:C:OP1	43:XL:117:ARG:NH2	2.33	0.43
32:XA:790:A:C6	32:XA:791:G:C6	3.06	0.43
1:YA:1110:G:H1'	1:YA:1111:A:H8	1.82	0.43
1:YA:2149:G:C2	1:YA:2150:U:H1'	2.53	0.43
1:YA:2286:A:H4'	1:YA:2287:A:O4'	2.18	0.43
1:YA:251:A:C5	1:YA:252:G:H1'	2.53	0.43
1:YA:2689:U:P	1:YA:2719:G:H22	2.41	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:394:A:C6	1:YA:395:U:C4	3.06	0.43
1:YA:1500:G:O2'	3:YD:100:GLY:O	2.32	0.43
14:YS:25:ARG:HD3	14:YS:42:ASP:OD2	2.18	0.43
32:QA:161:A:H8	32:QA:161:A:O5'	2.01	0.43
33:QB:109:SER:O	33:QB:112:VAL:HG22	2.18	0.43
53:QV:3:C:C2'	53:QV:4:G:H5'	2.48	0.43
55:QY:138:TYR:CD1	55:QY:336:LYS:HB2	2.54	0.43
1:RA:108:U:H2'	1:RA:109:G:H8	1.83	0.43
1:RA:1378:A:OP1	29:R7:10:ARG:NH2	2.52	0.43
1:RA:93:G:H2'	1:RA:94(A):C:C6	2.53	0.43
12:RQ:75:THR:HG21	12:RQ:87:LYS:HG2	1.99	0.43
32:XA:575:G:O2'	32:XA:821:G:H5'	2.18	0.43
32:XA:952:U:H4'	32:XA:964:A:N1	2.33	0.43
33:XB:179:LYS:HA	39:XH:72:PRO:HG3	2.00	0.43
38:XG:16:LEU:HD11	40:XI:45:ALA:HB2	2.00	0.43
32:XA:1202:G:H1'	45:YN:29:ARG:HD2	2.00	0.43
37:XF:91:VAL:HG11	49:XR:72:ARG:NH1	2.33	0.43
55:XY:263:GLN:O	55:XY:267:LYS:N	2.48	0.43
1:YA:1429:G:H2'	1:YA:1430:C:C6	2.53	0.43
1:YA:706:A:H2'	1:YA:707:G:O4'	2.18	0.43
2:YB:14:U:O3'	2:YB:108:U:O2'	2.33	0.43
4:YE:119:ARG:HD3	4:YE:160:TYR:HB2	2.00	0.43
5:YF:101:LEU:HD12	5:YF:102:PRO:HD2	2.00	0.43
6:YG:170:ARG:HH21	6:YG:180:PHE:CB	2.31	0.43
1:YA:2311:A:C2	6:YG:80:PHE:HB3	2.53	0.43
7:YH:137:ASP:HB3	7:YH:140:LYS:HB3	2.01	0.43
7:YH:33:LEU:HD11	7:YH:75:ALA:HB1	2.00	0.43
35:QD:15:GLU:OE2	35:QD:66:ARG:NH1	2.51	0.43
46:QO:71:GLN:HB2	46:QO:78:TYR:CG	2.54	0.43
42:QK:109:VAL:HG23	49:QR:85:LEU:O	2.18	0.43
1:RA:1472:A:H2'	1:RA:1473:G:O4'	2.18	0.43
1:RA:1423:G:OP1	1:RA:1492:G:O2'	2.35	0.43
1:RA:2543:G:H2'	1:RA:2544:G:C8	2.52	0.43
1:RA:2869:G:H2'	1:RA:2870:C:O4'	2.18	0.43
7:RH:137:ASP:HB3	7:RH:140:LYS:HB3	2.00	0.43
13:RR:24:GLN:HE21	13:RR:44:LEU:HG	1.82	0.43
32:XA:1346:A:N1	32:XA:1374:A:H5''	2.32	0.43
32:XA:176:C:H2'	32:XA:177:C:C6	2.54	0.43
32:XA:601:C:H2'	32:XA:602:A:C8	2.53	0.43
32:XA:757:U:H2'	32:XA:758:G:O4'	2.19	0.43
33:XB:114:ARG:NH1	33:XB:118:LEU:HG	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:XB:18:GLY:HA2	33:XB:42:ILE:HD12	1.99	0.43
34:XC:137:ALA:HA	34:XC:140:ARG:NH1	2.34	0.43
55:XY:121:GLY:O	55:XY:123:GLU:N	2.49	0.43
55:XY:177:PHE:CB	55:XY:321:ARG:HH22	2.30	0.43
1:YA:1410:G:H1	1:YA:1592:C:H42	1.65	0.43
1:YA:1587:A:H2'	1:YA:1588:C:C6	2.53	0.43
1:YA:2080:G:OP1	23:Y1:35:THR:HG21	2.18	0.43
1:YA:2186:G:C2	1:YA:2187:G:C5	3.06	0.43
1:YA:300:A:P	20:YY:86:ARG:HH21	2.41	0.43
1:YA:309:G:H21	1:YA:330:A:P	2.40	0.43
32:QA:1239:A:C4	32:QA:1298:C:N4	2.86	0.43
51:QT:39:LYS:HB2	51:QT:39:LYS:HE3	1.90	0.43
55:QY:123:GLU:HG3	55:QY:188:PRO:HB3	2.00	0.43
11:RP:62:LEU:O	30:R8:13:ARG:HD3	2.19	0.43
1:RA:1704:G:H5'	32:QA:1429:C:O2'	2.17	0.43
1:RA:2130:U:H2'	1:RA:2158:A:H61	1.83	0.43
1:RA:2130:U:H2'	1:RA:2158:A:N1	2.34	0.43
18:RW:33:ARG:NH2	18:RW:52:GLU:OE1	2.50	0.43
32:XA:926:G:H22	54:XX:15:A:H3'	1.83	0.43
34:XC:70:VAL:HG22	34:XC:72:LYS:H	1.84	0.43
35:XD:122:ARG:NH1	35:XD:136:PRO:HD3	2.34	0.43
42:XK:116:HIS:N	42:XK:117:ASN:HA	2.34	0.43
47:XP:20:VAL:HG21	47:XP:32:TYR:CD2	2.53	0.43
49:XR:58:LEU:HD12	49:XR:62:GLU:CG	2.48	0.43
1:YA:1080:C:H2'	1:YA:1081:U:C6	2.53	0.43
1:YA:2098:U:H2'	1:YA:2099:U:O4'	2.17	0.43
1:YA:2133:G:N2	1:YA:2157:G:H2'	2.34	0.43
4:YE:150:VAL:CG1	4:YE:154:LYS:HG3	2.47	0.43
4:YE:34:VAL:HG12	4:YE:72:VAL:HG21	2.00	0.43
7:YH:9:ILE:HG12	7:YH:69:ARG:HD3	2.01	0.43
32:QA:56:U:H2'	32:QA:57:G:H8	1.83	0.43
45:QN:3:ARG:HA	45:QN:3:ARG:HD3	1.77	0.43
51:QT:101:GLY:HA2	51:QT:102:GLY:HA2	1.68	0.43
53:QV:64:G:H2'	53:QV:65:C:C6	2.54	0.43
1:RA:2394:C:OP2	30:R8:30:ARG:HD2	2.18	0.43
1:RA:2114:A:H3'	1:RA:2115:G:H8	1.83	0.43
1:RA:2122:U:H3	1:RA:2176:A:N6	2.15	0.43
1:RA:657:U:H2'	1:RA:658:C:C6	2.54	0.43
6:RG:131:TYR:HB3	6:RG:159:VAL:CG1	2.48	0.43
8:RI:75:LEU:HD22	8:RI:105:HIS:ND1	2.33	0.43
32:XA:839:U:H3'	32:XA:840:C:C5	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:XP:75:ARG:HG3	47:XP:80:PHE:HD2	1.84	0.43
55:XY:138:TYR:CD1	55:XY:336:LYS:HB2	2.53	0.43
1:YA:1638:C:O3'	1:YA:2709:G:N2	2.51	0.43
1:YA:1790:C:H5''	1:YA:1791:A:OP1	2.18	0.43
1:YA:1810:A:H2'	1:YA:1811:G:O4'	2.19	0.43
1:YA:2184:G:N1	1:YA:2185:C:O2	2.51	0.43
9:YN:62:VAL:HG11	9:YN:66:LYS:HB2	2.00	0.43
32:QA:1493:A:H4'	55:QY:121:GLY:N	2.34	0.43
32:QA:575:G:N2	32:QA:881:G:H1'	2.33	0.43
34:QC:18:TRP:HZ2	45:QN:57:ARG:HB3	1.83	0.43
39:QH:41:ARG:NH1	39:QH:123:GLU:OE2	2.48	0.43
38:QG:150:ALA:HA	42:QK:59:TYR:HB3	2.01	0.43
46:QO:61:GLY:O	46:QO:65:ARG:HG3	2.19	0.43
26:R4:59:PHE:CE1	50:QS:64:GLU:HA	2.53	0.43
1:RA:577:G:O2'	1:RA:1254:A:OP1	2.33	0.43
1:RA:2086:U:H2'	1:RA:2087:G:C8	2.52	0.43
1:RA:2186:G:C2	1:RA:2187:G:C5	3.06	0.43
1:RA:321:G:O2'	1:RA:340:A:N3	2.51	0.43
6:RG:55:LYS:O	6:RG:59:GLU:HG3	2.18	0.43
11:RP:84:ASN:OD1	11:RP:117:GLU:HB2	2.19	0.43
12:RQ:16:ARG:HG2	12:RQ:18:LYS:HD3	2.00	0.43
13:RR:104:ARG:HD2	13:RR:107:ASP:OD1	2.19	0.43
1:RA:2319:G:H22	14:RS:3:ARG:CZ	2.32	0.43
14:RS:66:ALA:O	14:RS:69:VAL:HG22	2.19	0.43
16:RU:86:ALA:O	17:RV:49:THR:HG23	2.18	0.43
32:XA:1103:C:OP1	33:XB:96:ARG:NH1	2.50	0.43
32:XA:1402:4OC:H6	32:XA:1402:4OC:O5'	2.19	0.43
32:XA:864:A:H2'	32:XA:865:A:C8	2.54	0.43
34:XC:180:ALA:HB1	34:XC:203:PHE:CE1	2.53	0.43
22:Y0:50:ASN:HB3	22:Y0:63:VAL:HG22	2.00	0.43
1:YA:1073:A:O2'	1:YA:1074:G:O5'	2.36	0.43
1:YA:1404:C:H2'	1:YA:1405:U:H6	1.83	0.43
1:YA:1518:U:H2'	1:YA:1519:G:O4'	2.19	0.43
1:YA:2734:A:H2'	1:YA:2735:G:O4'	2.18	0.43
1:YA:873:G:H1	1:YA:904:C:H42	1.64	0.43
4:YE:59:VAL:HG12	4:YE:64:LYS:HG3	2.00	0.43
1:YA:911:A:H2'	12:YQ:9:TYR:OH	2.18	0.43
21:YZ:23:LYS:NZ	21:YZ:40:ASP:OD2	2.51	0.43
34:QC:36:ASP:OD1	34:QC:57:ILE:HG21	2.18	0.43
26:R4:50:VAL:HG13	44:QM:65:LYS:HG2	2.01	0.43
53:QV:4:G:O2'	53:QV:5:G:H8	2.02	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1029:A:N6	1:RA:1125:G:O2'	2.50	0.43
1:RA:184:C:H2'	1:RA:185:U:C6	2.53	0.43
1:RA:607:U:OP1	5:RF:102:PRO:HA	2.18	0.43
12:RQ:55:VAL:HG12	12:RQ:64:ILE:HD12	1.99	0.43
32:XA:1062:U:H2'	32:XA:1063:C:C6	2.53	0.43
32:XA:114:U:H2'	32:XA:115:G:C8	2.54	0.43
38:XG:50:ILE:HD11	38:XG:58:PRO:HA	2.00	0.43
41:XJ:45:ARG:HG2	41:XJ:47:PHE:CZ	2.54	0.43
32:XA:750:G:N3	46:XO:23:GLY:HA3	2.33	0.43
55:XY:229:SER:OG	55:XY:242:SER:O	2.37	0.43
1:YA:2526:G:C2'	31:Y9:1:MET:H1	2.28	0.43
1:YA:2693:A:H2'	1:YA:2694:G:C8	2.54	0.43
1:YA:370:G:H4'	1:YA:371:A:OP2	2.18	0.43
1:YA:78:A:H2'	1:YA:79:G:H8	1.83	0.43
5:YF:34:TRP:CH2	11:YP:8:PRO:HB3	2.54	0.43
6:YG:126:ASP:HB3	6:YG:128:ARG:H	1.84	0.43
6:YG:47:LYS:HG2	6:YG:48:GLU:N	2.34	0.43
9:YN:58:ASP:N	9:YN:58:ASP:OD1	2.49	0.43
16:YU:49:HIS:HA	16:YU:52:ARG:HB3	1.98	0.43
18:YW:19:LEU:HD23	27:Y5:25:LEU:HD21	2.00	0.43
32:QA:620:C:H2'	32:QA:621:A:O4'	2.19	0.43
42:QK:18:ARG:NH2	42:QK:35:PRO:O	2.52	0.43
53:QV:28:C:H2'	53:QV:29:G:H8	1.82	0.43
1:RA:1778:U:H2'	1:RA:1784:A:N6	2.33	0.43
1:RA:2106:G:C4	1:RA:2107:C:H1'	2.54	0.43
3:RD:145:VAL:HB	3:RD:155:LEU:HB2	2.01	0.43
1:RA:601:C:OP1	5:RF:108:LYS:HE3	2.18	0.43
6:RG:106:LEU:HA	6:RG:110:ALA:HB3	1.99	0.43
1:RA:1188:U:C4'	17:RV:79:VAL:HG22	2.49	0.43
32:XA:537:G:H5''	43:XL:113:ARG:NH1	2.34	0.43
32:XA:737:A:H2'	32:XA:738:C:H6	1.84	0.43
34:XC:148:GLY:HA3	34:XC:172:ARG:O	2.19	0.43
35:XD:153:ARG:HG2	35:XD:153:ARG:H	1.65	0.43
41:XJ:49:VAL:HG22	41:XJ:50:ILE:O	2.18	0.43
43:XL:32:PHE:CD2	43:XL:86:ARG:HB3	2.54	0.43
44:XM:15:VAL:O	44:XM:19:LEU:HD13	2.17	0.43
32:XA:273:A:H1'	48:XQ:16:GLN:NE2	2.33	0.43
55:XY:328:ARG:O	55:XY:329:LEU:HG	2.18	0.43
30:Y8:63:PRO:HG2	30:Y8:64:TYR:CD2	2.54	0.43
1:YA:1045:A:H8	1:YA:1047:G:N3	2.17	0.43
1:YA:1091:G:H2'	1:YA:1091:G:N3	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1359:A:N6	1:YA:1372:U:H3	2.15	0.43
1:YA:2119:A:O2'	1:YA:2120:G:H5'	2.18	0.43
1:YA:2348:U:O4	1:YA:2382:G:N1	2.52	0.43
1:YA:528:A:O2'	1:YA:529:A:H5'	2.19	0.43
3:YD:142:VAL:HG23	3:YD:193:VAL:HA	2.00	0.43
9:YN:131:GLN:CD	9:YN:131:GLN:H	2.21	0.43
1:YA:1287:A:H8	13:YR:104:ARG:HD3	1.83	0.43
15:YT:118:ARG:HH22	15:YT:121:ILE:HG21	1.84	0.43
32:QA:1323:G:H2'	32:QA:1324:A:C8	2.53	0.43
32:QA:567:G:H2'	32:QA:568:G:O4'	2.19	0.43
33:QB:124:SER:HA	33:QB:125:PRO:HA	1.71	0.43
37:QF:89:MET:HE1	49:QR:72:ARG:HB3	2.01	0.43
1:RA:1179:C:H2'	1:RA:1180:C:C6	2.54	0.43
1:RA:1530:C:N4	1:RA:1539:G:H1	2.16	0.43
1:RA:2389:G:H5''	1:RA:2390:U:O4'	2.19	0.43
1:RA:251:A:C5	1:RA:252:G:H1'	2.54	0.43
6:RG:114:ILE:HG12	6:RG:140:ILE:HG12	2.01	0.43
19:RX:41:ASN:O	19:RX:45:THR:HG23	2.18	0.43
20:RY:19:LYS:HE2	20:RY:19:LYS:HB3	1.86	0.43
33:XB:19:HIS:CG	33:XB:20:GLU:H	2.36	0.43
34:XC:180:ALA:HB1	34:XC:203:PHE:HE1	1.84	0.43
39:XH:73:ASP:OD1	39:XH:75:ARG:HD3	2.19	0.43
45:XN:4:LYS:O	45:XN:7:ILE:HG12	2.19	0.43
50:XS:30:LEU:HD11	50:XS:50:ALA:HB2	2.00	0.43
55:XY:103:LYS:HE2	55:XY:103:LYS:HB3	1.88	0.43
55:XY:165:LYS:HE2	55:XY:167:SER:OG	2.19	0.43
1:YA:1058:G:N2	1:YA:1080:C:N3	2.59	0.43
1:YA:1530:C:HO2'	1:YA:1531:C:P	2.38	0.43
1:YA:2119:A:N6	1:YA:2168:G:H21	2.16	0.43
1:YA:2137:C:H1'	1:YA:2154:G:H22	1.84	0.43
1:YA:336:C:O2'	20:YY:35:TYR:OH	2.34	0.43
1:YA:956:G:OP2	12:YQ:14:ARG:NH2	2.49	0.43
19:YX:56:THR:HB	19:YX:77:LYS:HE3	2.01	0.43
20:YY:87:LYS:HB3	20:YY:95:LYS:HD3	2.00	0.43
32:QA:46:G:H2'	32:QA:366:C:C5	2.54	0.43
36:QE:33:VAL:HG13	36:QE:112:LEU:HD12	2.01	0.43
55:QY:114:GLU:HB3	55:QY:163:ILE:HB	2.01	0.43
1:RA:2870:C:H2'	1:RA:2871:C:O4'	2.19	0.43
1:RA:492:A:H2'	1:RA:493:G:O4'	2.19	0.43
1:RA:1971:A:P	3:RD:242:ARG:HH22	2.41	0.43
12:RQ:110:THR:HG23	12:RQ:113:GLN:OE1	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:RT:60:THR:HG22	15:RT:77:PRO:HA	2.01	0.43
32:XA:1023:G:H3'	32:XA:1024:G:C8	2.50	0.43
32:XA:1039:C:C4	32:XA:1040:U:C4	3.06	0.43
32:XA:1342:C:H2'	32:XA:1343:G:C8	2.54	0.43
1:YA:1050:A:C2	1:YA:1051:G:C5	3.06	0.43
1:YA:1759:A:H1'	1:YA:2711:A:C2	2.54	0.43
7:YH:84:SER:HA	7:YH:133:VAL:O	2.18	0.43
9:YN:34:LEU:HD23	9:YN:107:LEU:HD11	2.01	0.43
9:YN:108:PRO:O	9:YN:113:GLY:HA3	2.19	0.43
32:QA:1065:U:H4'	32:QA:1066:C:O5'	2.19	0.42
32:QA:320:C:O2'	32:QA:1435:G:O2'	2.31	0.42
42:QK:20:TYR:HB2	42:QK:31:THR:HG23	2.01	0.42
44:QM:11:ARG:C	44:QM:13:LYS:H	2.23	0.42
32:QA:1047:G:H5''	45:QN:4:LYS:HD3	2.01	0.42
55:QY:119:THR:HG21	55:QY:303:ARG:HH11	1.83	0.42
26:R4:56:VAL:HB	26:R4:60:GLN:HG2	2.01	0.42
1:RA:1503:U:H2'	1:RA:1504:C:C6	2.54	0.42
1:RA:2355:C:H1'	22:R0:39:ARG:HH21	1.83	0.42
1:RA:476:G:H4'	1:RA:502:A:N1	2.34	0.42
1:RA:886:C:O2'	1:RA:889:C:N4	2.51	0.42
3:RD:206:LEU:HD22	3:RD:211:ARG:HG2	2.00	0.42
32:XA:1315:U:H2'	32:XA:1316:G:O4'	2.18	0.42
32:XA:779:C:H2'	32:XA:780:A:O4'	2.19	0.42
34:XC:164:ARG:HG2	34:XC:165:THR:H	1.83	0.42
34:XC:77:ILE:O	34:XC:84:ILE:N	2.47	0.42
34:XC:6:HIS:NE2	34:XC:8:ILE:HB	2.34	0.42
32:XA:1151:A:O4'	41:XJ:39:PRO:HB2	2.19	0.42
41:XJ:70:ARG:HD3	41:XJ:70:ARG:HA	1.88	0.42
1:YA:577:G:O2'	1:YA:1254:A:OP1	2.33	0.42
1:YA:1798:U:H5'	3:YD:259:THR:CG2	2.46	0.42
1:YA:2262:U:H4'	1:YA:2328:A:H2	1.83	0.42
1:YA:78:A:H2'	1:YA:79:G:C8	2.53	0.42
7:YH:72:ILE:O	7:YH:75:ALA:HB3	2.19	0.42
12:YQ:11:LYS:HE2	12:YQ:88:GLY:O	2.19	0.42
21:YZ:33:LEU:HD11	21:YZ:90:VAL:HG21	2.00	0.42
32:QA:159:G:H2'	32:QA:161:A:OP2	2.18	0.42
32:QA:576:G:N2	32:QA:760:G:OP1	2.52	0.42
36:QE:50:GLU:HB2	36:QE:53:LEU:HD13	2.01	0.42
42:QK:70:LYS:HB2	42:QK:70:LYS:HE2	1.86	0.42
47:QP:74:LEU:O	47:QP:79:VAL:HG22	2.19	0.42
53:QV:47:U:H3'	53:QV:48:C:C5'	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:R3:8:LEU:CD1	25:R3:31:LEU:HD22	2.49	0.42
1:RA:1053:C:O2'	1:RA:1054:A:O5'	2.37	0.42
1:RA:1091:G:H2'	1:RA:1091:G:N3	2.34	0.42
1:RA:1056:G:N1	1:RA:1102:C:OP2	2.45	0.42
1:RA:2051:A:H5'	1:RA:2578:G:O4'	2.19	0.42
1:RA:2390:U:O2'	1:RA:2391:G:H5'	2.19	0.42
1:RA:740:U:H2'	1:RA:741:G:C8	2.54	0.42
6:RG:170:ARG:O	6:RG:170:ARG:HD3	2.19	0.42
7:RH:86:GLU:HB3	7:RH:165:ALA:HB2	2.01	0.42
21:RZ:70:LEU:HG	21:RZ:91:LEU:HD21	2.01	0.42
32:XA:954:G:H21	32:XA:1227:A:H62	1.67	0.42
32:XA:1504:G:OP1	32:XA:1507:A:H4'	2.19	0.42
32:XA:65:U:H1'	32:XA:66:G:OP2	2.18	0.42
33:XB:71:VAL:HG12	33:XB:93:VAL:CG2	2.49	0.42
43:XL:117:ARG:HB3	43:XL:122:THR:O	2.19	0.42
55:XY:312:PHE:H	55:XY:313:PRO:HD2	1.83	0.42
25:Y3:24:LYS:HE2	25:Y3:24:LYS:HB2	1.89	0.42
6:YG:101:ILE:HD13	26:Y4:25:TYR:HB2	2.01	0.42
1:YA:2742:C:P	31:Y9:35:ARG:HH11	2.41	0.42
1:YA:1371:G:O2'	1:YA:1372:U:H5	2.02	0.42
1:YA:634:C:H2'	1:YA:635:C:C6	2.54	0.42
3:YD:38:LYS:HD2	3:YD:38:LYS:HA	1.82	0.42
6:YG:170:ARG:NH2	6:YG:182:LYS:O	2.51	0.42
6:YG:16:ARG:O	6:YG:20:ILE:HG13	2.19	0.42
12:YQ:60:ARG:NH2	21:YZ:181:GLU:OE1	2.49	0.42
32:QA:1084:G:C5	32:QA:1085:U:C4	3.08	0.42
37:QF:61:LEU:HD23	37:QF:63:TYR:OH	2.19	0.42
41:QJ:38:ILE:CG1	41:QJ:71:LEU:HB3	2.49	0.42
32:QA:790:A:H1'	53:QV:38:A:H4'	2.00	0.42
26:R4:59:PHE:CE1	50:QS:64:GLU:HG3	2.53	0.42
1:RA:1035:U:OP2	7:RH:59:ARG:NH2	2.52	0.42
8:RI:109:ILE:HA	8:RI:109:ILE:HD12	1.76	0.42
16:RU:49:HIS:HA	16:RU:52:ARG:HB3	2.01	0.42
19:RX:5:TYR:HD1	24:R2:33:MET:SD	2.42	0.42
32:XA:18:C:H4'	32:XA:1078:U:O2	2.19	0.42
33:XB:213:LEU:O	33:XB:217:ARG:HB2	2.20	0.42
40:XI:37:PHE:HB3	40:XI:43:ALA:CB	2.50	0.42
47:XP:21:VAL:HG11	47:XP:59:TRP:NE1	2.34	0.42
55:XY:309:THR:HG23	55:XY:320:HIS:NE2	2.34	0.42
23:Y1:85:LEU:HD23	23:Y1:89:GLU:HB3	2.01	0.42
1:YA:1153:C:H2'	1:YA:1154:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:234:C:H2'	1:YA:235:U:C6	2.54	0.42
1:YA:9:U:H3	1:YA:2629:A:H2	1.66	0.42
7:YH:9:ILE:HG12	7:YH:69:ARG:CD	2.50	0.42
19:YX:44:GLU:HG3	19:YX:51:VAL:HG23	2.01	0.42
20:YY:7:VAL:CG1	20:YY:27:VAL:HG21	2.49	0.42
32:QA:437:U:H5'	35:QD:155:LEU:HD21	2.01	0.42
32:QA:575:G:C5	32:QA:881:G:C2	3.07	0.42
37:QF:35:ALA:HA	37:QF:67:MET:HB3	2.01	0.42
32:QA:553:A:H5''	43:QL:24:VAL:HG21	2.01	0.42
44:QM:108:ARG:NH1	44:QM:112:GLY:O	2.48	0.42
55:QY:312:PHE:N	55:QY:313:PRO:HD2	2.35	0.42
1:RA:1400:G:H2'	1:RA:1401:G:C8	2.54	0.42
1:RA:2119:A:H61	1:RA:2168:G:H21	1.66	0.42
2:RB:90:A:N7	2:RB:91:C:H1'	2.34	0.42
12:RQ:35:VAL:CG1	12:RQ:130:LYS:HB3	2.49	0.42
32:XA:528:C:H5'	32:XA:529:G:OP2	2.19	0.42
32:XA:993:G:O6	32:XA:1045:C:N4	2.48	0.42
34:XC:64:VAL:O	34:XC:99:VAL:HA	2.19	0.42
39:XH:98:LYS:HE3	39:XH:98:LYS:HB2	1.80	0.42
41:XJ:21:GLN:O	41:XJ:25:GLU:HG2	2.20	0.42
47:XP:66:PRO:HG2	47:XP:71:ARG:NH1	2.34	0.42
1:YA:1036:G:H1	1:YA:1119:C:H42	1.67	0.42
1:YA:1493:C:C5	1:YA:2206:G:H2'	2.54	0.42
1:YA:2144:U:H1'	1:YA:2147:G:O6	2.19	0.42
1:YA:2693:A:H2'	1:YA:2694:G:H8	1.84	0.42
6:YG:9:ARG:NH1	6:YG:13:GLU:OE1	2.45	0.42
8:YI:48:GLU:HG3	8:YI:52:ARG:HH11	1.83	0.42
15:YT:28:VAL:HG13	15:YT:86:ILE:HG23	2.00	0.42
32:QA:1518:MA6:H93	32:QA:1519:MA6:H92	2.02	0.42
36:QE:57:LYS:HG2	36:QE:61:TYR:HE2	1.81	0.42
37:QF:23:LYS:NZ	37:QF:42:GLU:OE2	2.29	0.42
32:QA:1125:U:H4'	41:QJ:5:ARG:NH2	2.34	0.42
55:QY:184:VAL:O	55:QY:198:THR:HA	2.18	0.42
1:RA:1668:A:O2'	1:RA:1674:G:N7	2.48	0.42
1:RA:2320:A:N3	1:RA:2320:A:H2'	2.34	0.42
1:RA:493:G:H2'	1:RA:494:G:O4'	2.19	0.42
1:RA:828:U:H4'	1:RA:831:G:N1	2.34	0.42
3:RD:242:ARG:HD3	3:RD:242:ARG:N	2.34	0.42
11:RP:101:VAL:HA	11:RP:106:LEU:O	2.19	0.42
12:RQ:35:VAL:HG13	12:RQ:130:LYS:HB3	2.01	0.42
20:RY:20:TYR:O	20:RY:23:ARG:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:1004:A:H5'	32:XA:1025:U:C5	2.48	0.42
32:XA:1402:4OC:HM41	54:XX:18:G:OP2	2.18	0.42
40:XI:112:LYS:HE2	40:XI:117:HIS:O	2.19	0.42
32:XA:101:A:H5'	51:XT:10:LEU:HD21	2.02	0.42
1:YA:125:G:N3	29:Y7:48:LYS:HE2	2.34	0.42
1:YA:1019:U:H2'	1:YA:1020:A:C8	2.54	0.42
1:YA:2321:G:HO2'	1:YA:2322:A:P	2.40	0.42
1:YA:2390:U:O2'	1:YA:2391:G:H5'	2.20	0.42
1:YA:2757:A:N3	7:YH:63:SER:OG	2.52	0.42
1:YA:861:A:H2'	1:YA:862:G:O4'	2.19	0.42
1:YA:945:A:C4	1:YA:2448:A:C2	3.07	0.42
32:QA:1024:G:N3	32:QA:1024:G:H2'	2.34	0.42
35:QD:8:VAL:HG22	35:QD:21:LEU:HD13	2.01	0.42
38:QG:113:GLU:HG3	38:QG:118:VAL:HG12	2.00	0.42
44:QM:74:VAL:O	44:QM:78:ILE:HG13	2.20	0.42
55:QY:325:THR:O	55:QY:325:THR:OG1	2.34	0.42
26:R4:57:GLU:CB	26:R4:58:ARG:HA	2.48	0.42
1:RA:1291:C:H2'	1:RA:1292:U:C6	2.55	0.42
1:RA:1288:U:C2	1:RA:1327:C:O2	2.73	0.42
1:RA:1430:C:H2'	1:RA:1431:U:C6	2.55	0.42
1:RA:1504:C:H2'	1:RA:1505:C:C6	2.54	0.42
1:RA:330:A:HO2'	1:RA:331:A:H8	1.62	0.42
2:RB:14:U:O3'	2:RB:108:U:O2'	2.37	0.42
4:RE:116:VAL:HG13	4:RE:122:PHE:HB2	2.01	0.42
21:RZ:140:ASP:OD1	21:RZ:142:SER:OG	2.38	0.42
32:XA:1030(B):G:H21	32:XA:1030(D):G:H3'	1.84	0.42
32:XA:1301:U:O2'	32:XA:1302:U:H5'	2.19	0.42
32:XA:796:C:O5'	32:XA:796:C:H6	2.03	0.42
33:XB:118:LEU:HD23	33:XB:118:LEU:HA	1.87	0.42
33:XB:58:ILE:CG2	33:XB:222:ILE:HG22	2.50	0.42
33:XB:178:ARG:NH2	39:XH:74:PRO:HB3	2.35	0.42
39:XH:82:HIS:NE2	39:XH:84:ARG:HG2	2.35	0.42
46:XO:35:ARG:HH21	46:XO:59:MET:HE2	1.84	0.42
47:XP:4:ILE:HG23	47:XP:36:ILE:HD11	2.01	0.42
50:XS:20:LEU:HA	50:XS:23:ASN:HB2	2.02	0.42
55:XY:322:ILE:HD12	55:XY:324:LEU:HD13	2.02	0.42
1:YA:1065:U:H4'	1:YA:1066:U:C5'	2.48	0.42
1:YA:1092:C:O2	1:YA:1092:C:H2'	2.18	0.42
1:YA:1108:U:H3'	1:YA:1109:C:C6	2.54	0.42
1:YA:1139:G:O2'	1:YA:1143:A:N1	2.43	0.42
1:YA:1529:G:C6	1:YA:1530:C:N4	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1668:A:H4'	1:YA:1669:A:O5'	2.18	0.42
1:YA:1695:G:H1'	3:YD:8:PRO:O	2.20	0.42
1:YA:2109:U:H2'	1:YA:2110:G:C8	2.54	0.42
5:YF:135:LYS:HG3	5:YF:137:LYS:HG2	2.01	0.42
7:YH:154:PRO:HB3	7:YH:163:TYR:CE2	2.54	0.42
10:YO:26:LYS:O	10:YO:30:ALA:HB2	2.20	0.42
21:YZ:140:ASP:OD1	21:YZ:142:SER:OG	2.38	0.42
32:QA:1504:G:OP1	32:QA:1507:A:H4'	2.20	0.42
35:QD:188:LEU:HA	35:QD:189:PRO:HD3	1.90	0.42
35:QD:173:TRP:CG	35:QD:189:PRO:HG3	2.54	0.42
40:QI:46:ALA:HB2	40:QI:74:ILE:HG23	2.02	0.42
41:QJ:30:SER:OG	41:QJ:81:THR:HG22	2.18	0.42
32:QA:1302:U:C5	44:QM:17:VAL:HG21	2.55	0.42
45:QN:45:ARG:O	45:QN:49:HIS:HD2	2.01	0.42
1:RA:1057:A:N6	1:RA:1087:G:OP2	2.53	0.42
1:RA:1069:A:H5'	1:RA:1096:A:H5'	2.02	0.42
1:RA:1092:C:O2	1:RA:1092:C:H2'	2.18	0.42
1:RA:1022:G:C5	1:RA:1140:C:C4	3.08	0.42
1:RA:1418:G:H8	1:RA:1418:G:O5'	2.02	0.42
1:RA:1570:A:H2'	1:RA:1571:A:C8	2.54	0.42
1:RA:641:C:O2'	1:RA:2350:C:OP1	2.31	0.42
1:RA:250:G:C6	1:RA:251:A:C6	3.08	0.42
1:RA:582:G:H2'	1:RA:583:G:C8	2.54	0.42
8:RI:72:LEU:HD12	8:RI:138:ILE:HG21	2.01	0.42
15:RT:105:LEU:HA	15:RT:105:LEU:HD23	1.89	0.42
37:XF:10:LEU:HB2	37:XF:59:TYR:HB3	2.01	0.42
26:Y4:61:ARG:HD3	50:XS:67:VAL:HG12	2.02	0.42
51:XT:37:SER:O	51:XT:41:ILE:HG12	2.20	0.42
1:YA:1055:G:H2'	1:YA:1056:G:O4'	2.19	0.42
1:YA:1504:C:H2'	1:YA:1505:C:C6	2.54	0.42
1:YA:1641:A:H2'	1:YA:1642:G:O4'	2.19	0.42
1:YA:2112:G:H2'	1:YA:2113:U:C6	2.55	0.42
1:YA:724:U:H2'	1:YA:725:G:O4'	2.20	0.42
1:YA:875:G:H2'	1:YA:876:C:O4'	2.20	0.42
2:YB:78:A:C2	2:YB:100:A:C4	3.08	0.42
5:YF:129:PHE:O	5:YF:132:VAL:HG22	2.19	0.42
32:QA:571:U:H2'	32:QA:917:G:H4'	2.01	0.42
33:QB:51:LEU:HD23	33:QB:201:ILE:HD12	2.02	0.42
32:QA:1232:U:H5"	40:QI:124:GLN:O	2.20	0.42
45:QN:32:SER:HB3	45:QN:41:ARG:HG2	2.01	0.42
45:QN:4:LYS:HG3	45:QN:7:ILE:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:QP:79:VAL:HG23	47:QP:80:PHE:CD1	2.54	0.42
51:QT:92:LEU:O	51:QT:96:GLY:N	2.48	0.42
1:RA:1668:A:H4'	1:RA:1669:A:O5'	2.20	0.42
1:RA:196:A:H2'	1:RA:196:A:N3	2.35	0.42
1:RA:2119:A:N6	1:RA:2168:G:H21	2.16	0.42
1:RA:2118:U:H5	1:RA:2148:G:H1'	1.85	0.42
1:RA:2321:G:HO2'	1:RA:2322:A:P	2.42	0.42
1:RA:898:C:H2'	1:RA:899:A:O4'	2.20	0.42
2:RB:8:U:O3'	14:RS:25:ARG:NH2	2.38	0.42
3:RD:77:ALA:HB2	3:RD:97:TYR:CD2	2.55	0.42
10:RO:2:ILE:HD12	10:RO:6:THR:HG21	2.01	0.42
32:XA:1318:A:O2'	50:XS:37:ARG:HD2	2.19	0.42
51:XT:72:LEU:HD23	51:XT:72:LEU:HA	1.89	0.42
55:XY:341:ILE:O	55:XY:345:ILE:HG13	2.20	0.42
24:Y2:38:GLN:HB3	24:Y2:44:LEU:HB2	2.01	0.42
1:YA:760:G:H2'	1:YA:761:A:O4'	2.20	0.42
2:YB:78:A:H2'	2:YB:79:C:O4'	2.19	0.42
5:YF:129:PHE:CD2	5:YF:163:VAL:HG21	2.54	0.42
32:QA:1187:G:H4'	40:QI:111:ARG:NH1	2.35	0.42
32:QA:604:G:C6	32:QA:635:G:C6	3.08	0.42
1:RA:1045:A:N3	1:RA:1045:A:H2'	2.35	0.42
1:RA:1110:G:H1'	1:RA:1111:A:C8	2.54	0.42
1:RA:1292:U:H2'	1:RA:1293:C:C6	2.55	0.42
1:RA:1300:U:C2	1:RA:1626:G:C6	3.08	0.42
1:RA:276:A:H5''	1:RA:277:C:H5'	2.01	0.42
1:RA:334:C:OP1	1:RA:335:C:N4	2.53	0.42
1:RA:569:U:C4	1:RA:570:G:C6	3.08	0.42
1:RA:581:C:H2'	1:RA:582:G:C8	2.55	0.42
1:RA:612:C:H2'	1:RA:613:G:O4'	2.20	0.42
4:RE:101:ARG:CZ	4:RE:171:GLU:HB2	2.50	0.42
6:RG:66:GLN:HB3	6:RG:92:VAL:HG21	2.02	0.42
32:XA:1005:A:C5	32:XA:1006:C:H1'	2.55	0.42
32:XA:110:C:H2'	32:XA:111:G:O4'	2.19	0.42
32:XA:343:U:O3'	32:XA:344:A:H8	2.03	0.42
32:XA:688:G:H2'	32:XA:689:C:H6	1.84	0.42
34:XC:54:ARG:NH1	34:XC:54:ARG:HB3	2.35	0.42
41:XJ:19:SER:O	41:XJ:23:ILE:HG12	2.19	0.42
47:XP:17:TYR:HE1	47:XP:41:PRO:HG3	1.84	0.42
51:XT:43:LEU:HD13	51:XT:51:GLU:HB3	2.00	0.42
52:XU:12:LYS:HB3	52:XU:22:ARG:HD2	2.01	0.42
53:XV:3:C:C2'	53:XV:4:G:H5'	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:XY:123:GLU:HG3	55:XY:188:PRO:HB3	2.02	0.42
55:XY:333:MET:HG2	55:XY:333:MET:H	1.50	0.42
1:YA:468:G:N7	29:Y7:39:ARG:NH2	2.59	0.42
1:YA:1826:G:H4'	3:YD:242:ARG:NH1	2.35	0.42
12:YQ:32:TYR:OH	12:YQ:111:GLU:OE1	2.29	0.42
32:QA:1023:G:H2'	32:QA:1024:G:N7	2.35	0.42
35:QD:61:LYS:HD2	35:QD:207:TYR:OH	2.20	0.42
35:QD:57:ARG:HH22	36:QE:107:ARG:HD3	1.85	0.42
55:QY:312:PHE:H	55:QY:313:PRO:HD2	1.85	0.42
55:QY:311:ASN:ND2	55:QY:314:GLN:HB2	2.35	0.42
1:RA:1073:A:O2'	1:RA:1074:G:O5'	2.36	0.42
1:RA:1080:C:H2'	1:RA:1081:U:C6	2.55	0.42
1:RA:1607:C:N4	1:RA:1622:G:OP2	2.34	0.42
1:RA:2282:G:OP1	1:RA:2283:C:H1'	2.19	0.42
4:RE:150:VAL:CG1	4:RE:154:LYS:HG3	2.50	0.42
10:RO:26:LYS:O	10:RO:30:ALA:HB2	2.19	0.42
32:XA:1442(A):G:N3	32:XA:1442(A):G:H2'	2.34	0.42
32:XA:148:G:H2'	32:XA:149:A:C8	2.55	0.42
32:XA:148:G:H2'	32:XA:149:A:H8	1.85	0.42
32:XA:163:C:H2'	32:XA:164:U:O4'	2.19	0.42
32:XA:448:A:P	32:XA:485:G:H22	2.41	0.42
32:XA:567:G:H2'	32:XA:568:G:O4'	2.20	0.42
32:XA:745:C:H1'	32:XA:836:G:O2'	2.20	0.42
32:XA:1151:A:H5"	41:XJ:41:PRO:HA	2.02	0.42
50:XS:23:ASN:HA	50:XS:27:GLU:OE2	2.20	0.42
55:XY:101:LEU:H	55:XY:102:PRO:HD2	1.84	0.42
55:XY:211:ASP:OD1	55:XY:286:ARG:NH2	2.52	0.42
1:YA:1022:G:C5	1:YA:1140:C:C4	3.07	0.42
1:YA:1179:C:H2'	1:YA:1180:C:C6	2.55	0.42
1:YA:1510:G:H2'	1:YA:1511:C:C6	2.55	0.42
7:YH:90:LYS:HD3	7:YH:159:GLU:HG2	2.02	0.42
8:YI:129:THR:HA	8:YI:138:ILE:O	2.20	0.42
32:QA:107:G:H2'	32:QA:108:G:O4'	2.20	0.41
32:QA:112:G:H4'	32:QA:389:A:H4'	2.02	0.41
33:QB:47:THR:HA	33:QB:202:PRO:HG2	2.02	0.41
36:QE:69:VAL:HA	36:QE:70:PRO:HD3	1.78	0.41
42:QK:79:SER:HA	42:QK:104:GLN:HB2	2.01	0.41
44:QM:13:LYS:HA	44:QM:44:ARG:NH1	2.34	0.41
50:QS:52:TYR:HB2	50:QS:57:HIS:CD2	2.54	0.41
55:QY:222:LEU:HD13	55:QY:246:ILE:HG21	2.01	0.41
1:RA:1057:A:C2	1:RA:1058:G:C4	3.07	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:2188:C:H2'	1:RA:2189:U:O4'	2.20	0.41
1:RA:2648:C:H2'	1:RA:2649:U:C6	2.55	0.41
1:RA:2690:C:N4	1:RA:2713:A:H1'	2.35	0.41
32:XA:1003:G:H3'	32:XA:1003:G:N3	2.35	0.41
32:XA:1206:G:H2'	32:XA:1207:2MG:O4'	2.20	0.41
32:XA:501:C:H2'	32:XA:502:G:H8	1.83	0.41
32:XA:859:A:H2'	32:XA:860:A:O4'	2.20	0.41
34:XC:6:HIS:HB3	45:XN:49:HIS:ND1	2.35	0.41
40:X1:108:VAL:HG12	40:X1:109:VAL:H	1.85	0.41
41:XJ:16:LEU:HD13	41:XJ:70:ARG:HG2	2.02	0.41
32:XA:1492:A:O4'	43:XL:47:LYS:HD3	2.18	0.41
51:XT:42:GLN:O	51:XT:45:GLN:HB3	2.20	0.41
1:YA:1057:A:H62	1:YA:1087:G:P	2.43	0.41
1:YA:1068:G:H3'	1:YA:1096:A:OP2	2.20	0.41
1:YA:1166:C:H2'	1:YA:1167:U:C6	2.55	0.41
1:YA:1316:U:H2'	1:YA:1317:A:C8	2.55	0.41
1:YA:1753:G:OP1	15:YT:95:ARG:HD3	2.20	0.41
1:YA:180:G:OP2	29:Y7:32:LYS:HE3	2.20	0.41
1:YA:2271:G:OP1	22:Y0:18:ALA:HB1	2.20	0.41
1:YA:228:A:H8	1:YA:229:A:H5'	1.85	0.41
1:YA:30:G:H2'	1:YA:31:C:C6	2.54	0.41
7:YH:55:PRO:HG2	7:YH:61:HIS:ND1	2.35	0.41
9:YN:67:LEU:HD13	9:YN:67:LEU:HA	1.96	0.41
12:YQ:130:LYS:HB3	12:YQ:130:LYS:HE2	1.88	0.41
20:YY:20:TYR:CE1	20:YY:43:ASN:HA	2.55	0.41
32:QA:1077:G:N2	32:QA:1080:A:OP2	2.52	0.41
32:QA:110:C:H2'	32:QA:111:G:O4'	2.21	0.41
32:QA:713:G:H2'	32:QA:714:G:C8	2.55	0.41
34:QC:3:ASN:N	34:QC:3:ASN:OD1	2.52	0.41
39:QH:81:HIS:N	39:QH:138:TRP:O	2.53	0.41
55:QY:219:PRO:C	55:QY:221:ASP:H	2.24	0.41
23:R1:3:LYS:HG2	23:R1:61:ARG:NH1	2.34	0.41
1:RA:2420:C:H5''	28:R6:8:LYS:CD	2.50	0.41
1:RA:2461:C:H2'	1:RA:2462:U:C6	2.54	0.41
6:RG:138:GLN:HE22	6:RG:153:ARG:HD2	1.84	0.41
7:RH:98:LEU:HA	7:RH:98:LEU:HD12	1.93	0.41
32:XA:1151:A:O2'	32:XA:1152:A:O5'	2.34	0.41
32:XA:1068:G:N2	32:XA:1191:A:N3	2.61	0.41
32:XA:600:C:H2'	32:XA:601:C:C6	2.55	0.41
42:XK:92:GLU:O	42:XK:96:ARG:HG2	2.20	0.41
43:XL:117:ARG:NH2	43:XL:124:LYS:HB2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:523:A:N1	43:XL:92:0TD:H6	2.35	0.41
46:XO:61:GLY:O	46:XO:65:ARG:HG3	2.20	0.41
48:XQ:6:LEU:O	48:XQ:58:GLU:HA	2.20	0.41
29:Y7:12:ARG:NH2	29:Y7:44:PRO:HB3	2.36	0.41
1:YA:1053:C:H4'	1:YA:1054:A:OP1	2.20	0.41
1:YA:2810:A:N6	1:YA:2891:G:O2'	2.40	0.41
1:YA:478:A:C6	1:YA:480:A:C6	3.08	0.41
1:YA:748:G:OP1	1:YA:2612:C:N4	2.53	0.41
5:YF:53:THR:HG22	5:YF:56:GLU:OE2	2.20	0.41
6:YG:126:ASP:HB2	6:YG:130:ASN:O	2.20	0.41
7:YH:163:TYR:CE2	7:YH:169:VAL:HG22	2.55	0.41
7:YH:98:LEU:HD12	7:YH:98:LEU:HA	1.91	0.41
8:YI:62:LYS:HE2	8:YI:133:HIS:NE2	2.35	0.41
18:YW:9:TYR:HA	18:YW:100:THR:CG2	2.49	0.41
32:QA:1007:C:N3	32:QA:1022:G:O6	2.53	0.41
33:QB:8:LYS:HG2	33:QB:8:LYS:H	1.60	0.41
30:R8:33:ASN:HA	30:R8:36:LYS:HD2	2.02	0.41
1:RA:1405:U:H2'	1:RA:1406:U:C6	2.54	0.41
1:RA:458:G:O2'	1:RA:469:G:O6	2.22	0.41
9:RN:58:ASP:N	9:RN:58:ASP:OD1	2.52	0.41
1:RA:2820:A:P	13:RR:2:ARG:HH22	2.43	0.41
32:XA:1030(B):G:H1'	32:XA:1030(D):G:C5	2.55	0.41
32:XA:1065:U:H4'	32:XA:1066:C:O5'	2.20	0.41
32:XA:297:G:N2	32:XA:300:A:OP2	2.44	0.41
35:XD:189:PRO:HB2	35:XD:194:LEU:HD11	2.02	0.41
55:XY:195:ARG:HE	55:XY:197:HIS:CE1	2.38	0.41
55:XY:209:LEU:HD12	55:XY:209:LEU:HA	1.88	0.41
1:YA:1639:U:C2'	1:YA:1640:C:H5''	2.49	0.41
1:YA:2331:G:O2'	1:YA:2336:A:N1	2.45	0.41
1:YA:2785:C:O2'	4:YE:66:HIS:ND1	2.42	0.41
6:YG:115:ARG:HG2	6:YG:136:ARG:HH21	1.85	0.41
32:QA:1298:C:H4'	32:QA:1299:A:C4	2.55	0.41
32:QA:942:G:C2	32:QA:1342:C:C2	3.08	0.41
35:QD:156:GLU:O	35:QD:160:GLN:HG2	2.20	0.41
40:QI:108:VAL:HG12	40:QI:109:VAL:N	2.36	0.41
41:QJ:38:ILE:O	41:QJ:38:ILE:HG13	2.19	0.41
1:RA:1270:C:H5''	1:RA:1271:G:O5'	2.20	0.41
1:RA:1941:C:C5	1:RA:1942:5MC:HM52	2.56	0.41
1:RA:2695:C:H2'	1:RA:2696:U:C6	2.55	0.41
1:RA:337:C:H2'	1:RA:338:G:O4'	2.20	0.41
1:RA:721:C:H2'	1:RA:722:A:H8	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:955:C:OP1	12:RQ:87:LYS:HE2	2.20	0.41
1:RA:9:U:H3	1:RA:2629:A:H2	1.65	0.41
5:RF:101:LEU:HD12	5:RF:102:PRO:HD2	2.01	0.41
5:RF:116:ASP:OD1	5:RF:119:ARG:NH2	2.48	0.41
7:RH:12:PRO:O	7:RH:15:VAL:HG22	2.20	0.41
32:XA:1005:A:H5''	32:XA:1006:C:C6	2.55	0.41
32:XA:1070:U:H2'	32:XA:1071:C:H6	1.84	0.41
32:XA:262:A:C6	32:XA:263:A:C6	3.07	0.41
32:XA:552:U:O3'	43:XL:87:GLY:HA2	2.20	0.41
32:XA:560:U:H4'	32:XA:561:U:O5'	2.19	0.41
33:XB:127:ILE:HG12	33:XB:128:GLU:H	1.85	0.41
47:XP:19:ILE:HG22	47:XP:36:ILE:HG13	2.01	0.41
53:XV:10:G:N2	53:XV:26:G:H1'	2.35	0.41
53:XV:16:C:O2'	53:XV:61:C:OP1	2.34	0.41
55:XY:129:GLY:O	55:XY:133:ARG:HG2	2.20	0.41
55:XY:311:ASN:HD21	55:XY:313:PRO:HG2	1.85	0.41
1:YA:1030:G:N1	1:YA:1124:C:O2	2.50	0.41
1:YA:1449:A:N3	1:YA:1529:G:H1'	2.36	0.41
1:YA:1709:U:H2'	1:YA:1710:C:C6	2.54	0.41
1:YA:385:C:O2	11:YP:71:VAL:HG21	2.20	0.41
2:YB:33:G:C6	2:YB:34:U:C4	3.09	0.41
15:YT:16:ARG:HD3	15:YT:18:ASP:OD1	2.20	0.41
1:YA:1187:G:H5'	17:YV:81:TYR:CE1	2.55	0.41
32:QA:141:A:H1'	32:QA:182:U:O2	2.21	0.41
33:QB:224:GLN:HA	33:QB:228:GLY:O	2.21	0.41
38:QG:16:LEU:HD11	40:QI:45:ALA:HB2	2.02	0.41
23:R1:82:LEU:HA	23:R1:82:LEU:HD23	1.90	0.41
26:R4:13:ARG:HB3	26:R4:15:ILE:HD11	2.03	0.41
1:RA:1063:G:H2'	1:RA:1065:U:C6	2.55	0.41
1:RA:154(B):C:H42	1:RA:171:G:H1	1.68	0.41
1:RA:2680:C:OP2	4:RE:111:ARG:NH2	2.53	0.41
1:RA:27:G:C2	1:RA:512:G:N3	2.89	0.41
1:RA:370:G:H4'	1:RA:371:A:OP2	2.20	0.41
6:RG:77:ILE:HB	6:RG:82:LEU:HB3	2.02	0.41
1:RA:583:G:OP2	16:RU:10:ARG:HD2	2.20	0.41
20:RY:15:VAL:HG21	20:RY:42:VAL:HG11	2.02	0.41
21:RZ:91:LEU:HD12	21:RZ:130:PRO:HG3	2.03	0.41
32:XA:1201:A:H4'	32:XA:1202:G:H5''	2.03	0.41
32:XA:663:A:H5'	32:XA:836:G:OP1	2.21	0.41
36:XE:60:TYR:CZ	36:XE:64:ARG:HD3	2.56	0.41
40:XI:42:ARG:HB3	40:XI:42:ARG:HE	1.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:YN:50:LYS:HA	45:YN:50:LYS:HD2	1.79	0.41
45:YN:58:LYS:HE3	45:YN:58:LYS:HB3	1.88	0.41
32:XA:1305:G:H5'	52:XU:4:GLY:HA3	2.02	0.41
30:Y8:23:VAL:CG1	30:Y8:47:LYS:HD3	2.50	0.41
1:YA:1048:A:C5	1:YA:1049:C:C4	3.09	0.41
1:YA:1025:G:C4	1:YA:1135:C:H1'	2.55	0.41
1:YA:1802:A:N1	1:YA:1822:G:H1'	2.36	0.41
1:YA:2130:U:H2'	1:YA:2158:A:N1	2.36	0.41
1:YA:2591:C:H2'	1:YA:2592:G:C8	2.55	0.41
1:YA:2748:A:C2	1:YA:2749:A:C4	3.08	0.41
1:YA:2748:A:C6	1:YA:2749:A:C6	3.08	0.41
3:YD:134:ARG:NH1	3:YD:188:GLU:OE2	2.48	0.41
5:YF:184:TYR:CE1	11:YP:3:LEU:HD21	2.54	0.41
21:YZ:53:ILE:HG22	21:YZ:71:VAL:O	2.21	0.41
34:QC:15:THR:HG21	34:QC:181:ASN:HA	2.02	0.41
39:QH:34:GLU:OE1	39:QH:37:ARG:NH1	2.54	0.41
44:QM:80:ARG:O	44:QM:84:ILE:HG23	2.21	0.41
55:QY:214:LEU:N	55:QY:215:PRO:HD3	2.36	0.41
1:RA:1002:G:H2'	1:RA:1003:G:O4'	2.20	0.41
1:RA:1057:A:O2'	1:RA:1058:G:P	2.79	0.41
1:RA:1479:G:H1'	1:RA:1558:A:OP1	2.21	0.41
1:RA:1810:A:H2'	1:RA:1811:G:O4'	2.21	0.41
1:RA:1827:C:OP2	3:RD:222:ARG:HD2	2.20	0.41
1:RA:2306:C:C4	1:RA:2307:G:C6	3.08	0.41
1:RA:2336:A:H61	22:R0:43:THR:CG2	2.34	0.41
1:RA:2342:C:O2'	1:RA:2374:C:H5''	2.21	0.41
1:RA:2781:A:H5''	1:RA:2782:G:H5'	2.03	0.41
6:RG:126:ASP:HB3	6:RG:128:ARG:H	1.85	0.41
11:RP:96:THR:H	11:RP:99:LEU:HD12	1.86	0.41
32:XA:620:C:C2	35:XD:135:LEU:HG	2.55	0.41
32:XA:76:C:H42	32:XA:93:G:H1	1.67	0.41
32:XA:1104:G:O5'	33:XB:111:ARG:HD2	2.21	0.41
37:XF:11:ASN:HB3	37:XF:14:LEU:HG	2.03	0.41
38:XG:12:LEU:HD12	38:XG:12:LEU:H	1.85	0.41
41:XJ:25:GLU:O	41:XJ:29:ARG:HG2	2.20	0.41
44:XM:27:LYS:HA	44:XM:27:LYS:HD3	1.89	0.41
45:YN:6:LEU:HD23	45:YN:23:ARG:NH2	2.35	0.41
22:Y0:68:GLU:OE1	22:Y0:82:ARG:NH1	2.53	0.41
23:Y1:70:VAL:O	23:Y1:74:VAL:HG23	2.21	0.41
24:Y2:53:LEU:HD23	24:Y2:53:LEU:HA	1.88	0.41
1:YA:1047:G:H2'	1:YA:1110:G:H22	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:818:G:N1	1:YA:1188:U:OP2	2.33	0.41
1:YA:2114:A:H2'	1:YA:2115:G:O4'	2.21	0.41
1:YA:2181:G:H2'	1:YA:2182:G:O4'	2.20	0.41
1:YA:531:C:H4'	1:YA:532:A:H5''	2.03	0.41
1:YA:721:C:H2'	1:YA:722:A:H8	1.86	0.41
32:QA:1330:U:H2'	32:QA:1331:G:H5'	2.01	0.41
32:QA:1410:G:H2'	32:QA:1411:C:C6	2.55	0.41
32:QA:299:G:H2'	32:QA:300:A:C8	2.56	0.41
32:QA:302:G:O2'	32:QA:556:C:H5''	2.21	0.41
32:QA:685:G:O2'	32:QA:686:U:H5'	2.19	0.41
32:QA:900:A:H2'	32:QA:901:A:C8	2.55	0.41
33:QB:21:ARG:HD3	33:QB:21:ARG:N	2.35	0.41
34:QC:82:GLU:OE1	34:QC:85:ARG:NH2	2.47	0.41
36:QE:69:VAL:HG21	36:QE:113:ALA:HB1	2.03	0.41
42:QK:84:VAL:HG21	42:QK:95:ILE:HD11	2.02	0.41
43:QL:83:VAL:HG13	43:QL:100:ILE:HG23	2.02	0.41
49:QR:42:ARG:NH2	49:QR:42:ARG:HA	2.36	0.41
49:QR:66:LEU:O	49:QR:70:ILE:HG13	2.21	0.41
55:QY:311:ASN:HD22	55:QY:314:GLN:HB2	1.85	0.41
23:R1:3:LYS:O	23:R1:12:PRO:HD3	2.20	0.41
1:RA:1073:A:H4'	1:RA:1074:G:OP1	2.21	0.41
1:RA:2552:2MU:H6'3	1:RA:2554:U:C6	2.56	0.41
4:RE:47:VAL:HG23	4:RE:84:PHE:O	2.21	0.41
5:RF:183:VAL:O	5:RF:187:VAL:HG23	2.20	0.41
12:RQ:30:GLY:HA2	12:RQ:107:ALA:HB2	2.03	0.41
32:XA:922:G:H2'	32:XA:923:A:C8	2.56	0.41
36:XE:70:PRO:O	36:XE:72:GLN:NE2	2.54	0.41
42:XK:84:VAL:HG11	42:XK:91:ARG:HH11	1.85	0.41
44:XM:80:ARG:O	44:XM:84:ILE:HG23	2.20	0.41
50:XS:40:ILE:HB	50:XS:67:VAL:O	2.21	0.41
1:YA:1430:C:H2'	1:YA:1431:U:C6	2.55	0.41
1:YA:1495:A:H2'	1:YA:1496:A:C8	2.56	0.41
1:YA:2051:A:H8	1:YA:2051:A:OP2	2.03	0.41
1:YA:2136:C:C6	1:YA:2137:C:H5	2.38	0.41
1:YA:2144:U:O2'	1:YA:2147:G:N1	2.49	0.41
1:YA:2335:A:C8	1:YA:2337:G:C5	3.08	0.41
1:YA:566:U:H5''	11:YP:29:LYS:HE3	2.02	0.41
20:YY:40:GLU:O	20:YY:42:VAL:HG23	2.20	0.41
32:QA:1205:U:O2'	34:QC:195:VAL:HG23	2.20	0.41
32:QA:604:G:C5	32:QA:635:G:C6	3.08	0.41
34:QC:59:ARG:H	41:QJ:92:THR:CG2	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:QE:40:ARG:NH2	36:QE:68:GLU:OE1	2.54	0.41
39:QH:37:ARG:HH21	39:QH:41:ARG:HH21	1.69	0.41
42:QK:27:ASN:OD1	42:QK:28:THR:N	2.52	0.41
53:QV:21:A:N6	53:QV:46:G:H2'	2.35	0.41
55:QY:247:THR:HG23	55:QY:254:VAL:HG12	2.03	0.41
27:R5:37:LYS:HD3	27:R5:37:LYS:HA	1.90	0.41
1:RA:1079:C:N4	1:RA:1080:C:C2	2.82	0.41
1:RA:127:A:H5''	1:RA:128:C:O4'	2.21	0.41
1:RA:1641:A:H2'	1:RA:1642:G:O4'	2.20	0.41
1:RA:2119:A:O2'	1:RA:2120:G:H5'	2.20	0.41
1:RA:2259:G:C2	1:RA:2282:G:N1	2.89	0.41
1:RA:361:G:O2'	1:RA:362:U:H5'	2.21	0.41
1:RA:463:G:N2	1:RA:466:A:OP2	2.43	0.41
1:RA:635:C:H2'	1:RA:636:G:O4'	2.21	0.41
1:RA:644:A:H4'	1:RA:645:C:H5	1.84	0.41
1:RA:1695:G:H1'	3:RD:8:PRO:O	2.20	0.41
12:RQ:109:VAL:HG13	12:RQ:113:GLN:CB	2.51	0.41
18:RW:37:ARG:HD3	18:RW:38:TYR:CE2	2.56	0.41
18:RW:65:LEU:HD23	18:RW:65:LEU:HA	1.88	0.41
32:XA:1002:G:C4	32:XA:1003:G:C8	3.08	0.41
32:XA:384:G:H2'	32:XA:385:C:C6	2.55	0.41
34:XC:12:LEU:O	45:XN:57:ARG:NH2	2.41	0.41
48:XQ:19:VAL:HG23	48:XQ:44:ALA:HB3	2.02	0.41
53:XV:4:G:O2'	53:XV:5:G:H8	2.02	0.41
1:YA:1059:G:N2	1:YA:1079:C:N3	2.69	0.41
1:YA:2122:U:H2'	1:YA:2123:G:C8	2.56	0.41
1:YA:2869:G:H2'	1:YA:2870:C:O4'	2.21	0.41
1:YA:7:G:H2'	1:YA:8:A:H8	1.84	0.41
5:YF:33:LEU:HB3	11:YP:6:LEU:HD21	2.02	0.41
8:YI:62:LYS:HG2	8:YI:133:HIS:CD2	2.56	0.41
17:YV:40:LEU:HB2	17:YV:46:VAL:HG12	2.01	0.41
21:YZ:126:VAL:CG1	21:YZ:161:VAL:HG13	2.50	0.41
32:QA:1225:A:H2'	32:QA:1226:C:C5	2.56	0.41
32:QA:519:C:OP2	43:QL:50:SER:OG	2.23	0.41
32:QA:1148:U:O4'	40:QI:16:ARG:HD2	2.20	0.41
1:RA:1045:A:H8	1:RA:1047:G:N3	2.18	0.41
1:RA:2136:C:C6	1:RA:2137:C:H5	2.39	0.41
1:RA:2734:A:H2'	1:RA:2735:G:O4'	2.21	0.41
1:RA:2752:C:H2'	1:RA:2753:A:O4'	2.21	0.41
1:RA:2852:G:H2'	1:RA:2853:C:O4'	2.20	0.41
1:RA:588:U:H1'	5:RF:90:PHE:CG	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:RG:133:LEU:HD11	6:RG:157:ILE:HD12	2.03	0.41
6:RG:79:ASN:OD1	6:RG:79:ASN:N	2.53	0.41
9:RN:14:VAL:HG11	9:RN:138:LEU:HD12	2.01	0.41
17:RV:76:LYS:HB2	17:RV:81:TYR:HB3	2.03	0.41
32:XA:1084:G:H5'	32:XA:1102:A:OP2	2.21	0.41
32:XA:1216:G:H5''	45:YN:5:ALA:HB2	2.03	0.41
32:XA:155:C:H2'	32:XA:156:G:O4'	2.21	0.41
32:XA:691:G:H1'	32:XA:696:A:N6	2.35	0.41
23:Y1:51:VAL:HG11	23:Y1:74:VAL:CG2	2.51	0.41
1:YA:1083:U:H5''	1:YA:1084:A:OP1	2.21	0.41
1:YA:1301:A:C8	1:YA:1303:G:C8	3.09	0.41
1:YA:2330:G:H2'	1:YA:2331:G:O4'	2.21	0.41
1:YA:36:G:O2'	1:YA:450:G:H2'	2.21	0.41
2:YB:43:C:H5''	26:Y4:1:MET:HG2	2.02	0.41
4:YE:47:VAL:O	4:YE:80:GLU:HA	2.21	0.41
1:YA:2786:U:O2	4:YE:62:PRO:HB3	2.20	0.41
6:YG:43:LEU:HB3	6:YG:44:GLY:H	1.68	0.41
9:YN:99:LEU:HD23	9:YN:99:LEU:HA	1.85	0.41
21:YZ:14:LYS:HB3	21:YZ:14:LYS:HE2	1.79	0.41
32:QA:1277:C:HO2'	32:QA:1279:A:H8	1.64	0.41
32:QA:160:A:H2'	32:QA:161:A:O4'	2.20	0.41
32:QA:486:U:H2'	32:QA:487:A:C8	2.56	0.41
34:QC:181:ASN:HB3	34:QC:205:GLY:O	2.21	0.41
36:QE:116:THR:HG23	36:QE:117:ASP:OD2	2.21	0.41
1:RA:725:G:C6	1:RA:726:G:N1	2.89	0.41
1:RA:746:A:H2'	1:RA:2612:C:H5''	2.03	0.41
2:RB:24:G:N7	2:RB:56:G:H2'	2.36	0.41
2:RB:95:C:H2'	2:RB:96:U:C6	2.56	0.41
3:RD:132:PRO:HD3	3:RD:190:TYR:CZ	2.56	0.41
4:RE:28:ALA:HB3	4:RE:93:VAL:HG12	2.03	0.41
10:RO:8:LEU:HD13	10:RO:82:ASN:HB3	2.03	0.41
12:RQ:32:TYR:OH	12:RQ:111:GLU:OE1	2.22	0.41
15:YT:41:ARG:NH2	32:XA:346:G:OP1	2.38	0.41
32:XA:540:G:C6	32:XA:541:G:C5	3.09	0.41
32:XA:730:G:C5	32:XA:731:G:H1'	2.56	0.41
36:XE:110:LEU:HD13	36:XE:118:ILE:HG21	2.03	0.41
39:XH:14:ARG:O	39:XH:18:ARG:HD3	2.21	0.41
42:XK:82:VAL:HB	42:XK:108:ILE:HG12	2.03	0.41
26:Y4:61:ARG:HG2	50:XS:42:PRO:CG	2.51	0.41
1:YA:1268:A:H2'	1:YA:1269:A:O4'	2.21	0.41
1:YA:207:A:H2'	1:YA:208:C:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:954:G:O2'	1:YA:2274:A:N1	2.44	0.41
1:YA:24:G:H2'	1:YA:25:U:O4'	2.21	0.41
1:YA:972:G:C6	1:YA:973:A:C6	3.09	0.41
6:YG:114:ILE:HA	6:YG:136:ARG:HH22	1.86	0.41
32:QA:434:U:H2'	32:QA:435:C:C6	2.56	0.41
48:QQ:86:GLU:O	48:QQ:90:ILE:HG12	2.21	0.41
55:QY:233:GLY:HA3	55:QY:237:VAL:CG2	2.50	0.41
55:QY:341:ILE:O	55:QY:345:ILE:HG13	2.21	0.41
28:R6:8:LYS:HD3	30:R8:34:TRP:HB3	2.03	0.41
1:RA:1274:A:N3	1:RA:1297:C:H1'	2.36	0.41
1:RA:2112:G:H2'	1:RA:2113:U:C6	2.56	0.41
1:RA:2745:C:H2'	1:RA:2746:U:O4'	2.21	0.41
1:RA:286:C:H2'	1:RA:287:C:C6	2.56	0.41
8:RI:92:VAL:CG1	8:RI:120:ILE:HB	2.51	0.41
12:RQ:137:TYR:O	12:RQ:141:GLN:HG2	2.21	0.41
32:XA:1144:G:C6	32:XA:1145:C:C4	3.09	0.41
32:XA:1502:A:C8	32:XA:1505:G:N2	2.89	0.41
32:XA:411:A:O2'	32:XA:413:G:H5'	2.20	0.41
55:XY:183:ARG:HA	55:XY:200:ALA:HB2	2.02	0.41
55:XY:187:VAL:HG13	55:XY:196:ILE:HD13	2.03	0.41
26:Y4:8:LYS:HE2	26:Y4:8:LYS:HB3	1.85	0.41
1:YA:1073:A:H4'	1:YA:1074:G:OP1	2.22	0.41
1:YA:2328:A:H2'	1:YA:2329:G:C8	2.56	0.41
1:YA:2747:G:OP1	7:YH:138:LYS:NZ	2.51	0.41
1:YA:969:U:H2'	1:YA:970:C:C6	2.56	0.41
2:YB:73:A:C4	2:YB:105:A:C2	3.09	0.41
13:YR:87:TYR:OH	13:YR:117:VAL:O	2.26	0.41
18:YW:9:TYR:HA	18:YW:100:THR:HG23	2.01	0.41
32:QA:1081:G:H8	32:QA:1081:G:O5'	2.04	0.40
32:QA:102:G:O2'	32:QA:151:A:N3	2.43	0.40
32:QA:743:U:H2'	32:QA:744:C:C6	2.56	0.40
33:QB:19:HIS:HE1	33:QB:206:ASP:OD2	2.04	0.40
32:QA:4:U:C4	39:QH:105:ARG:HD3	2.56	0.40
41:QJ:4:ILE:N	41:QJ:100:THR:HG22	2.36	0.40
47:QP:5:ARG:HH21	47:QP:24:ALA:HA	1.85	0.40
24:R2:53:LEU:HD23	24:R2:53:LEU:HA	1.89	0.40
19:RX:60:ARG:NH1	29:R7:47:ARG:HH22	2.19	0.40
1:RA:1469:A:H2'	1:RA:1470:G:O4'	2.22	0.40
1:RA:2134:A:C5	1:RA:2157:G:H5'	2.56	0.40
1:RA:2647:U:H2'	1:RA:2648:C:C6	2.56	0.40
1:RA:2749:A:C6	1:RA:2750:A:C6	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:27:G:O2'	1:RA:28:A:OP2	2.36	0.40
1:RA:443:A:H1'	1:RA:1201:C:O4'	2.21	0.40
7:RH:20:ALA:HB1	7:RH:21:PRO:HD2	2.01	0.40
9:RN:42:TRP:CH2	9:RN:44:PRO:HB3	2.56	0.40
12:RQ:111:GLU:O	12:RQ:115:MET:HG2	2.21	0.40
13:RR:54:LEU:HD12	13:RR:54:LEU:HA	1.98	0.40
21:RZ:125:LEU:HG	21:RZ:164:ALA:HB3	2.02	0.40
32:XA:337:C:H2'	32:XA:338:A:C8	2.56	0.40
32:XA:411:A:OP1	35:XD:30:LYS:NZ	2.45	0.40
32:XA:501:C:H1'	32:XA:549:C:H1'	2.03	0.40
38:XG:108:ALA:O	38:XG:119:ARG:HD2	2.21	0.40
32:XA:663:A:H5"	49:XR:61:LYS:NZ	2.36	0.40
1:YA:1291:C:H2'	1:YA:1292:U:C6	2.56	0.40
1:YA:2505:G:O6	1:YA:2576:G:H2'	2.20	0.40
1:YA:656:G:H2'	1:YA:657:U:O4'	2.22	0.40
2:YB:13:A:O2'	2:YB:14:U:H3'	2.21	0.40
3:YD:232:PRO:HB3	3:YD:244:ARG:CZ	2.51	0.40
7:YH:13:LYS:HA	7:YH:14:GLY:HA2	1.79	0.40
14:YS:49:VAL:HG21	14:YS:77:ALA:HA	2.03	0.40
2:YB:77:U:OP1	21:YZ:19:ARG:NH2	2.54	0.40
32:QA:1353:G:C2	32:QA:1370:G:C2	3.09	0.40
32:QA:1417:G:O2'	32:QA:1483:A:N6	2.51	0.40
35:QD:31:CYS:O	35:QD:35:ARG:HG3	2.22	0.40
38:QG:102:ARG:O	38:QG:106:GLN:HG3	2.22	0.40
43:QL:124:LYS:HA	43:QL:125:PRO:HD3	1.94	0.40
32:QA:127:G:O2'	48:QQ:2:PRO:O	2.37	0.40
55:QY:143:ARG:NE	55:QY:143:ARG:HA	2.36	0.40
28:R6:8:LYS:HG2	30:R8:34:TRP:CD1	2.56	0.40
1:RA:1431:U:H2'	1:RA:1432:C:C6	2.56	0.40
1:RA:1689:A:H4'	32:QA:1475:G:H4'	2.03	0.40
1:RA:1790:C:H2'	1:RA:1791:A:C5	2.56	0.40
1:RA:2114:A:H2'	1:RA:2115:G:O4'	2.21	0.40
1:RA:2359:C:H2'	1:RA:2360:A:O4'	2.20	0.40
1:RA:2552:2MU:H6	1:RA:2552:2MU:O5'	2.21	0.40
1:RA:662:G:H5'	11:RP:14:LYS:O	2.22	0.40
32:XA:149:A:H2'	32:XA:150:C:C6	2.56	0.40
32:XA:1516:G:H2'	32:XA:1518:MA6:OP2	2.22	0.40
32:XA:561:U:HO2'	32:XA:562:C:P	2.44	0.40
32:XA:598:U:H4'	39:XH:94:TYR:CD2	2.57	0.40
32:XA:778:G:H2'	32:XA:779:C:O4'	2.21	0.40
33:XB:20:GLU:HB3	33:XB:21:ARG:H	1.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:XC:125:GLU:OE1	34:XC:190:ARG:HD3	2.20	0.40
55:XY:274:LEU:HA	55:XY:274:LEU:HD23	1.94	0.40
23:Y1:54:ALA:HB1	23:Y1:83:GLU:HG3	2.02	0.40
1:YA:2526:G:O2'	31:Y9:1:MET:HB2	2.21	0.40
1:YA:2370:G:C6	1:YA:2371:G:C6	3.09	0.40
1:YA:2522:U:O2'	1:YA:2647:U:OP1	2.30	0.40
1:YA:2660:A:H2'	1:YA:2661:G:O4'	2.22	0.40
1:YA:644:A:H4'	1:YA:645:C:H5	1.86	0.40
1:YA:674:G:O2'	5:YF:74:ARG:HD3	2.21	0.40
1:YA:686:G:N2	1:YA:788:A:H61	2.20	0.40
2:YB:75:G:N3	21:YZ:85:HIS:CE1	2.90	0.40
5:YF:110:LEU:HD13	5:YF:202:PHE:HE1	1.87	0.40
14:YS:23:ARG:NH1	14:YS:85:VAL:O	2.54	0.40
21:YZ:108:PRO:HA	21:YZ:142:SER:HA	2.03	0.40
32:QA:1035:A:H8	32:QA:1035:A:O5'	2.04	0.40
32:QA:1312:G:N7	50:QS:2:PRO:HD2	2.37	0.40
32:QA:195:A:C6	32:QA:196:A:N1	2.90	0.40
32:QA:429:U:H3'	35:QD:9:CYS:SG	2.61	0.40
48:QQ:22:LEU:HD13	48:QQ:41:LYS:HG3	2.03	0.40
53:QV:16:C:O2'	53:QV:61:C:OP1	2.36	0.40
1:RA:1614:A:P	1:RA:1614:A:H8	2.45	0.40
1:RA:1913:A:N7	32:QA:1493:A:O2'	2.43	0.40
1:RA:2144:U:H1'	1:RA:2147:G:O6	2.21	0.40
1:RA:2163:C:H5''	1:RA:2164:C:OP2	2.22	0.40
1:RA:2643:G:H2'	1:RA:2644:G:O4'	2.21	0.40
1:RA:900:A:H2'	1:RA:901:A:O4'	2.21	0.40
3:RD:72:LYS:HG3	3:RD:103:ARG:HH22	1.86	0.40
5:RF:150:GLY:HA2	5:RF:172:TRP:CD2	2.56	0.40
5:RF:20:LEU:HD13	5:RF:21:ALA:N	2.37	0.40
10:RO:64:ARG:NH2	10:RO:99:PHE:O	2.55	0.40
11:RP:83:VAL:HG12	11:RP:112:LEU:HD21	2.02	0.40
21:RZ:28:MET:HA	21:RZ:88:PHE:O	2.21	0.40
33:XB:92:TYR:CE1	33:XB:94:ASN:HB2	2.57	0.40
35:XD:111:ALA:HB2	35:XD:120:LEU:HD12	2.03	0.40
41:XJ:32:ALA:HB1	41:XJ:33:GLN:CD	2.42	0.40
55:XY:223:ARG:NH1	55:XY:225:ASP:OD2	2.54	0.40
1:YA:1075:C:N4	1:YA:1077:A:C5	2.89	0.40
1:YA:55:G:O2'	1:YA:127:A:N1	2.38	0.40
1:YA:2319:G:H1	14:YS:3:ARG:NH2	2.19	0.40
1:YA:2364:C:H2'	1:YA:2365:G:O4'	2.21	0.40
1:YA:2345:G:N3	1:YA:2381:C:H2'	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:322:A:OP1	5:YF:168:ARG:HD2	2.21	0.40
1:YA:639:U:H2'	1:YA:640:C:C6	2.56	0.40
1:YA:64:A:O3'	19:YX:71:GLY:HA3	2.22	0.40
2:YB:22:U:H2'	2:YB:23:G:C8	2.56	0.40
1:YA:784:A:N6	3:YD:229:VAL:HG11	2.36	0.40
32:QA:1020:U:H2'	32:QA:1021:G:H8	1.84	0.40
32:QA:1030(D):G:H2'	32:QA:1030(E):A:H8	1.86	0.40
32:QA:1030(D):G:C8	32:QA:1031:G:N2	2.89	0.40
32:QA:1183:A:H3'	32:QA:1184:G:H5''	2.02	0.40
32:QA:1263:C:H2'	32:QA:1264:C:C6	2.55	0.40
37:QF:45:LEU:HD12	37:QF:59:TYR:CD2	2.56	0.40
44:QM:88:ARG:HG3	44:QM:98:VAL:HG11	2.03	0.40
47:QP:57:ARG:NH2	47:QP:78:GLY:O	2.54	0.40
48:QQ:6:LEU:O	48:QQ:58:GLU:HA	2.22	0.40
23:R1:67:ILE:N	23:R1:68:PRO:HD2	2.37	0.40
1:RA:2181:G:H2'	1:RA:2182:G:O4'	2.22	0.40
1:RA:1637:A:H4'	1:RA:2711:A:O2'	2.21	0.40
1:RA:489:G:N7	18:RW:49:LYS:NZ	2.69	0.40
1:RA:1569:A:H5'	3:RD:61:LEU:HD11	2.02	0.40
11:RP:138:LEU:HD23	11:RP:145:PRO:HB3	2.03	0.40
1:RA:1653:G:C6	13:RR:9:LYS:HB2	2.56	0.40
21:RZ:24:LEU:HD21	21:RZ:86:VAL:HG13	2.03	0.40
32:XA:1014:A:C2	32:XA:1219:U:H1'	2.56	0.40
32:XA:1410:G:H2'	32:XA:1411:C:C6	2.56	0.40
32:XA:186:C:H5'	51:XT:78:ALA:HB1	2.03	0.40
33:XB:55:PHE:HD1	33:XB:55:PHE:HA	1.76	0.40
40:XI:7:THR:O	40:XI:83:ARG:HD2	2.22	0.40
32:XA:449:C:O2	47:XP:42:ARG:HD2	2.21	0.40
23:Y1:53:VAL:HG22	23:Y1:74:VAL:HG13	2.02	0.40
1:YA:1180:C:H2'	1:YA:1181:C:C6	2.57	0.40
1:YA:1638:C:H2'	1:YA:1639:U:O4'	2.22	0.40
1:YA:1847:A:H3'	1:YA:1848:A:H5'	2.02	0.40
1:YA:2114:A:H3'	1:YA:2115:G:H8	1.85	0.40
1:YA:2752:C:H2'	1:YA:2753:A:O4'	2.21	0.40
1:YA:372:G:H8	23:Y1:65:SER:O	2.04	0.40
4:YE:144:ARG:HB3	4:YE:145:LYS:H	1.53	0.40
5:YF:40:GLN:NE2	5:YF:182:ASN:HB2	2.36	0.40
1:YA:588:U:H1'	5:YF:90:PHE:CG	2.56	0.40
13:YR:13:HIS:CE1	13:YR:16:HIS:HB2	2.56	0.40
16:YU:104:GLN:CD	16:YU:104:GLN:H	2.25	0.40
20:YY:56:PRO:O	20:YY:57:GLN:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:1499:A:H1'	32:QA:1520:G:H5'	2.02	0.40
32:QA:126:G:O2'	32:QA:635:G:O4'	2.35	0.40
46:QO:21:ASP:OD1	46:QO:24:SER:HB3	2.22	0.40
1:RA:2344:U:OP2	28:R6:37:ARG:HB2	2.21	0.40
1:RA:1043:C:HO2'	1:RA:1048:A:HO2'	1.67	0.40
1:RA:1050:A:C2	1:RA:1051:G:C5	3.09	0.40
1:RA:1083:U:H5''	1:RA:1084:A:OP1	2.22	0.40
1:RA:115:C:HO2'	1:RA:127:A:HO2'	1.70	0.40
1:RA:1392:A:C6	1:RA:1393:A:C6	3.09	0.40
1:RA:1410:G:H2'	1:RA:1411:C:H6	1.85	0.40
1:RA:1495:A:H2'	1:RA:1496:A:C8	2.56	0.40
1:RA:1510:G:H2'	1:RA:1511:C:C6	2.57	0.40
1:RA:2311:A:H3'	1:RA:2312:U:C6	2.56	0.40
1:RA:2802:G:H2'	1:RA:2803:C:O4'	2.22	0.40
1:RA:350:U:H2'	1:RA:351:G:O4'	2.21	0.40
1:RA:752:A:H3'	29:R7:1:MET:CE	2.52	0.40
1:RA:783:A:O2'	1:RA:785:G:OP1	2.31	0.40
3:RD:70:TRP:HB3	3:RD:190:TYR:CE1	2.56	0.40
4:RE:119:ARG:HG2	4:RE:120:TRP:CE2	2.57	0.40
19:RX:12:VAL:HG22	19:RX:29:TRP:CE2	2.56	0.40
32:XA:1070:U:H2'	32:XA:1071:C:C6	2.57	0.40
32:XA:1143:G:H2'	32:XA:1144:G:H8	1.86	0.40
32:XA:719:C:H3'	32:XA:720:C:C6	2.56	0.40
32:XA:857:C:H2'	32:XA:858:G:O4'	2.20	0.40
35:XD:10:ARG:HB2	35:XD:40:PRO:HG3	2.04	0.40
32:XA:404:U:H5'	35:XD:122:ARG:HD3	2.03	0.40
37:XF:61:LEU:HD23	37:XF:63:TYR:OH	2.21	0.40
40:XI:6:GLY:HA3	40:XI:83:ARG:HB2	2.03	0.40
44:XM:89:GLY:O	44:XM:93:ARG:HG3	2.22	0.40
47:XP:3:LYS:O	47:XP:21:VAL:HA	2.22	0.40
32:XA:1236:A:OP2	52:XU:3:LYS:HD3	2.22	0.40
1:YA:1359:A:N1	1:YA:1372:U:O4	2.54	0.40
1:YA:1479:G:H5''	1:YA:1560:G:H4'	2.02	0.40
1:YA:2118:U:H5	1:YA:2148:G:H1'	1.86	0.40
1:YA:2144:U:O3'	1:YA:2145:C:H2'	2.22	0.40
1:YA:2282:G:OP1	1:YA:2283:C:H1'	2.21	0.40
2:YB:28:C:H2'	2:YB:29:A:O4'	2.21	0.40
11:YP:6:LEU:HA	11:YP:6:LEU:HD23	1.79	0.40
5:YF:34:TRP:CZ3	11:YP:8:PRO:HB3	2.57	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]	2.14	0.06

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	RD	273/276 (99%)	261 (96%)	12 (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%)	32	74
4	YE	202/206 (98%)	195 (96%)	7 (4%)	0	100	100
5	RF	201/210 (96%)	197 (98%)	4 (2%)	0	100	100
5	YF	201/210 (96%)	196 (98%)	3 (2%)	2 (1%)	18	61
6	RG	179/182 (98%)	166 (93%)	12 (7%)	1 (1%)	28	72
6	YG	179/182 (98%)	170 (95%)	8 (4%)	1 (1%)	28	72
7	RH	172/180 (96%)	167 (97%)	5 (3%)	0	100	100
7	YH	171/180 (95%)	164 (96%)	7 (4%)	0	100	100
8	RI	145/148 (98%)	135 (93%)	10 (7%)	0	100	100
8	YI	144/148 (97%)	137 (95%)	7 (5%)	0	100	100
9	RN	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
9	YN	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
10	RO	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
10	YO	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
11	RP	147/150 (98%)	142 (97%)	4 (3%)	1 (1%)	25	68
11	YP	147/150 (98%)	142 (97%)	4 (3%)	1 (1%)	25	68
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	YR	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
14	RS	108/112 (96%)	104 (96%)	3 (3%)	1 (1%)	20	64
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%)	113 (99%)	1 (1%)	0	100	100
16	YU	114/118 (97%)	114 (100%)	0	0	100	100
17	RV	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	18	61
17	YV	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	18	61
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%)	1 (1%)	0	100	100
20	RY	105/110 (96%)	99 (94%)	6 (6%)	0	100	100
20	YY	105/110 (96%)	102 (97%)	3 (3%)	0	100	100
21	RZ	187/206 (91%)	182 (97%)	5 (3%)	0	100	100
21	YZ	187/206 (91%)	181 (97%)	6 (3%)	0	100	100
22	R0	75/85 (88%)	73 (97%)	2 (3%)	0	100	100
22	Y0	75/85 (88%)	73 (97%)	2 (3%)	0	100	100
23	R1	95/98 (97%)	94 (99%)	0	1 (1%)	17	58
23	Y1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	17	58
24	R2	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
24	Y2	68/72 (94%)	67 (98%)	1 (2%)	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%)	56 (84%)	7 (10%)	4 (6%)	2	14
26	Y4	67/71 (94%)	55 (82%)	9 (13%)	3 (4%)	3	21
27	R5	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
27	Y5	57/60 (95%)	56 (98%)	1 (2%)	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	201 (88%)	24 (10%)	4 (2%)	11	48
33	XB	229/256 (90%)	205 (90%)	19 (8%)	5 (2%)	8	41
34	QC	204/239 (85%)	190 (93%)	14 (7%)	0	100	100
34	XC	204/239 (85%)	189 (93%)	15 (7%)	0	100	100
35	QD	206/209 (99%)	197 (96%)	9 (4%)	0	100	100
35	XD	206/209 (99%)	199 (97%)	7 (3%)	0	100	100
36	QE	146/162 (90%)	144 (99%)	2 (1%)	0	100	100
36	XE	146/162 (90%)	144 (99%)	2 (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%)	151 (99%)	2 (1%)	0	100	100
38	XG	153/156 (98%)	149 (97%)	3 (2%)	1 (1%)	25	68
39	QH	135/138 (98%)	132 (98%)	3 (2%)	0	100	100
39	XH	135/138 (98%)	132 (98%)	3 (2%)	0	100	100
40	QI	125/128 (98%)	116 (93%)	9 (7%)	0	100	100
40	XI	124/128 (97%)	113 (91%)	9 (7%)	2 (2%)	11	50
41	QJ	95/105 (90%)	83 (87%)	8 (8%)	4 (4%)	3	23
41	XJ	94/105 (90%)	84 (89%)	8 (8%)	2 (2%)	8	42
42	QK	112/129 (87%)	105 (94%)	6 (5%)	1 (1%)	20	64
42	XK	112/129 (87%)	106 (95%)	6 (5%)	0	100	100
43	QL	119/132 (90%)	117 (98%)	2 (2%)	0	100	100
43	XL	119/132 (90%)	116 (98%)	3 (2%)	0	100	100
44	QM	114/126 (90%)	105 (92%)	7 (6%)	2 (2%)	10	47
44	XM	112/126 (89%)	105 (94%)	6 (5%)	1 (1%)	20	64
45	QN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	2 (2%)	1 (1%)	18	61
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%)	65 (98%)	1 (2%)	0	100	100
50	QS	81/93 (87%)	78 (96%)	2 (2%)	1 (1%)	15	56
50	XS	81/93 (87%)	77 (95%)	4 (5%)	0	100	100
51	QT	94/106 (89%)	88 (94%)	5 (5%)	1 (1%)	17	58
51	XT	96/106 (91%)	89 (93%)	5 (5%)	2 (2%)	8	42
52	QU	21/27 (78%)	19 (90%)	2 (10%)	0	100	100
52	XU	21/27 (78%)	18 (86%)	2 (10%)	1 (5%)	2	20
55	QY	255/360 (71%)	224 (88%)	17 (7%)	14 (6%)	2	16
55	XY	256/360 (71%)	222 (87%)	25 (10%)	9 (4%)	4	28
All	All	11925/12848 (93%)	11396 (96%)	459 (4%)	70 (1%)	28	72

All (70) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	R4	49	PHE
33	QB	16	HIS
33	QB	22	LYS
51	QT	95	ALA
55	QY	215	PRO
55	QY	217	ILE
55	QY	241	ASP
55	QY	306	ARG
55	QY	322	ILE
23	Y1	3	LYS
33	XB	17	PHE
33	XB	20	GLU
33	XB	124	SER
40	XI	44	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
40	XI	54	ASP
55	XY	105	PRO
6	RG	51	ARG
14	RS	60	GLY
26	R4	45	GLY
26	R4	47	GLN
26	R4	55	ARG
41	QJ	31	GLY
41	QJ	78	ASN
55	QY	105	PRO
55	QY	121	GLY
55	QY	220	ALA
55	QY	299	GLY
5	YF	21	ALA
6	YG	81	LYS
26	Y4	60	GLN
33	XB	10	LEU
44	XM	67	GLU
51	XT	95	ALA
55	XY	322	ILE
33	QB	17	PHE
41	QJ	79	ARG
33	XB	125	PRO
41	XJ	78	ASN
41	XJ	79	ARG
55	XY	194	GLY
55	XY	303	ARG
55	XY	306	ARG
55	XY	323	ASN
4	RE	52	LEU
42	QK	117	ASN
44	QM	12	ASN
48	QQ	68	ARG
55	QY	329	LEU
55	XY	229	SER
11	RP	29	LYS
23	R1	3	LYS
55	QY	101	LEU
26	Y4	45	GLY
52	XU	7	ARG
33	QB	127	ILE
44	QM	67	GLU

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Mol	Chain	Res	Type
50	QS	12	ASP
55	QY	323	ASN
5	YF	130	ALA
11	YP	29	LYS
26	Y4	55	ARG
38	XG	7	ALA
51	XT	100	ILE
55	XY	241	ASP
55	XY	101	LEU
55	QY	162	ILE
17	RV	79	VAL
41	QJ	77	PRO
55	QY	194	GLY
17	YV	79	VAL

### 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%)	206 (96%)	8 (4%)	39	75
3	YD	215/218 (99%)	210 (98%)	5 (2%)	56	84
4	RE	164/166 (99%)	157 (96%)	7 (4%)	33	71
4	YE	164/166 (99%)	156 (95%)	8 (5%)	29	68
5	RF	160/166 (96%)	151 (94%)	9 (6%)	25	64
5	YF	159/166 (96%)	149 (94%)	10 (6%)	21	59
6	RG	144/156 (92%)	136 (94%)	8 (6%)	25	64
6	YG	142/156 (91%)	131 (92%)	11 (8%)	15	50
7	RH	144/148 (97%)	141 (98%)	3 (2%)	59	85
7	YH	143/148 (97%)	133 (93%)	10 (7%)	18	54
8	RI	111/124 (90%)	102 (92%)	9 (8%)	14	48
8	YI	108/124 (87%)	101 (94%)	7 (6%)	20	58
9	RN	119/119 (100%)	111 (93%)	8 (7%)	19	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	YN	118/119 (99%)	114 (97%)	4 (3%)	42	77
10	RO	100/100 (100%)	100 (100%)	0	100	100
10	YO	100/100 (100%)	100 (100%)	0	100	100
11	RP	115/116 (99%)	113 (98%)	2 (2%)	66	88
11	YP	115/116 (99%)	113 (98%)	2 (2%)	66	88
12	RQ	111/111 (100%)	108 (97%)	3 (3%)	50	82
12	YQ	111/111 (100%)	105 (95%)	6 (5%)	26	65
13	RR	101/101 (100%)	95 (94%)	6 (6%)	23	62
13	YR	101/101 (100%)	95 (94%)	6 (6%)	23	62
14	RS	87/88 (99%)	85 (98%)	2 (2%)	56	84
14	YS	85/88 (97%)	83 (98%)	2 (2%)	54	84
15	RT	115/127 (91%)	111 (96%)	4 (4%)	41	76
15	YT	113/127 (89%)	110 (97%)	3 (3%)	50	82
16	RU	93/94 (99%)	89 (96%)	4 (4%)	33	71
16	YU	93/94 (99%)	90 (97%)	3 (3%)	44	78
17	RV	81/82 (99%)	77 (95%)	4 (5%)	29	68
17	YV	80/82 (98%)	76 (95%)	4 (5%)	28	67
18	RW	90/92 (98%)	84 (93%)	6 (7%)	19	56
18	YW	90/92 (98%)	87 (97%)	3 (3%)	43	78
19	RX	77/78 (99%)	76 (99%)	1 (1%)	73	91
19	YX	77/78 (99%)	77 (100%)	0	100	100
20	RY	86/91 (94%)	84 (98%)	2 (2%)	56	84
20	YY	86/91 (94%)	83 (96%)	3 (4%)	41	76
21	RZ	159/179 (89%)	153 (96%)	6 (4%)	38	74
21	YZ	156/179 (87%)	150 (96%)	6 (4%)	38	74
22	R0	61/67 (91%)	59 (97%)	2 (3%)	43	78
22	Y0	61/67 (91%)	60 (98%)	1 (2%)	68	89
23	R1	79/83 (95%)	77 (98%)	2 (2%)	53	83
23	Y1	81/83 (98%)	77 (95%)	4 (5%)	29	68
24	R2	65/67 (97%)	63 (97%)	2 (3%)	45	79
24	Y2	66/67 (98%)	64 (97%)	2 (3%)	46	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	R3	51/52 (98%)	51 (100%)	0	100	100
25	Y3	50/52 (96%)	44 (88%)	6 (12%)	6	26
26	R4	58/63 (92%)	56 (97%)	2 (3%)	42	77
26	Y4	54/63 (86%)	46 (85%)	8 (15%)	3	16
27	R5	51/52 (98%)	49 (96%)	2 (4%)	37	74
27	Y5	50/52 (96%)	48 (96%)	2 (4%)	36	73
28	R6	51/52 (98%)	49 (96%)	2 (4%)	37	74
28	Y6	50/52 (96%)	50 (100%)	0	100	100
29	R7	41/42 (98%)	41 (100%)	0	100	100
29	Y7	41/42 (98%)	41 (100%)	0	100	100
30	R8	54/55 (98%)	51 (94%)	3 (6%)	25	64
30	Y8	54/55 (98%)	52 (96%)	2 (4%)	39	75
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%)	180 (94%)	11 (6%)	23	62
33	XB	187/220 (85%)	173 (92%)	14 (8%)	16	52
34	QC	144/188 (77%)	142 (99%)	2 (1%)	71	90
34	XC	140/188 (74%)	137 (98%)	3 (2%)	59	85
35	QD	171/181 (94%)	166 (97%)	5 (3%)	48	80
35	XD	172/181 (95%)	169 (98%)	3 (2%)	66	88
36	QE	114/123 (93%)	113 (99%)	1 (1%)	82	94
36	XE	114/123 (93%)	113 (99%)	1 (1%)	82	94
37	QF	85/90 (94%)	85 (100%)	0	100	100
37	XF	85/90 (94%)	84 (99%)	1 (1%)	75	91
38	QG	120/127 (94%)	114 (95%)	6 (5%)	28	67
38	XG	119/127 (94%)	115 (97%)	4 (3%)	42	77
39	QH	116/119 (98%)	113 (97%)	3 (3%)	51	83
39	XH	114/119 (96%)	110 (96%)	4 (4%)	41	76
40	QI	91/99 (92%)	83 (91%)	8 (9%)	12	42
40	XI	88/99 (89%)	83 (94%)	5 (6%)	24	63
41	QJ	68/92 (74%)	66 (97%)	2 (3%)	48	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	XJ	68/92 (74%)	67 (98%)	1 (2%)	70	90
42	QK	83/99 (84%)	81 (98%)	2 (2%)	54	84
42	XK	83/99 (84%)	83 (100%)	0	100	100
43	QL	96/108 (89%)	95 (99%)	1 (1%)	80	93
43	XL	96/108 (89%)	95 (99%)	1 (1%)	80	93
44	QM	90/101 (89%)	87 (97%)	3 (3%)	43	78
44	XM	87/101 (86%)	86 (99%)	1 (1%)	78	92
45	QN	49/50 (98%)	44 (90%)	5 (10%)	8	34
45	XN	49/50 (98%)	48 (98%)	1 (2%)	60	86
46	QO	78/80 (98%)	74 (95%)	4 (5%)	28	66
46	XO	78/80 (98%)	75 (96%)	3 (4%)	38	74
47	QP	69/74 (93%)	68 (99%)	1 (1%)	71	90
47	XP	68/74 (92%)	66 (97%)	2 (3%)	48	80
48	QQ	94/97 (97%)	94 (100%)	0	100	100
48	XQ	94/97 (97%)	94 (100%)	0	100	100
49	QR	59/77 (77%)	59 (100%)	0	100	100
49	XR	59/77 (77%)	58 (98%)	1 (2%)	66	88
50	QS	68/80 (85%)	66 (97%)	2 (3%)	48	80
50	XS	67/80 (84%)	67 (100%)	0	100	100
51	QT	71/82 (87%)	68 (96%)	3 (4%)	34	72
51	XT	70/82 (85%)	69 (99%)	1 (1%)	71	90
52	QU	18/22 (82%)	18 (100%)	0	100	100
52	XU	18/22 (82%)	17 (94%)	1 (6%)	25	64
55	QY	210/299 (70%)	200 (95%)	10 (5%)	30	68
55	XY	211/299 (71%)	198 (94%)	13 (6%)	21	60
All	All	9765/10662 (92%)	9411 (96%)	354 (4%)	40	76

All (354) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	RD	88	ARG
3	RD	94	LEU
3	RD	99	ASP

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Mol	Chain	Res	Type
3	RD	111	LEU
3	RD	126	GLN
3	RD	211	ARG
3	RD	242	ARG
3	RD	260	ARG
4	RE	9	VAL
4	RE	82	ARG
4	RE	111	ARG
4	RE	116	VAL
4	RE	119	ARG
4	RE	144	ARG
4	RE	184	VAL
5	RF	33	LEU
5	RF	60	SER
5	RF	74	ARG
5	RF	110	LEU
5	RF	125	LEU
5	RF	168	ARG
5	RF	170	LEU
5	RF	192	LEU
5	RF	205	ARG
6	RG	7	LEU
6	RG	31	VAL
6	RG	53	LEU
6	RG	79	ASN
6	RG	135	LEU
6	RG	146	TYR
6	RG	153	ARG
6	RG	170	ARG
7	RH	6	ARG
7	RH	23	ARG
7	RH	69	ARG
8	RI	10	GLU
8	RI	12	LEU
8	RI	57	ARG
8	RI	60	GLU
8	RI	61	ARG
8	RI	69	LYS
8	RI	75	LEU
8	RI	77	LEU
8	RI	101	LEU
9	RN	7	LYS

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Mol	Chain	Res	Type
9	RN	33	LEU
9	RN	48	MET
9	RN	61	ARG
9	RN	87	LEU
9	RN	99	LEU
9	RN	120	LEU
9	RN	131	GLN
11	RP	112	LEU
11	RP	119	GLU
12	RQ	21	THR
12	RQ	56	ARG
12	RQ	60	ARG
13	RR	18	LEU
13	RR	33	ARG
13	RR	44	LEU
13	RR	54	LEU
13	RR	75	LEU
13	RR	79	LEU
14	RS	43	GLU
14	RS	59	LYS
15	RT	6	LEU
15	RT	35	LYS
15	RT	53	ARG
15	RT	96	ARG
16	RU	5	LYS
16	RU	36	ARG
16	RU	74	LEU
16	RU	92	ARG
17	RV	18	LEU
17	RV	21	ARG
17	RV	62	LEU
17	RV	79	VAL
18	RW	4	LYS
18	RW	11	ARG
18	RW	15	ARG
18	RW	23	LEU
18	RW	51	LEU
18	RW	67	ASP
19	RX	66	LEU
20	RY	23	ARG
20	RY	102	CYS
21	RZ	61	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
21	RZ	72	ARG
21	RZ	150	LEU
21	RZ	156	LYS
21	RZ	171	ILE
21	RZ	185	GLU
22	R0	11	ARG
22	R0	55	ARG
23	R1	40	ARG
23	R1	52	ARG
24	R2	32	LEU
24	R2	53	LEU
26	R4	46	GLN
26	R4	58	ARG
27	R5	29	THR
27	R5	40	LYS
28	R6	6	ARG
28	R6	28	ARG
30	R8	31	HIS
30	R8	32	LEU
30	R8	34	TRP
33	QB	15	VAL
33	QB	16	HIS
33	QB	21	ARG
33	QB	24	TRP
33	QB	135	GLN
33	QB	144	ARG
33	QB	157	ARG
33	QB	163	PHE
33	QB	170	GLU
33	QB	187	LEU
33	QB	195	ASP
34	QC	36	ASP
34	QC	131	ARG
35	QD	8	VAL
35	QD	31	CYS
35	QD	49	ARG
35	QD	58	LEU
35	QD	188	LEU
36	QE	41	VAL
38	QG	15	ASP
38	QG	56	GLN
38	QG	57	GLU

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Mol	Chain	Res	Type
38	QG	86	GLN
38	QG	104	LEU
38	QG	114	ARG
39	QH	21	LYS
39	QH	63	LEU
39	QH	84	ARG
40	QI	2	GLU
40	QI	25	LYS
40	QI	42	ARG
40	QI	65	VAL
40	QI	66	ARG
40	QI	92	TYR
40	QI	93	ARG
40	QI	104	ARG
41	QJ	5	ARG
41	QJ	66	ARG
42	QK	48	ILE
42	QK	117	ASN
43	QL	33	ARG
44	QM	3	ARG
44	QM	11	ARG
44	QM	36	LYS
45	QN	3	ARG
45	QN	18	VAL
45	QN	33	VAL
45	QN	41	ARG
45	QN	57	ARG
46	QO	38	ARG
46	QO	39	LEU
46	QO	41	GLU
46	QO	48	LYS
47	QP	5	ARG
50	QS	41	VAL
50	QS	81	ARG
51	QT	10	LEU
51	QT	65	LYS
51	QT	84	LEU
55	QY	94	GLN
55	QY	95	GLN
55	QY	187	VAL
55	QY	193	GLN
55	QY	195	ARG

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Mol	Chain	Res	Type
55	QY	209	LEU
55	QY	257	CYS
55	QY	265	LYS
55	QY	329	LEU
55	QY	336	LYS
3	YD	88	ARG
3	YD	94	LEU
3	YD	211	ARG
3	YD	242	ARG
3	YD	260	ARG
4	YE	73	GLU
4	YE	75	VAL
4	YE	78	LEU
4	YE	82	ARG
4	YE	111	ARG
4	YE	116	VAL
4	YE	119	ARG
4	YE	144	ARG
5	YF	20	LEU
5	YF	33	LEU
5	YF	74	ARG
5	YF	106	ARG
5	YF	110	LEU
5	YF	170	LEU
5	YF	175	THR
5	YF	192	LEU
5	YF	197	ASP
5	YF	205	ARG
6	YG	3	LEU
6	YG	21	ARG
6	YG	31	VAL
6	YG	47	LYS
6	YG	55	LYS
6	YG	98	ARG
6	YG	135	LEU
6	YG	136	ARG
6	YG	146	TYR
6	YG	167	GLU
6	YG	170	ARG
7	YH	3	ARG
7	YH	33	LEU
7	YH	41	MET

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Mol	Chain	Res	Type
7	YH	46	GLU
7	YH	81	GLU
7	YH	84	SER
7	YH	88	LEU
7	YH	95	ARG
7	YH	140	LYS
7	YH	171	LEU
8	YI	44	LEU
8	YI	50	ARG
8	YI	68	LEU
8	YI	75	LEU
8	YI	77	LEU
8	YI	92	VAL
8	YI	116	LEU
9	YN	48	MET
9	YN	87	LEU
9	YN	99	LEU
9	YN	131	GLN
11	YP	70	GLN
11	YP	112	LEU
12	YQ	7	MET
12	YQ	21	THR
12	YQ	56	ARG
12	YQ	60	ARG
12	YQ	79	LEU
12	YQ	109	VAL
13	YR	28	LEU
13	YR	44	LEU
13	YR	65	LEU
13	YR	75	LEU
13	YR	79	LEU
13	YR	100	LEU
14	YS	20	ARG
14	YS	67	ARG
15	YT	23	ARG
15	YT	53	ARG
15	YT	96	ARG
16	YU	36	ARG
16	YU	74	LEU
16	YU	89	GLU
17	YV	6	LYS
17	YV	18	LEU

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Mol	Chain	Res	Type
17	YV	53	GLU
17	YV	62	LEU
18	YW	11	ARG
18	YW	23	LEU
18	YW	67	ASP
20	YY	6	HIS
20	YY	23	ARG
20	YY	102	CYS
21	YZ	6	LYS
21	YZ	46	LYS
21	YZ	72	ARG
21	YZ	91	LEU
21	YZ	150	LEU
21	YZ	156	LYS
22	Y0	35	ASN
23	Y1	21	ARG
23	Y1	40	ARG
23	Y1	52	ARG
23	Y1	85	LEU
24	Y2	32	LEU
24	Y2	53	LEU
25	Y3	3	ARG
25	Y3	23	LEU
25	Y3	30	ARG
25	Y3	44	ARG
25	Y3	54	VAL
25	Y3	55	ARG
26	Y4	46	GLN
26	Y4	48	ARG
26	Y4	58	ARG
26	Y4	60	GLN
26	Y4	61	ARG
26	Y4	62	ARG
26	Y4	67	TYR
26	Y4	69	LYS
27	Y5	29	THR
27	Y5	40	LYS
30	Y8	31	HIS
30	Y8	34	TRP
33	XB	8	LYS
33	XB	24	TRP
33	XB	76	GLN

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Mol	Chain	Res	Type
33	XB	118	LEU
33	XB	122	PHE
33	XB	127	ILE
33	XB	158	LEU
33	XB	163	PHE
33	XB	170	GLU
33	XB	187	LEU
33	XB	195	ASP
33	XB	212	GLN
33	XB	217	ARG
33	XB	224	GLN
34	XC	21	ARG
34	XC	105	GLU
34	XC	190	ARG
35	XD	8	VAL
35	XD	31	CYS
35	XD	122	ARG
36	XE	41	VAL
37	XF	28	ARG
38	XG	15	ASP
38	XG	78	ARG
38	XG	114	ARG
38	XG	115	ARG
39	XH	21	LYS
39	XH	63	LEU
39	XH	98	LYS
39	XH	112	LEU
40	XI	23	ASN
40	XI	65	VAL
40	XI	92	TYR
40	XI	102	LEU
40	XI	104	ARG
41	XJ	57	LYS
43	XL	41	ARG
44	XM	70	LEU
45	XN	57	ARG
46	XO	38	ARG
46	XO	39	LEU
46	XO	68	ARG
47	XP	8	ARG
47	XP	28	ARG
49	XR	58	LEU

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Mol	Chain	Res	Type
51	XT	84	LEU
52	XU	10	ARG
55	XY	107	ASP
55	XY	153	GLU
55	XY	187	VAL
55	XY	193	GLN
55	XY	274	LEU
55	XY	305	ASP
55	XY	306	ARG
55	XY	311	ASN
55	XY	318	THR
55	XY	325	THR
55	XY	326	LEU
55	XY	329	LEU
55	XY	336	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
11	RP	9	ASN
31	R9	20	HIS
9	YN	131	GLN
34	XC	6	HIS
40	XI	124	GLN
50	XS	23	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	RA	2855/2915 (97%)	442 (15%)	27 (0%)
1	YA	2855/2915 (97%)	439 (15%)	25 (0%)
2	RB	119/122 (97%)	9 (7%)	0
2	YB	119/122 (97%)	10 (8%)	0
32	QA	1494/1521 (98%)	229 (15%)	16 (1%)
32	XA	1498/1521 (98%)	227 (15%)	19 (1%)
53	QV	76/77 (98%)	15 (19%)	0
53	XV	76/77 (98%)	15 (19%)	1 (1%)
54	QX	9/25 (36%)	2 (22%)	0
54	XX	8/25 (32%)	3 (37%)	0
All	All	9109/9320 (97%)	1391 (15%)	88 (0%)



All (1391) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	RA	10	G
1	RA	11	G
1	RA	12	U
1	RA	15	G
1	RA	45	C
1	RA	71	A
1	RA	74	A
1	RA	75	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	131	G
1	RA	141	A
1	RA	157	U
1	RA	196	A
1	RA	199	A
1	RA	205	G
1	RA	215	G
1	RA	216	A
1	RA	221	A
1	RA	222	A
1	RA	229	A
1	RA	230	U
1	RA	248	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	279	C
1	RA	311	A
1	RA	317	G
1	RA	324	A

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Mol	Chain	Res	Type
1	RA	327	G
1	RA	329	G
1	RA	330	A
1	RA	342	G
1	RA	352	G
1	RA	362	U
1	RA	363(A)	G
1	RA	372	G
1	RA	386	G
1	RA	396	G
1	RA	405	U
1	RA	411	G
1	RA	412	A
1	RA	428	A
1	RA	444	C
1	RA	455	C
1	RA	456	C
1	RA	457	A
1	RA	470	A
1	RA	481	G
1	RA	505	A
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	563	G
1	RA	573	G
1	RA	575	A
1	RA	586	A
1	RA	603	A
1	RA	604	G
1	RA	607	U
1	RA	610	G
1	RA	615	G
1	RA	627	A
1	RA	634	C
1	RA	637	A
1	RA	645	C
1	RA	646	A
1	RA	652(C)	A

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Mol	Chain	Res	Type
1	RA	652(D)	G
1	RA	652(V)	G
1	RA	653	A
1	RA	669	G
1	RA	686	G
1	RA	715	G
1	RA	717	G
1	RA	730	C
1	RA	752	A
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	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	900	A
1	RA	901	A
1	RA	907	U
1	RA	910	A
1	RA	915	C
1	RA	917	A
1	RA	931	G
1	RA	932	G
1	RA	941	A
1	RA	945	A

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Mol	Chain	Res	Type
1	RA	946	G
1	RA	953	A
1	RA	959	A
1	RA	961	C
1	RA	974	G
1	RA	975(A)	C
1	RA	980	A
1	RA	983	A
1	RA	996	A
1	RA	1012	U
1	RA	1013	C
1	RA	1017	G
1	RA	1025	G
1	RA	1033	U
1	RA	1038	C
1	RA	1044	G
1	RA	1046	A
1	RA	1047	G
1	RA	1048	A
1	RA	1052	C
1	RA	1053	C
1	RA	1054	A
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	1072	C
1	RA	1073	A
1	RA	1074	G
1	RA	1076	C
1	RA	1077	A
1	RA	1078	U
1	RA	1079	C
1	RA	1082	U
1	RA	1083	U

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Mol	Chain	Res	Type
1	RA	1084	A
1	RA	1085	A
1	RA	1086	A
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	1098	A
1	RA	1109	C
1	RA	1110	G
1	RA	1111	A
1	RA	1112	G
1	RA	1126	A
1	RA	1130	U
1	RA	1135	C
1	RA	1136	G
1	RA	1142(B)	A
1	RA	1171	G
1	RA	1206	G
1	RA	1211	U
1	RA	1212	G
1	RA	1220	A
1	RA	1236	G
1	RA	1253	A
1	RA	1256	G
1	RA	1271	G
1	RA	1272	A
1	RA	1273	U
1	RA	1300	U
1	RA	1301	A
1	RA	1314	C
1	RA	1352	U
1	RA	1359	A
1	RA	1360	A
1	RA	1365	A
1	RA	1368	G
1	RA	1380	G
1	RA	1384	A
1	RA	1385	G
1	RA	1416	G

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Mol	Chain	Res	Type
1	RA	1417	C
1	RA	1420	U
1	RA	1421	G
1	RA	1428	C
1	RA	1445(A)	A
1	RA	1450(A)	G
1	RA	1455	G
1	RA	1459	G
1	RA	1467	C
1	RA	1471	A
1	RA	1482	G
1	RA	1493	C
1	RA	1494	A
1	RA	1497	U
1	RA	1508	A
1	RA	1509(A)	C
1	RA	1509(B)	A
1	RA	1531	C
1	RA	1542	A
1	RA	1543	C
1	RA	1547	C
1	RA	1558	A
1	RA	1559	G
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
1	RA	1609	A
1	RA	1610	A
1	RA	1640	C
1	RA	1648	C
1	RA	1674	G
1	RA	1696	G
1	RA	1700	A
1	RA	1701	A
1	RA	1721	G
1	RA	1722	A
1	RA	1740	G
1	RA	1750	G

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Mol	Chain	Res	Type
1	RA	1756	G
1	RA	1762	A
1	RA	1763	G
1	RA	1764	G
1	RA	1773	A
1	RA	1780	A
1	RA	1786	A
1	RA	1791	A
1	RA	1800	C
1	RA	1801	G
1	RA	1812	A
1	RA	1816	G
1	RA	1835	G
1	RA	1847	A
1	RA	1848	A
1	RA	1877	A
1	RA	1878	G
1	RA	1900	A
1	RA	1906	G
1	RA	1914	C
1	RA	1915	5MU
1	RA	1927	A
1	RA	1929	G
1	RA	1930	G
1	RA	1936	A
1	RA	1938	A
1	RA	1955	U
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	2043	C
1	RA	2055	C
1	RA	2056	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	RA	2060	A
1	RA	2061	G
1	RA	2062	A
1	RA	2069	G
1	RA	2096	U
1	RA	2099	U
1	RA	2103	C
1	RA	2105	C
1	RA	2107	C
1	RA	2108	C
1	RA	2109	U
1	RA	2112	G
1	RA	2115	G
1	RA	2116	G
1	RA	2117	A
1	RA	2118	U
1	RA	2119	A
1	RA	2121	G
1	RA	2123	G
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	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	2158	A
1	RA	2159	G
1	RA	2161	C
1	RA	2163	C
1	RA	2165	G
1	RA	2172	U
1	RA	2173	A
1	RA	2180	U
1	RA	2186	G
1	RA	2189	U

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Mol	Chain	Res	Type
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	2225	A
1	RA	2238	G
1	RA	2239	G
1	RA	2269	A
1	RA	2275	C
1	RA	2278	A
1	RA	2283	C
1	RA	2287	A
1	RA	2289	G
1	RA	2291	U
1	RA	2305	A
1	RA	2308	G
1	RA	2311	A
1	RA	2312	U
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	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	2406	U
1	RA	2410	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

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	RA	2439	A
1	RA	2441	C
1	RA	2448	A
1	RA	2465	C
1	RA	2466	C
1	RA	2474	C
1	RA	2476	A
1	RA	2478	A
1	RA	2502	G
1	RA	2504	U
1	RA	2505	G
1	RA	2506	U
1	RA	2518	A
1	RA	2527	C
1	RA	2529	G
1	RA	2554	U
1	RA	2555	U
1	RA	2566	A
1	RA	2567	G
1	RA	2573	C
1	RA	2574	G
1	RA	2602	A
1	RA	2603	G
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	2654	A
1	RA	2663	G
1	RA	2689	U
1	RA	2690	C
1	RA	2703	C
1	RA	2712(B)	A
1	RA	2713	A
1	RA	2714	G
1	RA	2726	U
1	RA	2732	G
1	RA	2733	A
1	RA	2744	G
1	RA	2751	G

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Mol	Chain	Res	Type
1	RA	2757	A
1	RA	2758	A
1	RA	2759	G
1	RA	2764	A
1	RA	2765	A
1	RA	2766	G
1	RA	2769	C
1	RA	2778	A
1	RA	2780	G
1	RA	2811	G
1	RA	2818	G
1	RA	2820	A
1	RA	2821	A
1	RA	2833	G
1	RA	2849	U
1	RA	2872	G
1	RA	2873	A
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	9	G
2	RB	13	A
2	RB	30	C
2	RB	56	G
2	RB	73	A
2	RB	84	C
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	47	C
32	QA	48	C
32	QA	50	A
32	QA	51	A
32	QA	61	G
32	QA	79	G

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Mol	Chain	Res	Type
32	QA	101	A
32	QA	116	A
32	QA	121	C
32	QA	131	C
32	QA	163	C
32	QA	174	C
32	QA	182	U
32	QA	189(F)	U
32	QA	195	A
32	QA	197	A
32	QA	202	U
32	QA	203	U
32	QA	204	U
32	QA	216	G
32	QA	247	G
32	QA	251	G
32	QA	266	G
32	QA	267	C
32	QA	289	G
32	QA	318	G
32	QA	321	A
32	QA	328	C
32	QA	332	G
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	398	C
32	QA	406	G
32	QA	412	A
32	QA	413	G
32	QA	423	G
32	QA	424	G
32	QA	429	U
32	QA	439	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
32	QA	442	C
32	QA	452	A
32	QA	458	C
32	QA	461	A
32	QA	470	C
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	518	C
32	QA	521	G
32	QA	527	7MG
32	QA	532	A
32	QA	547	A
32	QA	559	A
32	QA	561	U
32	QA	564	C
32	QA	572	A
32	QA	573	A
32	QA	575	G
32	QA	576	G
32	QA	577	G
32	QA	592	G
32	QA	596	C
32	QA	619	U
32	QA	630	G
32	QA	631	G
32	QA	632	A
32	QA	653	A
32	QA	661	G
32	QA	665	A
32	QA	687	A
32	QA	688	G
32	QA	695	A
32	QA	721	G
32	QA	723	U
32	QA	731	G
32	QA	753	A
32	QA	755	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
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	817	C
32	QA	818	G
32	QA	821	G
32	QA	828	A
32	QA	829	G
32	QA	838	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	926	G
32	QA	927	G
32	QA	931	C
32	QA	934	C
32	QA	942	G
32	QA	960	U
32	QA	961	U
32	QA	968	A
32	QA	969	A
32	QA	971	G
32	QA	972	C
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	1002	G
32	QA	1003	G
32	QA	1006	C
32	QA	1009	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
32	QA	1020	U
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(B)	G
32	QA	1030(C)	C
32	QA	1030(E)	A
32	QA	1032	G
32	QA	1033	G
32	QA	1037	C
32	QA	1042	G
32	QA	1044	A
32	QA	1054	C
32	QA	1065	U
32	QA	1066	C
32	QA	1068	G
32	QA	1081	G
32	QA	1094	G
32	QA	1095	U
32	QA	1101	A
32	QA	1125	U
32	QA	1130	A
32	QA	1134	G
32	QA	1136	U
32	QA	1139	G
32	QA	1140	C
32	QA	1152	A
32	QA	1158	C
32	QA	1159	U
32	QA	1166	G
32	QA	1183	A
32	QA	1184	G
32	QA	1196	U
32	QA	1197	G
32	QA	1202	G
32	QA	1208	C
32	QA	1213	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
32	QA	1224	G
32	QA	1227	A
32	QA	1238	A
32	QA	1250	A
32	QA	1256	A
32	QA	1257	U
32	QA	1258	G
32	QA	1270	C
32	QA	1278	U
32	QA	1280	A
32	QA	1281	U
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	1312	G
32	QA	1320	C
32	QA	1338	G
32	QA	1340	A
32	QA	1347	G
32	QA	1353	G
32	QA	1363(A)	C
32	QA	1364	U
32	QA	1370	G
32	QA	1394	A
32	QA	1397	C
32	QA	1399	C
32	QA	1401	G
32	QA	1419	G
32	QA	1442(A)	G
32	QA	1442(B)	G
32	QA	1446	U
32	QA	1447	A
32	QA	1452	C
32	QA	1487	G
32	QA	1492	A
32	QA	1493	A
32	QA	1497	G
32	QA	1499	A
32	QA	1503	A

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Mol	Chain	Res	Type
32	QA	1504	G
32	QA	1506	U
32	QA	1517	G
32	QA	1520	G
32	QA	1525	G
32	QA	1529	G
32	QA	1530	G
32	QA	1531	A
53	QV	2	G
53	QV	4	G
53	QV	5	G
53	QV	9	G
53	QV	17(A)	U
53	QV	18	G
53	QV	19	G
53	QV	21	A
53	QV	31	G
53	QV	47	U
53	QV	48	C
53	QV	52	G
53	QV	53	G
53	QV	54	U
53	QV	76	A
54	QX	21	A
54	QX	22	C
1	YA	10	G
1	YA	11	G
1	YA	12	U
1	YA	15	G
1	YA	45	C
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	102	G
1	YA	118	A
1	YA	119	A
1	YA	120	U
1	YA	131	G
1	YA	141	A

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Mol	Chain	Res	Type
1	YA	157	U
1	YA	196	A
1	YA	199	A
1	YA	205	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	248	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	279	C
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	352	G
1	YA	362	U
1	YA	363(A)	G
1	YA	372	G
1	YA	386	G
1	YA	396	G
1	YA	405	U
1	YA	411	G
1	YA	412	A
1	YA	428	A
1	YA	444	C
1	YA	455	C
1	YA	456	C

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Mol	Chain	Res	Type
1	YA	457	A
1	YA	470	A
1	YA	481	G
1	YA	505	A
1	YA	509	C
1	YA	530	G
1	YA	531	C
1	YA	532	A
1	YA	533	G
1	YA	545	G
1	YA	563	G
1	YA	573	G
1	YA	575	A
1	YA	586	A
1	YA	603	A
1	YA	604	G
1	YA	607	U
1	YA	610	G
1	YA	615	G
1	YA	627	A
1	YA	634	C
1	YA	637	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	717	G
1	YA	730	C
1	YA	752	A
1	YA	753	C
1	YA	764	A
1	YA	775	G
1	YA	776	G
1	YA	782	A
1	YA	784	A
1	YA	785	G
1	YA	792	G

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Mol	Chain	Res	Type
1	YA	805	G
1	YA	811	U
1	YA	812	C
1	YA	827	U
1	YA	828	U
1	YA	857	C
1	YA	859	G
1	YA	877	U
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	900	A
1	YA	901	A
1	YA	907	U
1	YA	910	A
1	YA	915	C
1	YA	917	A
1	YA	931	G
1	YA	932	G
1	YA	941	A
1	YA	945	A
1	YA	946	G
1	YA	953	A
1	YA	959	A
1	YA	961	C
1	YA	974	G
1	YA	975(A)	C
1	YA	980	A
1	YA	983	A
1	YA	996	A
1	YA	1012	U
1	YA	1013	C
1	YA	1017	G
1	YA	1025	G
1	YA	1033	U
1	YA	1038	C
1	YA	1046	A

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Mol	Chain	Res	Type
1	YA	1047	G
1	YA	1048	A
1	YA	1052	C
1	YA	1053	C
1	YA	1054	A
1	YA	1058	G
1	YA	1060	U
1	YA	1063	G
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	1109	C
1	YA	1110	G
1	YA	1111	A
1	YA	1112	G
1	YA	1126	A
1	YA	1130	U
1	YA	1135	C

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Mol	Chain	Res	Type
1	YA	1136	G
1	YA	1142(B)	A
1	YA	1171	G
1	YA	1206	G
1	YA	1212	G
1	YA	1220	A
1	YA	1236	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	1314	C
1	YA	1352	U
1	YA	1359	A
1	YA	1360	A
1	YA	1365	A
1	YA	1368	G
1	YA	1380	G
1	YA	1384	A
1	YA	1385	G
1	YA	1416	G
1	YA	1417	C
1	YA	1420	U
1	YA	1421	G
1	YA	1428	C
1	YA	1445(A)	A
1	YA	1450(A)	G
1	YA	1455	G
1	YA	1459	G
1	YA	1467	C
1	YA	1471	A
1	YA	1482	G
1	YA	1493	C
1	YA	1494	A
1	YA	1497	U
1	YA	1508	A
1	YA	1509(A)	C
1	YA	1509(B)	A
1	YA	1531	C

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Mol	Chain	Res	Type
1	YA	1542	A
1	YA	1543	C
1	YA	1547	C
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	1674	G
1	YA	1696	G
1	YA	1700	A
1	YA	1701	A
1	YA	1721	G
1	YA	1722	A
1	YA	1750	G
1	YA	1756	G
1	YA	1762	A
1	YA	1763	G
1	YA	1764	G
1	YA	1773	A
1	YA	1780	A
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	1835	G
1	YA	1847	A
1	YA	1848	A
1	YA	1877	A
1	YA	1878	G
1	YA	1900	A
1	YA	1906	G

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Mol	Chain	Res	Type
1	YA	1914	C
1	YA	1915	5MU
1	YA	1927	A
1	YA	1929	G
1	YA	1930	G
1	YA	1936	A
1	YA	1938	A
1	YA	1955	U
1	YA	1963	U
1	YA	1967	C
1	YA	1970	A
1	YA	1971	A
1	YA	1972	A
1	YA	1975	G
1	YA	1993	U
1	YA	1997	G
1	YA	2023	G
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	2104	G
1	YA	2105	C
1	YA	2107	C
1	YA	2108	C
1	YA	2109	U
1	YA	2112	G
1	YA	2115	G
1	YA	2116	G
1	YA	2117	A
1	YA	2118	U
1	YA	2119	A
1	YA	2121	G

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Mol	Chain	Res	Type
1	YA	2123	G
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	2148	G
1	YA	2151	G
1	YA	2158	A
1	YA	2159	G
1	YA	2161	C
1	YA	2163	C
1	YA	2165	G
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	2278	A
1	YA	2283	C
1	YA	2287	A
1	YA	2289	G
1	YA	2291	U
1	YA	2305	A

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Mol	Chain	Res	Type
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	2343	C
1	YA	2347	C
1	YA	2350	C
1	YA	2372	G
1	YA	2379	G
1	YA	2383	G
1	YA	2385	C
1	YA	2406	U
1	YA	2410	G
1	YA	2422	A
1	YA	2425	A
1	YA	2429	G
1	YA	2430	A
1	YA	2434	A
1	YA	2435	A
1	YA	2439	A
1	YA	2441	C
1	YA	2448	A
1	YA	2465	C
1	YA	2466	C
1	YA	2474	C
1	YA	2476	A
1	YA	2478	A
1	YA	2502	G
1	YA	2504	U
1	YA	2505	G
1	YA	2506	U
1	YA	2518	A
1	YA	2527	C
1	YA	2529	G
1	YA	2554	U
1	YA	2555	U
1	YA	2566	A
1	YA	2567	G

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Mol	Chain	Res	Type
1	YA	2573	C
1	YA	2602	A
1	YA	2609	U
1	YA	2611	U
1	YA	2612	C
1	YA	2615	U
1	YA	2629	A
1	YA	2630	G
1	YA	2654	A
1	YA	2663	G
1	YA	2689	U
1	YA	2690	C
1	YA	2702	U
1	YA	2703	C
1	YA	2712(B)	A
1	YA	2713	A
1	YA	2714	G
1	YA	2726	U
1	YA	2732	G
1	YA	2733	A
1	YA	2744	G
1	YA	2751	G
1	YA	2757	A
1	YA	2758	A
1	YA	2759	G
1	YA	2764	A
1	YA	2765	A
1	YA	2766	G
1	YA	2769	C
1	YA	2778	A
1	YA	2780	G
1	YA	2811	G
1	YA	2818	G
1	YA	2820	A
1	YA	2821	A
1	YA	2833	G
1	YA	2849	U
1	YA	2872	G
1	YA	2873	A
1	YA	2880	C
1	YA	2886	G
1	YA	2892	A

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Mol	Chain	Res	Type
1	YA	2894	G
1	YA	2897	U
2	YB	2	C
2	YB	8	U
2	YB	9	G
2	YB	13	A
2	YB	30	C
2	YB	56	G
2	YB	73	A
2	YB	84	C
2	YB	106	G
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	66	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	156	G
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

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
32	XA	266	G
32	XA	267	C
32	XA	289	G
32	XA	318	G
32	XA	321	A
32	XA	328	C
32	XA	332	G
32	XA	348	G
32	XA	350	G
32	XA	352	C
32	XA	353	A
32	XA	354	G
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	461	A
32	XA	470	C
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	521	G
32	XA	527	7MG
32	XA	532	A
32	XA	533	A
32	XA	547	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
32	XA	559	A
32	XA	561	U
32	XA	564	C
32	XA	572	A
32	XA	573	A
32	XA	575	G
32	XA	576	G
32	XA	577	G
32	XA	592	G
32	XA	596	C
32	XA	630	G
32	XA	631	G
32	XA	632	A
32	XA	653	A
32	XA	661	G
32	XA	665	A
32	XA	687	A
32	XA	688	G
32	XA	695	A
32	XA	721	G
32	XA	723	U
32	XA	731	G
32	XA	749	C
32	XA	753	A
32	XA	755	G
32	XA	774	G
32	XA	777	A
32	XA	787	A
32	XA	792	A
32	XA	793	U
32	XA	794	A
32	XA	817	C
32	XA	818	G
32	XA	821	G
32	XA	828	A
32	XA	829	G
32	XA	840	C
32	XA	841	U
32	XA	848	C
32	XA	851	G
32	XA	902	G
32	XA	914	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
32	XA	926	G
32	XA	927	G
32	XA	931	C
32	XA	934	C
32	XA	942	G
32	XA	960	U
32	XA	961	U
32	XA	968	A
32	XA	969	A
32	XA	971	G
32	XA	972	C
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	999	C
32	XA	1003	G
32	XA	1004	A
32	XA	1005	A
32	XA	1006	C
32	XA	1009	G
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	1029	C
32	XA	1030(B)	G
32	XA	1030(C)	C
32	XA	1033	G
32	XA	1036	G
32	XA	1041	A
32	XA	1044	A
32	XA	1054	C
32	XA	1055	A
32	XA	1065	U
32	XA	1066	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
32	XA	1068	G
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	1138	G
32	XA	1139	G
32	XA	1140	C
32	XA	1147	C
32	XA	1152	A
32	XA	1159	U
32	XA	1183	A
32	XA	1184	G
32	XA	1196	U
32	XA	1197	G
32	XA	1211	U
32	XA	1212	U
32	XA	1213	A
32	XA	1224	G
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	1278	U
32	XA	1279	A
32	XA	1280	A
32	XA	1281	U
32	XA	1286	A
32	XA	1287	A
32	XA	1300	G
32	XA	1305	G
32	XA	1320	C
32	XA	1340	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
32	XA	1347	G
32	XA	1353	G
32	XA	1363(A)	C
32	XA	1364	U
32	XA	1370	G
32	XA	1394	A
32	XA	1397	C
32	XA	1399	C
32	XA	1401	G
32	XA	1419	G
32	XA	1442(A)	G
32	XA	1442(B)	G
32	XA	1446	U
32	XA	1447	A
32	XA	1452	C
32	XA	1487	G
32	XA	1492	A
32	XA	1493	A
32	XA	1497	G
32	XA	1499	A
32	XA	1503	A
32	XA	1504	G
32	XA	1506	U
32	XA	1517	G
32	XA	1520	G
32	XA	1525	G
32	XA	1529	G
32	XA	1530	G
32	XA	1531	A
53	XV	2	G
53	XV	4	G
53	XV	5	G
53	XV	9	G
53	XV	17(A)	U
53	XV	18	G
53	XV	19	G
53	XV	21	A
53	XV	31	G
53	XV	47	U
53	XV	48	C
53	XV	52	G
53	XV	53	G

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Mol	Chain	Res	Type
53	XV	54	U
53	XV	76	A
54	XX	15	A
54	XX	21	A
54	XX	22	C

All (88) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	RA	9	U
1	RA	196	A
1	RA	272(M)	G
1	RA	277	C
1	RA	752	A
1	RA	856	C
1	RA	900	A
1	RA	1047	G
1	RA	1053	C
1	RA	1057	A
1	RA	1065	U
1	RA	1067	A
1	RA	1073	A
1	RA	1076	C
1	RA	1210	A
1	RA	1379	A
1	RA	1420	U
1	RA	1530	C
1	RA	1913	A
1	RA	1992	G
1	RA	2126	A
1	RA	2171	A
1	RA	2172	U
1	RA	2321	G
1	RA	2573	C
1	RA	2689	U
1	RA	2756	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

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Mol	Chain	Res	Type
32	QA	913	A
32	QA	991	U
32	QA	1065	U
32	QA	1067	A
32	QA	1201	A
32	QA	1207	2MG
32	QA	1256	A
32	QA	1281	U
32	QA	1285	A
32	QA	1442(A)	G
1	YA	9	U
1	YA	196	A
1	YA	272(M)	G
1	YA	277	C
1	YA	752	A
1	YA	827	U
1	YA	856	C
1	YA	900	A
1	YA	1047	G
1	YA	1053	C
1	YA	1057	A
1	YA	1065	U
1	YA	1067	A
1	YA	1073	A
1	YA	1076	C
1	YA	1379	A
1	YA	1420	U
1	YA	1530	C
1	YA	1992	G
1	YA	2126	A
1	YA	2171	A
1	YA	2172	U
1	YA	2321	G
1	YA	2689	U
1	YA	2756	U
32	XA	60	A
32	XA	65	U
32	XA	115	G
32	XA	266	G
32	XA	509	A
32	XA	560	U
32	XA	687	A

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Mol	Chain	Res	Type
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	1128	C
32	XA	1212	U
32	XA	1256	A
32	XA	1279	A
32	XA	1442(A)	G
53	XV	53	G

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

50 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	32,56	19,26,27	4.26	6 (31%)	20,38,41	2.76	8 (40%)
32	5MC	QA	1400	32	15,22,23	3.20	5 (33%)	17,32,35	1.12	2 (11%)
32	4OC	QA	1402	32	16,23,24	3.52	6 (37%)	19,32,35	1.64	1 (5%)
32	5MC	QA	1404	32	15,22,23	3.21	5 (33%)	17,32,35	1.17	3 (17%)
32	5MC	QA	1407	32	15,22,23	3.20	5 (33%)	17,32,35	1.13	2 (11%)
32	UR3	QA	1498	32	14,22,23	3.34	3 (21%)	16,32,35	0.77	0
32	MA6	QA	1518	32	16,26,27	1.19	2 (12%)	18,38,41	4.33	4 (22%)
32	MA6	QA	1519	32	16,26,27	1.17	2 (12%)	18,38,41	4.29	4 (22%)
32	PSU	QA	516	32,56	16,21,22	3.72	8 (50%)	20,30,33	3.51	6 (30%)
32	7MG	QA	527	32,56	20,26,27	4.88	8 (40%)	22,39,42	1.95	8 (36%)
32	M2G	QA	966	32	20,27,28	4.00	6 (30%)	21,40,43	2.65	8 (38%)
32	5MC	QA	967	32	15,22,23	3.26	5 (33%)	17,32,35	0.92	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
43	0TD	QL	92	43	5,9,10	1.53	1 (20%)	3,11,13	1.92	1 (33%)
55	MEQ	QY	235	55	9,9,10	1.03	0	7,10,12	1.50	2 (28%)
1	PSU	RA	1911	1	16,21,22	3.74	7 (43%)	20,30,33	3.71	5 (25%)
1	5MU	RA	1915	1	14,22,23	1.62	2 (14%)	16,32,35	2.72	3 (18%)
1	PSU	RA	1917	1	16,21,22	3.75	7 (43%)	20,30,33	3.85	6 (30%)
1	4OC	RA	1920	1	15,22,24	3.48	6 (40%)	19,31,35	0.88	1 (5%)
1	5MU	RA	1939	1	14,22,23	1.43	2 (14%)	16,32,35	3.00	3 (18%)
1	5MC	RA	1942	1,56	15,22,23	3.26	5 (33%)	17,32,35	1.00	1 (5%)
1	5MC	RA	1962	1,56	15,22,23	3.21	5 (33%)	17,32,35	1.01	1 (5%)
1	OMG	RA	2251	1,56,53	18,26,27	3.42	7 (38%)	22,38,41	2.39	8 (36%)
1	2MA	RA	2503	1,56	18,25,26	3.93	5 (27%)	17,37,40	2.87	4 (23%)
1	2MU	RA	2552	1,56	14,22,24	8.05	10 (71%)	18,31,36	1.56	2 (11%)
1	PSU	RA	2605	1	16,21,22	3.72	7 (43%)	20,30,33	3.45	6 (30%)
32	2MG	XA	1207	32	19,26,27	4.22	6 (31%)	20,38,41	2.61	7 (35%)
32	5MC	XA	1400	32	15,22,23	3.20	5 (33%)	17,32,35	0.95	1 (5%)
32	4OC	XA	1402	32	16,23,24	3.34	6 (37%)	19,32,35	2.69	1 (5%)
32	5MC	XA	1404	32	15,22,23	3.17	5 (33%)	17,32,35	1.12	2 (11%)
32	5MC	XA	1407	32	15,22,23	3.20	5 (33%)	17,32,35	0.99	1 (5%)
32	UR3	XA	1498	32,56	14,22,23	3.36	3 (21%)	16,32,35	0.78	0
32	MA6	XA	1518	32	16,26,27	1.11	2 (12%)	18,38,41	4.40	4 (22%)
32	MA6	XA	1519	32	16,26,27	1.15	2 (12%)	18,38,41	4.38	4 (22%)
32	PSU	XA	516	32	16,21,22	3.73	7 (43%)	20,30,33	3.61	6 (30%)
32	7MG	XA	527	32,56	20,26,27	4.91	9 (45%)	22,39,42	1.96	9 (40%)
32	M2G	XA	966	32	20,27,28	3.93	6 (30%)	21,40,43	2.63	7 (33%)
32	5MC	XA	967	32	15,22,23	3.22	5 (33%)	17,32,35	1.06	2 (11%)
43	0TD	XL	92	43	5,9,10	1.62	1 (20%)	3,11,13	2.17	1 (33%)
55	MEQ	XY	235	55	9,9,10	1.11	1 (11%)	7,10,12	1.49	1 (14%)
1	PSU	YA	1911	1	16,21,22	3.73	7 (43%)	20,30,33	3.72	6 (30%)
1	5MU	YA	1915	1,56	14,22,23	1.58	2 (14%)	16,32,35	2.75	3 (18%)
1	PSU	YA	1917	1	16,21,22	3.71	7 (43%)	20,30,33	3.70	6 (30%)
1	4OC	YA	1920	1	15,22,24	3.45	6 (40%)	19,31,35	0.85	1 (5%)
1	5MU	YA	1939	1,56	14,22,23	1.39	2 (14%)	16,32,35	3.03	3 (18%)
1	5MC	YA	1942	1	15,22,23	3.25	5 (33%)	17,32,35	1.07	2 (11%)
1	5MC	YA	1962	1,56	15,22,23	3.22	5 (33%)	17,32,35	0.96	1 (5%)
1	OMG	YA	2251	1,56,53	18,26,27	3.39	6 (33%)	22,38,41	2.34	8 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	2MA	YA	2503	1,56	18,25,26	3.97	5 (27%)	17,37,40	2.87	4 (23%)
1	2MU	YA	2552	1,56	14,22,24	8.08	10 (71%)	18,31,36	1.64	2 (11%)
1	PSU	YA	2605	1	16,21,22	3.70	7 (43%)	20,30,33	3.47	6 (30%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	2MG	QA	1207	32,56	-	0/5/27/28	0/3/3/3
32	5MC	QA	1400	32	-	0/3/25/26	0/2/2/2
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
55	MEQ	QY	235	55	-	0/7/9/11	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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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
55	MEQ	XY	235	55	-	0/7/9/11	0/0/0/0
1	PSU	YA	1911	1	-	0/7/25/26	0/2/2/2
1	5MU	YA	1915	1,56	-	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
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 (250) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	YA	2552	2MU	C6-C5	-9.63	1.17	1.38
1	RA	2552	2MU	C6-C5	-9.61	1.17	1.38
1	YA	2552	2MU	C3'-C2'	-8.59	1.33	1.53
1	RA	2552	2MU	C3'-C2'	-8.33	1.34	1.53
1	RA	2552	2MU	C4-N3	-6.87	1.20	1.33
1	YA	2552	2MU	C4-N3	-6.87	1.20	1.33
1	YA	2552	2MU	O4'-C4'	-5.47	1.32	1.45
1	RA	2552	2MU	O4'-C4'	-5.39	1.32	1.45
1	RA	1915	5MU	C4-N3	-4.51	1.24	1.33
1	YA	1915	5MU	C4-N3	-4.34	1.25	1.33
1	YA	1911	PSU	C5-C1'	-4.33	1.48	1.52
32	XA	516	PSU	C5-C1'	-4.23	1.48	1.52
1	RA	1917	PSU	C5-C1'	-3.83	1.48	1.52
1	YA	1917	PSU	C5-C1'	-3.79	1.49	1.52
1	RA	1939	5MU	C4-N3	-3.78	1.26	1.33
1	YA	1939	5MU	C4-N3	-3.63	1.26	1.33
1	RA	1911	PSU	C5-C1'	-3.62	1.49	1.52
1	RA	2605	PSU	C5-C1'	-3.56	1.49	1.52
1	YA	2605	PSU	C5-C1'	-3.55	1.49	1.52
1	YA	2251	OMG	O6-C6	-3.29	1.16	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	RA	2251	OMG	O6-C6	-3.27	1.16	1.24
32	QA	516	PSU	C5-C1'	-3.21	1.49	1.52
1	RA	2552	2MU	O5'-C5'	-3.20	1.40	1.44
1	YA	2552	2MU	O5'-C5'	-3.16	1.40	1.44
32	QA	1519	MA6	C5-C4	-2.45	1.35	1.40
32	XA	1518	MA6	C5-C4	-2.42	1.35	1.40
32	QA	1518	MA6	C5-C4	-2.37	1.35	1.40
32	XA	1519	MA6	C5-C4	-2.29	1.35	1.40
32	QA	516	PSU	O4-C4	-2.25	1.18	1.24
1	RA	2605	PSU	O4-C4	-2.24	1.18	1.24
1	YA	2605	PSU	O4-C4	-2.19	1.19	1.24
1	RA	1911	PSU	O4-C4	-2.17	1.19	1.24
32	XA	516	PSU	O4-C4	-2.15	1.19	1.24
1	RA	1917	PSU	O4-C4	-2.14	1.19	1.24
1	YA	1917	PSU	O4-C4	-2.11	1.19	1.24
1	YA	1911	PSU	O4-C4	-2.09	1.19	1.24
32	QA	516	PSU	O4'-C1'	-2.05	1.41	1.44
1	RA	2251	OMG	C2-N3	2.00	1.45	1.35
32	XA	527	7MG	C8-N7	2.07	1.53	1.43
55	XY	235	MEQ	CA-C	2.28	1.53	1.50
1	YA	1939	5MU	C6-C5	2.28	1.46	1.40
32	XA	1518	MA6	C2-N3	2.33	1.36	1.32
32	XA	1519	MA6	C2-N3	2.34	1.36	1.32
1	RA	1939	5MU	C6-C5	2.38	1.46	1.40
1	YA	2552	2MU	O2'-C2'	2.39	1.49	1.42
32	XA	527	7MG	C5-C4	2.41	1.45	1.39
1	RA	2552	2MU	O2'-C2'	2.42	1.49	1.42
1	YA	1915	5MU	C6-C5	2.47	1.46	1.40
32	QA	1518	MA6	C2-N3	2.49	1.36	1.32
1	RA	1915	5MU	C6-C5	2.52	1.46	1.40
32	QA	1519	MA6	C2-N3	2.54	1.36	1.32
32	QA	527	7MG	C5-C4	2.58	1.46	1.39
43	QL	92	0TD	CA-C	2.65	1.53	1.50
43	XL	92	0TD	CA-C	2.90	1.54	1.50
32	QA	1207	2MG	C2-N1	3.14	1.45	1.34
32	XA	1207	2MG	C2-N1	3.15	1.45	1.34
1	YA	1920	4OC	C4-N4	3.29	1.46	1.35
1	RA	1920	4OC	C4-N4	3.30	1.46	1.35
1	YA	1920	4OC	C5-C4	3.40	1.49	1.41
1	RA	1920	4OC	C5-C4	3.41	1.49	1.41
32	XA	1207	2MG	C2-N3	3.43	1.46	1.34
32	QA	1207	2MG	C2-N3	3.46	1.46	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	RA	2552	2MU	C2-N3	3.51	1.45	1.38
1	YA	1962	5MC	C6-C5	3.53	1.49	1.40
1	RA	1942	5MC	C6-C5	3.53	1.49	1.40
32	XA	1400	5MC	C6-C5	3.54	1.49	1.40
1	YA	1942	5MC	C6-C5	3.56	1.49	1.40
1	RA	1962	5MC	C6-C5	3.57	1.49	1.40
1	YA	2552	2MU	C2-N3	3.59	1.45	1.38
32	XA	1407	5MC	C6-C5	3.61	1.49	1.40
32	QA	1407	5MC	C6-C5	3.68	1.49	1.40
32	QA	967	5MC	C6-C5	3.68	1.49	1.40
32	XA	967	5MC	C6-C5	3.78	1.49	1.40
32	QA	1400	5MC	C6-C5	3.79	1.49	1.40
32	XA	1402	4OC	C4-N4	3.79	1.44	1.36
32	XA	1404	5MC	C6-C5	3.80	1.49	1.40
32	QA	1404	5MC	C6-C5	3.87	1.50	1.40
1	YA	2552	2MU	C3'-C4'	3.97	1.63	1.53
1	RA	2552	2MU	C3'-C4'	4.03	1.63	1.53
32	XA	1407	5MC	C4-N4	4.21	1.45	1.34
1	RA	1942	5MC	C4-N4	4.21	1.45	1.34
1	RA	1962	5MC	C4-N4	4.22	1.45	1.34
1	YA	1962	5MC	C4-N4	4.22	1.45	1.34
1	YA	1942	5MC	C4-N4	4.23	1.45	1.34
32	QA	1402	4OC	C4-N4	4.23	1.45	1.36
32	XA	1400	5MC	C4-N4	4.25	1.45	1.34
32	QA	1400	5MC	C4-N4	4.25	1.45	1.34
32	XA	1404	5MC	C4-N4	4.26	1.45	1.34
32	QA	1407	5MC	C4-N4	4.26	1.45	1.34
32	QA	967	5MC	C4-N4	4.27	1.45	1.34
32	XA	967	5MC	C4-N4	4.29	1.45	1.34
32	QA	1404	5MC	C4-N4	4.32	1.45	1.34
32	XA	1402	4OC	C5-C4	4.55	1.49	1.39
32	QA	1402	4OC	C5-C4	4.55	1.49	1.39
32	XA	966	M2G	C2-N3	4.71	1.46	1.33
32	XA	516	PSU	C6-N1	4.81	1.44	1.34
1	YA	1911	PSU	C6-N1	4.82	1.44	1.34
1	YA	2605	PSU	C6-N1	4.84	1.44	1.34
1	YA	1917	PSU	C6-N1	4.86	1.44	1.34
1	RA	2605	PSU	C6-N1	4.91	1.45	1.34
1	RA	1911	PSU	C6-N1	4.94	1.45	1.34
32	QA	966	M2G	C2-N3	4.95	1.47	1.33
32	XA	1402	4OC	C2-N3	4.96	1.48	1.38
32	XA	1402	4OC	C6-C5	4.99	1.48	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	RA	1917	PSU	C6-N1	5.01	1.45	1.34
32	QA	516	PSU	C6-N1	5.06	1.45	1.34
32	XA	1498	UR3	C6-C5	5.16	1.49	1.38
32	QA	1402	4OC	C6-C5	5.19	1.49	1.38
32	QA	1498	UR3	C6-C5	5.22	1.49	1.38
1	YA	1920	4OC	C6-C5	5.26	1.49	1.38
1	YA	2251	OMG	C2-N2	5.26	1.44	1.34
1	RA	1920	4OC	C6-C5	5.29	1.49	1.38
1	RA	2251	OMG	C2-N2	5.31	1.44	1.34
32	XA	1404	5MC	C2-N3	5.39	1.48	1.38
32	QA	527	7MG	C8-N9	5.44	1.53	1.45
32	QA	527	7MG	C2-N2	5.44	1.45	1.34
32	QA	1400	5MC	C2-N3	5.49	1.49	1.38
32	XA	1407	5MC	C2-N3	5.50	1.49	1.38
32	XA	527	7MG	C8-N9	5.50	1.53	1.45
32	QA	1404	5MC	C2-N3	5.50	1.49	1.38
1	YA	1920	4OC	C2-N3	5.53	1.49	1.38
32	QA	1407	5MC	C2-N3	5.54	1.49	1.38
32	QA	1402	4OC	C2-N3	5.54	1.49	1.38
1	RA	2503	2MA	C6-N1	5.54	1.45	1.34
32	XA	527	7MG	C2-N2	5.57	1.45	1.34
32	XA	967	5MC	C2-N3	5.58	1.49	1.38
1	RA	1962	5MC	C2-N3	5.62	1.49	1.38
1	RA	1920	4OC	C2-N3	5.62	1.49	1.38
1	RA	1942	5MC	C2-N3	5.66	1.49	1.38
32	XA	1400	5MC	C2-N3	5.66	1.49	1.38
32	QA	967	5MC	C2-N3	5.66	1.49	1.38
1	YA	2503	2MA	C6-N1	5.67	1.45	1.34
1	YA	1962	5MC	C2-N3	5.70	1.49	1.38
1	YA	2251	OMG	C6-N1	5.70	1.43	1.33
32	QA	516	PSU	C2-N3	5.70	1.49	1.38
1	RA	2605	PSU	C2-N3	5.72	1.49	1.38
1	YA	1942	5MC	C2-N3	5.77	1.49	1.38
1	RA	2251	OMG	C6-N1	5.77	1.43	1.33
1	RA	2503	2MA	C2-N1	5.78	1.44	1.34
1	YA	2503	2MA	C2-N1	5.79	1.44	1.34
32	XA	516	PSU	C2-N3	5.80	1.49	1.38
1	YA	2605	PSU	C2-N3	5.81	1.49	1.38
32	XA	1402	4OC	C4-N3	5.81	1.45	1.34
1	YA	1962	5MC	C5-C4	5.82	1.49	1.41
1	YA	1917	PSU	C2-N3	5.82	1.49	1.38
1	YA	1911	PSU	C2-N3	5.83	1.49	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	RA	1911	PSU	C2-N3	5.83	1.49	1.38
1	YA	2605	PSU	C2-N1	5.86	1.49	1.38
1	RA	1917	PSU	C2-N3	5.86	1.49	1.38
1	YA	1911	PSU	C2-N1	5.89	1.49	1.38
1	RA	1962	5MC	C5-C4	5.95	1.50	1.41
1	RA	2605	PSU	C2-N1	5.96	1.50	1.38
32	QA	1407	5MC	C5-C4	5.96	1.50	1.41
1	RA	1911	PSU	C2-N1	5.98	1.50	1.38
32	XA	516	PSU	C2-N1	6.00	1.50	1.38
32	XA	1400	5MC	C5-C4	6.00	1.50	1.41
32	XA	1407	5MC	C5-C4	6.00	1.50	1.41
32	QA	1400	5MC	C5-C4	6.01	1.50	1.41
32	QA	1404	5MC	C5-C4	6.02	1.50	1.41
1	YA	2251	OMG	C2-N1	6.04	1.46	1.35
1	YA	1942	5MC	C5-C4	6.04	1.50	1.41
1	YA	1917	PSU	C2-N1	6.05	1.50	1.38
32	QA	966	M2G	C2-N1	6.06	1.45	1.34
32	XA	1404	5MC	C5-C4	6.06	1.50	1.41
1	RA	2251	OMG	C2-N1	6.07	1.46	1.35
32	XA	966	M2G	C2-N1	6.08	1.45	1.34
32	XA	967	5MC	C5-C4	6.09	1.50	1.41
1	RA	1942	5MC	C5-C4	6.12	1.50	1.41
32	QA	516	PSU	C2-N1	6.12	1.50	1.38
1	YA	1920	4OC	C4-N3	6.14	1.46	1.35
1	RA	1920	4OC	C4-N3	6.17	1.46	1.35
1	RA	1917	PSU	C2-N1	6.17	1.50	1.38
32	XA	1207	2MG	C6-N1	6.18	1.44	1.33
32	QA	967	5MC	C5-C4	6.19	1.50	1.41
32	QA	1207	2MG	C6-N1	6.20	1.44	1.33
32	QA	1402	4OC	C4-N3	6.29	1.46	1.34
1	RA	1917	PSU	C6-C5	6.45	1.47	1.38
1	YA	1911	PSU	C6-C5	6.45	1.47	1.38
1	YA	2251	OMG	C6-C5	6.46	1.53	1.41
1	YA	1917	PSU	C6-C5	6.47	1.47	1.38
1	RA	2251	OMG	C6-C5	6.54	1.53	1.41
1	YA	2605	PSU	C6-C5	6.59	1.47	1.38
32	XA	516	PSU	C6-C5	6.59	1.47	1.38
1	RA	1911	PSU	C6-C5	6.59	1.47	1.38
32	QA	966	M2G	C6-N1	6.61	1.45	1.33
32	XA	966	M2G	C6-N1	6.61	1.45	1.33
32	QA	1207	2MG	C6-C5	6.61	1.53	1.41
32	XA	1207	2MG	C6-C5	6.68	1.54	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	QA	516	PSU	C6-C5	6.77	1.48	1.38
32	XA	1404	5MC	C4-N3	6.81	1.45	1.35
1	RA	2605	PSU	C6-C5	6.87	1.48	1.38
32	QA	1498	UR3	C4-N3	6.87	1.48	1.38
1	YA	2251	OMG	C4-N3	6.87	1.46	1.35
32	QA	966	M2G	C6-C5	6.88	1.54	1.41
1	YA	2503	2MA	C6-C5	6.88	1.53	1.41
32	XA	1498	UR3	C4-N3	6.94	1.48	1.38
32	XA	966	M2G	C6-C5	6.95	1.54	1.41
32	QA	1404	5MC	C4-N3	6.98	1.45	1.35
1	RA	2251	OMG	C4-N3	7.01	1.47	1.35
32	XA	967	5MC	C4-N3	7.02	1.45	1.35
32	QA	1407	5MC	C4-N3	7.03	1.45	1.35
32	QA	1400	5MC	C4-N3	7.05	1.45	1.35
32	XA	1407	5MC	C4-N3	7.10	1.45	1.35
32	XA	1400	5MC	C4-N3	7.13	1.45	1.35
1	RA	2503	2MA	C6-C5	7.14	1.53	1.41
32	XA	527	7MG	C2-N3	7.14	1.48	1.35
1	RA	1962	5MC	C4-N3	7.22	1.46	1.35
32	QA	527	7MG	C2-N3	7.23	1.48	1.35
32	QA	967	5MC	C4-N3	7.25	1.46	1.35
1	YA	1942	5MC	C4-N3	7.29	1.46	1.35
1	YA	1962	5MC	C4-N3	7.35	1.46	1.35
1	RA	1942	5MC	C4-N3	7.36	1.46	1.35
32	QA	527	7MG	C2-N1	7.44	1.48	1.35
32	XA	527	7MG	C2-N1	7.45	1.48	1.35
1	RA	2503	2MA	C2-N3	7.53	1.47	1.34
32	QA	516	PSU	C4-N3	7.53	1.46	1.33
1	YA	1920	4OC	C6-N1	7.54	1.46	1.35
1	RA	1920	4OC	C6-N1	7.57	1.46	1.35
32	XA	516	PSU	C4-N3	7.57	1.46	1.33
32	XA	1402	4OC	C6-N1	7.59	1.46	1.35
1	RA	2605	PSU	C4-N3	7.60	1.46	1.33
1	YA	2503	2MA	C2-N3	7.65	1.48	1.34
1	YA	1917	PSU	C4-N3	7.66	1.46	1.33
1	RA	1917	PSU	C4-N3	7.68	1.46	1.33
32	QA	1402	4OC	C6-N1	7.72	1.46	1.35
1	YA	1911	PSU	C4-N3	7.73	1.47	1.33
1	YA	2605	PSU	C4-N3	7.74	1.47	1.33
32	QA	527	7MG	C6-N1	7.78	1.47	1.33
1	RA	1911	PSU	C4-N3	7.82	1.47	1.33
32	XA	1207	2MG	C4-N3	7.85	1.48	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	XA	527	7MG	C6-N1	7.92	1.47	1.33
32	QA	1207	2MG	C4-N3	8.04	1.48	1.35
32	XA	966	M2G	C2-N2	8.53	1.48	1.34
32	QA	1498	UR3	C6-N1	8.57	1.47	1.35
32	XA	966	M2G	C4-N3	8.65	1.49	1.35
32	XA	1498	UR3	C6-N1	8.70	1.47	1.35
32	QA	966	M2G	C2-N2	8.76	1.49	1.34
32	QA	966	M2G	C4-N3	8.97	1.50	1.35
1	RA	2503	2MA	C4-N3	9.90	1.51	1.35
1	YA	2503	2MA	C4-N3	10.23	1.52	1.35
32	QA	527	7MG	C6-C5	10.67	1.53	1.41
32	XA	527	7MG	C4-N3	10.79	1.48	1.34
32	XA	527	7MG	C6-C5	10.81	1.54	1.41
32	QA	527	7MG	C4-N3	10.90	1.48	1.34
1	YA	2552	2MU	O4'-C1'	11.94	1.57	1.41
1	RA	2552	2MU	O4'-C1'	11.99	1.57	1.41
32	XA	1207	2MG	C2-N2	12.82	1.45	1.34
32	QA	1207	2MG	C2-N2	12.87	1.45	1.34
1	RA	2552	2MU	C6-N1	21.85	1.65	1.35
1	YA	2552	2MU	C6-N1	21.89	1.65	1.35

All (177) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	QA	1519	MA6	N1-C6-N6	-14.02	102.12	117.00
32	XA	1518	MA6	N1-C6-N6	-14.00	102.14	117.00
32	XA	1519	MA6	N1-C6-N6	-13.68	102.48	117.00
32	QA	1518	MA6	N1-C6-N6	-13.63	102.54	117.00
1	RA	1917	PSU	N1-C2-N3	-12.57	119.36	128.40
1	RA	1911	PSU	N1-C2-N3	-12.43	119.46	128.40
1	YA	1917	PSU	N1-C2-N3	-11.87	119.86	128.40
32	QA	516	PSU	N1-C2-N3	-11.87	119.86	128.40
1	YA	1911	PSU	N1-C2-N3	-11.86	119.87	128.40
32	XA	516	PSU	N1-C2-N3	-11.48	120.14	128.40
1	YA	2605	PSU	N1-C2-N3	-11.44	120.17	128.40
32	XA	1402	4OC	CM4-N4-C4	-11.39	113.10	122.94
1	RA	2605	PSU	N1-C2-N3	-11.11	120.41	128.40
1	RA	1939	5MU	C5-C6-N1	-10.20	111.10	122.15
1	YA	1939	5MU	C5-C6-N1	-10.04	111.28	122.15
32	XA	1519	MA6	N3-C2-N1	-9.54	120.55	128.86
32	QA	1518	MA6	N3-C2-N1	-9.23	120.82	128.86
1	YA	1915	5MU	C5-C6-N1	-9.04	112.36	122.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	XA	1518	MA6	N3-C2-N1	-9.01	121.01	128.86
1	RA	1915	5MU	C5-C6-N1	-8.96	112.44	122.15
32	QA	1519	MA6	N3-C2-N1	-8.43	121.51	128.86
1	YA	1911	PSU	C5-C4-N3	-8.41	118.53	125.43
32	QA	966	M2G	C1'-N9-C4	-8.29	112.31	126.64
32	XA	516	PSU	C5-C4-N3	-8.21	118.69	125.43
1	YA	1917	PSU	C5-C4-N3	-8.16	118.73	125.43
1	RA	1917	PSU	C5-C4-N3	-7.95	118.90	125.43
1	RA	1911	PSU	C5-C4-N3	-7.68	119.13	125.43
1	RA	2503	2MA	C1'-N9-C4	-7.63	113.46	126.64
1	YA	2503	2MA	C1'-N9-C4	-7.62	113.47	126.64
32	XA	966	M2G	C1'-N9-C4	-7.40	113.85	126.64
1	RA	2605	PSU	C5-C4-N3	-7.29	119.45	125.43
1	YA	2605	PSU	C5-C4-N3	-7.14	119.57	125.43
32	QA	516	PSU	C5-C4-N3	-7.06	119.64	125.43
32	QA	1402	4OC	CM4-N4-C4	-6.62	117.22	122.94
1	RA	2251	OMG	N3-C2-N1	-6.09	118.57	127.46
1	YA	2251	OMG	N3-C2-N1	-6.03	118.66	127.46
32	XA	1207	2MG	CM2-N2-C2	-5.65	116.76	123.63
32	QA	1207	2MG	CM2-N2-C2	-5.50	116.94	123.63
32	QA	1207	2MG	N3-C2-N1	-4.83	118.93	126.23
32	XA	527	7MG	N1-C2-N3	-4.67	117.88	125.45
32	XA	1207	2MG	N3-C2-N1	-4.59	119.29	126.23
32	QA	527	7MG	N1-C2-N3	-4.28	118.52	125.45
55	XY	235	MEQ	CB-CA-C	-3.50	105.88	111.65
32	QA	527	7MG	C5-C4-N3	-3.48	120.67	126.47
32	XA	966	M2G	CM1-N2-C2	-3.37	118.13	121.34
1	RA	1917	PSU	C5-C6-N1	-3.30	120.12	124.39
32	XA	527	7MG	C5-C4-N3	-3.24	121.06	126.47
1	RA	2605	PSU	C5-C6-N1	-3.24	120.19	124.39
1	YA	2605	PSU	C5-C6-N1	-3.19	120.26	124.39
32	QA	516	PSU	C5-C6-N1	-3.19	120.26	124.39
1	YA	2503	2MA	N3-C2-N1	-3.18	119.17	125.60
55	QY	235	MEQ	CB-CA-C	-3.12	106.51	111.65
1	RA	2503	2MA	N3-C2-N1	-3.12	119.29	125.60
1	YA	2552	2MU	C4'-O4'-C1'	-3.08	106.50	109.77
1	YA	1917	PSU	C5-C6-N1	-3.02	120.48	124.39
32	QA	527	7MG	C5-C6-N1	-2.96	118.73	123.37
1	YA	1911	PSU	C5-C6-N1	-2.94	120.58	124.39
32	XA	516	PSU	C5-C6-N1	-2.92	120.61	124.39
1	RA	2605	PSU	C5-C1'-C2'	-2.81	110.70	115.55
1	RA	1911	PSU	C5-C6-N1	-2.78	120.79	124.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	2605	PSU	C5-C1'-C2'	-2.77	110.77	115.55
32	XA	527	7MG	C5-C6-N1	-2.74	119.07	123.37
32	XA	966	M2G	C4-C5-N7	-2.66	106.84	109.41
1	YA	2251	OMG	C5-C6-N1	-2.65	119.70	123.48
1	RA	1917	PSU	C5-C1'-C2'	-2.65	110.97	115.55
1	RA	2251	OMG	C5-C6-N1	-2.65	119.71	123.48
1	RA	2251	OMG	C4-C5-N7	-2.62	106.88	109.41
32	XA	1404	5MC	C5-C6-N1	-2.61	119.33	122.15
32	XA	966	M2G	C5-C6-N1	-2.60	119.79	123.48
32	QA	1207	2MG	C5-C6-N1	-2.60	119.79	123.48
32	QA	1207	2MG	C4-C5-N7	-2.57	106.92	109.41
1	YA	1911	PSU	C5-C1'-C2'	-2.55	111.14	115.55
32	QA	1400	5MC	C5-C6-N1	-2.55	119.39	122.15
1	YA	1917	PSU	C5-C1'-C2'	-2.52	111.20	115.55
1	YA	2251	OMG	C6-C5-C4	-2.51	118.35	120.84
32	XA	1207	2MG	C4-C5-N7	-2.47	107.03	109.41
32	XA	1207	2MG	C5-C6-N1	-2.46	119.98	123.48
1	YA	1942	5MC	C5-C6-N1	-2.45	119.50	122.15
1	YA	2251	OMG	C4-C5-N7	-2.45	107.05	109.41
32	QA	1404	5MC	CM5-C5-C4	-2.44	119.14	121.65
55	QY	235	MEQ	CB-CG-CD	-2.44	107.66	113.18
32	QA	1404	5MC	C5-C6-N1	-2.43	119.52	122.15
1	RA	2552	2MU	C4'-O4'-C1'	-2.41	107.20	109.77
1	RA	1942	5MC	C5-C6-N1	-2.38	119.57	122.15
1	RA	1962	5MC	C5-C6-N1	-2.34	119.61	122.15
1	RA	2251	OMG	C6-C5-C4	-2.34	118.52	120.84
32	QA	966	M2G	C4-C5-N7	-2.32	107.17	109.41
32	QA	966	M2G	C5-C6-N1	-2.31	120.19	123.48
32	QA	966	M2G	CM2-N2-C2	-2.31	119.14	121.34
32	XA	1404	5MC	CM5-C5-C4	-2.24	119.35	121.65
1	RA	1920	4OC	C5-C4-N3	-2.14	119.14	121.68
32	QA	1407	5MC	C5-C6-N1	-2.12	119.85	122.15
1	YA	1920	4OC	C5-C4-N3	-2.10	119.18	121.68
32	XA	967	5MC	C5-C6-N1	-2.09	119.88	122.15
32	QA	1400	5MC	CM5-C5-C4	-2.09	119.50	121.65
32	XA	967	5MC	CM5-C5-C4	-2.09	119.51	121.65
32	QA	1404	5MC	N4-C4-N3	2.03	120.00	117.00
32	XA	527	7MG	C5-C4-N9	2.03	109.27	106.31
32	QA	1407	5MC	N4-C4-N3	2.03	120.01	117.00
32	QA	527	7MG	N2-C2-N3	2.05	120.52	117.24
32	XA	1407	5MC	N4-C4-N3	2.06	120.04	117.00
32	XA	527	7MG	N3-C4-N9	2.11	129.67	126.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	XA	527	7MG	N2-C2-N3	2.13	120.65	117.24
32	XA	1400	5MC	N4-C4-N3	2.13	120.15	117.00
1	YA	1942	5MC	N4-C4-N3	2.18	120.23	117.00
32	QA	1207	2MG	O3'-C3'-C2'	2.23	118.96	111.83
32	XA	516	PSU	O4'-C1'-C2'	2.23	108.04	104.45
32	QA	516	PSU	O4'-C1'-C2'	2.23	108.04	104.45
1	RA	1939	5MU	C5M-C5-C4	2.27	122.79	120.17
1	YA	1962	5MC	N4-C4-N3	2.28	120.37	117.00
32	QA	527	7MG	N2-C2-N1	2.33	120.97	117.24
1	RA	1915	5MU	C5M-C5-C4	2.43	122.97	120.17
1	RA	2503	2MA	CM2-C2-N3	2.44	121.20	117.22
32	XA	516	PSU	C6-N1-C2	2.51	119.38	115.36
32	QA	527	7MG	C2-N3-C4	2.54	121.08	113.95
1	RA	2251	OMG	N2-C2-N1	2.57	121.34	117.24
32	QA	527	7MG	N3-C4-N9	2.57	130.26	126.98
1	YA	2251	OMG	N2-C2-N1	2.57	121.35	117.24
1	YA	2503	2MA	CM2-C2-N3	2.60	121.46	117.22
1	YA	1915	5MU	C5M-C5-C4	2.61	123.18	120.17
1	RA	2605	PSU	C6-N1-C2	2.64	119.58	115.36
32	XA	966	M2G	C6-N1-C2	2.65	119.33	116.18
32	XA	527	7MG	N2-C2-N1	2.65	121.47	117.24
1	YA	1911	PSU	C6-N1-C2	2.67	119.63	115.36
32	XA	527	7MG	C2-N3-C4	2.70	121.52	113.95
32	XA	1207	2MG	C6-N1-C2	2.70	120.02	115.18
1	YA	1917	PSU	C6-N1-C2	2.70	119.68	115.36
32	QA	966	M2G	C6-N1-C2	2.74	119.44	116.18
32	QA	966	M2G	N1-C2-N2	2.75	119.99	117.16
32	QA	516	PSU	C6-N1-C2	2.83	119.89	115.36
1	RA	1911	PSU	C6-N1-C2	2.84	119.90	115.36
1	YA	2605	PSU	C6-N1-C2	2.87	119.96	115.36
43	QL	92	0TD	CSB-SB-CB	2.95	107.10	101.60
32	QA	1207	2MG	C6-N1-C2	2.98	120.52	115.18
1	RA	1917	PSU	C6-N1-C2	3.04	120.23	115.36
32	QA	1519	MA6	C2-N1-C6	3.10	119.42	111.82
32	QA	966	M2G	N3-C2-N2	3.15	120.40	117.15
1	RA	2251	OMG	C6-N1-C2	3.24	120.71	116.06
43	XL	92	0TD	CSB-SB-CB	3.24	107.64	101.60
1	YA	2251	OMG	C6-N1-C2	3.24	120.72	116.06
1	YA	1939	5MU	C5M-C5-C4	3.25	123.92	120.17
32	QA	1518	MA6	C2-N1-C6	3.44	120.26	111.82
32	XA	1518	MA6	C2-N1-C6	3.49	120.37	111.82
32	XA	1519	MA6	C2-N1-C6	3.51	120.44	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	QA	527	7MG	C6-N1-C2	3.94	121.72	116.06
32	XA	527	7MG	C6-N1-C2	4.02	121.84	116.06
1	RA	2552	2MU	C4-N3-C2	4.50	118.00	114.13
1	YA	2251	OMG	C1'-N9-C4	4.54	134.48	126.64
32	XA	966	M2G	N1-C2-N2	4.54	121.84	117.16
1	YA	2552	2MU	C4-N3-C2	4.56	118.05	114.13
32	QA	1207	2MG	C2-N3-C4	4.74	120.52	115.11
1	RA	2251	OMG	C1'-N9-C4	4.75	134.85	126.64
1	YA	2251	OMG	C2-N3-C4	4.77	120.72	115.16
1	YA	2605	PSU	C4-N3-C2	4.79	119.35	115.16
32	XA	1207	2MG	C2-N3-C4	4.85	120.64	115.11
1	RA	1915	5MU	C4-N3-C2	4.85	119.40	115.16
1	RA	2605	PSU	C4-N3-C2	4.93	119.47	115.16
1	RA	2251	OMG	C2-N3-C4	4.93	120.91	115.16
1	YA	1915	5MU	C4-N3-C2	4.95	119.49	115.16
1	YA	1939	5MU	C4-N3-C2	5.14	119.66	115.16
32	QA	966	M2G	C2-N3-C4	5.18	121.02	115.11
32	XA	966	M2G	C2-N3-C4	5.21	121.06	115.11
32	QA	516	PSU	C4-N3-C2	5.31	119.80	115.16
1	RA	1939	5MU	C4-N3-C2	5.33	119.82	115.16
32	XA	1207	2MG	N2-C2-N1	5.61	122.40	116.95
32	QA	1207	2MG	N2-C2-N1	5.64	122.43	116.95
32	XA	516	PSU	C4-N3-C2	5.68	120.13	115.16
1	YA	1917	PSU	C4-N3-C2	5.75	120.19	115.16
1	YA	1911	PSU	C4-N3-C2	5.88	120.30	115.16
1	RA	1911	PSU	C4-N3-C2	5.88	120.30	115.16
1	RA	1917	PSU	C4-N3-C2	5.92	120.34	115.16
32	QA	1519	MA6	C5-C6-N6	6.89	137.98	122.58
32	QA	1518	MA6	C5-C6-N6	6.95	138.12	122.58
32	XA	1519	MA6	C5-C6-N6	6.95	138.13	122.58
32	XA	1518	MA6	C5-C6-N6	7.18	138.62	122.58
1	YA	2503	2MA	C2-N3-C4	7.48	121.88	115.41
1	RA	2503	2MA	C2-N3-C4	7.65	122.02	115.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

21 monomers are involved in 33 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	QA	1402	4OC	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	QA	1518	MA6	1	0
32	QA	1519	MA6	3	0
32	QA	966	M2G	1	0
1	RA	1917	PSU	1	0
1	RA	1939	5MU	1	0
1	RA	1942	5MC	1	0
1	RA	1962	5MC	1	0
1	RA	2503	2MA	2	0
1	RA	2552	2MU	4	0
32	XA	1207	2MG	1	0
32	XA	1402	4OC	3	0
32	XA	1518	MA6	2	0
32	XA	1519	MA6	1	0
43	XL	92	0TD	1	0
1	YA	1917	PSU	1	0
1	YA	1939	5MU	1	0
1	YA	1942	5MC	1	0
1	YA	1962	5MC	1	0
1	YA	2503	2MA	2	0
1	YA	2552	2MU	4	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 2445 ligands modelled in this entry, 2443 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	-	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	-	-	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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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 is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

EDS failed to run properly - this section is therefore empty.

### 6.4 Ligands [i](#)

EDS failed to run properly - this section is therefore empty.

### 6.5 Other polymers [i](#)

EDS failed to run properly - this section is therefore empty.