



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 4, 2020 – 11:22 pm BST

PDB ID : 5J30
Title : Thermus thermophilus 70S termination complex containing E. coli RF1
Authors : Hoffer, E.D.; Dunham, C.M.
Deposited on : 2016-03-30
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : **FAILED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

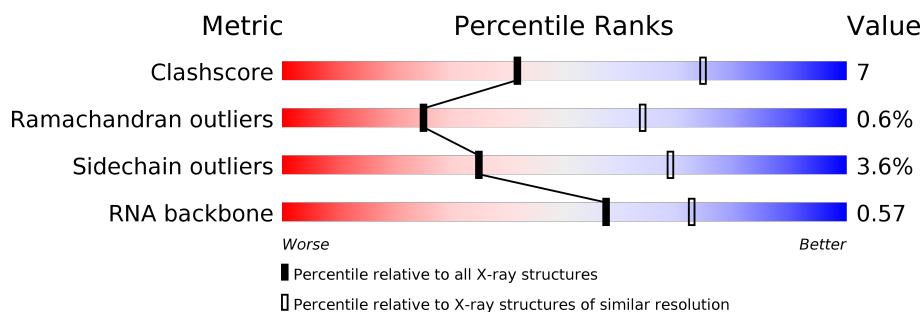
1 Overall quality at a glance

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	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RNA backbone	3102	1010 (3.50-2.90)















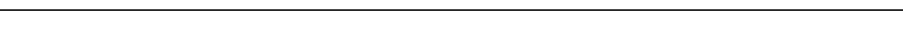




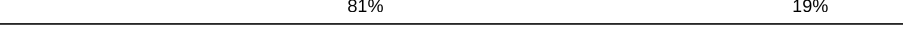





The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively.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

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	RA	2915	65% 27% 6% .
1	YA	2915	64% 27% 6% .
2	RB	122	82% 16% ..
2	YB	122	68% 26% . .
3	RD	276	82% 16% .
3	YD	276	84% 14% .
4	RE	206	81% 16% ..


























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Mol	Chain	Length	Quality of chain
4	YE	206	
5	RF	210	
5	YF	210	
6	RG	182	
6	YG	182	
7	RH	180	
7	YH	180	
8	RI	148	
8	YI	148	
9	RN	140	
9	YN	140	
10	RO	122	
10	YO	122	
11	RP	150	
11	YP	150	
12	RQ	141	
12	YQ	141	
13	RR	118	
13	YR	118	
14	RS	112	
14	YS	112	
15	RT	146	
15	YT	146	
16	RU	118	
16	YU	118	















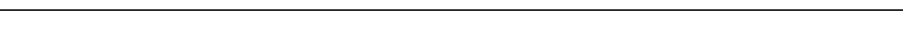




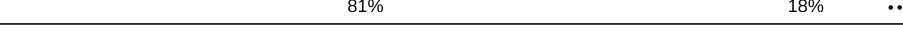





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Mol	Chain	Length	Quality of chain
17	RV	101	
17	YV	101	
18	RW	113	
18	YW	113	
19	RX	96	
19	YX	96	
20	RY	110	
20	YY	110	
21	RZ	206	
21	YZ	206	
22	R0	85	
22	Y0	85	
23	R1	98	
23	Y1	98	
24	R2	72	
24	Y2	72	
25	R3	60	
25	Y3	60	
26	R4	71	
26	Y4	71	
27	R5	60	
27	Y5	60	
28	R6	54	
28	Y6	54	
29	R7	49	


























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Mol	Chain	Length	Quality of chain
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	
41	XJ	105	



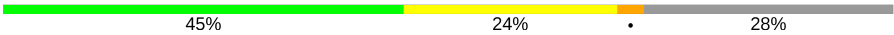
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Mol	Chain	Length	Quality of chain
42	QK	129	
42	XK	129	
43	QL	132	
43	XL	132	
44	QM	126	
44	XM	126	
45	QN	61	
45	XN	61	
46	QO	89	
46	XO	89	
47	QP	88	
47	XP	88	
48	QQ	105	
48	XQ	105	
49	QR	88	
49	XR	88	
50	QS	93	
50	XS	93	
51	QT	106	
51	XT	106	
52	QU	27	
52	XU	27	
53	QV	77	
53	XV	77	
54	QX	25	

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Mol	Chain	Length	Quality of chain
54	XX	25	 12% 16% 8% 64%
55	QY	360	 46% 23% • 28%
55	XY	360	 45% 24% • 28%

2 Entry composition

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	0	0	0
			1091	680	225	185			
15	YT	131	Total	C	N	O	0	0	0
			1083	675	224	183			

- 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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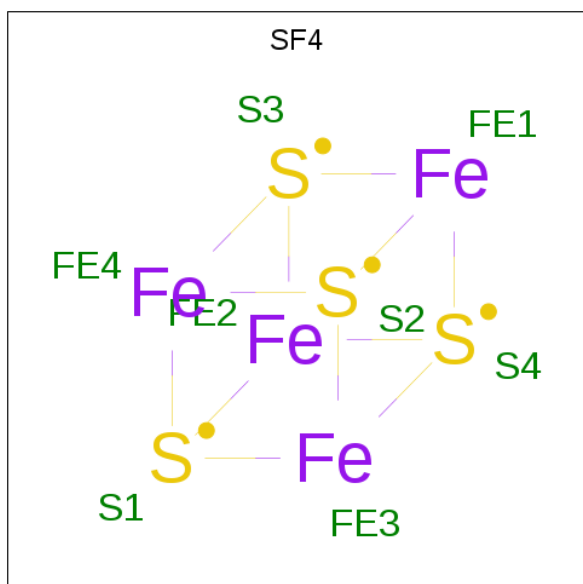
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	YF	3	Total 3	Mg 3	0	0
56	YP	1	Total 1	Mg 1	0	0
56	RZ	1	Total 1	Mg 1	0	0
56	QB	1	Total 1	Mg 1	0	0
56	Y5	1	Total 1	Mg 1	0	0
56	RE	8	Total 8	Mg 8	0	0
56	XK	1	Total 1	Mg 1	0	0
56	YB	18	Total 18	Mg 18	0	0
56	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: Fe₄S₄).



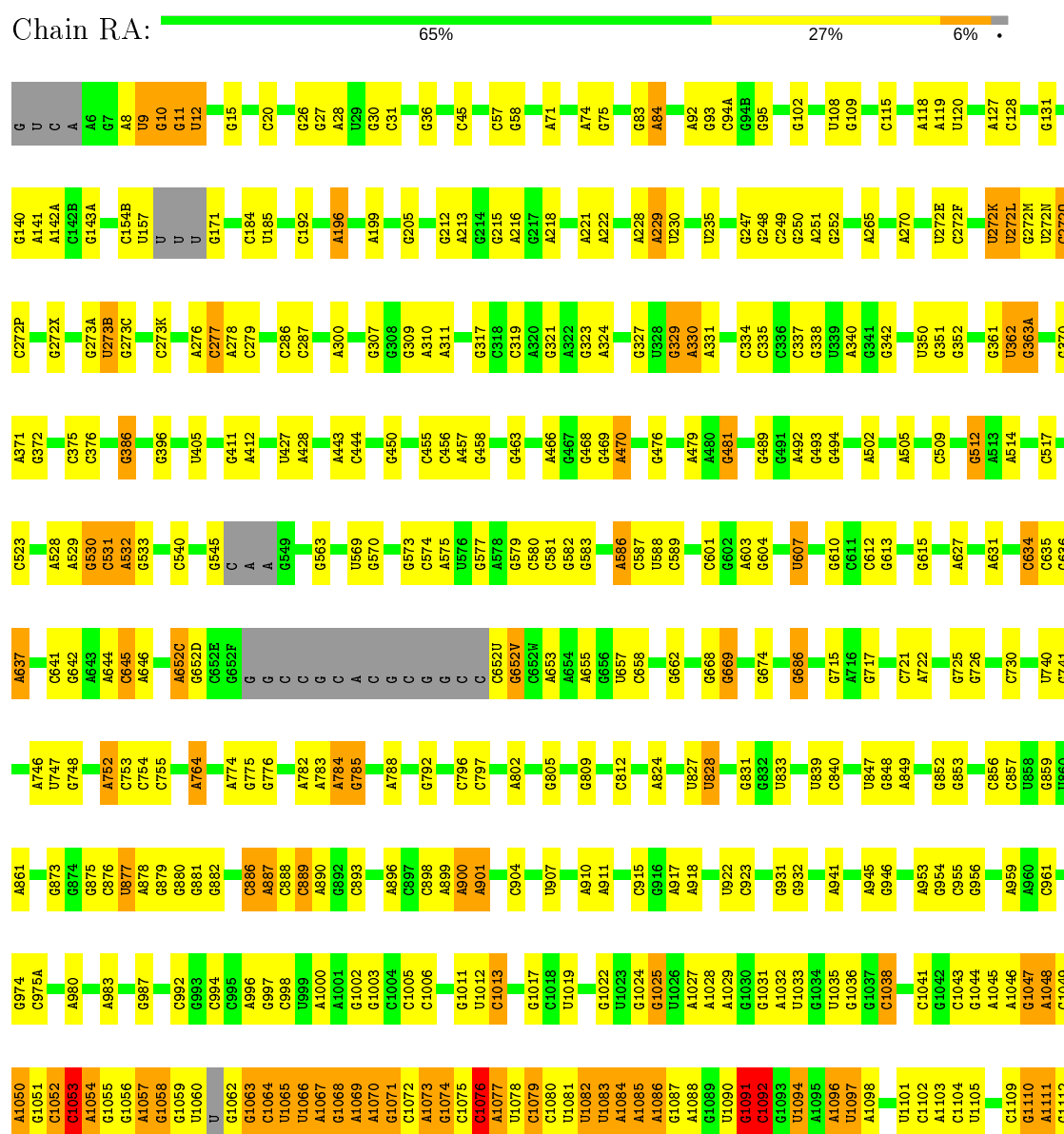
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
58	QD	1	Total 8	Fe 4	S 4	0	0
58	XD	1	Total 8	Fe 4	S 4	0	0

3 Residue-property plots [i](#)

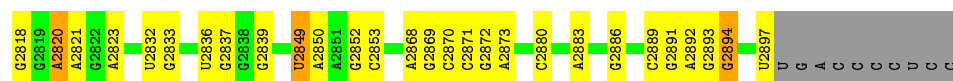
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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. 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

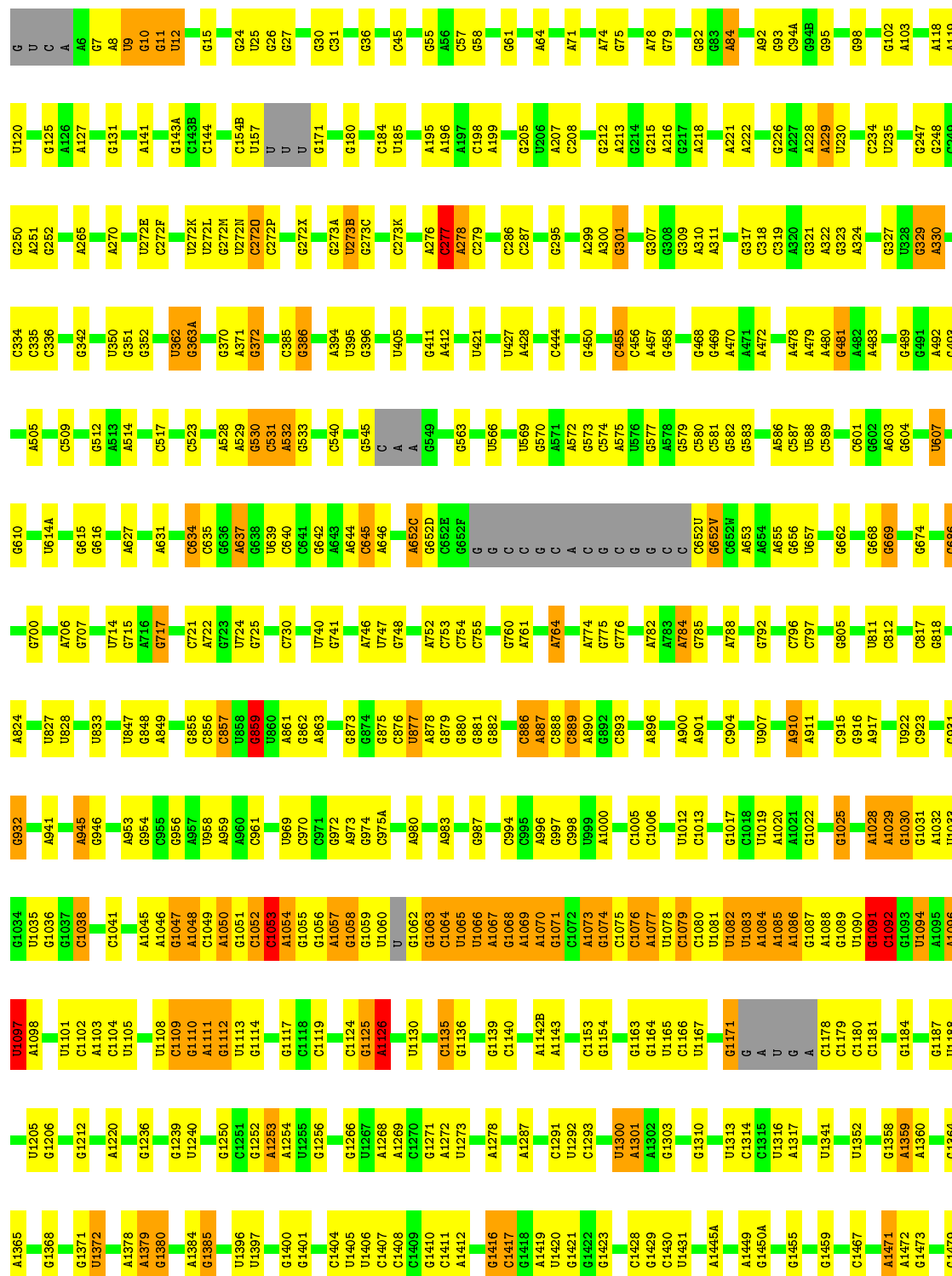


U2726	C2573	U2438	G2342	G2238	C2142	A2060	A1927	U1779	A1614	U1503	A1392	G1239	U1113
G2732	G2574	A2439	C2343	G2239	C2143	G2061	A1928	A1780	G1622	C1504	A1393	U1240	G1114
A2733	G2578	C2440	U2344	G2240	U2144	A2062	G1929	A1784	G1626	C1505	A1396	G1280	G1117
G2734	A2602	G2445	G2345	U2243	C2145	G2069	U1931	A1785	A1637	G1506	U1397	A1253	C1118
G2735	G2603	A2446	G2346	U2244	G2146	U2074	A1932	A1786	C1638	A1507	U1397	A1254	C1119
C2742	U2604	A2448	C2347	G2289	G2148	U2075	G1933	C1790	U1637	A1508	G1400	G1286	G1125
C2743	C2350	G2485	C2350	U2282	U2150	U2086	A1936	A1791	C1638	C1509A	G1401	A1256	A1126
G2744	G2354	G2485	G2354	U2282	G2151	U2086	A1937	U1794	U1638	C1509B	G1401	U1130	U1130
C2745	C2355	G2461	C2355	A2269	G2152	G2087	A1938	C1795	A1641	A1509C	C1404	G1270	G1135
U2746	G2355	U2462	C2355	A2269	G2153	U2092	U1939	C1795	G1642	C1511	U1405	G1271	G1136
G2747	C2355	G2462	C2355	A2269	G2154	U2092	U1940	U1796	G1648	U1514	U1406	C1270	G1135
A2748	G2358	G2463	G2358	A2274	G2155	G2093	C1941	C1797	G1648	G1515	C1407	G1271	G1136
G2749	C2359	C2464	C2359	G2275	G2156	G2093	C1942	U1798	G1653	C1530	G1410	U1273	G1139
A2750	C2361	C2465	A2360	G2276	G2157	U2096	U1955	C1800	G1657	C1531	C1411	A1274	U1140
G2751	C2361	C2466	A2360	G2277	G2158	U2096	U1955	C1801	C1658	C1532	G1416	A1278	U1141
C2752	C2364	C2365	C2365	G2278	G2159	U2097	C1962	A1802	G1667	G1533	U1417	U1288	U1142A
A2753	C2365	C2365	C2365	G2282	G2160	U2098	U1963	A1803	A1668	U	U1419	U1291	A1142B
U2756	G2372	G2476	G2372	G2282	G2161	U2099	C1967	C1804	A1669	A	G1422	U1292	A1143
A2757	G2373	C2477	C2373	G2284	C2162	C2102	U1970	A1810	G1674	G1536	G1422	C1293	G1154
A2758	C2374	A2478	C2374	G2285	C2163	C2103	A1971	G1811	C1686	A1542	C1428	C1297	U1165
G2759	G2375	G2498	G2375	A2286	G2165	U2102	A1972	A1812	G1687	C1543	C1428	U1300	C1166
U2764	G2376	C2498	G2376	A2287	G2166	C2105	A1972	A1813	U1688	C1547	G1429	U1301	U1167
A2765	G2377	C2498	G2377	A2288	G2167	C2106	U1993	G1824	U1693	C1557	C1432	G1309	G1171
G2766	G2378	G2498	G2378	A2289	G2168	C2107	U1997	C1827	C1694	A1588	U1431	G1310	G
C2769	G2379	U2391	G2379	U2291	A2171	C2108	A2001	G1835	G1695	G1559	A1445A	U1313	A
A2778	G2382	G2383	G2382	G2304	U2172	U2109	G2002	A1847	A1700	A1566	G1450A	C1314	C1178
U2779	G2383	G2383	G2383	A2305	A2173	C2111	G2010	A1848	A1701	A1569	U1453	G1327	C1179
G2780	G2384	G2385	G2384	A2306	G2176	U2112	G2012	U1877	G1704	A1570	G1453	U1340	C1180
A2781	G2385	G2385	G2385	A2307	A2177	C2113	G2011	G1878	G1721	A1571	G1459	U1341	U1188
G2782	G2389	U2390	G2389	G2308	U2180	U2115	A2001	A1877	A1722	U1578	C1467	U1352	C1201
C2785	G2391	G2391	G2391	U2311	G2181	G2116	G2012	G1878	A1739	A1580	G1468	G1358	U1205
U2786	C2394	C2394	C2394	U2312	G2182	U2118	G2011	G1878	G1740	C1582	A1471	A1360	G1206
C2789	G2394	C2394	C2394	C2313	G2185	A2119	G2012	A1889	A1741	U1583	G1470	U1365	U1211
A	G2394	C2394	C2394	C2314	G2186	G2120	G2013	A1890	G1750	C1584	A1472	A1365	G1212
C	G2394	C2394	C2394	C2315	G2187	G2122	G2014	A1900	G1756	A1586	G1473	G1368	A1220
G2792	G2394	C2394	C2394	C2316	G2188	U2123	G2015	A1900	G1757	C1587	G1479	U1372	G1223
G2793	G2394	C2394	C2394	C2317	G2189	U2124	G2016	A1900	G1758	C1588	G1482	A1379	G1225
C2794A	G2394	C2394	C2394	C2318	G2190	U2125	G2017	A1900	G1759	C1589	G1492	G1379	A1226
G	G2394	C2394	C2394	C2319	G2191	U2126	G2018	A1900	G1760	C1590	G1493	G1380	U1236
U	G2394	C2394	C2394	C2320	G2192	U2127	G2019	A1900	G1761	C1591	G1494	A1384	G1236
C	G2394	C2394	C2394	C2321	G2193	U2128	G2020	A1900	G1762	C1592	G1495	A1385	
A	G2394	C2394	C2394	C2322	G2194	U2129	G2021	A1900	G1763	C1593	G1496		
G2801B	G2394	C2394	C2394	C2323	G2195	U2130	G2022	A1900	G1764	C1594	G1497		
G2802	G2394	C2394	C2394	C2324	G2196	U2131	G2023	A1900	G1765	C1595	G1498		
C2803	G2394	C2394	C2394	C2325	G2197	U2132	G2024	A1900	G1766	C1596	G1499		
G2804	G2394	C2394	C2394	C2326	G2198	U2133	G2025	A1900	G1767	C1597	G1500		
G2805	G2394	C2394	C2394	C2327	G2199	U2134	G2026	A1900	G1768	C1598	G1501		
G2806	G2394	C2394	C2394	C2328	G2200	U2135	G2027	A1900	G1769	C1599	G1502		
G2807	G2394	C2394	C2394	C2329	G2201	U2136	G2028	A1900	G1770	C1600	G1503		
A2810	G2394	C2394	C2394	C2330	G2202	U2137	G2029	A1900	G1771	C1601	G1504		
G2811	G2394	C2394	C2394	C2331	G2203	U2138	G2030	A1900	G1772	C1602	G1505		
	G2394	C2394	C2394	C2332	G2204	U2139	G2031	A1900	G1773	C1603	G1506		
	G2394	C2394	C2394	C2333	G2205	U2140	G2032	A1900	G1774	C1604	G1507		
	G2394	C2394	C2394	C2334	G2206	U2141	G2033	A1900	G1775	C1605	G1508		
	G2394	C2394	C2394	C2335	G2207	U2142	G2034	A1900	G1776	C1606	G1509		
	G2394	C2394	C2394	C2336	G2208	U2143	G2035	A1900	G1777	C1607	G1510		
	G2394	C2394	C2394	C2337	G2209	U2144	G2036	A1900	G1778	C1608	G1511		
	G2394	C2394	C2394	C2338	G2210	U2145	G2037	A1900	G1779	C1609	G1512		
	G2394	C2394	C2394	C2339	G2211	U2146	G2038	A1900	G1780	C1610	G1513		
	G2394	C2394	C2394	C2340	G2212	U2147	G2039	A1900	G1781	C1611	G1514		
	G2394	C2394	C2394	C2341	G2213	U2148	G2040	A1900	G1782	C1612	G1515		
	G2394	C2394	C2394	C2342	G2214	U2149	G2041	A1900	G1783	C1613	G1516		
	G2394	C2394	C2394	C2343	G2215	U2150	G2042	A1900	G1784	C1614	G1517		
	G2394	C2394	C2394	C2344	G2216	U2151	G2043	A1900	G1785	C1615	G1518		
	G2394	C2394	C2394	C2345	G2217	U2152	G2044	A1900	G1786	C1616	G1519		
	G2394	C2394	C2394	C2346	G2218	U2153	G2045	A1900	G1787	C1617	G1520		
	G2394	C2394	C2394	C2347	G2219	U2154	G2046	A1900	G1788	C1618	G1521		
	G2394	C2394	C2394	C2348	G2220	U2155	G2047	A1900	G1789	C1619	G1522		
	G2394	C2394	C2394	C2349	G2221	U2156	G2048	A1900	G1790	C1620	G1523		
	G2394	C2394	C2394	C2350	G2222	U2157	G2049	A1900	G1791	C1621	G1524		
	G2394	C2394	C2394	C2351	G2223	U2158	G2050	A1900	G1792	C1622	G1525		
	G2394	C2394	C2394	C2352	G2224	U2159	G2051	A1900	G1793	C1623	G1526		
	G2394	C2394	C2394	C2353	G2225	U2160	G2052	A1900	G1794	C1624	G1527		
	G2394	C2394	C2394	C2354	G2226	U2161	G2053	A1900	G1795	C1625	G1528		
	G2394	C2394	C2394	C2355	G2227	U2162	G2054	A1900	G1796	C1626	G1529		
	G2394	C2394	C2394	C2356	G2228	U2163	G2055	A1900	G1797	C1627	G1530		
	G2394	C2394	C2394	C2357	G2229	U2164	G2056	A1900	G1798	C1628	G1531		
	G2394	C2394	C2394	C2358	G2230	U2165	G2057	A1900	G1799	C1629	G1532		
	G2394	C2394	C2394	C2359	G2231	U2166	G2058	A1900	G1800	C1630	G1533		
	G2394	C2394	C2394	C2360	G2232	U2167	G2059	A1900	G1801	C1631	G1534		
	G2394	C2394	C2394	C2361	G2233	U2168	G2060	A1900	G1802	C1632	G1535		
	G2394	C2394	C2394	C2362	G2234	U2169	G2061	A1900	G1803	C1633	G1536		
	G2394	C2394	C2394	C2363	G2235	U2170	G2062	A1900	G1804	C1634	G1537		
	G2394	C2394	C2394	C2364	G2236	U2171	G2063	A1900	G1805	C1635	G1538		
	G2394	C2394	C2394	C2365	G2237	U2172	G2064	A1900	G1806	C1636	G1539		
	G2394	C2394	C2394	C2366	G2238	U2173	G2065	A1900	G1807	C1637	G1540		
	G2394	C2394	C2394	C2367	G2239	U2174	G2066	A1900	G1808	C1638	G1541		
	G2394	C2394	C2394	C2368	G2240	U2175	G2067	A1900	G1809	C1639	G1542		
	G2394	C2394	C2394	C2369	G2241	U2176	G2068	A1900	G1810	C1640	G1543		
	G2394	C2394	C2394	C2370	G2242	U2177	G2069	A1900	G1811	C1641	G1544		
	G2394	C2394	C2394	C2371	G2243	U2178	G2070	A1900	G1812	C1642	G1545		
	G2394	C2394	C2394	C2372	G2244	U2179	G2071	A1900	G1813	C1643	G1546		
	G2394	C2394	C2394	C2373	G2245	U2180	G2072	A1900	G1814	C1644	G1547		
	G2394	C2394	C2394	C2374	G2246	U2181	G2073	A1900	G1815	C1645	G1548		
	G2394	C2394	C2394	C2375	G2247	U2182	G2074	A1900	G1816	C1646	G1549		
	G2394	C2394	C2394	C2376	G2248	U2183	G2075	A1900	G1817	C1647	G1550		
	G2394	C2394	C2394	C2377	G2249	U2184	G2076	A1900	G1818	C1648	G1551		
	G2394	C2394	C2394	C2378	G2250	U2185	G2077	A1900	G1819	C1649	G1552		
	G2394	C2394	C2394	C2379	G2251	U2186	G2078	A1900	G1820	C1650			



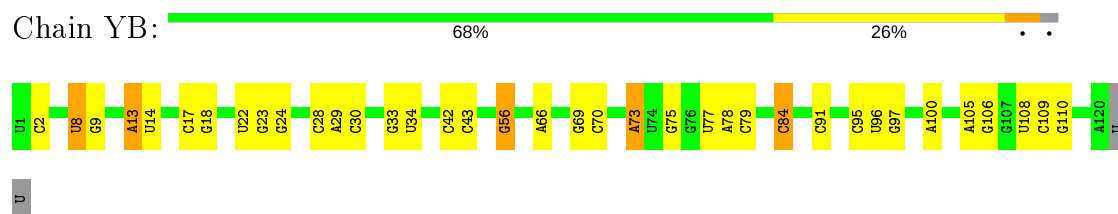
• Molecule 1: 23S rRNA

Chain YA: 64% 27% 6%

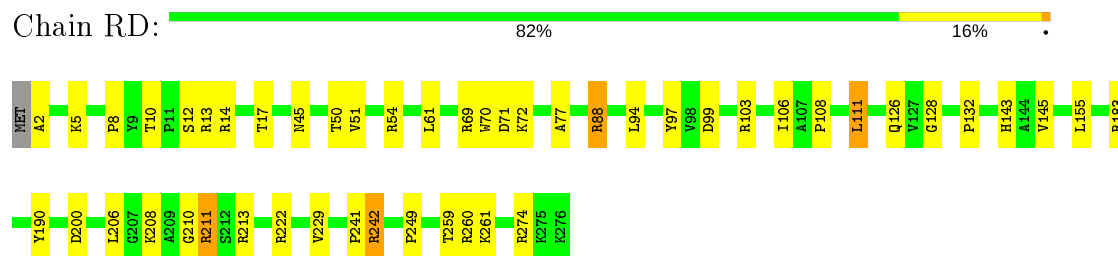


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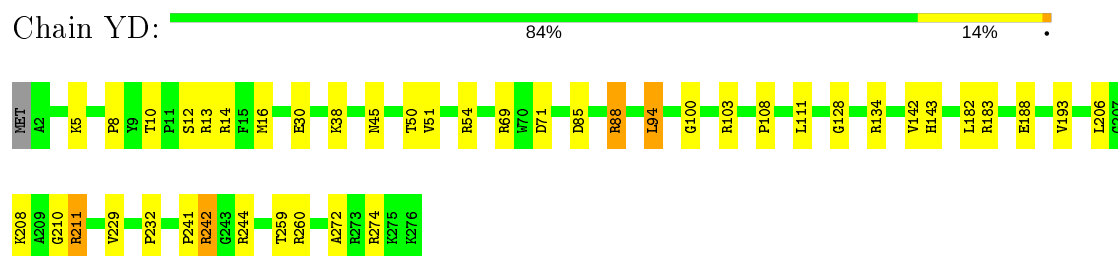
- Molecule 2: 5S rRNA



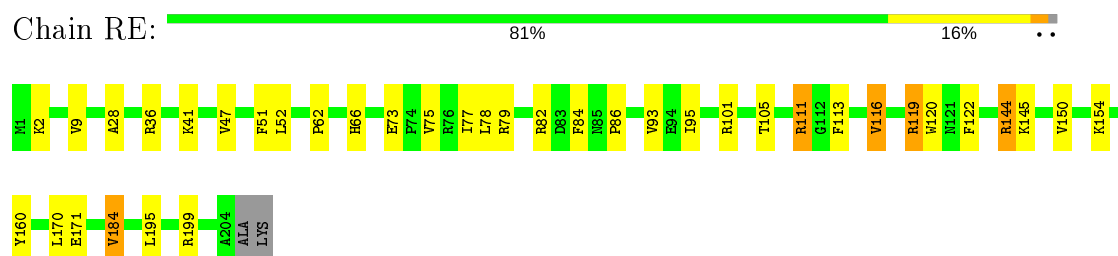
- Molecule 3: 50S ribosomal protein L2



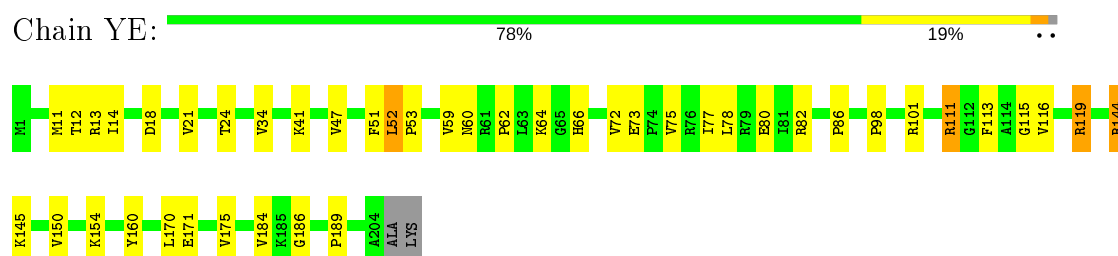
- Molecule 3: 50S ribosomal protein L2




- Molecule 4: 50S ribosomal protein L3

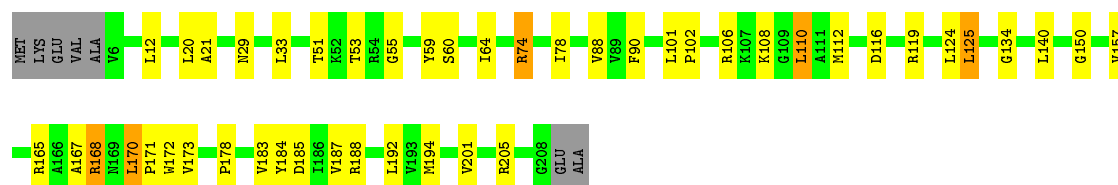


- Molecule 4: 50S ribosomal protein L3



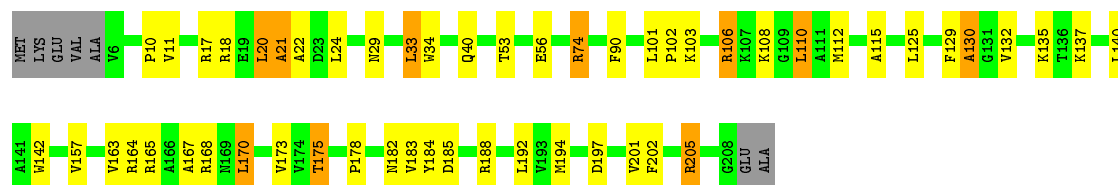
- Molecule 5: 50S ribosomal protein L4

Chain RF:  75% 20% ..



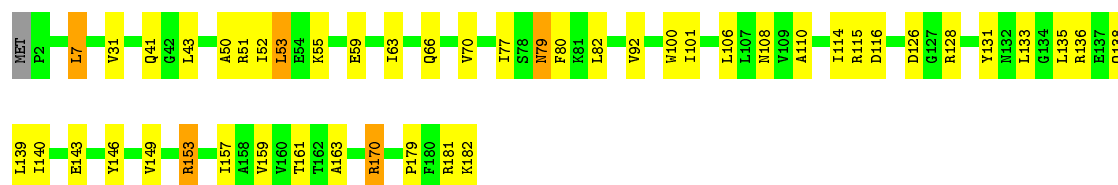
- Molecule 5: 50S ribosomal protein L4

Chain YF:  71% 20% 5% .



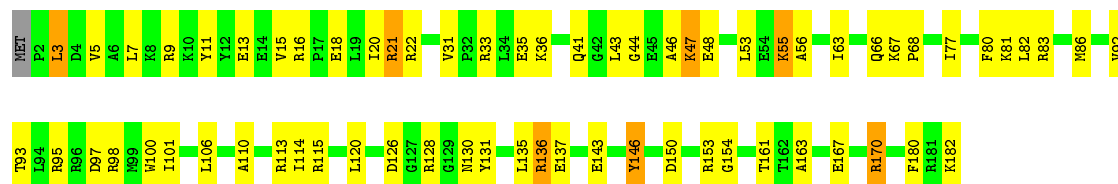
- Molecule 6: 50S ribosomal protein L5

Chain RG:  74% 23% ..




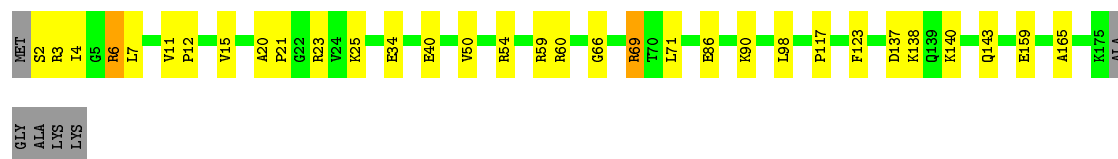
- Molecule 6: 50S ribosomal protein L5

Chain YG:  63% 32% ..



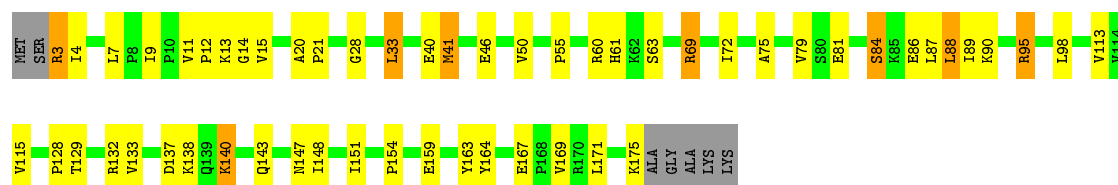
- Molecule 7: 50S ribosomal protein L6

Chain RH:  79% 17% ..




- Molecule 7: 50S ribosomal protein L6

Chain YH:  66% 26%




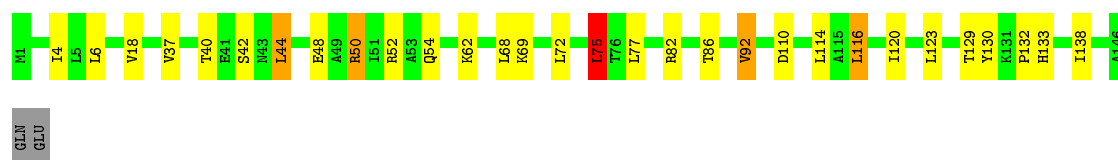
- Molecule 8: 50S ribosomal protein L9

Chain RI:  78% 20%




- Molecule 8: 50S ribosomal protein L9

Chain YI:  78% 17%




- Molecule 9: 50S ribosomal protein L13

Chain RN:  81% 16%



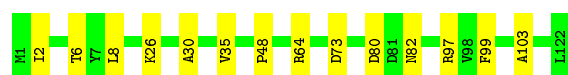
- Molecule 9: 50S ribosomal protein L13

Chain YN:  81% 17%




- Molecule 10: 50S ribosomal protein L14

Chain RO:  89% 11%

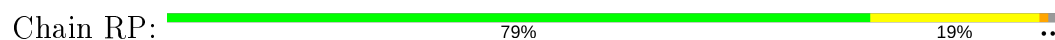


- Molecule 10: 50S ribosomal protein L14

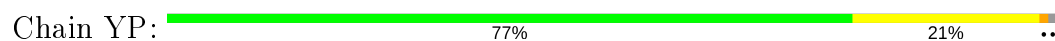
Chain YO:  86% 14%



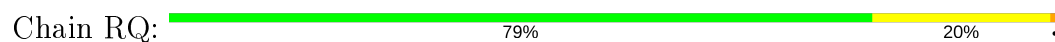
- Molecule 11: 50S ribosomal protein L15



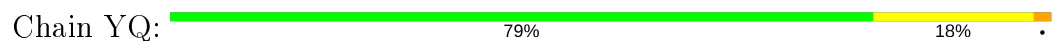
- Molecule 11: 50S ribosomal protein L15



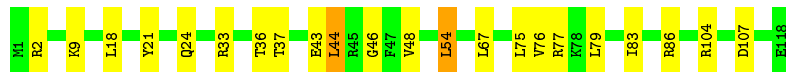
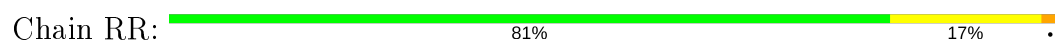
- Molecule 12: 50S ribosomal protein L16



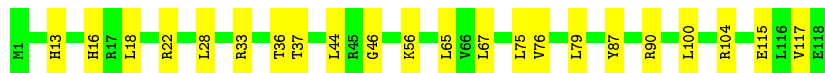
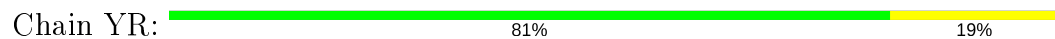
- Molecule 12: 50S ribosomal protein L16



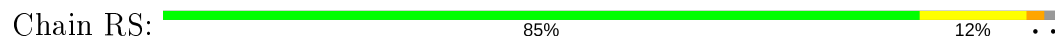
- Molecule 13: 50S ribosomal protein L17



- Molecule 13: 50S ribosomal protein L17



- Molecule 14: 50S ribosomal protein L18





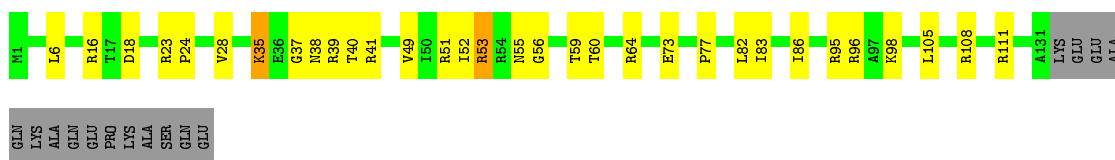
- Molecule 14: 50S ribosomal protein L18

Chain YS: 78% 20% ..



- Molecule 15: 50S ribosomal protein L19

Chain RT: 68% 21% • 10%



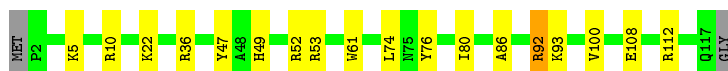
- Molecule 15: 50S ribosomal protein L19

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% ..




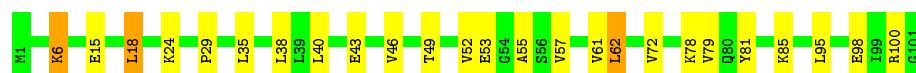
- Molecule 17: 50S ribosomal protein L21

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% .




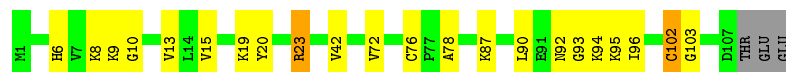
- Molecule 19: 50S ribosomal protein L23

Chain YX:  78% 21% .



- Molecule 20: 50S ribosomal protein L24

Chain RY:  77% 18% . .




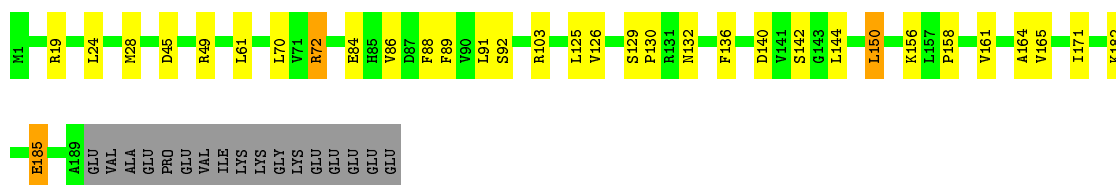
- Molecule 20: 50S ribosomal protein L24

Chain YY:  72% 24% . .



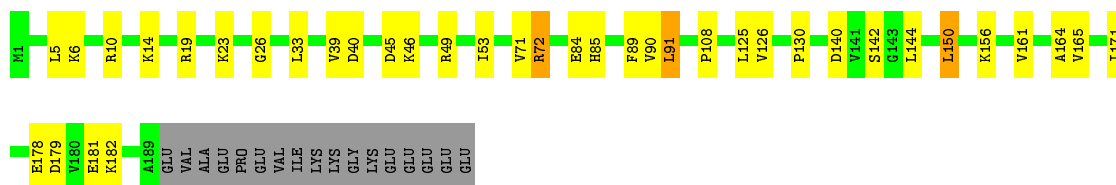
- Molecule 21: 50S ribosomal protein L25

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%




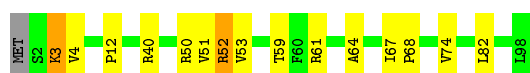
- Molecule 22: 50S ribosomal protein L27

Chain Y0:  72% 19% 9%



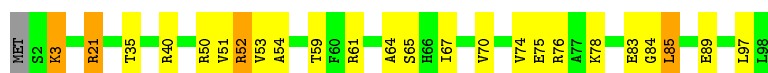
- Molecule 23: 50S ribosomal protein L28

Chain R1:  84% 13% ..



- Molecule 23: 50S ribosomal protein L28

Chain Y1:  74% 20% ..



- Molecule 24: 50S ribosomal protein L29

Chain R2:  88% 8% ..



- Molecule 24: 50S ribosomal protein L29

Chain Y2: 81% 15% ..



- Molecule 25: 50S ribosomal protein L30

Chain R3: 92% 7% .



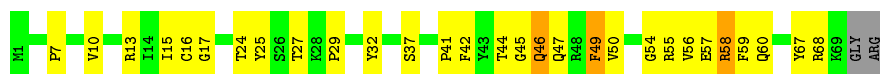
- Molecule 25: 50S ribosomal protein L30

Chain Y3: 77% 18% ..



- Molecule 26: 50S ribosomal protein L31

Chain R4: 56% 37% . .



- Molecule 26: 50S ribosomal protein L31

Chain Y4: 55% 37% 6% .



- Molecule 27: 50S ribosomal protein L32

Chain R5: 75% 22% ..



- Molecule 27: 50S ribosomal protein L32

Chain Y5: 85% 12% ..



- Molecule 28: 50S ribosomal protein L33

Chain R6: 76% 20%



- Molecule 28: 50S ribosomal protein L33

Chain Y6: 87% 11%



- Molecule 29: 50S ribosomal protein L34

Chain R7: 76% 22%



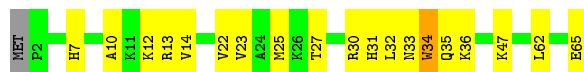
- Molecule 29: 50S ribosomal protein L34

Chain Y7: 78% 20%



- 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

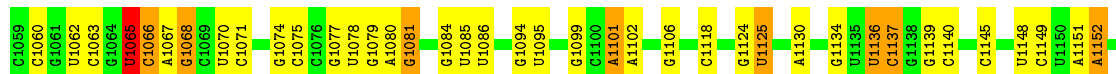
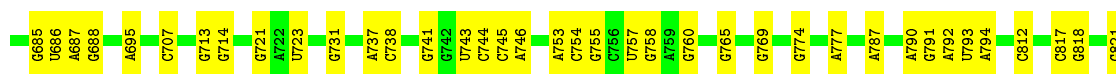
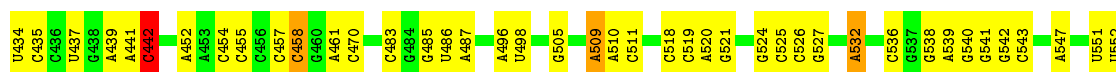
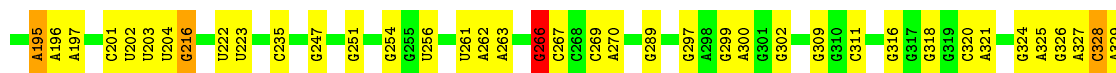
Chain R9: 81% 19%

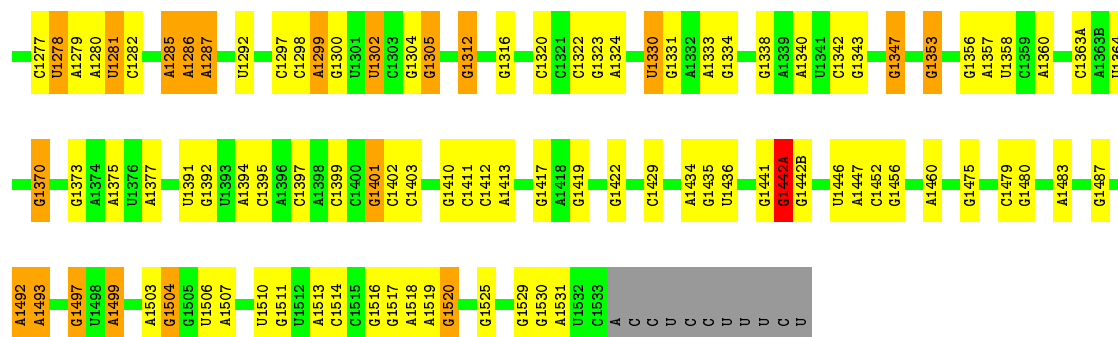


- Molecule 31: 50S ribosomal protein L36



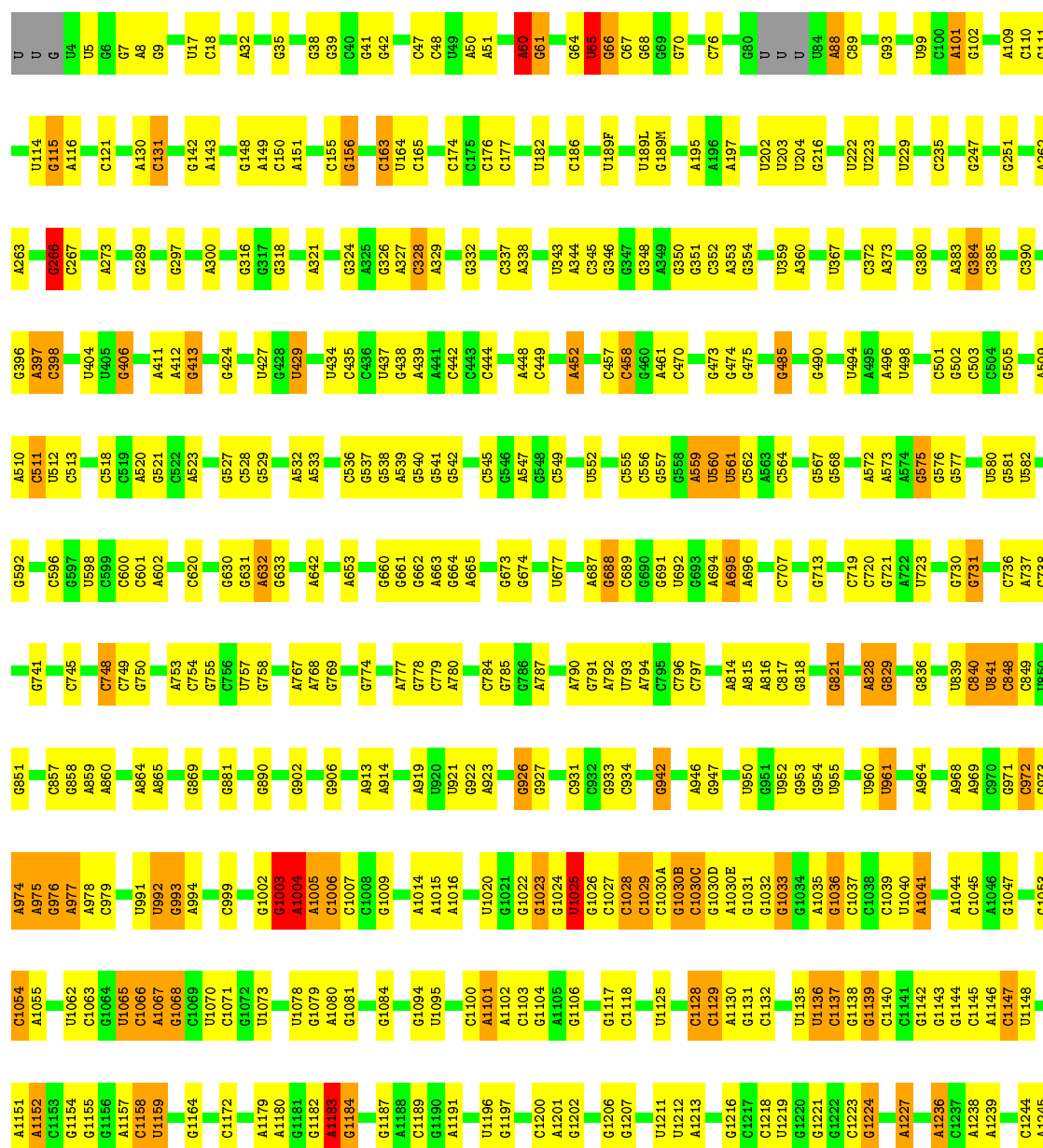
- Molecule 32: 16S rRNA

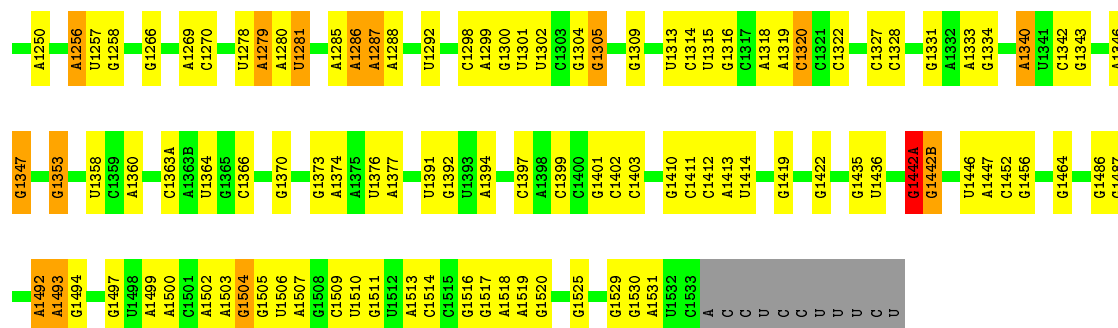




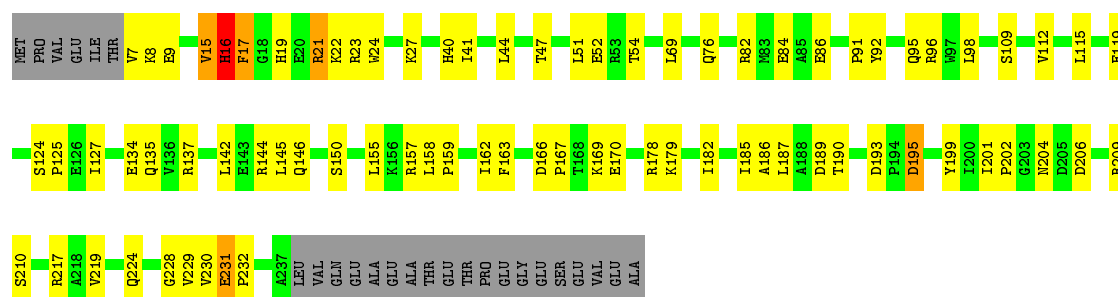
• Molecule 32: 16S rRNA

Chain XA: 63% 30% 6% ..

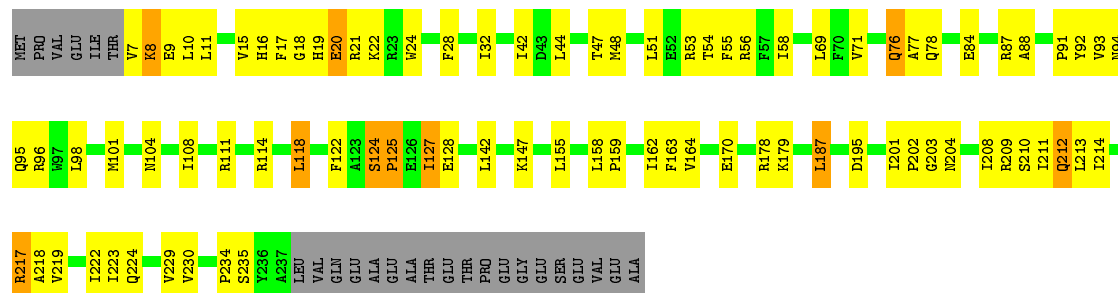




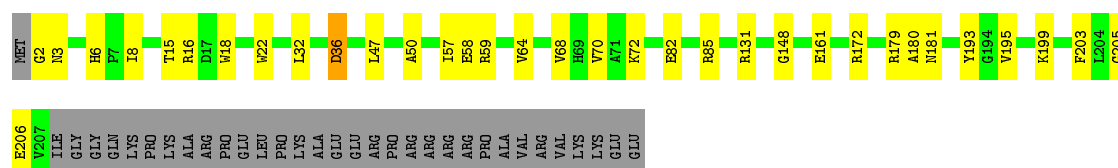
- Molecule 33: 30S ribosomal protein S2



- Molecule 33: 30S ribosomal protein S2

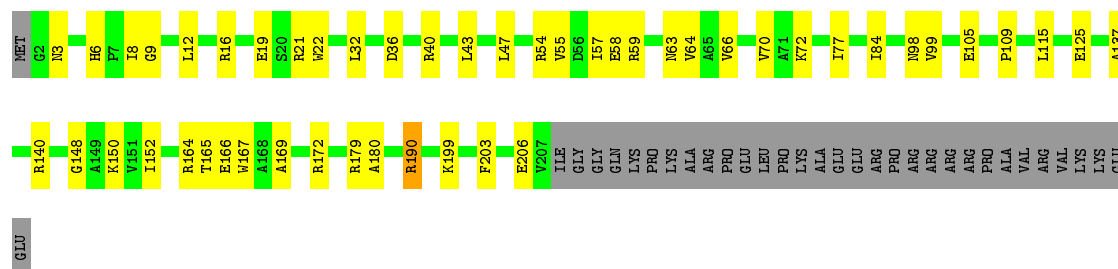


- Molecule 34: 30S ribosomal protein S3

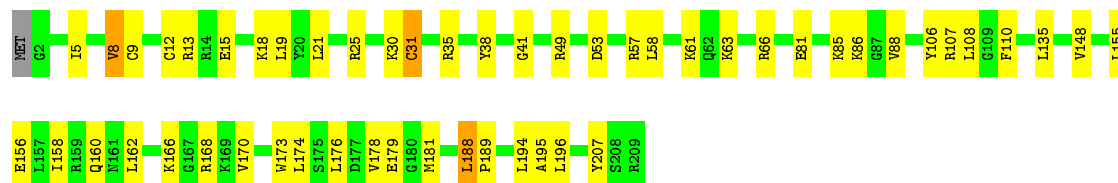
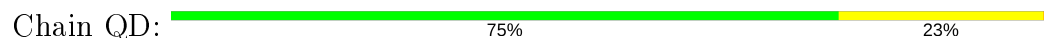


- Molecule 34: 30S ribosomal protein S3

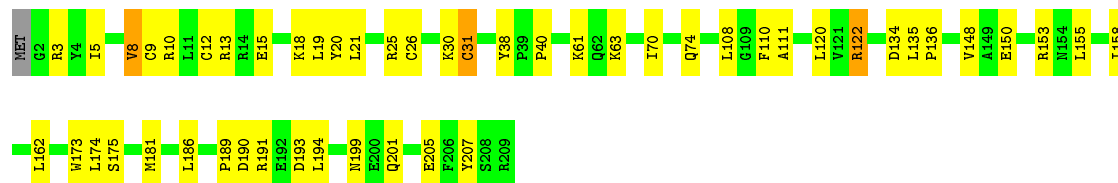
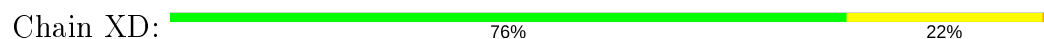




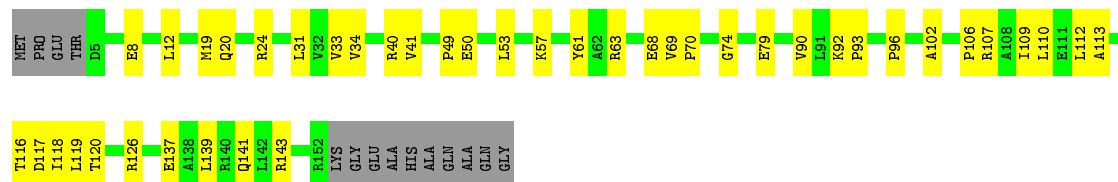
- Molecule 35: 30S ribosomal protein S4



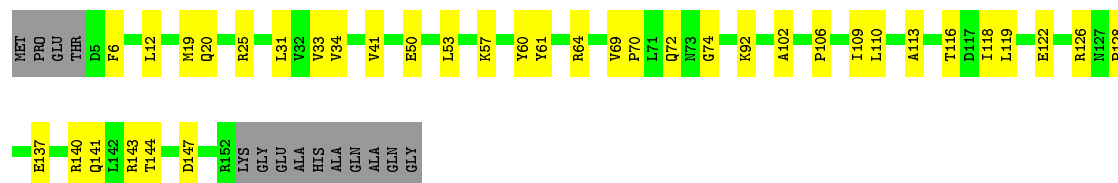
- Molecule 35: 30S ribosomal protein S4




- Molecule 36: 30S ribosomal protein S5

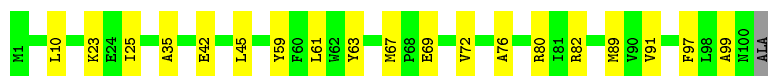


- Molecule 36: 30S ribosomal protein S5




- Molecule 37: 30S ribosomal protein S6

Chain QF:  80% 19%




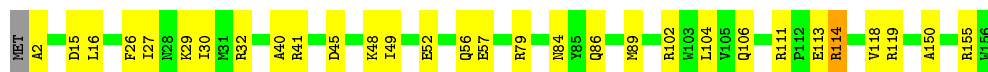
- Molecule 37: 30S ribosomal protein S6

Chain XF:  83% 16%




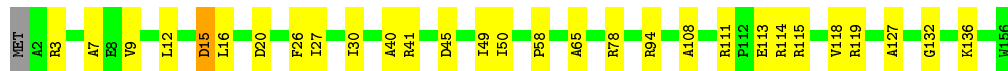
- Molecule 38: 30S ribosomal protein S7

Chain QG:  80% 19%




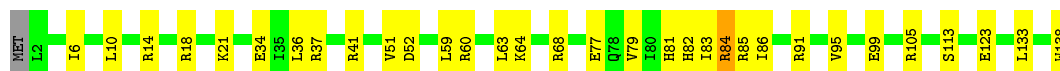
- Molecule 38: 30S ribosomal protein S7

Chain XG:  81% 18%




- Molecule 39: 30S ribosomal protein S8

Chain QH:  76% 22%



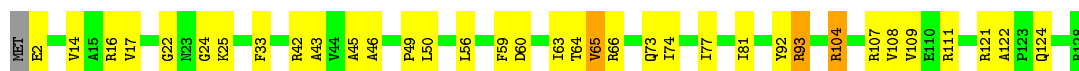
- Molecule 39: 30S ribosomal protein S8

Chain XH:  82% 16%

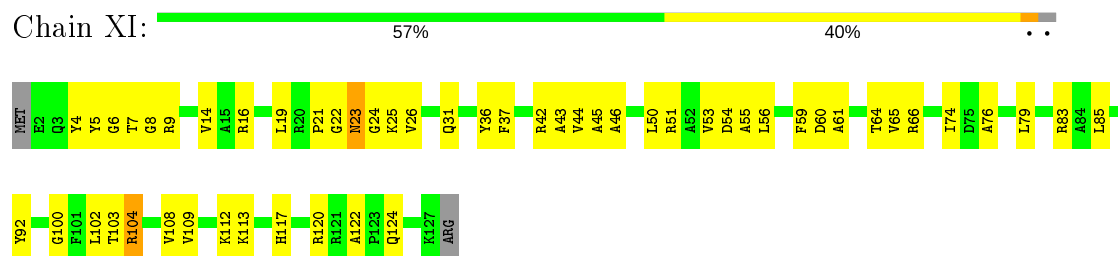


- Molecule 40: 30S ribosomal protein S9

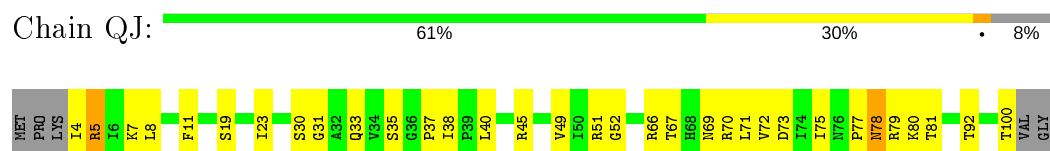
Chain QI:  72% 25%



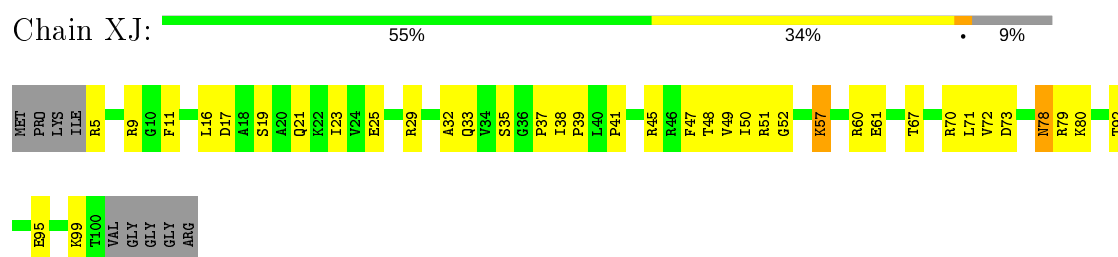
- Molecule 40: 30S ribosomal protein S9



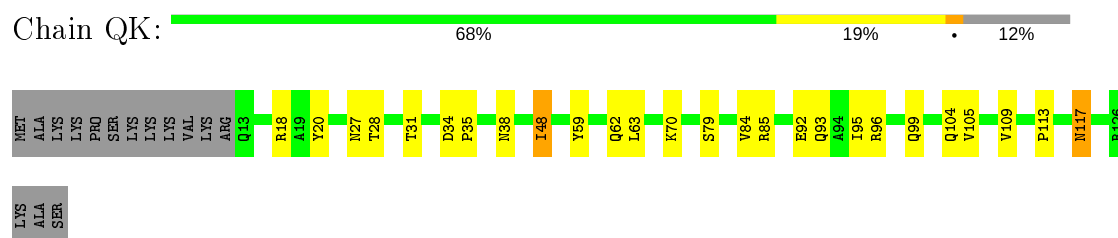
- Molecule 41: 30S ribosomal protein S10



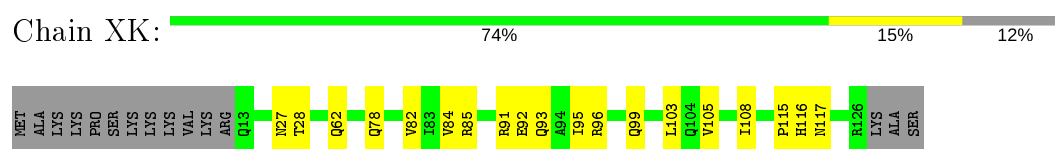
- Molecule 41: 30S ribosomal protein S10



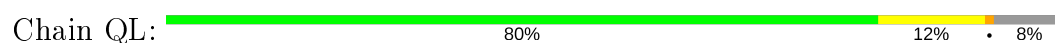
- Molecule 42: 30S ribosomal protein S11



- Molecule 42: 30S ribosomal protein S11



- Molecule 43: 30S ribosomal protein S12

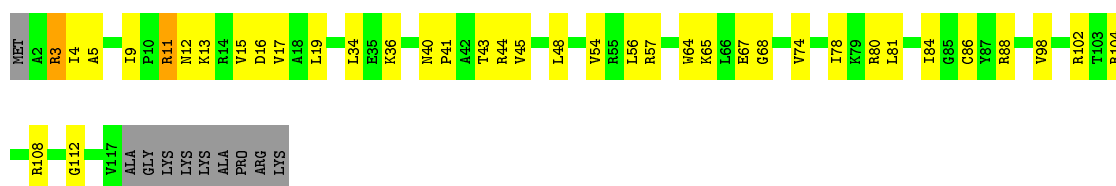




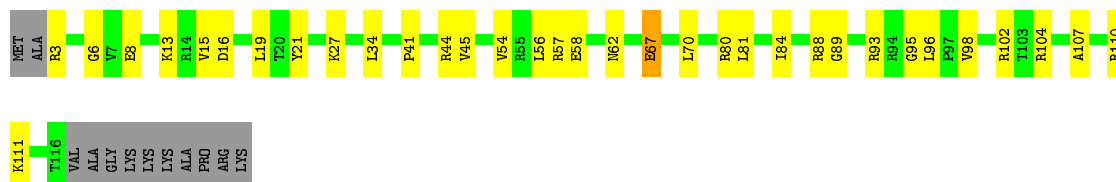
- Molecule 43: 30S ribosomal protein S12



- Molecule 44: 30S ribosomal protein S13



- Molecule 44: 30S ribosomal protein S13



- Molecule 45: 30S ribosomal protein S14 type Z

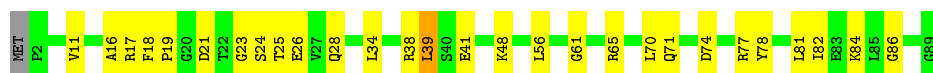


- Molecule 45: 30S ribosomal protein S14 type Z



- Molecule 46: 30S ribosomal protein S15





- Molecule 46: 30S ribosomal protein S15

Chain XO: 82% 15% ..



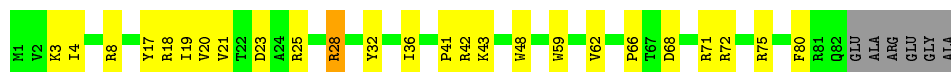
- Molecule 47: 30S ribosomal protein S16

Chain QP: 77% 15% 7%



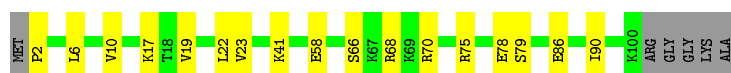
- Molecule 47: 30S ribosomal protein S16

Chain XP: 65% 27% 7%



- Molecule 48: 30S ribosomal protein S17

Chain QQ: 78% 16% 6%



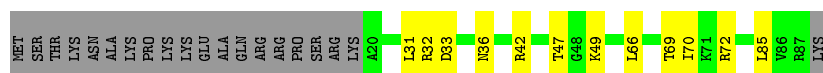
- Molecule 48: 30S ribosomal protein S17

Chain XQ: 86% 9% 6%



- Molecule 49: 30S ribosomal protein S18

Chain QR: 64% 14% 23%



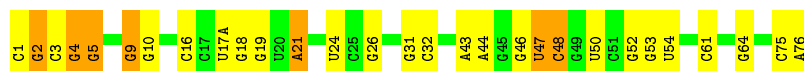
- Molecule 49: 30S ribosomal protein S18

Chain XR: 57% 19% 23%





- Molecule 53: P-site tRNA fMet



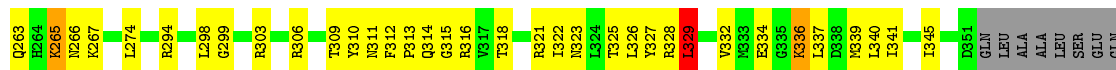
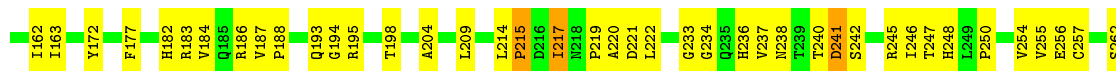
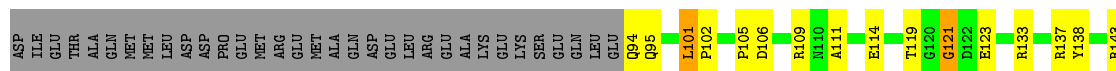
- Molecule 54: messenger RNA



- Molecule 54: messenger RNA



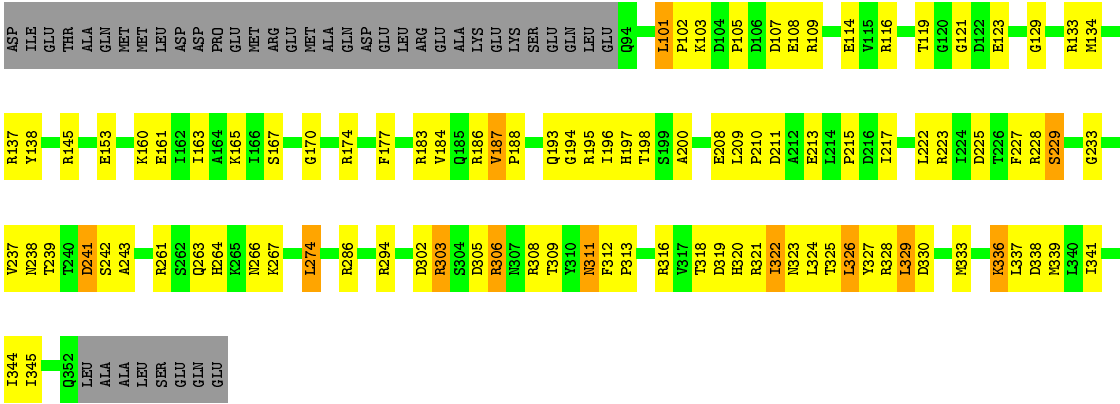
- Molecule 55: Peptide chain release factor 1



GLU

- Molecule 55: Peptide chain release factor 1





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, α , β , γ	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
$\langle I/\sigma(I) \rangle$ ¹	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 ²)	93.8	Xtriage
Anisotropy	0.251	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	294739	wwPDB-VP
Average B, all atoms (Å ²)	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.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, ZN, 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

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:1798:U:OP2	3:YD:274:ARG:NH2	2.16	0.78
1:YA:2756:U:H5''	31:Y9:19:ARG:HA	1.65	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:987:G:O2'	1:YA:1000:A:N3	2.29	0.66
1:YA:1064:C:H3'	1:YA:1065:U:H5'	1.77	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:1064:C:H3'	1:RA:1065:U:C5'	2.26	0.66
1:RA:1923:U:OP1	53:QV:24:U:O2'	2.14	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
5:RF:157:VAL:HB	5:RF:194:MET:HG2	1.79	0.64
1:RA:637:A:H8	11:RP:117:GLU:HG3	1.62	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:X1:50:LEU:HB2	40:X1:56: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
33:XB:101:MET:HA	33:XB:108:ILE:HG13	1.83	0.61
32:XA:1073:U:O2'	33:XB:104:ASN:OD1	2.19	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:2306:C:N4	6:YG:43:LEU:O	2.33	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
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:YN: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:2748:A:H5'	7:RH:4:ILE:HD12	1.84	0.59
1:RA:2749:A:H5'	7:RH:3:ARG:NH2	2.17	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:2747:G:OP1	7:RH:138:LYS:NZ	2.34	0.58
1:RA:652(U):C:H2'	1:RA:652(V):G:C8	2.37	0.58
1:YA:2218:U:O2	23:Y1:52:ARG:NH2	2.36	0.58
1:YA:1721:G:H2'	1:YA:1740:G:O6	2.04	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:662:G:H2'	32:XA:663:A:C8	2.40	0.57
32:XA:1191:A:OP2	34:XC:3:ASN:ND2	2.37	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:444:C:H42	32:XA:490:G:H1	1.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:411:A:OP2	35:XD:25:ARG:NH2	2.39	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: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
1:RA:250:G:P	30:R8:13:ARG:HH22	2.30	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:261:U:OP2	51:QT:79:ARG:NH2	2.40	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
1:RA:1803:A:O2'	3:RD:259:THR:HG21	2.07	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: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
1:RA:747:U:O2	1:RA:2014:A:H1'	2.08	0.54
19:RX:5:TYR:O	24:R2:36:ARG:NH2	2.39	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
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
6:YG:113:ARG:HH21	26:Y4:33:VAL:HG12	1.71	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:57:LYS:HE2	41:XJ:60:ARG:NH2	2.23	0.54
41:XJ:37:PRO:HA	41:XJ:72:VAL:HG12	1.89	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:1101:U:H2'	1:YA:1102:C:C6	2.43	0.54
1:YA:1049:C:O2	1:YA:1113:U:H4'	2.07	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
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:2354:G:H21	22:R0:36:ILE:HD11	1.73	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:1106:G:H5''	34:XC:172:ARG:HG2	1.89	0.54
32:XA:1151:A:O2'	32:XA:1152:A:H8	1.90	0.54
32:XA:452:A:N3	47:XP:72:ARG:NH1	2.56	0.54
34:XC:150:LYS:HG3	34:XC:169:ALA:HB2	1.90	0.54
38:XG:132:GLY:O	38:XG:136:LYS:HG2	2.06	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
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
32:XA:979:C:H42	45:XN:18:VAL:HG12	1.73	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
33:QB:15:VAL:HG23	33:QB:209:ARG:HB3	1.89	0.53
32:QA:411:A:OP2	35:QD:25:ARG:NH2	2.41	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:1492:A:OP2	43:XL:47:LYS:HG3	2.09	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
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
15:YT:39:ARG:HH22	32:XA:344:A:H4'	1.73	0.53
32:XA:707:C:OP1	42:XK:85:ARG:NH1	2.41	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:975:A:N1	41:XJ:48:THR:HB	2.24	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:YI:114:LEU:HD12	8:YI:116:LEU:HB2	1.89	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
32:XA:942:G:H21	40:XI:124:GLN:NE2	2.05	0.53
33:XB:69:LEU:HB3	33:XB:162:ILE:HG22	1.90	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:2526:G:H5'	1:RA:2742:C:O2'	2.09	0.53
1:RA:1824:G:O3'	3:RD:249:PRO:HD3	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: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:2756:U:H5''	31:R9:19:ARG:HA	1.91	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
51:QT:10:LEU:HB3	51:QT:12:ALA:H	1.74	0.52
26:R4:59:PHE:HE1	50:QS:64:GLU:HA	1.75	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
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
11:RP:63:PRO:HD3	30:R8:27:THR:HG22	1.91	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
18:RW:23:LEU:HD11	27:R5:25:LEU:HB2	1.92	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
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: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
32:QA:1360:A:OP2	45:QN:35:ARG:NH2	2.42	0.52
1:RA:1796:U:H2'	1:RA:1797:C:C6	2.45	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
1:YA:1310:G:OP2	29:Y7:9:ARG:HD2	2.09	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:2602:A:N1	55:XY:242:SER:OG	2.42	0.52
1:YA:1411:C:H2'	1:YA:1412:A:C8	2.45	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:1101:U:H2'	1:RA:1102:C:H6	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:2284:C:OP1	28:R6:5:VAL:HG13	2.09	0.51
1:RA:2758:A:C2	7:RH:71:LEU:HD21	2.45	0.51
21:RZ:126:VAL:HG11	21:RZ:161:VAL:HG23	1.92	0.51
21:RZ:129:SER:HB3	21:RZ:132:ASN:HB2	1.91	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
22:Y0:8:GLY:N	53:XV:2:G:H5'	2.25	0.51
55:XY:116:ARG:HH11	55:XY:161:GLU:HG3	1.75	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
19:RX:5:TYR:HB3	24:R2:33:MET:HB2	1.93	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
43:XL:28:LYS:N	43:XL:29:GLY:HA2	2.24	0.51
37:XF:95:GLU:O	49:XR:32:ARG:NH2	2.43	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:545:C:OP1	35:XD:61:LYS:NZ	2.44	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
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: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
32:XA:1309:G:OP1	44:XM:88:ARG:HD2	2.09	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
4:RE:105:THR:OG1	4:RE:199:ARG:NH2	2.44	0.51
1:RA:587:C:P	11:RP:21:ARG:HH22	2.34	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
32:XA:229:U:O2'	47:XP:23:ASP:OD2	2.28	0.51
36:XE:144:THR:H	36:XE:147:ASP:HB2	1.76	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)
7:YH:55:PRO:HG2	7:YH:61:HIS:CE1	2.45	0.51
1:YA:2683:C:OP1	15:YT:53:ARG:NH2	2.44	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:C8	2.46	0.51
32:QA:189(L):U:H2'	32:QA:189(M):G:H8	1.76	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: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
1:YA:61:G:H5'	24:Y2:50:ILE:HG21	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
19:RX:60:ARG:HH22	29:R7:47:ARG:HH22	1.57	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
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:300:A:OP1	20:YY:86:ARG:NH2	2.44	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
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: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
1:RA:321:G:H5'	5:RF:134:GLY:O	2.10	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
1:YA:997:G:OP1	16:YU:92:ARG:HG2	2.11	0.50
2:YB:66:A:H61	2:YB:109:C:H5'	1.76	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:1063:G:H2'	1:YA:1065:U:H6	1.76	0.50
1:YA:1058:G:H1	1:YA:1080:C:H42	1.60	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
1:YA:1364:G:OP2	23:Y1:3:LYS:HG3	2.11	0.50
25:Y3:23:LEU:HD22	25:Y3:50:VAL:HG11	1.93	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:1456:G:N1	51:XT:51:GLU:OE1	2.44	0.50
32:XA:429:U:H3'	35:XD:9:CYS:SG	2.52	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
1:YA:583:G:OP2	16:YU:10:ARG:HD2	2.12	0.50
14:YS:67:ARG:HG3	14:YS:71:ARG:NH1	2.27	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:764:A:H5'	3:YD:210:GLY:HA2	1.95	0.49
1:YA:8:A:H2'	1:YA:9:U:C6	2.48	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:950:U:OP2	44:QM:102:ARG:HD2	2.13	0.49
32:QA:1060:C:C4	34:QC:2:GLY:HA3	2.47	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: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
32:QA:235:C:H5'	48:QQ:70:ARG:HG2	1.93	0.49
1:RA:1065:U:H4'	1:RA:1066:U:H5'	1.94	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
1:RA:1224:C:O2'	17:RV:85:LYS:HA	2.13	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:1188:U:H4'	17:RV:79:VAL:HG22	1.95	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
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
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
6:RG:101:ILE:HD13	26:R4:25:TYR:HB2	1.94	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
6:YG:67:LYS:HE3	6:YG:68:PRO:O	2.13	0.48
11:YP:62:LEU:O	30:Y8:13:ARG:HD3	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
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
1:YA:587:C:OP2	11:YP:21:ARG:NH2	2.46	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: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
1:RA:2849:U:O4	15:RT:23:ARG:NH2	2.46	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:1826:G:H4'	3:YD:242:ARG:CZ	2.44	0.48
1:YA:273(A):G:N7	1:YA:421:U:H2'	2.29	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)
1:YA:2507:C:O4'	55:XY:238:ASN:HB3	2.13	0.48
26:Y4:20:ASN:ND2	26:Y4:38:LYS:HG3	2.28	0.48
1:YA:1803:A:O2'	3:YD:259:THR:HG21	2.13	0.48
1:YA:2115:G:N2	1:YA:2171:A:H61	2.12	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:1410:G:H2'	1:RA:1411:C:C6	2.48	0.48
1:RA:2611:U:C4	27:R5:3:LYS:HG2	2.48	0.48
5:RF:167:ALA:HB1	5:RF:173:VAL:HG11	1.96	0.48
5:RF:165:ARG:HA	5:RF:168:ARG:CD	2.44	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:2262:U:H4'	1:RA:2328:A:C2	2.49	0.47
1:RA:1814:G:H4'	3:RD:51:VAL:HG21	1.95	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: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
1:RA:2683:C:OP1	15:RT:53:ARG:NH2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
32:XA:972:C:O5'	41:XJ:57:LYS:HG2	2.14	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:2086:U:H2'	1:YA:2087:G:C8	2.49	0.47
1:YA:1278:A:OP1	13:YR:36:THR:HG23	2.14	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
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
11:RP:50:ARG:HD3	30:R8:7:HIS:CD2	2.50	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:26:PHE:O	38:XG:30:ILE:HG13	2.15	0.47
38:XG:65:ALA:HB1	38:XG:127:ALA:HB3	1.96	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:1665:A:H4'	10:YO:67:LYS:HB2	1.96	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: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:150:LEU:HB3	21:YZ:171:ILE:HD11	1.96	0.47
21:YZ:10:ARG:HH21	21:YZ:26:GLY:H	1.61	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:2820:A:OP2	13:RR:2:ARG:NH2	2.47	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
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:752:A:H3'	29:R7:1:MET:HE2	1.95	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
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:950:U:OP2	44:XM:102:ARG:HD3	2.15	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
1:YA:2158:A:H1'	1:YA:2159:G:C8	2.50	0.47
1:YA:2336:A:H61	22:Y0:43:THR:HG22	1.79	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:1805:U:O2	3:RD:50:THR:HB	2.14	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
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:581:C:H2'	1:YA:582:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:YA:529:A:OP2	9:YN:114:ARG:NH2	2.47	0.47
1:YA:295:G:OP1	20:YY:1:MET:HB2	2.15	0.47
40:QI:33:PHE:CE1	40:QI:43:ALA:HB1	2.50	0.47
53:QV:21:A:H61	53:QV:46:G:H2'	1.80	0.47
53:QV:43:A:H2'	53:QV:44:A:C8	2.49	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:2438:U:O2'	1:RA:2440:C:OP1	2.21	0.46
1:RA:2478:A:H5'	31:R9:31:LYS:HG2	1.98	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:98:G:H5'	24:Y2:3:LEU:HG	1.97	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
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:91:PHE:CE2	11:YP:99:LEU:HD21	2.50	0.46
11:YP:97:PRO:HA	11:YP:112:LEU:HD12	1.96	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:1971:A:C4	3:RD:241:PRO:HD3	2.50	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
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
33:QB:91:PRO:HG2	33:QB:155:LEU:HD23	1.96	0.46
33:QB:69:LEU:HB3	33:QB:162:ILE:HG22	1.97	0.46
39:QH:36:LEU:HD12	39:QH:59:LEU:HD13	1.97	0.46
32:QA:881:G:OP2	43:QL:12:ARG:NH2	2.49	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:4:U:O4	39:QH:105:ARG:HA	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: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:2693:A:H2'	1:RA:2694:G:H8	1.80	0.46
1:RA:10:G:H1'	1:RA:2801(B):A:N1	2.31	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:247:G:H4'	1:YA:386:G:C5	2.50	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: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:1343:G:H4'	40:QI:122:ALA:HB3	1.98	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
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
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
32:QA:1304:G:OP1	52:QU:2:GLY:N	2.49	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
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: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:2279:G:O6	22:Y0:14:ARG:HD2	2.15	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
1:YA:1341:U:O4'	19:YX:57:LEU:HD23	2.15	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: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
32:QA:657:G:H4'	46:QO:28:GLN:HG2	1.98	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
19:RX:60:ARG:NH2	29:R7:47:ARG:HH22	2.14	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
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:323:G:H1'	1:RA:1205:U:O2	2.16	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: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: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:1971:A:C4	3:YD:241:PRO:HD3	2.52	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
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
1:YA:144:C:H5'	19:YX:2:LYS:HE2	1.98	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:2128:C:H3'	1:RA:2129:C:H5''	1.98	0.45
1:RA:2107:C:H42	1:RA:2182:G:H1	1.65	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: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
32:QA:1058:G:OP1	34:QC:199:LYS:HE3	2.17	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:QI: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:2016:U:H1'	27:Y5:6:VAL:HG13	1.98	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: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: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:2420:C:OP1	30:R8:34:TRP:HB3	2.18	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:2016:U:H1'	27:R5:6:VAL:HG13	1.98	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
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
33:QB:9:GLU:CD	33:QB:217:ARG:HH22	2.20	0.44
37:QF:25:ILE:HG13	37:QF:82:ARG:HH12	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
32:QA:956:U:OP2	55:QY:137:ARG:NH2	2.51	0.44
1:RA:1041:C:N4	1:RA:1114:G:H1	2.04	0.44
1:RA:1309:G:P	29:R7:9:ARG:HD3	2.58	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: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:1239:A:C4	32:XA:1298:C:N4	2.86	0.44
32:XA:1492:A:C2'	55:XY:303:ARG:HH12	2.31	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
1:YA:1143:A:OP1	9:YN:25:ARG:NH2	2.51	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
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
14:YS:43:GLU:OE1	22:Y0:49:LYS:HE3	2.17	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
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:1202:G:H1'	45:YN:29:ARG:HD2	2.00	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
37:XF:91:VAL:HG11	49:XR:72:ARG:NH1	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
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
42:QK:109:VAL:HG23	49:QR:85:LEU:O	2.18	0.43
46:QO:71:GLN:HB2	46:QO:78:TYR:CG	2.54	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:2080:G:OP1	23:Y1:35:THR:HG21	2.18	0.43
1:YA:1587:A:H2'	1:YA:1588:C:C6	2.53	0.43
1:YA:1410:G:H1	1:YA:1592:C:H42	1.65	0.43
1:YA:2186:G:C2	1:YA:2187:G:C5	3.06	0.43
1:YA:309:G:H21	1:YA:330:A:P	2.40	0.43
1:YA:300:A:P	20:YY:86:ARG:HH21	2.41	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: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:2394:C:OP2	30:R8:30:ARG:HD2	2.18	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: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
1:YA:1638:C:O3'	1:YA:2709:G:N2	2.51	0.43
9:YN:62:VAL:HG11	9:YN:66:LYS:HB2	2.00	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
38:QG:150:ALA:HA	42:QK:59:TYR:HB3	2.01	0.43
39:QH:41:ARG:NH1	39:QH:123:GLU:OE2	2.48	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
32:QA:1493:A:H4'	55:QY:121:GLY:N	2.34	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
53:QV:4:G:O2'	53:QV:5:G:H8	2.02	0.43
26:R4:50:VAL:HG13	44:QM:65:LYS:HG2	2.01	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
32:XA:750:G:N3	46:XO:23:GLY:HA3	2.33	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
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:2137:C:H1'	1:YA:2154:G:H22	1.84	0.43
1:YA:2119:A:N6	1:YA:2168:G:H21	2.16	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:108:PRO:O	9:YN:113:GLY:HA3	2.19	0.43
9:YN:34:LEU:HD23	9:YN:107:LEU:HD11	2.01	0.43
32:QA:1047:G:H5'	45:QN:4:LYS:HD3	2.01	0.42
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
55:QY:119:THR:HG21	55:QY:303:ARG:HH11	1.83	0.42
1:RA:2355:C:H1'	22:R0:39:ARG:HH21	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: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:1151:A:O4'	41:XJ:39:PRO:HB2	2.19	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
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:2390:U:O2'	1:RA:2391:G:H5'	2.19	0.42
1:RA:2051:A:H5'	1:RA:2578:G:O4'	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: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
32:XA:954:G:H21	32:XA:1227:A:H62	1.67	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
32:QA:790:A:H1'	53:QV:38:A:H4'	2.00	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
26:R4:59:PHE:CE1	50:QS:64:GLU:HG3	2.53	0.42
19:RX:5:TYR:HD1	24:R2:33:MET:SD	2.42	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
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:575:G:C5	32:QA:881:G:C2	3.07	0.42
32:QA:437:U:H5'	35:QD:155:LEU:HD21	2.01	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:2144:U:H1'	1:YA:2147:G:O6	2.19	0.42
1:YA:1493:C:C5	1:YA:2206:G:H2'	2.54	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:1125:U:H4'	41:QJ:5:ARG:NH2	2.34	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
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:1019:U:H2'	1:YA:1020:A:C8	2.54	0.42
1:YA:125:G:N3	29:Y7:48:LYS:HE2	2.34	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:945:A:C4	1:YA:2448:A:C2	3.07	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
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:178:ARG:NH2	39:XH:74:PRO:HB3	2.35	0.42
33:XB:58:ILE:CG2	33:XB:222:ILE:HG22	2.50	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:1302:U:C5	44:QM:17:VAL:HG21	2.55	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
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:1092:C:O2	1:RA:1092:C:H2'	2.18	0.42
1:RA:1069:A:H5'	1:RA:1096:A:H5'	2.02	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:2118:U:H5	1:RA:2148:G:H1'	1.85	0.42
1:RA:2119:A:N6	1:RA:2168:G:H21	2.16	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:1151:A:H5''	41:XJ:41:PRO:HA	2.02	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
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:XI:108:VAL:HG12	40:XI: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:2271:G:OP1	22:Y0:18:ALA:HB1	2.20	0.41
1:YA:180:G:OP2	29:Y7:32:LYS:HE3	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: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
1:YA:1753:G:OP1	15:YT:95:ARG:HD3	2.20	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:370:G:H4'	1:RA:371:A:OP2	2.20	0.41
1:RA:27:G:C2	1:RA:512:G:N3	2.89	0.41
1:RA:583:G:OP2	16:RU:10:ARG:HD2	2.20	0.41
6:RG:77:ILE:HB	6:RG:82:LEU:HB3	2.02	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:1305:G:H5'	52:XU:4:GLY:HA3	2.02	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:XI:42:ARG:HB3	40:XI:42:ARG:HE	1.62	0.41
45:XN:50:LYS:HA	45:XN:50:LYS:HD2	1.79	0.41
45:XN:58:LYS:HE3	45:XN:58:LYS:HB3	1.88	0.41
30:Y8:23:VAL:CG1	30:Y8:47:LYS:HD3	2.50	0.41
1:YA:1025:G:C4	1:YA:1135:C:H1'	2.55	0.41
1:YA:1048:A:C5	1:YA:1049:C:C4	3.09	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: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
1:RA:1827:C:OP2	3:RD:222:ARG:HD2	2.20	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:XN:6:LEU:HD23	45:XN: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:604:G:C5	32:QA:635:G:C6	3.08	0.41
32:QA:1205:U:O2'	34:QC:195:VAL:HG23	2.20	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
8:YI:62:LYS:HG2	8:YI:133:HIS:CD2	2.56	0.41
5:YF:33:LEU:HB3	11:YP:6:LEU:HD21	2.02	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
1:YA:2786:U:O2	4:YE:62:PRO:HB3	2.20	0.41
4:YE:47:VAL:O	4:YE:80:GLU:HA	2.21	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:187:VAL:HG13	55:XY:196:ILE:HD13	2.03	0.41
55:XY:183:ARG:HA	55:XY:200:ALA:HB2	2.02	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
32:XA:663:A:H5''	49:XR:61:LYS:NZ	2.36	0.40
38:XG:108:ALA:O	38:XG:119:ARG:HD2	2.21	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
2:YB:77:U:OP1	21:YZ:19:ARG:NH2	2.54	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
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:1569:A:H5'	3:RD:61:LEU:HD11	2.02	0.40
1:RA:1653:G:C6	13:RR:9:LYS:HB2	2.56	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
11:RP:138:LEU:HD23	11:RP:145:PRO:HB3	2.03	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%)	29	67
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%)	15	54
6	RG	179/182 (98%)	166 (93%)	12 (7%)	1 (1%)	25	64
6	YG	179/182 (98%)	170 (95%)	8 (4%)	1 (1%)	25	64
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%)	22	61
11	YP	147/150 (98%)	142 (97%)	4 (3%)	1 (1%)	22	61
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%)	17	56
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%)	15	54
17	YV	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	15	54
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%)	14	51
23	Y1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	14	51
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%)	1	12
26	Y4	67/71 (94%)	55 (82%)	9 (13%)	3 (4%)	2	18
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%)	9	42
33	XB	229/256 (90%)	205 (90%)	19 (8%)	5 (2%)	6	35
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%)	22	61
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%)	9	43
41	QJ	95/105 (90%)	83 (87%)	8 (8%)	4 (4%)	3	20
41	XJ	94/105 (90%)	84 (89%)	8 (8%)	2 (2%)	7	37
42	QK	112/129 (87%)	105 (94%)	6 (5%)	1 (1%)	17	56
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%)	8	41
44	XM	112/126 (89%)	105 (94%)	6 (5%)	1 (1%)	17	56
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%)	15	54
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%)	13	49
50	XS	81/93 (87%)	77 (95%)	4 (5%)	0	100	100
51	QT	94/106 (89%)	88 (94%)	5 (5%)	1 (1%)	14	51
51	XT	96/106 (91%)	89 (93%)	5 (5%)	2 (2%)	7	37
52	QU	21/27 (78%)	19 (90%)	2 (10%)	0	100	100
52	XU	21/27 (78%)	18 (86%)	2 (10%)	1 (5%)	2	17
55	QY	255/360 (71%)	224 (88%)	17 (7%)	14 (6%)	2	14
55	XY	256/360 (71%)	222 (87%)	25 (10%)	9 (4%)	3	24
All	All	11925/12848 (93%)	11396 (96%)	459 (4%)	70 (1%)	25	64

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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Mol	Chain	Res	Type
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%)	34	68
3	YD	215/218 (99%)	210 (98%)	5 (2%)	50	78
4	RE	164/166 (99%)	157 (96%)	7 (4%)	29	64
4	YE	164/166 (99%)	156 (95%)	8 (5%)	25	61
5	RF	160/166 (96%)	151 (94%)	9 (6%)	21	57
5	YF	159/166 (96%)	149 (94%)	10 (6%)	18	52
6	RG	144/156 (92%)	136 (94%)	8 (6%)	21	57
6	YG	142/156 (91%)	131 (92%)	11 (8%)	13	44
7	RH	144/148 (97%)	141 (98%)	3 (2%)	53	79
7	YH	143/148 (97%)	133 (93%)	10 (7%)	15	48
8	RI	111/124 (90%)	102 (92%)	9 (8%)	11	42
8	YI	108/124 (87%)	101 (94%)	7 (6%)	17	51
9	RN	119/119 (100%)	111 (93%)	8 (7%)	16	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	YN	118/119 (99%)	114 (97%)	4 (3%)	37	70
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%)	60	83
11	YP	115/116 (99%)	113 (98%)	2 (2%)	60	83
12	RQ	111/111 (100%)	108 (97%)	3 (3%)	44	75
12	YQ	111/111 (100%)	105 (95%)	6 (5%)	22	58
13	RR	101/101 (100%)	95 (94%)	6 (6%)	19	54
13	YR	101/101 (100%)	95 (94%)	6 (6%)	19	54
14	RS	87/88 (99%)	85 (98%)	2 (2%)	50	78
14	YS	85/88 (97%)	83 (98%)	2 (2%)	49	77
15	RT	115/127 (91%)	111 (96%)	4 (4%)	36	69
15	YT	113/127 (89%)	110 (97%)	3 (3%)	44	75
16	RU	93/94 (99%)	89 (96%)	4 (4%)	29	64
16	YU	93/94 (99%)	90 (97%)	3 (3%)	39	71
17	RV	81/82 (99%)	77 (95%)	4 (5%)	25	61
17	YV	80/82 (98%)	76 (95%)	4 (5%)	24	60
18	RW	90/92 (98%)	84 (93%)	6 (7%)	16	50
18	YW	90/92 (98%)	87 (97%)	3 (3%)	38	71
19	RX	77/78 (99%)	76 (99%)	1 (1%)	69	87
19	YX	77/78 (99%)	77 (100%)	0	100	100
20	RY	86/91 (94%)	84 (98%)	2 (2%)	50	78
20	YY	86/91 (94%)	83 (96%)	3 (4%)	36	69
21	RZ	159/179 (89%)	153 (96%)	6 (4%)	33	67
21	YZ	156/179 (87%)	150 (96%)	6 (4%)	33	67
22	R0	61/67 (91%)	59 (97%)	2 (3%)	38	71
22	Y0	61/67 (91%)	60 (98%)	1 (2%)	62	84
23	R1	79/83 (95%)	77 (98%)	2 (2%)	47	77
23	Y1	81/83 (98%)	77 (95%)	4 (5%)	25	61
24	R2	65/67 (97%)	63 (97%)	2 (3%)	40	72
24	Y2	66/67 (98%)	64 (97%)	2 (3%)	41	73

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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%)	5	22
26	R4	58/63 (92%)	56 (97%)	2 (3%)	37	70
26	Y4	54/63 (86%)	46 (85%)	8 (15%)	3	14
27	R5	51/52 (98%)	49 (96%)	2 (4%)	32	67
27	Y5	50/52 (96%)	48 (96%)	2 (4%)	31	66
28	R6	51/52 (98%)	49 (96%)	2 (4%)	32	67
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%)	21	57
30	Y8	54/55 (98%)	52 (96%)	2 (4%)	34	68
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%)	20	55
33	XB	187/220 (85%)	173 (92%)	14 (8%)	13	45
34	QC	144/188 (77%)	142 (99%)	2 (1%)	67	86
34	XC	140/188 (74%)	137 (98%)	3 (2%)	53	79
35	QD	171/181 (94%)	166 (97%)	5 (3%)	42	74
35	XD	172/181 (95%)	169 (98%)	3 (2%)	60	83
36	QE	114/123 (93%)	113 (99%)	1 (1%)	78	91
36	XE	114/123 (93%)	113 (99%)	1 (1%)	78	91
37	QF	85/90 (94%)	85 (100%)	0	100	100
37	XF	85/90 (94%)	84 (99%)	1 (1%)	71	88
38	QG	120/127 (94%)	114 (95%)	6 (5%)	24	60
38	XG	119/127 (94%)	115 (97%)	4 (3%)	37	70
39	QH	116/119 (98%)	113 (97%)	3 (3%)	46	76
39	XH	114/119 (96%)	110 (96%)	4 (4%)	36	69
40	QI	91/99 (92%)	83 (91%)	8 (9%)	10	36
40	XI	88/99 (89%)	83 (94%)	5 (6%)	20	56
41	QJ	68/92 (74%)	66 (97%)	2 (3%)	42	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	XJ	68/92 (74%)	67 (98%)	1 (2%)	65	85
42	QK	83/99 (84%)	81 (98%)	2 (2%)	49	77
42	XK	83/99 (84%)	83 (100%)	0	100	100
43	QL	96/108 (89%)	95 (99%)	1 (1%)	76	90
43	XL	96/108 (89%)	95 (99%)	1 (1%)	76	90
44	QM	90/101 (89%)	87 (97%)	3 (3%)	38	71
44	XM	87/101 (86%)	86 (99%)	1 (1%)	73	88
45	QN	49/50 (98%)	44 (90%)	5 (10%)	7	29
45	XN	49/50 (98%)	48 (98%)	1 (2%)	55	80
46	QO	78/80 (98%)	74 (95%)	4 (5%)	24	60
46	XO	78/80 (98%)	75 (96%)	3 (4%)	33	67
47	QP	69/74 (93%)	68 (99%)	1 (1%)	67	86
47	XP	68/74 (92%)	66 (97%)	2 (3%)	42	74
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%)	60	83
50	QS	68/80 (85%)	66 (97%)	2 (3%)	42	74
50	XS	67/80 (84%)	67 (100%)	0	100	100
51	QT	71/82 (87%)	68 (96%)	3 (4%)	30	65
51	XT	70/82 (85%)	69 (99%)	1 (1%)	67	86
52	QU	18/22 (82%)	18 (100%)	0	100	100
52	XU	18/22 (82%)	17 (94%)	1 (6%)	21	57
55	QY	210/299 (70%)	200 (95%)	10 (5%)	25	61
55	XY	211/299 (71%)	198 (94%)	13 (6%)	18	53
All	All	9765/10662 (92%)	9411 (96%)	354 (4%)	35	69

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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Mol	Chain	Res	Type
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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Mol	Chain	Res	Type
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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Mol	Chain	Res	Type
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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Mol	Chain	Res	Type
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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Mol	Chain	Res	Type
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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Mol	Chain	Res	Type
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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Mol	Chain	Res	Type
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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Mol	Chain	Res	Type
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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Mol	Chain	Res	Type
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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Mol	Chain	Res	Type
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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Mol	Chain	Res	Type
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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Mol	Chain	Res	Type
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	5MC	XA	1400	32	15,22,23	3.23	5 (33%)	19,32,35	1.31	2 (10%)
1	PSU	YA	1917	1	17,21,22	3.72	8 (47%)	20,30,33	3.24	6 (30%)
43	0TD	QL	92	43	4,9,10	1.15	0	3,11,13	2.83	2 (66%)
32	UR3	QA	1498	32	14,22,23	3.49	3 (21%)	15,32,35	0.74	0
32	M2G	QA	966	32	20,27,28	4.15	6 (30%)	22,40,43	2.54	8 (36%)
32	2MG	QA	1207	32,56	19,26,27	4.42	6 (31%)	21,38,41	2.67	8 (38%)
32	5MC	QA	1400	32	15,22,23	3.22	5 (33%)	19,32,35	1.39	3 (15%)
1	5MU	RA	1915	1	15,22,23	2.86	3 (20%)	16,32,35	2.66	2 (12%)
32	2MG	XA	1207	32	19,26,27	4.38	6 (31%)	21,38,41	2.52	7 (33%)
1	2MA	YA	2503	1,56	17,25,26	4.23	6 (35%)	19,37,40	2.89	5 (26%)
1	5MC	YA	1962	1,56	15,22,23	3.25	5 (33%)	19,32,35	1.35	2 (10%)
55	MEQ	XY	235	55	8,9,10	0.90	0	5,10,12	0.80	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	2MU	YA	2552	1,56	14,22,24	8.48	9 (64%)	14,31,36	1.04	0
1	4OC	RA	1920	1	15,22,24	3.63	6 (40%)	17,31,35	1.67	3 (17%)
32	PSU	XA	516	32	17,21,22	3.73	9 (52%)	20,30,33	3.15	6 (30%)
1	5MC	RA	1942	1,56	15,22,23	3.28	5 (33%)	19,32,35	1.25	3 (15%)
55	MEQ	QY	235	55	8,9,10	0.93	0	5,10,12	1.08	1 (20%)
1	5MU	RA	1939	1	15,22,23	2.80	3 (20%)	16,32,35	2.99	2 (12%)
32	4OC	QA	1402	32	16,23,24	3.56	6 (37%)	17,32,35	1.75	1 (5%)
1	2MA	RA	2503	1,56	17,25,26	4.19	6 (35%)	19,37,40	2.87	5 (26%)
32	MA6	QA	1519	32	19,26,27	1.13	2 (10%)	18,38,41	3.55	2 (11%)
1	2MU	RA	2552	1,56	14,22,24	8.46	9 (64%)	14,31,36	1.03	0
1	5MC	RA	1962	1,56	15,22,23	3.24	5 (33%)	19,32,35	1.33	3 (15%)
32	PSU	QA	516	32,56	17,21,22	3.71	9 (52%)	20,30,33	3.11	6 (30%)
32	MA6	XA	1519	32	19,26,27	1.12	2 (10%)	18,38,41	3.54	2 (11%)
32	5MC	QA	1404	32	15,22,23	3.22	5 (33%)	19,32,35	1.47	4 (21%)
1	PSU	YA	2605	1	17,21,22	3.69	8 (47%)	20,30,33	3.07	6 (30%)
32	7MG	QA	527	32,56	22,26,27	4.67	10 (45%)	28,39,42	1.99	11 (39%)
1	PSU	RA	1911	1	17,21,22	3.74	9 (52%)	20,30,33	3.27	5 (25%)
1	4OC	YA	1920	1	15,22,24	3.61	6 (40%)	17,31,35	1.61	3 (17%)
32	UR3	XA	1498	32,56	14,22,23	3.52	3 (21%)	15,32,35	0.76	0
32	5MC	QA	967	32	15,22,23	3.28	5 (33%)	19,32,35	1.30	2 (10%)
1	OMG	RA	2251	1,56,53	18,26,27	3.57	7 (38%)	20,38,41	2.54	8 (40%)
32	MA6	QA	1518	32	19,26,27	1.14	2 (10%)	18,38,41	3.50	2 (11%)
1	5MU	YA	1939	1,56	15,22,23	2.79	3 (20%)	16,32,35	2.96	2 (12%)
1	PSU	YA	1911	1	17,21,22	3.74	8 (47%)	20,30,33	3.25	6 (30%)
32	5MC	XA	1404	32	15,22,23	3.17	5 (33%)	19,32,35	1.42	3 (15%)
32	M2G	XA	966	32	20,27,28	4.08	6 (30%)	22,40,43	2.53	7 (31%)
1	PSU	RA	1917	1	17,21,22	3.75	8 (47%)	20,30,33	3.40	6 (30%)
32	5MC	QA	1407	32	15,22,23	3.21	5 (33%)	19,32,35	1.47	3 (15%)
1	5MC	YA	1942	1	15,22,23	3.27	5 (33%)	19,32,35	1.32	3 (15%)
1	PSU	RA	2605	1	17,21,22	3.70	8 (47%)	20,30,33	3.05	6 (30%)
1	OMG	YA	2251	1,56,53	18,26,27	3.54	7 (38%)	20,38,41	2.48	8 (40%)
32	4OC	XA	1402	32	16,23,24	3.38	6 (37%)	17,32,35	2.87	1 (5%)
32	7MG	XA	527	32,56	22,26,27	4.67	10 (45%)	28,39,42	1.92	11 (39%)
43	0TD	XL	92	43	4,9,10	1.14	0	3,11,13	2.75	2 (66%)
32	5MC	XA	1407	32	15,22,23	3.21	5 (33%)	19,32,35	1.30	2 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	5MC	XA	967	32	15,22,23	3.23	5 (33%)	19,32,35	1.37	4 (21%)
1	5MU	YA	1915	1,56	15,22,23	2.87	3 (20%)	16,32,35	2.68	2 (12%)
32	MA6	XA	1518	32	19,26,27	1.06	2 (10%)	18,38,41	3.59	2 (11%)

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	5MC	XA	1400	32	-	4/5/25/26	0/2/2/2
1	PSU	YA	1917	1	-	0/7/25/26	0/2/2/2
43	0TD	QL	92	43	-	1/3/12/14	-
32	UR3	QA	1498	32	-	0/5/25/26	0/2/2/2
32	M2G	QA	966	32	-	0/7/29/30	0/3/3/3
32	2MG	QA	1207	32,56	-	0/5/27/28	0/3/3/3
32	5MC	QA	1400	32	-	2/5/25/26	0/2/2/2
1	5MU	RA	1915	1	-	2/5/25/26	0/2/2/2
32	2MG	XA	1207	32	-	0/5/27/28	0/3/3/3
1	2MA	YA	2503	1,56	-	1/3/25/26	0/3/3/3
1	5MC	YA	1962	1,56	-	2/5/25/26	0/2/2/2
55	MEQ	XY	235	55	-	4/8/9/11	-
1	2MU	YA	2552	1,56	-	0/7/27/28	0/2/2/2
1	4OC	RA	1920	1	-	0/7/27/30	0/2/2/2
32	PSU	XA	516	32	-	0/7/25/26	0/2/2/2
1	5MC	RA	1942	1,56	-	0/5/25/26	0/2/2/2
55	MEQ	QY	235	55	-	2/8/9/11	-
1	5MU	RA	1939	1	-	0/5/25/26	0/2/2/2
32	4OC	QA	1402	32	-	3/9/29/30	0/2/2/2
1	2MA	RA	2503	1,56	-	1/3/25/26	0/3/3/3
32	MA6	QA	1519	32	-	2/7/29/30	0/3/3/3
1	2MU	RA	2552	1,56	-	0/7/27/28	0/2/2/2
1	5MC	RA	1962	1,56	-	2/5/25/26	0/2/2/2
32	PSU	QA	516	32,56	-	0/7/25/26	0/2/2/2
32	MA6	XA	1519	32	-	2/7/29/30	0/3/3/3
32	5MC	QA	1404	32	-	0/5/25/26	0/2/2/2
1	PSU	YA	2605	1	-	0/7/25/26	0/2/2/2
32	7MG	QA	527	32,56	-	2/7/37/38	0/3/3/3
1	PSU	RA	1911	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	4OC	YA	1920	1	-	1/7/27/30	0/2/2/2
32	UR3	XA	1498	32,56	-	0/5/25/26	0/2/2/2
32	5MC	QA	967	32	-	0/5/25/26	0/2/2/2
1	OMG	RA	2251	1,56,53	-	0/5/27/28	0/3/3/3
32	MA6	QA	1518	32	-	0/7/29/30	0/3/3/3
1	5MU	YA	1939	1,56	-	0/5/25/26	0/2/2/2
1	PSU	YA	1911	1	-	0/7/25/26	0/2/2/2
32	5MC	XA	1404	32	-	0/5/25/26	0/2/2/2
32	M2G	XA	966	32	-	0/7/29/30	0/3/3/3
1	PSU	RA	1917	1	-	0/7/25/26	0/2/2/2
32	5MC	QA	1407	32	-	0/5/25/26	0/2/2/2
1	5MC	YA	1942	1	-	0/5/25/26	0/2/2/2
1	PSU	RA	2605	1	-	0/7/25/26	0/2/2/2
1	OMG	YA	2251	1,56,53	-	0/5/27/28	0/3/3/3
32	4OC	XA	1402	32	-	2/9/29/30	0/2/2/2
32	7MG	XA	527	32,56	-	2/7/37/38	0/3/3/3
43	0TD	XL	92	43	-	2/3/12/14	-
32	5MC	XA	1407	32	-	0/5/25/26	0/2/2/2
32	5MC	XA	967	32	-	0/5/25/26	0/2/2/2
1	5MU	YA	1915	1,56	-	2/5/25/26	0/2/2/2
32	MA6	XA	1518	32	-	0/7/29/30	0/3/3/3

All (265) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	YA	2552	2MU	C6-N1	24.02	1.65	1.35
1	RA	2552	2MU	C6-N1	23.98	1.65	1.35
32	QA	1207	2MG	C2-N2	13.10	1.45	1.34
32	XA	1207	2MG	C2-N2	13.04	1.45	1.34
1	RA	2552	2MU	O4'-C1'	12.01	1.57	1.41
1	YA	2552	2MU	O4'-C1'	11.96	1.57	1.41
32	QA	527	7MG	C4-N3	11.04	1.48	1.34
32	XA	527	7MG	C4-N3	10.94	1.48	1.34
1	YA	2503	2MA	C4-N3	10.62	1.52	1.35
1	RA	2503	2MA	C4-N3	10.28	1.51	1.35
1	YA	1939	5MU	C4-C5	9.54	1.61	1.41
32	XA	1498	UR3	C6-N1	9.52	1.47	1.35
1	RA	1939	5MU	C4-C5	9.51	1.61	1.41
1	YA	1915	5MU	C4-C5	9.46	1.61	1.41
1	YA	2552	2MU	C6-C5	-9.43	1.17	1.38
1	RA	2552	2MU	C6-C5	-9.42	1.17	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	QA	1498	UR3	C6-N1	9.38	1.47	1.35
1	RA	1915	5MU	C4-C5	9.35	1.61	1.41
32	QA	966	M2G	C4-N3	9.31	1.50	1.35
32	XA	527	7MG	C6-C5	9.27	1.54	1.41
32	QA	527	7MG	C6-C5	9.15	1.53	1.41
32	XA	966	M2G	C4-N3	8.99	1.49	1.35
32	QA	966	M2G	C2-N2	8.70	1.49	1.34
1	YA	2552	2MU	C3'-C2'	-8.57	1.33	1.52
32	XA	966	M2G	C2-N2	8.47	1.48	1.34
32	QA	1402	4OC	C6-N1	8.44	1.46	1.35
32	QA	1207	2MG	C4-N3	8.35	1.48	1.35
1	RA	2552	2MU	C3'-C2'	-8.31	1.34	1.52
32	XA	1402	4OC	C6-N1	8.30	1.46	1.35
1	RA	1920	4OC	C6-N1	8.28	1.46	1.35
1	YA	1920	4OC	C6-N1	8.25	1.46	1.35
32	XA	527	7MG	C6-N1	8.23	1.47	1.33
32	XA	1207	2MG	C4-N3	8.16	1.48	1.35
1	RA	1911	PSU	C4-N3	8.13	1.47	1.33
32	QA	527	7MG	C6-N1	8.09	1.47	1.33
1	YA	2605	PSU	C4-N3	8.04	1.47	1.33
1	YA	1911	PSU	C4-N3	8.03	1.47	1.33
1	RA	1917	PSU	C4-N3	7.98	1.46	1.33
1	YA	1917	PSU	C4-N3	7.96	1.46	1.33
1	RA	2605	PSU	C4-N3	7.90	1.46	1.33
1	YA	2503	2MA	C2-N3	7.90	1.48	1.34
1	RA	2503	2MA	C6-C5	7.88	1.53	1.41
32	XA	516	PSU	C4-N3	7.87	1.46	1.33
32	QA	516	PSU	C4-N3	7.83	1.46	1.33
1	RA	1942	5MC	C4-N3	7.81	1.46	1.35
1	YA	1962	5MC	C4-N3	7.80	1.46	1.35
1	RA	2503	2MA	C2-N3	7.77	1.47	1.34
1	YA	1942	5MC	C4-N3	7.73	1.46	1.35
32	QA	967	5MC	C4-N3	7.70	1.46	1.35
1	RA	1962	5MC	C4-N3	7.67	1.46	1.35
32	XA	966	M2G	C6-C5	7.66	1.54	1.41
1	YA	2503	2MA	C6-C5	7.60	1.53	1.41
32	XA	527	7MG	C2-N1	7.60	1.48	1.35
32	QA	527	7MG	C2-N1	7.59	1.48	1.35
32	QA	966	M2G	C6-C5	7.58	1.54	1.41
32	XA	1400	5MC	C4-N3	7.56	1.45	1.35
32	XA	1407	5MC	C4-N3	7.54	1.45	1.35
32	QA	1400	5MC	C4-N3	7.48	1.45	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	QA	1407	5MC	C4-N3	7.46	1.45	1.35
32	XA	967	5MC	C4-N3	7.45	1.45	1.35
32	QA	1404	5MC	C4-N3	7.41	1.45	1.35
32	QA	527	7MG	C2-N3	7.38	1.48	1.35
32	XA	1207	2MG	C6-C5	7.36	1.54	1.41
32	QA	1207	2MG	C6-C5	7.29	1.53	1.41
1	RA	2251	OMG	C4-N3	7.29	1.47	1.35
32	XA	527	7MG	C2-N3	7.28	1.48	1.35
32	XA	1404	5MC	C4-N3	7.23	1.45	1.35
1	RA	2251	OMG	C6-C5	7.21	1.53	1.41
1	YA	2251	OMG	C4-N3	7.15	1.46	1.35
1	YA	2251	OMG	C6-C5	7.13	1.53	1.41
1	RA	2552	2MU	C4-N3	-7.12	1.20	1.33
1	YA	2552	2MU	C4-N3	-7.12	1.20	1.33
32	XA	1498	UR3	C4-N3	7.10	1.48	1.38
32	QA	1498	UR3	C4-N3	7.03	1.48	1.38
32	QA	966	M2G	C6-N1	6.87	1.45	1.33
32	XA	966	M2G	C6-N1	6.87	1.45	1.33
1	RA	1920	4OC	C4-N3	6.53	1.46	1.35
1	YA	1920	4OC	C4-N3	6.50	1.46	1.35
1	RA	2605	PSU	C6-C5	6.48	1.48	1.38
32	QA	1207	2MG	C6-N1	6.44	1.44	1.33
32	XA	1207	2MG	C6-N1	6.43	1.44	1.33
32	QA	516	PSU	C6-C5	6.39	1.48	1.38
32	XA	966	M2G	C2-N1	6.22	1.45	1.34
1	RA	1911	PSU	C6-C5	6.22	1.47	1.38
32	XA	516	PSU	C6-C5	6.21	1.47	1.38
1	YA	2605	PSU	C6-C5	6.21	1.47	1.38
32	QA	966	M2G	C2-N1	6.20	1.45	1.34
1	RA	2251	OMG	C2-N1	6.19	1.46	1.35
1	RA	1917	PSU	C2-N1	6.17	1.50	1.38
1	YA	2251	OMG	C2-N1	6.15	1.46	1.35
32	QA	516	PSU	C2-N1	6.12	1.50	1.38
1	YA	1917	PSU	C6-C5	6.10	1.47	1.38
1	YA	1911	PSU	C6-C5	6.08	1.47	1.38
1	RA	1917	PSU	C6-C5	6.08	1.47	1.38
1	YA	1917	PSU	C2-N1	6.05	1.50	1.38
1	RA	2251	OMG	C6-N1	6.00	1.43	1.33
32	XA	516	PSU	C2-N1	6.00	1.50	1.38
1	RA	1911	PSU	C2-N1	5.98	1.50	1.38
1	YA	2503	2MA	C2-N1	5.97	1.44	1.34
32	QA	1402	4OC	C4-N3	5.97	1.46	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	RA	2503	2MA	C2-N1	5.96	1.44	1.34
1	RA	2605	PSU	C2-N1	5.96	1.50	1.38
1	YA	2251	OMG	C6-N1	5.93	1.43	1.33
32	QA	967	5MC	C5-C4	5.92	1.50	1.41
1	YA	1911	PSU	C2-N1	5.89	1.49	1.38
1	RA	1917	PSU	C2-N3	5.86	1.49	1.38
1	YA	2605	PSU	C2-N1	5.86	1.49	1.38
1	RA	1942	5MC	C5-C4	5.85	1.50	1.41
1	RA	1911	PSU	C2-N3	5.83	1.49	1.38
1	YA	1911	PSU	C2-N3	5.83	1.49	1.38
32	XA	967	5MC	C5-C4	5.82	1.50	1.41
1	YA	1917	PSU	C2-N3	5.82	1.49	1.38
1	YA	2605	PSU	C2-N3	5.81	1.49	1.38
32	XA	516	PSU	C2-N3	5.80	1.49	1.38
32	XA	1404	5MC	C5-C4	5.79	1.50	1.41
32	XA	527	7MG	C2-N2	5.79	1.45	1.33
1	YA	1942	5MC	C5-C4	5.77	1.50	1.41
1	YA	1942	5MC	C2-N3	5.77	1.49	1.38
32	QA	1404	5MC	C5-C4	5.75	1.50	1.41
32	QA	1400	5MC	C5-C4	5.74	1.50	1.41
32	XA	1400	5MC	C5-C4	5.73	1.50	1.41
32	XA	1407	5MC	C5-C4	5.73	1.50	1.41
1	RA	2605	PSU	C2-N3	5.72	1.49	1.38
32	QA	516	PSU	C2-N3	5.70	1.49	1.38
1	YA	1962	5MC	C2-N3	5.70	1.49	1.38
32	QA	1407	5MC	C5-C4	5.69	1.50	1.41
1	RA	1962	5MC	C5-C4	5.68	1.50	1.41
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	RA	1942	5MC	C2-N3	5.66	1.49	1.38
32	QA	527	7MG	C2-N2	5.65	1.45	1.33
1	RA	1920	4OC	C2-N3	5.62	1.49	1.38
1	RA	1962	5MC	C2-N3	5.62	1.49	1.38
32	XA	967	5MC	C2-N3	5.58	1.49	1.38
1	YA	1962	5MC	C5-C4	5.55	1.49	1.41
32	QA	1402	4OC	C2-N3	5.54	1.49	1.38
32	QA	1407	5MC	C2-N3	5.54	1.49	1.38
1	YA	1920	4OC	C2-N3	5.53	1.49	1.38
1	YA	2552	2MU	O4'-C4'	-5.53	1.32	1.45
32	QA	966	M2G	C2-N3	5.53	1.47	1.33
1	RA	2251	OMG	C2-N2	5.52	1.44	1.33
32	XA	1402	4OC	C4-N3	5.51	1.45	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	QA	1404	5MC	C2-N3	5.50	1.49	1.38
32	XA	1407	5MC	C2-N3	5.50	1.49	1.38
32	QA	1400	5MC	C2-N3	5.49	1.49	1.38
1	YA	2251	OMG	C2-N2	5.46	1.44	1.33
1	RA	2552	2MU	O4'-C4'	-5.46	1.32	1.45
1	YA	2503	2MA	C6-N1	5.40	1.45	1.35
32	XA	1404	5MC	C2-N3	5.39	1.48	1.38
1	RA	2503	2MA	C6-N1	5.28	1.45	1.35
32	XA	966	M2G	C2-N3	5.26	1.46	1.33
1	RA	1920	4OC	C6-C5	5.17	1.49	1.38
32	QA	516	PSU	C6-N1	5.15	1.45	1.34
1	YA	1920	4OC	C6-C5	5.14	1.49	1.38
32	QA	1498	UR3	C6-C5	5.10	1.49	1.38
1	RA	1917	PSU	C6-N1	5.10	1.45	1.34
32	QA	1402	4OC	C6-C5	5.07	1.49	1.38
32	XA	1498	UR3	C6-C5	5.04	1.49	1.38
1	RA	1911	PSU	C6-N1	5.02	1.45	1.34
1	RA	2605	PSU	C6-N1	5.00	1.45	1.34
32	XA	1402	4OC	C2-N3	4.96	1.48	1.38
1	YA	1917	PSU	C6-N1	4.95	1.44	1.34
1	YA	2605	PSU	C6-N1	4.93	1.44	1.34
1	YA	1911	PSU	C6-N1	4.90	1.44	1.34
32	XA	516	PSU	C6-N1	4.89	1.44	1.34
32	XA	1402	4OC	C6-C5	4.87	1.48	1.38
32	QA	527	7MG	C4-N9	4.78	1.47	1.38
1	RA	1915	5MU	C4-N3	-4.66	1.24	1.33
32	QA	1404	5MC	C4-N4	4.51	1.45	1.34
1	YA	1915	5MU	C4-N3	-4.49	1.25	1.33
32	XA	967	5MC	C4-N4	4.48	1.45	1.34
32	XA	527	7MG	C4-N9	4.47	1.46	1.38
32	QA	967	5MC	C4-N4	4.46	1.45	1.34
32	QA	1407	5MC	C4-N4	4.45	1.45	1.34
32	XA	1404	5MC	C4-N4	4.45	1.45	1.34
32	QA	1402	4OC	C5-C4	4.44	1.49	1.39
32	QA	1400	5MC	C4-N4	4.44	1.45	1.34
32	XA	1402	4OC	C5-C4	4.44	1.49	1.39
32	XA	1400	5MC	C4-N4	4.44	1.45	1.34
1	YA	1942	5MC	C4-N4	4.41	1.45	1.34
1	YA	1962	5MC	C4-N4	4.41	1.45	1.34
1	RA	1962	5MC	C4-N4	4.41	1.45	1.34
1	YA	1911	PSU	C5-C1'	-4.41	1.48	1.52
1	RA	1942	5MC	C4-N4	4.40	1.45	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	XA	1407	5MC	C4-N4	4.40	1.45	1.34
32	XA	516	PSU	C5-C1'	-4.31	1.48	1.52
32	QA	1402	4OC	C4-N4	4.20	1.45	1.36
1	RA	2552	2MU	C3'-C4'	4.13	1.63	1.53
1	YA	2552	2MU	C3'-C4'	4.07	1.63	1.53
32	XA	527	7MG	C5-N7	3.94	1.46	1.39
1	RA	1939	5MU	C4-N3	-3.91	1.26	1.33
1	RA	1917	PSU	C5-C1'	-3.90	1.48	1.52
1	RA	1917	PSU	C4-C5	3.87	1.49	1.41
1	YA	1917	PSU	C5-C1'	-3.86	1.49	1.52
1	YA	1917	PSU	C4-C5	3.82	1.49	1.41
32	QA	1207	2MG	C2-N3	3.81	1.46	1.34
32	XA	1207	2MG	C2-N3	3.78	1.46	1.34
1	YA	1911	PSU	C4-C5	3.77	1.49	1.41
32	XA	1402	4OC	C4-N4	3.77	1.44	1.36
1	YA	1939	5MU	C4-N3	-3.76	1.26	1.33
32	XA	516	PSU	C4-C5	3.76	1.49	1.41
1	RA	1911	PSU	C4-C5	3.73	1.49	1.41
32	QA	527	7MG	C5-N7	3.70	1.46	1.39
1	RA	1911	PSU	C5-C1'	-3.69	1.49	1.52
32	QA	516	PSU	C4-C5	3.67	1.49	1.41
1	YA	2605	PSU	C4-C5	3.67	1.49	1.41
1	RA	1920	4OC	C4-N4	3.66	1.46	1.35
1	YA	1920	4OC	C4-N4	3.66	1.46	1.35
1	RA	2605	PSU	C5-C1'	-3.62	1.49	1.52
1	YA	2605	PSU	C5-C1'	-3.61	1.49	1.52
32	QA	1404	5MC	C6-C5	3.61	1.50	1.40
32	QA	527	7MG	C5-C4	3.60	1.46	1.39
1	YA	2552	2MU	C2-N3	3.59	1.45	1.38
32	XA	1404	5MC	C6-C5	3.55	1.49	1.40
32	QA	1400	5MC	C6-C5	3.54	1.49	1.40
32	XA	967	5MC	C6-C5	3.53	1.49	1.40
1	RA	2552	2MU	C2-N3	3.51	1.45	1.38
1	RA	1920	4OC	C5-C4	3.50	1.49	1.41
1	YA	1920	4OC	C5-C4	3.49	1.49	1.41
1	RA	2605	PSU	C4-C5	3.49	1.48	1.41
32	XA	1207	2MG	C2-N1	3.47	1.45	1.34
32	QA	1207	2MG	C2-N1	3.47	1.45	1.34
32	QA	967	5MC	C6-C5	3.44	1.49	1.40
32	QA	1407	5MC	C6-C5	3.44	1.49	1.40
32	XA	1407	5MC	C6-C5	3.38	1.49	1.40
32	XA	527	7MG	C5-C4	3.37	1.45	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	RA	1962	5MC	C6-C5	3.33	1.49	1.40
1	YA	1942	5MC	C6-C5	3.32	1.49	1.40
32	XA	1400	5MC	C6-C5	3.30	1.49	1.40
1	RA	1942	5MC	C6-C5	3.30	1.49	1.40
1	YA	1962	5MC	C6-C5	3.30	1.49	1.40
1	YA	2251	OMG	O6-C6	-3.29	1.16	1.24
1	RA	2251	OMG	O6-C6	-3.27	1.16	1.24
32	QA	516	PSU	C5-C1'	-3.27	1.49	1.52
32	XA	527	7MG	C8-N9	3.25	1.53	1.45
32	QA	527	7MG	C8-N9	3.21	1.53	1.45
32	QA	1519	MA6	C2-N3	2.69	1.36	1.32
32	QA	1518	MA6	C2-N3	2.64	1.36	1.32
1	RA	2552	2MU	O2'-C2'	2.55	1.49	1.42
1	YA	2552	2MU	O2'-C2'	2.51	1.49	1.42
32	XA	1519	MA6	C2-N3	2.48	1.36	1.32
32	XA	1518	MA6	C2-N3	2.47	1.36	1.32
1	RA	1915	5MU	C6-C5	2.35	1.46	1.40
1	RA	2251	OMG	C2-N3	2.32	1.45	1.34
1	YA	1915	5MU	C6-C5	2.30	1.46	1.40
1	YA	2251	OMG	C2-N3	2.27	1.45	1.34
32	QA	1519	MA6	C5-C4	-2.25	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
32	XA	1518	MA6	C5-C4	-2.23	1.35	1.40
1	RA	1939	5MU	C6-C5	2.22	1.46	1.40
1	YA	2605	PSU	O4-C4	-2.19	1.19	1.24
32	QA	1518	MA6	C5-C4	-2.18	1.35	1.40
1	RA	1911	PSU	O4-C4	-2.17	1.19	1.24
32	QA	516	PSU	O4'-C1'	-2.17	1.41	1.44
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	1939	5MU	C6-C5	2.12	1.46	1.40
32	XA	1519	MA6	C5-C4	-2.11	1.35	1.40
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	XA	516	PSU	O4'-C1'	-2.08	1.41	1.44
1	YA	2503	2MA	CM2-C2	2.08	1.55	1.49
1	RA	1911	PSU	O4'-C1'	-2.05	1.41	1.44
1	RA	2503	2MA	CM2-C2	2.03	1.55	1.49

All (188) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	QA	1519	MA6	N1-C6-N6	-14.19	102.12	117.06
32	XA	1518	MA6	N1-C6-N6	-14.17	102.14	117.06
32	XA	1519	MA6	N1-C6-N6	-13.85	102.48	117.06
32	QA	1518	MA6	N1-C6-N6	-13.80	102.54	117.06
32	XA	1402	4OC	CM4-N4-C4	-11.49	113.10	122.97
1	RA	1917	PSU	N1-C2-N3	-11.41	119.36	128.43
1	RA	1911	PSU	N1-C2-N3	-11.28	119.46	128.43
1	YA	1917	PSU	N1-C2-N3	-10.78	119.86	128.43
32	QA	516	PSU	N1-C2-N3	-10.77	119.86	128.43
1	YA	1911	PSU	N1-C2-N3	-10.77	119.87	128.43
32	XA	516	PSU	N1-C2-N3	-10.43	120.14	128.43
1	YA	2605	PSU	N1-C2-N3	-10.39	120.17	128.43
1	RA	1939	5MU	C5-C6-N1	-10.29	111.10	122.19
1	YA	1939	5MU	C5-C6-N1	-10.13	111.28	122.19
1	RA	2605	PSU	N1-C2-N3	-10.09	120.41	128.43
1	YA	1915	5MU	C5-C6-N1	-9.12	112.36	122.19
1	RA	1915	5MU	C5-C6-N1	-9.05	112.44	122.19
32	QA	966	M2G	C1'-N9-C4	-8.16	112.31	126.64
1	RA	2503	2MA	C2-N3-C4	8.00	122.02	115.52
1	YA	2503	2MA	C2-N3-C4	7.82	121.88	115.52
1	RA	2503	2MA	C1'-N9-C4	-7.50	113.46	126.64
1	YA	2503	2MA	C1'-N9-C4	-7.50	113.47	126.64
32	XA	966	M2G	C1'-N9-C4	-7.28	113.85	126.64
32	QA	1402	4OC	CM4-N4-C4	-6.69	117.22	122.97
1	RA	2251	OMG	N3-C2-N1	-6.49	118.57	127.22
1	YA	2251	OMG	N3-C2-N1	-6.42	118.66	127.22
1	RA	1917	PSU	C4-N3-C2	6.15	120.34	115.14
1	RA	1911	PSU	C4-N3-C2	6.11	120.30	115.14
1	YA	1911	PSU	C4-N3-C2	6.11	120.30	115.14
1	YA	1917	PSU	C4-N3-C2	5.98	120.19	115.14
32	XA	516	PSU	C4-N3-C2	5.91	120.13	115.14
32	QA	1207	2MG	N2-C2-N1	5.70	122.43	116.96
32	XA	1207	2MG	CM2-N2-C2	-5.67	116.76	123.59
32	XA	1207	2MG	N2-C2-N1	5.66	122.40	116.96
1	RA	1939	5MU	C4-N3-C2	5.54	119.82	115.14
1	RA	1920	4OC	C2-N3-C4	5.54	121.95	116.34
32	QA	516	PSU	C4-N3-C2	5.52	119.80	115.14
32	QA	1207	2MG	CM2-N2-C2	-5.51	116.94	123.59
1	YA	1939	5MU	C4-N3-C2	5.34	119.66	115.14
1	YA	1920	4OC	C2-N3-C4	5.34	121.76	116.34
1	YA	1911	PSU	C5-C4-N3	-5.30	118.53	125.36
32	XA	1519	MA6	N3-C2-N1	-5.20	120.55	128.68
32	XA	516	PSU	C5-C4-N3	-5.18	118.69	125.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	1915	5MU	C4-N3-C2	5.15	119.49	115.14
1	YA	1917	PSU	C5-C4-N3	-5.14	118.73	125.36
1	RA	2605	PSU	C4-N3-C2	5.12	119.47	115.14
32	XA	966	M2G	C2-N3-C4	5.09	121.06	115.28
32	QA	966	M2G	C2-N3-C4	5.06	121.02	115.28
1	RA	1915	5MU	C4-N3-C2	5.04	119.40	115.14
32	QA	1518	MA6	N3-C2-N1	-5.03	120.82	128.68
1	RA	1917	PSU	C5-C4-N3	-5.01	118.90	125.36
1	YA	2605	PSU	C4-N3-C2	4.98	119.35	115.14
32	XA	1518	MA6	N3-C2-N1	-4.91	121.01	128.68
1	RA	2251	OMG	C2-N3-C4	4.87	120.91	115.36
1	RA	1911	PSU	C5-C4-N3	-4.83	119.13	125.36
32	XA	527	7MG	N1-C2-N3	-4.81	117.88	125.42
32	XA	1207	2MG	C2-N3-C4	4.72	120.64	115.28
1	YA	2251	OMG	C2-N3-C4	4.70	120.72	115.36
1	RA	2251	OMG	C1'-N9-C4	4.67	134.85	126.64
32	QA	1207	2MG	N3-C2-N1	-4.61	118.93	126.23
32	QA	1207	2MG	C2-N3-C4	4.61	120.52	115.28
32	XA	966	M2G	N1-C2-N2	4.59	121.84	117.19
1	RA	2605	PSU	C5-C4-N3	-4.59	119.45	125.36
32	QA	1519	MA6	N3-C2-N1	-4.58	121.51	128.68
1	YA	2605	PSU	C5-C4-N3	-4.49	119.57	125.36
1	YA	2251	OMG	C1'-N9-C4	4.46	134.48	126.64
32	QA	516	PSU	C5-C4-N3	-4.44	119.64	125.36
32	QA	527	7MG	N1-C2-N3	-4.40	118.52	125.42
32	XA	1207	2MG	N3-C2-N1	-4.39	119.29	126.23
32	QA	1407	5MC	C2-N3-C4	4.35	121.27	116.02
1	YA	1962	5MC	C2-N3-C4	4.02	120.87	116.02
32	QA	1404	5MC	C2-N3-C4	4.00	120.85	116.02
32	XA	1400	5MC	C2-N3-C4	3.98	120.82	116.02
32	QA	967	5MC	C2-N3-C4	3.97	120.81	116.02
43	QL	92	0TD	CB-CA-N	-3.95	100.68	109.10
32	XA	1404	5MC	C2-N3-C4	3.89	120.72	116.02
32	XA	1407	5MC	C2-N3-C4	3.85	120.66	116.02
32	QA	527	7MG	C6-C5-C4	3.82	119.30	115.20
32	XA	967	5MC	C2-N3-C4	3.81	120.61	116.02
1	RA	1962	5MC	C2-N3-C4	3.80	120.60	116.02
32	XA	527	7MG	C6-N1-C2	3.72	121.84	115.93
32	QA	527	7MG	C6-N1-C2	3.64	121.72	115.93
1	YA	1942	5MC	C2-N3-C4	3.61	120.37	116.02
32	QA	527	7MG	C5-C4-N3	-3.57	120.67	126.49
1	YA	2503	2MA	N3-C2-N1	-3.56	119.17	125.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	QA	1400	5MC	C2-N3-C4	3.55	120.31	116.02
1	RA	1942	5MC	C2-N3-C4	3.55	120.30	116.02
1	RA	1917	PSU	C5-C6-N1	-3.52	120.12	124.44
1	RA	2503	2MA	N3-C2-N1	-3.49	119.29	125.72
1	RA	2605	PSU	C5-C6-N1	-3.46	120.19	124.44
43	XL	92	0TD	CB-CA-N	-3.43	101.78	109.10
1	YA	2605	PSU	C5-C6-N1	-3.40	120.26	124.44
32	QA	516	PSU	C5-C6-N1	-3.40	120.26	124.44
32	XA	527	7MG	C5-C4-N3	-3.32	121.06	126.49
32	XA	966	M2G	CM1-N2-C2	-3.31	118.13	121.29
1	YA	2503	2MA	C5-C6-N1	-3.29	119.61	123.06
1	YA	1917	PSU	C5-C6-N1	-3.22	120.48	124.44
32	XA	527	7MG	C6-C5-C4	3.19	118.62	115.20
32	QA	966	M2G	N3-C2-N2	3.17	120.40	117.18
1	YA	1911	PSU	C5-C6-N1	-3.14	120.58	124.44
32	XA	516	PSU	C5-C6-N1	-3.12	120.61	124.44
1	YA	2251	OMG	C6-N1-C2	3.02	120.72	115.93
1	RA	2251	OMG	C6-N1-C2	3.01	120.71	115.93
32	QA	1207	2MG	C6-N1-C2	2.98	120.52	115.18
1	RA	1911	PSU	C5-C6-N1	-2.97	120.79	124.44
1	RA	1917	PSU	C6-N1-C2	2.95	120.23	115.36
43	XL	92	0TD	CSB-SB-CB	2.94	107.64	101.85
1	RA	2503	2MA	C5-C6-N1	-2.82	120.10	123.06
1	YA	2605	PSU	C6-N1-C2	2.79	119.96	115.36
32	QA	966	M2G	N1-C2-N2	2.77	119.99	117.19
1	YA	2503	2MA	CM2-C2-N3	2.77	121.46	117.16
32	XA	527	7MG	C2-N3-C4	2.76	121.52	113.89
32	QA	527	7MG	N7-C8-N9	2.76	107.33	103.38
1	RA	1911	PSU	C6-N1-C2	2.75	119.90	115.36
32	QA	516	PSU	C6-N1-C2	2.74	119.89	115.36
32	QA	966	M2G	C6-N1-C2	2.74	119.44	116.18
1	YA	2251	OMG	C5-C6-N1	-2.72	119.70	123.43
1	RA	2251	OMG	C5-C6-N1	-2.72	119.71	123.43
32	XA	527	7MG	N2-C2-N1	2.71	121.47	117.25
32	XA	1207	2MG	C6-N1-C2	2.70	120.02	115.18
43	QL	92	0TD	CSB-SB-CB	2.67	107.10	101.85
32	XA	966	M2G	C5-C6-N1	-2.67	119.79	123.43
32	QA	1207	2MG	C5-C6-N1	-2.66	119.79	123.43
32	XA	1404	5MC	C5-C6-N1	-2.66	119.33	122.19
32	XA	966	M2G	C6-N1-C2	2.65	119.33	116.18
1	YA	2251	OMG	N2-C2-N1	2.64	121.35	117.25
1	RA	2251	OMG	N2-C2-N1	2.63	121.34	117.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YA	1917	PSU	C6-N1-C2	2.62	119.68	115.36
32	QA	527	7MG	N3-C4-N9	2.61	130.26	126.91
32	QA	527	7MG	C2-N3-C4	2.60	121.08	113.89
32	QA	1400	5MC	C5-C6-N1	-2.60	119.39	122.19
1	RA	2503	2MA	CM2-C2-N3	2.60	121.20	117.16
1	YA	1911	PSU	C6-N1-C2	2.59	119.63	115.36
1	RA	2605	PSU	C5-C1'-C2'	-2.59	110.70	115.32
1	YA	2251	OMG	C6-C5-C4	-2.56	118.35	120.80
1	RA	2605	PSU	C6-N1-C2	2.56	119.58	115.36
32	QA	1404	5MC	CM5-C5-C4	-2.55	119.14	121.72
1	YA	2605	PSU	C5-C1'-C2'	-2.55	110.77	115.32
32	XA	1207	2MG	C5-C6-N1	-2.52	119.98	123.43
1	YA	1942	5MC	C5-C6-N1	-2.50	119.50	122.19
32	QA	527	7MG	C4-C5-N7	2.50	110.79	106.98
32	QA	1404	5MC	C5-C6-N1	-2.48	119.52	122.19
32	XA	966	M2G	C4-C5-N7	-2.46	106.84	109.40
1	RA	1917	PSU	C5-C1'-C2'	-2.44	110.97	115.32
32	XA	516	PSU	C6-N1-C2	2.44	119.38	115.36
1	RA	1942	5MC	C5-C6-N1	-2.44	119.57	122.19
1	RA	2251	OMG	C4-C5-N7	-2.42	106.88	109.40
55	QY	235	MEQ	CB-CG-CD	-2.41	107.66	113.04
1	RA	1962	5MC	C5-C6-N1	-2.40	119.61	122.19
1	RA	2251	OMG	C6-C5-C4	-2.39	118.52	120.80
32	QA	527	7MG	N2-C2-N1	2.39	120.97	117.25
32	QA	1207	2MG	C4-C5-N7	-2.37	106.92	109.40
32	QA	966	M2G	C5-C6-N1	-2.37	120.19	123.43
1	YA	1962	5MC	N4-C4-N3	2.36	120.37	117.03
32	XA	1404	5MC	CM5-C5-C4	-2.35	119.35	121.72
1	YA	1911	PSU	C5-C1'-C2'	-2.34	111.14	115.32
1	YA	1917	PSU	C5-C1'-C2'	-2.31	111.20	115.32
32	XA	527	7MG	C4-C5-N7	2.29	110.47	106.98
32	XA	1207	2MG	C4-C5-N7	-2.28	107.03	109.40
1	YA	1942	5MC	N4-C4-N3	2.26	120.23	117.03
1	YA	2251	OMG	C4-C5-N7	-2.26	107.05	109.40
32	QA	966	M2G	CM2-N2-C2	-2.26	119.14	121.29
1	RA	1920	4OC	C5-C4-N3	-2.24	119.14	121.72
32	QA	1207	2MG	O3'-C3'-C2'	2.21	118.96	111.82
32	XA	1400	5MC	N4-C4-N3	2.21	120.15	117.03
1	YA	1920	4OC	C5-C4-N3	-2.20	119.18	121.72
32	QA	1400	5MC	CM5-C5-C4	-2.19	119.50	121.72
32	XA	967	5MC	CM5-C5-C4	-2.19	119.51	121.72
32	XA	527	7MG	N2-C2-N3	2.18	120.65	117.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	QA	1407	5MC	C5-C6-N1	-2.17	119.85	122.19
32	XA	527	7MG	N3-C4-N9	2.15	129.67	126.91
32	QA	527	7MG	C5-C6-N1	-2.15	118.73	123.14
32	XA	967	5MC	C5-C6-N1	-2.14	119.88	122.19
32	QA	966	M2G	C4-C5-N7	-2.14	107.17	109.40
32	XA	1407	5MC	N4-C4-N3	2.13	120.04	117.03
1	RA	1920	4OC	N4-C4-N3	2.11	119.82	116.49
32	QA	1407	5MC	N4-C4-N3	2.10	120.01	117.03
32	QA	1404	5MC	N4-C4-N3	2.10	120.00	117.03
32	QA	527	7MG	N2-C2-N3	2.10	120.52	117.25
32	QA	516	PSU	O4'-C1'-C2'	2.09	108.04	104.66
32	XA	516	PSU	O4'-C1'-C2'	2.09	108.04	104.66
32	XA	527	7MG	N7-C8-N9	2.08	106.36	103.38
32	XA	967	5MC	N4-C4-N3	2.06	119.95	117.03
1	RA	1942	5MC	N4-C4-N3	2.06	119.94	117.03
32	QA	967	5MC	N4-C4-N3	2.05	119.93	117.03
1	RA	1962	5MC	N4-C4-N3	2.04	119.91	117.03
32	XA	527	7MG	C5-C4-N9	2.01	109.27	106.44
1	YA	1920	4OC	N4-C4-N3	2.01	119.67	116.49

There are no chirality outliers.

All (39) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
32	XA	1400	5MC	O4'-C1'-N1-C6
32	XA	1400	5MC	C2'-C1'-N1-C6
43	QL	92	0TD	CG-CB-SB-CSB
1	RA	1915	5MU	O4'-C4'-C5'-O5'
1	YA	1962	5MC	O4'-C1'-N1-C6
1	YA	1962	5MC	C2'-C1'-N1-C6
55	QY	235	MEQ	O-C-CA-CB
32	QA	1402	4OC	O4'-C4'-C5'-O5'
32	QA	1402	4OC	O4'-C1'-N1-C6
32	QA	1519	MA6	O4'-C4'-C5'-O5'
1	RA	1962	5MC	O4'-C1'-N1-C6
1	RA	1962	5MC	C2'-C1'-N1-C6
32	XA	1519	MA6	O4'-C4'-C5'-O5'
32	QA	527	7MG	C3'-C4'-C5'-O5'
1	YA	1920	4OC	C2'-C1'-N1-C6
32	XA	1402	4OC	O4'-C4'-C5'-O5'
32	XA	1402	4OC	C3'-C4'-C5'-O5'
32	XA	527	7MG	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
43	XL	92	0TD	CG-CB-SB-CSB
1	YA	1915	5MU	C3'-C4'-C5'-O5'
1	YA	1915	5MU	O4'-C4'-C5'-O5'
1	RA	1915	5MU	C3'-C4'-C5'-O5'
32	QA	1402	4OC	C3'-C4'-C5'-O5'
32	QA	1519	MA6	C3'-C4'-C5'-O5'
32	XA	1519	MA6	C3'-C4'-C5'-O5'
32	QA	1400	5MC	O4'-C4'-C5'-O5'
32	QA	1400	5MC	C3'-C4'-C5'-O5'
32	QA	527	7MG	O4'-C4'-C5'-O5'
55	XY	235	MEQ	CA-CB-CG-CD
32	XA	527	7MG	O4'-C4'-C5'-O5'
55	XY	235	MEQ	C-CA-CB-CG
55	QY	235	MEQ	CA-CB-CG-CD
55	XY	235	MEQ	OE1-CD-CG-CB
43	XL	92	0TD	CA-CB-SB-CSB
32	XA	1400	5MC	O4'-C4'-C5'-O5'
55	XY	235	MEQ	NE2-CD-CG-CB
32	XA	1400	5MC	C3'-C4'-C5'-O5'
1	YA	2503	2MA	O4'-C4'-C5'-O5'
1	RA	2503	2MA	O4'-C4'-C5'-O5'

There are no ring outliers.

21 monomers are involved in 33 short contacts:

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

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	RA	1917	PSU	1	0
1	YA	1942	5MC	1	0
32	XA	1402	4OC	3	0
43	XL	92	0TD	1	0
32	XA	1518	MA6	2	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	-	-		
58	SF4	XD	301	-	0,12,12	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	-	-	0/6/5/5
58	SF4	XD	301	-	-	-	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

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

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

6.3 Carbohydrates ⓘ

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

6.4 Ligands ⓘ

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

6.5 Other polymers ⓘ

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