



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 18, 2014 – 07:13 AM EDT

PDB ID : 4LNT
Title : Crystal Structure of tRNA Proline (CGG) Bound to Codon CCC-U on the Ribosome
Authors : Maehigashi, T.; Dunkle, J.A.; Dunham, C.M.
Deposited on : 2013-07-12
Resolution : 2.94 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

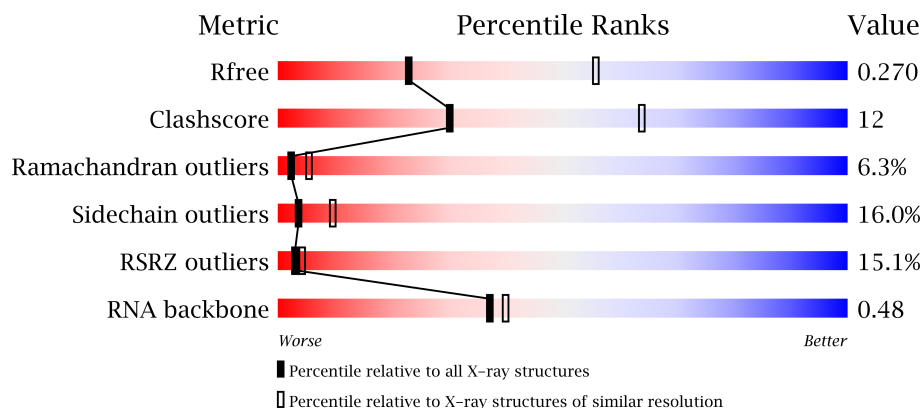
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable23489
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable23489

1 Overall quality at a glance

The reported resolution of this entry is 2.94 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))
R_{free}	66092	1424 (2.98-2.90)
Clashscore	79885	1761 (2.98-2.90)
Ramachandran outliers	78287	1708 (2.98-2.90)
Sidechain outliers	78261	1710 (2.98-2.90)
RSRZ outliers	66119	1425 (2.98-2.90)
RNA backbone	1838	1002 (3.44-2.44)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	QA	1522	
1	XA	1522	
2	QB	256	
2	XB	256	
3	QC	239	
3	XC	239	
4	QD	209	
4	XD	209	
5	QE	162	
5	XE	162	
6	QF	101	

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Mol	Chain	Length	Quality of chain
6	XF	101	
7	QG	156	
7	XG	156	
8	QH	138	
8	XH	138	
9	QI	128	
9	XI	128	
10	QJ	105	
10	XJ	105	
11	QK	129	
11	XK	129	
12	QL	132	
12	XL	132	
13	QM	126	
13	XM	126	
14	QN	61	
14	XN	61	
15	QO	89	
15	XO	89	
16	QP	88	
16	XP	88	
17	QQ	105	
17	XQ	105	
18	QR	88	
18	XR	88	
19	QS	93	
19	XS	93	
20	QT	106	
20	XT	106	
21	QU	27	
21	XU	27	
22	QV	77	
22	XV	77	
23	QY	17	
23	XY	17	
24	QX	25	
24	XX	25	
25	RA	2916	
25	YA	2916	
26	RB	122	
26	YB	122	
27	RD	276	

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Mol	Chain	Length	Quality of chain
27	YD	276	
28	RE	206	
28	YE	206	
29	RF	210	
29	YF	210	
30	RG	182	
30	YG	182	
31	RH	180	
31	YH	180	
32	RI	148	
32	YI	148	
33	RN	140	
33	YN	140	
34	RO	122	
34	YO	122	
35	RP	150	
35	YP	150	
36	RQ	141	
36	YQ	141	
37	RR	118	
37	YR	118	
38	RS	112	
38	YS	112	
39	RT	146	
39	YT	146	
40	RU	118	
40	YU	118	
41	RV	101	
41	YV	101	
42	RW	113	
42	YW	113	
43	RX	96	
43	YX	96	
44	RY	110	
44	YY	110	
45	RZ	206	
45	YZ	206	
46	R0	85	
46	Y0	85	
47	R1	98	
47	Y1	98	
48	R2	72	

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Mol	Chain	Length	Quality of chain
48	Y2	72	
49	R3	60	
49	Y3	60	
50	R4	71	
50	Y4	71	
51	R5	60	
51	Y5	60	
52	R6	54	
52	Y6	54	
53	R7	49	
53	Y7	49	
54	R8	65	
54	Y8	65	
55	R9	37	
55	Y9	37	
56	Z6	3	
56	Z8	3	

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 291993 atoms, of which 0 are hydrogen and 0 are deuterium.

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 16S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	QA	1500	Total	C	N	O	P	0	0	0
			32247	14353	5981	10414	1499			
1	XA	1500	Total	C	N	O	P	0	0	0
			32249	14354	5984	10412	1499			

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	QB	237	Total	C	N	O	S	0	0	0
			1924	1228	344	347	5			
2	XB	237	Total	C	N	O	S	0	0	0
			1924	1228	344	347	5			

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	QC	205	Total	C	N	O	S	0	0	0
			1605	1011	313	280	1			
3	XC	205	Total	C	N	O	S	0	0	0
			1605	1011	313	280	1			

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	QD	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			
4	XD	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	QE	151	Total	C	N	O	S	0	0	0
			1155	729	218	204	4			
5	XE	151	Total	C	N	O	S	0	0	0
			1155	729	218	204	4			

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	QF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			
6	XF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	QG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			
7	XG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	QH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			
8	XH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	QI	127	Total	C	N	O		0	0	0
			1010	639	197	174				
9	XI	127	Total	C	N	O		0	0	0
			1010	639	197	174				

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	QJ	99	Total	C	N	O	S	0	0	0
			801	504	157	139	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	XJ	99	Total	C	N	O	S	0	0	0
			801	504	157	139	1			

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	QK	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			
11	XK	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	QL	125	Total	C	N	O	S	0	0	0
			975	614	196	164	1			
12	XL	125	Total	C	N	O	S	0	0	0
			975	614	196	164	1			

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	QM	121	Total	C	N	O	S	0	0	0
			964	597	199	166	2			
13	XM	121	Total	C	N	O	S	0	0	0
			964	597	199	166	2			

- Molecule 14 is a protein called 30S ribosomal protein S14.

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

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	QO	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			
15	XO	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	QP	84	Total	C	N	O	S	0	0	0
			705	446	140	118	1			
16	XP	84	Total	C	N	O	S	0	0	0
			705	446	140	118	1			

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	QQ	100	Total	C	N	O	S	0	0	0
			834	534	155	143	2			
17	XQ	100	Total	C	N	O	S	0	0	0
			834	534	155	143	2			

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	QR	70	Total	C	N	O	0	0	0
			574	367	112	95			
18	XR	70	Total	C	N	O	0	0	0
			574	367	112	95			

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	QS	84	Total	C	N	O	S	0	0	0
			674	430	126	116	2			
19	XS	84	Total	C	N	O	S	0	0	0
			674	430	126	116	2			

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	QT	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			
20	XT	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	QU	25	Total	C	N	O	0	0	0
			217	134	52	31			
21	XU	25	Total	C	N	O	0	0	0
			217	134	52	31			

- Molecule 22 is a RNA chain called P-site tRNA fMet.

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

- Molecule 23 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	QY	15	Total	C	N	O	P	0	0	0
			323	144	58	106	15			
23	XY	15	Total	C	N	O	P	0	0	0
			323	144	58	106	15			

- Molecule 24 is a RNA chain called A-site ASL SufA6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	QX	8	Total	C	N	O	P	0	0	0
			167	75	28	56	8			
24	XX	8	Total	C	N	O	P	0	0	0
			167	75	28	56	8			

- Molecule 25 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	RA	2882	Total	C	N	O	P	0	0	0
			62071	27627	11611	19952	2881			
25	YA	2883	Total	C	N	O	P	0	0	0
			62091	27636	11613	19960	2882			

- Molecule 26 is a RNA chain called 5S rRNA.

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

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

- Molecule 27 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	RD	272	Total	C	N	O	S	0	0	0
			2115	1335	420	357	3			
27	YD	272	Total	C	N	O	S	0	0	0
			2115	1335	420	357	3			

- Molecule 28 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	RE	205	Total	C	N	O	S	0	0	0
			1568	991	300	271	6			
28	YE	205	Total	C	N	O	S	0	0	0
			1568	991	300	271	6			

- Molecule 29 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	RF	202	Total	C	N	O	S	0	0	0
			1585	1011	297	275	2			
29	YF	202	Total	C	N	O	S	0	0	0
			1585	1011	297	275	2			

- Molecule 30 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	RG	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			
30	YG	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			

- Molecule 31 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	RH	170	Total	C	N	O	S	0	0	0
			1307	829	245	232	1			
31	YH	170	Total	C	N	O	S	0	0	0
			1307	829	245	232	1			

- Molecule 32 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	RI	146	Total	C	N	O	S	0	0	0
			1136	726	201	208	1			
32	YI	146	Total	C	N	O	S	0	0	0
			1136	726	201	208	1			

- Molecule 33 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	RN	138	Total	C	N	O	S	0	0	0
			1104	712	206	182	4			
33	YN	138	Total	C	N	O	S	0	0	0
			1104	712	206	182	4			

- Molecule 34 is a protein called 50S ribosomal protein L14.

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

- Molecule 35 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	RP	150	Total	C	N	O	S	0	0	0
			1145	712	232	198	3			
35	YP	150	Total	C	N	O	S	0	0	0
			1145	712	232	198	3			

- Molecule 36 is a protein called 50S ribosomal protein L16.

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

- Molecule 37 is a protein called 50S ribosomal protein L17.

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

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	RS	111	Total	C	N	O	S	0	0	0
			882	556	176	150				
38	YS	111	Total	C	N	O	S	0	0	0
			882	556	176	150				

- Molecule 39 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	RT	137	Total	C	N	O	S	0	0	0
			1141	710	234	196	1			
39	YT	137	Total	C	N	O	S	0	0	0
			1141	710	234	196	1			

- Molecule 40 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	RU	117	Total	C	N	O	S	0	0	0
			964	610	202	151	1			
40	YU	117	Total	C	N	O	S	0	0	0
			964	610	202	151	1			

- Molecule 41 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	RV	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			
41	YV	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			

- Molecule 42 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	RW	113	Total	C	N	O	S	0	0	0
			900	566	177	155	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	YW	113	Total	C	N	O	S	0	0	0
			900	566	177	155	2			

- Molecule 43 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	RX	92	Total	C	N	O		0	0	0
			725	471	131	123				
43	YX	92	Total	C	N	O		0	0	0
			725	471	131	123				

- Molecule 44 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	RY	102	Total	C	N	O	S	0	0	0
			785	505	150	125	5			
44	YY	102	Total	C	N	O	S	0	0	0
			785	505	150	125	5			

- Molecule 45 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	RZ	183	Total	C	N	O	S	0	0	0
			1461	933	260	265	3			
45	YZ	183	Total	C	N	O	S	0	0	0
			1461	933	260	265	3			

- Molecule 46 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	R0	82	Total	C	N	O	S	0	0	0
			648	401	138	108	1			
46	Y0	82	Total	C	N	O	S	0	0	0
			648	401	138	108	1			

- Molecule 47 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	R1	97	Total	C	N	O	S	0	0	0
			763	481	150	131	1			
47	Y1	97	Total	C	N	O	S	0	0	0
			763	481	150	131	1			

- Molecule 48 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	R2	69	Total	C	N	O	S	0	0	0
			581	358	118	104	1			
48	Y2	69	Total	C	N	O	S	0	0	0
			581	358	118	104	1			

- Molecule 49 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
49	R3	59	Total	C	N	O	0	0	0
			469	298	90	81			
49	Y3	59	Total	C	N	O	0	0	0
			469	298	90	81			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	R4	71	Total	C	N	O	S	0	0	0
			581	364	108	104	5			
50	Y4	71	Total	C	N	O	S	0	0	0
			581	364	108	104	5			

- Molecule 51 is a protein called 50S ribosomal protein L32.

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

- Molecule 52 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	R6	49	Total	C	N	O	S	0	0	0
			424	264	87	69	4			
52	Y6	49	Total	C	N	O	S	0	0	0
			424	264	87	69	4			

- Molecule 53 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	R7	49	Total	C	N	O	S	0	0	0
			430	263	108	57	2			
53	Y7	49	Total	C	N	O	S	0	0	0
			430	263	108	57	2			

- Molecule 54 is a protein called 50S ribosomal protein L35.

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

- Molecule 55 is a protein called 50S ribosomal protein L36.

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

- Molecule 56 is a RNA chain called tRNA acceptor end mimic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	Z6	3	Total	C	N	O	P	0	0	0
			74	40	13	19	2			
56	Z8	3	Total	C	N	O	P	0	0	0
			74	40	13	19	2			

- Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	QA	65	Total	Mg	0	0
			65	65		
57	RP	2	Total	Mg	0	0
			2	2		
57	QX	1	Total	Mg	0	0
			1	1		
57	YA	268	Total	Mg	0	0
			268	268		
57	QM	1	Total	Mg	0	0
			1	1		

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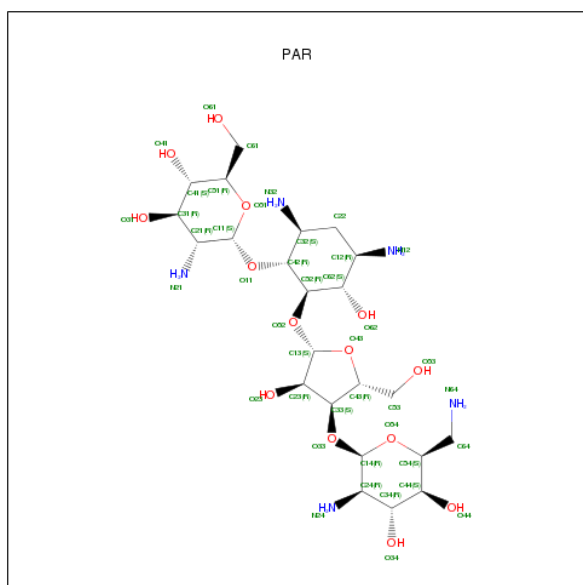
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	XX	1	Total 1	Mg 1	0	0
57	QV	1	Total 1	Mg 1	0	0
57	XA	72	Total 72	Mg 72	0	0
57	R0	1	Total 1	Mg 1	0	0
57	RU	1	Total 1	Mg 1	0	0
57	QH	1	Total 1	Mg 1	0	0
57	YQ	1	Total 1	Mg 1	0	0
57	R8	1	Total 1	Mg 1	0	0
57	YX	1	Total 1	Mg 1	0	0
57	RR	1	Total 1	Mg 1	0	0
57	RD	1	Total 1	Mg 1	0	0
57	QF	1	Total 1	Mg 1	0	0
57	R5	1	Total 1	Mg 1	0	0
57	RA	242	Total 242	Mg 242	0	0
57	YP	2	Total 2	Mg 2	0	0
57	Y5	1	Total 1	Mg 1	0	0
57	RE	2	Total 2	Mg 2	0	0
57	YB	3	Total 3	Mg 3	0	0
57	XV	1	Total 1	Mg 1	0	0
57	RB	2	Total 2	Mg 2	0	0
57	RF	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	XM	1	Total	Mg	0	0
			1	1		
57	YE	1	Total	Mg	0	0
			1	1		

- Molecule 58 is PAROMOMYCIN (three-letter code: PAR) (formula: $C_{23}H_{45}N_5O_{14}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
58	QA	1	Total	C	N	O	0	0
			42	23	5	14		
58	XA	1	Total	C	N	O	0	0
			42	23	5	14		

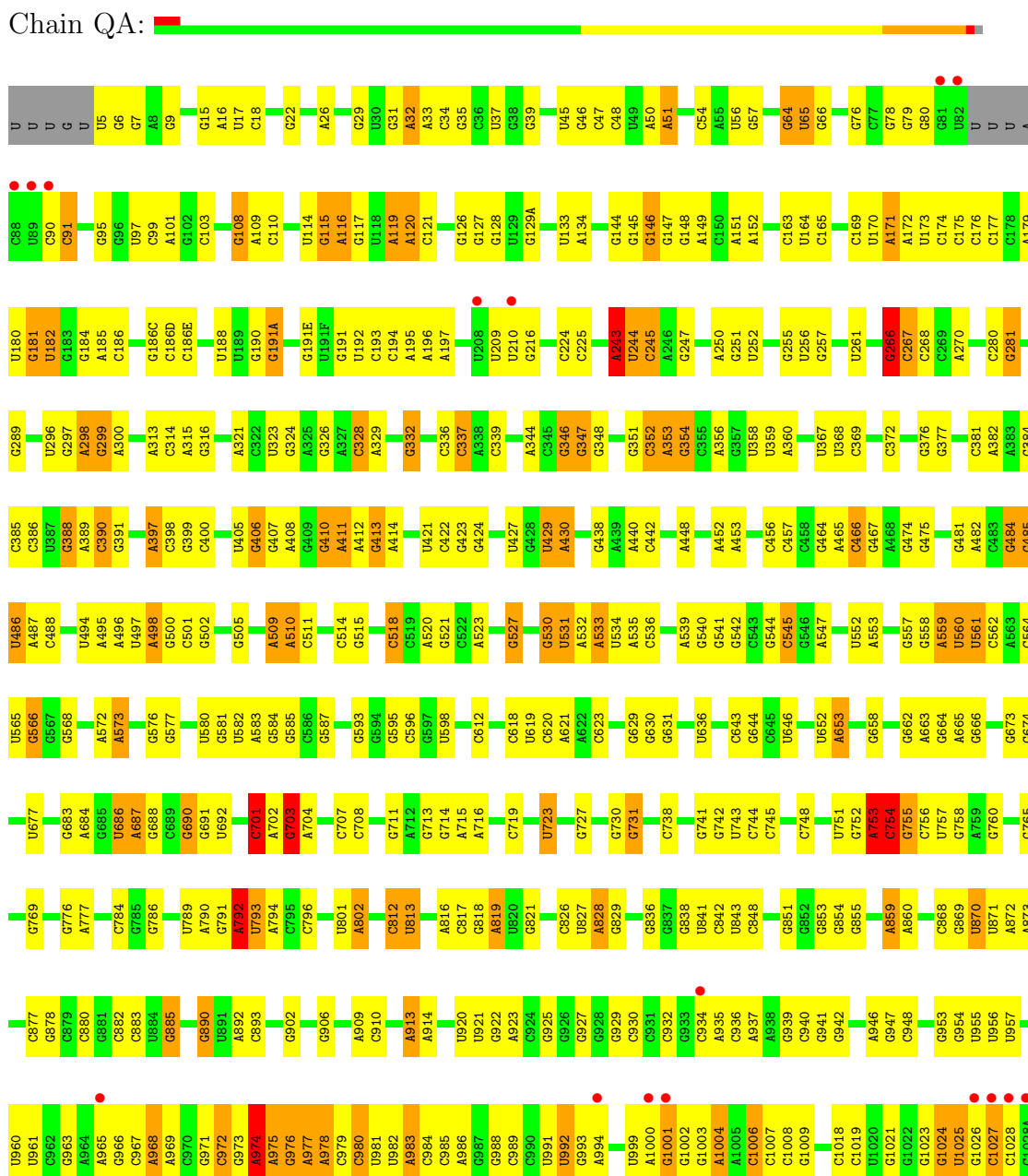
- Molecule 59 is ZINC ION (three-letter code: ZN) (formula: Zn).

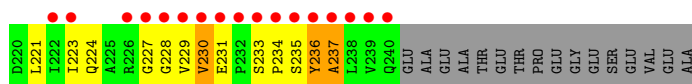
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	XD	1	Total	Zn	0	0
			1	1		
59	QD	1	Total	Zn	0	0
			1	1		
59	QN	1	Total	Zn	0	0
			1	1		
59	XN	1	Total	Zn	0	0
			1	1		

3 Residue-property plots

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

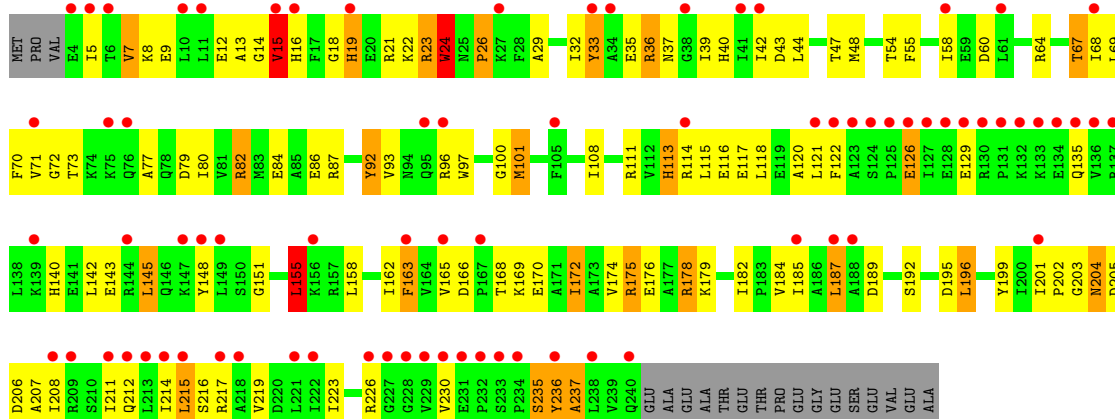
• Molecule 1: 16S rRNA





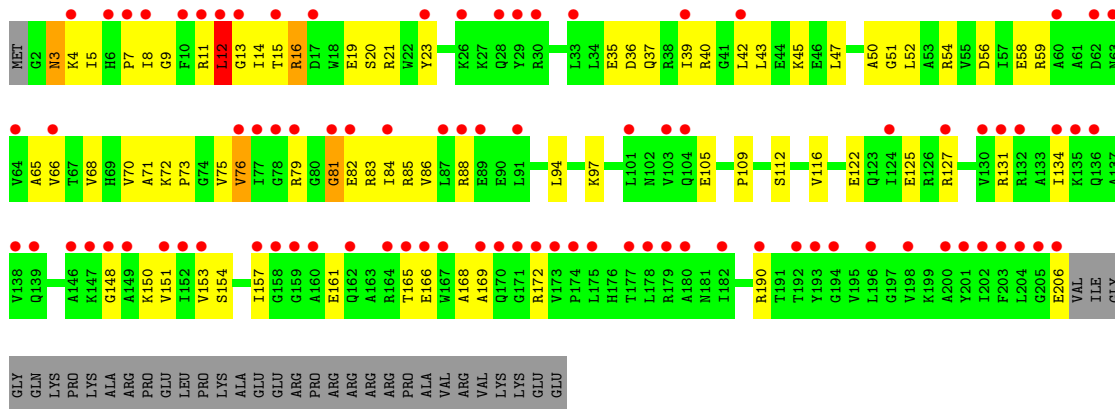
• Molecule 2: 30S ribosomal protein S2

Chain XB:



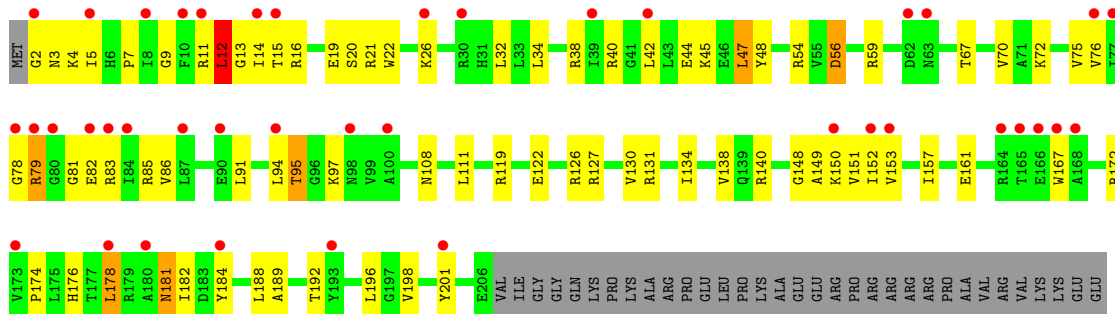
• Molecule 3: 30S ribosomal protein S3

Chain QC:



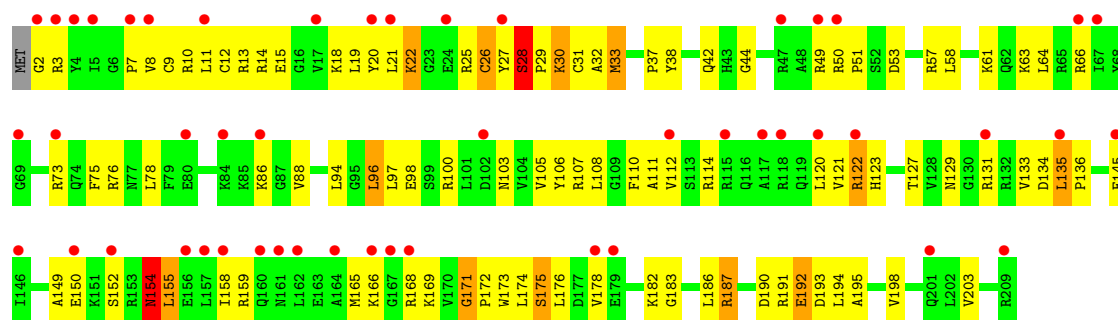
• Molecule 3: 30S ribosomal protein S3

Chain XC:



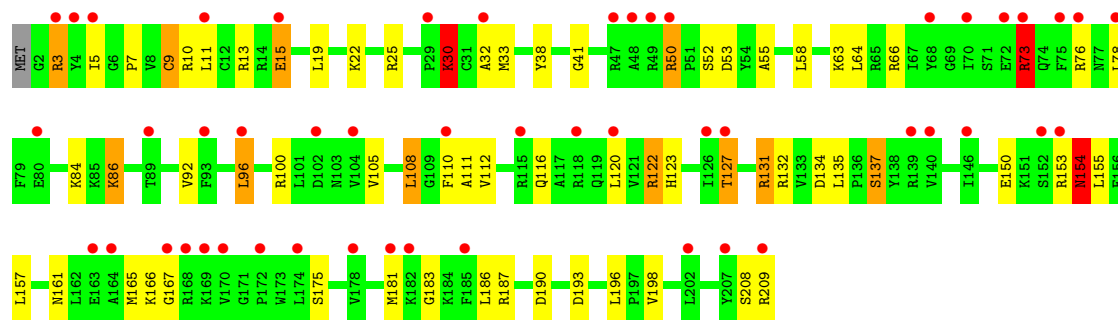
• Molecule 4: 30S ribosomal protein S4

Chain QD:



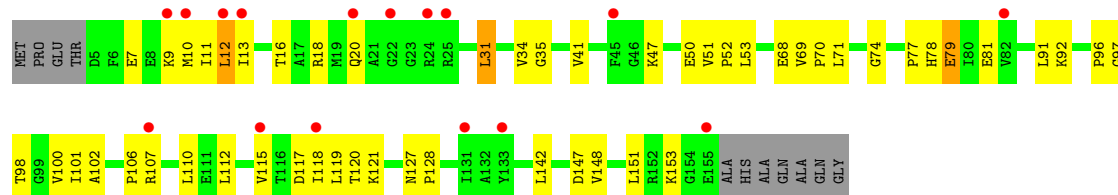
- Molecule 4: 30S ribosomal protein S4

Chain XD:



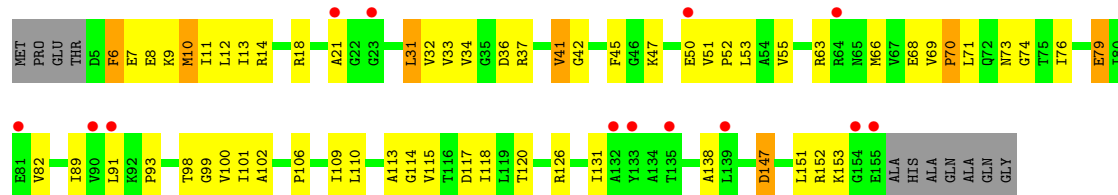
- Molecule 5: 30S ribosomal protein S5

Chain QE:



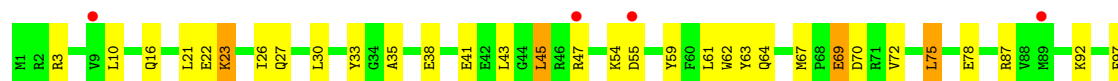
- Molecule 5: 30S ribosomal protein S5

Chain XE:



- Molecule 6: 30S ribosomal protein S6

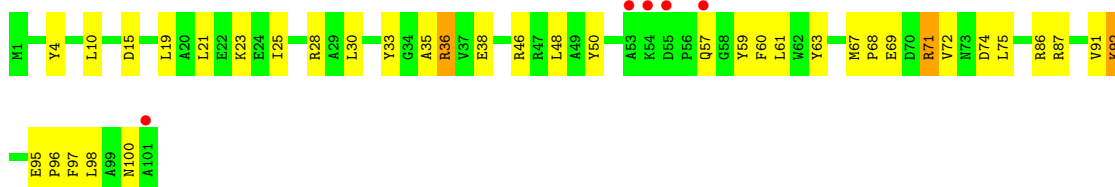
Chain QF:





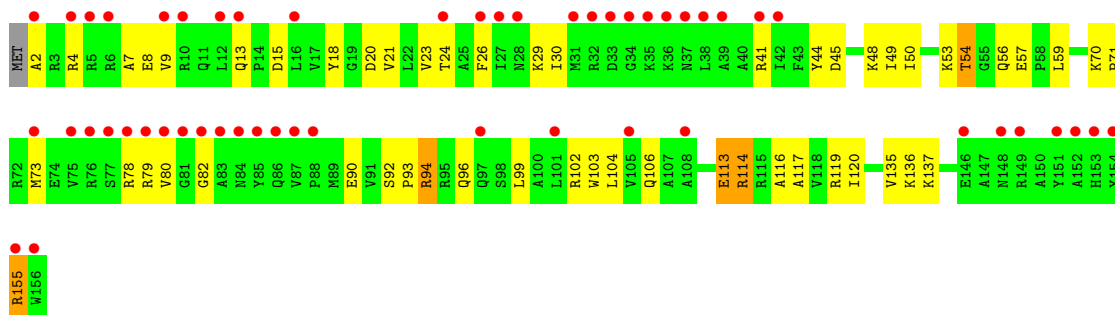
- Molecule 6: 30S ribosomal protein S6

Chain XF:



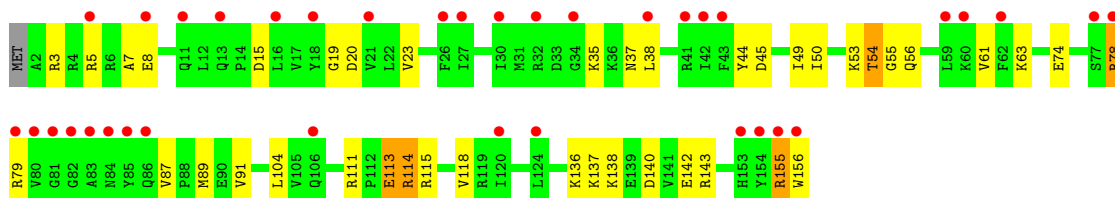
- Molecule 7: 30S ribosomal protein S7

Chain QG:



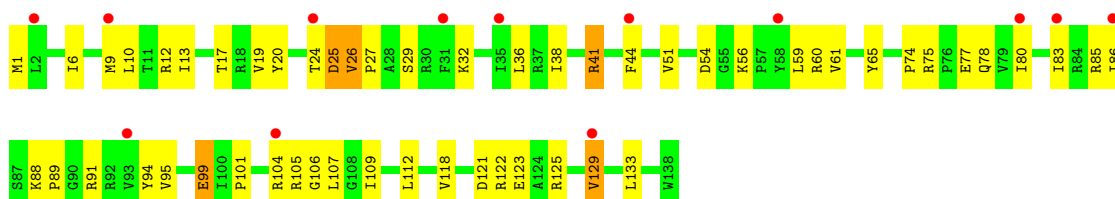
- Molecule 7: 30S ribosomal protein S7

Chain XG:



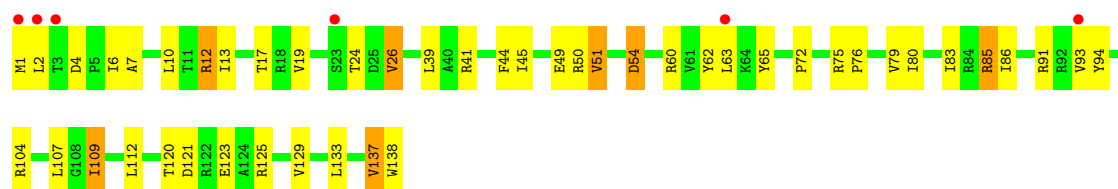
- Molecule 8: 30S ribosomal protein S8

Chain QH:



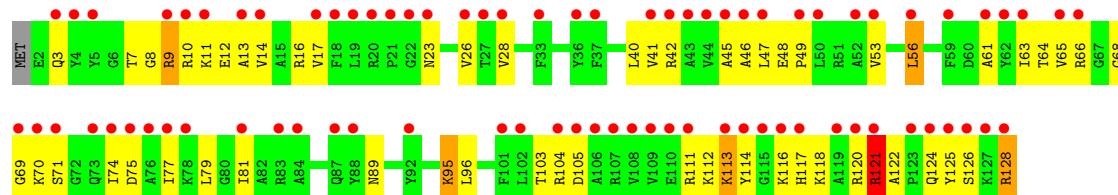
- Molecule 8: 30S ribosomal protein S8

Chain XH:



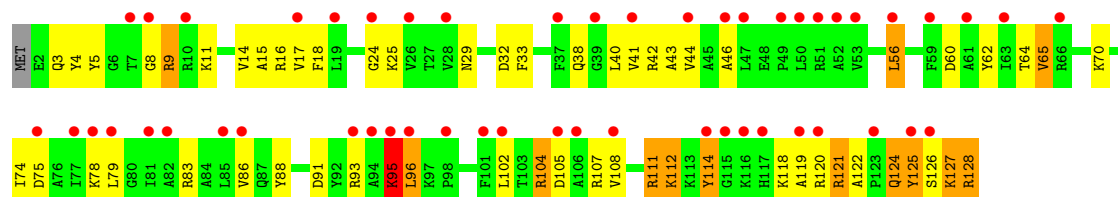
- Molecule 9: 30S ribosomal protein S9

Chain QI:



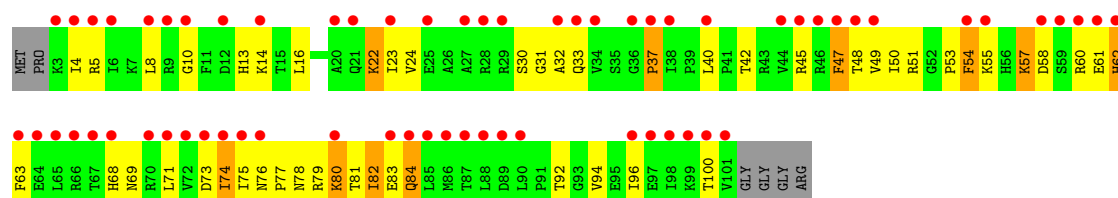
- Molecule 9: 30S ribosomal protein S9

Chain XI:



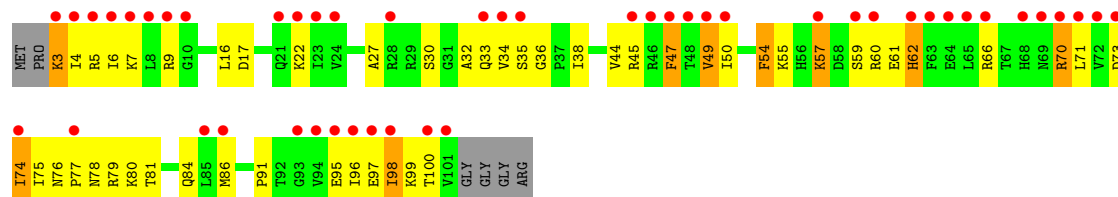
- Molecule 10: 30S ribosomal protein S10

Chain QJ:



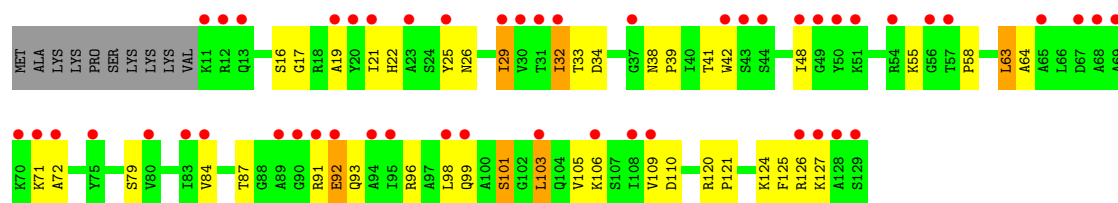
- Molecule 10: 30S ribosomal protein S10

Chain XJ:



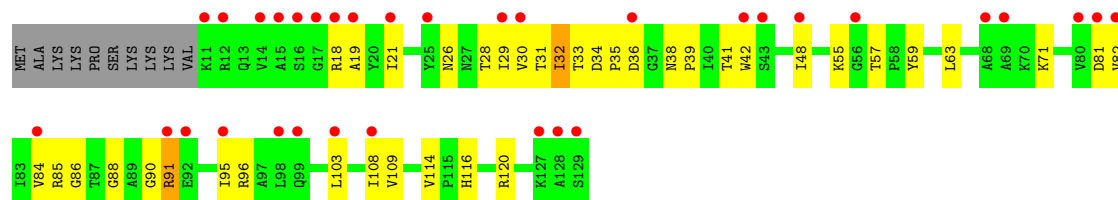
- Molecule 11: 30S ribosomal protein S11

Chain QK:



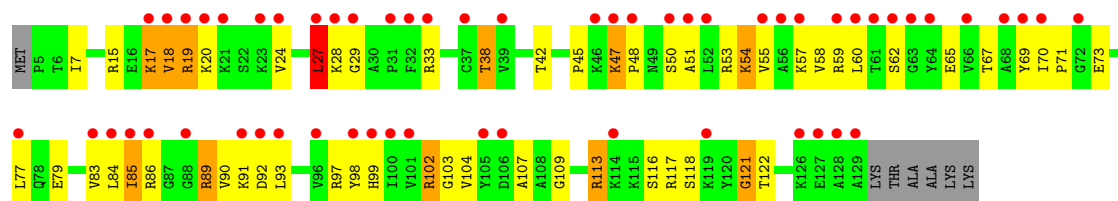
- Molecule 11: 30S ribosomal protein S11

Chain XK:



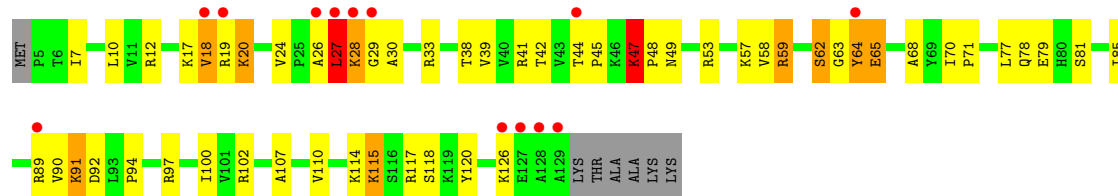
- Molecule 12: 30S ribosomal protein S12

Chain QL:



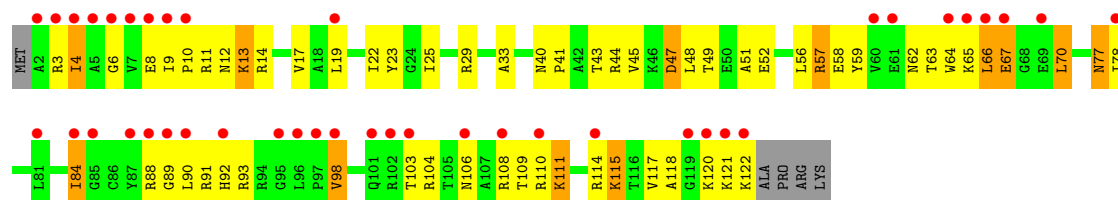
- Molecule 12: 30S ribosomal protein S12

Chain XL:



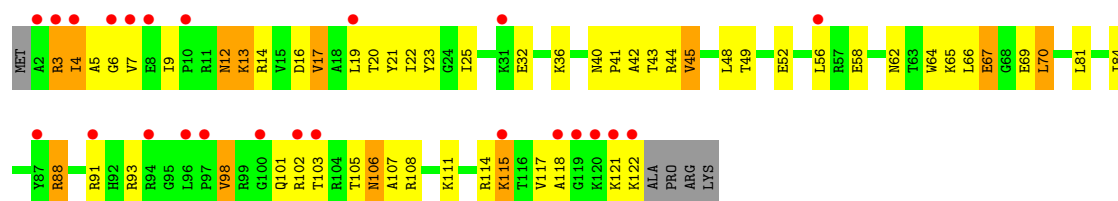
- Molecule 13: 30S ribosomal protein S13

Chain QM:



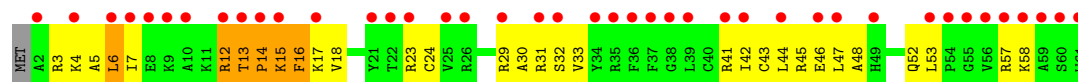
- Molecule 13: 30S ribosomal protein S13

Chain XM:



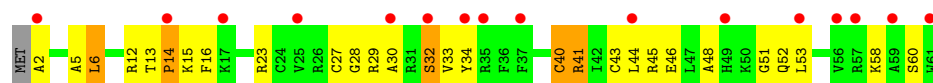
- Molecule 14: 30S ribosomal protein S14

Chain QN:



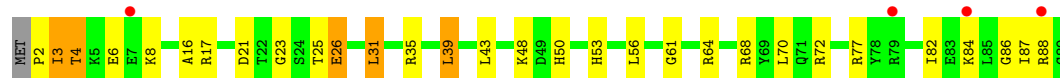
- Molecule 14: 30S ribosomal protein S14

Chain XN:



- Molecule 15: 30S ribosomal protein S15

Chain QO:



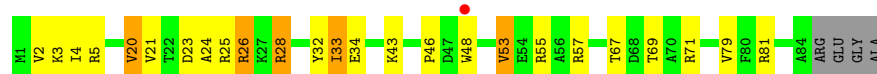
- Molecule 15: 30S ribosomal protein S15

Chain XO:



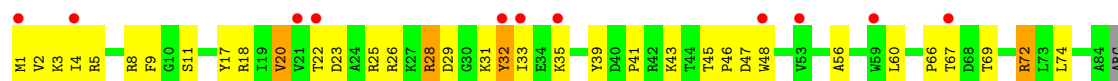
- Molecule 16: 30S ribosomal protein S16

Chain QP:



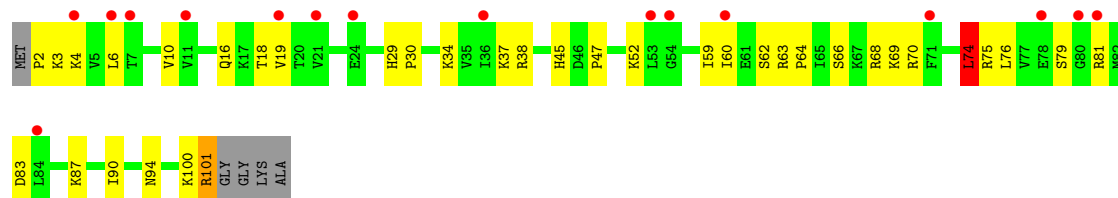
- Molecule 16: 30S ribosomal protein S16

Chain XP:



- Molecule 17: 30S ribosomal protein S17

Chain QQ: 



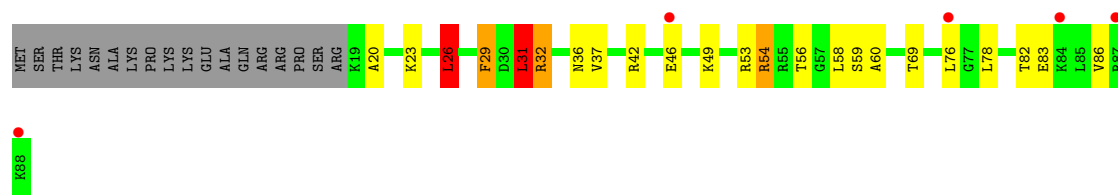
- Molecule 17: 30S ribosomal protein S17

Chain XQ: 



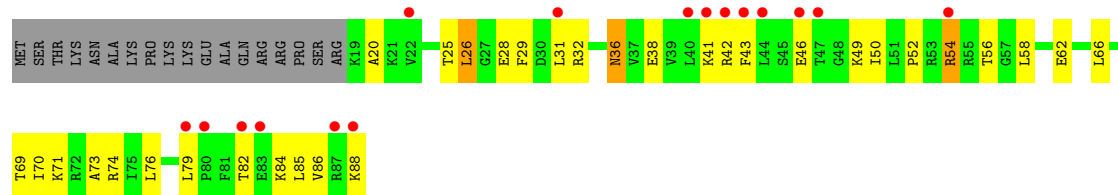
- Molecule 18: 30S ribosomal protein S18

Chain QR: 



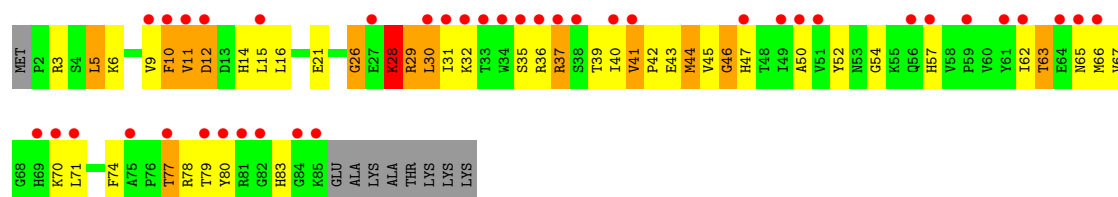
- Molecule 18: 30S ribosomal protein S18

Chain XR: 



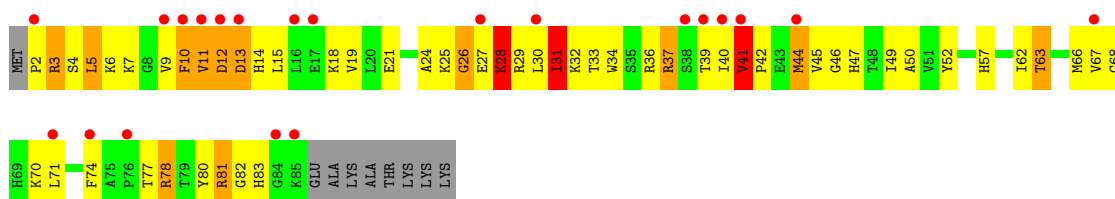
- Molecule 19: 30S ribosomal protein S19

Chain QS: 



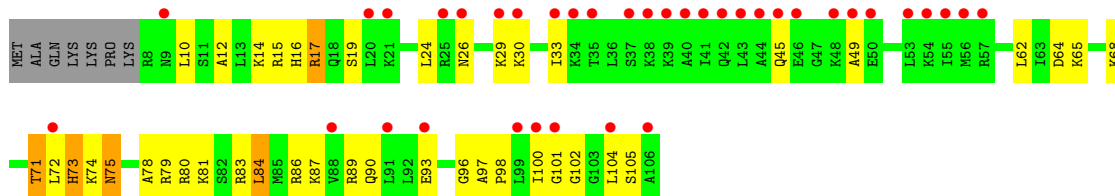
- Molecule 19: 30S ribosomal protein S19

Chain XS: 



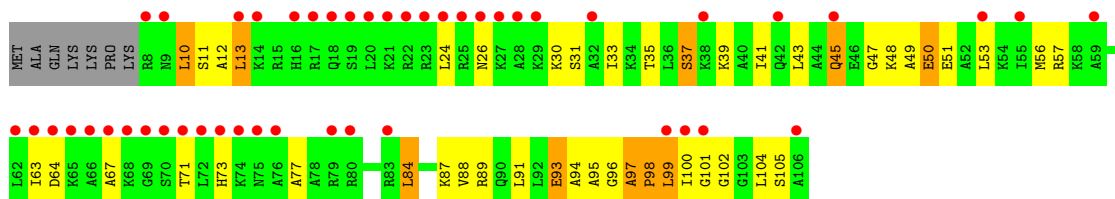
- Molecule 20: 30S ribosomal protein S20

Chain QT:



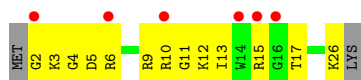
- Molecule 20: 30S ribosomal protein S20

Chain XT:



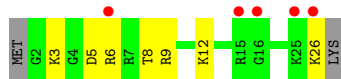
- Molecule 21: 30S ribosomal protein S21

Chain QU:



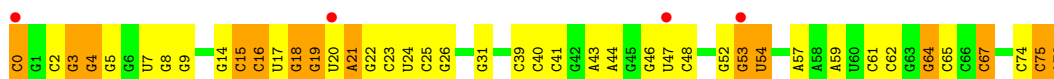
- Molecule 21: 30S ribosomal protein S21

Chain XU:



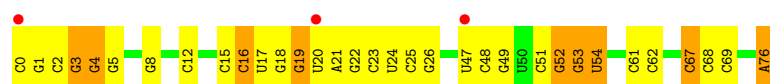
- Molecule 22: P-site tRNA fMet

Chain QV:



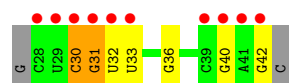
- Molecule 22: P-site tRNA fMet

Chain XV:



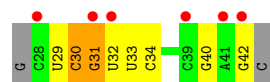
- Molecule 23: messenger RNA

Chain QY:



- Molecule 23: messenger RNA

Chain XY:



- Molecule 24: A-site ASL SufA6

Chain QX:



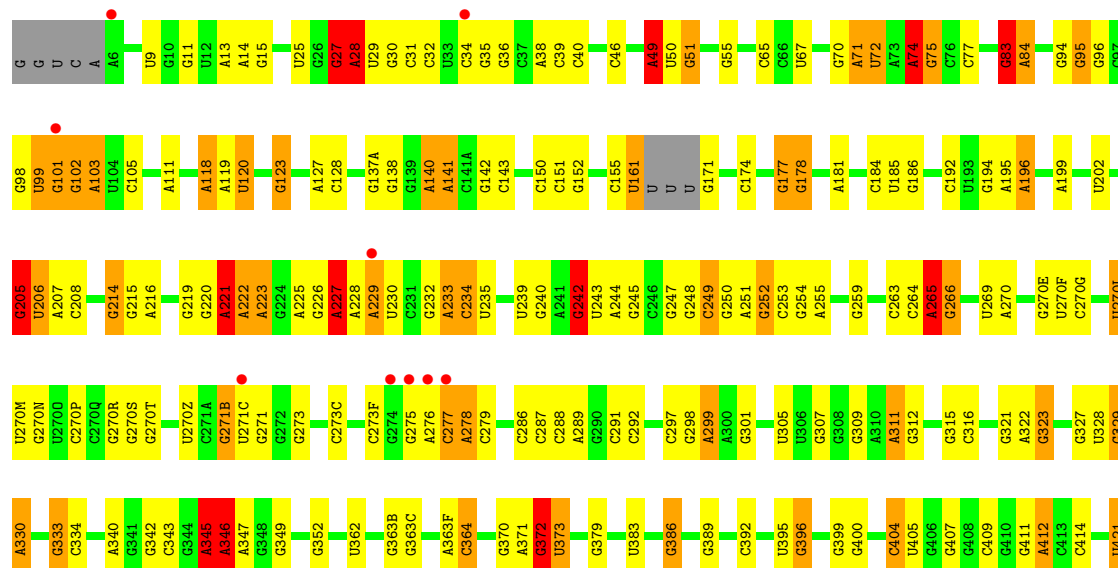
- Molecule 24: A-site ASL SufA6

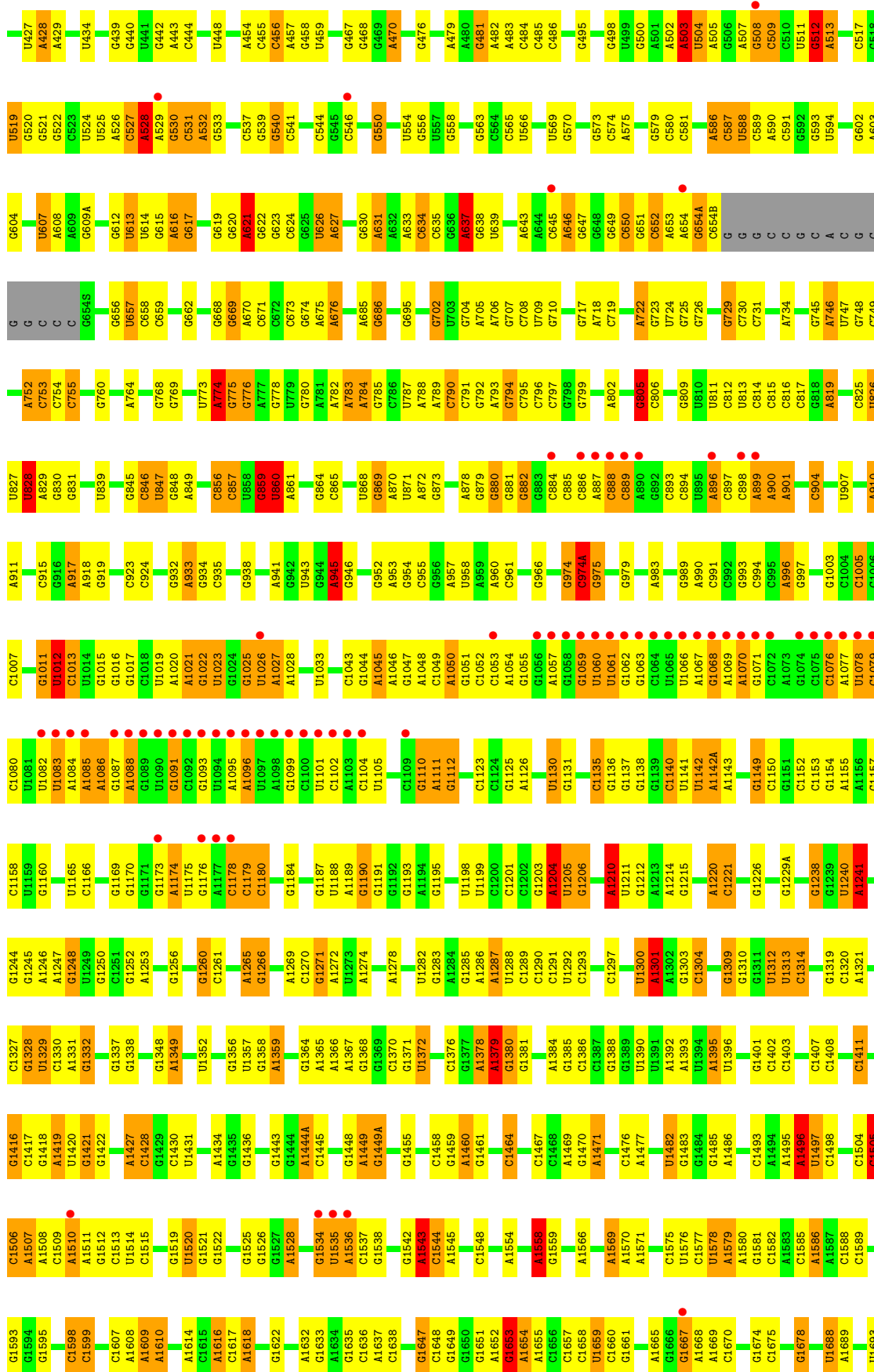
Chain XX:



- Molecule 25: 23S rRNA

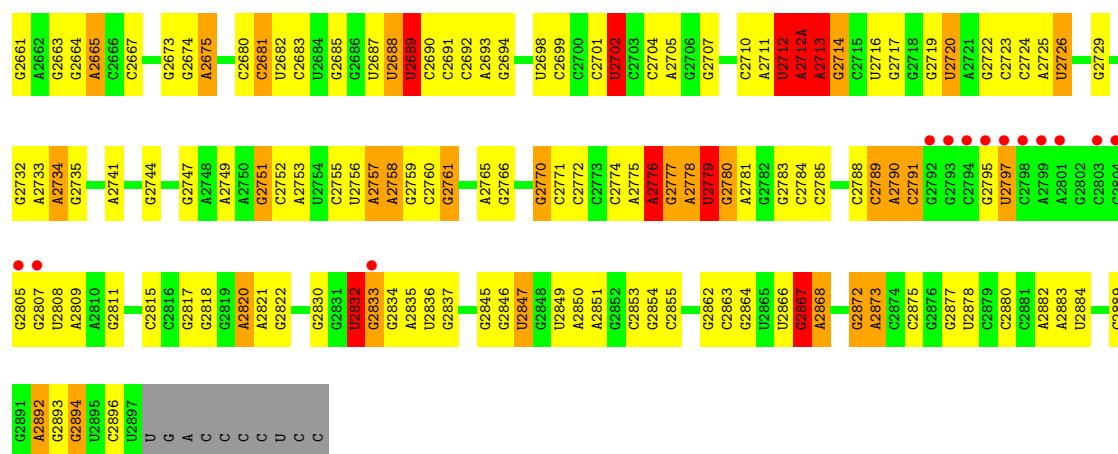
Chain RA:





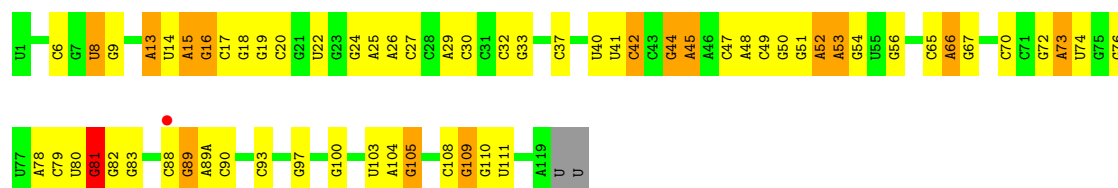


WORLDWIDE
PDB
PROTEIN DATA BANK



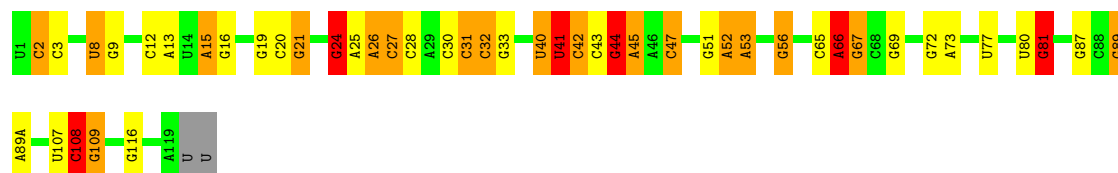
- Molecule 26: 5S rRNA

Chain RB:



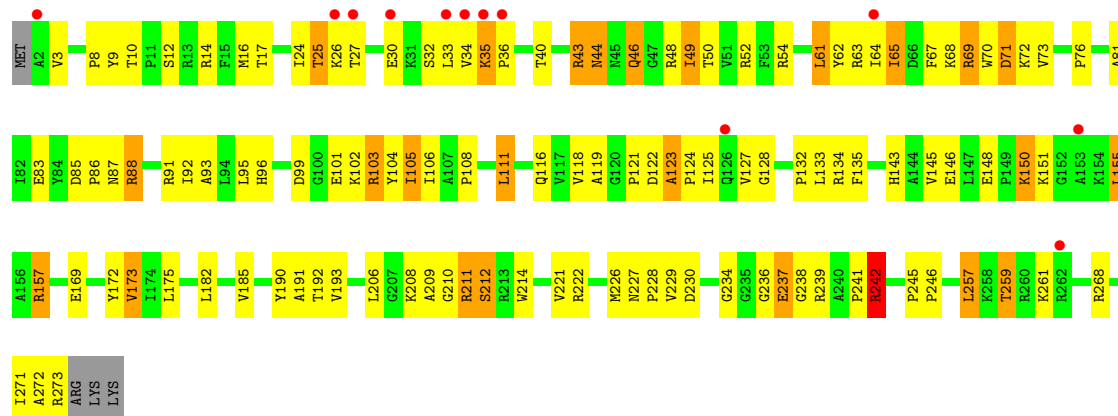
- Molecule 26: 5S rRNA

Chain YB:



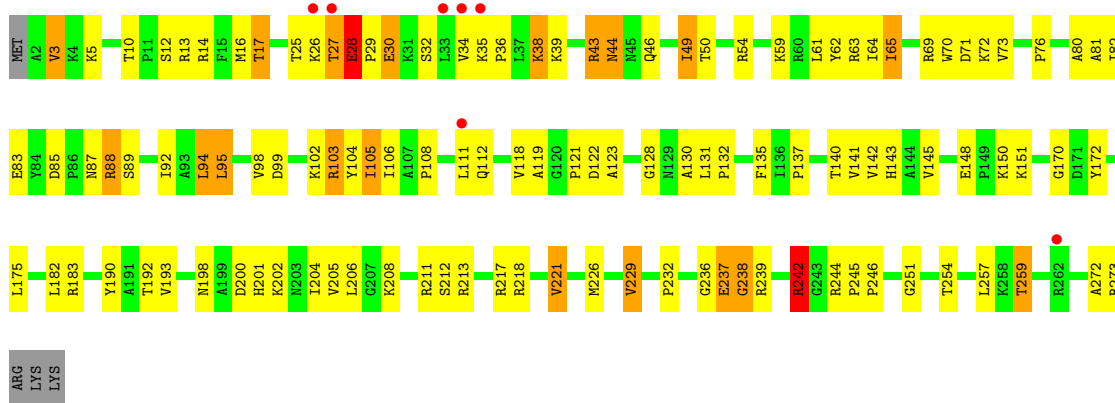
- Molecule 27: 50S ribosomal protein L2

Chain RD:



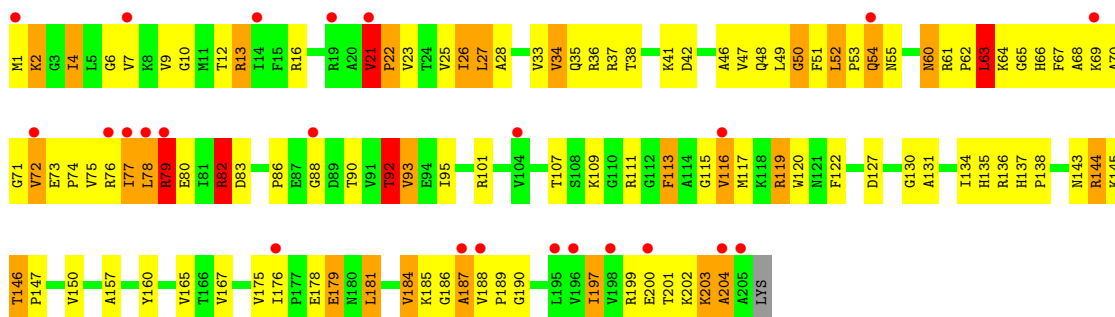
- Molecule 27: 50S ribosomal protein L2

Chain YD:



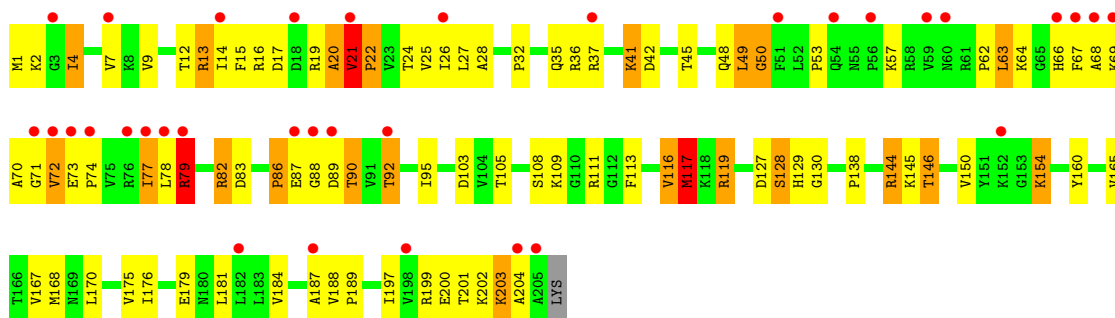
- Molecule 28: 50S ribosomal protein L3

Chain RE:



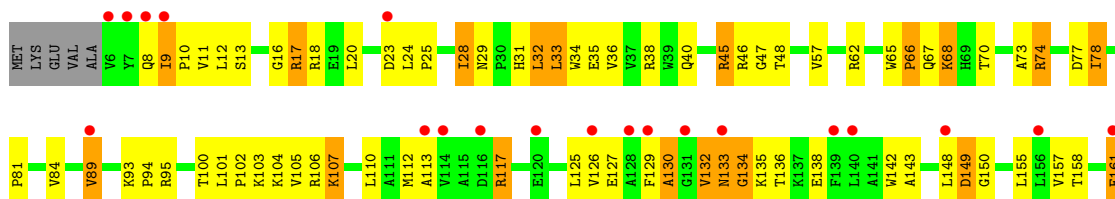
- Molecule 28: 50S ribosomal protein L3

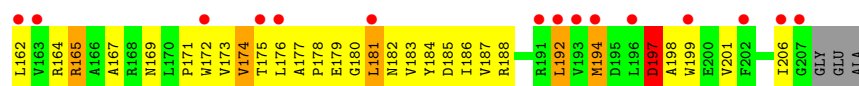
Chain YE:



- Molecule 29: 50S ribosomal protein L4

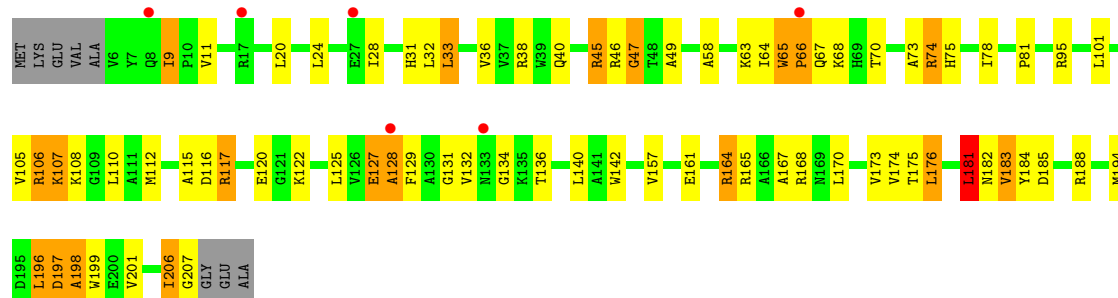
Chain RF:





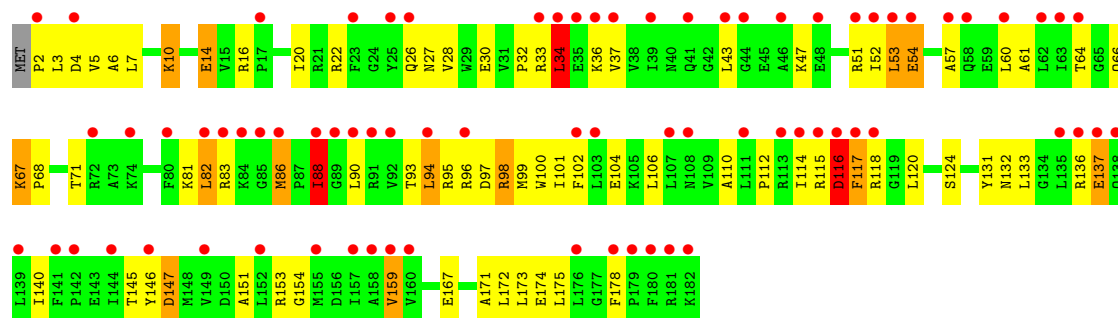
• Molecule 29: 50S ribosomal protein L4

Chain YF:



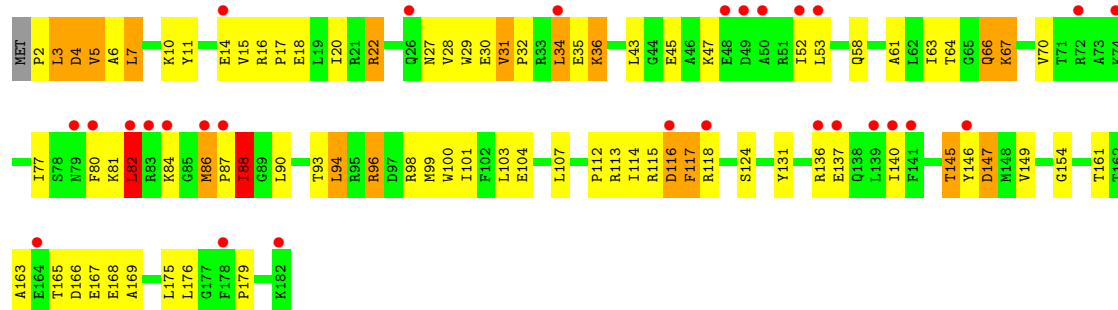
• Molecule 30: 50S ribosomal protein L5

Chain RG:



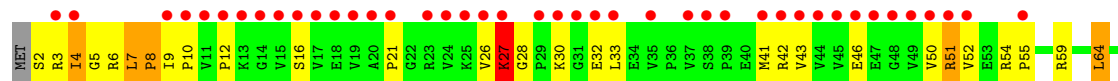
• Molecule 30: 50S ribosomal protein L5

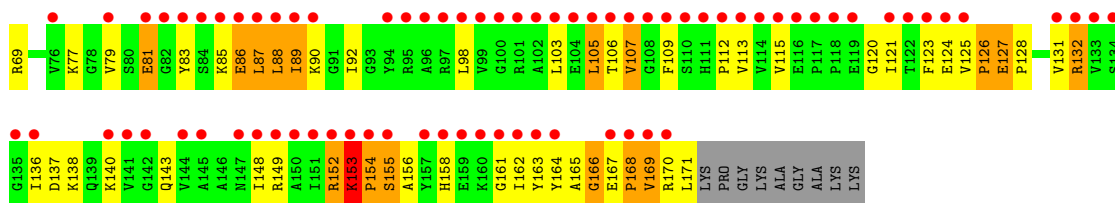
Chain YG:



• Molecule 31: 50S ribosomal protein L6

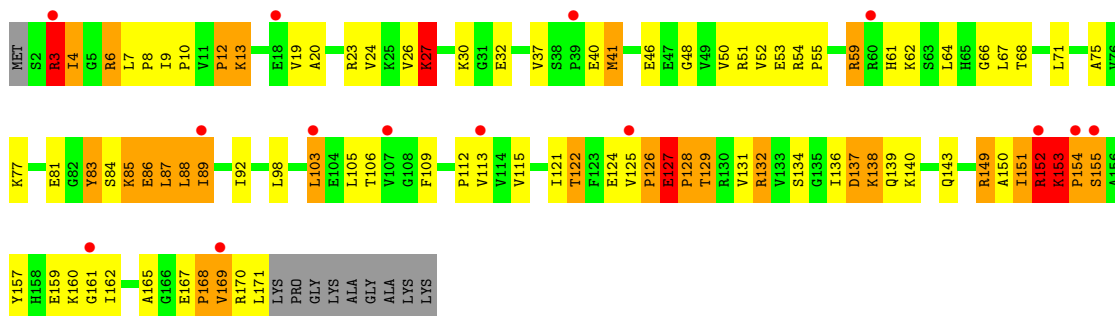
Chain RH:





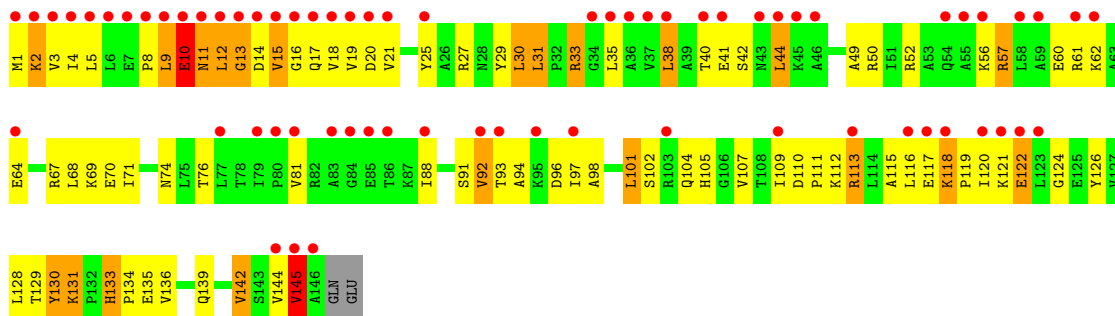
• Molecule 31: 50S ribosomal protein L6

Chain YH:



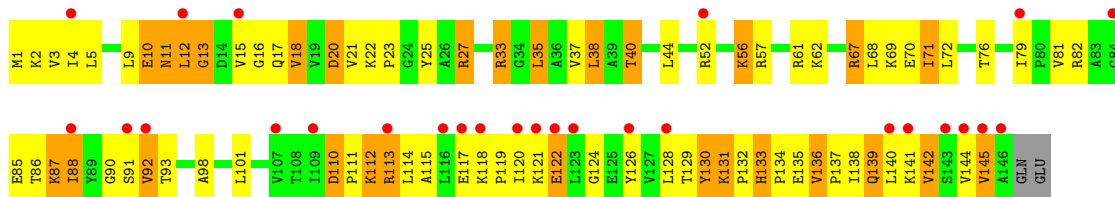
• Molecule 32: 50S ribosomal protein L9

Chain RI:



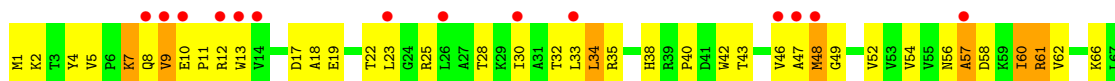
• Molecule 32: 50S ribosomal protein L9

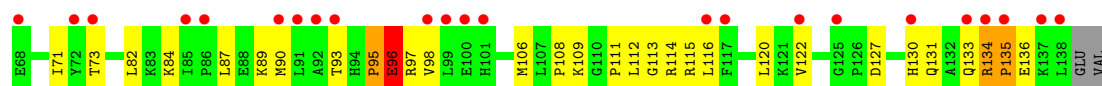
Chain YI:



• Molecule 33: 50S ribosomal protein L13

Chain RN:





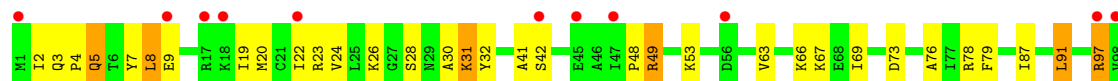
- Molecule 33: 50S ribosomal protein L13

Chain YN:



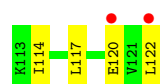
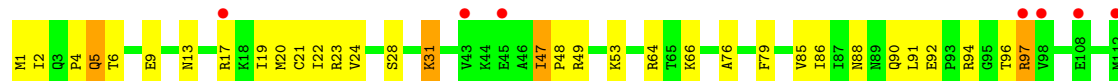
- Molecule 34: 50S ribosomal protein L14

Chain RO:



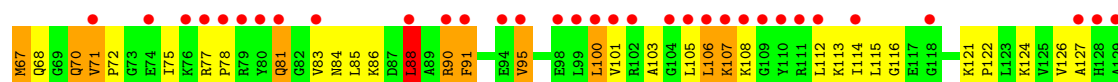
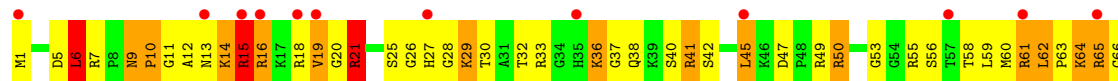
- Molecule 34: 50S ribosomal protein L14

Chain YO:



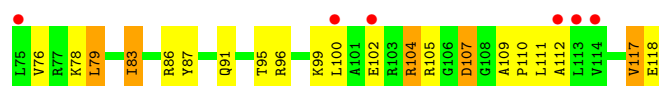
- Molecule 35: 50S ribosomal protein L15

Chain RP:



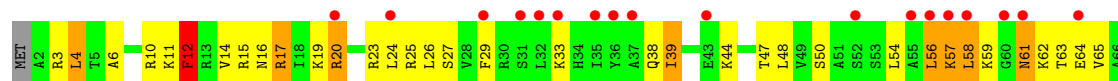
- Molecule 35: 50S ribosomal protein L15

Chain YP:



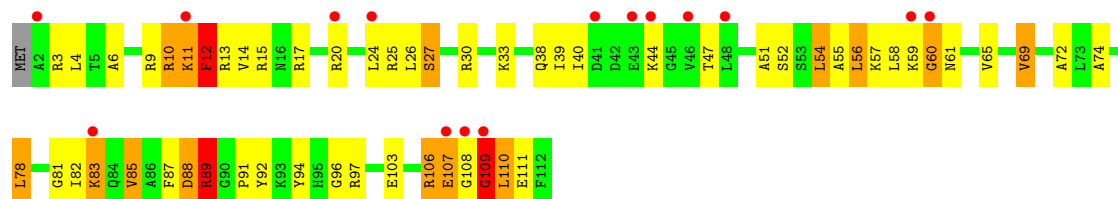
- Molecule 38: 50S ribosomal protein L18

Chain RS:



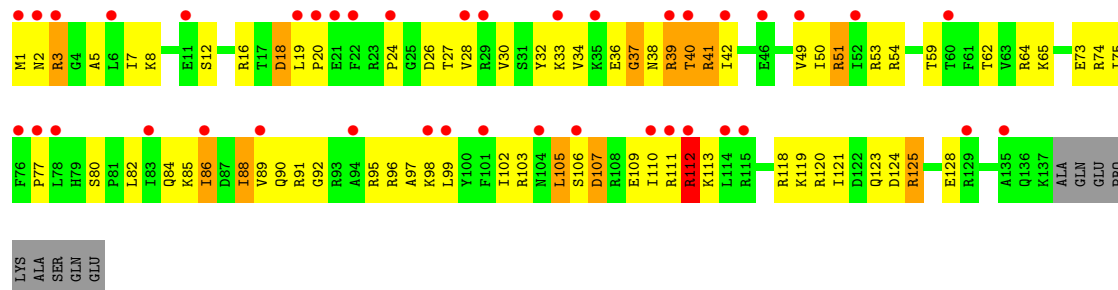
- Molecule 38: 50S ribosomal protein L18

Chain YS:



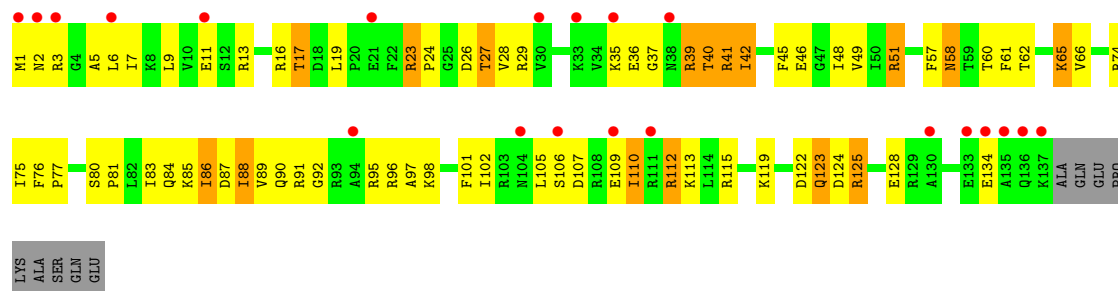
- Molecule 39: 50S ribosomal protein L19

Chain RT:



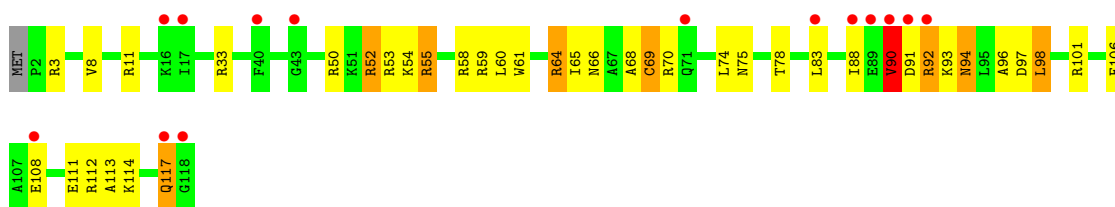
- Molecule 39: 50S ribosomal protein L19

Chain YT:



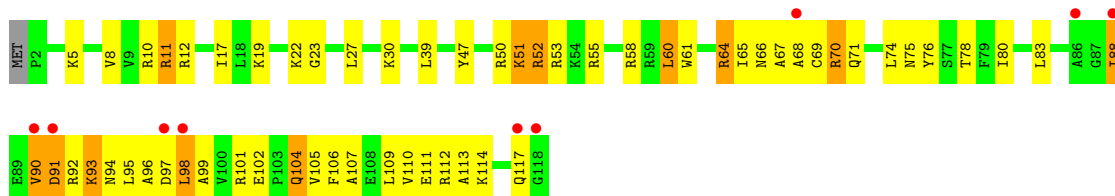
- Molecule 40: 50S ribosomal protein L20

Chain RU:



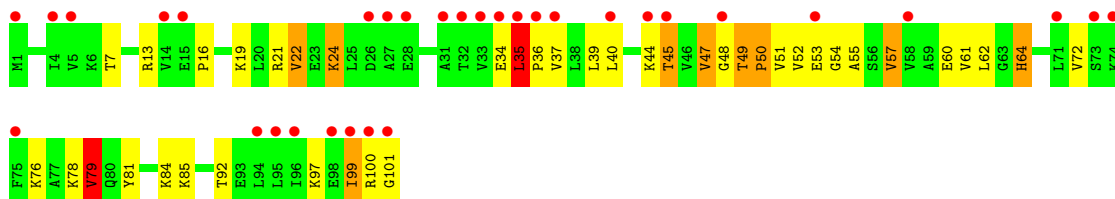
- Molecule 40: 50S ribosomal protein L20

Chain YU:



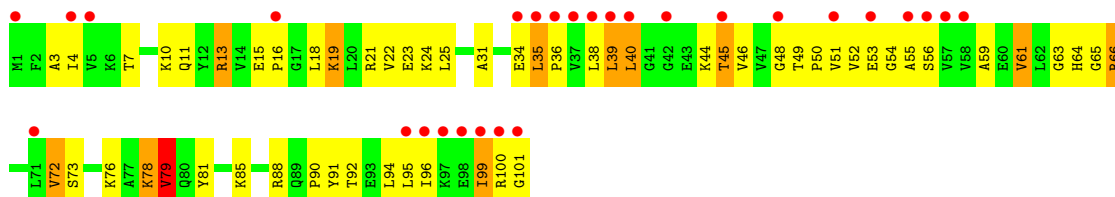
- Molecule 41: 50S ribosomal protein L21

Chain RV:



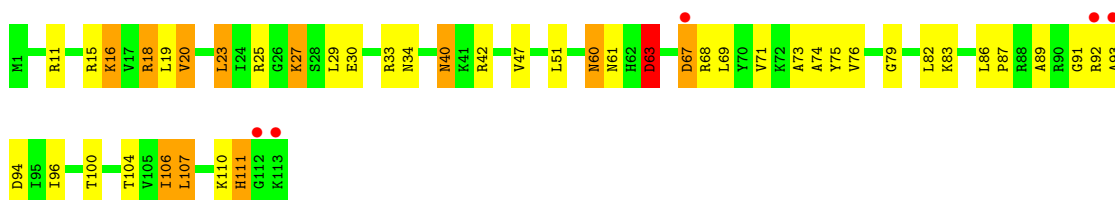
- Molecule 41: 50S ribosomal protein L21

Chain YV:



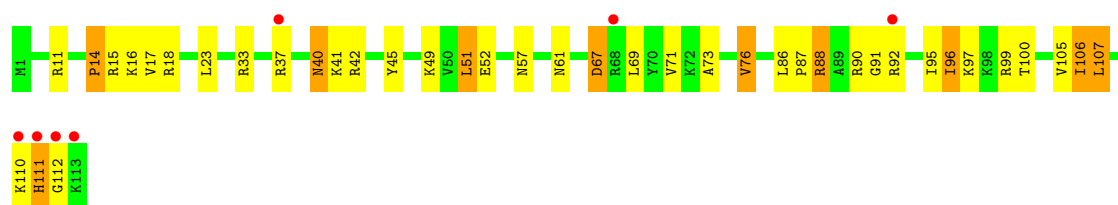
- Molecule 42: 50S ribosomal protein L22

Chain RW:



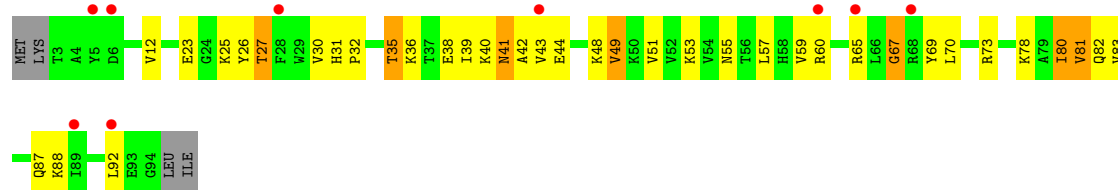
- Molecule 42: 50S ribosomal protein L22

Chain YW:



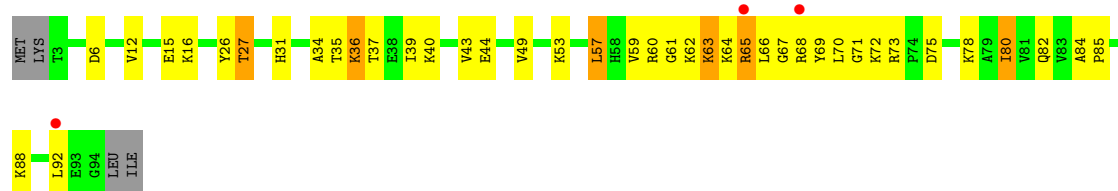
- Molecule 43: 50S ribosomal protein L23

Chain RX:



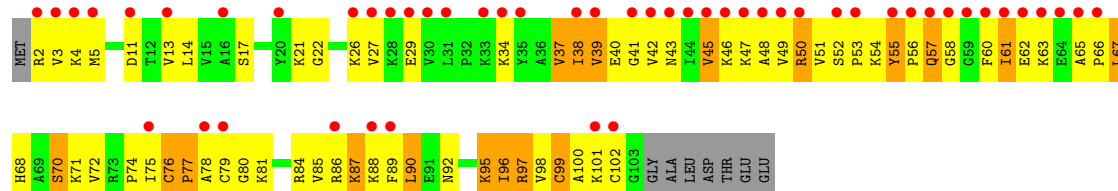
- Molecule 43: 50S ribosomal protein L23

Chain YX:



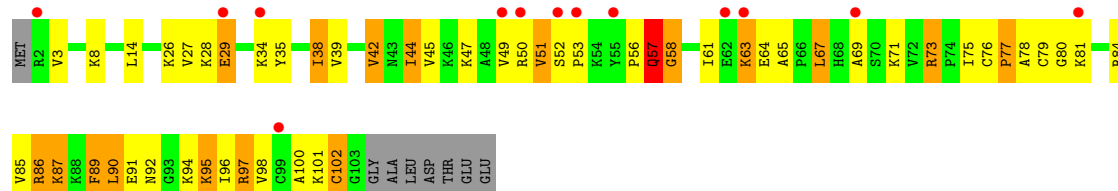
- Molecule 44: 50S ribosomal protein L24

Chain RY:



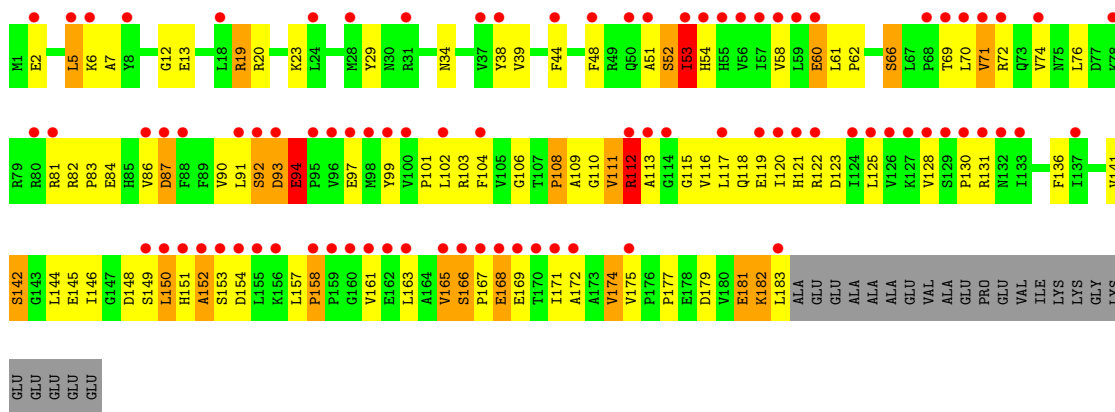
- Molecule 44: 50S ribosomal protein L24

Chain YY:



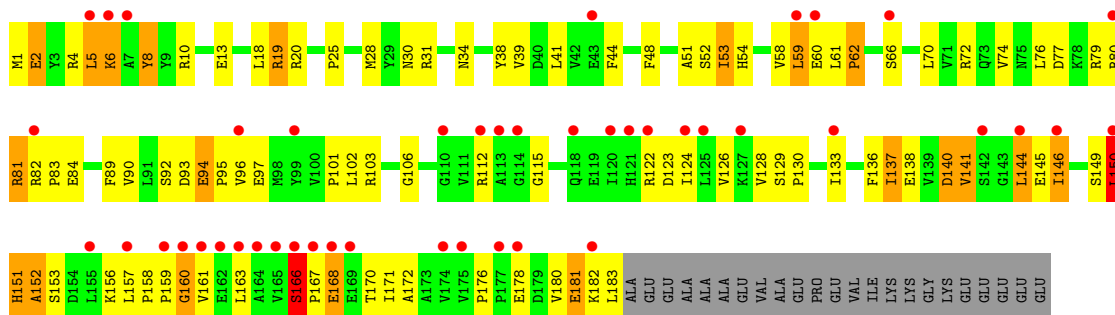
- Molecule 45: 50S ribosomal protein L25

Chain RZ:



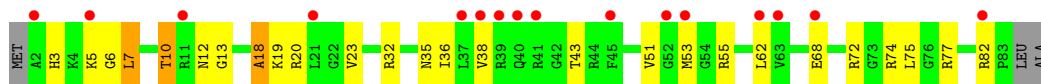
- Molecule 45: 50S ribosomal protein L25

Chain YZ:



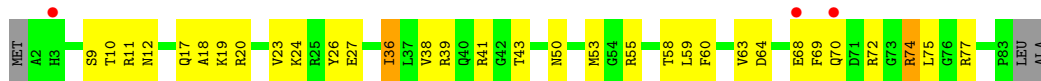
- Molecule 46: 50S ribosomal protein L27

Chain R0:



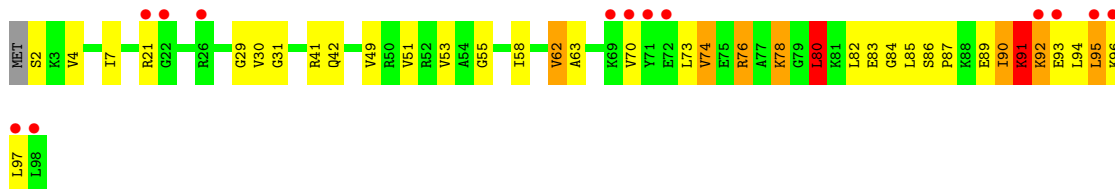
- Molecule 46: 50S ribosomal protein L27

Chain Y0:



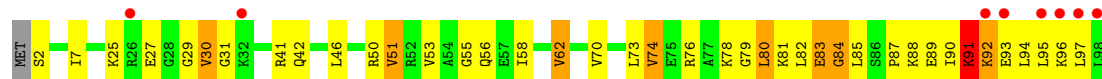
- Molecule 47: 50S ribosomal protein L28

Chain R1:



- Molecule 47: 50S ribosomal protein L28

Chain Y1:



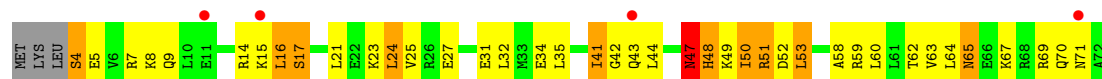
- Molecule 48: 50S ribosomal protein L29

Chain R2:



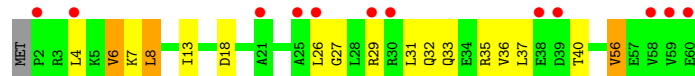
- Molecule 48: 50S ribosomal protein L29

Chain Y2:



- Molecule 49: 50S ribosomal protein L30

Chain R3:



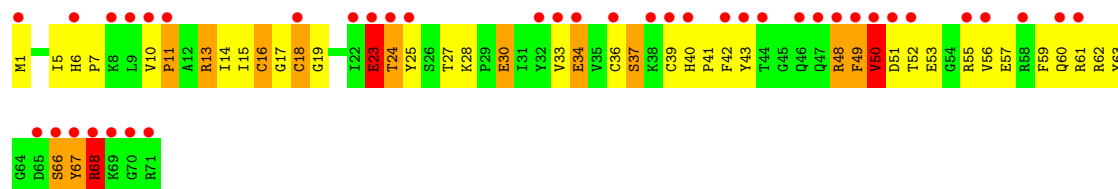
- Molecule 49: 50S ribosomal protein L30

Chain Y3:



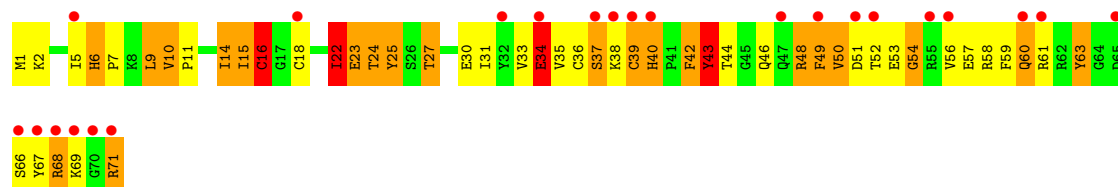
- Molecule 50: 50S ribosomal protein L31

Chain R4:



- Molecule 50: 50S ribosomal protein L31

Chain Y4:



- Molecule 51: 50S ribosomal protein L32

Chain R5:



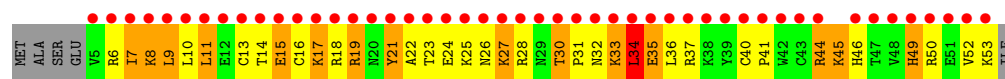
- Molecule 51: 50S ribosomal protein L32

Chain Y5:



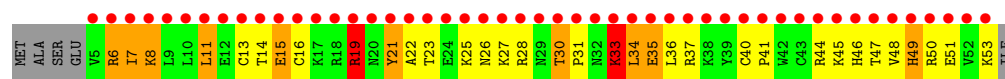
- Molecule 52: 50S ribosomal protein L33

Chain R6:



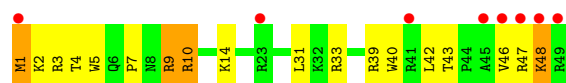
- Molecule 52: 50S ribosomal protein L33

Chain Y6:



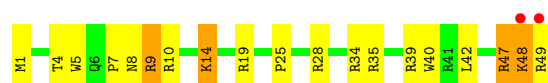
- Molecule 53: 50S ribosomal protein L34

Chain R7:



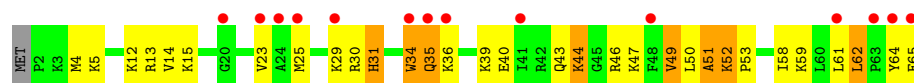
- Molecule 53: 50S ribosomal protein L34

Chain Y7:



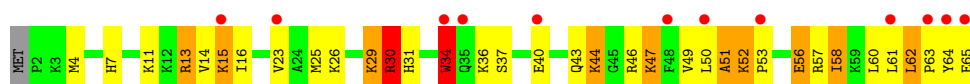
- Molecule 54: 50S ribosomal protein L35

Chain R8:



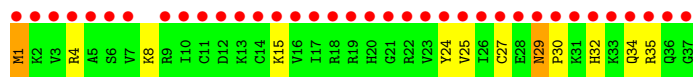
- Molecule 54: 50S ribosomal protein L35

Chain Y8:



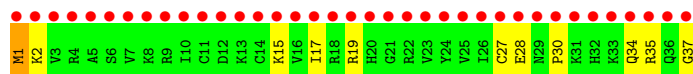
- Molecule 55: 50S ribosomal protein L36

Chain R9:



- Molecule 55: 50S ribosomal protein L36

Chain Y9:



- Molecule 56: tRNA acceptor end mimic

Chain Z6:



- Molecule 56: tRNA acceptor end mimic

Chain Z8:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.81Å 449.41Å 620.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	155.22 – 2.94 181.78 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.6 (155.22-2.94) 98.0 (181.78-2.80)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 2.82Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.219 , 0.265 0.230 , 0.270	Depositor DCC
R_{free} test set	64589 reflections (4.86%)	DCC
Wilson B-factor (Å ²)	50.1	Xtriage
Anisotropy	0.137	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 18.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Outliers	1 of 1394065 reflections (0.000%)	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	291993	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.57% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG, PAR, 1MG, PPU

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	QA	0.46	0/36098	1.01	71/56341 (0.1%)
1	XA	0.54	0/36101	1.09	114/56346 (0.2%)
2	QB	0.31	0/1959	0.52	0/2642
2	XB	0.32	0/1959	0.54	0/2642
3	QC	0.31	0/1629	0.53	0/2195
3	XC	0.36	0/1629	0.56	0/2195
4	QD	0.38	0/1733	0.58	1/2318 (0.0%)
4	XD	0.40	0/1733	0.60	0/2318
5	QE	0.35	0/1171	0.56	0/1576
5	XE	0.39	0/1171	0.59	0/1576
6	QF	0.38	0/856	0.54	0/1154
6	XF	0.38	0/856	0.58	0/1154
7	QG	0.33	0/1276	0.50	0/1709
7	XG	0.34	0/1276	0.50	0/1709
8	QH	0.33	0/1136	0.55	0/1527
8	XH	0.38	0/1136	0.58	0/1527
9	QI	0.31	0/1029	0.55	0/1379
9	XI	0.33	0/1029	0.57	0/1379
10	QJ	0.33	0/814	0.54	0/1095
10	XJ	0.35	0/814	0.59	0/1095
11	QK	0.36	0/900	0.57	0/1213
11	XK	0.38	0/900	0.58	0/1213
12	QL	0.37	0/991	0.61	0/1327
12	XL	0.45	0/991	0.74	1/1327 (0.1%)
13	QM	0.32	0/974	0.59	0/1303
13	XM	0.36	0/974	0.63	0/1303
14	QN	0.41	0/501	0.60	0/664
14	XN	0.42	0/501	0.66	0/664
15	QO	0.35	0/745	0.53	0/992
15	XO	0.39	0/745	0.54	0/992
16	QP	0.36	0/721	0.56	0/970
16	XP	0.35	0/721	0.57	0/970

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	QQ	0.35	0/847	0.53	0/1131
17	XQ	0.35	0/847	0.54	0/1131
18	QR	0.35	0/579	0.64	1/768 (0.1%)
18	XR	0.37	0/579	0.59	0/768
19	QS	0.33	0/689	0.60	0/926
19	XS	0.37	0/689	0.69	1/926 (0.1%)
20	QT	0.35	0/765	0.63	0/1007
20	XT	0.31	0/765	0.59	0/1007
21	QU	0.30	0/221	0.54	0/288
21	XU	0.31	0/221	0.61	0/288
22	QV	0.52	1/1836 (0.1%)	0.98	4/2859 (0.1%)
22	XV	0.59	1/1836 (0.1%)	1.06	4/2859 (0.1%)
23	QY	0.34	0/333	0.91	0/517
23	XY	0.40	0/333	0.94	0/517
24	QX	0.44	0/185	1.15	2/285 (0.7%)
24	XX	0.67	0/185	1.08	0/285
25	RA	0.63	8/69521 (0.0%)	1.16	318/108529 (0.3%)
25	YA	0.72	19/69543 (0.0%)	1.26	504/108563 (0.5%)
26	RB	0.49	0/2878	1.05	6/4490 (0.1%)
26	YB	0.56	0/2878	1.15	18/4490 (0.4%)
27	RD	0.50	0/2165	0.70	0/2919
27	YD	0.58	0/2165	0.78	1/2919 (0.0%)
28	RE	0.43	0/1601	0.73	3/2160 (0.1%)
28	YE	0.46	0/1601	0.75	2/2160 (0.1%)
29	RF	0.42	0/1620	0.62	0/2194
29	YF	0.48	0/1620	0.71	1/2194 (0.0%)
30	RG	0.31	0/1499	0.57	1/2016 (0.0%)
30	YG	0.39	0/1499	0.60	0/2016
31	RH	0.28	0/1332	0.58	0/1802
31	YH	0.45	0/1332	0.73	0/1802
32	RI	0.35	0/1151	0.67	0/1558
32	YI	0.35	0/1151	0.66	0/1558
33	RN	0.41	0/1131	0.62	0/1525
33	YN	0.43	0/1131	0.64	0/1525
34	RO	0.41	0/943	0.62	1/1269 (0.1%)
34	YO	0.49	0/943	0.65	0/1269
35	RP	0.43	0/1162	0.81	1/1544 (0.1%)
35	YP	0.49	0/1162	0.90	2/1544 (0.1%)
36	RQ	0.47	0/1143	0.73	2/1527 (0.1%)
36	YQ	0.57	0/1143	0.80	1/1527 (0.1%)
37	RR	0.42	0/982	0.69	0/1312
37	YR	0.44	0/982	0.73	0/1312
38	RS	0.36	0/892	0.64	0/1187

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	YS	0.40	0/892	0.75	1/1187 (0.1%)
39	RT	0.42	0/1155	0.63	0/1542
39	YT	0.44	0/1155	0.67	0/1542
40	RU	0.39	0/982	0.65	0/1306
40	YU	0.50	0/982	0.68	0/1306
41	RV	0.38	0/790	0.61	1/1057 (0.1%)
41	YV	0.45	0/790	0.73	1/1057 (0.1%)
42	RW	0.49	0/911	0.67	0/1220
42	YW	0.45	0/911	0.68	0/1220
43	RX	0.47	0/739	0.62	0/993
43	YX	0.50	0/739	0.66	0/993
44	RY	0.44	0/798	0.68	0/1064
44	YY	0.46	0/798	0.69	0/1064
45	RZ	0.34	0/1493	0.59	0/2026
45	YZ	0.37	0/1493	0.64	2/2026 (0.1%)
46	R0	0.45	0/657	0.65	0/874
46	Y0	0.48	0/657	0.69	0/874
47	R1	0.44	0/770	0.66	0/1022
47	Y1	0.46	0/770	0.69	0/1022
48	R2	0.39	0/583	0.65	0/771
48	Y2	0.52	0/583	0.73	0/771
49	R3	0.35	0/474	0.57	0/635
49	Y3	0.41	0/474	0.59	0/635
50	R4	0.33	0/594	0.68	0/795
50	Y4	0.37	0/594	0.68	0/795
51	R5	0.43	0/473	0.73	0/639
51	Y5	0.43	0/473	0.77	1/639 (0.2%)
52	R6	0.35	0/431	0.69	0/575
52	Y6	0.37	0/431	0.67	0/575
53	R7	0.49	0/438	0.68	0/575
53	Y7	0.57	0/438	0.71	0/575
54	R8	0.55	0/525	0.79	0/691
54	Y8	0.58	0/525	0.82	0/691
55	R9	0.26	0/310	0.45	0/407
55	Y9	0.32	0/310	0.48	0/407
56	Z6	0.80	0/40	1.80	1/60 (1.7%)
56	Z8	0.78	0/40	1.81	1/60 (1.7%)
All	All	0.56	29/316367 (0.0%)	1.04	1068/472979 (0.2%)

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
12	QL	0	1
12	XL	0	1
28	RE	0	1
28	YE	0	1
29	YF	0	1
31	RH	0	2
31	YH	0	2
38	YS	0	1
45	YZ	0	1
48	Y2	0	1
54	R8	0	2
54	Y8	0	2
All	All	0	16

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	QV	0	C	OP3-P	-10.50	1.48	1.61
22	XV	0	C	OP3-P	-10.49	1.48	1.61
25	YA	528	A	N9-C4	-9.10	1.32	1.37
25	YA	783	A	N9-C4	-7.66	1.33	1.37
25	YA	783	A	N3-C4	-7.55	1.30	1.34
25	YA	676	A	N9-C4	-7.13	1.33	1.37
25	RA	774	A	N9-C4	-7.10	1.33	1.37
25	YA	1786	A	N3-C4	-6.80	1.30	1.34
25	YA	1142(A)	A	N9-C4	-6.74	1.33	1.37
25	YA	71	A	N9-C4	-6.52	1.33	1.37
25	YA	2287	A	N9-C4	-6.37	1.34	1.37
25	RA	528	A	N9-C4	-6.27	1.34	1.37
25	YA	783	A	C5-C6	-6.22	1.35	1.41
25	RA	783	A	N9-C4	-6.05	1.34	1.37
25	RA	2518	A	N9-C4	-6.03	1.34	1.37
25	YA	1021	A	N9-C4	-5.71	1.34	1.37
25	YA	1786	A	N9-C4	-5.66	1.34	1.37
25	YA	783	A	N9-C8	5.56	1.42	1.37
25	RA	2053	G	C8-N7	5.55	1.34	1.30
25	YA	74	A	N9-C4	-5.53	1.34	1.37
25	YA	776	G	N7-C5	5.51	1.42	1.39
25	RA	2713	A	N9-C4	-5.35	1.34	1.37
25	YA	1950	G	C2-N3	5.31	1.36	1.32
25	YA	49	A	N7-C5	-5.29	1.36	1.39
25	YA	1991	U	C2-N3	-5.27	1.34	1.37
25	YA	974	G	C8-N7	5.21	1.34	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	RA	2287	A	N9-C4	-5.12	1.34	1.37
25	YA	774	A	C5-C6	-5.07	1.36	1.41
25	RA	1616	A	N9-C4	-5.04	1.34	1.37

All (1068) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	YA	1786	A	N7-C8-N9	13.21	120.41	113.80
25	YA	528	A	C2-N3-C4	-13.10	104.05	110.60
25	YA	783	A	C2-N3-C4	-12.39	104.41	110.60
25	YA	1786	A	C5-N7-C8	-12.26	97.77	103.90
25	YA	1786	A	C2-N3-C4	-11.73	104.73	110.60
25	YA	783	A	C5-N7-C8	-11.48	98.16	103.90
25	YA	1899	G	N3-C2-N2	11.37	127.86	119.90
25	RA	1899	G	N1-C2-N2	-11.25	106.07	116.20
25	YA	774	A	N1-C6-N6	11.19	125.32	118.60
25	YA	1991	U	N3-C4-O4	-10.91	111.76	119.40
25	YA	265	A	O4'-C1'-N9	10.83	116.86	108.20
25	RA	1786	A	N7-C8-N9	10.49	119.05	113.80
25	YA	774	A	C2-N3-C4	-10.47	105.36	110.60
25	RA	1786	A	C5-N7-C8	-10.46	98.67	103.90
25	YA	1899	G	N1-C2-N2	-10.44	106.80	116.20
25	YA	1678	G	C4-C5-N7	10.44	114.97	110.80
25	RA	2490	G	C4-C5-N7	10.37	114.95	110.80
25	RA	1899	G	N3-C2-N2	10.29	127.11	119.90
25	YA	2430	A	C2-N3-C4	-10.26	105.47	110.60
25	RA	2430	A	C2-N3-C4	-10.12	105.54	110.60
25	RA	2614	A	C6-N1-C2	-9.91	112.65	118.60
25	RA	2614	A	N1-C2-N3	9.86	134.23	129.30
25	YA	74	A	C2-N3-C4	-9.86	105.67	110.60
25	YA	71	A	C2-N3-C4	-9.80	105.70	110.60
25	YA	1678	G	C5-N7-C8	-9.77	99.42	104.30
25	YA	530	G	N3-C2-N2	9.56	126.59	119.90
1	QA	328	C	N1-C2-O2	9.46	124.58	118.90
25	YA	945	A	N1-C6-N6	9.44	124.27	118.60
25	YA	1786	A	N1-C2-N3	9.42	134.01	129.30
25	YA	1786	A	C8-N9-C4	-9.39	102.04	105.80
25	RA	1786	A	C2-N3-C4	-9.32	105.94	110.60
25	YA	676	A	C5-N7-C8	-9.30	99.25	103.90
25	YA	1021	A	C2-N3-C4	-9.21	105.99	110.60
25	YA	528	A	N3-C4-N9	-9.17	120.06	127.40
25	RA	774	A	C2-N3-C4	-9.14	106.03	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	RA	1931	U	N3-C2-O2	-9.08	115.84	122.20
25	RA	1359	A	N9-C4-C5	-9.04	102.18	105.80
25	YA	676	A	C2-N3-C4	-9.02	106.09	110.60
25	RA	783	A	C2-N3-C4	-8.93	106.13	110.60
25	YA	1332	G	C6-C5-N7	-8.90	125.06	130.40
25	RA	1359	A	N1-C6-N6	8.90	123.94	118.60
25	YA	528	A	N3-C4-C5	8.90	133.03	126.80
1	QA	1322	C	C2-N1-C1'	8.83	128.52	118.80
25	YA	783	A	C4-C5-N7	8.79	115.09	110.70
25	YA	1824	G	O5'-P-OP2	-8.79	97.79	105.70
25	RA	1332	G	C2-N3-C4	-8.78	107.51	111.90
25	YA	1979	C	C6-N1-C2	-8.66	116.84	120.30
25	RA	783	A	C5-N7-C8	-8.65	99.58	103.90
25	YA	2287	A	C2-N3-C4	-8.64	106.28	110.60
25	RA	2490	G	C6-C5-N7	-8.63	125.22	130.40
1	QA	1297	C	P-O3'-C3'	8.61	130.03	119.70
25	YA	530	G	N1-C6-O6	-8.60	114.74	119.90
25	YA	372	G	O4'-C1'-N9	8.59	115.08	108.20
25	YA	776	G	C5-N7-C8	-8.56	100.02	104.30
25	RA	1396	U	N3-C2-O2	-8.55	116.21	122.20
25	RA	2287	A	C2-N3-C4	-8.52	106.34	110.60
25	YA	945	A	C5-N7-C8	-8.52	99.64	103.90
25	YA	776	G	N1-C6-O6	-8.51	114.79	119.90
25	YA	1950	G	N7-C8-N9	8.49	117.35	113.10
25	YA	1678	G	C6-C5-N7	-8.46	125.32	130.40
25	YA	530	G	N1-C2-N2	-8.44	108.60	116.20
25	RA	776	G	C5-N7-C8	-8.42	100.09	104.30
25	RA	1204	A	C2-N3-C4	-8.41	106.39	110.60
25	RA	1931	U	C5-C4-O4	8.41	130.94	125.90
25	YA	1204	A	O4'-C1'-N9	8.41	114.92	108.20
25	YA	945	A	C4-C5-N7	8.39	114.90	110.70
25	YA	774	A	N1-C2-N3	8.38	133.49	129.30
25	RA	2053	G	C5-N7-C8	-8.38	100.11	104.30
25	YA	776	G	N7-C8-N9	8.36	117.28	113.10
1	XA	1336	C	C2-N1-C1'	8.34	127.98	118.80
1	XA	792	A	O4'-C1'-N9	8.34	114.87	108.20
25	YA	974(A)	C	N3-C2-O2	-8.34	116.06	121.90
25	YA	2490	G	C4-C5-N7	8.31	114.12	110.80
25	RA	1980	G	P-O3'-C3'	8.31	129.67	119.70
25	YA	1332	G	C4-C5-N7	8.31	114.12	110.80
25	YA	120	U	C5-C6-N1	-8.28	118.56	122.70
25	YA	2490	G	C5-N7-C8	-8.28	100.16	104.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	XA	518	C	C2-N3-C4	-8.27	115.76	119.90
25	YA	1991	U	N3-C4-C5	8.26	119.56	114.60
25	YA	1210	A	C8-N9-C4	-8.21	102.52	105.80
25	YA	2702	U	C2-N1-C1'	8.21	127.55	117.70
1	QA	1158	C	C2-N1-C1'	8.20	127.82	118.80
25	YA	330	A	C2-N3-C4	-8.17	106.52	110.60
1	QA	1158	C	N1-C2-O2	8.16	123.80	118.90
25	YA	1899	G	C6-C5-N7	-8.16	125.50	130.40
25	YA	74	A	N1-C2-N3	8.13	133.37	129.30
1	XA	963	G	N3-C4-C5	-8.09	124.55	128.60
25	RA	1130	U	P-O3'-C3'	8.09	129.40	119.70
25	YA	783	A	N7-C8-N9	8.08	117.84	113.80
25	YA	774	A	C6-C5-N7	-8.08	126.65	132.30
1	XA	1301	U	C2-N1-C1'	8.03	127.34	117.70
25	YA	141	A	N7-C8-N9	8.03	117.82	113.80
25	YA	1496	A	N7-C8-N9	8.03	117.81	113.80
25	YA	1616	A	C5-N7-C8	-8.01	99.90	103.90
25	RA	2307	G	O4'-C1'-N9	8.00	114.60	108.20
25	RA	2335	A	O4'-C1'-N9	7.99	114.59	108.20
25	YA	1950	G	C4-N9-C1'	7.98	136.88	126.50
25	RA	2307	G	C4-N9-C1'	7.96	136.85	126.50
25	YA	1678	G	N7-C8-N9	7.95	117.07	113.10
25	RA	776	G	N7-C8-N9	7.95	117.07	113.10
25	YA	2490	G	C6-C5-N7	-7.94	125.63	130.40
25	RA	1937	A	O4'-C1'-N9	7.94	114.55	108.20
25	RA	2490	G	C5-N7-C8	-7.91	100.34	104.30
25	RA	1396	U	N1-C2-O2	7.88	128.32	122.80
1	QA	1301	U	C2-N1-C1'	7.87	127.15	117.70
25	YA	1786	A	C6-C5-N7	-7.87	126.79	132.30
1	XA	792	A	N1-C6-N6	7.87	123.32	118.60
25	YA	2712(A)	A	N7-C8-N9	7.87	117.73	113.80
25	YA	2447	G	C8-N9-C4	-7.85	103.26	106.40
25	YA	2544	G	N1-C6-O6	7.84	124.61	119.90
25	YA	945	A	C6-C5-N7	-7.84	126.81	132.30
25	YA	1396	U	N3-C2-O2	-7.83	116.72	122.20
1	XA	1054	C	C2-N1-C1'	7.82	127.41	118.80
25	YA	2584	U	N3-C2-O2	-7.82	116.73	122.20
1	QA	1322	C	N1-C2-O2	7.78	123.56	118.90
25	YA	1210	A	N7-C8-N9	7.77	117.69	113.80
1	XA	328	C	C2-N1-C1'	7.77	127.34	118.80
25	YA	1819	A	P-O3'-C3'	7.75	129.00	119.70
25	YA	1142(A)	A	C2-N3-C4	-7.74	106.73	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	YA	1899	G	N3-C4-N9	7.74	130.64	126.00
1	XA	812	C	P-O3'-C3'	7.68	128.92	119.70
25	YA	1190	G	C5-N7-C8	-7.68	100.46	104.30
25	RA	1929	G	OP1-P-O3'	7.67	122.06	105.20
25	YA	470	A	O5'-P-OP1	-7.64	98.82	105.70
25	RA	774	A	N3-C4-C5	7.61	132.12	126.80
25	RA	2688	U	N3-C2-O2	-7.61	116.88	122.20
1	QA	1322	C	C6-N1-C1'	-7.59	111.69	120.80
25	YA	1678	G	C2-N3-C4	-7.59	108.11	111.90
25	YA	1678	G	N1-C6-O6	7.59	124.45	119.90
25	RA	2490	G	C4-N9-C1'	7.55	136.32	126.50
25	YA	1698	A	C2-N3-C4	-7.55	106.83	110.60
25	YA	1130	U	P-O3'-C3'	7.54	128.75	119.70
25	YA	676	A	N3-C4-C5	7.52	132.06	126.80
25	YA	1404	C	O5'-P-OP1	-7.52	98.93	105.70
25	RA	528	A	C2-N3-C4	-7.51	106.85	110.60
25	YA	1396	U	N1-C2-O2	7.50	128.05	122.80
25	YA	1204	A	N1-C2-N3	7.49	133.05	129.30
25	RA	1786	A	C4-C5-N7	7.47	114.44	110.70
25	YA	2713	A	C5-N7-C8	-7.46	100.17	103.90
25	YA	2688	U	C4-C5-C6	7.46	124.17	119.70
25	YA	450	G	C5-C6-N1	-7.44	107.78	111.50
25	RA	1786	A	C6-C5-N7	-7.43	127.09	132.30
25	YA	2346	A	C2-N3-C4	-7.43	106.88	110.60
25	YA	1931	U	C5-C4-O4	7.42	130.35	125.90
1	XA	1302	U	C2-N1-C1'	7.42	126.61	117.70
25	YA	774	A	C5-N7-C8	-7.42	100.19	103.90
25	YA	1950	G	N3-C2-N2	7.40	125.08	119.90
22	QV	16	C	C2-N1-C1'	7.38	126.92	118.80
25	YA	2490	G	N7-C8-N9	7.38	116.79	113.10
1	XA	1158	C	C2-N1-C1'	7.38	126.92	118.80
25	YA	1332	G	C4-N9-C1'	7.38	136.09	126.50
25	YA	774	A	C4-C5-N7	7.37	114.39	110.70
25	YA	1332	G	C5-N7-C8	-7.37	100.62	104.30
25	YA	2429	G	OP2-P-O3'	7.36	121.38	105.20
1	XA	1498	U	C2-N1-C1'	7.35	126.52	117.70
1	XA	792	A	C4-C5-N7	7.34	114.37	110.70
25	YA	2688	U	N3-C2-O2	-7.33	117.07	122.20
25	RA	2060	A	P-O3'-C3'	7.33	128.49	119.70
1	XA	753	A	P-O3'-C3'	7.33	128.49	119.70
25	RA	1204	A	O4'-C1'-N9	7.32	114.06	108.20
25	RA	1304	C	N1-C2-O2	7.32	123.29	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	YA	1382	G	N1-C6-O6	7.32	124.29	119.90
25	RA	372	G	O4'-C1'-N9	7.32	114.05	108.20
25	RA	676	A	O4'-C1'-N9	7.31	114.05	108.20
25	YA	1332	G	N7-C8-N9	7.30	116.75	113.10
25	YA	140	A	N7-C8-N9	7.30	117.45	113.80
25	YA	371	A	O5'-P-OP1	-7.29	99.14	105.70
25	YA	1950	G	O4'-C1'-N9	7.28	114.02	108.20
25	YA	1204	A	C2-N3-C4	-7.28	106.96	110.60
25	YA	856	C	C6-N1-C2	-7.26	117.39	120.30
25	YA	512	G	O4'-C1'-N9	7.26	114.01	108.20
25	YA	1021	A	C5-N7-C8	-7.26	100.27	103.90
25	YA	120	U	C4-C5-C6	7.25	124.05	119.70
25	RA	28	A	N7-C8-N9	7.24	117.42	113.80
25	YA	1950	G	C8-N9-C4	-7.24	103.50	106.40
25	YA	676	A	O4'-C1'-N9	7.24	113.99	108.20
25	YA	141	A	C8-N9-C4	-7.22	102.91	105.80
25	YA	1799	G	P-O3'-C3'	7.22	128.36	119.70
25	YA	1936	A	N9-C4-C5	-7.22	102.91	105.80
25	RA	1931	U	N3-C4-O4	-7.20	114.36	119.40
25	YA	1929	G	OP1-P-O3'	7.20	121.04	105.20
22	QV	16	C	N1-C2-O2	7.18	123.21	118.90
28	YE	21	VAL	C-N-CD	-7.18	104.80	120.60
1	XA	1151	A	O4'-C1'-N9	7.18	113.94	108.20
25	YA	1313	U	C2-N1-C1'	7.17	126.31	117.70
25	RA	2490	G	N7-C8-N9	7.17	116.68	113.10
25	RA	2439	A	C8-N9-C4	-7.17	102.93	105.80
25	YA	621	A	C2-N3-C4	-7.16	107.02	110.60
25	YA	1616	A	N7-C8-N9	7.16	117.38	113.80
25	RA	1786	A	N1-C6-N6	7.16	122.89	118.60
25	RA	2702	U	C2-N1-C1'	7.14	126.27	117.70
12	XL	47	LYS	C-N-CD	-7.14	104.90	120.60
25	YA	141	A	C5-N7-C8	-7.13	100.33	103.90
25	RA	1929	G	C4-C5-N7	7.12	113.65	110.80
25	RA	1698	A	C2-N3-C4	-7.10	107.05	110.60
25	YA	140	A	C5-N7-C8	-7.09	100.36	103.90
25	YA	446	G	N1-C6-O6	7.07	124.14	119.90
25	YA	1931	U	N3-C2-O2	-7.06	117.26	122.20
25	RA	470	A	O5'-P-OP1	-7.05	99.36	105.70
25	RA	2036	C	O5'-P-OP2	-7.04	99.36	105.70
25	RA	2053	G	C4-C5-N7	7.04	113.62	110.80
26	YB	31	C	C6-N1-C2	-7.03	117.49	120.30
25	YA	1496	A	C8-N9-C4	-7.02	102.99	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	RA	242	G	P-O3'-C3'	7.01	128.11	119.70
25	RA	2726	U	C2-N1-C1'	7.01	126.11	117.70
25	YA	2688	U	C5-C4-O4	7.00	130.10	125.90
25	RA	2307	G	C6-C5-N7	-7.00	126.20	130.40
25	RA	1694	C	P-O3'-C3'	7.00	128.10	119.70
25	YA	974(A)	C	N1-C2-O2	6.99	123.09	118.90
25	RA	1786	A	C5-C6-N1	-6.98	114.21	117.70
1	XA	328	C	C6-N1-C2	-6.97	117.51	120.30
25	YA	1614	A	C5-N7-C8	-6.96	100.42	103.90
25	YA	1427	A	P-O3'-C3'	6.96	128.05	119.70
25	RA	1899	G	C6-C5-N7	-6.96	126.22	130.40
25	YA	1653	G	P-O3'-C3'	6.93	128.01	119.70
1	XA	1336	C	C6-N1-C2	-6.91	117.54	120.30
1	QA	1302	U	C2-N1-C1'	6.91	125.99	117.70
25	RA	1332	G	N3-C4-C5	6.90	132.05	128.60
25	YA	1929	G	C4-C5-N7	6.89	113.56	110.80
25	RA	2518	A	C2-N3-C4	-6.89	107.16	110.60
25	YA	621	A	N7-C8-N9	6.89	117.24	113.80
25	YA	2587	A	N1-C6-N6	-6.88	114.47	118.60
25	YA	974(A)	C	N3-C4-N4	-6.88	113.18	118.00
25	RA	74	A	C2-N3-C4	-6.86	107.17	110.60
25	YA	1889	A	O5'-P-OP1	-6.85	99.54	105.70
1	QA	792	A	P-O3'-C3'	6.84	127.91	119.70
25	YA	2311	A	C2-N3-C4	-6.84	107.18	110.60
1	XA	1054	C	C6-N1-C1'	-6.84	112.59	120.80
25	RA	2584	U	N3-C2-O2	-6.83	117.42	122.20
25	YA	2689	U	N3-C4-O4	-6.83	114.62	119.40
25	RA	1930	G	C4-N9-C1'	-6.83	117.62	126.50
25	RA	2544	G	N1-C6-O6	6.83	124.00	119.90
25	YA	2481	G	P-O3'-C3'	6.83	127.89	119.70
56	Z8	74	C	N1-C2-O2	6.82	122.99	118.90
1	XA	328	C	N1-C2-O2	6.82	122.99	118.90
1	XA	1065	U	P-O3'-C3'	6.81	127.88	119.70
1	XA	1128	C	C6-N1-C2	-6.80	117.58	120.30
25	YA	783	A	N3-C4-C5	6.80	131.56	126.80
25	YA	1428	C	O5'-P-OP2	6.80	118.86	110.70
25	RA	503	A	P-O3'-C3'	6.79	127.85	119.70
1	XA	1200	C	P-O3'-C3'	6.79	127.85	119.70
25	YA	1528	A	N7-C8-N9	6.79	117.19	113.80
56	Z6	74	C	N1-C2-O2	6.77	122.96	118.90
26	RB	44	G	C4-N9-C1'	-6.76	117.71	126.50
25	RA	2559	C	N1-C2-O2	6.76	122.95	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	YA	676	A	N3-C4-N9	-6.76	121.99	127.40
25	YA	1929	G	N1-C6-O6	6.75	123.95	119.90
25	YA	1955	U	P-O3'-C3'	6.75	127.80	119.70
1	XA	1108	G	C5-C6-N1	-6.74	108.13	111.50
25	RA	1653	G	P-O3'-C3'	6.74	127.79	119.70
25	YA	676	A	N7-C8-N9	6.74	117.17	113.80
1	XA	963	G	N3-C4-N9	6.74	130.04	126.00
25	YA	828	U	N3-C2-O2	-6.74	117.48	122.20
1	QA	703	G	N3-C4-C5	-6.73	125.23	128.60
25	RA	2490	G	O4'-C1'-N9	6.73	113.58	108.20
25	YA	242	G	P-O3'-C3'	6.71	127.76	119.70
25	YA	245	G	O5'-P-OP1	-6.71	99.66	105.70
25	RA	1266	G	C8-N9-C4	6.71	109.08	106.40
26	YB	44	G	C4-N9-C1'	-6.71	117.78	126.50
25	RA	2307	G	N7-C8-N9	6.70	116.45	113.10
25	YA	71	A	N3-C4-C5	6.70	131.49	126.80
25	YA	2430	A	N1-C2-N3	6.70	132.65	129.30
25	YA	860	U	N3-C2-O2	-6.69	117.52	122.20
1	QA	1065	U	OP2-P-O3'	6.69	119.91	105.20
25	RA	974(A)	C	N3-C2-O2	-6.68	117.22	121.90
25	YA	1616	A	O4'-C1'-N9	6.67	113.54	108.20
25	RA	774	A	N3-C4-N9	-6.67	122.06	127.40
1	XA	1298	C	P-O3'-C3'	6.67	127.71	119.70
25	RA	783	A	C4-C5-N7	6.66	114.03	110.70
25	YA	776	G	C4-C5-C6	-6.66	114.81	118.80
1	QA	1065	U	P-O3'-C3'	6.65	127.68	119.70
25	YA	528	A	N1-C2-N3	6.64	132.62	129.30
25	RA	2318	G	O4'-C1'-N9	6.64	113.51	108.20
1	QA	328	C	N3-C2-O2	-6.63	117.26	121.90
1	QA	1301	U	N1-C2-O2	6.63	127.44	122.80
25	YA	828	U	C5-C4-O4	6.63	129.88	125.90
25	YA	99	U	P-O3'-C3'	6.62	127.65	119.70
25	YA	2439	A	N7-C8-N9	6.62	117.11	113.80
25	YA	2609	U	C5-C6-N1	-6.62	119.39	122.70
25	RA	1698	A	N1-C6-N6	6.61	122.57	118.60
25	RA	2702	U	O4'-C1'-N1	6.61	113.49	108.20
25	YA	588	U	O5'-P-OP1	-6.61	99.75	105.70
25	YA	238	C	C5-C6-N1	-6.61	117.69	121.00
22	XV	16	C	C2-N1-C1'	6.61	126.07	118.80
25	RA	1698	A	C6-C5-N7	-6.60	127.68	132.30
25	YA	27	G	N3-C4-N9	-6.59	122.05	126.00
25	RA	2420	C	O5'-P-OP1	-6.58	99.77	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	YA	1929	G	C5-C6-O6	-6.58	124.65	128.60
1	XA	1200	C	OP2-P-O3'	6.58	119.67	105.20
25	RA	2026	C	N3-C4-C5	6.58	124.53	121.90
25	YA	1786	A	C4-C5-N7	6.57	113.99	110.70
25	RA	1359	A	C4-C5-N7	6.57	113.98	110.70
25	RA	1905	C	N3-C4-C5	6.56	124.52	121.90
25	RA	1332	G	N3-C4-N9	-6.55	122.07	126.00
25	YA	1213	A	N1-C6-N6	6.55	122.53	118.60
1	XA	703	G	N3-C4-C5	-6.55	125.32	128.60
25	YA	2713	A	N1-C6-N6	6.55	122.53	118.60
1	QA	328	C	C2-N1-C1'	6.55	126.00	118.80
22	XV	16	C	N1-C2-O2	6.55	122.83	118.90
25	RA	1496	A	N7-C8-N9	6.55	117.07	113.80
25	YA	1496	A	C5-N7-C8	-6.54	100.63	103.90
25	YA	503	A	P-O3'-C3'	6.53	127.54	119.70
25	YA	2070	G	N1-C6-O6	-6.53	115.98	119.90
25	RA	1931	U	O5'-P-OP1	-6.53	99.83	105.70
25	YA	372	G	C4-N9-C1'	-6.53	118.02	126.50
25	YA	1694	C	P-O3'-C3'	6.53	127.53	119.70
25	YA	1428	C	O5'-P-OP1	-6.52	99.83	105.70
38	YS	56	LEU	CA-CB-CG	6.52	130.30	115.30
25	RA	140	A	N7-C8-N9	6.52	117.06	113.80
28	RE	21	VAL	C-N-CD	-6.52	106.26	120.60
25	RA	2392	A	C2-N3-C4	-6.51	107.34	110.60
25	YA	860	U	C4-C5-C6	6.51	123.61	119.70
1	XA	1336	C	N1-C2-O2	6.51	122.81	118.90
25	YA	783	A	C6-C5-N7	-6.51	127.75	132.30
25	YA	1786	A	C5-C6-N1	-6.50	114.45	117.70
25	YA	1021	A	N7-C8-N9	6.50	117.05	113.80
25	RA	530	G	N3-C2-N2	6.49	124.44	119.90
25	RA	2518	A	N1-C6-N6	6.49	122.49	118.60
1	XA	117	G	N1-C6-O6	6.48	123.79	119.90
25	RA	2447	G	C8-N9-C1'	6.48	135.43	127.00
25	YA	528	A	C5-C6-N1	-6.48	114.46	117.70
25	RA	1929	G	C5-N7-C8	-6.48	101.06	104.30
25	RA	1396	U	C2-N1-C1'	6.48	125.47	117.70
1	XA	690	G	O4'-C1'-N9	6.48	113.38	108.20
25	YA	2713	A	C4-C5-N7	6.48	113.94	110.70
25	YA	570	G	C5-C6-N1	-6.47	108.26	111.50
25	RA	1790	C	C6-N1-C2	6.47	122.89	120.30
1	XA	410	G	P-O3'-C3'	6.46	127.45	119.70
25	RA	2490	G	C8-N9-C1'	-6.46	118.61	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	RA	790	C	C6-N1-C2	6.46	122.88	120.30
25	YA	1899	G	N3-C4-C5	-6.46	125.37	128.60
1	XA	1297	C	P-O3'-C3'	6.45	127.44	119.70
25	YA	195	A	C5-N7-C8	-6.44	100.68	103.90
25	YA	621	A	C5-N7-C8	-6.44	100.68	103.90
25	YA	783	A	N1-C6-N6	6.44	122.46	118.60
25	RA	1123	C	C6-N1-C2	6.43	122.87	120.30
25	RA	945	A	C5-N7-C8	-6.43	100.69	103.90
25	YA	1969	A	C8-N9-C4	6.43	108.37	105.80
25	YA	679	C	C6-N1-C2	6.43	122.87	120.30
25	YA	2458	G	N3-C4-C5	-6.42	125.39	128.60
25	RA	2307	G	C8-N9-C1'	-6.42	118.65	127.00
25	YA	1925	C	N1-C2-O2	-6.42	115.05	118.90
25	YA	2032	G	C5-N7-C8	-6.42	101.09	104.30
25	RA	2702	U	N1-C2-O2	6.42	127.29	122.80
1	XA	108	G	C4-C5-N7	6.42	113.37	110.80
1	XA	792	A	N9-C4-C5	-6.41	103.23	105.80
1	XA	1053	G	C4-N9-C1'	-6.41	118.17	126.50
1	XA	827	U	N3-C2-O2	-6.41	117.72	122.20
25	YA	1153	C	N1-C2-O2	-6.41	115.06	118.90
25	RA	1992	G	C8-N9-C4	-6.40	103.84	106.40
25	RA	974(A)	C	P-O3'-C3'	6.40	127.38	119.70
25	YA	1799	G	N3-C4-C5	-6.40	125.40	128.60
25	YA	761	A	N1-C6-N6	6.40	122.44	118.60
25	YA	2587	A	C8-N9-C4	-6.39	103.24	105.80
25	YA	1021	A	N1-C2-N3	6.39	132.50	129.30
25	YA	1950	G	C6-C5-N7	-6.38	126.57	130.40
25	RA	2346	A	C2-N3-C4	-6.38	107.41	110.60
1	QA	1158	C	N3-C2-O2	-6.38	117.44	121.90
1	QA	328	C	P-O3'-C3'	6.37	127.34	119.70
25	YA	1528	A	C8-N9-C4	-6.37	103.25	105.80
1	XA	914	A	O5'-P-OP1	-6.37	99.97	105.70
25	YA	1955	U	C5-C4-O4	6.36	129.72	125.90
25	YA	2779	U	N3-C2-O2	-6.36	117.75	122.20
25	YA	2502	G	O5'-P-OP1	-6.36	99.98	105.70
26	YB	108	C	O4'-C1'-N1	6.35	113.28	108.20
25	YA	1992	G	P-O3'-C3'	6.35	127.32	119.70
25	YA	783	A	C8-N9-C4	-6.35	103.26	105.80
24	QX	3	G	P-O3'-C3'	6.34	127.31	119.70
25	YA	27	G	N9-C4-C5	6.34	107.93	105.40
25	YA	1210	A	C5-N7-C8	-6.33	100.73	103.90
25	YA	2584	U	C5-C4-O4	6.33	129.70	125.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	YA	2832	U	P-O3'-C3'	6.33	127.30	119.70
1	XA	576	G	O5'-P-OP2	-6.32	100.01	105.70
25	YA	577	G	N1-C6-O6	6.32	123.69	119.90
25	RA	2346	A	N1-C2-N3	6.32	132.46	129.30
25	YA	2598	A	OP2-P-O3'	6.32	119.09	105.20
25	YA	372	G	OP2-P-O3'	6.31	119.09	105.20
25	YA	2638	G	N3-C4-N9	6.31	129.79	126.00
25	YA	2712	U	O4'-C1'-N1	6.31	113.25	108.20
25	YA	2318	G	C6-C5-N7	-6.30	126.62	130.40
25	YA	2430	A	C5-N7-C8	-6.30	100.75	103.90
1	QA	723	U	C2-N1-C1'	6.30	125.26	117.70
25	RA	265	A	O4'-C1'-N9	6.30	113.24	108.20
25	RA	2712(A)	A	N7-C8-N9	6.30	116.95	113.80
25	RA	1786	A	N9-C1'-C2'	6.30	122.19	114.00
1	QA	890	G	O4'-C1'-N9	6.29	113.24	108.20
25	YA	860	U	C5-C6-N1	-6.29	119.56	122.70
25	RA	372	G	C4-N9-C1'	-6.28	118.34	126.50
25	YA	1142(A)	A	N3-C4-C5	6.28	131.19	126.80
25	RA	1905	C	C6-N1-C2	6.27	122.81	120.30
1	XA	960	U	N3-C2-O2	-6.26	117.82	122.20
25	RA	2318	G	C4-N9-C1'	6.26	134.64	126.50
25	RA	783	A	N7-C8-N9	6.26	116.93	113.80
25	YA	774	A	C5-C6-N6	-6.25	118.70	123.70
25	RA	794	G	N1-C6-O6	-6.24	116.16	119.90
25	RA	2702	U	N3-C2-O2	-6.24	117.83	122.20
1	QA	974	A	O4'-C1'-N9	6.24	113.19	108.20
25	YA	1614	A	C4-C5-N7	6.24	113.82	110.70
1	QA	913	A	P-O3'-C3'	6.21	127.16	119.70
25	RA	1359	A	C5-C6-N6	-6.21	118.73	123.70
25	RA	915	C	C6-N1-C2	-6.20	117.82	120.30
1	XA	1158	C	C6-N1-C2	-6.20	117.82	120.30
25	RA	1313	U	C2-N1-C1'	6.20	125.14	117.70
25	RA	1314	C	N1-C2-O2	6.19	122.61	118.90
25	YA	2712	U	C2-N1-C1'	6.19	125.12	117.70
1	XA	913	A	P-O3'-C3'	6.18	127.11	119.70
1	XA	1302	U	N1-C2-O2	6.18	127.12	122.80
25	RA	1633	G	C8-N9-C4	-6.17	103.93	106.40
26	YB	66	A	P-O3'-C3'	6.17	127.11	119.70
25	RA	1543	A	O4'-C1'-N9	6.17	113.13	108.20
25	YA	140	A	C8-N9-C4	-6.17	103.33	105.80
1	QA	687	A	P-O3'-C3'	6.16	127.10	119.70
25	YA	1899	G	C4-N9-C1'	6.16	134.51	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	YA	2447	G	C8-N9-C1'	6.15	135.00	127.00
25	YA	2702	U	C5-C6-N1	6.15	125.78	122.70
25	YA	1544	C	O5'-P-OP1	-6.15	100.17	105.70
25	RA	860	U	C4-C5-C6	6.15	123.39	119.70
25	RA	805	G	C4-C5-N7	6.15	113.26	110.80
25	RA	1653	G	N3-C4-C5	-6.14	125.53	128.60
1	XA	115	G	P-O3'-C3'	6.14	127.06	119.70
25	YA	1314	C	C2-N1-C1'	6.14	125.55	118.80
25	YA	1614	A	N1-C6-N6	6.13	122.28	118.60
1	QA	1528	U	P-O3'-C3'	6.13	127.06	119.70
1	XA	1301	U	N1-C2-O2	6.13	127.09	122.80
25	RA	2318	G	N7-C8-N9	6.13	116.16	113.10
25	RA	372	G	C8-N9-C1'	6.12	134.96	127.00
25	RA	2392	A	C5-N7-C8	-6.12	100.84	103.90
25	RA	2056	G	C5-N7-C8	-6.11	101.24	104.30
25	YA	945	A	C5-C6-N6	-6.11	118.81	123.70
1	XA	703	G	N3-C4-N9	6.11	129.66	126.00
26	YB	24	G	P-O3'-C3'	6.10	127.02	119.70
25	YA	227	A	C8-N9-C4	-6.09	103.36	105.80
25	YA	2681	C	P-O3'-C3'	6.09	127.01	119.70
25	RA	974(A)	C	C6-N1-C2	-6.09	117.86	120.30
25	RA	2392	A	N7-C8-N9	6.09	116.85	113.80
25	YA	446	G	C5-C6-O6	-6.09	124.94	128.60
25	RA	1929	G	N3-C4-C5	6.09	131.65	128.60
1	QA	1158	C	C6-N1-C2	-6.09	117.86	120.30
25	RA	2490	G	N9-C4-C5	-6.09	102.97	105.40
25	YA	859	G	P-O3'-C3'	6.09	127.00	119.70
25	RA	676	A	C5-N7-C8	-6.08	100.86	103.90
25	RA	2079	U	O5'-P-OP1	-6.08	100.23	105.70
25	YA	2307	G	O4'-C1'-N9	6.08	113.06	108.20
29	YF	74	ARG	NE-CZ-NH1	6.08	123.34	120.30
25	RA	1653	G	C8-N9-C4	-6.08	103.97	106.40
25	YA	570	G	C4-C5-N7	-6.08	108.37	110.80
25	RA	945	A	C4-C5-N7	6.07	113.74	110.70
25	RA	372	G	OP2-P-O3'	6.07	118.56	105.20
25	YA	140	A	C2-N3-C4	-6.07	107.57	110.60
25	RA	752	A	P-O3'-C3'	6.07	126.98	119.70
25	YA	1698	A	C5-N7-C8	-6.07	100.87	103.90
25	RA	221	A	C8-N9-C4	-6.06	103.38	105.80
25	RA	2712	U	N3-C2-O2	-6.06	117.96	122.20
25	YA	1991	U	C4-C5-C6	-6.05	116.07	119.70
25	YA	1647	G	O5'-P-OP1	-6.05	100.25	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	YA	2496	C	N3-C4-C5	6.05	124.32	121.90
36	RQ	79	LEU	CA-CB-CG	6.04	129.20	115.30
25	RA	1786	A	C8-N9-C4	-6.04	103.38	105.80
25	YA	2610	C	P-O3'-C3'	6.04	126.95	119.70
25	RA	530	G	O4'-C1'-N9	6.04	113.03	108.20
26	YB	108	C	C2-N1-C1'	-6.04	112.16	118.80
25	RA	828	U	N3-C2-O2	-6.03	117.98	122.20
25	RA	2053	G	C8-N9-C1'	6.02	134.83	127.00
25	RA	140	A	C8-N9-C4	-6.02	103.39	105.80
1	QA	812	C	P-O3'-C3'	6.01	126.92	119.70
25	YA	621	A	O4'-C1'-N9	6.01	113.01	108.20
25	RA	2776	A	P-O3'-C3'	6.01	126.91	119.70
25	RA	773	U	C5-C6-N1	-6.00	119.70	122.70
25	RA	1632	A	N1-C6-N6	6.00	122.20	118.60
25	YA	140	A	C6-C5-N7	-6.00	128.10	132.30
30	RG	34	LEU	CA-CB-CG	6.00	129.10	115.30
25	YA	1332	G	C8-N9-C1'	-6.00	119.20	127.00
26	RB	6	C	C6-N1-C2	5.99	122.70	120.30
1	QA	1200	C	OP2-P-O3'	5.99	118.38	105.20
25	RA	1012	U	P-O3'-C3'	5.99	126.89	119.70
25	RA	2430	A	N1-C2-N3	5.99	132.30	129.30
25	RA	2490	G	N3-C4-N9	5.99	129.59	126.00
1	XA	703	G	C4-N9-C1'	5.99	134.28	126.50
25	YA	2518	A	C2-N3-C4	-5.98	107.61	110.60
25	RA	74	A	N1-C6-N6	5.97	122.19	118.60
25	YA	1007	C	O5'-P-OP1	-5.97	100.32	105.70
25	YA	271(B)	G	P-O3'-C3'	5.97	126.87	119.70
25	YA	1559	G	N1-C6-O6	5.97	123.48	119.90
25	YA	177	G	O4'-C1'-N9	5.97	112.98	108.20
25	YA	1332	G	O4'-C1'-N9	-5.97	103.42	108.20
25	RA	2506	U	N3-C2-O2	-5.96	118.03	122.20
25	RA	2556	C	C6-N1-C2	-5.96	117.92	120.30
25	RA	1930	G	C8-N9-C1'	5.96	134.75	127.00
25	YA	1970	A	O5'-P-OP2	-5.96	100.34	105.70
25	RA	2439	A	N7-C8-N9	5.96	116.78	113.80
25	YA	140	A	O4'-C1'-N9	5.96	112.96	108.20
25	YA	1328	G	N3-C4-N9	5.95	129.57	126.00
41	YV	35	LEU	CA-CB-CG	5.95	128.99	115.30
25	YA	2702	U	C6-N1-C1'	-5.93	112.89	121.20
25	YA	74	A	P-O3'-C3'	5.93	126.81	119.70
25	RA	1359	A	C6-C5-N7	-5.92	128.15	132.30
25	YA	930	U	C5-C4-O4	5.92	129.46	125.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	YA	2287	A	N3-C4-C5	5.92	130.95	126.80
25	RA	2392	A	C6-C5-N7	-5.92	128.16	132.30
1	QA	1200	C	P-O3'-C3'	5.91	126.80	119.70
25	RA	1309	G	N1-C6-O6	5.91	123.44	119.90
25	YA	1696	G	C8-N9-C4	-5.91	104.04	106.40
25	YA	2589	A	C8-N9-C4	5.90	108.16	105.80
25	RA	2439	A	P-O3'-C3'	5.89	126.77	119.70
1	XA	328	C	N3-C2-O2	-5.89	117.78	121.90
1	XA	1094	G	OP2-P-O3'	5.89	118.16	105.20
26	YB	31	C	N3-C2-O2	-5.89	117.78	121.90
25	RA	1309	G	C5-C6-O6	-5.89	125.07	128.60
25	RA	2056	G	C4-C5-N7	5.89	113.16	110.80
25	RA	1304	C	N3-C2-O2	-5.89	117.78	121.90
25	YA	97	C	N1-C2-O2	5.88	122.43	118.90
25	YA	1558	A	P-O3'-C3'	5.88	126.76	119.70
1	XA	974	A	O4'-C1'-N9	5.88	112.91	108.20
25	RA	783	A	N1-C6-N6	5.88	122.13	118.60
25	RA	1914	C	C2-N1-C1'	5.88	125.27	118.80
25	YA	575	A	O5'-P-OP1	-5.88	100.41	105.70
25	RA	637	A	P-O3'-C3'	5.87	126.75	119.70
25	RA	1954	G	C8-N9-C4	5.87	108.75	106.40
25	YA	446	G	N9-C4-C5	-5.87	103.05	105.40
25	RA	530	G	N1-C2-N2	-5.87	110.92	116.20
25	YA	930	U	N3-C4-O4	-5.86	115.30	119.40
25	YA	228	A	C8-N9-C4	-5.86	103.45	105.80
25	RA	1632	A	C5-N7-C8	-5.86	100.97	103.90
25	RA	621	A	C2-N3-C4	-5.86	107.67	110.60
25	YA	2050	C	N1-C2-O2	-5.85	115.39	118.90
25	RA	27	G	C4-N9-C1'	-5.85	118.89	126.50
25	RA	1799	G	P-O3'-C3'	5.85	126.72	119.70
25	YA	1698	A	N1-C2-N3	5.85	132.22	129.30
1	QA	789	U	N3-C2-O2	-5.85	118.11	122.20
25	YA	330	A	C4-C5-N7	5.84	113.62	110.70
25	YA	1313	U	C6-N1-C2	-5.84	117.49	121.00
25	RA	27	G	P-O3'-C3'	5.84	126.71	119.70
1	QA	703	G	C8-N9-C4	-5.84	104.06	106.40
25	RA	512	G	O4'-C1'-N9	5.83	112.86	108.20
25	YA	1698	A	O4'-C1'-N9	5.83	112.86	108.20
25	YA	2440	C	O5'-P-OP2	5.83	117.70	110.70
25	YA	2447	G	N9-C4-C5	5.83	107.73	105.40
25	YA	2481	G	OP2-P-O3'	5.83	118.03	105.20
28	RE	63	LEU	CA-CB-CG	5.82	128.68	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	QA	1297	C	C2-N1-C1'	5.82	125.20	118.80
25	YA	2031	A	O4'-C1'-N9	5.82	112.85	108.20
25	YA	372	G	C8-N9-C1'	5.81	134.56	127.00
25	RA	74	A	C5-N7-C8	-5.81	101.00	103.90
25	RA	1950	G	C8-N9-C4	-5.81	104.08	106.40
1	XA	1347	G	C4-N9-C1'	-5.81	118.95	126.50
25	RA	1733	G	N1-C6-O6	5.80	123.38	119.90
1	XA	792	A	C5-N7-C8	-5.80	101.00	103.90
25	YA	27	G	P-O3'-C3'	5.80	126.66	119.70
25	YA	974	G	N9-C4-C5	5.80	107.72	105.40
25	RA	1647	G	O5'-P-OP1	-5.80	100.48	105.70
25	YA	1559	G	C4-C5-N7	5.80	113.12	110.80
25	YA	2439	A	P-O3'-C3'	5.79	126.65	119.70
25	YA	1950	G	N1-C2-N2	-5.79	110.99	116.20
25	RA	2447	G	C5-N7-C8	-5.79	101.41	104.30
25	YA	195	A	C8-N9-C4	-5.79	103.49	105.80
1	QA	243	A	P-O3'-C3'	5.78	126.64	119.70
25	YA	450	G	N1-C6-O6	5.78	123.37	119.90
25	YA	2490	G	C4-N9-C1'	5.78	134.01	126.50
1	QA	1302	U	N1-C2-O2	5.78	126.85	122.80
25	YA	2067	G	C8-N9-C4	-5.78	104.09	106.40
25	RA	270(Z)	U	C2-N1-C1'	-5.78	110.77	117.70
25	RA	1930	G	O4'-C1'-N9	5.78	112.82	108.20
25	YA	1698	A	N7-C8-N9	5.77	116.69	113.80
25	RA	2071	A	C8-N9-C4	-5.77	103.49	105.80
25	RA	2832	U	P-O3'-C3'	5.77	126.62	119.70
25	YA	1899	G	N7-C8-N9	5.77	115.98	113.10
25	YA	1022	G	P-O3'-C3'	5.76	126.61	119.70
1	XA	243	A	P-O3'-C3'	5.76	126.61	119.70
25	YA	982	C	C6-N1-C2	-5.76	118.00	120.30
25	YA	2439	A	C8-N9-C4	-5.75	103.50	105.80
25	RA	746	A	C8-N9-C4	-5.75	103.50	105.80
1	XA	1065	U	OP2-P-O3'	5.75	117.85	105.20
1	XA	687	A	P-O3'-C3'	5.75	126.60	119.70
25	YA	1528	A	O4'-C1'-N9	5.75	112.80	108.20
25	YA	2583	G	C4-C5-N7	-5.74	108.50	110.80
25	YA	783	A	N3-C4-N9	-5.74	122.81	127.40
25	YA	1698	A	C8-N9-C4	-5.74	103.50	105.80
25	YA	2503	A	C2-N3-C4	5.74	113.47	110.60
25	RA	2440	C	C6-N1-C2	5.74	122.59	120.30
25	RA	1021	A	C2-N3-C4	-5.73	107.73	110.60
25	YA	1528	A	C5-N7-C8	-5.73	101.03	103.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	RA	704	G	C8-N9-C4	5.72	108.69	106.40
25	YA	2307	G	C4-N9-C1'	5.72	133.94	126.50
25	YA	2867	G	P-O3'-C3'	5.72	126.56	119.70
36	YQ	82	ARG	N-CA-C	5.72	126.44	111.00
25	RA	1931	U	N1-C2-N3	5.72	118.33	114.90
25	RA	528	A	N3-C4-C5	5.72	130.80	126.80
25	RA	1528	A	O4'-C1'-N9	5.72	112.77	108.20
25	RA	2610	C	P-O3'-C3'	5.72	126.56	119.70
25	YA	444	C	C6-N1-C2	-5.71	118.01	120.30
25	YA	2430	A	N1-C6-N6	5.71	122.03	118.60
1	QA	1301	U	N3-C2-O2	-5.71	118.21	122.20
25	YA	1313	U	C5-C6-N1	5.71	125.55	122.70
25	YA	2712	U	C6-N1-C1'	-5.70	113.22	121.20
25	YA	238	C	C2-N3-C4	-5.70	117.05	119.90
25	YA	752	A	P-O3'-C3'	5.70	126.54	119.70
25	YA	330	A	C5-N7-C8	-5.70	101.05	103.90
1	QA	703	G	C4-N9-C1'	5.69	133.90	126.50
25	RA	1633	G	N9-C4-C5	5.69	107.67	105.40
1	XA	246	A	C8-N9-C4	5.69	108.07	105.80
35	YP	59	LEU	CA-CB-CG	5.69	128.38	115.30
25	RA	1395	A	O4'-C1'-N9	5.68	112.75	108.20
25	YA	1950	G	C8-N9-C1'	-5.68	119.62	127.00
25	YA	195	A	N7-C8-N9	5.67	116.64	113.80
25	RA	1992	G	P-O3'-C3'	5.67	126.51	119.70
25	RA	227	A	N7-C8-N9	5.67	116.64	113.80
1	XA	768	A	C8-N9-C4	5.67	108.07	105.80
1	XA	1302	U	C6-N1-C1'	-5.66	113.27	121.20
25	YA	2335	A	O4'-C1'-N9	5.66	112.73	108.20
25	RA	1411	C	N1-C2-O2	5.66	122.30	118.90
25	YA	573	G	O5'-P-OP2	-5.66	100.61	105.70
26	YB	44	G	C6-C5-N7	5.66	133.80	130.40
25	YA	195	A	P-O3'-C3'	5.66	126.49	119.70
25	RA	1925	C	N1-C2-O2	-5.66	115.51	118.90
1	XA	558	G	N1-C6-O6	5.66	123.29	119.90
25	YA	2028	U	C5-C4-O4	-5.65	122.51	125.90
25	YA	512	G	C8-N9-C1'	5.65	134.35	127.00
25	YA	789	A	N1-C6-N6	-5.65	115.21	118.60
25	YA	1398	C	N3-C4-C5	5.65	124.16	121.90
25	YA	124	G	C5-C6-O6	-5.65	125.21	128.60
25	YA	2468	G	C8-N9-C4	-5.64	104.14	106.40
25	RA	383	U	O4'-C1'-N1	5.64	112.71	108.20
25	YA	1616	A	C8-N9-C4	-5.64	103.55	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	RA	755	C	N3-C4-C5	5.63	124.15	121.90
25	YA	46	C	O5'-P-OP1	-5.63	100.64	105.70
25	YA	2318	G	O4'-C1'-N9	5.63	112.70	108.20
25	RA	1899	G	N3-C4-N9	5.62	129.38	126.00
25	YA	860	U	C2-N1-C1'	5.62	124.45	117.70
1	QA	1397	C	C6-N1-C2	-5.62	118.05	120.30
25	RA	1012	U	OP2-P-O3'	5.62	117.57	105.20
25	RA	2287	A	N3-C4-C5	5.62	130.74	126.80
25	YA	2307	G	C6-C5-N7	-5.62	127.03	130.40
25	YA	2447	G	N7-C8-N9	5.62	115.91	113.10
25	RA	2689	U	P-O3'-C3'	5.62	126.44	119.70
25	YA	676	A	C4-C5-N7	5.61	113.51	110.70
25	RA	1328	G	N9-C4-C5	-5.61	103.16	105.40
25	RA	404	C	P-O3'-C3'	5.61	126.43	119.70
1	XA	328	C	C5-C6-N1	5.61	123.80	121.00
25	YA	783	A	N1-C2-N3	5.61	132.10	129.30
25	RA	1819	A	P-O3'-C3'	5.60	126.42	119.70
1	XA	1347	G	OP2-P-O3'	5.60	117.52	105.20
1	XA	910	C	C6-N1-C2	5.60	122.54	120.30
25	YA	1678	G	C5-C6-O6	-5.59	125.24	128.60
1	XA	1094	G	P-O3'-C3'	5.59	126.41	119.70
25	YA	102	G	P-O3'-C3'	5.59	126.41	119.70
25	RA	2506	U	N1-C2-O2	5.59	126.71	122.80
25	RA	1210	A	C5-N7-C8	-5.59	101.11	103.90
35	YP	25	SER	N-CA-C	-5.59	95.92	111.00
25	YA	930	U	N3-C2-O2	-5.58	118.29	122.20
27	YD	229	VAL	CB-CA-C	-5.58	100.79	111.40
25	RA	1950	G	O4'-C1'-N9	5.58	112.66	108.20
25	RA	227	A	C8-N9-C4	-5.58	103.57	105.80
25	RA	1558	A	P-O3'-C3'	5.58	126.39	119.70
25	RA	613	U	N3-C2-O2	-5.57	118.30	122.20
25	YA	330	A	N1-C6-N6	5.57	121.94	118.60
25	RA	2053	G	C4-N9-C1'	-5.57	119.26	126.50
1	XA	1301	U	C6-N1-C1'	-5.57	113.41	121.20
25	YA	974	G	C8-N9-C1'	5.57	134.24	127.00
25	YA	2071	A	O5'-P-OP2	5.57	117.38	110.70
1	QA	533	A	P-O3'-C3'	5.57	126.38	119.70
25	RA	205	G	O4'-C1'-N9	5.55	112.64	108.20
25	RA	1950	G	N7-C8-N9	5.55	115.88	113.10
25	YA	2496	C	C6-N1-C2	5.55	122.52	120.30
25	RA	676	A	N7-C8-N9	5.55	116.58	113.80
25	YA	1786	A	N9-C1'-C2'	5.54	121.21	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	YA	1799	G	C5-C6-O6	5.54	131.93	128.60
25	RA	372	G	N3-C4-N9	-5.54	122.67	126.00
25	YA	2566	A	P-O3'-C3'	5.54	126.35	119.70
25	YA	1941	C	C6-N1-C2	-5.54	118.08	120.30
25	RA	1899	G	N7-C8-N9	5.54	115.87	113.10
25	YA	1667	G	C8-N9-C4	-5.54	104.19	106.40
26	RB	44	G	C8-N9-C1'	5.54	134.20	127.00
25	YA	1616	A	C4-C5-N7	5.54	113.47	110.70
25	YA	1835	G	N3-C4-N9	5.54	129.32	126.00
25	YA	2713	A	N7-C8-N9	5.54	116.57	113.80
25	YA	945	A	N7-C8-N9	5.53	116.57	113.80
25	YA	1930	G	C4-N9-C1'	-5.53	119.31	126.50
1	XA	1336	C	N3-C2-O2	-5.53	118.03	121.90
1	XA	681	C	N3-C2-O2	-5.53	118.03	121.90
25	YA	1647	G	O4'-C1'-N9	-5.53	103.78	108.20
25	YA	2712(A)	A	C5-N7-C8	-5.53	101.14	103.90
25	RA	2702	U	C5-C6-N1	5.52	125.46	122.70
24	QX	3	G	OP2-P-O3'	5.52	117.35	105.20
25	YA	1142(A)	A	C5-N7-C8	-5.52	101.14	103.90
1	XA	1301	U	C5-C6-N1	5.52	125.46	122.70
25	YA	2318	G	C4-N9-C1'	5.52	133.68	126.50
1	XA	792	A	C3'-C2'-C1'	-5.52	97.09	101.50
1	QA	108	G	C4-N9-C1'	5.51	133.67	126.50
1	XA	1108	G	C5-C6-O6	5.51	131.90	128.60
25	YA	1929	G	C6-C5-N7	-5.51	127.10	130.40
25	YA	2056	G	C5-N7-C8	-5.51	101.55	104.30
25	YA	1698	A	C6-C5-N7	-5.50	128.45	132.30
1	QA	690	G	C5-N7-C8	-5.50	101.55	104.30
1	QA	1336	C	C6-N1-C2	-5.50	118.10	120.30
25	RA	2432	A	N1-C6-N6	5.50	121.90	118.60
25	YA	2688	U	N1-C2-N3	5.50	118.20	114.90
1	XA	345	C	P-O3'-C3'	5.50	126.30	119.70
25	RA	2032	G	C5-N7-C8	-5.50	101.55	104.30
25	YA	38	A	N1-C6-N6	-5.50	115.30	118.60
25	YA	621	A	N1-C2-N3	5.50	132.05	129.30
25	RA	345	A	OP1-P-O3'	5.49	117.28	105.20
25	YA	1191	G	N7-C8-N9	-5.49	110.35	113.10
25	YA	1790	C	C6-N1-C2	5.49	122.50	120.30
1	QA	108	G	O4'-C1'-N9	5.49	112.59	108.20
1	XA	1336	C	C5-C6-N1	5.49	123.74	121.00
25	YA	1565	C	C6-N1-C2	5.49	122.50	120.30
25	YA	1905	C	N1-C2-O2	5.49	122.19	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	RA	1535	U	N1-C2-O2	5.48	126.64	122.80
25	YA	1947	C	N3-C4-C5	5.48	124.09	121.90
25	YA	1969	A	N7-C8-N9	-5.48	111.06	113.80
25	RA	2447	G	OP1-P-OP2	-5.48	111.38	119.60
25	RA	2566	A	P-O3'-C3'	5.48	126.27	119.70
1	XA	1446	A	P-O3'-C3'	5.48	126.27	119.70
25	YA	214	G	O4'-C1'-N9	5.48	112.58	108.20
25	YA	1419	A	O4'-C1'-N9	5.47	112.58	108.20
25	RA	503	A	C8-N9-C4	-5.47	103.61	105.80
25	RA	1190	G	C5-N7-C8	-5.47	101.56	104.30
28	RE	27	LEU	CA-CB-CG	5.47	127.88	115.30
25	YA	2506	U	C2-N1-C1'	5.47	124.26	117.70
1	QA	1322	C	C5-C6-N1	5.46	123.73	121.00
25	RA	234	C	N1-C2-O2	5.46	122.18	118.90
26	YB	44	G	C8-N9-C1'	5.46	134.10	127.00
25	RA	794	G	C5-C6-O6	5.46	131.88	128.60
25	RA	1936	A	O4'-C1'-N9	5.46	112.57	108.20
25	YA	2655	G	P-O3'-C3'	5.46	126.25	119.70
25	RA	1204	A	N1-C2-N3	5.46	132.03	129.30
35	RP	88	LEU	CA-CB-CG	5.46	127.85	115.30
25	YA	222	A	P-O3'-C3'	5.46	126.25	119.70
25	YA	1395	A	O4'-C1'-N9	5.45	112.56	108.20
25	YA	1786	A	N1-C6-N6	5.45	121.87	118.60
25	RA	214	G	O4'-C1'-N9	5.45	112.56	108.20
25	YA	831	G	N1-C6-O6	5.45	123.17	119.90
25	YA	1674	G	C5-C6-O6	-5.45	125.33	128.60
25	YA	2254	C	N1-C2-O2	-5.45	115.63	118.90
25	YA	2463	C	N3-C4-C5	5.45	124.08	121.90
25	RA	1781	C	C6-N1-C2	-5.45	118.12	120.30
25	YA	1774	C	N3-C4-C5	5.45	124.08	121.90
25	YA	2720	U	O5'-P-OP1	-5.45	100.80	105.70
25	YA	196	A	O4'-C1'-N9	5.45	112.56	108.20
25	YA	2468	G	N7-C8-N9	5.45	115.82	113.10
25	YA	958	U	C6-N1-C2	-5.44	117.73	121.00
25	YA	865	C	O5'-P-OP1	-5.44	100.80	105.70
25	YA	238	C	C6-N1-C2	5.44	122.48	120.30
25	YA	383	U	O4'-C1'-N1	5.44	112.55	108.20
1	XA	1370	G	N1-C6-O6	5.44	123.16	119.90
1	QA	1347	G	P-O3'-C3'	5.44	126.22	119.70
25	YA	2031	A	C4-N9-C1'	5.43	136.08	126.30
25	YA	97	C	N3-C2-O2	-5.43	118.10	121.90
25	RA	1558	A	N1-C2-N3	5.43	132.01	129.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	YA	250	G	C4-C5-N7	5.43	112.97	110.80
1	QA	754	C	C2-N1-C1'	5.43	124.77	118.80
25	RA	1899	G	C4-N9-C1'	5.43	133.56	126.50
1	XA	435	C	C6-N1-C2	-5.43	118.13	120.30
1	XA	1336	C	C6-N1-C1'	-5.42	114.29	120.80
25	YA	2031	A	C8-N9-C1'	-5.42	117.94	127.70
25	YA	2692	C	N3-C2-O2	-5.42	118.10	121.90
25	RA	1241	A	C2-N3-C4	-5.42	107.89	110.60
25	YA	841	A	N1-C6-N6	5.42	121.85	118.60
25	YA	1309	G	N1-C6-O6	5.42	123.15	119.90
25	YA	2468	G	C4-N9-C1'	5.42	133.55	126.50
1	QA	1158	C	C6-N1-C1'	-5.42	114.30	120.80
25	YA	1570	A	C8-N9-C4	5.41	107.97	105.80
25	YA	762	U	C2-N1-C1'	5.41	124.19	117.70
1	QA	252	U	N3-C2-O2	-5.41	118.41	122.20
25	YA	1930	G	C6-C5-N7	5.41	133.65	130.40
1	XA	1053	G	C8-N9-C4	5.41	108.56	106.40
26	YB	30	C	N3-C2-O2	-5.41	118.11	121.90
1	QA	1053	G	O4'-C1'-N9	5.41	112.53	108.20
25	RA	530	G	N1-C6-O6	-5.40	116.66	119.90
25	RA	1535	U	C2-N1-C1'	5.40	124.19	117.70
25	RA	1902	C	N3-C4-C5	5.40	124.06	121.90
26	RB	66	A	P-O3'-C3'	5.40	126.18	119.70
25	YA	58	G	C8-N9-C4	-5.40	104.24	106.40
25	YA	1359	A	N9-C4-C5	-5.40	103.64	105.80
25	YA	2318	G	N7-C8-N9	5.40	115.80	113.10
1	XA	1496	C	C6-N1-C2	5.39	122.46	120.30
25	YA	27	G	N3-C2-N2	-5.39	116.12	119.90
25	RA	1698	A	C4-C5-N7	5.39	113.40	110.70
25	YA	2713	A	C6-C5-N7	-5.39	128.53	132.30
25	YA	512	G	C4-N9-C1'	-5.39	119.50	126.50
25	YA	974(A)	C	P-O3'-C3'	5.39	126.17	119.70
25	RA	2490	G	N3-C2-N2	5.39	123.67	119.90
25	RA	270(Z)	U	C5-C6-N1	-5.38	120.01	122.70
25	YA	1929	G	N9-C4-C5	-5.38	103.25	105.40
25	YA	2070	G	C5-C6-O6	5.38	131.83	128.60
25	YA	1950	G	C5-N7-C8	-5.38	101.61	104.30
25	RA	1899	G	C5-C6-O6	5.38	131.83	128.60
25	YA	242	G	OP2-P-O3'	5.38	117.03	105.20
25	YA	2609	U	C2-N1-C1'	-5.38	111.25	117.70
25	RA	49	A	C4-C5-C6	5.37	119.69	117.00
45	YZ	115	GLY	N-CA-C	-5.37	99.67	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	RA	2763	G	N3-C4-C5	-5.37	125.91	128.60
25	YA	974(A)	C	C5-C4-N4	5.37	123.96	120.20
25	YA	1396	U	C2-N1-C1'	5.37	124.15	117.70
25	YA	1603	A	C8-N9-C4	-5.37	103.65	105.80
25	RA	141	A	C2-N3-C4	-5.37	107.92	110.60
25	RA	2053	G	C5-C6-N1	5.37	114.18	111.50
1	XA	701	C	P-O3'-C3'	5.37	126.14	119.70
1	XA	518	C	N1-C2-N3	5.36	122.95	119.20
1	XA	1517	G	O5'-P-OP2	-5.36	100.88	105.70
25	RA	805	G	C5-C6-O6	-5.36	125.39	128.60
25	RA	2278	A	O4'-C1'-N9	5.36	112.49	108.20
25	YA	2346	A	N1-C2-N3	5.36	131.98	129.30
1	QA	701	C	P-O3'-C3'	5.35	126.12	119.70
25	YA	2446	G	OP2-P-O3'	5.35	116.97	105.20
25	YA	626	U	C6-N1-C2	-5.35	117.79	121.00
25	YA	773	U	C5-C6-N1	-5.35	120.03	122.70
25	YA	2045	C	C6-N1-C2	5.35	122.44	120.30
1	QA	299	G	C5-C6-N1	-5.35	108.83	111.50
25	RA	1210	A	N7-C8-N9	5.35	116.47	113.80
25	RA	2713	A	C5-N7-C8	-5.35	101.23	103.90
1	XA	115	G	N3-C4-C5	-5.35	125.93	128.60
25	YA	2587	A	N9-C4-C5	5.34	107.94	105.80
1	XA	1108	G	C4-C5-N7	-5.33	108.67	110.80
25	YA	364	C	C6-N1-C2	-5.33	118.17	120.30
25	YA	2445	G	C5-C6-O6	5.33	131.80	128.60
25	YA	1309	G	C8-N9-C4	5.32	108.53	106.40
25	YA	846	C	C2-N1-C1'	5.32	124.65	118.80
25	YA	1559	G	C5-C6-O6	-5.32	125.41	128.60
1	XA	703	G	P-O3'-C3'	5.32	126.08	119.70
1	QA	1301	U	C6-N1-C1'	-5.32	113.76	121.20
25	RA	227	A	P-O3'-C3'	5.32	126.08	119.70
25	RA	675	A	N1-C6-N6	5.32	121.79	118.60
25	YA	1191	G	C8-N9-C4	5.32	108.53	106.40
25	RA	1698	A	N1-C2-N3	5.31	131.96	129.30
1	QA	1346	A	P-O3'-C3'	5.31	126.08	119.70
25	RA	2712	U	C2-N1-C1'	5.31	124.07	117.70
25	YA	270(Z)	U	O4'-C1'-N1	5.31	112.45	108.20
25	YA	1970	A	O4'-C1'-N9	-5.31	103.95	108.20
25	RA	2438	U	O5'-P-OP2	-5.31	100.92	105.70
25	YA	458	G	O4'-C1'-N9	5.30	112.44	108.20
25	YA	514	A	C8-N9-C4	5.30	107.92	105.80
25	YA	2501	C	C2-N1-C1'	-5.30	112.97	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	YB	41	U	C5-C6-N1	-5.30	120.05	122.70
25	RA	1241	A	O4'-C1'-N9	5.30	112.44	108.20
25	YA	213	A	OP2-P-O3'	5.30	116.86	105.20
1	XA	1502	A	C5-N7-C8	-5.30	101.25	103.90
25	RA	799	G	C5-C6-O6	-5.30	125.42	128.60
1	QA	108	G	C4-C5-N7	5.29	112.92	110.80
25	YA	795	C	C2-N3-C4	-5.29	117.26	119.90
25	RA	621	A	O4'-C1'-N9	5.29	112.43	108.20
25	RA	760	G	C4-C5-N7	-5.29	108.69	110.80
25	YA	1781	C	C6-N1-C1'	-5.28	114.46	120.80
25	RA	1992	G	C2-N3-C4	5.28	114.54	111.90
25	YA	670	A	OP1-P-O3'	5.28	116.82	105.20
25	YA	1396	U	C5-C4-O4	5.28	129.07	125.90
25	YA	141	A	O4'-C1'-N9	5.28	112.42	108.20
1	QA	1302	U	N3-C2-O2	-5.28	118.51	122.20
25	RA	1647	G	O4'-C1'-N9	-5.28	103.98	108.20
25	YA	776	G	C6-C5-N7	5.28	133.56	130.40
25	YA	793	A	C8-N9-C4	-5.28	103.69	105.80
18	QR	31	LEU	CA-CB-CG	5.27	127.43	115.30
1	XA	1222	G	N3-C2-N2	-5.27	116.21	119.90
25	YA	621	A	C8-N9-C4	-5.27	103.69	105.80
25	YA	2406	U	O4'-C1'-N1	-5.27	103.98	108.20
25	YA	2610	C	OP2-P-O3'	5.27	116.79	105.20
1	XA	266	G	P-O3'-C3'	5.26	126.01	119.70
1	XA	792	A	C6-C5-N7	-5.26	128.62	132.30
25	YA	99	U	OP2-P-O3'	5.26	116.78	105.20
25	YA	812	C	N1-C2-O2	-5.26	115.74	118.90
51	Y5	4	HIS	C-N-CD	5.26	139.44	128.40
25	YA	2822	G	C5-C6-O6	-5.26	125.44	128.60
1	QA	1054	C	C2-N1-C1'	5.26	124.58	118.80
25	RA	141	A	N7-C8-N9	5.25	116.43	113.80
25	RA	1312	U	P-O3'-C3'	5.25	126.01	119.70
25	RA	1659	U	N1-C2-O2	-5.25	119.12	122.80
25	YA	1359	A	C4-C5-N7	5.25	113.33	110.70
25	YA	2265	U	C5-C4-O4	-5.25	122.75	125.90
25	RA	1632	A	C4-C5-N7	5.25	113.33	110.70
1	XA	792	A	N9-C1'-C2'	5.25	120.83	114.00
1	XA	723	U	N1-C2-O2	5.25	126.47	122.80
25	YA	739	G	C8-N9-C4	5.25	108.50	106.40
25	RA	2726	U	C6-N1-C1'	-5.25	113.85	121.20
25	YA	1786	A	C4-N9-C1'	5.25	135.74	126.30
25	YA	67	U	C2-N3-C4	5.25	130.15	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	YA	917	A	C2-N3-C4	-5.25	107.98	110.60
25	YA	2600	A	O5'-P-OP2	-5.25	100.98	105.70
25	YA	2544	G	C5-C6-N1	-5.24	108.88	111.50
25	RA	346	A	O5'-P-OP2	-5.24	100.98	105.70
25	RA	2688	U	N1-C2-O2	5.24	126.47	122.80
1	XA	1498	U	P-O3'-C3'	5.24	125.99	119.70
25	YA	140	A	C4-C5-N7	5.24	113.32	110.70
1	XA	328	C	P-O3'-C3'	5.23	125.98	119.70
25	RA	2717	G	N3-C4-C5	-5.23	125.98	128.60
1	XA	681	C	C6-N1-C2	-5.23	118.21	120.30
1	QA	1297	C	OP2-P-O3'	5.23	116.70	105.20
25	YA	2655	G	C4-N9-C1'	-5.23	119.70	126.50
25	YA	2330	G	C5-C6-O6	-5.22	125.47	128.60
26	YB	108	C	C6-N1-C1'	5.22	127.07	120.80
25	RA	2021	C	C6-N1-C2	-5.22	118.21	120.30
25	RA	1379	A	O4'-C1'-N9	5.22	112.38	108.20
1	XA	888	G	C5-C6-O6	-5.22	125.47	128.60
1	QA	690	G	O4'-C1'-N9	5.22	112.37	108.20
25	RA	1301	A	O5'-P-OP1	-5.21	101.01	105.70
25	RA	2867	G	P-O3'-C3'	5.21	125.96	119.70
1	QA	753	A	P-O3'-C3'	5.21	125.95	119.70
25	RA	974	G	C8-N9-C4	-5.21	104.32	106.40
25	YA	1647	G	O5'-P-OP2	5.21	116.95	110.70
25	RA	1954	G	N7-C8-N9	-5.20	110.50	113.10
19	XS	41	VAL	C-N-CD	-5.20	109.15	120.60
25	YA	46	C	C6-N1-C2	-5.20	118.22	120.30
25	RA	1210	A	N1-C6-N6	5.20	121.72	118.60
26	YB	31	C	N3-C4-C5	-5.20	119.82	121.90
25	YA	1190	G	C4-C5-N7	5.20	112.88	110.80
25	YA	2392	A	C5-N7-C8	-5.20	101.30	103.90
25	YA	1799	G	N1-C6-O6	-5.19	116.78	119.90
34	RO	8	LEU	CA-CB-CG	5.19	127.24	115.30
1	QA	1053	G	C4-N9-C1'	-5.19	119.75	126.50
22	QV	16	C	N3-C2-O2	-5.19	118.27	121.90
25	RA	270(Z)	U	O4'-C1'-N1	5.19	112.35	108.20
25	YA	481	G	O5'-P-OP2	-5.19	101.03	105.70
25	RA	1779	U	O4'-C1'-N1	5.19	112.35	108.20
1	XA	108	G	N9-C4-C5	-5.18	103.33	105.40
25	YA	1142(A)	A	N3-C4-N9	-5.18	123.25	127.40
25	YA	2427	C	O5'-P-OP1	-5.18	101.03	105.70
1	QA	498	A	O4'-C1'-N9	5.18	112.34	108.20
22	QV	16	C	C6-N1-C1'	-5.18	114.58	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	RA	1496	A	C5-N7-C8	-5.18	101.31	103.90
1	XA	690	G	N3-C2-N2	-5.18	116.27	119.90
25	RA	1807	G	N3-C4-C5	5.18	131.19	128.60
25	YA	1914	C	C2-N1-C1'	5.18	124.50	118.80
25	YA	2498	C	N3-C4-C5	5.18	123.97	121.90
25	RA	83	G	P-O3'-C3'	5.17	125.91	119.70
25	YA	2307	G	C4-C5-N7	5.17	112.87	110.80
25	YA	805	G	C5-C6-O6	-5.17	125.50	128.60
1	XA	1506	U	N1-C2-O2	-5.17	119.18	122.80
25	RA	1411	C	C2-N1-C1'	5.17	124.49	118.80
25	YA	1882	C	C2-N1-C1'	5.17	124.49	118.80
1	XA	1347	G	O4'-C1'-N9	5.17	112.33	108.20
25	YA	1012	U	P-O3'-C3'	5.16	125.89	119.70
25	YA	2469	A	C2-N3-C4	-5.16	108.02	110.60
1	XA	318	G	N1-C6-O6	5.16	123.00	119.90
25	RA	1496	A	C8-N9-C4	-5.16	103.74	105.80
25	YA	1023	U	O5'-P-OP1	-5.16	101.06	105.70
25	YA	1256	G	N9-C4-C5	-5.16	103.34	105.40
1	XA	858	G	N7-C8-N9	5.16	115.68	113.10
1	XA	1285	A	P-O3'-C3'	5.16	125.89	119.70
25	YA	2584	U	N1-C2-N3	5.16	118.00	114.90
25	YA	138	G	O4'-C1'-N9	5.15	112.32	108.20
25	YA	395	U	O4'-C1'-N1	5.15	112.32	108.20
25	YA	2126	A	P-O3'-C3'	5.15	125.88	119.70
25	YA	364	C	C5-C6-N1	5.15	123.58	121.00
1	QA	1201	A	P-O3'-C3'	5.15	125.88	119.70
1	XA	1346	A	P-O3'-C3'	5.15	125.88	119.70
25	RA	2063	C	O5'-P-OP2	-5.14	101.07	105.70
22	XV	16	C	C6-N1-C2	-5.14	118.24	120.30
25	YA	1899	G	C4-C5-C6	5.14	121.89	118.80
25	YA	2330	G	C4-C5-N7	5.14	112.86	110.80
25	YA	74	A	C5-C6-N1	-5.14	115.13	117.70
25	YA	1800	C	O5'-P-OP2	5.14	116.86	110.70
25	RA	729	G	N1-C6-O6	5.14	122.98	119.90
25	YA	2023	G	O5'-P-OP1	-5.13	101.08	105.70
25	YA	2584	U	C6-N1-C2	-5.13	117.92	121.00
25	YA	1328	G	N9-C4-C5	-5.13	103.35	105.40
25	RA	2430	A	N3-C4-C5	5.13	130.39	126.80
25	YA	676	A	C5-C6-N1	-5.13	115.14	117.70
1	QA	1285	A	P-O3'-C3'	5.12	125.85	119.70
1	XA	690	G	C2-N3-C4	-5.12	109.34	111.90
25	YA	2430	A	C6-C5-N7	-5.12	128.71	132.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	QD	28	SER	C-N-CD	5.12	139.15	128.40
41	RV	35	LEU	CA-CB-CG	5.12	127.06	115.30
1	XA	812	C	OP2-P-O3'	5.12	116.45	105.20
25	RA	1616	A	C4-C5-N7	5.11	113.26	110.70
25	YA	1300	U	N1-C2-N3	5.11	117.97	114.90
26	YB	81	G	N7-C8-N9	5.11	115.66	113.10
25	YA	1683	C	C6-N1-C2	-5.11	118.25	120.30
25	RA	685	A	N1-C6-N6	-5.11	115.53	118.60
25	YA	1835	G	C4-N9-C1'	5.11	133.14	126.50
26	YB	31	C	N1-C2-O2	5.11	121.96	118.90
25	YA	577	G	C6-C5-N7	-5.10	127.34	130.40
25	YA	1930	G	OP2-P-O3'	5.10	116.43	105.20
1	QA	337	C	C6-N1-C2	-5.10	118.26	120.30
25	RA	2779	U	O4'-C1'-N1	5.10	112.28	108.20
25	YA	783	A	N9-C1'-C2'	-5.10	106.39	112.00
25	YA	1929	G	O4'-C1'-N9	-5.10	104.12	108.20
25	YA	2402	C	O4'-C1'-N1	5.10	112.28	108.20
1	XA	1502	A	C2-N3-C4	-5.10	108.05	110.60
25	YA	810	U	O5'-P-OP2	-5.10	101.11	105.70
25	YA	1905	C	N3-C2-O2	-5.10	118.33	121.90
1	QA	1504	G	O5'-P-OP1	-5.09	101.12	105.70
25	RA	140	A	C5-N7-C8	-5.09	101.36	103.90
25	RA	2763	G	N3-C4-N9	5.09	129.06	126.00
1	XA	1027	C	OP1-P-O3'	5.09	116.40	105.20
22	XV	16	C	N3-C2-O2	-5.09	118.34	121.90
25	YA	404	C	P-O3'-C3'	5.09	125.81	119.70
25	RA	1359	A	C8-N9-C4	5.09	107.84	105.80
25	RA	2311	A	C2-N3-C4	-5.09	108.06	110.60
25	RA	1535	U	N3-C2-O2	-5.09	118.64	122.20
1	XA	890	G	O4'-C1'-N9	5.09	112.27	108.20
25	YA	2681	C	C6-N1-C2	-5.09	118.27	120.30
1	QA	1027	C	P-O3'-C3'	5.08	125.80	119.70
1	QA	690	G	N7-C8-N9	5.08	115.64	113.10
25	YA	528	A	C5-N7-C8	-5.08	101.36	103.90
25	RA	2518	A	N3-C4-C5	5.08	130.35	126.80
25	RA	1558	A	C2-N3-C4	-5.08	108.06	110.60
25	YA	503	A	C8-N9-C4	-5.08	103.77	105.80
25	YA	2619	C	O5'-P-OP2	-5.07	101.13	105.70
26	YB	56	G	C8-N9-C4	-5.07	104.37	106.40
1	QA	1347	G	OP2-P-O3'	5.07	116.36	105.20
25	YA	2318	G	C4-C5-N7	5.07	112.83	110.80
25	YA	2688	U	N3-C4-C5	-5.07	111.56	114.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	QA	117	G	N9-C4-C5	-5.07	103.37	105.40
25	RA	856	C	C6-N1-C2	-5.07	118.27	120.30
25	RA	791	C	C2-N1-C1'	-5.07	113.22	118.80
25	YA	27	G	C8-N9-C1'	5.07	133.59	127.00
25	YA	2250	G	N3-C4-C5	-5.07	126.07	128.60
25	RA	205	G	P-O3'-C3'	5.07	125.78	119.70
25	RA	619	G	N1-C6-O6	-5.07	116.86	119.90
25	RA	2026	C	C6-N1-C2	5.07	122.33	120.30
25	RA	1505	C	N1-C2-O2	5.06	121.94	118.90
25	RA	859	G	P-O3'-C3'	5.06	125.77	119.70
1	XA	1498	U	N3-C2-O2	-5.06	118.66	122.20
25	YA	795	C	C5-C6-N1	-5.06	118.47	121.00
26	YB	43	C	C2-N1-C1'	5.06	124.36	118.80
25	YA	62	C	C6-N1-C2	5.05	122.32	120.30
25	YA	71	A	N3-C4-N9	-5.05	123.36	127.40
25	YA	2246	G	C8-N9-C4	5.05	108.42	106.40
25	YA	2611	U	O5'-P-OP2	-5.05	101.15	105.70
25	YA	2751	G	C5-N7-C8	-5.05	101.77	104.30
1	QA	266	G	P-O3'-C3'	5.05	125.76	119.70
1	XA	1054	C	P-O3'-C3'	5.05	125.76	119.70
25	YA	812	C	N3-C4-C5	-5.05	119.88	121.90
25	YA	1698	A	C4-C5-N7	5.05	113.23	110.70
28	YE	117	MET	CA-CB-CG	5.05	121.89	113.30
25	RA	2500	U	N3-C2-O2	-5.05	118.67	122.20
1	XA	542	G	O5'-P-OP1	-5.05	101.16	105.70
1	XA	971	G	O4'-C1'-N9	5.05	112.24	108.20
25	YA	2655	G	OP2-P-O3'	5.05	116.31	105.20
25	RA	783	A	N3-C4-C5	5.05	130.33	126.80
25	RA	1781	C	N3-C2-O2	-5.05	118.37	121.90
25	YA	1839	G	C8-N9-C1'	-5.05	120.44	127.00
25	RA	271(B)	G	N3-C4-C5	-5.04	126.08	128.60
25	RA	2307	G	C4-C5-N7	5.04	112.82	110.80
25	YA	2523	G	C8-N9-C4	-5.04	104.38	106.40
1	XA	410	G	OP1-P-O3'	5.04	116.29	105.20
1	QA	893	C	N1-C2-O2	5.04	121.92	118.90
25	RA	825	C	OP1-P-O3'	5.04	116.29	105.20
1	XA	330	C	N1-C2-O2	5.04	121.92	118.90
25	YA	740	U	N3-C4-C5	5.04	117.62	114.60
25	YA	1781	C	O4'-C1'-N1	5.04	112.23	108.20
25	RA	1260	G	C8-N9-C4	5.04	108.42	106.40
25	YA	1253	A	C5-N7-C8	-5.04	101.38	103.90
25	RA	1678	G	C5-N7-C8	-5.03	101.78	104.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	RA	1599	C	N3-C2-O2	-5.03	118.38	121.90
25	YA	2776	A	P-O3'-C3'	5.03	125.74	119.70
25	YA	1535	U	C2-N1-C1'	5.03	123.73	117.70
25	YA	530	G	C5-C6-N1	5.03	114.01	111.50
25	RA	783	A	N1-C2-N3	5.02	131.81	129.30
25	RA	783	A	C6-C5-N7	-5.02	128.78	132.30
1	XA	960	U	C2-N1-C1'	5.02	123.73	117.70
1	QA	328	C	C6-N1-C1'	-5.02	114.77	120.80
25	YA	472	A	C5-C6-N1	-5.02	115.19	117.70
25	RA	826	U	N1-C2-N3	5.02	117.91	114.90
25	RA	979	G	N7-C8-N9	5.02	115.61	113.10
25	RA	2126	A	P-O3'-C3'	5.02	125.72	119.70
36	RQ	82	ARG	N-CA-C	5.02	124.55	111.00
1	QA	992	U	P-O3'-C3'	5.02	125.72	119.70
25	RA	1988	C	C5-C4-N4	-5.02	116.69	120.20
25	YA	1799	G	C8-N9-C4	-5.02	104.39	106.40
26	RB	81	G	C8-N9-C4	-5.01	104.39	106.40
25	YA	781	A	C8-N9-C4	5.01	107.81	105.80
45	YZ	150	LEU	CA-CB-CG	5.01	126.83	115.30
25	YA	1382	G	C5-C6-O6	-5.01	125.59	128.60
26	RB	44	G	N3-C4-N9	-5.01	123.00	126.00
1	XA	481	G	P-O3'-C3'	5.01	125.71	119.70
1	XA	1347	G	C8-N9-C1'	5.01	133.51	127.00
25	YA	2444	G	O5'-P-OP2	-5.00	101.20	105.70
26	YB	81	G	C5-N7-C8	-5.00	101.80	104.30

There are no chirality outliers.

All (16) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	QL	47	LYS	Peptide
54	R8	30	ARG	Peptide
54	R8	35	GLN	Peptide
28	RE	21	VAL	Peptide
31	RH	127	GLU	Peptide
31	RH	153	LYS	Peptide
12	XL	47	LYS	Peptide
48	Y2	17	SER	Peptide
54	Y8	30	ARG	Peptide
54	Y8	51	ALA	Peptide
28	YE	21	VAL	Peptide
29	YF	47	GLY	Peptide

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Mol	Chain	Res	Type	Group
31	YH	127	GLU	Peptide
31	YH	153	LYS	Peptide
38	YS	109	GLY	Peptide
45	YZ	181	GLU	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	QA	32247	0	16278	492	0
1	XA	32249	0	16279	529	1
2	QB	1924	0	1975	64	0
2	XB	1924	0	1975	80	0
3	QC	1605	0	1668	41	0
3	XC	1605	0	1668	63	0
4	QD	1703	0	1763	63	0
4	XD	1703	0	1764	47	0
5	QE	1155	0	1213	28	0
5	XE	1155	0	1213	42	0
6	QF	843	0	857	20	0
6	XF	843	0	857	23	0
7	QG	1257	0	1296	37	0
7	XG	1257	0	1296	24	0
8	QH	1116	0	1175	37	0
8	XH	1116	0	1177	25	0
9	QI	1010	0	1037	34	0
9	XI	1010	0	1037	50	0
10	QJ	801	0	849	48	0
10	XJ	801	0	849	42	0
11	QK	885	0	904	25	0
11	XK	885	0	904	28	0
12	QL	975	0	1062	35	0
12	XL	975	0	1062	46	0
13	QM	964	0	1034	40	0
13	XM	964	0	1034	39	0
14	QN	492	0	529	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	XN	492	0	529	17	0
15	QO	734	0	771	21	0
15	XO	734	0	771	19	0
16	QP	705	0	725	18	0
16	XP	705	0	725	26	0
17	QQ	834	0	904	19	0
17	XQ	834	0	904	19	0
18	QR	574	0	644	11	0
18	XR	574	0	644	21	0
19	QS	674	0	699	40	0
19	XS	674	0	699	44	0
20	QT	763	0	860	26	0
20	XT	763	0	861	36	0
21	QU	217	0	234	11	0
21	XU	217	0	234	4	0
22	QV	1644	0	836	26	0
22	XV	1644	0	836	18	0
23	QY	323	0	165	3	0
23	XY	323	0	165	4	0
24	QX	167	0	87	0	0
24	XX	167	0	87	0	0
25	RA	62071	0	31288	921	1
25	YA	62091	0	31295	872	0
26	RB	2573	0	1306	40	1
26	YB	2573	0	1306	32	0
27	RD	2115	0	2195	96	0
27	YD	2115	0	2195	97	0
28	RE	1568	0	1634	72	0
28	YE	1568	0	1634	64	0
29	RF	1585	0	1632	80	0
29	YF	1585	0	1632	64	0
30	RG	1474	0	1535	54	0
30	YG	1474	0	1535	57	0
31	RH	1307	0	1382	61	0
31	YH	1307	0	1382	66	0
32	RI	1136	0	1223	59	1
32	YI	1136	0	1223	49	0
33	RN	1104	0	1180	40	0
33	YN	1104	0	1180	50	0
34	RO	933	0	996	26	0
34	YO	933	0	996	25	0
35	RP	1145	0	1227	87	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	YP	1145	0	1227	94	0
36	RQ	1122	0	1179	61	0
36	YQ	1122	0	1178	48	0
37	RR	968	0	1033	48	0
37	YR	968	0	1033	36	0
38	RS	882	0	943	48	0
38	YS	882	0	943	40	0
39	RT	1141	0	1202	53	0
39	YT	1141	0	1202	50	0
40	RU	964	0	1022	30	0
40	YU	964	0	1022	58	0
41	RV	779	0	852	20	0
41	YV	779	0	852	42	0
42	RW	900	0	964	27	0
42	YW	900	0	964	28	0
43	RX	725	0	778	28	0
43	YX	725	0	778	25	0
44	RY	785	0	878	52	0
44	YY	785	0	878	39	0
45	RZ	1461	0	1493	59	0
45	YZ	1461	0	1493	56	0
46	R0	648	0	672	20	0
46	Y0	648	0	672	27	0
47	R1	763	0	848	26	0
47	Y1	763	0	848	28	0
48	R2	581	0	629	19	0
48	Y2	581	0	629	26	0
49	R3	469	0	518	7	0
49	Y3	469	0	518	17	0
50	R4	581	0	574	25	0
50	Y4	581	0	574	45	0
51	R5	459	0	480	25	0
51	Y5	459	0	480	33	0
52	R6	424	0	450	27	0
52	Y6	424	0	450	30	0
53	R7	430	0	480	14	0
53	Y7	430	0	480	17	0
54	R8	517	0	582	30	0
54	Y8	517	0	582	40	0
55	R9	307	0	338	9	0
55	Y9	307	0	338	7	0
56	Z6	74	0	51	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	Z8	74	0	51	5	0
57	QA	65	0	0	0	0
57	QF	1	0	0	0	0
57	QH	1	0	0	0	0
57	QM	1	0	0	0	0
57	QV	1	0	0	0	0
57	QX	1	0	0	0	0
57	R0	1	0	0	0	0
57	R5	1	0	0	0	0
57	R8	1	0	0	0	0
57	RA	242	0	0	0	0
57	RB	2	0	0	0	0
57	RD	1	0	0	0	0
57	RE	2	0	0	0	0
57	RF	1	0	0	0	0
57	RP	2	0	0	0	0
57	RR	1	0	0	0	0
57	RU	1	0	0	0	0
57	XA	72	0	0	0	0
57	XM	1	0	0	0	0
57	XV	1	0	0	0	0
57	XX	1	0	0	0	0
57	Y5	1	0	0	0	0
57	YA	268	0	0	0	0
57	YB	3	0	0	0	0
57	YE	1	0	0	0	0
57	YP	2	0	0	0	0
57	YQ	1	0	0	0	0
57	YX	1	0	0	0	0
58	QA	42	0	45	2	0
58	XA	42	0	45	1	0
59	QD	1	0	0	0	0
59	QN	1	0	0	0	0
59	XD	1	0	0	0	0
59	XN	1	0	0	0	0
All	All	291993	0	198359	5830	2

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 12.

All (5830) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:QD:22:LYS:HG3	4:QD:26:CYS:SG	1.85	1.16
25:RA:2701:C:H3'	25:RA:2702:U:H5''	1.30	1.13
25:YA:2701:C:H3'	25:YA:2702:U:H5''	1.32	1.07
25:RA:1359:A:N6	25:RA:1372:U:O4	1.87	1.07
27:YD:43:ARG:NH1	27:YD:44:ASN:OD1	1.86	1.06
25:YA:1359:A:N6	25:YA:1372:U:O4	1.92	1.02
25:RA:1310:G:OP2	53:R7:9:ARG:NH1	1.94	0.99
25:YA:1771:C:HO2'	25:YA:1786:A:H8	1.01	0.98
1:XA:963:G:N3	10:XJ:55:LYS:NZ	2.11	0.97
25:YA:1496:A:H8	25:YA:1577:C:HO2'	1.10	0.97
4:QD:9:CYS:SG	4:QD:22:LYS:CE	2.52	0.97
25:RA:2298:A:H62	25:RA:2318:G:H8	1.14	0.95
4:QD:9:CYS:SG	4:QD:22:LYS:HE3	2.07	0.95
25:YA:1138:G:H21	33:YN:106:MET:HE3	1.30	0.95
2:QB:185:ILE:HG22	2:QB:199:TYR:HB2	1.48	0.93
25:YA:483:A:H4'	44:YY:49:VAL:HA	1.51	0.92
25:YA:774:A:H2	25:YA:787:U:HO2'	1.00	0.92
1:QA:559:A:H4'	1:QA:560:U:H3'	1.50	0.92
25:YA:620:G:H4'	25:YA:621:A:H5''	1.50	0.92
25:RA:1138:G:H21	33:RN:106:MET:HE3	1.31	0.92
35:RP:58:THR:O	35:RP:61:ARG:NE	2.03	0.92
25:RA:1689:A:H62	25:RA:1698:A:H2	1.18	0.91
1:QA:963:G:N3	10:QJ:55:LYS:NZ	2.18	0.91
25:YA:1728:G:H8	25:YA:1732:A:H62	1.15	0.91
25:YA:67:U:H3	25:YA:74:A:H2	1.11	0.91
28:YE:24:THR:HG21	28:YE:188:VAL:HG11	1.52	0.91
45:YZ:151:HIS:HB3	45:YZ:170:THR:HA	1.54	0.89
28:YE:50:GLY:HA2	28:YE:77:ILE:HA	1.53	0.89
51:R5:55:ARG:HG3	51:R5:57:VAL:H	1.37	0.89
25:RA:1403:C:H5''	25:RA:1471:A:H1'	1.55	0.89
44:YY:79:CYS:SG	44:YY:80:GLY:N	2.45	0.88
39:RT:26:ASP:HB3	39:RT:92:GLY:H	1.36	0.88
25:YA:1021:A:OP2	33:YN:65:LYS:NZ	2.06	0.88
25:RA:2580:U:H4'	28:RE:130:GLY:HA3	1.56	0.88
25:YA:2451:A:C6	56:Z8:76:PPU:HE2	2.09	0.87
35:RP:64:LYS:O	35:RP:66:GLY:N	2.07	0.87
1:XA:1502:A:H2	1:XA:1505:G:H1	1.22	0.87
25:RA:1464:C:HO2'	25:RA:1528:A:H8	1.22	0.87
35:YP:58:THR:O	35:YP:61:ARG:NE	2.08	0.87
44:YY:76:CYS:HB3	44:YY:96:ILE:HD13	1.57	0.87
25:RA:676:A:H8	25:RA:2069:G:H21	1.22	0.87
1:XA:664:G:H22	1:XA:741:G:H1	1.22	0.86
51:Y5:40:LYS:HG2	51:Y5:47:PRO:HD2	1.56	0.86

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:993:G:OP1	40:YU:50:ARG:NH2	2.09	0.86
35:RP:19:VAL:HG13	35:RP:21:ARG:H	1.40	0.86
4:XD:157:LEU:O	4:XD:161:ASN:ND2	2.07	0.86
25:YA:528:A:O2'	25:YA:529:A:H5'	1.75	0.86
27:RD:43:ARG:NH1	27:RD:44:ASN:OD1	2.08	0.86
25:YA:498:G:N3	44:YY:47:LYS:NZ	2.24	0.86
26:RB:80:U:H2'	26:RB:81:G:H21	1.41	0.85
25:RA:27:G:N2	25:RA:513:A:OP2	2.09	0.85
45:YZ:94:GLU:HB2	45:YZ:130:PRO:HD2	1.58	0.85
5:QE:50:GLU:HB3	5:QE:53:LEU:HD13	1.59	0.85
25:RA:1019:U:H3	25:RA:1142(A):A:H62	1.24	0.85
25:YA:1689:A:H62	25:YA:1698:A:H2	1.21	0.85
22:QV:75:C:OP1	25:RA:2602:A:OP1	1.94	0.85
42:YW:18:ARG:HG3	42:YW:76:VAL:HG13	1.58	0.84
44:RY:79:CYS:SG	44:RY:80:GLY:N	2.45	0.84
25:YA:1479:G:N7	25:YA:1510:A:N6	2.25	0.84
25:YA:780:G:H21	25:YA:783:A:H62	1.19	0.84
45:YZ:145:GLU:HG3	45:YZ:146:ILE:HG12	1.59	0.84
1:XA:501:C:OP1	12:XL:117:ARG:NH2	2.10	0.84
25:RA:1332:G:N2	25:RA:1609:A:HO2'	1.76	0.84
39:YT:26:ASP:HB3	39:YT:92:GLY:H	1.42	0.84
1:QA:1316:G:H22	1:QA:1319:A:H5''	1.40	0.84
1:QA:1305:G:H22	1:QA:1331:G:H2'	1.42	0.83
33:YN:4:TYR:O	40:YU:64:ARG:NH1	2.10	0.83
25:RA:617:G:OP1	29:RF:40:GLN:NE2	2.10	0.83
25:YA:1728:G:N1	25:YA:1730:U:OP2	2.11	0.83
2:QB:80:ILE:HD11	2:QB:208:ILE:HG23	1.58	0.83
1:XA:971:G:HO2'	1:XA:1365:G:HO2'	1.24	0.83
30:YG:27:ASN:HB3	30:YG:30:GLU:HG3	1.60	0.83
25:RA:2393:A:H5'	35:RP:62:LEU:HB3	1.61	0.83
25:YA:2580:U:H4'	28:YE:130:GLY:HA3	1.58	0.83
25:YA:265:A:N6	25:YA:427:U:O2'	2.12	0.83
1:XA:448:A:OP2	1:XA:485:G:N2	2.10	0.83
35:YP:19:VAL:HG13	35:YP:21:ARG:H	1.41	0.83
1:XA:1298:C:OP2	7:XG:114:ARG:NH2	2.10	0.83
25:YA:674:G:H1'	29:YF:74:ARG:HD3	1.61	0.83
51:R5:4:HIS:HB3	51:R5:5:PRO:HD3	1.61	0.82
40:YU:90:VAL:O	40:YU:92:ARG:N	2.11	0.82
25:YA:1310:G:OP2	53:Y7:9:ARG:NH1	2.11	0.82
25:RA:2392:A:H2	25:RA:2424:C:H42	1.26	0.82
51:R5:16:ARG:NH1	51:R5:17:ASP:OD1	2.13	0.82
29:RF:197:ASP:O	29:RF:199:TRP:N	2.12	0.82

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
44:RY:29:GLU:HB3	44:RY:38:ILE:HG12	1.62	0.82
47:Y1:7:ILE:HD12	47:Y1:62:VAL:HG11	1.62	0.82
45:RZ:94:GLU:HB2	45:RZ:130:PRO:HD2	1.60	0.81
51:Y5:16:ARG:NH1	51:Y5:17:ASP:OD1	2.13	0.81
48:Y2:47:ASN:O	48:Y2:49:LYS:N	2.12	0.81
35:RP:62:LEU:HD21	54:R8:25:MET:HB2	1.61	0.81
25:YA:630:G:OP1	54:Y8:46:ARG:NH1	2.13	0.81
29:RF:103:LYS:HA	29:RF:106:ARG:HG3	1.63	0.81
25:YA:631:A:OP2	54:Y8:46:ARG:NH2	2.13	0.81
33:YN:4:TYR:OH	33:YN:7:LYS:NZ	2.14	0.81
48:R2:47:ASN:O	48:R2:49:LYS:N	2.13	0.81
2:XB:69:LEU:HB3	2:XB:162:ILE:HG22	1.61	0.81
13:QM:14:ARG:H	13:QM:44:ARG:HD3	1.45	0.80
25:RA:2701:C:H3'	25:RA:2702:U:C5'	2.10	0.80
28:RE:201:THR:HG22	28:RE:203:LYS:H	1.45	0.80
25:RA:141:A:H8	25:RA:1595:G:H21	1.29	0.80
39:RT:24:PRO:HA	39:RT:49:VAL:HG13	1.61	0.80
1:XA:1305:G:N2	1:XA:1331:G:H2'	1.96	0.80
33:RN:42:TRP:O	40:RU:64:ARG:NH2	2.15	0.80
25:YA:1403:C:H5''	25:YA:1471:A:H1'	1.61	0.80
28:RE:50:GLY:HA2	28:RE:77:ILE:HA	1.64	0.80
1:XA:1086:U:H3	1:XA:1099:G:H22	1.29	0.80
1:QA:1502:A:H2	1:QA:1505:G:H1	1.29	0.80
32:YI:92:VAL:HG13	32:YI:120:ILE:HG23	1.64	0.80
44:YY:76:CYS:SG	44:YY:77:PRO:HD2	2.22	0.80
13:QM:3:ARG:HA	13:QM:9:ILE:HG21	1.62	0.80
25:RA:1332:G:N2	25:RA:1609:A:O2'	2.14	0.80
25:YA:138:G:N2	43:YX:44:GLU:OE2	2.11	0.80
25:YA:2015:A:H1'	51:Y5:2:ALA:HA	1.64	0.80
25:RA:1012:U:O2'	25:RA:1013:C:OP2	1.99	0.79
1:QA:346:G:OP1	39:RT:41:ARG:NH2	2.14	0.79
13:XM:65:LYS:HD3	13:XM:69:GLU:HG3	1.63	0.79
45:YZ:182:LYS:HG3	45:YZ:183:LEU:HD23	1.62	0.79
3:XC:32:LEU:HD13	3:XC:59:ARG:HD3	1.64	0.79
43:YX:67:GLY:O	43:YX:69:TYR:N	2.15	0.79
11:QK:21:ILE:HB	11:QK:84:VAL:HG12	1.65	0.79
37:RR:104:ARG:HD2	37:RR:111:LEU:HD21	1.63	0.79
1:XA:1002:G:H1	1:XA:1038:C:H42	1.28	0.79
20:XT:33:ILE:O	20:XT:37:SER:OG	2.01	0.79
1:QA:1298:C:OP2	7:QG:114:ARG:NH2	2.15	0.79
15:QO:26:GLU:OE2	15:QO:77:ARG:NH1	2.16	0.79
25:RA:857:C:H4'	46:R0:23:VAL:HG21	1.63	0.79

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:XB:77:ALA:HB2	2:XB:211:ILE:HD13	1.64	0.79
25:YA:2701:C:H3'	25:YA:2702:U:C5'	2.13	0.79
25:RA:1754:C:OP1	39:RT:96:ARG:NH1	2.15	0.79
32:YI:130:TYR:HB3	32:YI:136:VAL:HG13	1.62	0.78
25:RA:1080:C:N4	25:RA:1088:A:OP2	2.15	0.78
25:RA:1210:A:H5''	25:RA:1210:A:H8	1.48	0.78
3:XC:59:ARG:HH12	3:XC:97:LYS:HE3	1.48	0.78
4:XD:9:CYS:SG	4:XD:22:LYS:NZ	2.52	0.78
45:YZ:144:LEU:HD11	45:YZ:149:SER:HA	1.63	0.78
1:XA:1053:G:H5'	1:XA:1054:C:H5'	1.65	0.78
25:RA:2832:U:H4'	25:RA:2833:G:H5''	1.63	0.78
33:RN:95:PRO:O	33:RN:97:ARG:N	2.15	0.78
25:YA:2849:U:OP2	39:YT:95:ARG:NH1	2.17	0.78
35:RP:126:VAL:HG12	35:RP:147:LEU:HD21	1.63	0.78
50:Y4:1:MET:SD	50:Y4:6:HIS:NE2	2.56	0.78
20:QT:100:ILE:HG13	20:QT:102:GLY:H	1.48	0.78
27:RD:69:ARG:NH2	27:RD:128:GLY:O	2.17	0.78
10:QJ:50:ILE:HA	10:QJ:60:ARG:HG2	1.66	0.78
25:RA:958:U:OP2	36:RQ:14:ARG:NH1	2.15	0.78
34:YO:88:ASN:HD21	34:YO:92:GLU:HB2	1.47	0.78
25:RA:1980:G:O2'	25:RA:1982:C:OP2	2.00	0.78
25:RA:819:A:OP2	25:RA:1187:G:N2	2.15	0.78
26:RB:33:G:H5'	30:RG:2:PRO:HG3	1.64	0.78
1:XA:339:C:OP2	34:YO:97:ARG:NH1	2.18	0.77
32:RI:4:ILE:HD11	32:RI:44:LEU:HD12	1.66	0.77
13:XM:14:ARG:H	13:XM:44:ARG:HD3	1.49	0.77
1:XA:1128:C:H5'	9:XI:16:ARG:HH22	1.50	0.77
25:YA:607:U:H3	25:YA:621:A:H2	1.33	0.77
3:XC:20:SER:HB2	3:XC:40:ARG:HH22	1.50	0.77
25:YA:900:A:H3'	25:YA:901:A:H8	1.49	0.77
27:YD:69:ARG:NH2	27:YD:128:GLY:O	2.18	0.77
25:RA:2287:A:H62	25:RA:2344:U:H3	1.32	0.77
29:RF:66:PRO:O	29:RF:68:LYS:N	2.18	0.77
1:XA:880:C:OP1	12:XL:12:ARG:NH1	2.18	0.77
33:YN:95:PRO:O	33:YN:97:ARG:N	2.18	0.77
25:RA:1543:A:O2'	25:RA:1544:C:H3'	1.85	0.77
1:QA:1297:C:O2'	1:QA:1298:C:OP2	2.02	0.77
35:YP:47:ASP:OD1	35:YP:50:ARG:NH2	2.17	0.77
1:XA:1139:G:N2	1:XA:1143:G:O6	2.18	0.77
1:QA:1002:G:H2'	1:QA:1003:G:H8	1.50	0.76
25:YA:2306:C:H3'	25:YA:2307:G:H5''	1.67	0.76
37:RR:3:HIS:O	37:RR:5:LYS:N	2.19	0.76

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:XA:58:C:O2'	1:XA:388:G:N7	2.17	0.76
28:RE:9:VAL:HB	28:RE:25:VAL:HG23	1.66	0.76
16:XP:45:THR:HG22	16:XP:47:ASP:H	1.51	0.76
38:RS:62:LYS:HB3	38:RS:97:ARG:HD3	1.67	0.76
29:YF:197:ASP:O	29:YF:199:TRP:N	2.19	0.76
25:YA:1996:C:OP1	34:YO:31:LYS:NZ	2.19	0.76
37:YR:74:LYS:O	37:YR:76:VAL:N	2.18	0.76
25:RA:49:A:N7	25:RA:120:U:H5	1.83	0.76
25:YA:128:C:H4'	53:Y7:49:ARG:HH12	1.51	0.76
31:YH:153:LYS:HG2	31:YH:162:ILE:HG13	1.67	0.75
1:XA:1178:G:N2	1:XA:1181:G:N7	2.33	0.75
25:RA:996:A:H4'	40:RU:92:ARG:HE	1.50	0.75
44:RY:95:LYS:HB3	44:RY:100:ALA:HA	1.68	0.75
1:XA:1002:G:H2'	1:XA:1003:G:H8	1.52	0.75
25:RA:1899:G:H21	25:RA:1902:C:N4	1.85	0.75
1:XA:532:A:H2	1:XA:1206:G:H21	1.34	0.75
25:RA:2438:U:O3'	25:RA:2439:A:H3'	1.87	0.75
1:XA:356:A:N3	1:XA:368:U:O2'	2.19	0.75
52:R6:41:PRO:HG2	52:R6:45:LYS:H	1.52	0.75
44:RY:87:LYS:HD3	44:RY:92:ASN:HB3	1.69	0.75
25:YA:1434:A:H61	25:YA:1558:A:N6	1.85	0.75
25:YA:2392:A:H2	25:YA:2424:C:H42	1.35	0.75
39:YT:57:PHE:O	39:YT:58:ASN:ND2	2.20	0.75
25:RA:910:A:N3	25:RA:2264:C:O2'	2.20	0.75
35:RP:14:LYS:O	35:RP:16:ARG:N	2.20	0.75
39:YT:27:THR:HG23	39:YT:90:GLN:HB3	1.67	0.75
40:YU:92:ARG:O	40:YU:94:ASN:N	2.20	0.75
53:R7:9:ARG:HH21	53:R7:48:LYS:HD2	1.52	0.75
33:YN:13:TRP:HB2	33:YN:133:GLN:HG3	1.69	0.75
37:RR:56:LYS:NZ	37:RR:90:ARG:O	2.20	0.74
44:RY:86:ARG:HB2	44:RY:95:LYS:HD2	1.69	0.74
41:YV:24:LYS:HA	41:YV:92:THR:HG23	1.68	0.74
5:QE:102:ALA:HB1	5:QE:106:PRO:HG2	1.69	0.74
37:RR:74:LYS:O	37:RR:76:VAL:N	2.18	0.74
25:RA:483:A:H4'	44:RY:49:VAL:HA	1.67	0.74
17:XQ:66:SER:O	17:XQ:70:ARG:NH1	2.21	0.74
45:RZ:60:GLU:HA	45:RZ:66:SER:HA	1.68	0.74
25:YA:2849:U:O4	39:YT:23:ARG:NH2	2.21	0.74
25:RA:1332:G:H21	25:RA:1610:A:H8	1.34	0.74
30:RG:34:LEU:HB2	30:RG:172:LEU:HD21	1.68	0.74
38:YS:78:LEU:HD21	38:YS:108:GLY:HA3	1.68	0.74
5:QE:7:GLU:HG2	5:QE:112:LEU:HD22	1.69	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:1048:A:H2	25:RA:1112:G:H21	1.36	0.74
1:XA:971:G:N2	1:XA:1363:A:OP2	2.20	0.74
45:YZ:30:ASN:HD22	45:YZ:90:VAL:HB	1.51	0.74
26:YB:15:A:H5'	26:YB:16:G:C8	2.22	0.74
39:YT:51:ARG:HG2	39:YT:98:LYS:HG3	1.70	0.74
25:YA:482:A:H4'	44:YY:47:LYS:HD2	1.70	0.74
25:RA:780:G:H21	25:RA:783:A:H62	1.33	0.74
1:XA:619:U:H3	4:XD:135:LEU:HD23	1.52	0.74
30:YG:161:THR:HG22	30:YG:163:ALA:H	1.53	0.74
1:QA:1124:G:H3'	1:QA:1145:C:N4	2.03	0.74
8:QH:29:SER:HB3	8:QH:32:LYS:HG3	1.69	0.74
1:QA:973:G:OP1	10:QJ:57:LYS:NZ	2.21	0.74
25:RA:2392:A:H8	35:RP:60:MET:HG2	1.52	0.74
1:XA:1305:G:H22	1:XA:1331:G:H2'	1.52	0.74
1:XA:1321:C:H3'	1:XA:1322:C:H5''	1.69	0.74
28:RE:62:PRO:O	28:RE:64:LYS:N	2.20	0.74
5:QE:100:VAL:O	5:QE:107:ARG:NH2	2.20	0.73
1:XA:1314:C:N4	19:XS:3:ARG:O	2.18	0.73
25:RA:2115:G:N2	25:RA:2165:G:N7	2.35	0.73
25:RA:631:A:OP2	54:R8:46:ARG:NH2	2.22	0.73
25:RA:1542:G:O6	25:RA:1543:A:N6	2.21	0.73
50:Y4:9:LEU:H	50:Y4:27:THR:HG23	1.53	0.73
25:YA:483:A:H5'	44:YY:49:VAL:HG22	1.69	0.73
25:RA:1496:A:H8	25:RA:1577:C:HO2'	1.37	0.73
35:YP:14:LYS:O	35:YP:16:ARG:N	2.22	0.73
43:YX:27:THR:HB	43:YX:80:ILE:HB	1.69	0.73
25:YA:1667:G:O2'	25:YA:1991:U:O4	2.04	0.73
25:YA:2287:A:H62	25:YA:2344:U:H3	1.34	0.73
4:XD:7:PRO:HB2	4:XD:10:ARG:HD2	1.69	0.73
25:YA:49:A:N7	25:YA:120:U:H5	1.86	0.73
31:YH:86:GLU:HG3	31:YH:165:ALA:H	1.53	0.73
36:YQ:111:GLU:OE1	36:YQ:133:ARG:NH2	2.22	0.73
3:QC:58:GLU:HB2	3:QC:65:ALA:HB3	1.70	0.73
4:QD:175:SER:HB3	4:QD:186:LEU:HD21	1.69	0.73
32:RI:5:LEU:HD11	32:RI:19:VAL:HG12	1.70	0.73
25:YA:2849:U:O2'	25:YA:2866:U:O2	2.07	0.73
36:YQ:104:PHE:HE1	36:YQ:125:LEU:HD11	1.54	0.73
36:YQ:24:GLY:O	36:YQ:26:TYR:N	2.19	0.73
1:QA:677:U:H3	1:QA:713:G:H22	1.36	0.72
1:QA:1189:C:OP1	10:QJ:51:ARG:NH2	2.21	0.72
3:QC:20:SER:HB2	3:QC:40:ARG:HH22	1.54	0.72
7:QG:9:VAL:HG13	7:QG:94:ARG:HH21	1.54	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:1210:A:H8	25:YA:1210:A:H5'	1.52	0.72
1:QA:1494:G:N7	58:QA:1666:PAR:N32	2.38	0.72
50:Y4:48:ARG:HH12	50:Y4:52:THR:HG22	1.54	0.72
25:RA:1443:G:H1	25:RA:1548:C:H42	1.37	0.72
25:RA:1582:C:HO2'	25:RA:1586:A:H8	1.37	0.72
25:RA:530:G:C2	25:RA:2022:U:OP1	2.42	0.72
30:YG:64:THR:HG23	30:YG:66:GLN:H	1.55	0.72
25:RA:1728:G:H3'	25:RA:1729:A:H5''	1.71	0.72
25:RA:590:A:OP1	29:RF:95:ARG:NH1	2.22	0.72
30:YG:6:ALA:H	50:Y4:23:GLU:HG2	1.54	0.72
27:YD:35:LYS:HD2	27:YD:104:TYR:CE1	2.25	0.72
25:RA:2112:G:O6	25:RA:2169:A:N6	2.22	0.72
32:RI:98:ALA:HB2	32:RI:111:PRO:HB3	1.72	0.72
48:Y2:42:GLY:O	48:Y2:44:LEU:N	2.20	0.72
25:YA:2753:A:O2'	55:Y9:15:LYS:NZ	2.22	0.72
25:YA:2789:C:H1'	25:YA:2892:A:H2	1.55	0.72
31:YH:129:THR:OG1	31:YH:129:THR:O	2.08	0.72
44:YY:51:VAL:HG13	44:YY:52:SER:H	1.54	0.72
17:QQ:4:LYS:HE3	17:QQ:6:LEU:HD21	1.72	0.72
25:RA:1286:A:O2'	25:RA:1288:U:OP2	2.07	0.72
25:RA:140:A:H8	25:RA:1408:C:HO2'	1.35	0.72
5:XE:10:MET:HB3	5:XE:32:VAL:HG22	1.70	0.71
34:YO:47:ILE:HG13	34:YO:48:PRO:HD2	1.72	0.71
45:YZ:102:LEU:HG	45:YZ:123:ASP:HA	1.72	0.71
25:RA:900:A:H3'	25:RA:901:A:H8	1.55	0.71
9:XI:114:TYR:HE1	10:XJ:60:ARG:H	1.38	0.71
25:YA:2469:A:H2	25:YA:2481:G:H21	1.36	0.71
1:QA:1243:C:OP2	21:QU:10:ARG:NH2	2.23	0.71
46:R0:68:GLU:OE1	46:R0:82:ARG:NH1	2.23	0.71
45:RZ:166:SER:HB2	45:RZ:168:GLU:N	2.05	0.71
6:XF:50:TYR:OH	18:XR:74:ARG:O	2.06	0.71
25:YA:910:A:H62	36:YQ:12:GLN:HA	1.56	0.71
28:YE:170:LEU:HD21	28:YE:187:ALA:HB3	1.72	0.71
2:QB:115:LEU:HB2	2:QB:145:LEU:HD12	1.73	0.71
4:QD:28:SER:HB3	4:QD:29:PRO:HD3	1.72	0.71
26:RB:15:A:H5'	26:RB:16:G:C8	2.26	0.71
25:RA:2849:U:OP1	39:RT:95:ARG:NH1	2.23	0.71
26:YB:52:A:O2'	26:YB:53:A:N7	2.24	0.71
33:YN:89:LYS:O	33:YN:93:THR:HG22	1.90	0.71
25:YA:2415:G:H4'	35:YP:67:MET:N	2.06	0.71
49:R3:8:LEU:HD13	49:R3:31:LEU:HD23	1.71	0.71
30:RG:61:ALA:HB2	30:RG:68:PRO:HD3	1.72	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:2760:C:H2'	25:YA:2761:G:H5''	1.71	0.71
52:R6:17:LYS:HB3	52:R6:44:ARG:HH22	1.55	0.71
25:RA:252:G:OP2	35:RP:50:ARG:NH1	2.23	0.71
35:RP:38:GLN:HG2	35:RP:45:LEU:HD12	1.72	0.71
1:XA:974:A:OP2	14:XN:29:ARG:NH2	2.23	0.71
8:XH:10:LEU:HD22	8:XH:83:ILE:HD11	1.72	0.71
25:YA:1019:U:H3	25:YA:1142(A):A:H62	1.37	0.71
25:YA:259:G:H21	25:YA:621:A:H8	1.39	0.71
44:YY:29:GLU:HB3	44:YY:38:ILE:HG23	1.70	0.71
1:QA:1286:A:H5''	21:QU:26:LYS:HD2	1.73	0.71
20:XT:45:GLN:HB2	20:XT:91:LEU:HD13	1.73	0.71
25:YA:918:A:N3	26:YB:80:U:O2'	2.23	0.71
1:QA:1224:G:C6	1:QA:1322:C:H1'	2.25	0.71
10:QJ:61:GLU:OE2	14:QN:45:ARG:NH1	2.23	0.71
25:RA:994:C:OP2	40:RU:54:LYS:NZ	2.23	0.71
32:RI:93:THR:HG22	32:RI:119:PRO:HB3	1.71	0.71
25:YA:372:G:O2'	25:YA:373:U:OP2	2.08	0.71
32:YI:144:VAL:HG13	32:YI:145:VAL:HG13	1.70	0.71
38:YS:106:ARG:HA	38:YS:110:LEU:HD21	1.73	0.71
38:YS:24:LEU:HB2	38:YS:85:VAL:HG12	1.70	0.71
39:YT:77:PRO:HB2	39:YT:80:SER:HB2	1.72	0.71
34:YO:2:ILE:HD12	34:YO:6:THR:HG21	1.72	0.71
44:YY:42:VAL:HG12	44:YY:65:ALA:HB3	1.71	0.71
25:RA:2405:G:O2'	25:RA:2411:A:N6	2.23	0.70
36:RQ:81:VAL:O	36:RQ:82:ARG:NE	2.22	0.70
1:XA:1129:C:N4	1:XA:1133:G:O6	2.24	0.70
54:Y8:58:ILE:HD13	54:Y8:61:LEU:HD21	1.73	0.70
25:YA:2334:G:H5'	38:YS:9:ARG:HG2	1.72	0.70
25:RA:2839:G:H5'	37:RR:46:GLY:HA2	1.73	0.70
48:R2:29:LYS:HE3	48:R2:57:ILE:HG21	1.73	0.70
39:RT:18:ASP:N	39:RT:18:ASP:OD1	2.19	0.70
1:XA:1298:C:HO2'	1:XA:1299:A:P	2.13	0.70
30:YG:47:LYS:HD3	30:YG:81:LYS:HB2	1.73	0.70
1:QA:411:A:H62	1:QA:413:G:H21	1.37	0.70
19:QS:40:ILE:HD11	19:QS:62:ILE:HD12	1.74	0.70
19:QS:41:VAL:HB	19:QS:42:PRO:HA	1.74	0.70
1:QA:261:U:OP2	20:QT:79:ARG:NH2	2.23	0.70
42:RW:29:LEU:HD22	42:RW:69:LEU:HD11	1.72	0.70
25:YA:860:U:H5	25:YA:917:A:C2	2.10	0.70
1:XA:1129:C:H4'	1:XA:1130:A:H5'	1.73	0.70
10:XJ:50:ILE:HA	10:XJ:60:ARG:HG2	1.72	0.70
10:XJ:61:GLU:OE2	14:XN:45:ARG:NH1	2.25	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
45:YZ:141:VAL:HG23	45:YZ:144:LEU:HB2	1.74	0.70
1:QA:1322:C:O2'	1:QA:1323:G:H5'	1.90	0.70
31:RH:106:THR:HG22	31:RH:112:PRO:HB3	1.72	0.70
18:XR:58:LEU:HD23	18:XR:62:GLU:HB3	1.74	0.70
42:YW:17:VAL:HG12	42:YW:76:VAL:HG11	1.72	0.70
13:QM:59:TYR:O	13:QM:63:THR:OG1	2.07	0.70
25:RA:1184:G:OP1	49:R3:29:ARG:NH1	2.25	0.70
25:RA:2747:G:H21	25:RA:2757:A:H62	1.37	0.70
25:YA:2633:G:H1'	28:YE:62:PRO:HG2	1.73	0.70
29:YF:185:ASP:HA	29:YF:188:ARG:HD3	1.72	0.70
45:YZ:103:ARG:HB2	45:YZ:138:GLU:HG2	1.72	0.70
25:RA:2392:A:C8	35:RP:60:MET:HG2	2.27	0.70
25:YA:226:G:O2'	25:YA:227:A:O5'	2.09	0.70
28:RE:119:ARG:HB3	28:RE:120:TRP:CD1	2.27	0.70
14:YN:48:ALA:HB2	14:YN:53:LEU:HD12	1.73	0.70
27:YD:43:ARG:HB3	27:YD:54:ARG:HB2	1.74	0.70
2:XB:185:ILE:HG22	2:XB:199:TYR:HB2	1.74	0.70
25:YA:2292:C:P	38:YS:17:ARG:HH22	2.14	0.70
45:YZ:80:ARG:HH21	45:YZ:82:ARG:HH22	1.39	0.69
10:QJ:48:THR:HA	10:QJ:62:HIS:HB3	1.73	0.69
25:RA:2636:U:OP1	28:RE:79:ARG:HA	1.91	0.69
27:RD:93:ALA:HB3	27:RD:105:ILE:HG22	1.74	0.69
1:QA:336:C:H2'	1:QA:337:C:H6	1.55	0.69
50:R4:18:CYS:SG	50:R4:19:GLY:N	2.66	0.69
1:XA:1200:C:O2'	1:XA:1201:A:OP2	2.09	0.69
4:XD:105:VAL:HG13	4:XD:110:PHE:HB2	1.74	0.69
19:XS:10:PHE:HB2	19:XS:39:THR:H	1.54	0.69
25:YA:221:A:H4'	25:YA:222:A:O5'	1.91	0.69
29:YF:182:ASN:ND2	29:YF:185:ASP:OD2	2.19	0.69
6:XF:68:PRO:HG2	6:XF:71:ARG:HG3	1.74	0.69
25:YA:1754:C:OP1	39:YT:96:ARG:NH1	2.26	0.69
27:YD:182:LEU:H	27:YD:272:ALA:HB3	1.56	0.69
20:XT:100:ILE:HG13	20:XT:102:GLY:H	1.56	0.69
25:YA:1338:G:N7	43:YX:62:LYS:NZ	2.40	0.69
25:YA:252:G:OP2	35:YP:50:ARG:NH1	2.26	0.69
50:R4:7:PRO:HB2	50:R4:27:THR:HG21	1.74	0.69
52:Y6:11:LEU:HD11	52:Y6:51:GLU:HG3	1.75	0.69
25:YA:1019:U:HO2'	25:YA:1021:A:H2	1.39	0.69
25:YA:676:A:H8	25:YA:2069:G:H21	1.38	0.69
27:YD:71:ASP:HB2	27:YD:103:ARG:HH22	1.58	0.69
29:YF:110:LEU:HD11	29:YF:181:LEU:HD13	1.74	0.69
1:QA:1077:G:N2	1:QA:1080:A:OP2	2.24	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
51:R5:41:PRO:O	51:R5:44:THR:OG1	2.10	0.69
25:RA:2547:U:O2	34:RO:23:ARG:NH2	2.26	0.69
1:XA:130:A:N3	1:XA:263:A:O2'	2.24	0.69
29:YF:184:TYR:O	29:YF:188:ARG:HG3	1.93	0.69
36:RQ:37:LEU:HD21	36:RQ:130:LYS:HE3	1.74	0.69
1:XA:963:G:N2	1:XA:972:C:N3	2.34	0.69
25:YA:2401:U:H2'	25:YA:2402:C:H5''	1.75	0.69
28:YE:128:SER:OG	28:YE:129:HIS:N	2.24	0.69
4:QD:57:ARG:HH22	5:QE:107:ARG:HD3	1.58	0.69
28:RE:2:LYS:HD3	28:RE:95:ILE:HG22	1.75	0.69
42:RW:29:LEU:HG	42:RW:33:ARG:HD2	1.74	0.69
25:YA:704:G:O2'	25:YA:726:G:N2	2.25	0.69
1:QA:1053:G:H5'	1:QA:1054:C:H5'	1.74	0.68
27:RD:25:THR:O	27:RD:27:THR:N	2.26	0.68
47:Y1:73:LEU:HD13	47:Y1:90:ILE:HG22	1.76	0.68
25:YA:141:A:H8	25:YA:1595:G:H21	1.39	0.68
29:YF:157:VAL:HB	29:YF:194:MET:HB3	1.75	0.68
35:YP:64:LYS:C	35:YP:66:GLY:H	1.96	0.68
25:RA:2131:G:H4'	25:RA:2132:U:H4'	1.75	0.68
31:RH:86:GLU:HG3	31:RH:165:ALA:H	1.56	0.68
25:YA:1509:C:H3'	25:YA:1510:A:H5''	1.75	0.68
25:YA:2712:U:HO2'	25:YA:2712(A):A:H8	1.40	0.68
3:QC:3:ASN:N	3:QC:3:ASN:OD1	2.27	0.68
39:YT:123:GLN:O	39:YT:125:ARG:N	2.26	0.68
1:QA:620:C:H2'	1:QA:621:A:O4'	1.94	0.68
30:RG:66:GLN:NE2	30:RG:93:THR:O	2.26	0.68
30:RG:47:LYS:HD3	30:RG:81:LYS:HB2	1.76	0.68
14:XN:13:THR:N	14:XN:14:PRO:HD2	2.09	0.68
27:YD:25:THR:O	27:YD:27:THR:N	2.26	0.68
25:RA:1245:G:OP1	35:RP:13:ASN:ND2	2.25	0.68
25:YA:2527:C:H5''	55:Y9:30:PRO:HB2	1.73	0.68
25:YA:1049:C:H2'	25:YA:1050:A:H5''	1.76	0.68
25:YA:1094:U:O2'	25:YA:1096:A:OP1	2.09	0.68
1:QA:1204:A:OP1	14:QN:3:ARG:NH2	2.27	0.68
16:QP:4:ILE:HG12	16:QP:21:VAL:HG12	1.75	0.68
37:RR:38:VAL:HG22	37:RR:112:ALA:HB2	1.75	0.68
2:XB:235:SER:OG	2:XB:236:TYR:N	2.25	0.68
28:YE:95:ILE:H	28:YE:95:ILE:HD12	1.59	0.68
1:QA:542:G:OP1	4:QD:10:ARG:NH2	2.26	0.68
1:QA:973:G:H3'	1:QA:974:A:H5''	1.75	0.68
5:QE:11:ILE:HG13	5:QE:31:LEU:HB3	1.76	0.68
11:QK:58:PRO:HB2	11:QK:93:GLN:HG3	1.75	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
36:RQ:12:GLN:HG2	36:RQ:73:PRO:HD2	1.75	0.68
27:YD:142:VAL:HG23	27:YD:193:VAL:HA	1.75	0.68
35:YP:64:LYS:C	35:YP:66:GLY:N	2.48	0.68
33:YN:133:GLN:HB2	33:YN:135:PRO:HD3	1.76	0.68
36:YQ:37:LEU:HD21	36:YQ:130:LYS:HE3	1.74	0.68
1:QA:662:G:O2'	1:QA:836:G:OP1	2.11	0.68
1:QA:686:U:O4	1:QA:703:G:H1'	1.93	0.68
25:RA:1169:G:H1	25:RA:1180:C:H42	1.42	0.68
30:RG:83:ARG:H	30:RG:86:MET:HG3	1.58	0.68
35:YP:39:LYS:HG3	35:YP:45:LEU:HD22	1.75	0.68
25:RA:2451:A:C6	56:Z6:76:PPU:HE2	2.29	0.68
2:QB:27:LYS:HD2	2:QB:193:ASP:HB2	1.75	0.67
25:RA:768:G:O2'	25:RA:1379:A:N6	2.26	0.67
45:RZ:108:PRO:HA	45:RZ:142:SER:HA	1.75	0.67
25:RA:249:C:O2	54:R8:12:LYS:NZ	2.26	0.67
19:XS:40:ILE:HG12	19:XS:41:VAL:HG13	1.76	0.67
54:Y8:29:LYS:O	54:Y8:31:HIS:N	2.27	0.67
25:YA:2636:U:OP1	28:YE:79:ARG:HA	1.93	0.67
32:YI:5:LEU:HD21	32:YI:12:LEU:HB3	1.77	0.67
1:QA:1392:G:H21	1:QA:1502:A:H8	1.42	0.67
4:QD:154:ASN:OD1	4:QD:154:ASN:N	2.26	0.67
19:QS:29:ARG:HD3	19:QS:30:LEU:HD13	1.77	0.67
25:RA:221:A:H4'	25:RA:222:A:O5'	1.93	0.67
25:RA:442:G:H1'	29:RF:48:THR:HG21	1.76	0.67
25:RA:674:G:H1'	29:RF:74:ARG:HD3	1.75	0.67
31:RH:152:ARG:HG3	31:RH:153:LYS:HD2	1.77	0.67
31:RH:41:MET:HE1	31:RH:64:LEU:HD22	1.76	0.67
25:RA:2308:G:H22	25:RA:2311:A:H2	1.40	0.67
25:RA:84:A:N1	25:RA:98:G:O2'	2.28	0.67
25:RA:2712:U:HO2'	25:RA:2712(A):A:H8	1.42	0.67
25:RA:2779:U:O2'	25:RA:2781:A:N7	2.28	0.67
5:XE:31:LEU:HD23	5:XE:45:PHE:CD1	2.30	0.67
28:YE:1:MET:N	28:YE:83:ASP:O	2.28	0.67
31:YH:137:ASP:OD1	31:YH:138:LYS:N	2.27	0.67
36:YQ:89:ASN:O	36:YQ:92:GLY:N	2.18	0.67
26:YB:52:A:H62	38:YS:33:LYS:HG3	1.60	0.67
1:QA:582:U:OP1	15:QO:68:ARG:NH2	2.22	0.67
1:QA:954:G:H21	1:QA:1227:A:H62	1.42	0.67
25:RA:2114:A:N6	25:RA:2119:A:N7	2.42	0.67
27:RD:182:LEU:H	27:RD:272:ALA:HB3	1.59	0.67
8:XH:120:THR:H	8:XH:123:GLU:HB2	1.59	0.67
25:YA:2393:A:H5'	35:YP:62:LEU:HB3	1.77	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:270(T):G:H5''	47:Y1:97:LEU:HD22	1.76	0.67
25:YA:888:C:H3'	25:YA:889:C:H4'	1.76	0.67
1:QA:1255:G:OP1	10:QJ:45:ARG:NH2	2.27	0.67
29:RF:143:ALA:HB1	29:RF:148:LEU:HB2	1.75	0.67
41:RV:72:VAL:HG13	41:RV:85:LYS:HB3	1.75	0.67
1:XA:396:G:O2'	1:XA:398:C:OP1	2.09	0.67
2:XB:174:VAL:HG13	2:XB:184:VAL:HG11	1.75	0.67
5:XE:37:ARG:HA	5:XE:114:GLY:H	1.58	0.67
25:YA:2114:A:N6	25:YA:2119:A:N7	2.43	0.67
39:YT:16:ARG:NH2	39:YT:83:ILE:O	2.27	0.67
27:RD:49:ILE:HD11	27:RD:52:ARG:HA	1.77	0.67
39:RT:84:GLN:HG2	39:RT:85:LYS:HG2	1.76	0.67
1:XA:826:C:H2'	1:XA:827:U:O2	1.94	0.67
2:XB:168:THR:HB	2:XB:192:SER:HB2	1.77	0.67
41:YV:52:VAL:HG21	41:YV:55:ALA:HB3	1.76	0.67
1:QA:1321:C:H5''	1:QA:1322:C:H5''	1.77	0.67
25:YA:1021:A:H8	25:YA:1022:G:H5''	1.60	0.67
25:YA:2123:G:H2'	25:YA:2124:G:H8	1.58	0.67
27:YD:35:LYS:HG2	27:YD:64:ILE:H	1.59	0.67
36:RQ:30:GLY:HA2	36:RQ:107:ALA:HB2	1.77	0.66
1:XA:266:G:H5''	1:XA:267:C:C5	2.30	0.66
37:YR:78:LYS:HE2	37:YR:83:ILE:HD11	1.77	0.66
25:RA:2790:A:H2'	25:RA:2791:C:H5''	1.78	0.66
25:RA:857:C:OP2	46:R0:77:ARG:NH2	2.26	0.66
32:RI:4:ILE:HG12	32:RI:18:VAL:HG22	1.77	0.66
1:XA:1218:C:H2'	1:XA:1219:U:C6	2.30	0.66
51:Y5:4:HIS:HB3	51:Y5:5:PRO:HD3	1.77	0.66
25:YA:1796:U:H2'	25:YA:1797:C:C6	2.31	0.66
25:YA:587:C:OP2	35:YP:21:ARG:NH2	2.28	0.66
45:RZ:19:ARG:NH1	45:RZ:84:GLU:O	2.28	0.66
45:RZ:52:SER:O	45:RZ:52:SER:OG	2.12	0.66
32:YI:4:ILE:HG12	32:YI:18:VAL:HG22	1.76	0.66
25:YA:142:G:H1'	43:YX:37:THR:HG21	1.75	0.66
1:QA:922:G:H4'	5:QE:20:GLN:HA	1.77	0.66
55:R9:27:CYS:SG	55:R9:29:ASN:ND2	2.69	0.66
32:RI:3:VAL:HG12	32:RI:38:LEU:HA	1.77	0.66
25:YA:2685:G:N2	25:YA:2724:C:O2	2.19	0.66
42:YW:45:TYR:CZ	42:YW:49:LYS:HD2	2.30	0.66
1:QA:826:C:H2'	1:QA:827:U:O2	1.95	0.66
3:QC:70:VAL:HG12	3:QC:72:LYS:H	1.60	0.66
47:R1:7:ILE:HG12	47:R1:91:LYS:NZ	2.11	0.66
25:RA:631:A:H61	25:RA:2402:C:N4	1.94	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:695:G:H4'	25:RA:1380:G:H5'	1.78	0.66
1:XA:561:U:O2'	1:XA:562:C:OP2	2.11	0.66
10:XJ:7:LYS:HB2	10:XJ:97:GLU:HB2	1.76	0.66
13:XM:105:THR:O	13:XM:107:ALA:N	2.29	0.66
25:YA:2636:U:OP2	28:YE:79:ARG:NH1	2.29	0.66
31:YH:86:GLU:HG3	31:YH:165:ALA:N	2.10	0.66
44:YY:49:VAL:O	44:YY:51:VAL:N	2.29	0.66
19:QS:39:THR:HG22	19:QS:40:ILE:H	1.61	0.66
1:XA:390:C:O3'	16:XP:28:ARG:NH2	2.28	0.66
45:YZ:128:VAL:HB	45:YZ:161:VAL:HG13	1.78	0.66
1:XA:564:C:O2'	8:XH:91:ARG:NH2	2.29	0.66
25:YA:1899:G:H21	25:YA:1902:C:N4	1.94	0.66
25:YA:74:A:H4'	25:YA:75:G:O5'	1.95	0.66
44:YY:97:ARG:HE	44:YY:98:VAL:HB	1.61	0.66
1:QA:974:A:OP2	14:QN:41:ARG:NH1	2.29	0.66
30:RG:6:ALA:H	50:R4:23:GLU:HG2	1.61	0.66
28:RE:63:LEU:HD13	28:RE:65:GLY:H	1.60	0.66
44:RY:49:VAL:O	44:RY:51:VAL:N	2.29	0.66
25:YA:2308:G:H22	25:YA:2311:A:H2	1.43	0.66
33:YN:35:ARG:O	33:YN:37:LYS:N	2.29	0.66
35:YP:105:LEU:O	35:YP:106:LEU:HB2	1.95	0.66
45:YZ:60:GLU:HA	45:YZ:66:SER:HA	1.76	0.66
1:QA:890:G:O2'	1:QA:906:G:O6	2.13	0.66
39:RT:102:ILE:HB	39:RT:110:ILE:HD13	1.78	0.66
19:XS:50:ALA:HB1	19:XS:57:HIS:HB3	1.77	0.66
25:RA:242:G:H5''	54:R8:62:LEU:HD13	1.78	0.65
36:RQ:135:ASP:OD1	36:RQ:135:ASP:N	2.23	0.65
25:RA:2713:A:OP1	37:RR:14:SER:OG	2.12	0.65
25:YA:2444:G:OP2	29:YF:68:LYS:HE3	1.96	0.65
25:YA:363(B):G:H2'	25:YA:363(C):G:H8	1.61	0.65
41:YV:21:ARG:HD2	41:YV:91:TYR:CD1	2.31	0.65
27:RD:108:PRO:HG2	27:RD:111:LEU:HG	1.78	0.65
45:RZ:150:LEU:HD21	45:RZ:172:ALA:HB3	1.77	0.65
1:XA:547:A:OP1	4:XD:73:ARG:NH2	2.30	0.65
47:Y1:29:GLY:O	47:Y1:31:GLY:N	2.30	0.65
39:YT:16:ARG:HD3	39:YT:19:LEU:HD11	1.77	0.65
25:RA:1289:C:H2'	25:RA:1290:C:C6	2.31	0.65
25:RA:2469:A:H2	25:RA:2481:G:H21	1.44	0.65
1:XA:559:A:OP1	5:XE:126:ARG:NH2	2.30	0.65
1:XA:674:G:H2'	1:XA:675:A:H8	1.60	0.65
1:XA:1342:C:H4'	9:XI:125:TYR:HB3	1.78	0.65
25:YA:2306:C:H2'	25:YA:2307:G:H21	1.62	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:1863:G:HO2'	25:YA:2411:A:HO2'	1.44	0.65
1:QA:1080:A:H5''	5:QE:16:THR:HG21	1.79	0.65
50:R4:1:MET:SD	50:R4:6:HIS:NE2	2.69	0.65
27:RD:27:THR:HG21	27:RD:81:ALA:HB1	1.78	0.65
35:RP:59:LEU:HA	35:RP:61:ARG:NE	2.12	0.65
1:XA:67:C:H2'	1:XA:68:G:C8	2.31	0.65
25:YA:1771:C:H1'	25:YA:1786:A:C8	2.32	0.65
25:YA:780:G:N2	25:YA:783:A:H62	1.94	0.65
40:YU:8:VAL:HG23	40:YU:11:ARG:HH21	1.62	0.65
2:QB:82:ARG:HA	2:QB:92:TYR:CE2	2.31	0.65
1:QA:191:G:H1'	20:QT:105:SER:HB3	1.79	0.65
52:R6:11:LEU:HD23	52:R6:26:ASN:HB3	1.78	0.65
25:YA:1287:A:N7	37:YR:107:ASP:HB2	2.11	0.65
25:RA:1204:A:H2	25:RA:1241:A:N1	1.94	0.65
44:RY:38:ILE:HG22	44:RY:66:PRO:HA	1.79	0.65
48:Y2:50:ILE:HD12	48:Y2:51:ARG:H	1.62	0.65
51:Y5:40:LYS:HZ1	51:Y5:48:GLU:HB2	1.61	0.65
25:YA:443:A:H3'	29:YF:45:ARG:NH1	2.11	0.65
3:QC:9:GLY:HA2	3:QC:12:LEU:HD23	1.78	0.65
25:RA:846:C:O2'	25:RA:847:U:OP2	2.13	0.65
1:XA:1126:U:H5	1:XA:1127:G:C4	2.14	0.65
25:YA:768:G:N2	25:YA:1379:A:O2'	2.30	0.65
31:YH:20:ALA:HB3	31:YH:23:ARG:HG2	1.77	0.65
1:QA:612:C:O2	1:QA:629:G:N2	2.29	0.65
35:RP:71:VAL:HG13	35:RP:72:PRO:HD3	1.78	0.65
1:XA:243:A:H4'	1:XA:244:U:O5'	1.97	0.65
2:XB:178:ARG:NH1	2:XB:196:LEU:O	2.29	0.65
5:XE:152:ARG:NH2	8:XH:107:LEU:O	2.28	0.65
11:XK:21:ILE:HB	11:XK:84:VAL:HG12	1.78	0.65
20:XT:97:ALA:O	20:XT:99:LEU:N	2.30	0.65
1:XA:1286:A:H5''	21:XU:26:LYS:HD2	1.78	0.65
46:Y0:10:THR:HG22	46:Y0:12:ASN:H	1.62	0.65
25:YA:31:C:O3'	25:YA:1238:G:H5''	1.97	0.65
16:QP:53:VAL:HG12	16:QP:79:VAL:HG22	1.77	0.65
22:QV:76:A:H2'	25:RA:2602:A:N6	2.11	0.65
25:RA:1817:G:OP1	27:RD:88:ARG:NH2	2.28	0.65
1:QA:1175:G:H2'	1:QA:1176:A:C8	2.32	0.65
22:QV:23:C:H2'	22:QV:24:U:C6	2.31	0.65
25:RA:2439:A:C8	25:RA:2439:A:H5'	2.31	0.65
35:RP:47:ASP:OD1	35:RP:50:ARG:NH2	2.30	0.65
35:RP:85:LEU:HA	35:RP:88:LEU:HD22	1.79	0.65
51:Y5:56:LYS:HD2	51:Y5:56:LYS:H	1.60	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:YD:44:ASN:HB3	27:YD:49:ILE:HA	1.78	0.65
31:YH:153:LYS:HG3	31:YH:161:GLY:HA2	1.78	0.65
1:QA:1002:G:H2'	1:QA:1003:G:C8	2.30	0.64
51:R5:58:LEU:HD13	51:R5:60:VAL:HG12	1.78	0.64
34:RO:4:PRO:O	34:RO:5:GLN:HB2	1.96	0.64
3:XC:122:GLU:OE1	3:XC:126:ARG:NH2	2.29	0.64
25:YA:1190:G:OP1	35:YP:30:THR:OG1	2.15	0.64
25:YA:2853:C:H2'	25:YA:2854:G:H8	1.61	0.64
27:YD:80:ALA:HB3	27:YD:94:LEU:HD13	1.79	0.64
29:YF:107:LYS:HD2	29:YF:207:GLY:H	1.62	0.64
1:QA:1095:U:P	1:QA:1108:G:H1	2.19	0.64
1:QA:1135:U:H4'	1:QA:1136:U:H5	1.62	0.64
13:QM:3:ARG:HD2	13:QM:9:ILE:HG12	1.79	0.64
22:QV:23:C:H2'	22:QV:24:U:H6	1.62	0.64
25:YA:1639:U:H2'	25:YA:1640:C:H5''	1.79	0.64
1:QA:1152:A:H5''	10:QJ:13:HIS:CD2	2.32	0.64
25:RA:1329:U:H5''	25:RA:1330:C:H5	1.62	0.64
45:YZ:182:LYS:HG3	45:YZ:183:LEU:HA	1.78	0.64
25:RA:1059:G:O6	25:RA:1079:C:N4	2.30	0.64
25:RA:330:A:H2	25:RA:1210:A:H2'	1.60	0.64
25:RA:1678:G:H22	25:RA:1989:G:H22	1.44	0.64
27:RD:65:ILE:HD11	27:RD:67:PHE:CE1	2.31	0.64
15:XO:26:GLU:OE2	15:XO:77:ARG:NH1	2.31	0.64
27:YD:30:GLU:HG3	27:YD:63:ARG:NH2	2.12	0.64
31:YH:153:LYS:HB3	31:YH:162:ILE:H	1.63	0.64
36:YQ:78:PRO:O	36:YQ:79:LEU:HB2	1.97	0.64
5:QE:11:ILE:HD11	5:QE:31:LEU:HD12	1.80	0.64
25:RA:270(T):G:H5''	47:R1:97:LEU:HD22	1.78	0.64
27:RD:8:PRO:HB3	27:RD:14:ARG:HB2	1.79	0.64
27:RD:35:LYS:HG2	27:RD:64:ILE:N	2.12	0.64
1:XA:1226:C:O2'	13:XM:111:LYS:NZ	2.30	0.64
25:YA:2543:G:H2'	25:YA:2544:G:C8	2.33	0.64
40:YU:88:ILE:HG22	40:YU:90:VAL:HG23	1.79	0.64
1:QA:1055:A:N7	1:QA:1200:C:N4	2.46	0.64
1:QA:673:G:H2'	1:QA:674:G:C8	2.33	0.64
1:QA:953:G:H5'	1:QA:965:A:H61	1.63	0.64
26:RB:52:A:O2'	26:RB:53:A:N7	2.31	0.64
1:XA:664:G:N2	1:XA:741:G:H1	1.93	0.64
10:QJ:77:PRO:O	10:QJ:79:ARG:NH1	2.30	0.64
10:QJ:53:PRO:HA	14:QN:42:ILE:HD12	1.79	0.64
25:RA:155:C:H42	25:RA:171:G:H1	1.44	0.64
29:RF:192:LEU:HD22	29:RF:194:MET:HG2	1.80	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:YE:9:VAL:HB	28:YE:25:VAL:HG23	1.80	0.64
1:QA:963:G:H1	1:QA:972:C:H42	1.43	0.64
36:RQ:17:LEU:HD21	36:RQ:41:TRP:CD1	2.33	0.64
40:RU:90:VAL:O	40:RU:92:ARG:N	2.30	0.64
1:XA:963:G:H1	1:XA:972:C:H42	1.45	0.64
25:YA:2646:C:OP2	25:YA:2732:G:O2'	2.15	0.64
1:XA:1443:G:N2	25:YA:2864:G:OP1	2.27	0.64
37:YR:51:LEU:HD13	37:YR:66:VAL:HG13	1.79	0.64
2:QB:5:ILE:HG21	2:QB:221:LEU:HD23	1.78	0.64
1:XA:1095:U:P	1:XA:1108:G:H1	2.21	0.64
25:YA:1063:G:H22	25:YA:1076:C:H1'	1.62	0.64
1:QA:114:U:H2'	1:QA:115:G:C8	2.32	0.64
50:R4:48:ARG:O	50:R4:50:VAL:N	2.31	0.64
25:RA:2111:C:N3	25:RA:2118:U:O2'	2.30	0.64
27:RD:35:LYS:HG2	27:RD:64:ILE:H	1.63	0.64
31:RH:88:LEU:HD11	31:RH:165:ALA:HB2	1.80	0.64
36:RQ:83:MET:HB2	46:R0:7:LEU:HD12	1.79	0.64
3:XC:11:ARG:O	3:XC:13:GLY:N	2.30	0.64
3:XC:19:GLU:O	3:XC:40:ARG:NH2	2.30	0.64
8:XH:7:ALA:HB2	8:XH:85:ARG:HD3	1.80	0.64
25:YA:127:A:H5''	25:YA:128:C:C6	2.33	0.64
27:YD:35:LYS:NZ	27:YD:64:ILE:O	2.31	0.64
30:YG:112:PRO:HB3	50:Y4:37:SER:HB2	1.80	0.64
39:YT:36:GLU:HG3	39:YT:41:ARG:HE	1.62	0.64
1:QA:752:G:H1'	1:QA:754:C:H41	1.63	0.63
37:RR:104:ARG:HD3	37:RR:109:ALA:HB3	1.79	0.63
1:XA:701:C:O2'	1:XA:702:A:OP2	2.14	0.63
25:YA:1568:G:H4'	27:YD:59:LYS:HB3	1.80	0.63
1:QA:1318:A:H4'	19:QS:11:VAL:HG11	1.79	0.63
10:QJ:4:ILE:HB	10:QJ:74:ILE:HG13	1.81	0.63
25:RA:2107:C:H42	25:RA:2182:G:H1	1.47	0.63
25:RA:997:G:OP1	40:RU:93:LYS:HD3	1.98	0.63
38:RS:26:LEU:HB3	38:RS:87:PHE:HA	1.81	0.63
25:RA:2293:C:H5''	38:RS:89:ARG:HH12	1.63	0.63
43:RX:43:VAL:HG13	43:RX:51:VAL:HG21	1.79	0.63
48:Y2:41:ILE:HD11	48:Y2:44:LEU:HG	1.80	0.63
25:YA:72:U:N3	48:Y2:62:THR:HG22	2.14	0.63
25:YA:468:G:N7	53:Y7:39:ARG:NH2	2.44	0.63
54:Y8:16:ILE:HD13	54:Y8:57:ARG:HG2	1.80	0.63
35:YP:58:THR:HG22	35:YP:61:ARG:HG3	1.80	0.63
4:QD:7:PRO:HB2	4:QD:10:ARG:HD2	1.81	0.63
47:R1:29:GLY:O	47:R1:31:GLY:N	2.29	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:1061:U:H5'	25:RA:1070:A:H1'	1.80	0.63
25:RA:2327:A:H2'	25:RA:2328:A:C8	2.34	0.63
2:XB:187:LEU:HA	2:XB:201:ILE:HB	1.79	0.63
19:QS:40:ILE:HG23	19:QS:41:VAL:HG22	1.79	0.63
48:R2:65:ASN:HB3	48:R2:69:ARG:HH22	1.61	0.63
25:RA:1694:C:H4'	25:RA:1695:G:O5'	1.96	0.63
45:RZ:165:VAL:HG11	45:RZ:169:GLU:HB2	1.80	0.63
2:XB:79:ASP:HA	2:XB:82:ARG:HB2	1.80	0.63
5:XE:98:THR:HB	5:XE:117:ASP:HB3	1.79	0.63
27:YD:25:THR:HG23	27:YD:27:THR:HB	1.80	0.63
1:QA:411:A:N6	1:QA:413:G:H21	1.95	0.63
2:QB:24:TRP:HD1	2:QB:24:TRP:H	1.46	0.63
25:RA:806:C:OP2	35:RP:41:ARG:NH1	2.26	0.63
37:RR:33:ARG:HG3	37:RR:115:GLU:HB3	1.79	0.63
4:QD:27:TYR:OH	6:XF:15:ASP:OD2	2.09	0.63
13:XM:91:ARG:HB2	13:XM:98:VAL:HG13	1.80	0.63
50:Y4:48:ARG:O	50:Y4:50:VAL:N	2.31	0.63
25:YA:1405:U:H2'	25:YA:1406:U:H6	1.63	0.63
27:YD:35:LYS:HG2	27:YD:64:ILE:N	2.13	0.63
38:YS:59:LYS:HD3	38:YS:60:GLY:H	1.62	0.63
44:YY:91:GLU:HG3	44:YY:92:ASN:H	1.63	0.63
1:QA:1305:G:N2	1:QA:1331:G:H2'	2.11	0.63
1:QA:346:G:H1'	1:QA:347:G:H5'	1.80	0.63
1:QA:448:A:OP2	1:QA:485:G:N2	2.28	0.63
1:QA:877:C:H5''	8:QH:88:LYS:HD3	1.81	0.63
1:QA:690:G:H22	11:QK:55:LYS:HZ1	1.47	0.63
35:RP:95:VAL:HG13	35:RP:100:LEU:HD21	1.79	0.63
38:RS:15:ARG:HH11	38:RS:25:ARG:HH21	1.44	0.63
50:Y4:23:GLU:O	50:Y4:25:TYR:N	2.31	0.63
53:Y7:9:ARG:HH21	53:Y7:48:LYS:HD2	1.63	0.63
25:YA:1652:A:OP1	37:YR:8:ARG:NH1	2.30	0.63
31:YH:83:TYR:CZ	31:YH:138:LYS:HD2	2.34	0.63
35:YP:13:ASN:O	35:YP:15:ARG:N	2.32	0.63
25:YA:2470:G:H5'	36:YQ:56:ARG:HH22	1.62	0.63
1:QA:339:C:OP2	34:RO:97:ARG:NH1	2.31	0.63
1:QA:1292:U:OP1	7:QG:41:ARG:NH2	2.32	0.63
8:QH:10:LEU:HD22	8:QH:83:ILE:HD11	1.80	0.63
25:RA:1289:C:H2'	25:RA:1290:C:H6	1.64	0.63
25:RA:270(R):G:N3	47:R1:78:LYS:NZ	2.46	0.63
40:RU:66:ASN:O	40:RU:70:ARG:HB2	1.98	0.63
1:XA:427:U:OP1	4:XD:13:ARG:NH2	2.31	0.63
5:XE:147:ASP:O	5:XE:151:LEU:HG	1.97	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:2315:G:OP1	30:YG:36:LYS:NZ	2.31	0.63
25:YA:1786:A:H2	25:YA:2606:C:H1'	1.63	0.63
40:YU:83:LEU:HD12	40:YU:113:ALA:HB2	1.79	0.63
42:YW:41:LYS:HE3	51:Y5:25:LEU:HD21	1.80	0.63
1:QA:1023:G:H3'	1:QA:1024:G:H5''	1.79	0.63
1:QA:78:G:O6	1:QA:91:C:N4	2.31	0.63
25:RA:2683:C:OP1	39:RT:53:ARG:NH2	2.31	0.63
33:RN:133:GLN:HB2	33:RN:135:PRO:HD3	1.79	0.63
33:RN:13:TRP:HB2	33:RN:133:GLN:HG3	1.81	0.63
1:XA:299:G:H2'	1:XA:300:A:C8	2.34	0.63
13:XM:23:TYR:HB3	13:XM:67:GLU:HA	1.81	0.63
31:YH:152:ARG:HG3	31:YH:153:LYS:HD2	1.81	0.63
34:YO:13:ASN:ND2	34:YO:96:THR:O	2.30	0.63
25:RA:622:G:OP2	35:RP:108:LYS:NZ	2.27	0.63
44:RY:51:VAL:HG13	44:RY:52:SER:H	1.64	0.63
1:XA:975:A:H8	1:XA:975:A:H5'	1.64	0.63
52:Y6:41:PRO:HG2	52:Y6:45:LYS:H	1.63	0.63
25:YA:2068:U:H3	25:YA:2430:A:H2	1.46	0.63
25:YA:84:A:O5'	44:YY:8:LYS:HD3	1.99	0.63
7:QG:155:ARG:HD3	7:QG:155:ARG:H	1.64	0.62
25:RA:273(C):C:H42	25:RA:363(C):G:H1	1.47	0.62
25:RA:2633:G:O2'	28:RE:60:ASN:ND2	2.32	0.62
10:XJ:32:ALA:HB3	10:XJ:76:ASN:HB2	1.79	0.62
25:YA:1068:G:O2'	25:YA:1096:A:N3	2.32	0.62
25:YA:1348:G:H2'	25:YA:1349:A:H5''	1.81	0.62
25:YA:2394:C:OP1	35:YP:63:PRO:HD2	1.99	0.62
25:RA:1899:G:H21	25:RA:1902:C:H42	1.47	0.62
25:RA:2788:C:O2'	25:RA:2809:A:N3	2.32	0.62
25:RA:307:G:H21	25:RA:330:A:H62	1.47	0.62
25:RA:2680:C:H5'	28:RE:189:PRO:HA	1.80	0.62
29:RF:12:LEU:HD12	29:RF:17:ARG:HG2	1.80	0.62
9:XI:24:GLY:N	9:XI:60:ASP:OD1	2.29	0.62
25:YA:2817:G:OP1	37:YR:99:LYS:NZ	2.27	0.62
1:QA:1352:C:OP1	21:QU:3:LYS:NZ	2.26	0.62
28:RE:119:ARG:HG2	28:RE:160:TYR:HB2	1.80	0.62
1:XA:1125:U:OP2	1:XA:1145:C:N4	2.33	0.62
2:XB:92:TYR:CE1	2:XB:151:GLY:HA3	2.34	0.62
31:YH:26:VAL:HG11	31:YH:75:ALA:HB1	1.81	0.62
25:YA:996:A:H4'	40:YU:92:ARG:HE	1.65	0.62
1:QA:1435:G:H2'	1:QA:1436:U:C6	2.34	0.62
25:RA:2836:U:H2'	25:RA:2837:G:C8	2.33	0.62
26:RB:15:A:H5'	26:RB:16:G:H8	1.64	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
45:RZ:110:GLY:HA2	45:RZ:111:VAL:O	2.00	0.62
1:XA:62:U:O2'	1:XA:379:C:O2	2.14	0.62
2:XB:212:GLN:NE2	2:XB:235:SER:HB2	2.15	0.62
30:YG:115:ARG:NH2	30:YG:137:GLU:OE1	2.33	0.62
32:YI:124:GLY:H	32:YI:142:VAL:HG23	1.63	0.62
25:YA:2864:G:OP1	39:YT:119:LYS:HD2	1.99	0.62
1:QA:565:U:H5''	1:QA:566:G:H2'	1.81	0.62
1:QA:1152:A:OP1	10:QJ:68:HIS:NE2	2.31	0.62
47:R1:7:ILE:HG12	47:R1:91:LYS:HZ1	1.61	0.62
25:RA:1287:A:N7	37:RR:107:ASP:HB2	2.14	0.62
43:RX:53:LYS:HB2	43:RX:82:GLN:HB3	1.80	0.62
1:XA:1298:C:O2'	1:XA:1299:A:OP2	2.12	0.62
2:XB:12:GLU:O	2:XB:16:HIS:ND1	2.22	0.62
10:XJ:5:ARG:HH21	10:XJ:99:LYS:HD2	1.63	0.62
19:XS:13:ASP:N	19:XS:13:ASP:OD1	2.32	0.62
25:YA:2032:G:H21	28:YE:146:THR:HG23	1.64	0.62
29:YF:46:ARG:HG2	29:YF:46:ARG:HH11	1.65	0.62
30:YG:3:LEU:HD12	30:YG:4:ASP:H	1.64	0.62
32:YI:81:VAL:HG21	32:YI:88:ILE:HD12	1.80	0.62
39:YT:1:MET:O	39:YT:3:ARG:N	2.29	0.62
1:QA:816:A:OP1	1:QA:1526:G:O2'	2.17	0.62
1:QA:1152:A:H5''	10:QJ:13:HIS:HD2	1.64	0.62
25:RA:1579:A:H2'	25:RA:1580:A:C8	2.35	0.62
25:RA:1796:U:H2'	25:RA:1797:C:C6	2.34	0.62
25:RA:2776:A:OP1	25:RA:2776:A:H3'	2.00	0.62
39:RT:54:ARG:HA	39:RT:59:THR:HG23	1.82	0.62
2:XB:54:THR:HG21	2:XB:201:ILE:HD11	1.82	0.62
1:QA:1055:A:O2'	3:QC:161:GLU:OE2	2.13	0.62
11:QK:98:LEU:O	11:QK:101:SER:OG	2.14	0.62
25:RA:1827:C:OP2	27:RD:222:ARG:NH1	2.29	0.62
1:XA:1130:A:O2'	9:XI:3:GLN:NE2	2.28	0.62
1:XA:976:G:H5''	1:XA:1358:U:O2'	1.98	0.62
7:XG:111:ARG:NH1	7:XG:113:GLU:OE2	2.32	0.62
25:YA:265:A:O2'	25:YA:266:G:H4'	2.00	0.62
1:QA:792:A:H4'	1:QA:793:U:O5'	1.99	0.62
1:XA:1023:G:H3'	1:XA:1024:G:H5''	1.82	0.62
1:QA:243:A:H4'	1:QA:244:U:O5'	2.00	0.62
8:QH:6:ILE:HB	8:QH:85:ARG:NH1	2.15	0.62
12:QL:57:LYS:HG2	12:QL:67:THR:HG22	1.81	0.62
25:RA:2070:G:H2'	25:RA:2071:A:C8	2.35	0.62
50:Y4:37:SER:HB3	50:Y4:42:PHE:CD1	2.35	0.62
17:QQ:66:SER:O	17:QQ:70:ARG:NH1	2.33	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:265:A:N6	25:RA:427:U:O2'	2.33	0.62
27:RD:35:LYS:HD2	27:RD:104:TYR:CD1	2.35	0.62
4:XD:111:ALA:HB2	4:XD:120:LEU:HD12	1.82	0.62
5:XE:42:GLY:HA3	5:XE:66:MET:HG2	1.82	0.62
9:XI:29:ASN:OD1	9:XI:65:VAL:N	2.29	0.62
54:Y8:23:VAL:HG11	54:Y8:46:ARG:HD3	1.81	0.62
25:RA:607:U:H3	25:RA:621:A:H2	1.43	0.61
29:RF:28:ILE:HG22	29:RF:112:MET:HB3	1.80	0.61
1:XA:677:U:H3	1:XA:713:G:H22	1.47	0.61
46:Y0:27:GLU:HG3	46:Y0:68:GLU:HA	1.82	0.61
25:YA:1364:G:N7	47:Y1:2:SER:N	2.48	0.61
11:QK:121:PRO:HD2	11:QK:126:ARG:HD3	1.80	0.61
14:QN:13:THR:N	14:QN:14:PRO:HD2	2.15	0.61
28:RE:51:PHE:CD1	28:RE:52:LEU:HG	2.34	0.61
25:RA:2744:G:N2	31:RH:143:GLN:OE1	2.29	0.61
25:YA:2776:A:OP1	25:YA:2776:A:H3'	2.00	0.61
25:RA:94:G:N3	48:R2:47:ASN:ND2	2.48	0.61
28:RE:67:PHE:O	28:RE:69:LYS:N	2.33	0.61
20:XT:100:ILE:HG13	20:XT:102:GLY:N	2.15	0.61
25:YA:1062:G:H2'	25:YA:1063:G:C8	2.35	0.61
38:YS:83:LYS:C	38:YS:109:GLY:HA3	2.21	0.61
40:YU:92:ARG:HD2	41:YV:11:GLN:HB2	1.82	0.61
10:QJ:40:LEU:HB2	10:QJ:69:ASN:HB3	1.82	0.61
47:R1:53:VAL:HG22	47:R1:74:VAL:HG13	1.83	0.61
55:R9:25:VAL:HB	55:R9:34:GLN:HB2	1.82	0.61
25:RA:2298:A:N6	25:RA:2318:G:H8	1.94	0.61
25:RA:443:A:N7	29:RF:45:ARG:HD2	2.16	0.61
32:RI:104:GLN:O	32:RI:105:HIS:ND1	2.33	0.61
1:XA:542:G:OP1	4:XD:10:ARG:NH2	2.33	0.61
29:YF:197:ASP:N	29:YF:197:ASP:OD2	2.33	0.61
25:YA:1216:G:OP2	40:YU:12:ARG:NH2	2.31	0.61
1:QA:1346:A:O2'	1:QA:1347:G:OP2	2.11	0.61
11:QK:22:HIS:HB3	11:QK:29:ILE:HG23	1.83	0.61
45:RZ:166:SER:HB2	45:RZ:168:GLU:H	1.64	0.61
25:YA:2610:C:H4'	25:YA:2611:U:OP2	1.98	0.61
3:QC:14:ILE:O	3:QC:16:ARG:N	2.33	0.61
32:RI:5:LEU:HD13	32:RI:17:GLN:HB3	1.81	0.61
1:XA:1347:G:HO2'	1:XA:1373:G:H1	1.46	0.61
4:QD:30:LYS:C	4:QD:32:ALA:H	2.03	0.61
25:RA:530:G:N1	25:RA:2022:U:OP1	2.34	0.61
25:YA:1020:A:N1	25:YA:1141:U:H2'	2.15	0.61
25:YA:2451:A:N1	56:Z8:76:PPU:HE2	2.15	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:QA:17:U:H2'	1:QA:18:C:C6	2.35	0.61
14:QN:6:LEU:HD23	14:QN:23:ARG:HH22	1.64	0.61
15:QO:82:ILE:O	15:QO:86:GLY:N	2.33	0.61
21:QU:6:ARG:HE	21:QU:15:ARG:NH2	1.99	0.61
25:RA:1026:U:H4'	25:RA:1027:A:OP1	2.01	0.61
35:RP:84:ASN:HB3	35:RP:86:LYS:HG2	1.83	0.61
36:RQ:65:PHE:O	36:RQ:67:ARG:N	2.34	0.61
1:XA:250:A:H4'	1:XA:251:G:O5'	2.00	0.61
1:XA:973:G:H3'	1:XA:974:A:H5''	1.81	0.61
2:XB:67:THR:HG21	2:XB:155:LEU:HG	1.81	0.61
8:XH:4:ASP:OD1	8:XH:85:ARG:NH1	2.33	0.61
15:XO:87:ILE:HG22	15:XO:88:ARG:H	1.64	0.61
25:YA:1728:G:H3'	25:YA:1729:A:H5''	1.83	0.61
25:YA:751:A:H5'	42:YW:90:ARG:HA	1.82	0.61
22:QV:15:C:O2'	22:QV:61:C:OP1	2.19	0.61
1:XA:686:U:O4	1:XA:703:G:H1'	1.99	0.61
47:Y1:83:GLU:O	47:Y1:85:LEU:N	2.34	0.61
25:YA:99:U:H4'	25:YA:101:G:H5''	1.81	0.61
1:QA:1133:G:H2'	1:QA:1134:G:H8	1.64	0.61
25:RA:630:G:OP1	54:R8:46:ARG:NH1	2.33	0.61
25:RA:1607:C:N4	25:RA:1622:G:OP2	2.30	0.61
45:RZ:54:HIS:CD2	45:RZ:101:PRO:HG3	2.36	0.61
25:YA:1055:G:H1	25:YA:1104:C:H42	1.49	0.61
25:YA:71:A:H2	43:YX:31:HIS:HE2	1.49	0.61
40:YU:52:ARG:HA	40:YU:55:ARG:HG3	1.83	0.61
25:RA:1771:C:O2'	25:RA:1786:A:H8	1.83	0.60
1:XA:64:G:N2	1:XA:68:G:O6	2.34	0.60
25:YA:1093:G:H4'	31:YH:170:ARG:NH2	2.16	0.60
3:QC:8:ILE:HG23	3:QC:16:ARG:HG2	1.84	0.60
25:RA:1019:U:HO2'	25:RA:1021:A:H2	1.49	0.60
25:RA:1149:G:H2'	25:RA:1150:C:C6	2.36	0.60
31:RH:8:PRO:HG2	31:RH:69:ARG:HE	1.66	0.60
38:RS:88:ASP:O	38:RS:89:ARG:HB3	2.01	0.60
39:RT:77:PRO:HB2	39:RT:80:SER:HB2	1.83	0.60
40:RU:90:VAL:HG11	41:RV:40:LEU:HD12	1.82	0.60
51:Y5:16:ARG:HH11	51:Y5:16:ARG:HG2	1.66	0.60
27:YD:72:LYS:NZ	27:YD:99:ASP:OD1	2.33	0.60
31:YH:113:VAL:HG11	31:YH:151:ILE:HD12	1.83	0.60
36:YQ:35:VAL:HG13	36:YQ:130:LYS:HB3	1.83	0.60
1:QA:191:G:O2'	20:QT:101:GLY:O	2.20	0.60
1:QA:45:U:H2'	1:QA:46:G:C8	2.36	0.60
3:QC:11:ARG:O	3:QC:13:GLY:N	2.34	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:607:U:OP1	29:RF:102:PRO:HA	2.00	0.60
25:RA:1693:U:O2'	27:RD:14:ARG:NH2	2.34	0.60
37:RR:70:LEU:O	37:RR:72:ASP:N	2.31	0.60
1:XA:438:G:H4'	4:XD:123:HIS:CD2	2.35	0.60
17:XQ:11:VAL:HG12	17:XQ:85:VAL:HG13	1.83	0.60
50:Y4:56:VAL:HA	50:Y4:60:GLN:HB2	1.84	0.60
25:YA:1165:U:H2'	25:YA:1166:C:C6	2.36	0.60
27:YD:108:PRO:HB3	27:YD:143:HIS:CE1	2.35	0.60
25:YA:443:A:H3'	29:YF:45:ARG:HH12	1.65	0.60
35:YP:95:VAL:HG13	35:YP:100:LEU:HD21	1.83	0.60
9:QI:13:ALA:HB2	9:QI:68:GLY:HA3	1.82	0.60
14:QN:24:CYS:HB3	14:QN:29:ARG:H	1.66	0.60
25:RA:686:G:H21	25:RA:788:A:H61	1.49	0.60
25:RA:910:A:C5	36:RQ:13:GLN:HG3	2.35	0.60
52:Y6:25:LYS:HZ2	54:Y8:34:TRP:HZ2	1.48	0.60
25:YA:528:A:C2	25:YA:2042:A:H2'	2.36	0.60
27:YD:35:LYS:HD2	27:YD:104:TYR:CD1	2.35	0.60
4:QD:105:VAL:HG13	4:QD:110:PHE:HB2	1.83	0.60
1:QA:754:C:H5'	15:QO:72:ARG:HH22	1.65	0.60
25:RA:507:A:H5''	25:RA:508:G:H5'	1.83	0.60
25:RA:873:G:H1	25:RA:904:C:H42	1.48	0.60
27:RD:44:ASN:HB3	27:RD:49:ILE:HA	1.83	0.60
1:XA:328:C:H4'	1:XA:329:A:H5'	1.83	0.60
1:XA:991:U:O2'	1:XA:992:U:O5'	2.18	0.60
25:YA:229:A:OP1	25:YA:229:A:H4'	2.00	0.60
39:YT:84:GLN:OE1	39:YT:85:LYS:NZ	2.34	0.60
15:QO:39:LEU:HD13	15:QO:56:LEU:HB2	1.83	0.60
50:R4:23:GLU:O	50:R4:25:TYR:N	2.34	0.60
44:RY:87:LYS:O	44:RY:88:LYS:NZ	2.33	0.60
1:XA:1280:A:O2'	1:XA:1281:U:OP1	2.20	0.60
25:YA:443:A:N7	29:YF:45:ARG:HD2	2.17	0.60
34:YO:96:THR:O	34:YO:97:ARG:HB3	2.01	0.60
7:QG:26:PHE:O	7:QG:30:ILE:HG12	2.01	0.60
10:QJ:42:THR:HG23	10:QJ:68:HIS:HA	1.83	0.60
25:RA:2271:G:OP1	46:R0:18:ALA:HB1	2.02	0.60
51:R5:16:ARG:HH11	51:R5:16:ARG:HG2	1.66	0.60
37:RR:33:ARG:NH2	51:R5:55:ARG:HG2	2.16	0.60
25:RA:1497:U:H5''	25:RA:1498:C:H5	1.67	0.60
25:RA:1657:C:H2'	25:RA:1658:C:H6	1.67	0.60
25:RA:2053:G:O6	25:RA:2614:A:H2	1.85	0.60
1:XA:1446:A:O2'	1:XA:1447:G:O5'	2.20	0.60
55:Y9:35:ARG:HH21	55:Y9:37:GLY:HA3	1.67	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:1057:A:H62	25:YA:1086:A:H2'	1.66	0.60
30:YG:28:VAL:HG23	30:YG:29:TRP:CD1	2.36	0.60
31:YH:4:ILE:HB	31:YH:6:ARG:HG2	1.82	0.60
45:YZ:58:VAL:O	45:YZ:60:GLU:N	2.34	0.60
1:QA:690:G:H2'	1:QA:691:G:O4'	2.02	0.60
2:QB:15:VAL:H	2:QB:16:HIS:CE1	2.20	0.60
25:RA:1266:G:O5'	42:RW:15:ARG:NH2	2.34	0.60
25:RA:2543:G:H21	25:RA:2646:C:H5''	1.67	0.60
13:QM:93:ARG:NH1	25:RA:887:A:OP1	2.34	0.60
25:RA:2404:C:O3'	35:RP:77:ARG:NH2	2.35	0.60
1:XA:828:A:H2'	1:XA:829:G:O4'	2.02	0.60
1:XA:963:G:H21	10:XJ:55:LYS:HE2	1.67	0.60
25:YA:528:A:N1	25:YA:2042:A:H2'	2.17	0.60
35:YP:147:LEU:O	35:YP:148:LEU:HB2	2.02	0.60
12:QL:84:LEU:HD22	12:QL:104:VAL:HG11	1.84	0.60
25:RA:118:A:N3	25:RA:178:G:H1'	2.16	0.60
27:RD:70:TRP:CH2	27:RD:150:LYS:HA	2.36	0.60
30:RG:114:ILE:HD13	30:RG:140:ILE:HG21	1.83	0.60
31:RH:154:PRO:HD3	31:RH:162:ILE:N	2.16	0.60
45:RZ:87:ASP:OD2	45:RZ:87:ASP:N	2.34	0.60
1:XA:1435:G:H2'	1:XA:1436:U:C6	2.37	0.60
54:Y8:50:LEU:HD12	54:Y8:51:ALA:H	1.67	0.60
25:YA:1430:C:H2'	25:YA:1431:U:C6	2.37	0.60
25:YA:1434:A:H61	25:YA:1558:A:H62	1.48	0.60
25:YA:2698:U:H2'	25:YA:2699:C:C6	2.37	0.60
1:QA:1002:G:H1	1:QA:1038:C:H42	1.47	0.60
25:RA:270(F):U:H2'	25:RA:270(G):C:C6	2.36	0.60
30:RG:64:THR:HG23	30:RG:66:GLN:H	1.66	0.60
25:RA:631:A:OP1	35:RP:64:LYS:HE2	2.02	0.60
1:XA:963:G:H21	10:XJ:55:LYS:CE	2.14	0.60
2:XB:235:SER:O	2:XB:237:ALA:N	2.35	0.60
37:YR:42:LYS:HA	37:YR:45:ARG:HD2	1.84	0.60
25:RA:1022:G:H22	25:RA:1142(A):A:H2	1.49	0.59
32:RI:57:ARG:HA	32:RI:60:GLU:HB3	1.84	0.59
45:RZ:144:LEU:HG	45:RZ:150:LEU:HD12	1.84	0.59
1:XA:1262:C:H2'	1:XA:1263:C:C6	2.37	0.59
1:XA:690:G:H22	11:XK:55:LYS:NZ	2.00	0.59
13:XM:3:ARG:HA	13:XM:9:ILE:HG21	1.83	0.59
1:QA:1118:C:H1'	1:QA:1179:A:C4	2.37	0.59
1:QA:1128:C:OP1	9:QI:66:ARG:NH2	2.33	0.59
1:QA:1054:C:OP2	1:QA:1197:G:OP2	2.20	0.59
1:QA:1277:C:HO2'	1:QA:1279:A:H8	1.50	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:2010:G:H5''	42:RW:42:ARG:HB2	1.85	0.59
25:RA:389:G:N1	35:RP:70:GLN:HB3	2.17	0.59
32:YI:21:VAL:HG21	32:YI:25:TYR:HD1	1.66	0.59
1:QA:56:U:H4'	32:YI:82:ARG:HH22	1.67	0.59
25:YA:831:G:O2'	35:YP:38:GLN:NE2	2.35	0.59
13:QM:3:ARG:HB3	50:R4:34:GLU:HB3	1.83	0.59
54:R8:29:LYS:HB2	54:R8:44:LYS:HG2	1.84	0.59
39:RT:105:LEU:O	39:RT:107:ASP:N	2.36	0.59
6:XF:61:LEU:HB3	6:XF:63:TYR:HE2	1.66	0.59
22:XV:2:C:H2'	22:XV:3:G:H5'	1.83	0.59
25:YA:593:G:O4'	54:Y8:4:MET:HE1	2.02	0.59
25:YA:1980:G:O2'	25:YA:1982:C:OP2	2.19	0.59
42:YW:86:LEU:HD12	42:YW:87:PRO:HD2	1.83	0.59
1:QA:539:A:H2'	1:QA:540:G:C8	2.38	0.59
4:QD:64:LEU:HB2	4:QD:198:VAL:HG11	1.83	0.59
9:QI:9:ARG:HB3	9:QI:14:VAL:HG13	1.84	0.59
25:RA:1187:G:H5''	41:RV:81:TYR:CE2	2.37	0.59
1:XA:347:G:O2'	1:XA:348:G:OP2	2.19	0.59
1:XA:411:A:C4	1:XA:413:G:H1'	2.37	0.59
2:XB:92:TYR:HE1	2:XB:151:GLY:HA3	1.65	0.59
25:YA:775:G:O5'	25:YA:777:A:H1'	2.02	0.59
3:QC:50:ALA:HB2	3:QC:75:VAL:HB	1.85	0.59
22:QV:5:G:H1	22:QV:67:C:H42	1.50	0.59
25:RA:94:G:H21	48:R2:47:ASN:HD22	1.50	0.59
25:RA:1332:G:N2	25:RA:1610:A:C8	2.70	0.59
38:RS:38:GLN:OE1	38:RS:47:THR:OG1	2.18	0.59
1:XA:271:C:H2'	1:XA:272:C:H6	1.67	0.59
1:XA:973:G:OP1	10:XJ:57:LYS:NZ	2.34	0.59
25:YA:1932:A:H2'	25:YA:1933:G:O4'	2.03	0.59
25:YA:2314:C:H2'	25:YA:2315:G:H8	1.67	0.59
25:YA:2031:A:C6	25:YA:2498:C:H1'	2.37	0.59
31:YH:98:LEU:HD22	31:YH:125:VAL:HB	1.83	0.59
32:YI:129:THR:HG22	32:YI:137:PRO:HB3	1.84	0.59
37:YR:33:ARG:NH2	51:Y5:55:ARG:HG2	2.17	0.59
1:QA:501:C:H2'	1:QA:502:G:H8	1.68	0.59
1:QA:662:G:H2'	1:QA:663:A:C8	2.37	0.59
25:RA:918:A:N3	26:RB:80:U:O2'	2.33	0.59
30:RG:67:LYS:HE2	50:R4:6:HIS:CE1	2.38	0.59
25:RA:389:G:H1	35:RP:70:GLN:HB3	1.66	0.59
53:Y7:35:ARG:HG3	53:Y7:42:LEU:HD11	1.85	0.59
25:YA:1081:U:H3'	25:YA:1082:U:H4'	1.84	0.59
25:YA:1048:A:OP2	25:YA:1110:G:N2	2.35	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
42:YW:111:HIS:CD2	42:YW:112:GLY:H	2.20	0.59
13:QM:49:THR:HB	13:QM:52:GLU:HG3	1.85	0.59
50:R4:16:CYS:SG	50:R4:17:GLY:N	2.75	0.59
52:R6:52:VAL:HG22	52:R6:53:LYS:HG3	1.84	0.59
25:RA:2818:G:OP2	37:RR:42:LYS:NZ	2.35	0.59
25:RA:309:G:N3	25:RA:329:G:O2'	2.35	0.59
25:RA:590:A:H2'	25:RA:591:C:C6	2.37	0.59
31:RH:105:LEU:HD13	31:RH:105:LEU:H	1.67	0.59
1:XA:166:G:H2'	1:XA:167:G:H8	1.67	0.59
5:XE:45:PHE:CE2	5:XE:47:LYS:HD2	2.38	0.59
49:Y3:6:VAL:HG13	49:Y3:56:VAL:HG13	1.84	0.59
28:YE:36:ARG:HH21	28:YE:88:GLY:HA2	1.68	0.59
36:RQ:109:VAL:HG12	36:RQ:114:ALA:HB2	1.83	0.59
42:RW:86:LEU:HD12	42:RW:87:PRO:HD2	1.85	0.59
1:XA:1062:U:H2'	1:XA:1063:C:C6	2.38	0.59
31:YH:6:ARG:NH2	31:YH:54:ARG:HH22	2.01	0.59
35:YP:26:GLY:O	35:YP:28:GLY:N	2.35	0.59
25:RA:2364:C:OP1	46:R0:55:ARG:NH1	2.36	0.59
31:RH:121:ILE:HG13	31:RH:140:LYS:HD2	1.84	0.59
4:XD:9:CYS:SG	4:XD:22:LYS:HE2	2.39	0.59
25:YA:2291:U:H2'	25:YA:2292:C:C6	2.38	0.59
25:YA:2795:G:H3'	25:YA:2797:U:C5'	2.33	0.59
25:YA:372:G:O2'	25:YA:373:U:P	2.61	0.59
1:QA:686:U:H1'	11:QK:42:TRP:HE1	1.68	0.59
27:RD:85:ASP:HB2	27:RD:92:ILE:HD13	1.84	0.59
25:RA:2250:G:C4	36:RQ:82:ARG:HG3	2.37	0.59
10:XJ:76:ASN:O	10:XJ:78:ASN:ND2	2.36	0.59
14:XN:23:ARG:HD2	14:XN:28:GLY:O	2.03	0.59
20:XT:10:LEU:HG	20:XT:12:ALA:H	1.67	0.59
25:YA:943:U:OP2	35:YP:36:LYS:NZ	2.36	0.59
38:YS:26:LEU:HB3	38:YS:87:PHE:HA	1.85	0.59
1:QA:664:G:H22	1:QA:741:G:H1	1.49	0.58
1:QA:753:A:H4'	1:QA:754:C:O5'	2.03	0.58
7:QG:73:MET:HG2	7:QG:90:GLU:HA	1.83	0.58
25:RA:1857:G:O2'	25:RA:1885:A:N6	2.36	0.58
25:RA:345:A:H2'	25:RA:347:A:H62	1.68	0.58
25:RA:620:G:H4'	25:RA:621:A:H5''	1.84	0.58
1:XA:243:A:H4'	1:XA:244:U:H3'	1.84	0.58
25:YA:1012:U:O2'	25:YA:1013:C:OP2	2.16	0.58
25:YA:1364:G:C8	47:Y1:2:SER:N	2.70	0.58
30:YG:136:ARG:O	30:YG:154:GLY:HA2	2.02	0.58
38:YS:106:ARG:HA	38:YS:110:LEU:HD11	1.85	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:YN:40:PRO:HB3	40:YU:68:ALA:HB2	1.85	0.58
1:QA:1376:U:OP1	7:QG:94:ARG:NH1	2.36	0.58
47:R1:92:LYS:HG3	47:R1:96:LYS:HB2	1.84	0.58
25:RA:111:A:H4'	48:R2:69:ARG:NH2	2.18	0.58
25:RA:1178:C:H2'	25:RA:1179:C:C6	2.38	0.58
25:RA:2445:G:OP1	29:RF:74:ARG:NH2	2.37	0.58
27:RD:44:ASN:CB	27:RD:49:ILE:HA	2.33	0.58
45:RZ:158:PRO:HG2	45:RZ:161:VAL:HG21	1.85	0.58
36:RQ:137:TYR:CE2	45:RZ:83:PRO:HG3	2.38	0.58
51:Y5:4:HIS:HB3	51:Y5:5:PRO:CD	2.32	0.58
25:YA:250:G:OP2	54:Y8:13:ARG:NH2	2.35	0.58
25:YA:1103:A:H5'	25:YA:1104:C:H5	1.66	0.58
27:YD:28:GLU:OE1	27:YD:29:PRO:HD2	2.03	0.58
32:YI:67:ARG:HH21	32:YI:68:LEU:HB2	1.68	0.58
37:YR:67:LEU:HD13	37:YR:76:VAL:HG21	1.84	0.58
45:YZ:146:ILE:HG22	45:YZ:176:PRO:HD3	1.85	0.58
4:QD:111:ALA:HB2	4:QD:120:LEU:HD12	1.85	0.58
27:RD:71:ASP:OD2	27:RD:103:ARG:NH2	2.36	0.58
1:XA:7:G:H5'	1:XA:298:A:O4'	2.03	0.58
12:XL:38:THR:HG23	12:XL:57:LYS:HB3	1.84	0.58
47:Y1:51:VAL:HG11	47:Y1:74:VAL:HG21	1.84	0.58
25:YA:1665:A:H1'	34:YO:1:MET:HG3	1.83	0.58
43:YX:61:GLY:N	43:YX:75:ASP:OD2	2.36	0.58
1:QA:501:C:H2'	1:QA:502:G:C8	2.38	0.58
25:RA:1348:G:H2'	25:RA:1349:A:H5''	1.85	0.58
1:XA:1175:G:H2'	1:XA:1176:A:C8	2.38	0.58
3:XC:14:ILE:HG12	3:XC:15:THR:H	1.67	0.58
13:XM:13:LYS:HA	13:XM:44:ARG:HD2	1.83	0.58
25:YA:2115:G:N2	25:YA:2165:G:N7	2.45	0.58
25:YA:612:G:N2	25:YA:616:A:O2'	2.37	0.58
41:YV:44:LYS:O	41:YV:46:VAL:N	2.36	0.58
1:QA:643:C:H2'	1:QA:644:G:H8	1.69	0.58
1:QA:711:G:OP1	6:QF:54:LYS:NZ	2.32	0.58
10:QJ:49:VAL:HG13	14:QN:41:ARG:HB2	1.85	0.58
16:QP:21:VAL:O	16:QP:33:ILE:HG12	2.03	0.58
27:RD:35:LYS:HD2	27:RD:104:TYR:CE1	2.39	0.58
1:QA:1422:G:H5''	34:RO:48:PRO:HB3	1.84	0.58
1:XA:1291:G:OP1	7:XG:37:ASN:ND2	2.36	0.58
20:XT:63:ILE:HG22	20:XT:77:ALA:HB1	1.86	0.58
20:XT:56:MET:HG3	20:XT:88:VAL:HG21	1.85	0.58
31:YH:153:LYS:HB3	31:YH:154:PRO:HD3	1.85	0.58
1:QA:1298:C:O2'	1:QA:1299:A:OP2	2.20	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:QB:77:ALA:HB2	2:QB:211:ILE:HD13	1.86	0.58
25:RA:635:C:O2'	25:RA:639:U:OP1	2.19	0.58
30:RG:136:ARG:O	30:RG:154:GLY:HA2	2.03	0.58
2:XB:15:VAL:H	2:XB:16:HIS:CE1	2.22	0.58
2:XB:72:GLY:HA2	2:XB:165:VAL:HG22	1.86	0.58
2:XB:96:ARG:H	2:XB:96:ARG:HD2	1.67	0.58
9:XI:43:ALA:HA	9:XI:74:ILE:HD13	1.85	0.58
50:Y4:42:PHE:O	50:Y4:44:THR:N	2.36	0.58
25:YA:1278:A:H4'	37:YR:34:ILE:HD12	1.85	0.58
25:YA:2294:C:OP2	38:YS:13:ARG:NH1	2.37	0.58
1:QA:192:U:H2'	1:QA:193:C:H6	1.68	0.58
25:RA:1204:A:O2'	25:RA:1205:U:O5'	2.21	0.58
25:RA:1496:A:H8	25:RA:1577:C:O2'	1.85	0.58
27:RD:182:LEU:N	27:RD:272:ALA:HB3	2.18	0.58
25:RA:1803:A:O2'	27:RD:259:THR:HG21	2.03	0.58
30:RG:112:PRO:HB3	50:R4:37:SER:HB2	1.85	0.58
31:RH:89:ILE:O	31:RH:89:ILE:HG12	2.04	0.58
6:XF:36:ARG:NH1	6:XF:38:GLU:OE2	2.37	0.58
8:XH:39:LEU:HB3	8:XH:45:ILE:HG12	1.86	0.58
25:YA:1048:A:P	25:YA:1110:G:H22	2.25	0.58
25:YA:780:G:H21	25:YA:783:A:N6	1.98	0.58
37:YR:27:SER:HB3	37:YR:34:ILE:HD11	1.84	0.58
8:QH:121:ASP:N	8:QH:121:ASP:OD1	2.35	0.58
12:QL:53:ARG:HD3	12:QL:93:LEU:HD21	1.86	0.58
1:QA:552:U:O2'	12:QL:86:ARG:O	2.17	0.58
25:RA:1525:G:H2'	25:RA:1526:G:H8	1.69	0.58
25:RA:2070:G:H2'	25:RA:2071:A:H8	1.68	0.58
31:RH:87:LEU:HD22	31:RH:162:ILE:HG22	1.85	0.58
1:XA:1065:U:O2'	1:XA:1066:C:OP2	2.16	0.58
1:XA:680:C:H2'	1:XA:681:C:H6	1.69	0.58
3:XC:95:THR:HG22	3:XC:97:LYS:HG3	1.84	0.58
25:YA:2655:G:O2'	25:YA:2656:U:OP2	2.21	0.58
13:XM:93:ARG:NH1	25:YA:887:A:OP1	2.37	0.58
25:YA:1191:G:OP1	35:YP:32:THR:HB	2.04	0.58
33:RN:13:TRP:O	33:RN:135:PRO:HD2	2.03	0.58
26:RB:50:G:H5"	38:RS:61:ASN:HD21	1.68	0.58
2:XB:93:VAL:HG11	2:XB:97:TRP:HD1	1.68	0.58
19:XS:80:TYR:O	19:XS:82:GLY:N	2.36	0.58
25:YA:49:A:N7	25:YA:120:U:C5	2.70	0.58
25:YA:813:U:H2'	25:YA:814:C:C6	2.39	0.58
26:YB:41:U:C4	30:YG:70:VAL:HG23	2.38	0.58
29:YF:127:GLU:O	29:YF:129:PHE:N	2.32	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
34:YO:64:ARG:HG2	34:YO:79:PHE:CG	2.38	0.58
45:YZ:5:LEU:HD11	45:YZ:39:VAL:HB	1.85	0.58
7:QG:26:PHE:CE2	7:QG:30:ILE:HD11	2.38	0.58
13:QM:58:GLU:O	13:QM:62:ASN:ND2	2.31	0.58
27:RD:24:ILE:HD11	27:RD:91:ARG:HD2	1.84	0.58
32:RI:5:LEU:H	32:RI:5:LEU:HD12	1.69	0.58
35:RP:47:ASP:OD1	35:RP:49:ARG:NH1	2.37	0.58
5:XE:91:LEU:HD12	5:XE:120:THR:HG22	1.85	0.58
29:YF:28:ILE:HG22	29:YF:112:MET:HB3	1.85	0.58
37:YR:24:GLN:OE1	37:YR:36:THR:HG21	2.04	0.58
39:YT:24:PRO:HA	39:YT:49:VAL:HG13	1.85	0.58
40:YU:92:ARG:HD3	40:YU:94:ASN:HB3	1.85	0.58
25:RA:414:C:O2	25:RA:1864:U:O2'	2.18	0.57
33:RN:54:VAL:HB	33:RN:122:VAL:HG22	1.85	0.57
42:RW:71:VAL:HA	42:RW:107:LEU:HD12	1.86	0.57
7:XG:89:MET:HE1	7:XG:156:TRP:H	1.69	0.57
37:YR:117:VAL:HG22	37:YR:118:GLU:H	1.68	0.57
38:YS:59:LYS:HD3	38:YS:60:GLY:N	2.19	0.57
3:QC:134:ILE:HG23	3:QC:151:VAL:HB	1.85	0.57
25:RA:2015:A:H1'	51:R5:2:ALA:HA	1.85	0.57
25:RA:2651:C:H42	25:RA:2669:G:H1	1.53	0.57
25:RA:1637:A:H4'	25:RA:2711:A:O2'	2.04	0.57
28:RE:131:ALA:HB1	28:RE:135:HIS:HE1	1.69	0.57
44:RY:95:LYS:NZ	44:RY:99:CYS:O	2.37	0.57
1:XA:522:C:H41	12:XL:53:ARG:HH22	1.50	0.57
4:XD:9:CYS:HB3	4:XD:32:ALA:HB2	1.86	0.57
25:YA:72:U:H3	48:Y2:62:THR:HG22	1.68	0.57
30:YG:67:LYS:HE2	50:Y4:6:HIS:CE1	2.38	0.57
32:YI:33:ARG:HB3	32:YI:35:LEU:HG	1.86	0.57
36:YQ:66:ILE:HA	36:YQ:104:PHE:HA	1.85	0.57
42:YW:73:ALA:HB3	42:YW:106:ILE:HD13	1.84	0.57
1:QA:1376:U:P	7:QG:94:ARG:HH12	2.27	0.57
1:QA:1513:A:H2'	1:QA:1514:C:C6	2.39	0.57
54:R8:36:LYS:HB3	54:R8:40:GLU:HG2	1.85	0.57
25:RA:1771:C:H1'	25:RA:1786:A:C8	2.40	0.57
25:RA:2655:G:N2	25:RA:2665:A:OP2	2.37	0.57
30:RG:68:PRO:HB2	30:RG:90:LEU:HD12	1.86	0.57
1:XA:539:A:OP1	12:XL:114:LYS:NZ	2.22	0.57
1:XA:753:A:H4'	1:XA:754:C:O5'	2.03	0.57
17:XQ:55:ASP:HA	17:XQ:79:SER:HA	1.85	0.57
27:YD:65:ILE:H	27:YD:65:ILE:HD13	1.68	0.57
28:YE:35:GLN:HB3	28:YE:48:GLN:HB2	1.87	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:YG:98:ARG:NH1	50:Y4:1:MET:SD	2.77	0.57
1:QA:1129:C:H4'	1:QA:1130:A:H5'	1.86	0.57
7:QG:15:ASP:OD2	7:QG:44:TYR:OH	2.22	0.57
13:QM:14:ARG:N	13:QM:44:ARG:HD3	2.18	0.57
31:RH:153:LYS:HB3	31:RH:154:PRO:CD	2.34	0.57
37:RR:117:VAL:O	37:RR:118:GLU:HB2	2.04	0.57
3:XC:70:VAL:HG21	3:XC:76:VAL:HG11	1.85	0.57
11:XK:21:ILE:HG13	11:XK:30:VAL:HG12	1.86	0.57
46:Y0:50:ASN:HB3	46:Y0:63:VAL:HG22	1.86	0.57
25:YA:83:G:N2	25:YA:103:A:OP2	2.22	0.57
25:YA:1103:A:H5'	25:YA:1104:C:C5	2.39	0.57
25:YA:242:G:H5''	54:Y8:62:LEU:HD13	1.86	0.57
36:YQ:116:GLU:O	36:YQ:120:ILE:HG12	2.05	0.57
38:YS:10:ARG:NH2	38:YS:91:PRO:O	2.36	0.57
3:QC:134:ILE:HG22	3:QC:168:ALA:HB3	1.86	0.57
25:RA:1043:C:N3	25:RA:1112:G:N2	2.43	0.57
1:XA:673:G:H2'	1:XA:674:G:C8	2.39	0.57
25:YA:2405:G:O2'	25:YA:2411:A:N6	2.36	0.57
25:YA:259:G:N2	25:YA:621:A:H8	2.02	0.57
32:YI:40:THR:O	32:YI:44:LEU:HB2	2.04	0.57
45:YZ:158:PRO:O	45:YZ:160:GLY:N	2.37	0.57
7:QG:79:ARG:HH12	7:QG:82:GLY:HA2	1.69	0.57
25:RA:1798:U:H5'	27:RD:259:THR:HG22	1.86	0.57
44:RY:76:CYS:SG	44:RY:77:PRO:HD2	2.45	0.57
1:XA:701:C:H1'	1:XA:703:G:C6	2.39	0.57
2:XB:96:ARG:HD3	2:XB:148:TYR:HE1	1.70	0.57
4:XD:154:ASN:OD1	4:XD:154:ASN:N	2.37	0.57
1:XA:1453:G:H2'	20:XT:39:LYS:HE2	1.84	0.57
30:YG:98:ARG:HH12	50:Y4:1:MET:HB3	1.69	0.57
25:YA:2233:U:H2'	25:YA:2234:G:C8	2.39	0.57
46:R0:18:ALA:O	46:R0:20:ARG:NH1	2.36	0.57
25:RA:2306:C:H3'	25:RA:2307:G:H5''	1.86	0.57
25:RA:923:C:H2'	25:RA:924:C:C6	2.40	0.57
27:RD:145:VAL:HG13	27:RD:191:ALA:HB2	1.87	0.57
27:RD:241:PRO:O	27:RD:242:ARG:HB2	2.04	0.57
1:XA:1016:A:H2'	1:XA:1017:G:O4'	2.04	0.57
26:YB:12:C:O2'	46:Y0:74:ARG:HG3	2.04	0.57
25:YA:1309:G:H4'	53:Y7:7:PRO:HB2	1.85	0.57
25:YA:443:A:H1'	25:YA:1201:C:O4'	2.03	0.57
31:YH:149:ARG:HG3	31:YH:162:ILE:O	2.05	0.57
45:YZ:19:ARG:NH1	45:YZ:84:GLU:O	2.35	0.57
6:QF:3:ARG:NH1	6:QF:38:GLU:OE2	2.37	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:QM:23:TYR:HB3	13:QM:67:GLU:HG2	1.87	0.57
30:RG:22:ARG:HH21	30:RG:171:ALA:HB1	1.69	0.57
35:RP:58:THR:C	35:RP:61:ARG:HE	2.06	0.57
16:XP:20:VAL:HG23	16:XP:35:LYS:HA	1.86	0.57
19:XS:32:LYS:HA	19:XS:50:ALA:HB3	1.86	0.57
22:XV:51:C:H2'	22:XV:52:G:O4'	2.05	0.57
25:YA:1405:U:H2'	25:YA:1406:U:C6	2.40	0.57
27:YD:71:ASP:CB	27:YD:103:ARG:HH22	2.18	0.57
25:YA:1142(A):A:H4'	33:YN:25:ARG:HH22	1.70	0.57
35:YP:135:LEU:O	35:YP:139:LYS:HB2	2.04	0.57
2:QB:51:LEU:HD23	2:QB:201:ILE:HD12	1.86	0.57
25:RA:140:A:H8	25:RA:1408:C:O2'	1.88	0.57
25:RA:2146:C:H4'	25:RA:2147:G:C8	2.39	0.57
25:RA:372:G:O2'	25:RA:373:U:P	2.62	0.57
43:RX:60:ARG:NH1	53:R7:47:ARG:HH22	2.03	0.57
1:XA:96:G:H2'	1:XA:97:U:O4'	2.03	0.57
25:YA:1204:A:H2	25:YA:1241:A:N1	2.01	0.57
25:YA:2298:A:H62	25:YA:2318:G:H8	1.51	0.57
1:QA:1175:G:H2'	1:QA:1176:A:H8	1.68	0.57
12:QL:117:ARG:HB3	12:QL:122:THR:HB	1.86	0.57
25:RA:220:G:O2'	25:RA:233:A:N3	2.37	0.57
25:RA:2781:A:H5''	25:RA:2782:G:H5'	1.86	0.57
27:RD:44:ASN:HB2	27:RD:48:ARG:O	2.05	0.57
1:XA:1443:G:H5''	1:XA:1446:A:H2	1.69	0.57
9:XI:15:ALA:HB2	9:XI:65:VAL:HG23	1.86	0.57
25:YA:1412:A:H2'	25:YA:1413:G:C8	2.40	0.57
25:YA:1590:U:H2'	25:YA:1591:G:C8	2.39	0.57
32:YI:56:LYS:HE3	32:YI:57:ARG:HA	1.87	0.57
45:YZ:77:ASP:OD2	45:YZ:80:ARG:HD3	2.05	0.57
1:QA:620:C:C2	4:QD:135:LEU:HG	2.40	0.56
3:QC:73:PRO:HG3	3:QC:105:GLU:HG3	1.88	0.56
19:QS:41:VAL:HB	19:QS:42:PRO:CA	2.35	0.56
25:RA:1525:G:H2'	25:RA:1526:G:C8	2.40	0.56
25:RA:2645:G:H3'	25:RA:2646:C:H5'	1.86	0.56
41:RV:52:VAL:HG21	41:RV:55:ALA:HB3	1.87	0.56
1:XA:1347:G:C8	9:XI:107:ARG:HB3	2.40	0.56
50:Y4:71:ARG:HB2	50:Y4:71:ARG:HH11	1.68	0.56
25:YA:2815:C:H5'	51:Y5:29:THR:HG21	1.87	0.56
25:YA:1266:G:O5'	42:YW:15:ARG:NH2	2.38	0.56
25:YA:1359:A:N6	25:YA:1372:U:C4	2.72	0.56
25:YA:2011:U:OP1	42:YW:42:ARG:NH1	2.37	0.56
25:YA:2111:C:N3	25:YA:2118:U:O2'	2.38	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:654(A):G:H8	25:YA:654(A):G:OP2	1.88	0.56
36:YQ:85:LYS:O	36:YQ:87:LYS:N	2.38	0.56
25:RA:1378:A:OP1	53:R7:10:ARG:NH2	2.37	0.56
25:RA:1614:A:H62	42:RW:93:ALA:HB2	1.70	0.56
27:RD:108:PRO:HB3	27:RD:143:HIS:CE1	2.40	0.56
27:RD:148:GLU:HB2	27:RD:151:LYS:HD2	1.87	0.56
29:RF:11:VAL:HG12	29:RF:12:LEU:H	1.69	0.56
32:RI:116:LEU:O	32:RI:118:LYS:N	2.38	0.56
36:RQ:32:TYR:HE1	36:RQ:133:ARG:HG3	1.69	0.56
1:XA:128:G:O2'	17:XQ:3:LYS:NZ	2.33	0.56
10:XJ:50:ILE:HD11	10:XJ:57:LYS:HD3	1.85	0.56
25:YA:1359:A:H2'	25:YA:1360:A:H5'	1.88	0.56
25:YA:372:G:HO2'	25:YA:400:G:H1	1.53	0.56
25:YA:551:G:H5'	25:YA:1220:A:H1'	1.87	0.56
29:YF:107:LYS:HD2	29:YF:206:ILE:HA	1.86	0.56
30:YG:81:LYS:O	30:YG:82:LEU:HB2	2.04	0.56
34:YO:85:VAL:HG11	34:YO:114:ILE:HD11	1.87	0.56
25:RA:1885:A:H5'	25:RA:1886:C:OP2	2.05	0.56
25:RA:2116:G:N1	25:RA:2162:G:OP1	2.38	0.56
25:RA:2032:G:H1'	28:RE:145:LYS:HD3	1.86	0.56
32:RI:69:LYS:HG3	32:RI:136:VAL:HB	1.87	0.56
36:RQ:43:THR:HA	36:RQ:94:VAL:HG12	1.87	0.56
1:XA:27:G:H4'	4:XD:209:ARG:HG3	1.86	0.56
1:XA:1232:U:OP1	9:XI:124:GLN:NE2	2.38	0.56
22:XV:68:C:H2'	22:XV:69:C:C6	2.41	0.56
25:YA:1204:A:H1'	25:YA:1206:G:C8	2.40	0.56
25:YA:27:G:N2	25:YA:512:G:O2'	2.38	0.56
25:YA:2849:U:P	39:YT:95:ARG:HH12	2.28	0.56
35:YP:101:VAL:HG23	35:YP:106:LEU:HB3	1.88	0.56
39:YT:60:THR:HG22	39:YT:77:PRO:HA	1.86	0.56
41:YV:59:ALA:HB2	41:YV:96:ILE:HD13	1.87	0.56
25:YA:518:G:H5'	42:YW:18:ARG:HH12	1.70	0.56
1:QA:1465:C:H2'	1:QA:1466:C:O4'	2.05	0.56
17:QQ:90:ILE:O	17:QQ:94:ASN:ND2	2.38	0.56
25:RA:1028:A:N6	25:RA:1125:G:H2'	2.20	0.56
25:RA:1300:U:H4'	25:RA:1301:A:H5''	1.87	0.56
25:RA:1285:G:N2	25:RA:1329:U:OP1	2.38	0.56
25:RA:507:A:C5'	25:RA:508:G:H5'	2.34	0.56
32:RI:94:ALA:H	32:RI:116:LEU:HD13	1.70	0.56
35:RP:106:LEU:O	35:RP:107:LYS:HB2	2.05	0.56
28:RE:10:GLY:HA3	39:RT:8:LYS:HD2	1.85	0.56
25:YA:1061:U:H4'	25:YA:1070:A:H1'	1.87	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:1188:U:H4'	41:YV:79:VAL:HG22	1.86	0.56
1:QA:1367:C:H4'	10:QJ:48:THR:HG21	1.88	0.56
25:RA:960:A:H61	36:RQ:82:ARG:HH12	1.53	0.56
25:RA:2311:A:C8	30:RG:88:ILE:HD11	2.41	0.56
37:RR:67:LEU:HD13	37:RR:76:VAL:HG21	1.86	0.56
38:RS:106:ARG:HA	38:RS:110:LEU:HD11	1.87	0.56
44:RY:81:LYS:HZ3	44:RY:98:VAL:HG11	1.69	0.56
2:XB:178:ARG:HG3	8:XH:72:PRO:HA	1.86	0.56
52:Y6:25:LYS:HE2	52:Y6:27:LYS:HE3	1.87	0.56
41:YV:66:ARG:HH11	41:YV:88:ARG:HD3	1.71	0.56
45:YZ:152:ALA:HB2	45:YZ:168:GLU:HA	1.87	0.56
1:QA:336:C:H2'	1:QA:337:C:C6	2.39	0.56
8:QH:91:ARG:HB2	12:QL:7:ILE:HG13	1.87	0.56
25:RA:1798:U:C5'	27:RD:259:THR:HG22	2.35	0.56
25:RA:2392:A:H2	25:RA:2424:C:N4	2.00	0.56
25:RA:764:A:H5'	27:RD:210:GLY:HA2	1.86	0.56
36:RQ:24:GLY:O	36:RQ:26:TYR:N	2.36	0.56
41:RV:44:LYS:HE2	41:RV:45:THR:H	1.70	0.56
1:XA:343:U:HO2'	1:XA:344:A:H8	1.53	0.56
36:YQ:137:TYR:CE2	45:YZ:83:PRO:HG3	2.41	0.56
25:YA:2882:A:OP1	37:YR:96:ARG:NH1	2.38	0.56
42:YW:71:VAL:HA	42:YW:107:LEU:HD12	1.87	0.56
25:RA:74:A:H4'	25:RA:75:G:O5'	2.06	0.56
25:RA:859:G:O2'	25:RA:860:U:O2	2.16	0.56
28:RE:4:ILE:HD12	28:RE:28:ALA:HB1	1.88	0.56
25:RA:2404:C:H1'	35:RP:67:MET:HE1	1.87	0.56
36:RQ:66:ILE:HA	36:RQ:104:PHE:HA	1.87	0.56
1:XA:1392:G:H21	1:XA:1502:A:H8	1.52	0.56
3:XC:174:PRO:HD2	3:XC:182:ILE:HD11	1.88	0.56
7:XG:54:THR:O	7:XG:56:GLN:N	2.39	0.56
16:XP:20:VAL:HG21	16:XP:32:TYR:CD1	2.40	0.56
25:YA:1819:A:H4'	25:YA:1820:U:O5'	2.06	0.56
25:YA:860:U:C5	25:YA:917:A:C2	2.94	0.56
1:QA:128:G:O2'	17:QQ:3:LYS:NZ	2.35	0.56
2:QB:82:ARG:HA	2:QB:92:TYR:HE2	1.71	0.56
25:RA:1578:U:H2'	25:RA:1579:A:H5'	1.86	0.56
25:RA:1786:A:H2	25:RA:2606:C:H1'	1.70	0.56
25:RA:993:G:OP1	40:RU:50:ARG:NH2	2.38	0.56
43:RX:31:HIS:CD2	43:RX:32:PRO:HD2	2.40	0.56
1:XA:1368:G:OP1	9:XI:111:ARG:NH2	2.34	0.56
1:XA:437:U:H2'	1:XA:438:G:O4'	2.04	0.56
2:XB:84:GLU:HB3	2:XB:219:VAL:HG21	1.86	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:XB:21:ARG:O	2:XB:23:ARG:HD3	2.05	0.56
1:XA:191:G:O2'	20:XT:101:GLY:O	2.23	0.56
22:XV:61:C:H2'	22:XV:62:C:H6	1.71	0.56
31:YH:92:ILE:HD12	31:YH:92:ILE:H	1.71	0.56
32:YI:79:ILE:HB	32:YI:142:VAL:HA	1.88	0.56
34:YO:97:ARG:HA	34:YO:117:LEU:HD22	1.88	0.56
8:QH:106:GLY:O	8:QH:122:ARG:NH2	2.36	0.56
12:QL:45:PRO:HB3	12:QL:92:ASP:HB3	1.87	0.56
35:RP:68:GLN:HG2	54:R8:12:LYS:HD3	1.88	0.56
32:RI:8:PRO:HD3	32:RI:15:VAL:HG13	1.87	0.56
1:XA:1060:C:C4	3:XC:2:GLY:HA2	2.41	0.56
22:XV:3:G:O2'	22:XV:4:G:H8	1.88	0.56
25:YA:1693:U:O2'	27:YD:14:ARG:NH2	2.39	0.56
25:YA:2123:G:H1	25:YA:2175:C:H42	1.53	0.56
25:YA:2168:G:N2	25:YA:2170:A:N7	2.52	0.56
25:YA:2585:U:H5	56:Z8:76:PPU:HO2'	1.52	0.56
1:QA:1446:A:O2'	1:QA:1447:G:O5'	2.24	0.56
1:QA:266:G:H5''	1:QA:267:C:C5	2.40	0.56
10:QJ:5:ARG:HG3	10:QJ:71:LEU:HD11	1.87	0.56
25:RA:2630:G:N2	25:RA:2788:C:O2	2.38	0.56
25:RA:67:U:H3	25:RA:74:A:H2	1.48	0.56
32:RI:29:TYR:HD2	32:RI:30:LEU:HD23	1.71	0.56
25:RA:637:A:O5'	35:RP:116:GLY:HA2	2.06	0.56
40:RU:94:ASN:C	40:RU:94:ASN:HD22	2.08	0.56
1:XA:890:G:O2'	1:XA:906:G:O6	2.22	0.56
25:YA:573:G:OP2	41:YV:78:LYS:NZ	2.38	0.56
36:YQ:81:VAL:C	36:YQ:82:ARG:HG2	2.25	0.56
44:YY:95:LYS:HB3	44:YY:100:ALA:HA	1.87	0.56
4:QD:187:ARG:NH2	4:QD:193:ASP:OD2	2.38	0.56
12:QL:89:ARG:HB3	12:QL:97:ARG:HA	1.88	0.56
25:RA:1794:U:H2'	25:RA:1795:C:C6	2.41	0.56
25:RA:550:G:O2'	25:RA:1220:A:O2'	2.18	0.56
29:RF:110:LEU:HD11	29:RF:181:LEU:HD12	1.88	0.56
35:RP:121:LYS:HD3	35:RP:122:PRO:HD2	1.88	0.56
45:RZ:182:LYS:H	45:RZ:182:LYS:HD3	1.70	0.56
1:XA:522:C:H41	12:XL:53:ARG:NH2	2.04	0.56
3:XC:130:VAL:O	3:XC:134:ILE:HG12	2.06	0.56
3:XC:9:GLY:HA2	3:XC:12:LEU:HD23	1.88	0.56
4:XD:122:ARG:NH1	4:XD:134:ASP:O	2.39	0.56
4:XD:11:LEU:HD13	4:XD:66:ARG:HG2	1.87	0.56
25:YA:1952:A:C6	34:YO:22:ILE:HD12	2.41	0.56
31:YH:41:MET:HE1	31:YH:64:LEU:HB3	1.86	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:YN:40:PRO:O	40:YU:64:ARG:HD2	2.06	0.56
1:QA:1510:U:H2'	1:QA:1511:G:C8	2.42	0.55
2:QB:71:VAL:HG12	2:QB:93:VAL:HB	1.88	0.55
1:QA:953:G:N7	13:QM:104:ARG:NH2	2.54	0.55
51:R5:4:HIS:HB3	51:R5:5:PRO:CD	2.32	0.55
52:R6:36:LEU:HB2	52:R6:50:ARG:HA	1.89	0.55
25:RA:2543:G:H2'	25:RA:2544:G:C8	2.41	0.55
32:RI:41:GLU:HA	32:RI:44:LEU:HB2	1.86	0.55
42:RW:86:LEU:HD22	42:RW:96:ILE:HD11	1.88	0.55
1:XA:266:G:H5''	1:XA:267:C:H5	1.70	0.55
1:XA:674:G:H2'	1:XA:675:A:C8	2.41	0.55
1:XA:953:G:H5'	1:XA:965:A:H61	1.71	0.55
25:YA:1077:A:H5'	25:YA:1078:U:H5''	1.88	0.55
25:YA:1427:A:H4'	25:YA:1428:C:O5'	2.05	0.55
25:YA:1678:G:H8	25:YA:1678:G:O5'	1.90	0.55
33:YN:56:ASN:N	33:YN:125:GLY:O	2.22	0.55
39:YT:29:ARG:HB2	39:YT:46:GLU:HG3	1.88	0.55
1:QA:266:G:H5''	1:QA:267:C:H5	1.70	0.55
1:QA:411:A:C4	1:QA:413:G:H1'	2.42	0.55
10:QJ:16:LEU:HD23	10:QJ:94:VAL:HG13	1.88	0.55
10:QJ:78:ASN:O	10:QJ:81:THR:OG1	2.24	0.55
25:RA:1816:G:H8	27:RD:62:TYR:CZ	2.24	0.55
25:RA:1769:G:O2'	25:RA:1958:C:OP1	2.17	0.55
25:RA:2308:G:N2	25:RA:2311:A:H2	2.04	0.55
39:RT:26:ASP:O	39:RT:49:VAL:HG12	2.07	0.55
1:XA:1450:U:O2'	1:XA:1451:A:N7	2.35	0.55
1:XA:188:U:H2'	1:XA:189:U:H5''	1.88	0.55
10:XJ:34:VAL:HG22	10:XJ:74:ILE:HG22	1.89	0.55
27:YD:232:PRO:HB3	27:YD:244:ARG:NH1	2.21	0.55
39:YT:39:ARG:HG2	39:YT:40:THR:H	1.72	0.55
1:QA:1104:G:H4'	2:QB:111:ARG:NH1	2.21	0.55
47:R1:53:VAL:HG11	47:R1:90:ILE:HD11	1.88	0.55
25:RA:2150:U:H2'	25:RA:2151:G:C8	2.42	0.55
25:RA:2618:G:H21	28:RE:150:VAL:HG21	1.70	0.55
28:RE:63:LEU:CD1	28:RE:65:GLY:H	2.20	0.55
34:RO:78:ARG:HH21	39:RT:103:ARG:NH2	2.03	0.55
2:XB:158:LEU:HD13	2:XB:182:ILE:HD11	1.89	0.55
25:YA:1285:G:N2	25:YA:1329:U:OP1	2.35	0.55
25:YA:1798:U:H5'	27:YD:259:THR:HG22	1.88	0.55
50:R4:24:THR:OG1	50:R4:25:TYR:N	2.38	0.55
25:RA:898:C:H2'	25:RA:899:A:H5'	1.88	0.55
41:RV:7:THR:HG23	41:RV:22:VAL:HG11	1.88	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:XE:37:ARG:HA	5:XE:114:GLY:N	2.21	0.55
5:XE:50:GLU:HB3	5:XE:53:LEU:HD13	1.88	0.55
15:XO:18:PHE:CE1	15:XO:21:ASP:HB2	2.41	0.55
6:XF:97:PHE:HD2	18:XR:31:LEU:HD21	1.70	0.55
54:Y8:50:LEU:HD12	54:Y8:51:ALA:N	2.21	0.55
25:YA:264:C:C2'	25:YA:265:A:H5''	2.37	0.55
25:YA:2788:C:O2'	25:YA:2809:A:N3	2.39	0.55
25:YA:287:C:H2'	25:YA:288:C:H6	1.71	0.55
29:YF:101:LEU:O	29:YF:106:ARG:NH1	2.40	0.55
30:YG:67:LYS:HZ1	50:Y4:6:HIS:CD2	2.24	0.55
41:YV:38:LEU:H	41:YV:51:VAL:HG13	1.70	0.55
1:QA:1336:C:H1'	1:QA:1337:G:C2	2.41	0.55
1:QA:683:G:H2'	1:QA:684:A:C8	2.41	0.55
1:QA:757:U:H2'	1:QA:758:G:O4'	2.07	0.55
8:QH:86:ILE:HG13	8:QH:133:LEU:HD22	1.89	0.55
9:QI:77:ILE:O	9:QI:81:ILE:HG12	2.07	0.55
32:RI:92:VAL:HG13	32:RI:120:ILE:HG23	1.87	0.55
36:RQ:30:GLY:CA	36:RQ:107:ALA:HB2	2.37	0.55
44:RY:81:LYS:HB2	44:RY:96:ILE:HG22	1.89	0.55
1:XA:404:U:H2'	1:XA:405:U:H6	1.71	0.55
20:XT:49:ALA:HB1	20:XT:99:LEU:HB2	1.89	0.55
25:YA:1026:U:H1'	25:YA:1027:A:O5'	2.05	0.55
25:YA:1637:A:H4'	25:YA:2711:A:O2'	2.06	0.55
25:YA:2680:C:H5'	28:YE:189:PRO:HA	1.88	0.55
31:YH:121:ILE:HG12	31:YH:140:LYS:HD2	1.89	0.55
2:QB:5:ILE:HD12	2:QB:224:GLN:HG2	1.89	0.55
25:RA:1434:A:H61	25:RA:1558:A:H62	1.54	0.55
25:RA:2418:A:OP2	54:R8:29:LYS:HE2	2.06	0.55
25:RA:626:U:H5''	25:RA:627:A:H5'	1.89	0.55
29:RF:101:LEU:O	29:RF:106:ARG:NH1	2.40	0.55
44:RY:37:VAL:HG21	44:RY:72:VAL:HG21	1.88	0.55
1:XA:200:G:H1	1:XA:217:C:H42	1.54	0.55
2:XB:82:ARG:NH1	2:XB:86:GLU:OE2	2.40	0.55
1:XA:619:U:N3	4:XD:135:LEU:HD23	2.21	0.55
23:XY:30:C:H2'	23:XY:31:G:H8	1.71	0.55
52:Y6:28:ARG:HB3	52:Y6:30:THR:H	1.71	0.55
28:YE:63:LEU:HD12	28:YE:64:LYS:N	2.22	0.55
35:YP:52:GLU:HG3	35:YP:57:THR:HG22	1.88	0.55
39:YT:3:ARG:HG3	39:YT:7:ILE:HG12	1.88	0.55
50:R4:16:CYS:SG	50:R4:36:CYS:N	2.79	0.55
25:RA:1786:A:C2	25:RA:2606:C:H1'	2.42	0.55
25:RA:1266:G:O2'	25:RA:2012:G:O6	2.18	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:2068:U:H3	25:RA:2430:A:H2	1.51	0.55
27:RD:35:LYS:NZ	27:RD:104:TYR:HB2	2.22	0.55
32:RI:21:VAL:HG21	32:RI:25:TYR:HD1	1.71	0.55
25:RA:2816:C:O3'	37:RR:99:LYS:NZ	2.38	0.55
40:RU:52:ARG:HA	40:RU:55:ARG:HG3	1.88	0.55
44:RY:95:LYS:CB	44:RY:100:ALA:HA	2.36	0.55
44:RY:96:ILE:HG12	44:RY:101:LYS:HB2	1.88	0.55
1:XA:1298:C:H4'	1:XA:1299:A:C4	2.41	0.55
1:XA:1422:G:H5''	34:YO:48:PRO:HB3	1.88	0.55
1:XA:266:G:O2'	1:XA:267:C:OP2	2.23	0.55
46:Y0:27:GLU:HB2	46:Y0:69:PHE:HD1	1.72	0.55
25:YA:459:U:H5''	53:Y7:40:TRP:CD2	2.42	0.55
54:Y8:60:LEU:HB3	54:Y8:63:PRO:HG2	1.89	0.55
25:YA:2126:A:H4'	25:YA:2127:G:O5'	2.07	0.55
25:YA:527:C:OP2	25:YA:2779:U:H5	1.90	0.55
31:YH:157:TYR:HA	31:YH:171:LEU:O	2.06	0.55
35:YP:62:LEU:HD12	54:Y8:30:ARG:NH1	2.22	0.55
41:YV:34:GLU:O	41:YV:36:PRO:HD3	2.06	0.55
1:QA:34:C:H2'	1:QA:35:G:H8	1.72	0.55
1:QA:828:A:H2'	1:QA:829:G:O4'	2.06	0.55
10:QJ:51:ARG:NH2	14:QN:58:LYS:HZ1	2.04	0.55
14:QN:48:ALA:HB2	14:QN:53:LEU:HD12	1.89	0.55
51:R5:56:LYS:H	51:R5:56:LYS:HD2	1.72	0.55
25:RA:242:G:C8	54:R8:5:LYS:HG2	2.42	0.55
25:RA:50:U:H4'	25:RA:51:G:OP2	2.07	0.55
31:RH:109:PHE:HZ	31:RH:152:ARG:HG2	1.72	0.55
43:RX:25:LYS:HD3	43:RX:80:ILE:HD11	1.89	0.55
8:XH:86:ILE:HG22	8:XH:93:VAL:HG21	1.89	0.55
11:XK:34:ASP:OD1	11:XK:38:ASN:N	2.39	0.55
25:YA:1093:G:H5'	31:YH:170:ARG:NH1	2.22	0.55
25:YA:1939:U:OP1	25:YA:2604:U:O2'	2.20	0.55
25:YA:2286:A:H4'	25:YA:2287:A:O4'	2.07	0.55
25:YA:2790:A:H2'	25:YA:2791:C:H5''	1.89	0.55
25:YA:863:A:H2'	25:YA:864:G:C8	2.41	0.55
25:YA:863:A:H2'	25:YA:864:G:H8	1.72	0.55
25:YA:958:U:OP2	36:YQ:14:ARG:NH1	2.40	0.55
27:YD:43:ARG:HD2	27:YD:44:ASN:OD1	2.07	0.55
32:YI:129:THR:HA	32:YI:137:PRO:HA	1.88	0.55
32:YI:3:VAL:HG12	32:YI:38:LEU:HA	1.87	0.55
39:YT:26:ASP:O	39:YT:49:VAL:HG12	2.07	0.55
1:QA:1356:G:H2'	1:QA:1357:A:C8	2.42	0.55
25:RA:1427:A:H4'	25:RA:1428:C:O5'	2.06	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:2273:A:O2'	25:RA:2274:A:H5'	2.07	0.55
25:RA:2585:U:H5	56:Z6:76:PPU:HO2'	1.55	0.55
1:XA:606:G:N2	1:XA:631:G:H8	2.04	0.55
9:XI:16:ARG:HB2	9:XI:64:THR:HB	1.89	0.55
35:YP:71:VAL:HG13	35:YP:72:PRO:HD3	1.89	0.55
42:YW:14:PRO:O	42:YW:17:VAL:N	2.40	0.55
45:YZ:48:PHE:CE2	45:YZ:52:SER:HA	2.42	0.55
1:QA:56:U:H4'	32:YI:82:ARG:NH2	2.21	0.55
9:QI:26:VAL:HG22	9:QI:61:ALA:HB3	1.89	0.55
25:RA:1434:A:H61	25:RA:1558:A:N6	2.05	0.55
25:RA:223:A:N1	25:RA:407:G:O2'	2.31	0.55
25:RA:301:G:H1	25:RA:316:C:H42	1.53	0.55
1:XA:1356:G:H2'	1:XA:1357:A:C8	2.42	0.55
1:XA:339:C:H2'	1:XA:340:U:H6	1.71	0.55
1:XA:1223:C:P	19:XS:78:ARG:HH12	2.30	0.55
25:YA:141:A:C8	25:YA:1408:C:H1'	2.41	0.55
25:YA:1688:U:H1'	25:YA:1701:A:C6	2.42	0.55
25:YA:860:U:OP2	25:YA:916:G:N1	2.37	0.55
25:YA:2820:A:C8	28:YE:109:LYS:HE2	2.42	0.55
41:YV:61:VAL:HG23	41:YV:63:GLY:H	1.71	0.55
1:QA:359:U:H2'	1:QA:360:A:C8	2.42	0.54
10:QJ:13:HIS:CE1	10:QJ:14:LYS:HE3	2.42	0.54
25:RA:1444(A):A:H4'	25:RA:1460:A:O2'	2.07	0.54
25:RA:1482:U:H3	25:RA:1512:G:H1	1.55	0.54
25:RA:2068:U:N3	25:RA:2430:A:H2	2.05	0.54
29:RF:184:TYR:CE2	29:RF:188:ARG:HD2	2.42	0.54
31:RH:124:GLU:HB3	31:RH:132:ARG:HG3	1.89	0.54
1:XA:1129:C:H5'	1:XA:1130:A:OP1	2.08	0.54
4:XD:92:VAL:O	4:XD:96:LEU:HD22	2.07	0.54
8:XH:54:ASP:OD1	8:XH:54:ASP:N	2.39	0.54
12:XL:70:ILE:HG12	12:XL:100:ILE:HD12	1.88	0.54
25:YA:1292:U:H2'	25:YA:1293:C:C6	2.41	0.54
25:YA:2777:G:OP2	25:YA:2781:A:O2'	2.20	0.54
25:YA:330:A:HO2'	25:YA:331:A:H8	1.52	0.54
29:YF:116:ASP:OD2	35:YP:1:MET:N	2.26	0.54
25:YA:1649:G:O2'	37:YR:107:ASP:OD1	2.14	0.54
39:YT:62:THR:HG22	39:YT:75:ILE:HG12	1.89	0.54
25:YA:996:A:OP2	40:YU:92:ARG:NH2	2.40	0.54
10:QJ:8:LEU:HB3	10:QJ:16:LEU:HD21	1.87	0.54
54:R8:29:LYS:HD3	54:R8:44:LYS:HB2	1.88	0.54
25:RA:1210:A:H5''	25:RA:1210:A:C8	2.36	0.54
25:RA:1930:G:H22	25:RA:1969:A:H5''	1.72	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:686:G:N2	25:RA:788:A:H61	2.04	0.54
25:RA:468:G:H4'	29:RF:62:ARG:HH12	1.72	0.54
32:RI:113:ARG:HG3	32:RI:131:LYS:NZ	2.23	0.54
33:RN:40:PRO:HB3	40:RU:68:ALA:HB2	1.89	0.54
39:RT:1:MET:O	39:RT:3:ARG:N	2.40	0.54
45:RZ:146:ILE:HA	45:RZ:174:VAL:HB	1.90	0.54
1:XA:1453:G:H8	20:XT:39:LYS:HE2	1.72	0.54
3:XC:150:LYS:HE2	3:XC:152:ILE:HD11	1.88	0.54
25:YA:2656:U:H3	25:YA:2665:A:H2	1.54	0.54
25:YA:740:U:H2'	25:YA:741:G:C8	2.42	0.54
25:YA:898:C:H2'	25:YA:899:A:H5'	1.88	0.54
27:YD:12:SER:O	27:YD:16:MET:HB2	2.08	0.54
33:YN:42:TRP:O	40:YU:64:ARG:NH2	2.41	0.54
36:YQ:109:VAL:HG13	36:YQ:113:GLN:HB3	1.89	0.54
37:YR:55:ALA:HB2	37:YR:79:LEU:HD13	1.89	0.54
37:YR:56:LYS:NZ	37:YR:87:TYR:O	2.40	0.54
1:QA:652:U:H1'	1:QA:653:A:H2	1.73	0.54
47:R1:58:ILE:HD11	47:R1:86:SER:HB2	1.88	0.54
25:RA:177:G:N3	25:RA:177:G:H5''	2.22	0.54
25:RA:2126:A:H4'	25:RA:2127:G:O5'	2.07	0.54
25:RA:630:G:N2	25:RA:633:A:OP2	2.34	0.54
33:RN:30:ILE:HG22	33:RN:34:LEU:HD22	1.88	0.54
36:RQ:54:MET:HG3	36:RQ:117:ALA:HB1	1.89	0.54
36:RQ:31:ASP:O	36:RQ:134:ARG:HB2	2.07	0.54
45:RZ:58:VAL:O	45:RZ:60:GLU:N	2.39	0.54
45:RZ:53:ILE:H	45:RZ:71:VAL:HG13	1.72	0.54
10:XJ:33:GLN:HB2	10:XJ:75:ILE:HD11	1.89	0.54
51:Y5:55:ARG:HG3	51:Y5:57:VAL:H	1.73	0.54
25:YA:1113:U:H2'	25:YA:1114:G:C8	2.42	0.54
25:YA:2131:G:H4'	25:YA:2132:U:H4'	1.88	0.54
1:QA:1200:C:O2'	1:QA:1201:A:OP2	2.22	0.54
1:QA:985:C:H2'	1:QA:986:A:H8	1.73	0.54
5:QE:78:HIS:CE1	5:QE:142:LEU:HD23	2.42	0.54
25:RA:379:G:N2	47:R1:42:GLN:OE1	2.33	0.54
25:RA:1927:A:H2'	25:RA:1928:A:C8	2.43	0.54
25:RA:2444:G:OP2	29:RF:68:LYS:HE3	2.08	0.54
25:RA:2451:A:N1	56:Z6:76:PPU:HE2	2.23	0.54
25:RA:2496:C:P	36:RQ:81:VAL:HG12	2.48	0.54
27:RD:35:LYS:HZ1	27:RD:104:TYR:HB2	1.71	0.54
28:RE:35:GLN:HE21	28:RE:37:ARG:CZ	2.21	0.54
1:XA:1525:G:P	11:XK:120:ARG:HH22	2.29	0.54
5:XE:100:VAL:HG22	5:XE:118:ILE:HG22	1.90	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:XM:22:ILE:HD12	13:XM:25:ILE:HD12	1.89	0.54
18:XR:31:LEU:H	18:XR:31:LEU:HD23	1.73	0.54
1:XA:1455:G:H5''	20:XT:31:SER:HB2	1.88	0.54
46:Y0:20:ARG:O	46:Y0:24:LYS:NZ	2.39	0.54
25:YA:987:G:O2'	25:YA:1000:A:N3	2.38	0.54
26:YB:40:U:H1'	26:YB:45:A:H61	1.72	0.54
45:YZ:149:SER:HB2	45:YZ:172:ALA:O	2.07	0.54
5:QE:7:GLU:N	5:QE:35:GLY:O	2.36	0.54
9:QI:121:ARG:NH1	9:QI:122:ALA:O	2.40	0.54
48:R2:42:GLY:O	48:R2:44:LEU:N	2.35	0.54
48:R2:50:ILE:HD12	48:R2:51:ARG:H	1.72	0.54
32:RI:93:THR:O	32:RI:97:ILE:HG12	2.06	0.54
37:RR:103:ARG:NH1	37:RR:108:GLY:O	2.41	0.54
40:RU:112:ARG:NH2	41:RV:47:VAL:HG13	2.23	0.54
43:RX:83:VAL:CG1	43:RX:87:GLN:HB2	2.38	0.54
45:RZ:110:GLY:HA2	45:RZ:111:VAL:C	2.28	0.54
5:XE:12:LEU:HD21	5:XE:14:ARG:HD3	1.89	0.54
50:Y4:54:GLY:O	50:Y4:59:PHE:HB2	2.07	0.54
25:YA:1085:A:O2'	25:YA:1086:A:OP1	2.23	0.54
25:YA:530:G:H1'	25:YA:2021:C:O2'	2.07	0.54
25:YA:540:G:H5'	25:YA:541:C:OP2	2.07	0.54
33:YN:35:ARG:HB2	33:YN:42:TRP:CH2	2.42	0.54
35:YP:64:LYS:O	35:YP:66:GLY:N	2.41	0.54
40:YU:76:TYR:CZ	40:YU:80:ILE:HG13	2.43	0.54
45:YZ:5:LEU:HD21	45:YZ:44:PHE:HA	1.89	0.54
13:QM:22:ILE:HB	13:QM:25:ILE:HD12	1.89	0.54
1:QA:1223:C:P	19:QS:78:ARG:HH12	2.31	0.54
51:R5:40:LYS:HG2	51:R5:47:PRO:HD2	1.90	0.54
25:RA:1190:G:H5'	35:RP:32:THR:HA	1.90	0.54
25:RA:259:G:H21	25:RA:621:A:H8	1.55	0.54
30:RG:16:ARG:NH2	30:RG:28:VAL:O	2.41	0.54
1:XA:339:C:H2'	1:XA:340:U:C6	2.42	0.54
1:XA:598:U:H4'	8:XH:94:TYR:CD2	2.43	0.54
1:XA:807:A:H2'	1:XA:808:C:C6	2.42	0.54
12:XL:115:LYS:O	12:XL:117:ARG:N	2.35	0.54
48:Y2:35:LEU:HD12	48:Y2:53:LEU:HD12	1.89	0.54
1:QA:1053:G:N7	1:QA:1200:C:H5''	2.23	0.54
1:QA:978:A:O2'	1:QA:1322:C:N3	2.40	0.54
1:QA:977:A:O2'	1:QA:981:U:N3	2.37	0.54
25:RA:2116:G:H1	25:RA:2162:G:P	2.30	0.54
25:RA:2648:C:H2'	25:RA:2649:U:C6	2.42	0.54
25:RA:2751:G:N7	31:RH:2:SER:HB3	2.22	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
39:RT:111:ARG:O	39:RT:112:ARG:HG3	2.08	0.54
1:XA:1008:C:H42	1:XA:1021:G:H1	1.55	0.54
3:XC:150:LYS:HB3	3:XC:201:TYR:HB2	1.90	0.54
7:XG:20:ASP:HB3	7:XG:23:VAL:HG23	1.89	0.54
7:XG:49:ILE:O	7:XG:53:LYS:HB3	2.08	0.54
10:XJ:9:ARG:HB2	10:XJ:95:GLU:HB3	1.88	0.54
25:YA:141(A):C:H2'	25:YA:142:G:O4'	2.08	0.54
25:YA:287:C:H2'	25:YA:288:C:C6	2.42	0.54
25:YA:518:G:H5'	42:YW:18:ARG:NH1	2.23	0.54
45:YZ:82:ARG:HG3	45:YZ:83:PRO:HD2	1.90	0.54
2:QB:84:GLU:HB3	2:QB:219:VAL:HG21	1.89	0.54
25:RA:1101:U:H2'	25:RA:1102:C:H6	1.73	0.54
25:RA:586:A:H5'	29:RF:89:VAL:HG21	1.90	0.54
26:RB:51:G:N7	38:RS:62:LYS:NZ	2.47	0.54
35:RP:9:ASN:HB2	35:RP:10:PRO:HD2	1.90	0.54
1:XA:1189:C:H5''	1:XA:1190:G:OP2	2.08	0.54
1:XA:35:G:O2'	12:XL:118:SER:O	2.20	0.54
22:XV:23:C:H2'	22:XV:24:U:C6	2.43	0.54
25:YA:2022:U:O2'	25:YA:2617:C:H5'	2.08	0.54
25:YA:2089:U:H6	25:YA:2089:U:H5''	1.73	0.54
25:YA:460:A:H2'	25:YA:461:C:O4'	2.07	0.54
1:QA:1065:U:O2'	1:QA:1066:C:OP2	2.23	0.54
1:QA:1347:G:H22	1:QA:1374:A:P	2.30	0.54
1:QA:1106:G:H5''	3:QC:172:ARG:HG2	1.90	0.54
25:RA:1309:G:H4'	53:R7:7:PRO:HB2	1.89	0.54
25:RA:1063:G:N2	25:RA:1076:C:O2'	2.41	0.54
26:RB:40:U:H1'	26:RB:45:A:H61	1.72	0.54
32:RI:57:ARG:O	32:RI:61:ARG:HG2	2.08	0.54
35:RP:38:GLN:HG2	35:RP:45:LEU:CD1	2.36	0.54
37:RR:45:ARG:HA	37:RR:95:THR:HG21	1.90	0.54
45:RZ:82:ARG:HG3	45:RZ:83:PRO:HD2	1.90	0.54
1:XA:1510:U:H2'	1:XA:1511:G:C8	2.42	0.54
3:XC:15:THR:HG23	3:XC:181:ASN:HD22	1.73	0.54
1:XA:707:C:OP1	11:XK:85:ARG:NH1	2.41	0.54
13:XM:3:ARG:HA	13:XM:9:ILE:CG2	2.37	0.54
16:XP:43:LYS:HG2	16:XP:48:TRP:CE3	2.42	0.54
25:YA:125:G:H5''	53:Y7:19:ARG:HD3	1.90	0.54
30:YG:15:VAL:HG21	30:YG:176:LEU:HD23	1.90	0.54
33:YN:6:PRO:HG3	33:YN:41:ASP:HB2	1.89	0.54
25:RA:1141:U:O2'	25:RA:1142:U:OP2	2.25	0.54
25:RA:2133:G:H1'	25:RA:2158:A:H61	1.73	0.54
25:RA:2527:C:H5''	55:R9:30:PRO:HB2	1.90	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:479:A:N3	25:RA:481:G:H5''	2.23	0.54
28:RE:111:ARG:HG3	28:RE:160:TYR:CD1	2.43	0.54
32:RI:33:ARG:HB3	32:RI:35:LEU:HD23	1.90	0.54
35:RP:14:LYS:O	35:RP:16:ARG:HG2	2.08	0.54
39:RT:37:GLY:O	39:RT:39:ARG:N	2.34	0.54
36:RQ:134:ARG:NH2	45:RZ:122:ARG:HD2	2.23	0.54
10:XJ:32:ALA:H	10:XJ:78:ASN:HD21	1.55	0.54
25:YA:1341:U:OP2	25:YA:1394:U:O2'	2.22	0.54
25:YA:1929:G:H4'	25:YA:1930:G:OP1	2.08	0.54
25:YA:1678:G:N2	25:YA:1989:G:H22	2.05	0.54
25:YA:2126:A:N6	25:YA:2163:C:O2'	2.41	0.54
25:YA:649:G:H2'	25:YA:650:C:C6	2.42	0.54
1:QA:1255:G:O2'	1:QA:1258:G:O2'	2.23	0.53
1:QA:22:G:H4'	1:QA:885:G:C8	2.43	0.53
2:QB:235:SER:O	2:QB:237:ALA:N	2.41	0.53
4:QD:149:ALA:HB3	4:QD:152:SER:HB2	1.90	0.53
4:QD:194:LEU:HD12	4:QD:195:ALA:H	1.73	0.53
19:QS:10:PHE:HE2	19:QS:16:LEU:HD22	1.73	0.53
20:QT:75:ASN:N	20:QT:75:ASN:OD1	2.40	0.53
50:R4:56:VAL:HA	50:R4:60:GLN:HB2	1.89	0.53
25:RA:2544:G:O5'	25:RA:2544:G:H8	1.91	0.53
1:XA:1234:C:O2'	1:XA:1235:U:H5'	2.08	0.53
35:YP:62:LEU:HD12	54:Y8:30:ARG:HH11	1.72	0.53
25:YA:2212:A:H1'	25:YA:2215:G:C5	2.43	0.53
25:YA:2712:U:O2'	25:YA:2712(A):A:OP1	2.26	0.53
25:YA:528:A:HO2'	25:YA:529:A:H5'	1.73	0.53
27:YD:70:TRP:CH2	27:YD:150:LYS:HA	2.43	0.53
28:YE:111:ARG:HD2	28:YE:160:TYR:CD1	2.42	0.53
28:YE:78:LEU:HG	28:YE:79:ARG:NE	2.23	0.53
35:YP:88:LEU:HD12	35:YP:95:VAL:HG11	1.90	0.53
25:YA:996:A:H4'	40:YU:92:ARG:NE	2.22	0.53
1:QA:510:A:OP2	4:QD:49:ARG:NH2	2.41	0.53
2:QB:204:ASN:HD22	2:QB:206:ASP:H	1.56	0.53
25:RA:27:G:N2	25:RA:512:G:H1'	2.22	0.53
27:RD:44:ASN:HD22	27:RD:44:ASN:N	2.06	0.53
25:RA:321:G:H5''	29:RF:136:THR:HG23	1.90	0.53
39:RT:33:LYS:HD2	39:RT:82:LEU:HA	1.89	0.53
2:XB:162:ILE:O	2:XB:185:ILE:HG12	2.08	0.53
2:XB:82:ARG:HA	2:XB:92:TYR:CE2	2.43	0.53
3:XC:14:ILE:O	3:XC:16:ARG:N	2.35	0.53
1:XA:1314:C:N4	19:XS:2:PRO:O	2.40	0.53
25:YA:2114:A:N6	25:YA:2119:A:H62	2.07	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:2712:U:O2'	25:YA:2712(A):A:H8	1.90	0.53
25:YA:2832:U:H4'	25:YA:2833:G:H5''	1.90	0.53
27:YD:43:ARG:CB	27:YD:54:ARG:HB2	2.38	0.53
41:YV:66:ARG:NH1	41:YV:88:ARG:HD3	2.23	0.53
1:QA:957:U:H4'	19:QS:79:THR:HB	1.91	0.53
3:QC:84:ILE:HD11	3:QC:88:ARG:HH21	1.73	0.53
25:RA:1051:G:H2'	25:RA:1052:C:O4'	2.07	0.53
25:RA:1203:G:H3'	25:RA:1204:A:H5''	1.89	0.53
25:RA:1688:U:H1'	25:RA:1701:A:C6	2.44	0.53
25:RA:2061:G:OP2	25:RA:2502:G:H5'	2.09	0.53
25:RA:2469:A:H5'	25:RA:2470:G:OP2	2.08	0.53
25:RA:278:A:H61	25:RA:362:U:H3	1.56	0.53
35:RP:61:ARG:HD2	54:R8:13:ARG:HD2	1.90	0.53
45:RZ:152:ALA:O	45:RZ:154:ASP:N	2.40	0.53
45:RZ:166:SER:H	45:RZ:167:PRO:HA	1.74	0.53
1:XA:1305:G:O2'	1:XA:1306:A:C8	2.61	0.53
1:XA:346:G:H1'	1:XA:347:G:H5'	1.90	0.53
1:XA:691:G:H2'	1:XA:692:U:C6	2.44	0.53
10:XJ:4:ILE:HG12	10:XJ:100:THR:HG22	1.89	0.53
25:YA:2564:A:C2	25:YA:2647:U:H4'	2.43	0.53
25:YA:443:A:H5''	25:YA:444:C:OP1	2.09	0.53
33:YN:30:ILE:HG23	33:YN:52:VAL:HG11	1.91	0.53
1:QA:411:A:H62	1:QA:413:G:N2	2.06	0.53
12:QL:55:VAL:HG12	12:QL:69:TYR:HA	1.90	0.53
15:QO:6:GLU:OE2	15:QO:6:GLU:N	2.35	0.53
25:RA:2753:A:O2'	55:R9:15:LYS:NZ	2.42	0.53
25:RA:2772:C:H2'	25:RA:2773:C:H6	1.74	0.53
25:RA:2772:C:H2'	25:RA:2773:C:C6	2.43	0.53
25:RA:372:G:O2'	25:RA:373:U:OP2	2.27	0.53
25:RA:859:G:O2'	25:RA:860:U:P	2.67	0.53
29:RF:32:LEU:O	29:RF:36:VAL:HG23	2.09	0.53
34:RO:2:ILE:HD13	34:RO:8:LEU:HD11	1.90	0.53
25:RA:943:U:OP2	35:RP:36:LYS:HG2	2.08	0.53
36:RQ:32:TYR:CE1	36:RQ:133:ARG:HG3	2.43	0.53
41:RV:99:ILE:O	41:RV:101:GLY:N	2.42	0.53
42:RW:25:ARG:NH2	42:RW:74:ALA:O	2.33	0.53
1:XA:1301:U:H3'	1:XA:1302:U:H5'	1.91	0.53
1:XA:1399:C:C2	1:XA:1502:A:N6	2.77	0.53
1:XA:64:G:H5'	1:XA:65:U:H5'	1.90	0.53
17:XQ:4:LYS:HE3	17:XQ:6:LEU:HD21	1.90	0.53
19:XS:36:ARG:NH1	19:XS:52:TYR:O	2.42	0.53
48:Y2:15:LYS:H	48:Y2:67:LYS:HE2	1.73	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:1019:U:O2'	25:YA:1021:A:H2	1.91	0.53
25:YA:2853:C:H2'	25:YA:2854:G:C8	2.40	0.53
25:YA:796:C:H2'	25:YA:797:C:C6	2.43	0.53
27:YD:244:ARG:HB2	27:YD:245:PRO:HD2	1.90	0.53
27:YD:30:GLU:HG3	27:YD:63:ARG:HH21	1.72	0.53
32:YI:62:LYS:HE3	32:YI:134:PRO:HG2	1.90	0.53
35:YP:92:GLU:HA	35:YP:123:LEU:HD23	1.89	0.53
25:YA:2467:C:H4'	36:YQ:123:HIS:CD2	2.42	0.53
36:YQ:12:GLN:HG2	36:YQ:73:PRO:HD2	1.90	0.53
25:YA:1614:A:N6	42:YW:88:ARG:H	2.05	0.53
3:QC:35:GLU:HG2	3:QC:59:ARG:NH2	2.24	0.53
8:QH:51:VAL:HG11	8:QH:60:ARG:HG3	1.90	0.53
48:R2:10:LEU:O	48:R2:13:ALA:N	2.40	0.53
25:RA:1021:A:H8	25:RA:1022:G:H5''	1.72	0.53
25:RA:1020:A:N1	25:RA:1141:U:O2'	2.40	0.53
25:RA:229:A:H4'	25:RA:229:A:OP1	2.07	0.53
29:RF:135:LYS:HB3	29:RF:138:GLU:HG3	1.90	0.53
31:RH:149:ARG:HE	31:RH:154:PRO:HG2	1.72	0.53
32:RI:88:ILE:O	32:RI:121:LYS:NZ	2.40	0.53
38:RS:106:ARG:HA	38:RS:110:LEU:HD21	1.91	0.53
1:XA:881:G:P	12:XL:12:ARG:HH22	2.32	0.53
1:XA:933:G:O6	7:XG:3:ARG:NH2	2.41	0.53
2:XB:60:ASP:O	2:XB:64:ARG:HG2	2.09	0.53
9:XI:111:ARG:NE	9:XI:112:LYS:O	2.38	0.53
11:XK:84:VAL:HG11	11:XK:95:ILE:HD11	1.90	0.53
1:XA:949:A:N7	13:XM:106:ASN:ND2	2.56	0.53
55:Y9:27:CYS:SG	55:Y9:28:GLU:N	2.82	0.53
25:YA:1570:A:H2'	25:YA:1571:A:C8	2.42	0.53
25:YA:2150:U:H2'	25:YA:2151:G:C8	2.44	0.53
25:YA:2438:U:O3'	25:YA:2439:A:H3'	2.08	0.53
25:YA:2469:A:O2'	36:YQ:56:ARG:HG2	2.08	0.53
39:YT:105:LEU:O	39:YT:107:ASP:N	2.42	0.53
39:YT:112:ARG:NE	39:YT:112:ARG:O	2.39	0.53
39:YT:51:ARG:CG	39:YT:98:LYS:HG3	2.38	0.53
1:QA:976:G:H5''	1:QA:1358:U:O2'	2.09	0.53
1:QA:1348:U:H4'	9:QI:120:ARG:HD2	1.91	0.53
26:RB:72:G:O2'	26:RB:104:A:N6	2.41	0.53
32:RI:144:VAL:HG22	32:RI:145:VAL:H	1.73	0.53
44:RY:98:VAL:HG13	44:RY:99:CYS:SG	2.48	0.53
1:XA:130:A:N6	1:XA:233:C:O2	2.42	0.53
25:YA:2277:G:OP2	46:Y0:10:THR:HG21	2.08	0.53
25:YA:528:A:C2	25:YA:2043:C:H4'	2.44	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:226:G:O2'	25:YA:227:A:C8	2.61	0.53
25:YA:2567:G:H2'	25:YA:2568:C:C6	2.43	0.53
25:YA:782:A:H5'	25:YA:783:A:C2	2.44	0.53
25:YA:888:C:H3'	25:YA:889:C:C4'	2.38	0.53
1:QA:673:G:O3'	6:QF:87:ARG:NH2	2.41	0.53
6:QF:10:LEU:HD13	6:QF:61:LEU:HD13	1.90	0.53
1:QA:690:G:H22	11:QK:55:LYS:NZ	2.05	0.53
25:RA:1101:U:H2'	25:RA:1102:C:C6	2.44	0.53
25:RA:1509:C:H3'	25:RA:1510:A:H5''	1.90	0.53
45:RZ:76:LEU:HD23	45:RZ:76:LEU:H	1.73	0.53
1:XA:1002:G:H2'	1:XA:1003:G:C8	2.40	0.53
1:XA:966:G:O2'	9:XI:127:LYS:O	2.27	0.53
8:XH:121:ASP:HB2	8:XH:125:ARG:NH2	2.24	0.53
20:XT:95:ALA:O	20:XT:97:ALA:N	2.42	0.53
25:YA:1178:C:H2'	25:YA:1179:C:C6	2.44	0.53
25:YA:2757:A:OP1	55:Y9:19:ARG:HA	2.09	0.53
32:YI:79:ILE:N	32:YI:141:LYS:O	2.40	0.53
1:QA:1238:A:H62	1:QA:1299:A:N6	2.07	0.53
1:QA:405:U:O4	4:QD:2:GLY:N	2.41	0.53
1:QA:474:G:H2'	1:QA:475:G:C8	2.44	0.53
1:QA:520:A:N1	1:QA:536:C:H1'	2.24	0.53
9:QI:71:SER:HA	9:QI:74:ILE:HD12	1.90	0.53
19:QS:44:MET:O	19:QS:46:GLY:N	2.40	0.53
48:R2:65:ASN:HB3	48:R2:69:ARG:NH2	2.24	0.53
25:RA:1771:C:HO2'	25:RA:1786:A:H8	1.56	0.53
25:RA:1858:G:O2'	25:RA:1884:A:N6	2.42	0.53
35:RP:113:LYS:HG2	35:RP:115:LEU:HD23	1.90	0.53
45:RZ:5:LEU:HD11	45:RZ:39:VAL:HB	1.91	0.53
1:XA:1277:C:O2'	1:XA:1279:A:H1'	2.09	0.53
1:XA:1318:A:H4'	19:XS:11:VAL:CG1	2.39	0.53
25:YA:1061:U:H3'	25:YA:1062:G:H5''	1.89	0.53
25:YA:2877:G:H2'	25:YA:2878:U:O4'	2.09	0.53
27:YD:206:LEU:O	27:YD:211:ARG:HD3	2.09	0.53
30:YG:179:PRO:HG3	50:Y4:38:LYS:NZ	2.24	0.53
32:YI:93:THR:HG22	32:YI:119:PRO:HB3	1.91	0.53
33:YN:96:GLU:HG2	33:YN:97:ARG:N	2.24	0.53
39:YT:16:ARG:HE	39:YT:19:LEU:HD21	1.73	0.53
40:YU:102:GLU:OE1	41:YV:13:ARG:NH2	2.42	0.53
1:QA:1053:G:O6	1:QA:1199:U:H2'	2.08	0.53
1:QA:119:A:H4'	1:QA:120:A:O5'	2.07	0.53
1:QA:1304:G:N2	1:QA:1332:A:OP2	2.38	0.53
1:QA:1336:C:O2'	1:QA:1337:G:O5'	2.25	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:1050:A:H2'	25:RA:1051:G:O4'	2.08	0.53
42:RW:110:LYS:HG3	42:RW:111:HIS:ND1	2.23	0.53
1:XA:633:G:H5'	1:XA:634:C:OP2	2.08	0.53
18:XR:25:THR:HB	18:XR:26:LEU:HD23	1.91	0.53
19:XS:31:ILE:HG23	19:XS:49:ILE:HA	1.91	0.53
52:Y6:26:ASN:ND2	52:Y6:35:GLU:OE2	2.42	0.53
25:YA:1093:G:OP1	31:YH:170:ARG:NH1	2.42	0.53
25:YA:1697:G:OP2	25:YA:1698:A:O2'	2.12	0.53
25:YA:2629:A:O2'	25:YA:2630:G:H5''	2.09	0.53
25:YA:2667:C:H1'	31:YH:109:PHE:CD2	2.43	0.53
31:YH:149:ARG:NH1	31:YH:167:GLU:OE1	2.42	0.53
1:QA:410:G:H3'	4:QD:25:ARG:HH21	1.74	0.53
4:QD:78:LEU:HD22	4:QD:96:LEU:HB3	1.89	0.53
1:QA:1320:C:N4	19:QS:36:ARG:HG3	2.23	0.53
1:QA:1222:G:OP1	19:QS:77:THR:HG21	2.09	0.53
47:R1:80:LEU:HD23	47:R1:80:LEU:H	1.74	0.53
51:R5:40:LYS:NZ	51:R5:46:CYS:HB3	2.24	0.53
25:RA:459:U:H5''	53:R7:40:TRP:CD2	2.44	0.53
25:RA:1937:A:O2'	25:RA:1939:U:OP2	2.18	0.53
25:RA:2273:A:H2'	25:RA:2274:A:C8	2.43	0.53
25:RA:2023:G:H5'	25:RA:2617:C:H4'	1.91	0.53
28:RE:203:LYS:HE3	28:RE:204:ALA:HB2	1.91	0.53
29:RF:157:VAL:HB	29:RF:194:MET:HB3	1.91	0.53
25:RA:1261:C:OP2	42:RW:83:LYS:NZ	2.42	0.53
1:XA:1191:A:H5''	3:XC:4:LYS:HZ2	1.74	0.53
1:XA:818:G:O2'	1:XA:819:A:H5'	2.09	0.53
12:XL:7:ILE:HD13	12:XL:10:LEU:HD12	1.90	0.53
1:XA:1014:A:H4'	19:XS:14:HIS:CD2	2.43	0.53
48:Y2:47:ASN:ND2	48:Y2:47:ASN:H	2.05	0.53
52:Y6:40:CYS:HB2	52:Y6:45:LYS:HD3	1.90	0.53
25:YA:1184:G:OP1	49:Y3:29:ARG:NH1	2.42	0.53
25:YA:2469:A:H2	25:YA:2481:G:N2	2.05	0.53
25:YA:286:C:H2'	25:YA:287:C:C6	2.44	0.53
25:YA:363(F):A:H4'	25:YA:364:C:H5''	1.91	0.53
33:YN:13:TRP:O	33:YN:135:PRO:HD2	2.08	0.53
38:YS:10:ARG:O	38:YS:12:PHE:N	2.42	0.53
1:QA:1286:A:H8	1:QA:1287:A:H4'	1.73	0.52
1:QA:1317:C:N3	19:QS:37:ARG:NH2	2.52	0.52
25:RA:1582:C:O2'	25:RA:1586:A:H8	1.92	0.52
25:RA:247:G:H4'	25:RA:386:G:C5	2.44	0.52
25:RA:2540:C:H2'	25:RA:2541:A:O4'	2.09	0.52
25:RA:796:C:H2'	25:RA:797:C:C6	2.45	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:RE:1:MET:N	28:RE:83:ASP:O	2.41	0.52
1:XA:1221:G:O3'	19:XS:77:THR:HG21	2.08	0.52
2:XB:44:LEU:HD12	2:XB:44:LEU:H	1.74	0.52
7:XG:15:ASP:HB3	7:XG:19:GLY:H	1.74	0.52
20:XT:47:GLY:O	20:XT:49:ALA:N	2.41	0.52
25:YA:414:C:H2'	25:YA:415:A:C8	2.43	0.52
27:YD:85:ASP:OD2	27:YD:88:ARG:HD2	2.08	0.52
32:YI:20:ASP:N	32:YI:20:ASP:OD2	2.39	0.52
25:YA:2496:C:P	36:YQ:81:VAL:HG12	2.49	0.52
1:QA:7:G:H5'	1:QA:298:A:O4'	2.08	0.52
13:QM:66:LEU:HA	13:QM:70:LEU:HB2	1.91	0.52
14:QN:24:CYS:HB3	14:QN:29:ARG:N	2.23	0.52
25:RA:1329:U:H5''	25:RA:1330:C:C5	2.42	0.52
26:RB:65:C:H41	26:RB:108:C:H2'	1.73	0.52
31:RH:10:PRO:HD2	31:RH:50:VAL:HG13	1.89	0.52
25:YA:1354:A:OP1	27:YD:38:LYS:HE2	2.09	0.52
30:YG:96:ARG:O	30:YG:98:ARG:N	2.42	0.52
33:YN:110:GLY:O	33:YN:114:ARG:HG3	2.09	0.52
44:YY:35:TYR:CE1	44:YY:69:ALA:HB3	2.44	0.52
4:QD:98:GLU:OE2	4:QD:107:ARG:NE	2.43	0.52
48:R2:4:SER:OG	48:R2:5:GLU:OE2	2.16	0.52
25:RA:1292:U:H2'	25:RA:1293:C:C6	2.44	0.52
29:RF:134:GLY:HA3	29:RF:165:ARG:NH1	2.25	0.52
31:RH:46:GLU:OE2	31:RH:51:ARG:NH1	2.42	0.52
32:RI:11:ASN:O	32:RI:12:LEU:HB2	2.09	0.52
41:RV:60:GLU:HB2	41:RV:97:LYS:HE3	1.92	0.52
1:XA:1129:C:O2'	1:XA:1131:G:N7	2.41	0.52
1:XA:1321:C:H5''	1:XA:1322:C:C5'	2.39	0.52
1:XA:524:G:H2'	1:XA:525:C:C6	2.45	0.52
3:XC:40:ARG:O	3:XC:44:GLU:HB2	2.09	0.52
25:YA:1059:G:H3'	25:YA:1060:U:H5''	1.90	0.52
25:YA:1332:G:C8	25:YA:1332:G:H5'	2.44	0.52
25:YA:2667:C:H1'	31:YH:109:PHE:HD2	1.74	0.52
26:YB:42:C:O2	30:YG:93:THR:N	2.27	0.52
27:YD:132:PRO:HD3	27:YD:190:TYR:CZ	2.44	0.52
1:QA:1298:C:H4'	1:QA:1299:A:C4	2.45	0.52
1:QA:397:A:N3	1:QA:397:A:H3'	2.24	0.52
3:QC:37:GLN:NE2	14:QN:52:GLN:OE1	2.32	0.52
25:RA:467:G:OP1	53:R7:33:ARG:NH1	2.41	0.52
25:RA:2287:A:N6	25:RA:2344:U:H3	2.03	0.52
25:RA:192:C:O2'	25:RA:802:A:N3	2.37	0.52
27:RD:206:LEU:O	27:RD:211:ARG:NH1	2.38	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:RD:35:LYS:NZ	27:RD:64:ILE:O	2.41	0.52
30:RG:82:LEU:HA	30:RG:86:MET:SD	2.48	0.52
1:XA:1299:A:H2'	1:XA:1301:U:H1'	1.91	0.52
25:YA:184:C:H2'	25:YA:185:U:C6	2.45	0.52
25:YA:2867:G:OP2	39:YT:119:LYS:NZ	2.25	0.52
25:YA:729:G:C6	27:YD:208:LYS:HB2	2.44	0.52
25:YA:848:G:H2'	25:YA:849:A:C8	2.43	0.52
25:YA:2599:G:OP2	27:YD:236:GLY:HA2	2.09	0.52
38:YS:6:ALA:O	38:YS:10:ARG:HD3	2.09	0.52
1:QA:765:G:N2	1:QA:813:U:OP2	2.37	0.52
2:QB:134:GLU:HA	2:QB:137:ARG:HB3	1.92	0.52
1:QA:390:C:O3'	16:QP:28:ARG:NH2	2.41	0.52
25:RA:1443:G:H1	25:RA:1548:C:N4	2.04	0.52
27:RD:133:LEU:HB3	27:RD:173:VAL:HG11	1.91	0.52
31:RH:86:GLU:HG3	31:RH:165:ALA:N	2.25	0.52
37:RR:59:ASP:OD1	37:RR:61:HIS:HB3	2.08	0.52
1:XA:404:U:H2'	1:XA:405:U:C6	2.44	0.52
52:Y6:13:CYS:O	52:Y6:21:TYR:HA	2.09	0.52
25:YA:1149:G:H2'	25:YA:1150:C:C6	2.44	0.52
25:YA:1448:G:O2'	25:YA:1528:A:N6	2.43	0.52
25:YA:1728:G:H2'	25:YA:1731:G:O6	2.10	0.52
25:YA:1906:G:OP2	25:YA:1929:G:O2'	2.27	0.52
25:YA:2262:U:OP1	25:YA:2387:U:O2'	2.27	0.52
25:YA:2389:G:H5''	25:YA:2390:U:O4'	2.09	0.52
25:YA:507:A:C5'	25:YA:508:G:H5'	2.40	0.52
25:YA:1569:A:O5'	27:YD:61:LEU:HD21	2.10	0.52
1:QA:192:U:H2'	1:QA:193:C:C6	2.44	0.52
25:RA:1667:G:O2'	25:RA:1669:A:N6	2.43	0.52
25:RA:1973:G:H2'	25:RA:1974:C:C6	2.45	0.52
29:RF:150:GLY:HA2	29:RF:172:TRP:CE3	2.44	0.52
32:RI:133:HIS:HB2	32:RI:134:PRO:HD2	1.92	0.52
25:RA:2292:C:P	38:RS:17:ARG:HH22	2.33	0.52
1:XA:439:A:OP2	1:XA:493:G:N1	2.39	0.52
16:XP:8:ARG:O	16:XP:9:PHE:HD2	1.93	0.52
20:XT:53:LEU:O	20:XT:57:ARG:NH1	2.42	0.52
49:Y3:40:THR:HB	49:Y3:43:ILE:HG12	1.92	0.52
25:YA:444:C:H4'	29:YF:49:ALA:HB2	1.92	0.52
29:YF:63:LYS:HE2	29:YF:67:GLN:HB2	1.91	0.52
30:YG:88:ILE:O	30:YG:88:ILE:HD13	2.09	0.52
35:YP:20:GLY:HA2	35:YP:27:HIS:O	2.10	0.52
1:QA:1301:U:H3'	1:QA:1302:U:H5'	1.92	0.52
25:RA:2277:G:OP2	46:R0:10:THR:HG21	2.10	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:2585:U:H5	56:Z6:76:PPU:O2'	1.92	0.52
25:RA:476:G:N1	25:RA:479:A:OP2	2.41	0.52
27:RD:108:PRO:HB3	27:RD:143:HIS:HE1	1.73	0.52
44:RY:84:ARG:O	44:RY:95:LYS:HD3	2.09	0.52
3:XC:189:ALA:HB3	3:XC:196:LEU:HB2	1.91	0.52
1:XA:1123:A:H4'	10:XJ:36:GLY:HA3	1.92	0.52
10:XJ:78:ASN:O	10:XJ:81:THR:OG1	2.25	0.52
14:XN:43:CYS:HA	14:XN:46:GLU:HG3	1.92	0.52
25:YA:2327:A:H2'	25:YA:2328:A:C8	2.44	0.52
25:YA:363:G:H2'	25:YA:363(A):A:H8	1.74	0.52
25:YA:223:A:O4'	25:YA:422:A:H5'	2.10	0.52
25:YA:581:C:H2'	25:YA:582:G:H8	1.74	0.52
25:YA:581:C:H2'	25:YA:582:G:C8	2.45	0.52
25:YA:764:A:N3	27:YD:213:ARG:NH1	2.57	0.52
29:YF:24:LEU:HD23	29:YF:115:ALA:HA	1.91	0.52
25:YA:2585:U:H5	56:Z8:76:PPU:O2'	1.91	0.52
1:QA:1326:C:OP1	21:QU:17:THR:OG1	2.18	0.52
1:QA:64:G:H4'	1:QA:65:U:O5'	2.09	0.52
19:QS:28:LYS:HB2	19:QS:47:HIS:CD2	2.45	0.52
25:RA:2006:C:O2'	25:RA:2823:A:N3	2.37	0.52
25:RA:517:C:OP1	51:R5:16:ARG:NH2	2.42	0.52
25:RA:623:G:H2'	25:RA:624:C:C6	2.44	0.52
32:RI:110:ASP:N	32:RI:130:TYR:OH	2.30	0.52
1:XA:1005:A:HO2'	1:XA:1037:C:HO2'	1.55	0.52
2:XB:35:GLU:O	2:XB:36:ARG:HD3	2.10	0.52
19:XS:19:VAL:HG11	19:XS:44:MET:HG2	1.91	0.52
25:YA:857:C:OP2	46:Y0:77:ARG:NH2	2.43	0.52
25:YA:1184:G:OP1	49:Y3:30:ARG:HD2	2.10	0.52
54:Y8:11:LYS:NZ	54:Y8:63:PRO:HG3	2.24	0.52
25:YA:1210:A:C8	25:YA:1210:A:H5'	2.40	0.52
25:YA:1771:C:H1'	25:YA:1786:A:H8	1.75	0.52
25:YA:2774:C:H2'	25:YA:2775:A:O4'	2.10	0.52
25:YA:286:C:H2'	25:YA:287:C:H6	1.74	0.52
25:RA:2392:A:OP2	54:R8:31:HIS:HD2	1.92	0.52
25:RA:588:U:H2'	25:RA:589:C:C6	2.45	0.52
25:RA:994:C:OP1	40:RU:53:ARG:NH2	2.42	0.52
27:RD:206:LEU:HD22	27:RD:211:ARG:HG2	1.92	0.52
41:RV:34:GLU:O	41:RV:36:PRO:HD3	2.10	0.52
44:RY:87:LYS:HA	44:RY:92:ASN:HB3	1.91	0.52
1:XA:1034:G:H2'	1:XA:1035:A:H8	1.75	0.52
1:XA:555:C:OP2	12:XL:20:LYS:NZ	2.42	0.52
1:XA:561:U:HO2'	1:XA:562:C:P	2.30	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:XB:29:ALA:O	2:XB:32:ILE:HG22	2.10	0.52
4:XD:13:ARG:HD2	4:XD:38:TYR:O	2.10	0.52
7:XG:78:ARG:HG3	7:XG:79:ARG:N	2.25	0.52
48:Y2:58:ALA:O	48:Y2:62:THR:HG23	2.10	0.52
52:Y6:7:ILE:HG13	52:Y6:8:LYS:H	1.75	0.52
25:YA:2015:A:H1'	51:Y5:2:ALA:CA	2.38	0.52
25:YA:2123:G:H2'	25:YA:2124:G:C8	2.43	0.52
26:YB:77:U:P	45:YZ:19:ARG:HH22	2.33	0.52
32:YI:110:ASP:N	32:YI:130:TYR:OH	2.43	0.52
25:YA:1339:G:H5''	43:YX:16:LYS:HD3	1.92	0.52
45:YZ:124:ILE:HG22	45:YZ:126:VAL:HG13	1.92	0.52
4:QD:12:CYS:HA	4:QD:19:LEU:HD23	1.92	0.52
5:QE:91:LEU:HD12	5:QE:120:THR:HG22	1.92	0.52
1:QA:1240:U:OP1	7:QG:119:ARG:NH2	2.43	0.52
11:QK:32:ILE:HG13	11:QK:72:ALA:HB2	1.92	0.52
11:QK:96:ARG:HA	11:QK:99:GLN:HE21	1.75	0.52
47:R1:2:SER:HB2	47:R1:4:VAL:HG12	1.92	0.52
25:RA:2466:C:OP1	55:R9:4:ARG:HB2	2.10	0.52
25:RA:1657:C:H2'	25:RA:1658:C:C6	2.45	0.52
25:RA:288:C:H2'	25:RA:289:A:C8	2.45	0.52
39:RT:111:ARG:C	39:RT:113:LYS:H	2.12	0.52
42:RW:60:ASN:HD22	42:RW:60:ASN:H	1.56	0.52
1:XA:991:U:HO2'	1:XA:992:U:P	2.32	0.52
4:XD:108:LEU:HB3	4:XD:110:PHE:CE1	2.45	0.52
1:XA:719:C:O2'	18:XR:50:ILE:O	2.16	0.52
47:Y1:83:GLU:HG2	47:Y1:84:GLY:N	2.24	0.52
42:YW:40:ASN:O	42:YW:41:LYS:HG2	2.10	0.52
1:QA:429:U:H1'	1:QA:430:A:H5''	1.92	0.51
8:QH:77:GLU:HG2	8:QH:78:GLN:H	1.74	0.51
25:RA:847:U:H5	25:RA:933:A:N1	2.08	0.51
27:RD:12:SER:HB2	27:RD:208:LYS:HB3	1.92	0.51
29:RF:150:GLY:HA2	29:RF:172:TRP:CD2	2.45	0.51
37:RR:33:ARG:HD3	37:RR:113:LEU:HG	1.92	0.51
43:RX:59:VAL:HG21	43:RX:78:LYS:HE3	1.91	0.51
2:XB:170:GLU:O	2:XB:174:VAL:HG23	2.10	0.51
3:XC:47:LEU:HD11	3:XC:76:VAL:HB	1.91	0.51
12:XL:77:LEU:HD21	12:XL:107:ALA:HA	1.92	0.51
20:XT:26:ASN:HB2	20:XT:71:THR:HG23	1.92	0.51
26:YB:44:G:H1'	26:YB:47:C:N4	2.25	0.51
25:YA:2239:G:H5'	27:YD:251:GLY:HA3	1.92	0.51
25:YA:1952:A:C5	34:YO:22:ILE:HD12	2.44	0.51
39:YT:88:ILE:HD12	39:YT:90:GLN:N	2.25	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:QA:1074:G:O2'	1:QA:1101:A:N1	2.40	0.51
1:QA:1127:G:H21	1:QA:1147:C:H41	1.59	0.51
1:QA:179:A:H2'	1:QA:180:U:C6	2.44	0.51
25:RA:1534:G:H2'	25:RA:1534:G:N3	2.25	0.51
25:RA:593:G:H2'	25:RA:594:U:C6	2.45	0.51
25:RA:845:G:OP2	25:RA:845:G:H8	1.94	0.51
31:RH:153:LYS:HG2	31:RH:162:ILE:HG13	1.92	0.51
45:RZ:5:LEU:HD21	45:RZ:44:PHE:HA	1.92	0.51
1:XA:143:A:H2	1:XA:220:G:H1	1.57	0.51
1:XA:148:G:H2'	1:XA:149:A:H8	1.75	0.51
1:XA:321:A:H62	1:XA:328:C:H1'	1.74	0.51
1:XA:405:U:OP2	4:XD:3:ARG:NH2	2.44	0.51
48:Y2:24:LEU:HD13	48:Y2:60:LEU:HD11	1.92	0.51
54:Y8:51:ALA:N	54:Y8:53:PRO:HD2	2.25	0.51
25:YA:1786:A:C2	25:YA:2606:C:H1'	2.45	0.51
31:YH:26:VAL:HG13	31:YH:27:LYS:H	1.75	0.51
40:YU:107:ALA:O	40:YU:110:VAL:HB	2.10	0.51
41:YV:25:LEU:H	41:YV:92:THR:HG21	1.74	0.51
1:QA:1203:C:H2'	1:QA:1204:A:C8	2.45	0.51
1:QA:176:C:H2'	1:QA:177:C:H6	1.75	0.51
1:QA:920:U:H2'	1:QA:921:U:C6	2.45	0.51
25:RA:222:A:H3'	25:RA:421:U:H5'	1.92	0.51
25:RA:277:C:H4'	25:RA:278:A:OP2	2.11	0.51
26:RB:76:G:N2	26:RB:100:G:O6	2.32	0.51
29:RF:47:GLY:HA3	29:RF:95:ARG:O	2.10	0.51
35:RP:10:PRO:O	35:RP:12:ALA:N	2.43	0.51
1:XA:1327:C:OP2	21:XU:12:LYS:NZ	2.35	0.51
1:XA:165:C:H2'	1:XA:166:G:H8	1.74	0.51
5:XE:102:ALA:HB1	5:XE:106:PRO:HG2	1.93	0.51
5:XE:13:ILE:HD11	5:XE:55:VAL:HG22	1.91	0.51
25:YA:1533:C:H42	25:YA:1538:G:H1	1.57	0.51
25:YA:2151:G:H2'	25:YA:2152:G:C8	2.45	0.51
27:YD:148:GLU:HB2	27:YD:151:LYS:HD2	1.92	0.51
29:YF:127:GLU:OE1	29:YF:196:LEU:HB2	2.11	0.51
30:YG:77:ILE:HD13	30:YG:82:LEU:HD12	1.93	0.51
31:YH:88:LEU:H	31:YH:88:LEU:HD22	1.75	0.51
35:YP:96:THR:HG22	35:YP:126:VAL:HB	1.93	0.51
37:YR:83:ILE:HG22	37:YR:87:TYR:HE2	1.76	0.51
10:QJ:31:GLY:HA3	10:QJ:78:ASN:ND2	2.26	0.51
42:RW:67:ASP:OD2	42:RW:67:ASP:N	2.33	0.51
43:RX:35:THR:HG23	43:RX:38:GLU:HG2	1.93	0.51
44:RY:74:PRO:O	44:RY:80:GLY:HA2	2.10	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:XF:4:TYR:HD1	6:XF:92:LYS:HA	1.76	0.51
9:XI:70:LYS:O	9:XI:74:ILE:HG13	2.10	0.51
13:XM:14:ARG:N	13:XM:44:ARG:HD3	2.21	0.51
51:Y5:42:PRO:HB2	51:Y5:43:HIS:ND1	2.25	0.51
25:YA:1245:G:OP1	35:YP:13:ASN:ND2	2.40	0.51
25:YA:26:G:C6	25:YA:27:G:N1	2.77	0.51
25:YA:324:A:N6	25:YA:338:G:O2'	2.41	0.51
33:YN:38:HIS:O	40:YU:67:ALA:HB1	2.10	0.51
41:YV:65:GLY:HA3	41:YV:91:TYR:CZ	2.46	0.51
1:QA:255:G:H1'	17:QQ:16:GLN:NE2	2.25	0.51
1:QA:523:A:H61	12:QL:53:ARG:HH12	1.59	0.51
4:QD:61:LYS:HB2	4:QD:203:VAL:HG13	1.93	0.51
18:QR:32:ARG:HA	18:QR:69:THR:HG21	1.91	0.51
25:RA:1497:U:H3'	25:RA:1498:C:H6	1.75	0.51
25:RA:1796:U:H2'	25:RA:1797:C:H6	1.72	0.51
25:RA:2502:G:H5''	25:RA:2503:A:H5''	1.91	0.51
25:RA:2795:G:H3'	25:RA:2797:U:C5'	2.39	0.51
25:RA:288:C:H2'	25:RA:289:A:H8	1.74	0.51
31:RH:86:GLU:H	31:RH:86:GLU:CD	2.12	0.51
1:XA:1318:A:H4'	19:XS:11:VAL:HG11	1.93	0.51
9:XI:11:LYS:H	9:XI:104:ARG:HH21	1.58	0.51
20:XT:89:ARG:HH21	20:XT:104:LEU:HD11	1.76	0.51
47:Y1:70:VAL:O	47:Y1:74:VAL:HG23	2.10	0.51
51:Y5:38:ALA:HB3	51:Y5:40:LYS:HE3	1.92	0.51
51:Y5:56:LYS:HD3	51:Y5:58:LEU:HD23	1.90	0.51
25:YA:2734:A:H5'	25:YA:2735:G:OP2	2.11	0.51
25:YA:569:U:C4	25:YA:570:G:C6	2.97	0.51
30:YG:16:ARG:O	30:YG:20:ILE:HG12	2.10	0.51
40:YU:47:TYR:HA	40:YU:50:ARG:NH2	2.26	0.51
45:YZ:89:PHE:HE1	45:YZ:96:VAL:HG21	1.75	0.51
1:QA:1129:C:H5'	1:QA:1130:A:OP1	2.11	0.51
21:QU:6:ARG:HE	21:QU:15:ARG:HH21	1.59	0.51
25:RA:528:A:C2	25:RA:2042:A:H2'	2.45	0.51
25:RA:2760:C:H2'	25:RA:2761:G:H5''	1.92	0.51
25:RA:718:A:H3'	25:RA:719:C:C6	2.46	0.51
1:XA:1424:C:H2'	1:XA:1425:U:O4'	2.11	0.51
2:XB:21:ARG:HB2	2:XB:39:ILE:HA	1.91	0.51
7:XG:155:ARG:O	7:XG:155:ARG:NH2	2.43	0.51
17:XQ:100:LYS:O	17:XQ:101:ARG:NE	2.42	0.51
48:Y2:65:ASN:HB3	48:Y2:69:ARG:NH2	2.26	0.51
25:YA:2151:G:H2'	25:YA:2152:G:H8	1.74	0.51
25:YA:2572:A:N7	28:YE:145:LYS:HB2	2.24	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:YE:62:PRO:O	28:YE:64:LYS:N	2.43	0.51
36:YQ:2:LEU:H	36:YQ:2:LEU:HD23	1.76	0.51
38:YS:11:LYS:HB2	38:YS:91:PRO:HB3	1.93	0.51
39:YT:109:GLU:O	39:YT:113:LYS:HB2	2.11	0.51
40:YU:92:ARG:NH1	41:YV:11:GLN:O	2.44	0.51
12:QL:38:THR:HG23	12:QL:57:LYS:HB3	1.93	0.51
25:RA:1270:C:H5''	25:RA:1271:G:O5'	2.11	0.51
25:RA:2401:U:H2'	25:RA:2402:C:H5''	1.92	0.51
25:RA:2566:A:H4'	25:RA:2567:G:O5'	2.11	0.51
25:RA:27:G:O2'	25:RA:28:A:P	2.69	0.51
25:RA:813:U:H2'	25:RA:814:C:C6	2.46	0.51
29:RF:185:ASP:HA	29:RF:188:ARG:HD3	1.93	0.51
39:RT:28:VAL:HG23	39:RT:88:ILE:HA	1.92	0.51
40:RU:90:VAL:HG22	41:RV:39:LEU:HB3	1.93	0.51
1:XA:266:G:H5'	1:XA:268:C:H41	1.75	0.51
1:XA:1106:G:H5''	3:XC:172:ARG:HG2	1.92	0.51
19:XS:15:LEU:O	19:XS:19:VAL:N	2.36	0.51
20:XT:10:LEU:O	20:XT:13:LEU:HG	2.11	0.51
49:Y3:43:ILE:O	49:Y3:47:VAL:HG23	2.10	0.51
25:YA:1069:A:H4'	25:YA:1070:A:H5''	1.93	0.51
25:YA:2182:G:H2'	25:YA:2183:C:C6	2.46	0.51
25:YA:2328:A:H2'	25:YA:2329:G:C8	2.46	0.51
25:YA:2331:G:H4'	46:Y0:43:THR:H	1.75	0.51
25:YA:2795:G:H3'	25:YA:2797:U:H5'	1.93	0.51
31:YH:6:ARG:NE	31:YH:54:ARG:HH12	2.09	0.51
36:YQ:60:ARG:HA	45:YZ:178:GLU:O	2.11	0.51
1:QA:1305:G:H5'	21:QU:4:GLY:HA3	1.93	0.51
1:QA:983:A:H5''	1:QA:984:C:OP2	2.10	0.51
25:RA:152:G:H1	25:RA:174:C:H42	1.57	0.51
25:RA:1929:G:H4'	25:RA:1930:G:OP1	2.11	0.51
25:RA:1939:U:OP1	25:RA:2604:U:O2'	2.26	0.51
25:RA:593:G:O2'	54:R8:61:LEU:HD13	2.10	0.51
25:RA:1805:U:O2	27:RD:50:THR:HB	2.11	0.51
28:RE:134:ILE:HA	28:RE:137:HIS:CD2	2.45	0.51
29:RF:149:ASP:N	29:RF:149:ASP:OD1	2.27	0.51
29:RF:20:LEU:HD23	29:RF:125:LEU:HD12	1.93	0.51
38:RS:56:LEU:HD23	38:RS:58:LEU:HD22	1.92	0.51
1:XA:1200:C:H4'	1:XA:1201:A:H5'	1.93	0.51
1:XA:486:U:H2'	1:XA:487:A:C8	2.45	0.51
1:XA:757:U:H2'	1:XA:758:G:O4'	2.11	0.51
4:XD:78:LEU:HD22	4:XD:96:LEU:HB3	1.92	0.51
6:XF:97:PHE:CD2	18:XR:31:LEU:HD21	2.46	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
51:Y5:45:VAL:HG11	51:Y5:57:VAL:HG12	1.93	0.51
25:YA:1154:G:OP2	40:YU:58:ARG:NH1	2.41	0.51
25:YA:1548:C:H2'	25:YA:1549:C:H6	1.76	0.51
25:YA:524:U:H2'	25:YA:525:U:C6	2.45	0.51
27:YD:35:LYS:NZ	27:YD:104:TYR:HB2	2.26	0.51
37:YR:104:ARG:HD3	37:YR:111:LEU:HD21	1.92	0.51
25:YA:1654:A:OP2	37:YR:2:ARG:HD2	2.11	0.51
42:YW:106:ILE:O	42:YW:106:ILE:HG12	2.07	0.51
44:YY:81:LYS:HG2	44:YY:97:ARG:HD3	1.93	0.51
1:QA:1004:A:O5'	1:QA:1025:U:N3	2.43	0.51
6:QF:69:GLU:H	6:QF:69:GLU:CD	2.15	0.51
1:QA:719:C:O2'	18:QR:49:LYS:HB3	2.10	0.51
20:QT:14:LYS:HA	20:QT:17:ARG:HG3	1.91	0.51
25:RA:558:G:OP1	33:RN:111:PRO:HD2	2.11	0.51
43:RX:40:LYS:HG3	43:RX:51:VAL:HB	1.92	0.51
1:XA:1228:C:OP1	13:XM:115:LYS:HE3	2.11	0.51
1:XA:201:C:H42	1:XA:216:G:H1	1.59	0.51
15:XO:33:THR:HG21	15:XO:85:LEU:HD22	1.93	0.51
19:XS:26:GLY:O	19:XS:28:LYS:N	2.43	0.51
54:Y8:23:VAL:CG1	54:Y8:46:ARG:HD3	2.40	0.51
25:YA:2789:C:H1'	25:YA:2892:A:C2	2.42	0.51
25:YA:467:G:OP2	53:Y7:34:ARG:NH1	2.42	0.51
25:YA:673:C:H5''	29:YF:81:PRO:HD2	1.92	0.51
8:QH:20:TYR:HE2	8:QH:75:ARG:HD2	1.76	0.51
1:QA:1330:U:H4'	13:QM:23:TYR:CE2	2.45	0.51
16:QP:3:LYS:HG3	16:QP:24:ALA:HB2	1.92	0.51
30:RG:88:ILE:HD13	30:RG:88:ILE:O	2.10	0.51
25:RA:957:A:H5'	36:RQ:76:LYS:HD2	1.92	0.51
25:RA:2690:C:OP2	37:RR:14:SER:HB3	2.11	0.51
39:RT:19:LEU:HD22	39:RT:86:ILE:HG22	1.93	0.51
45:RZ:111:VAL:HG13	45:RZ:112:ARG:H	1.75	0.51
1:XA:1391:U:H2'	1:XA:1392:G:C8	2.46	0.51
1:XA:201:C:N4	1:XA:209:U:O2	2.43	0.51
1:XA:953:G:H2'	1:XA:954:G:O4'	2.10	0.51
1:XA:538:G:H5''	12:XL:114:LYS:HB2	1.93	0.51
25:YA:107:C:H2'	25:YA:108:U:H6	1.75	0.51
25:YA:1359:A:H61	25:YA:1372:U:H3	1.59	0.51
26:YB:8:U:O2'	38:YS:40:ILE:HD13	2.10	0.51
31:YH:89:ILE:HG12	31:YH:89:ILE:O	2.10	0.51
1:QA:1095:U:H5''	1:QA:1109:C:O2	2.10	0.50
1:QA:1348:U:C4	1:QA:1374:A:H2	2.30	0.50
1:QA:619:U:N3	4:QD:134:ASP:OD2	2.43	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
51:R5:3:LYS:HA	51:R5:3:LYS:NZ	2.27	0.50
35:RP:62:LEU:CD2	54:R8:25:MET:HB2	2.37	0.50
25:RA:729:G:H2'	25:RA:1775:U:H1'	1.94	0.50
25:RA:2150:U:H2'	25:RA:2151:G:H8	1.74	0.50
25:RA:2867:G:O2'	25:RA:2868:A:P	2.68	0.50
25:RA:29:U:H2'	25:RA:30:G:C8	2.47	0.50
25:RA:1188:U:H4'	41:RV:79:VAL:HG22	1.93	0.50
1:XA:1060:C:C5	3:XC:2:GLY:HA2	2.46	0.50
1:XA:412:A:H4'	1:XA:413:G:O5'	2.11	0.50
3:XC:138:VAL:HG22	3:XC:151:VAL:HG23	1.93	0.50
11:XK:41:THR:HG21	11:XK:71:LYS:HB3	1.93	0.50
25:YA:1412:A:H2'	25:YA:1413:G:H8	1.76	0.50
25:YA:1614:A:N1	42:YW:91:GLY:HA2	2.25	0.50
25:YA:2335:A:HO2'	25:YA:2336:A:P	2.34	0.50
25:YA:2524:G:H5'	25:YA:2525:G:OP2	2.11	0.50
26:YB:15:A:H1'	26:YB:109:G:C8	2.46	0.50
36:YQ:66:ILE:O	36:YQ:104:PHE:N	2.39	0.50
1:QA:1316:G:N2	1:QA:1319:A:H5''	2.20	0.50
9:QI:8:GLY:HA2	9:QI:79:LEU:HD12	1.92	0.50
11:QK:33:THR:HG22	11:QK:39:PRO:HA	1.92	0.50
13:QM:33:ALA:HA	13:QM:59:TYR:HE2	1.76	0.50
25:RA:1357:U:H2'	25:RA:1358:G:O4'	2.12	0.50
36:RQ:17:LEU:HD23	36:RQ:96:VAL:HG23	1.92	0.50
39:RT:118:ARG:HH21	39:RT:121:ILE:HG21	1.76	0.50
1:XA:93:U:H2'	1:XA:95:G:O4'	2.11	0.50
2:XB:80:ILE:HD11	2:XB:208:ILE:HG23	1.93	0.50
6:XF:86:ARG:O	6:XF:87:ARG:HG2	2.11	0.50
25:YA:2064:C:H2'	25:YA:2065:C:C6	2.45	0.50
25:YA:2758:A:C2	25:YA:2759:G:H1'	2.46	0.50
42:YW:57:ASN:O	42:YW:61:ASN:HB2	2.10	0.50
56:Z6:76:PPU:HN2	56:Z6:76:PPU:HD2	1.76	0.50
1:QA:1004:A:P	1:QA:1025:U:H3	2.35	0.50
1:QA:1443:G:N2	39:RT:119:LYS:HB2	2.26	0.50
1:QA:184:G:H2'	1:QA:185:A:C8	2.47	0.50
22:QV:14:G:H2'	22:QV:59:A:N1	2.27	0.50
25:RA:1247:A:OP1	29:RF:95:ARG:NH2	2.45	0.50
25:RA:1588:C:H2'	25:RA:1589:C:H6	1.77	0.50
25:RA:2599:G:OP2	27:RD:236:GLY:HA2	2.10	0.50
28:RE:176:ILE:HG23	28:RE:178:GLU:OE2	2.11	0.50
33:RN:46:VAL:HG13	33:RN:48:MET:HG3	1.93	0.50
1:XA:1346:A:H1'	1:XA:1348:U:C6	2.46	0.50
1:XA:89:U:O2'	1:XA:90:C:OP1	2.28	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:XB:9:GLU:HB3	2:XB:48:MET:SD	2.50	0.50
3:XC:54:ARG:HD3	3:XC:56:ASP:OD1	2.10	0.50
54:Y8:58:ILE:HA	54:Y8:61:LEU:HD21	1.92	0.50
25:YA:265:A:C8	25:YA:266:G:H1'	2.47	0.50
32:YI:11:ASN:O	32:YI:12:LEU:HB2	2.11	0.50
35:YP:62:LEU:N	35:YP:62:LEU:HD23	2.26	0.50
36:YQ:89:ASN:O	36:YQ:91:GLU:N	2.44	0.50
38:YS:30:ARG:HG3	38:YS:97:ARG:NH2	2.26	0.50
41:YV:52:VAL:HG23	41:YV:55:ALA:H	1.76	0.50
1:QA:1151:A:H2'	1:QA:1152:A:H8	1.76	0.50
1:QA:1306:A:N6	1:QA:1331:G:H1'	2.26	0.50
5:QE:148:VAL:HG21	8:QH:107:LEU:HD22	1.92	0.50
7:QG:116:ALA:O	7:QG:120:ILE:HG12	2.11	0.50
10:QJ:47:PHE:CE1	10:QJ:63:PHE:HB2	2.47	0.50
25:RA:1085:A:O2'	25:RA:1086:A:OP1	2.28	0.50
25:RA:1332:G:N2	25:RA:1610:A:H8	2.07	0.50
25:RA:297:C:H5''	44:RY:85:VAL:HG21	1.93	0.50
25:RA:774:A:O2'	25:RA:775:G:O5'	2.28	0.50
27:RD:62:TYR:CE1	27:RD:64:ILE:HA	2.46	0.50
28:RE:6:GLY:HA2	28:RE:51:PHE:CZ	2.46	0.50
35:RP:14:LYS:HD3	35:RP:14:LYS:O	2.12	0.50
25:RA:1244:G:H4'	35:RP:7:ARG:HB2	1.93	0.50
44:RY:97:ARG:HH21	44:RY:98:VAL:HB	1.77	0.50
1:XA:1347:G:O2'	1:XA:1348:U:OP2	2.25	0.50
1:XA:568:G:O2'	1:XA:574:A:N1	2.38	0.50
1:XA:57:G:H2'	1:XA:58:C:C6	2.46	0.50
1:XA:686:U:H1'	11:XK:42:TRP:HE1	1.77	0.50
1:XA:67:C:H2'	1:XA:68:G:H8	1.74	0.50
2:XB:114:ARG:O	2:XB:117:GLU:HB2	2.10	0.50
2:XB:189:ASP:HB3	2:XB:203:GLY:O	2.12	0.50
19:XS:4:SER:O	19:XS:5:LEU:HD13	2.11	0.50
19:XS:40:ILE:HG23	19:XS:67:VAL:O	2.12	0.50
50:Y4:10:VAL:HG22	50:Y4:11:PRO:HD2	1.94	0.50
30:YG:67:LYS:HZ1	50:Y4:1:MET:HB2	1.77	0.50
25:YA:530:G:C5	25:YA:2022:U:H5''	2.47	0.50
25:YA:2057:A:H2'	25:YA:2058:A:O4'	2.12	0.50
28:YE:111:ARG:HA	37:YR:1:MET:CG	2.40	0.50
32:YI:13:GLY:HA3	32:YI:17:GLN:OE1	2.12	0.50
45:YZ:72:ARG:NH2	45:YZ:97:GLU:O	2.27	0.50
1:QA:181:G:O2'	1:QA:182:U:O5'	2.25	0.50
1:QA:244:U:OP2	17:QQ:100:LYS:NZ	2.44	0.50
2:QB:162:ILE:HD11	2:QB:184:VAL:HG22	1.93	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:QK:17:GLY:N	11:QK:79:SER:O	2.44	0.50
12:QL:54:LYS:HD2	12:QL:54:LYS:H	1.75	0.50
12:QL:69:TYR:CG	12:QL:90:VAL:HG21	2.46	0.50
47:R1:62:VAL:HG23	47:R1:63:ALA:O	2.11	0.50
51:R5:46:CYS:HB2	51:R5:50:GLY:HA3	1.93	0.50
25:RA:1198:U:H2'	25:RA:1199:U:C6	2.46	0.50
25:RA:1678:G:H22	25:RA:1989:G:N2	2.08	0.50
25:RA:2031:A:C6	25:RA:2498:C:H1'	2.45	0.50
25:RA:2867:G:HO2'	25:RA:2868:A:P	2.34	0.50
42:RW:60:ASN:HD22	42:RW:60:ASN:N	2.09	0.50
43:RX:60:ARG:HH12	53:R7:47:ARG:HH22	1.58	0.50
1:XA:987:G:H1	1:XA:1218:C:H42	1.60	0.50
1:XA:1513:A:H2'	1:XA:1514:C:C6	2.47	0.50
2:XB:111:ARG:HH21	2:XB:114:ARG:HG2	1.76	0.50
2:XB:21:ARG:O	2:XB:23:ARG:N	2.44	0.50
4:XD:108:LEU:HD21	4:XD:183:GLY:HA3	1.93	0.50
1:XA:130:A:C8	17:XQ:63:ARG:HG3	2.46	0.50
25:YA:1771:C:C1'	25:YA:1786:A:H8	2.25	0.50
25:YA:1858:G:O2'	25:YA:1884:A:N6	2.44	0.50
25:YA:229:A:OP1	25:YA:230:U:H5'	2.12	0.50
25:YA:704:G:H1'	25:YA:727:A:N6	2.27	0.50
25:YA:877:U:H3	25:YA:899:A:H2	1.60	0.50
25:YA:900:A:H3'	25:YA:901:A:C8	2.39	0.50
25:YA:958:U:O2	26:YB:89(A):A:O2'	2.26	0.50
29:YF:167:ALA:HB1	29:YF:173:VAL:HG11	1.93	0.50
30:YG:5:VAL:HG11	30:YG:100:TRP:HB3	1.93	0.50
34:YO:120:GLU:HG2	34:YO:122:LEU:HG	1.94	0.50
35:YP:58:THR:O	35:YP:61:ARG:CZ	2.59	0.50
9:QL:53:VAL:HB	9:QL:95:LYS:HE3	1.92	0.50
53:R7:5:TRP:NE1	53:R7:7:PRO:HG3	2.26	0.50
25:RA:1598:C:H5'	43:RX:36:LYS:HB2	1.94	0.50
25:RA:2334:G:H4'	25:RA:2335:A:OP2	2.11	0.50
25:RA:39:C:H2'	25:RA:40:C:C6	2.47	0.50
36:RQ:89:ASN:O	36:RQ:92:GLY:N	2.42	0.50
1:XA:1321:C:H5''	1:XA:1322:C:H5''	1.93	0.50
1:XA:1347:G:H22	1:XA:1373:G:H2'	1.76	0.50
1:XA:353:A:H8	1:XA:353:A:H5'	1.77	0.50
22:XV:68:C:H2'	22:XV:69:C:H6	1.76	0.50
25:YA:1639:U:C2'	25:YA:1640:C:H5''	2.40	0.50
41:YV:61:VAL:HA	41:YV:94:LEU:HD23	1.93	0.50
1:QA:256:U:H2'	1:QA:257:G:C8	2.47	0.50
1:QA:715:A:H2'	1:QA:716:A:C8	2.47	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:QA:745:C:OP1	1:QA:851:G:O2'	2.29	0.50
9:QI:95:LYS:NZ	9:QI:96:LEU:HD13	2.26	0.50
13:QM:40:ASN:ND2	13:QM:43:THR:HG23	2.27	0.50
54:R8:23:VAL:HG11	54:R8:46:ARG:HD3	1.93	0.50
25:RA:363(B):G:H2'	25:RA:363(C):G:H8	1.76	0.50
25:RA:49:A:N7	25:RA:120:U:C5	2.74	0.50
31:RH:132:ARG:HH11	31:RH:132:ARG:HB2	1.76	0.50
35:RP:26:GLY:O	35:RP:28:GLY:N	2.45	0.50
39:RT:111:ARG:O	39:RT:113:LYS:N	2.42	0.50
1:XA:1525:G:OP1	11:XK:120:ARG:NH2	2.45	0.50
15:XO:67:LEU:HB3	15:XO:78:TYR:HE1	1.76	0.50
53:Y7:5:TRP:NE1	53:Y7:7:PRO:HG3	2.26	0.50
29:YF:108:LYS:O	29:YF:112:MET:HG3	2.11	0.50
29:YF:65:TRP:O	29:YF:67:GLN:N	2.43	0.50
31:YH:4:ILE:HG13	31:YH:6:ARG:NE	2.26	0.50
31:YH:84:SER:O	31:YH:85:LYS:HB2	2.11	0.50
35:YP:36:LYS:HB3	35:YP:40:SER:HB3	1.94	0.50
1:QA:1128:C:H4'	9:QI:16:ARG:HH12	1.76	0.50
1:QA:34:C:H2'	1:QA:35:G:C8	2.47	0.50
1:QA:713:G:H2'	1:QA:714:G:C8	2.46	0.50
1:QA:940:C:H2'	1:QA:941:G:C8	2.47	0.50
2:QB:231:GLU:HG3	2:QB:233:SER:H	1.77	0.50
10:QJ:22:LYS:HZ2	10:QJ:23:ILE:HA	1.77	0.50
13:QM:92:HIS:HD2	13:QM:110:ARG:HH21	1.58	0.50
13:QM:40:ASN:HD22	13:QM:43:THR:HG23	1.77	0.50
25:RA:1436:G:H1'	25:RA:1477:A:O2'	2.11	0.50
26:RB:80:U:H2'	26:RB:81:G:N2	2.19	0.50
32:RI:29:TYR:O	32:RI:33:ARG:HB2	2.12	0.50
38:RS:67:ARG:O	38:RS:71:ARG:HG3	2.12	0.50
39:RT:39:ARG:HG2	39:RT:40:THR:H	1.76	0.50
45:RZ:54:HIS:CG	45:RZ:101:PRO:HG3	2.47	0.50
1:XA:1015:A:H2'	1:XA:1016:A:C8	2.46	0.50
2:XB:32:ILE:HD11	2:XB:40:HIS:HB3	1.94	0.50
4:XD:112:VAL:HG12	4:XD:116:GLN:OE1	2.12	0.50
5:XE:76:ILE:HG13	5:XE:93:PRO:HB3	1.94	0.50
11:XK:86:GLY:O	11:XK:91:ARG:HD3	2.11	0.50
13:XM:49:THR:HB	13:XM:52:GLU:H	1.77	0.50
52:Y6:47:THR:HG22	52:Y6:48:VAL:HG12	1.94	0.50
25:YA:1424:G:H2'	25:YA:1425:G:O4'	2.12	0.50
25:YA:1590:U:H2'	25:YA:1591:G:H8	1.75	0.50
25:YA:1798:U:C5'	27:YD:259:THR:HG22	2.41	0.50
25:YA:2875:C:H4'	39:YT:5:ALA:HB2	1.93	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:YN:58:ASP:N	33:YN:58:ASP:OD1	2.45	0.50
1:QA:1296:C:OP1	13:QM:44:ARG:NH2	2.45	0.50
1:QA:1375:A:H4'	7:QG:29:LYS:HE3	1.94	0.50
3:QC:14:ILE:HG12	3:QC:15:THR:N	2.27	0.50
4:QD:33:MET:CE	4:QD:37:PRO:HA	2.41	0.50
9:QI:118:LYS:O	9:QI:120:ARG:N	2.40	0.50
1:QA:376:G:H5''	16:QP:5:ARG:HD2	1.94	0.50
25:RA:1140:C:OP2	33:RN:66:LYS:NZ	2.42	0.50
25:RA:1204:A:C2	25:RA:1241:A:N1	2.78	0.50
25:RA:1291:C:H2'	25:RA:1292:U:C6	2.47	0.50
25:RA:2416:C:H2'	25:RA:2417:C:C6	2.46	0.50
29:RF:16:GLY:O	29:RF:18:ARG:N	2.45	0.50
33:RN:34:LEU:O	33:RN:49:GLY:HA3	2.12	0.50
39:RT:34:VAL:HG12	39:RT:36:GLU:HG2	1.94	0.50
43:RX:26:TYR:HB3	43:RX:92:LEU:HD12	1.93	0.50
1:XA:371:G:H2'	1:XA:372:C:O4'	2.12	0.50
1:XA:973:G:C4	10:XJ:55:LYS:HE2	2.47	0.50
2:XB:162:ILE:HD11	2:XB:184:VAL:HG22	1.94	0.50
54:Y8:25:MET:O	54:Y8:47:LYS:NZ	2.44	0.50
25:YA:1778:U:H2'	25:YA:1784:A:N6	2.27	0.50
25:YA:2336:A:H61	46:Y0:43:THR:CG2	2.24	0.50
25:YA:278:A:H2'	25:YA:279:C:C6	2.47	0.50
25:YA:1805:U:O2	27:YD:50:THR:HB	2.12	0.50
35:YP:126:VAL:HG13	35:YP:145:PRO:HB2	1.94	0.50
36:YQ:66:ILE:HG13	36:YQ:67:ARG:N	2.27	0.50
43:YX:60:ARG:HH22	53:Y7:47:ARG:HH12	1.60	0.50
44:YY:97:ARG:HH21	44:YY:98:VAL:HB	1.76	0.50
2:QB:235:SER:OG	2:QB:236:TYR:N	2.46	0.49
19:QS:41:VAL:HA	19:QS:44:MET:HG3	1.93	0.49
25:RA:1416:G:H2'	25:RA:1417:C:C6	2.47	0.49
25:RA:225:A:H5'	25:RA:226:G:OP2	2.11	0.49
36:RQ:20:ALA:HB1	36:RQ:99:PRO:HD2	1.94	0.49
43:RX:40:LYS:O	43:RX:42:ALA:N	2.45	0.49
1:XA:17:U:H2'	1:XA:18:C:C6	2.47	0.49
1:XA:1314:C:OP1	19:XS:6:LYS:HE3	2.12	0.49
20:XT:64:ASP:HA	20:XT:67:ALA:HB3	1.93	0.49
25:YA:1872:A:H5'	25:YA:1878:G:OP2	2.12	0.49
25:YA:1878:G:H2'	25:YA:1879:C:C6	2.47	0.49
28:YE:103:ASP:OD1	28:YE:201:THR:HG23	2.12	0.49
25:YA:1138:G:N2	33:YN:106:MET:HE3	2.13	0.49
25:YA:2820:A:O5'	37:YR:4:LEU:HD23	2.12	0.49
1:QA:985:C:H2'	1:QA:986:A:C8	2.47	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:QB:204:ASN:ND2	2:QB:206:ASP:O	2.45	0.49
9:QI:46:ALA:HB2	9:QI:74:ILE:HG23	1.94	0.49
1:QA:194:C:H5''	20:QT:65:LYS:HG3	1.94	0.49
25:RA:1047:G:H2'	25:RA:1110:G:N1	2.26	0.49
25:RA:2844:G:H3'	25:RA:2845:G:H8	1.77	0.49
25:RA:826:U:H2'	25:RA:828:U:O4'	2.11	0.49
25:RA:860:U:H5	25:RA:917:A:C2	2.30	0.49
25:RA:900:A:H5'	25:RA:901:A:OP2	2.11	0.49
25:RA:443:A:H3'	29:RF:45:ARG:NH1	2.27	0.49
31:RH:155:SER:OG	31:RH:156:ALA:N	2.45	0.49
37:RR:44:LEU:HD22	37:RR:48:VAL:HG23	1.94	0.49
38:RS:15:ARG:NH1	38:RS:25:ARG:HH21	2.11	0.49
1:XA:523:A:H61	12:XL:92:ASP:HB2	1.77	0.49
14:XN:23:ARG:NH1	14:XN:30:ALA:HB2	2.27	0.49
16:XP:28:ARG:NH1	16:XP:29:ASP:OD1	2.45	0.49
1:XA:452:A:H4'	16:XP:72:ARG:NH2	2.28	0.49
6:XF:97:PHE:HB2	18:XR:32:ARG:CZ	2.41	0.49
46:Y0:70:GLN:OE1	46:Y0:72:ARG:HD3	2.12	0.49
25:YA:1520:U:H2'	25:YA:1521:G:O4'	2.12	0.49
25:YA:1535:U:H5''	25:YA:1537:C:C4	2.47	0.49
25:YA:2299:G:N2	25:YA:2318:G:H1'	2.27	0.49
25:YA:363(B):G:H2'	25:YA:363(C):G:C8	2.45	0.49
28:YE:73:GLU:HG3	28:YE:74:PRO:HD2	1.92	0.49
40:YU:83:LEU:HG	40:YU:88:ILE:HG13	1.93	0.49
56:Z8:76:PPU:HN2	56:Z8:76:PPU:HD2	1.76	0.49
1:QA:399:G:H2'	1:QA:400:C:C6	2.46	0.49
3:QC:157:ILE:HD11	3:QC:166:GLU:HB2	1.94	0.49
8:QH:9:MET:HG3	8:QH:26:VAL:HG21	1.94	0.49
6:QF:97:PHE:O	18:QR:31:LEU:HD23	2.12	0.49
25:RA:1062:G:H2'	25:RA:1063:G:C8	2.48	0.49
25:RA:1278:A:H4'	37:RR:34:ILE:HD12	1.93	0.49
25:RA:2328:A:H2'	25:RA:2329:G:C8	2.46	0.49
25:RA:482:A:H4'	44:RY:47:LYS:HD2	1.94	0.49
29:RF:9:ILE:HD11	29:RF:125:LEU:HG	1.94	0.49
36:RQ:11:LYS:HE2	36:RQ:86:GLY:O	2.11	0.49
1:XA:160:A:H1'	1:XA:344:A:C5	2.47	0.49
1:XA:620:C:H2'	1:XA:621:A:O4'	2.13	0.49
9:XI:40:LEU:C	9:XI:42:ARG:H	2.15	0.49
11:XK:82:VAL:HB	11:XK:108:ILE:HG12	1.94	0.49
12:XL:71:PRO:O	12:XL:102:ARG:HD3	2.12	0.49
13:XM:20:THR:C	13:XM:22:ILE:H	2.15	0.49
19:XS:41:VAL:HB	19:XS:42:PRO:CA	2.42	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:140:A:C8	25:YA:1408:C:O2'	2.62	0.49
25:YA:2023:G:H5'	25:YA:2617:C:H4'	1.93	0.49
25:YA:2687:U:C4	25:YA:2688:U:C5	2.99	0.49
25:YA:247:G:H4'	25:YA:386:G:C5	2.47	0.49
28:YE:35:GLN:HG2	28:YE:37:ARG:HE	1.77	0.49
25:YA:1093:G:H4'	31:YH:170:ARG:HH22	1.76	0.49
33:YN:7:LYS:HD2	33:YN:7:LYS:N	2.28	0.49
43:YX:53:LYS:HB3	43:YX:82:GLN:HB3	1.93	0.49
3:QC:14:ILE:HG12	3:QC:15:THR:H	1.76	0.49
1:QA:1226:C:H2'	13:QM:103:THR:HB	1.93	0.49
1:QA:196:A:OP1	20:QT:68:LYS:NZ	2.44	0.49
27:RD:175:LEU:HD12	27:RD:185:VAL:HG21	1.93	0.49
30:RG:115:ARG:NH2	30:RG:137:GLU:OE1	2.45	0.49
30:RG:110:ALA:HB1	30:RG:140:ILE:HD12	1.94	0.49
32:RI:2:LYS:HA	32:RI:20:ASP:HA	1.95	0.49
1:XA:108:G:H5''	1:XA:109:A:H5''	1.94	0.49
1:XA:165:C:H2'	1:XA:166:G:C8	2.47	0.49
50:Y4:15:ILE:HD13	50:Y4:15:ILE:H	1.76	0.49
25:YA:1021:A:H3'	25:YA:1021:A:C8	2.46	0.49
25:YA:2308:G:N2	25:YA:2311:A:H2	2.09	0.49
25:YA:2704:C:H2'	25:YA:2705:A:O4'	2.12	0.49
25:YA:2770:G:H5''	25:YA:2771:C:OP2	2.13	0.49
25:YA:754:C:H2'	25:YA:755:C:C6	2.47	0.49
27:YD:121:PRO:HB3	27:YD:135:PHE:CE1	2.47	0.49
1:QA:1176:A:H2'	1:QA:1177:G:H5'	1.94	0.49
3:QC:73:PRO:O	3:QC:76:VAL:HG22	2.12	0.49
7:QG:20:ASP:HB3	7:QG:23:VAL:HG23	1.94	0.49
8:QH:95:VAL:HB	8:QH:99:GLU:O	2.13	0.49
18:QR:26:LEU:HD22	18:QR:42:ARG:HD2	1.94	0.49
22:QV:61:C:H2'	22:QV:62:C:H6	1.78	0.49
25:RA:1510:A:O2'	25:RA:1511:A:N7	2.44	0.49
25:RA:2022:U:O2'	25:RA:2617:C:H5'	2.11	0.49
25:RA:2495:G:H5''	36:RQ:81:VAL:HG13	1.94	0.49
25:RA:244:A:C2	25:RA:255:A:C4	3.01	0.49
25:RA:270(L):U:H2'	32:RI:50:ARG:HD2	1.94	0.49
29:RF:178:PRO:HG2	29:RF:179:GLU:OE2	2.13	0.49
32:RI:5:LEU:HD23	32:RI:9:LEU:HD11	1.94	0.49
1:XA:426:G:OP1	4:XD:38:TYR:OH	2.24	0.49
10:XJ:49:VAL:HG22	14:XN:41:ARG:HB2	1.94	0.49
13:XM:81:LEU:HD13	13:XM:88:ARG:HD2	1.94	0.49
25:YA:153:C:OP1	47:Y1:88:LYS:HE2	2.12	0.49
25:YA:1007:C:H4'	33:YN:108:PRO:HD3	1.94	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:177:G:H3'	25:YA:178:G:H8	1.77	0.49
25:YA:2257:U:O2'	25:YA:2258:C:H5'	2.13	0.49
25:YA:2854:G:H2'	25:YA:2855:C:C6	2.47	0.49
25:YA:34:C:H41	25:YA:447:A:H61	1.58	0.49
25:YA:860:U:H5	25:YA:917:A:N1	2.09	0.49
29:YF:31:HIS:HB2	35:YP:9:ASN:OD1	2.12	0.49
33:YN:34:LEU:HD21	33:YN:120:LEU:HB2	1.94	0.49
33:YN:17:ASP:O	33:YN:56:ASN:HB2	2.12	0.49
40:YU:61:TRP:CD2	40:YU:94:ASN:HA	2.47	0.49
40:YU:95:LEU:HD22	41:YV:4:ILE:HD12	1.93	0.49
1:QA:988:G:H2'	1:QA:989:C:O4'	2.12	0.49
1:QA:564:C:P	12:QL:15:ARG:HH21	2.36	0.49
14:QN:15:LYS:HD2	14:QN:16:PHE:CE2	2.47	0.49
49:R3:6:VAL:HG13	49:R3:56:VAL:HG13	1.94	0.49
53:R7:31:LEU:HD22	53:R7:42:LEU:HD13	1.95	0.49
25:RA:1678:G:N2	25:RA:1989:G:H22	2.09	0.49
25:RA:2507:C:H2'	25:RA:2508:G:O4'	2.13	0.49
25:RA:631:A:H61	25:RA:2402:C:H42	1.61	0.49
25:RA:974(A):C:H4'	25:RA:975:G:O5'	2.13	0.49
26:RB:17:C:H2'	26:RB:18:G:O4'	2.11	0.49
30:RG:54:GLU:HA	30:RG:57:ALA:HB3	1.93	0.49
32:RI:74:ASN:OD1	32:RI:74:ASN:N	2.44	0.49
33:RN:134:ARG:N	33:RN:135:PRO:HD3	2.28	0.49
36:RQ:69:PHE:CD1	36:RQ:70:PRO:HD2	2.46	0.49
40:RU:92:ARG:O	40:RU:92:ARG:HG2	2.13	0.49
43:RX:27:THR:HB	43:RX:80:ILE:HB	1.94	0.49
45:RZ:102:LEU:HB3	45:RZ:104:PHE:HE1	1.78	0.49
1:XA:163:C:H2'	1:XA:164:U:C6	2.48	0.49
22:XV:25:C:H2'	22:XV:26:G:O4'	2.12	0.49
52:Y6:41:PRO:HD2	52:Y6:46:HIS:N	2.28	0.49
25:YA:77:C:OP1	48:Y2:59:ARG:HD3	2.13	0.49
27:YD:76:PRO:HG2	27:YD:98:VAL:HG21	1.94	0.49
27:YD:27:THR:HG21	27:YD:83:GLU:HG2	1.94	0.49
28:YE:179:GLU:HB3	28:YE:181:LEU:HD23	1.94	0.49
25:YA:617:G:OP1	29:YF:40:GLN:NE2	2.46	0.49
30:YG:94:LEU:HD12	30:YG:99:MET:HA	1.95	0.49
44:YY:86:ARG:HB2	44:YY:95:LYS:HD2	1.93	0.49
3:QC:47:LEU:HD23	3:QC:68:VAL:HG11	1.94	0.49
1:QA:963:G:H21	10:QJ:55:LYS:CE	2.26	0.49
22:QV:74:C:C2'	22:QV:75:C:H5'	2.42	0.49
46:R0:32:ARG:H	46:R0:35:ASN:ND2	2.10	0.49
52:R6:15:GLU:CD	52:R6:41:PRO:HB3	2.32	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:747:U:O2	25:RA:2014:A:H1'	2.12	0.49
26:RB:8:U:O3'	38:RS:25:ARG:NH2	2.40	0.49
28:RE:70:ALA:O	28:RE:72:VAL:N	2.46	0.49
29:RF:132:VAL:HG23	29:RF:133:ASN:OD1	2.12	0.49
30:RG:60:LEU:O	30:RG:64:THR:HG22	2.11	0.49
25:RA:2415:G:H4'	35:RP:67:MET:N	2.28	0.49
36:RQ:89:ASN:O	36:RQ:91:GLU:N	2.45	0.49
44:RY:47:LYS:HG2	44:RY:60:PHE:HD1	1.77	0.49
1:XA:1075:C:OP1	2:XB:179:LYS:HE2	2.13	0.49
1:XA:520:A:N1	1:XA:536:C:H1'	2.28	0.49
2:XB:24:TRP:CZ3	2:XB:26:PRO:HA	2.48	0.49
12:XL:62:SER:HB2	12:XL:64:TYR:HD1	1.76	0.49
23:XY:30:C:H2'	23:XY:31:G:C8	2.48	0.49
52:Y6:21:TYR:HE1	52:Y6:53:LYS:HE3	1.77	0.49
35:YP:63:PRO:HD3	54:Y8:13:ARG:HD3	1.95	0.49
25:YA:1021:A:H3'	25:YA:1021:A:H8	1.78	0.49
25:YA:1291:C:H5'	25:YA:1536:A:H5'	1.95	0.49
25:YA:589:C:H2'	25:YA:590:A:C8	2.48	0.49
1:QA:1529:G:OP2	1:QA:1529:G:H3'	2.13	0.49
1:QA:427:U:OP1	4:QD:13:ARG:NH2	2.45	0.49
20:QT:79:ARG:O	20:QT:83:ARG:HG3	2.12	0.49
23:QY:30:C:H2'	23:QY:31:G:C8	2.47	0.49
25:RA:263:C:H2'	25:RA:264:C:O4'	2.12	0.49
25:RA:2665:A:H2'	25:RA:2666:C:O4'	2.13	0.49
25:RA:27:G:O2'	25:RA:28:A:C8	2.66	0.49
25:RA:345:A:O2'	25:RA:347:A:N7	2.46	0.49
25:RA:774:A:H2	25:RA:787:U:HO2'	1.60	0.49
25:RA:811:U:OP2	35:RP:29:LYS:N	2.45	0.49
27:RD:228:PRO:HD3	27:RD:234:GLY:C	2.33	0.49
27:RD:35:LYS:HZ1	27:RD:65:ILE:HA	1.76	0.49
1:XA:1432:G:OP1	39:YT:107:ASP:HB2	2.13	0.49
1:XA:833:U:H3	1:XA:853:G:H1	1.61	0.49
3:XC:148:GLY:HA3	3:XC:172:ARG:O	2.12	0.49
11:XK:59:TYR:CZ	11:XK:63:LEU:HD11	2.47	0.49
13:XM:14:ARG:HG2	13:XM:17:VAL:HG23	1.95	0.49
20:XT:89:ARG:NH2	20:XT:104:LEU:HD11	2.27	0.49
52:Y6:41:PRO:O	52:Y6:45:LYS:HE3	2.12	0.49
25:YA:1113:U:H2'	25:YA:1114:G:H8	1.78	0.49
25:YA:1509:C:N3	25:YA:1511:A:N6	2.61	0.49
25:YA:152:G:H2'	25:YA:153:C:C6	2.48	0.49
25:YA:760:G:H4'	25:YA:1776:G:OP1	2.13	0.49
25:YA:185:U:H4'	25:YA:218:A:H4'	1.95	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:2031:A:N3	25:YA:2455:G:O2'	2.42	0.49
43:YX:57:LEU:HD11	43:YX:78:LYS:HD2	1.94	0.49
2:QB:96:ARG:H	2:QB:96:ARG:HD2	1.76	0.49
4:QD:129:ASN:HA	4:QD:145:GLU:HB2	1.94	0.49
12:QL:24:VAL:HG13	12:QL:98:TYR:HE2	1.77	0.49
17:QQ:18:THR:HG23	17:QQ:69:LYS:HE3	1.94	0.49
52:R6:14:THR:O	52:R6:49:HIS:HA	2.12	0.49
25:RA:1366:A:H2'	25:RA:1367:A:O4'	2.13	0.49
25:RA:1636:C:H2'	25:RA:1637:A:C8	2.48	0.49
25:RA:2210:G:H3'	25:RA:2211:G:C8	2.48	0.49
25:RA:2593:U:H2'	25:RA:2594:C:C6	2.48	0.49
25:RA:586:A:N1	25:RA:809:G:O2'	2.37	0.49
25:RA:848:G:H2'	25:RA:849:A:C8	2.48	0.49
31:RH:4:ILE:HG13	31:RH:6:ARG:NE	2.28	0.49
39:RT:16:ARG:HD3	39:RT:19:LEU:HD11	1.93	0.49
1:XA:632:A:C8	1:XA:633:G:C8	3.00	0.49
1:XA:686:U:O2'	11:XK:42:TRP:NE1	2.45	0.49
1:XA:762:C:H2'	1:XA:763:G:H8	1.78	0.49
2:XB:47:THR:HA	2:XB:202:PRO:HG2	1.95	0.49
5:XE:10:MET:SD	5:XE:13:ILE:HD13	2.53	0.49
10:XJ:35:SER:OG	10:XJ:73:ASP:HB2	2.13	0.49
19:XS:68:GLY:HA3	50:Y4:68:ARG:HB2	1.93	0.49
46:Y0:53:MET:HA	46:Y0:58:THR:O	2.13	0.49
25:YA:1667:G:OP2	25:YA:1667:G:H8	1.95	0.49
25:YA:2805:G:N2	25:YA:2893:G:O6	2.40	0.49
27:YD:170:GLY:C	27:YD:172:TYR:H	2.16	0.49
25:YA:1257:C:OP1	29:YF:75:HIS:HE1	1.95	0.49
31:YH:12:PRO:HG3	31:YH:48:GLY:HA2	1.95	0.49
1:QA:376:G:H5''	16:QP:5:ARG:HB2	1.95	0.49
2:QB:21:ARG:O	2:QB:23:ARG:N	2.46	0.49
10:QJ:24:VAL:HG21	10:QJ:37:PRO:HD3	1.95	0.49
15:QO:87:ILE:HG22	15:QO:88:ARG:H	1.78	0.49
25:RA:1021:A:H62	25:RA:1141:U:H3	1.61	0.49
25:RA:1169:G:H1	25:RA:1180:C:N4	2.08	0.49
25:RA:503:A:H4'	25:RA:504:U:H5''	1.95	0.49
6:XF:19:LEU:HD21	6:XF:59:TYR:CE2	2.47	0.49
35:YP:61:ARG:HD3	54:Y8:13:ARG:HD2	1.94	0.49
25:YA:1607:C:N4	25:YA:1622:G:OP2	2.39	0.49
25:YA:1870:C:H2'	25:YA:1871:A:O4'	2.13	0.49
25:YA:211:A:H2'	25:YA:212:G:O4'	2.13	0.49
25:YA:70:G:H21	25:YA:71:A:H62	1.59	0.49
25:YA:1803:A:O2'	27:YD:259:THR:HG21	2.13	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:YD:61:LEU:O	27:YD:63:ARG:NH1	2.45	0.49
29:YF:176:LEU:HD21	29:YF:181:LEU:HA	1.94	0.49
1:QA:109:A:C6	1:QA:326:G:C6	3.01	0.48
1:QA:297:G:N2	1:QA:300:A:OP2	2.45	0.48
7:QG:155:ARG:NH2	7:QG:155:ARG:O	2.46	0.48
15:QO:16:ALA:HB1	15:QO:21:ASP:HB3	1.94	0.48
19:QS:77:THR:HG22	19:QS:78:ARG:HD3	1.95	0.48
52:R6:25:LYS:HE2	52:R6:27:LYS:HD3	1.94	0.48
25:RA:2074:U:H2'	25:RA:2075:U:C6	2.48	0.48
25:RA:2243:U:H2'	25:RA:2244:U:C6	2.48	0.48
25:RA:2291:U:O2'	25:RA:2374:C:O2	2.24	0.48
25:RA:2689:U:H5'	25:RA:2713:A:C2	2.48	0.48
25:RA:2875:C:H4'	39:RT:5:ALA:HB2	1.94	0.48
25:RA:2882:A:OP1	37:RR:96:ARG:NH1	2.36	0.48
1:XA:690:G:H2'	1:XA:691:G:O4'	2.12	0.48
1:XA:883:C:C2'	1:XA:884:U:H5'	2.43	0.48
3:XC:134:ILE:HG23	3:XC:151:VAL:HB	1.94	0.48
3:XC:79:ARG:HH12	3:XC:82:GLU:HG3	1.77	0.48
5:XE:31:LEU:HD23	5:XE:45:PHE:HD1	1.78	0.48
6:XF:35:ALA:HA	6:XF:67:MET:HB3	1.94	0.48
25:YA:207:A:H2'	25:YA:208:C:O4'	2.13	0.48
25:YA:2470:G:H5'	36:YQ:56:ARG:NH2	2.28	0.48
25:YA:2712:U:O2'	25:YA:2712(A):A:P	2.71	0.48
25:YA:278:A:O2'	25:YA:279:C:O4'	2.30	0.48
25:YA:639:U:H2'	25:YA:640:C:C6	2.47	0.48
26:YB:15:A:H5'	26:YB:16:G:H8	1.73	0.48
30:YG:166:ASP:HA	30:YG:169:ALA:HB3	1.95	0.48
31:YH:98:LEU:HD13	31:YH:125:VAL:HB	1.94	0.48
34:YO:4:PRO:O	34:YO:5:GLN:HB2	2.11	0.48
36:YQ:104:PHE:CE1	36:YQ:125:LEU:HD11	2.41	0.48
39:YT:107:ASP:H	39:YT:110:ILE:HG22	1.78	0.48
42:YW:51:LEU:HD23	42:YW:105:VAL:HG11	1.94	0.48
2:QB:80:ILE:HG21	2:QB:212:GLN:HA	1.95	0.48
4:QD:27:TYR:HE2	6:XF:15:ASP:HB3	1.78	0.48
12:QL:58:VAL:O	12:QL:65:GLU:HA	2.13	0.48
21:QU:5:ASP:O	21:QU:11:GLY:HA3	2.13	0.48
47:R1:53:VAL:HB	47:R1:58:ILE:HD12	1.94	0.48
25:RA:2019:A:OP2	51:R5:9:LYS:NZ	2.45	0.48
25:RA:722:A:H5'	25:RA:723:G:OP2	2.12	0.48
29:RF:178:PRO:HB2	29:RF:201:VAL:HG11	1.94	0.48
30:RG:98:ARG:HE	30:RG:98:ARG:HB2	1.38	0.48
31:RH:152:ARG:HH21	31:RH:153:LYS:HZ1	1.61	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
31:RH:41:MET:HG3	31:RH:54:ARG:HA	1.96	0.48
44:RY:47:LYS:HG2	44:RY:60:PHE:CD1	2.48	0.48
1:XA:1135:U:H4'	1:XA:1136:U:H5	1.77	0.48
1:XA:413:G:HO2'	1:XA:414:A:P	2.35	0.48
5:XE:33:VAL:HG11	5:XE:109:ILE:HA	1.95	0.48
16:XP:26:ARG:HH21	16:XP:31:LYS:HB3	1.77	0.48
23:XY:29:U:H2'	23:XY:30:C:C6	2.48	0.48
25:YA:107:C:H2'	25:YA:108:U:C6	2.48	0.48
25:YA:1506:C:H3'	25:YA:1507:A:H5''	1.94	0.48
25:YA:2725:A:O2'	25:YA:2726:U:OP2	2.29	0.48
27:YD:35:LYS:HD3	27:YD:63:ARG:CB	2.43	0.48
28:YE:21:VAL:HG23	28:YE:22:PRO:HD3	1.95	0.48
29:YF:185:ASP:OD1	29:YF:188:ARG:NH1	2.35	0.48
31:YH:55:PRO:HG2	31:YH:61:HIS:CE1	2.48	0.48
35:YP:135:LEU:HD13	35:YP:139:LYS:HE2	1.94	0.48
40:YU:98:LEU:O	40:YU:102:GLU:N	2.37	0.48
1:QA:1372:U:H2'	1:QA:1373:G:O4'	2.13	0.48
1:QA:411:A:C5	1:QA:413:G:H1'	2.49	0.48
1:QA:560:U:H4'	1:QA:561:U:O5'	2.12	0.48
1:QA:692:U:OP1	11:QK:124:LYS:NZ	2.22	0.48
2:QB:163:PHE:HD2	2:QB:185:ILE:HG13	1.78	0.48
4:QD:100:ARG:NH2	4:QD:136:PRO:O	2.47	0.48
7:QG:113:GLU:HG3	7:QG:119:ARG:HG2	1.94	0.48
10:QJ:32:ALA:HB3	10:QJ:76:ASN:HB2	1.95	0.48
13:QM:49:THR:HG22	13:QM:51:ALA:H	1.79	0.48
13:QM:23:TYR:HE1	13:QM:70:LEU:HD12	1.77	0.48
25:RA:1188:U:O2'	25:RA:1189:A:H5'	2.14	0.48
25:RA:142:G:H5''	25:RA:1598:C:O2'	2.13	0.48
25:RA:2262:U:H4'	25:RA:2328:A:C2	2.48	0.48
25:RA:2506:U:OP1	28:RE:144:ARG:NH2	2.47	0.48
29:RF:155:LEU:HD12	29:RF:174:VAL:HG22	1.94	0.48
35:RP:58:THR:O	35:RP:61:ARG:CZ	2.61	0.48
35:RP:59:LEU:HA	35:RP:61:ARG:HE	1.76	0.48
43:RX:39:ILE:O	43:RX:43:VAL:HG12	2.13	0.48
1:XA:1128:C:N3	1:XA:1144:G:N2	2.37	0.48
1:XA:1486:G:H2'	1:XA:1487:G:O4'	2.14	0.48
1:XA:1499:A:H1'	1:XA:1520:G:H5'	1.94	0.48
1:XA:406:G:H5'	4:XD:5:ILE:HD13	1.95	0.48
3:XC:130:VAL:HG21	3:XC:157:ILE:HG23	1.94	0.48
3:XC:7:PRO:O	3:XC:11:ARG:HG2	2.13	0.48
25:YA:1109:C:HO2'	25:YA:1110:G:P	2.35	0.48
25:YA:1329:U:H5''	25:YA:1330:C:H5	1.77	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:1510:A:N3	25:YA:1510:A:H2'	2.29	0.48
25:YA:1733:G:H5'	25:YA:1734:C:OP2	2.13	0.48
25:YA:754:C:H2'	25:YA:755:C:H6	1.77	0.48
34:YO:76:ALA:HB3	39:YT:75:ILE:HD12	1.95	0.48
35:YP:82:GLY:HA2	35:YP:113:LYS:O	2.12	0.48
1:QA:999:U:H2'	1:QA:1000:A:C8	2.48	0.48
1:QA:791:G:H2'	1:QA:792:A:H5'	1.96	0.48
3:QC:150:LYS:HG3	3:QC:169:ALA:HB2	1.95	0.48
25:RA:1403:C:H5''	25:RA:1471:A:C1'	2.38	0.48
25:RA:526:A:OP1	25:RA:527:C:OP1	2.31	0.48
25:RA:71:A:H5'	25:RA:72:U:H3'	1.94	0.48
25:RA:873:G:H1	25:RA:904:C:N4	2.11	0.48
26:RB:15:A:H1'	26:RB:109:G:N9	2.28	0.48
30:RG:81:LYS:O	30:RG:82:LEU:HB2	2.12	0.48
25:RA:811:U:O2'	35:RP:21:ARG:HG3	2.13	0.48
1:XA:1256:A:OP2	3:XC:26:LYS:NZ	2.34	0.48
2:XB:101:MET:HA	2:XB:108:ILE:HG13	1.95	0.48
5:XE:50:GLU:HG3	5:XE:52:PRO:HD2	1.95	0.48
6:XF:36:ARG:CZ	6:XF:38:GLU:HG2	2.44	0.48
47:Y1:41:ARG:HG3	47:Y1:41:ARG:HH11	1.79	0.48
25:YA:1026:U:H4'	25:YA:1027:A:OP1	2.14	0.48
25:YA:2593:U:H2'	25:YA:2594:C:H6	1.79	0.48
25:YA:2862:G:H2'	25:YA:2863:C:H6	1.79	0.48
25:YA:507:A:H5''	25:YA:508:G:H5'	1.95	0.48
31:YH:137:ASP:HB3	31:YH:140:LYS:HB3	1.94	0.48
41:YV:15:GLU:O	41:YV:18:LEU:HB2	2.14	0.48
45:YZ:182:LYS:CG	45:YZ:183:LEU:HA	2.44	0.48
1:QA:1286:A:C8	1:QA:1287:A:H4'	2.48	0.48
1:QA:1379:G:O6	7:QG:2:ALA:HB3	2.12	0.48
1:QA:145:G:H2'	1:QA:146:G:O4'	2.13	0.48
1:QA:755:G:H2'	1:QA:756:C:H6	1.78	0.48
1:QA:838:G:C5	1:QA:842:C:H1'	2.49	0.48
12:QL:7:ILE:HG21	17:QQ:34:LYS:HB2	1.95	0.48
16:QP:43:LYS:HA	16:QP:48:TRP:HB3	1.95	0.48
19:QS:26:GLY:O	19:QS:28:LYS:N	2.41	0.48
49:R3:4:LEU:O	49:R3:36:VAL:HA	2.13	0.48
25:RA:1091:G:N2	25:RA:1101:U:H1'	2.28	0.48
25:RA:1889:A:O2'	25:RA:2087:G:H5'	2.14	0.48
25:RA:2563:U:H2'	25:RA:2565:A:OP2	2.13	0.48
25:RA:2629:A:O2'	25:RA:2630:G:H5''	2.13	0.48
25:RA:270:A:H1'	25:RA:370:G:C2	2.49	0.48
33:RN:4:TYR:O	40:RU:64:ARG:NH1	2.46	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
37:RR:97:VAL:HG22	37:RR:114:VAL:CG2	2.44	0.48
37:RR:2:ARG:HA	37:RR:5:LYS:HE3	1.95	0.48
44:RY:81:LYS:NZ	44:RY:98:VAL:HG11	2.28	0.48
1:XA:1319:A:H2'	1:XA:1323:G:N7	2.29	0.48
1:XA:56:U:H2'	1:XA:57:G:C8	2.48	0.48
1:XA:868:C:H2'	1:XA:869:G:O4'	2.12	0.48
2:XB:73:THR:OG1	2:XB:170:GLU:OE2	2.23	0.48
11:XK:18:ARG:NH2	11:XK:35:PRO:O	2.45	0.48
20:XT:93:GLU:OE1	20:XT:94:ALA:N	2.46	0.48
51:Y5:41:PRO:O	51:Y5:44:THR:OG1	2.32	0.48
28:YE:111:ARG:HG2	37:YR:1:MET:SD	2.54	0.48
39:YT:102:ILE:HB	39:YT:110:ILE:HD13	1.95	0.48
43:YX:63:LYS:O	43:YX:64:LYS:HD2	2.14	0.48
1:QA:1065:U:O5'	1:QA:1190:G:N2	2.47	0.48
1:QA:963:G:N2	1:QA:972:C:N3	2.44	0.48
7:QG:57:GLU:OE1	7:QG:57:GLU:N	2.41	0.48
9:QI:17:VAL:HG11	9:QI:81:ILE:HA	1.95	0.48
10:QJ:80:LYS:HD3	10:QJ:80:LYS:HA	1.69	0.48
11:QK:48:ILE:HD11	11:QK:64:ALA:HA	1.95	0.48
12:QL:17:LYS:HG2	12:QL:19:ARG:HG2	1.94	0.48
25:RA:1660:C:H2'	25:RA:1661:G:H8	1.78	0.48
25:RA:2053:G:H5'	28:RE:144:ARG:O	2.13	0.48
38:RS:64:GLU:O	38:RS:68:GLN:HG3	2.14	0.48
28:RE:181:LEU:HD21	39:RT:7:ILE:HG23	1.95	0.48
44:RY:51:VAL:O	44:RY:56:PRO:HA	2.14	0.48
1:XA:1347:G:N2	1:XA:1373:G:H2'	2.28	0.48
1:XA:701:C:HO2'	1:XA:702:A:P	2.35	0.48
2:XB:204:ASN:ND2	2:XB:206:ASP:H	2.11	0.48
9:XI:9:ARG:HB2	9:XI:14:VAL:HA	1.96	0.48
15:XO:70:LEU:HD11	15:XO:77:ARG:HG3	1.96	0.48
23:XY:29:U:H2'	23:XY:30:C:H6	1.78	0.48
25:YA:218:A:C2	25:YA:235:U:H4'	2.48	0.48
25:YA:2544:G:O5'	25:YA:2544:G:H8	1.95	0.48
28:YE:20:ALA:HB3	28:YE:21:VAL:HG13	1.95	0.48
35:YP:14:LYS:O	35:YP:16:ARG:HG2	2.13	0.48
35:YP:52:GLU:O	35:YP:55:ARG:HG2	2.14	0.48
25:YA:2496:C:OP2	36:YQ:81:VAL:HG12	2.12	0.48
38:YS:74:ALA:HB1	38:YS:107:GLU:HB3	1.95	0.48
40:YU:60:LEU:O	40:YU:60:LEU:HD22	2.14	0.48
41:YV:76:LYS:HB2	41:YV:81:TYR:HB3	1.95	0.48
1:QA:1151:A:H2'	1:QA:1152:A:C8	2.48	0.48
4:QD:88:VAL:HG13	5:QE:97:GLY:HA3	1.94	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:QT:12:ALA:O	20:QT:15:ARG:HB2	2.14	0.48
54:R8:51:ALA:N	54:R8:53:PRO:HD2	2.29	0.48
25:RA:2122:U:H2'	25:RA:2123:G:H8	1.79	0.48
25:RA:512:G:H4'	25:RA:513:A:O5'	2.12	0.48
25:RA:530:G:C5	25:RA:2022:U:H5''	2.49	0.48
29:RF:197:ASP:N	29:RF:197:ASP:OD2	2.46	0.48
45:RZ:52:SER:O	45:RZ:54:HIS:N	2.46	0.48
1:XA:1122:U:O4	1:XA:1123:A:N6	2.47	0.48
1:XA:95:G:C6	1:XA:96:G:C6	3.02	0.48
1:XA:403:C:OP1	4:XD:137:SER:OG	2.32	0.48
6:XF:10:LEU:HD22	6:XF:61:LEU:HD11	1.94	0.48
19:XS:39:THR:HG22	19:XS:40:ILE:H	1.78	0.48
25:YA:1050:A:C8	25:YA:2751:G:C4	3.02	0.48
25:YA:1533:C:H2'	25:YA:1534:G:N7	2.29	0.48
25:YA:2287:A:N6	25:YA:2344:U:H3	2.05	0.48
25:YA:27:G:H22	25:YA:512:G:C2'	2.27	0.48
25:YA:459:U:H2'	25:YA:460:A:H8	1.78	0.48
25:YA:576:U:H2'	25:YA:577:G:C8	2.48	0.48
26:YB:89:G:C6	26:YB:89(A):A:C6	3.01	0.48
27:YD:254:THR:O	27:YD:254:THR:OG1	2.30	0.48
40:YU:97:ASP:OD1	40:YU:101:ARG:NH1	2.46	0.48
42:YW:67:ASP:OD2	42:YW:67:ASP:N	2.46	0.48
1:QA:1220:G:O3'	19:QS:36:ARG:HD3	2.14	0.48
1:QA:1343:G:H2'	1:QA:1344:C:C6	2.48	0.48
1:QA:1352:C:H2'	1:QA:1353:G:C8	2.48	0.48
1:QA:406:G:C2	1:QA:407:G:C8	3.02	0.48
1:QA:892:A:O2'	1:QA:1415:G:H4'	2.14	0.48
9:QI:40:LEU:O	9:QI:42:ARG:N	2.46	0.48
12:QL:38:THR:O	12:QL:79:GLU:HG3	2.14	0.48
15:QO:26:GLU:H	15:QO:26:GLU:HG2	1.42	0.48
17:QQ:100:LYS:O	17:QQ:101:ARG:NE	2.47	0.48
50:R4:23:GLU:HG3	50:R4:25:TYR:CE2	2.49	0.48
51:R5:55:ARG:HG3	51:R5:57:VAL:N	2.17	0.48
25:RA:184:C:H2'	25:RA:185:U:C6	2.48	0.48
25:RA:2455:G:H2'	25:RA:2456:C:C6	2.49	0.48
22:QV:75:C:OP1	25:RA:2602:A:P	2.72	0.48
29:RF:102:PRO:HB2	29:RF:105:VAL:HG23	1.95	0.48
30:RG:82:LEU:HD21	30:RG:88:ILE:HG13	1.96	0.48
31:RH:154:PRO:HD3	31:RH:162:ILE:H	1.77	0.48
32:RI:133:HIS:HB2	32:RI:134:PRO:CD	2.43	0.48
35:RP:36:LYS:HB3	35:RP:40:SER:HB3	1.95	0.48
25:RA:671:C:OP1	35:RP:42:SER:O	2.31	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:XA:1094:G:O2'	1:XA:1095:U:OP2	2.22	0.48
1:XA:892:A:O2'	1:XA:1415:G:H4'	2.13	0.48
1:XA:688:G:H2'	1:XA:689:C:H6	1.79	0.48
1:XA:692:U:H5'	1:XA:797:C:H5'	1.95	0.48
5:XE:110:LEU:HD13	5:XE:118:ILE:HG21	1.94	0.48
9:XI:114:TYR:CD2	9:XI:114:TYR:N	2.81	0.48
52:Y6:27:LYS:HB2	52:Y6:27:LYS:NZ	2.28	0.48
25:YA:1385:G:H1'	25:YA:1386:C:C6	2.49	0.48
25:YA:1557:C:OP2	25:YA:1558:A:O2'	2.26	0.48
25:YA:776:G:H4'	25:YA:777:A:O5'	2.13	0.48
32:YI:69:LYS:HG3	32:YI:136:VAL:HB	1.96	0.48
40:YU:90:VAL:HG22	41:YV:39:LEU:HB3	1.96	0.48
44:YY:35:TYR:CD1	44:YY:69:ALA:HB3	2.49	0.48
1:QA:1143:G:H2'	1:QA:1144:G:C8	2.49	0.48
1:QA:452:A:O2'	1:QA:453:A:O4'	2.31	0.48
10:QJ:78:ASN:O	10:QJ:82:ILE:HG12	2.14	0.48
22:QV:61:C:H2'	22:QV:62:C:C6	2.49	0.48
52:R6:18:ARG:HB2	52:R6:44:ARG:HH12	1.77	0.48
25:RA:1019:U:O2'	25:RA:1021:A:H2	1.96	0.48
25:RA:1165:U:H2'	25:RA:1166:C:C6	2.49	0.48
25:RA:1520:U:H2'	25:RA:1521:G:O4'	2.13	0.48
25:RA:2119:A:N6	25:RA:2170:A:N7	2.60	0.48
27:RD:25:THR:O	27:RD:27:THR:HG22	2.14	0.48
31:RH:86:GLU:OE1	31:RH:86:GLU:N	2.43	0.48
32:RI:13:GLY:HA3	32:RI:17:GLN:CD	2.33	0.48
25:RA:1226:G:H4'	41:RV:84:LYS:HG2	1.96	0.48
1:XA:1151:A:O2'	1:XA:1152:A:O5'	2.23	0.48
1:XA:407:G:H2'	1:XA:408:A:H8	1.77	0.48
16:XP:22:THR:HA	16:XP:33:ILE:HG12	1.96	0.48
1:XA:110:C:O2'	16:XP:25:ARG:O	2.22	0.48
1:XA:564:C:C6	17:XQ:31:LEU:HD11	2.49	0.48
51:Y5:58:LEU:HD22	51:Y5:60:VAL:HB	1.96	0.48
25:YA:1156:A:C8	40:YU:51:LYS:HG3	2.49	0.48
25:YA:128:C:H4'	53:Y7:49:ARG:NH1	2.26	0.48
25:YA:1545(A):A:H2'	25:YA:1546:C:O4'	2.14	0.48
25:YA:1882:C:H5'	25:YA:1883:G:OP2	2.13	0.48
25:YA:2352:A:C4	25:YA:2366:A:C2	3.01	0.48
25:YA:861:A:C2	25:YA:917:A:C5	3.02	0.48
31:YH:6:ARG:HA	31:YH:66:GLY:HA2	1.95	0.48
32:YI:76:THR:OG1	32:YI:139:GLN:OE1	2.31	0.48
35:YP:46:LYS:HB3	35:YP:46:LYS:HE3	1.54	0.48
35:YP:98:GLU:HA	35:YP:101:VAL:HB	1.96	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
40:YU:92:ARG:CZ	41:YV:11:GLN:H	2.26	0.48
1:QA:1032(A):G:H2'	1:QA:1032(B):G:C8	2.48	0.48
1:QA:1327:C:OP2	21:QU:12:LYS:NZ	2.47	0.48
1:QA:738:C:OP2	6:QF:92:LYS:NZ	2.47	0.48
1:QA:909:A:H2'	1:QA:910:C:O4'	2.14	0.48
1:QA:946:A:N6	1:QA:1234:C:H42	2.11	0.48
2:QB:97:TRP:CH2	2:QB:173:ALA:HA	2.49	0.48
5:QE:69:VAL:O	5:QE:71:LEU:N	2.47	0.48
35:RP:61:ARG:CD	54:R8:13:ARG:HD2	2.44	0.48
25:RA:1012:U:O4	33:RN:25:ARG:HA	2.14	0.48
25:RA:1794:U:H2'	25:RA:1795:C:H6	1.77	0.48
25:RA:1870:C:H2'	25:RA:1871:A:O4'	2.14	0.48
25:RA:2164:C:H2'	25:RA:2165:G:O4'	2.13	0.48
25:RA:2563:U:H4'	34:RO:28:SER:HA	1.96	0.48
25:RA:2584:U:H2'	25:RA:2585:U:C6	2.49	0.48
25:RA:2823:A:OP1	28:RE:113:PHE:HB2	2.14	0.48
25:RA:323:G:H2'	29:RF:169:ASN:ND2	2.29	0.48
25:RA:38:A:H2'	25:RA:39:C:C6	2.48	0.48
29:RF:183:VAL:O	29:RF:187:VAL:HG23	2.13	0.48
33:RN:7:LYS:HD2	33:RN:7:LYS:H	1.79	0.48
43:RX:83:VAL:HG11	43:RX:87:GLN:HB2	1.96	0.48
1:XA:33:A:H2'	1:XA:34:C:C6	2.49	0.48
1:XA:407:G:H2'	1:XA:408:A:C8	2.48	0.48
1:XA:659:U:H2'	1:XA:660:G:H8	1.79	0.48
3:XC:70:VAL:HG12	3:XC:72:LYS:H	1.79	0.48
5:XE:6:PHE:CE2	5:XE:36:ASP:HB3	2.48	0.48
8:XH:49:GLU:HG2	8:XH:62:TYR:HE2	1.78	0.48
25:YA:1404:C:C2'	25:YA:1405:U:H5'	2.44	0.48
25:YA:603:A:O4'	25:YA:655:A:N6	2.46	0.48
33:YN:134:ARG:N	33:YN:135:PRO:HD3	2.29	0.48
38:YS:65:VAL:O	38:YS:69:VAL:HG12	2.14	0.48
44:YY:44:ILE:HG13	44:YY:45:VAL:N	2.28	0.48
1:QA:1179:A:H2'	1:QA:1180:A:O4'	2.14	0.47
1:QA:1213:A:N6	1:QA:1215:G:N3	2.62	0.47
1:QA:184:G:H2'	1:QA:185:A:H8	1.79	0.47
4:QD:106:TYR:HE1	4:QD:112:VAL:O	1.97	0.47
13:QM:57:ARG:HH11	13:QM:57:ARG:HB2	1.79	0.47
25:RA:1569:A:H2'	25:RA:1570:A:O4'	2.13	0.47
25:RA:321:G:OP1	29:RF:135:LYS:NZ	2.44	0.47
25:RA:483:A:H5'	44:RY:49:VAL:HG22	1.95	0.47
29:RF:167:ALA:HB1	29:RF:173:VAL:HG11	1.95	0.47
30:RG:145:THR:O	30:RG:147:ASP:N	2.47	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:1614:A:N1	42:RW:91:GLY:HA2	2.29	0.47
1:XA:1149:C:OP1	9:XI:9:ARG:NH2	2.41	0.47
1:XA:1241:G:H2'	1:XA:1242:C:C6	2.48	0.47
1:XA:1319:A:H5'	1:XA:1320:C:OP1	2.14	0.47
1:XA:28:G:O2'	1:XA:296:U:OP1	2.30	0.47
10:XJ:38:ILE:HD11	10:XJ:71:LEU:HD23	1.96	0.47
51:Y5:46:CYS:O	51:Y5:48:GLU:N	2.38	0.47
25:YA:264:C:H2'	25:YA:265:A:H5''	1.95	0.47
25:YA:2655:G:N2	25:YA:2665:A:OP2	2.47	0.47
26:YB:44:G:H1'	26:YB:47:C:H42	1.78	0.47
27:YD:35:LYS:HZ1	27:YD:104:TYR:HB2	1.79	0.47
1:QA:1321:C:H3'	1:QA:1322:C:H5''	1.95	0.47
1:QA:484:G:H4'	1:QA:485:G:O5'	2.14	0.47
2:QB:70:PHE:O	2:QB:93:VAL:N	2.48	0.47
4:QD:26:CYS:HA	4:QD:31:CYS:HA	1.96	0.47
6:QF:41:GLU:HB2	6:QF:62:TRP:CE3	2.50	0.47
48:R2:41:ILE:HD11	48:R2:44:LEU:HD12	1.96	0.47
55:R9:27:CYS:SG	55:R9:32:HIS:HB2	2.55	0.47
25:RA:1575:C:H2'	25:RA:1576:U:O4'	2.15	0.47
25:RA:2114:A:N6	25:RA:2119:A:H62	2.12	0.47
25:RA:363(B):G:H2'	25:RA:363(C):G:C8	2.49	0.47
25:RA:27:G:H22	25:RA:512:G:H1'	1.78	0.47
32:RI:49:ALA:O	32:RI:52:ARG:HG2	2.14	0.47
35:RP:127:ALA:HB3	35:RP:130:PHE:CZ	2.49	0.47
1:QA:1432:G:OP1	39:RT:107:ASP:HB2	2.14	0.47
1:XA:31:G:O2'	1:XA:48:C:N4	2.46	0.47
2:XB:84:GLU:OE1	2:XB:87:ARG:NH2	2.43	0.47
18:XR:36:ASN:ND2	18:XR:36:ASN:O	2.41	0.47
25:YA:1036:G:OP1	31:YH:59:ARG:HB2	2.14	0.47
25:YA:1535:U:N3	25:YA:1537:C:H1'	2.29	0.47
26:YB:27:C:H5'	26:YB:28:C:OP2	2.14	0.47
35:YP:144:GLU:N	35:YP:144:GLU:OE1	2.40	0.47
41:YV:44:LYS:O	41:YV:46:VAL:HG12	2.13	0.47
1:QA:1388:C:H2'	1:QA:1389:C:H6	1.79	0.47
1:QA:836:G:C6	1:QA:851:G:C6	3.02	0.47
1:QA:983:A:N1	1:QA:1222:G:N2	2.63	0.47
2:QB:25:ASN:O	2:QB:27:LYS:N	2.47	0.47
14:QN:41:ARG:CZ	14:QN:42:ILE:HD11	2.44	0.47
25:RA:1083:U:O2'	25:RA:1085:A:H5''	2.14	0.47
25:RA:1833:U:O2'	25:RA:1969:A:N1	2.30	0.47
25:RA:2494:G:H2'	25:RA:2495:G:H8	1.80	0.47
25:RA:860:U:C5	25:RA:917:A:C2	3.02	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
36:RQ:136:ALA:C	36:RQ:138:ASP:H	2.18	0.47
1:XA:1412:C:H2'	1:XA:1413:A:C8	2.49	0.47
1:XA:179:A:H2'	1:XA:180:U:C6	2.50	0.47
1:XA:109:A:H2'	1:XA:326:G:N2	2.29	0.47
3:XC:34:LEU:HD23	3:XC:38:ARG:HG3	1.95	0.47
3:XC:79:ARG:NH1	3:XC:82:GLU:HG3	2.29	0.47
4:XD:15:GLU:HG2	4:XD:63:LYS:HB2	1.97	0.47
1:XA:1298:C:C4	7:XG:114:ARG:HD2	2.50	0.47
9:XI:121:ARG:NH1	9:XI:122:ALA:O	2.47	0.47
9:XI:126:SER:O	9:XI:128:ARG:N	2.43	0.47
18:XR:66:LEU:O	18:XR:70:ILE:HG13	2.14	0.47
47:Y1:91:LYS:HB3	47:Y1:92:LYS:H	1.44	0.47
48:Y2:59:ARG:O	48:Y2:63:VAL:HG23	2.15	0.47
25:YA:2245:U:H5'	25:YA:2246:G:H5'	1.96	0.47
25:YA:2688:U:H5	25:YA:2720:U:OP2	1.97	0.47
25:YA:2849:U:H4'	25:YA:2868:A:C2	2.49	0.47
27:YD:71:ASP:HB2	27:YD:103:ARG:NH2	2.27	0.47
29:YF:36:VAL:HG11	29:YF:183:VAL:HG11	1.95	0.47
36:YQ:21:THR:HB	36:YQ:22:LYS:H	1.40	0.47
39:YT:11:GLU:N	39:YT:11:GLU:OE1	2.43	0.47
6:QF:61:LEU:HB3	6:QF:63:TYR:HE2	1.79	0.47
12:QL:51:ALA:HB3	12:QL:53:ARG:HE	1.80	0.47
20:QT:30:LYS:O	20:QT:33:ILE:HB	2.14	0.47
47:R1:91:LYS:O	47:R1:94:LEU:N	2.36	0.47
51:R5:46:CYS:O	51:R5:48:GLU:N	2.47	0.47
25:RA:83:G:N2	25:RA:103:A:OP2	2.37	0.47
25:RA:1421:G:C2	25:RA:1422:G:C8	3.02	0.47
25:RA:2064:C:H2'	25:RA:2065:C:C6	2.48	0.47
25:RA:2532:G:H1'	25:RA:2663:G:N2	2.29	0.47
25:RA:888:C:O2'	25:RA:889:C:H4'	2.14	0.47
36:RQ:63:LYS:HG2	36:RQ:65:PHE:CE2	2.50	0.47
39:RT:64:ARG:HD2	39:RT:73:GLU:OE1	2.14	0.47
40:RU:97:ASP:OD1	40:RU:101:ARG:NH1	2.48	0.47
1:XA:1004:A:H1'	1:XA:1036:G:N2	2.30	0.47
3:XC:22:TRP:CD1	3:XC:59:ARG:HD2	2.49	0.47
3:XC:81:GLY:O	3:XC:85:ARG:HB2	2.14	0.47
12:XL:24:VAL:HG12	12:XL:24:VAL:O	2.14	0.47
12:XL:7:ILE:HA	12:XL:7:ILE:HD13	1.82	0.47
20:XT:98:PRO:O	20:XT:100:ILE:N	2.46	0.47
47:Y1:53:VAL:HG22	47:Y1:74:VAL:HG13	1.96	0.47
35:YP:50:ARG:HE	54:Y8:7:HIS:HE2	1.63	0.47
25:YA:1379:A:H4'	25:YA:1380:G:OP2	2.14	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:2056:G:H1	51:Y5:4:HIS:HD2	1.62	0.47
25:YA:226:G:HO2'	25:YA:227:A:H8	1.55	0.47
25:YA:846:C:O2'	25:YA:847:U:OP2	2.26	0.47
25:YA:2467:C:H4'	36:YQ:123:HIS:CG	2.49	0.47
1:QA:1124:G:H5''	1:QA:1145:C:H41	1.78	0.47
1:QA:32:A:C2	1:QA:33:A:C4	3.03	0.47
2:QB:211:ILE:O	2:QB:215:LEU:HB2	2.14	0.47
2:QB:85:ALA:HB3	2:QB:92:TYR:HD2	1.79	0.47
4:QD:12:CYS:HA	4:QD:19:LEU:CD2	2.45	0.47
7:QG:99:LEU:HD22	7:QG:103:TRP:CZ2	2.49	0.47
25:RA:1220:A:H5'	25:RA:1221:C:OP2	2.14	0.47
25:RA:155:C:N4	25:RA:171:G:H1	2.11	0.47
25:RA:1871:A:H2'	25:RA:1872:A:C8	2.50	0.47
25:RA:958:U:OP1	36:RQ:74:TYR:OH	2.29	0.47
30:RG:3:LEU:HD11	50:R4:25:TYR:CE1	2.48	0.47
32:RI:98:ALA:HA	32:RI:109:ILE:HD11	1.97	0.47
5:XE:8:GLU:OE2	5:XE:63:ARG:NH2	2.46	0.47
6:XF:69:GLU:O	6:XF:72:VAL:HG12	2.14	0.47
9:XI:4:TYR:CZ	9:XI:88:TYR:HB2	2.49	0.47
12:XL:27:LEU:O	12:XL:29:GLY:N	2.46	0.47
15:XO:66:LEU:HD12	15:XO:66:LEU:HA	1.66	0.47
20:XT:35:THR:O	20:XT:39:LYS:HG3	2.14	0.47
54:Y8:36:LYS:HB3	54:Y8:40:GLU:HG2	1.95	0.47
25:YA:7:G:H1	25:YA:2896:C:H42	1.62	0.47
26:YB:24:G:H1'	26:YB:26:A:H62	1.79	0.47
27:YD:28:GLU:HB2	27:YD:29:PRO:CD	2.45	0.47
25:YA:1454:U:H5'	37:YR:63:ARG:NE	2.30	0.47
42:YW:110:LYS:HG3	42:YW:111:HIS:H	1.80	0.47
1:QA:1350:A:OP2	9:QI:118:LYS:NZ	2.48	0.47
1:QA:683:G:H2'	1:QA:684:A:H8	1.78	0.47
9:QI:28:VAL:HG22	9:QI:63:ILE:HB	1.96	0.47
25:RA:103:A:H8	25:RA:103:A:O5'	1.98	0.47
25:RA:1045:A:N3	25:RA:1047:G:N2	2.63	0.47
25:RA:1497:U:H5''	25:RA:1498:C:C5	2.49	0.47
25:RA:2294:C:OP2	38:RS:89:ARG:NH2	2.47	0.47
25:RA:27:G:O2'	25:RA:28:A:H8	1.97	0.47
25:RA:298:G:H5''	25:RA:299:A:OP1	2.15	0.47
25:RA:443:A:C5	29:RF:45:ARG:HD2	2.50	0.47
25:RA:484:C:OP1	44:RY:51:VAL:HG11	2.15	0.47
26:RB:42:C:O2	30:RG:93:THR:N	2.34	0.47
26:RB:52:A:N6	38:RS:33:LYS:HG3	2.29	0.47
28:RE:73:GLU:HG3	28:RE:74:PRO:HD2	1.95	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:960:A:H61	36:RQ:82:ARG:NH1	2.12	0.47
42:RW:63:ASP:OD1	42:RW:63:ASP:N	2.48	0.47
44:RY:21:LYS:HG3	44:RY:22:GLY:N	2.30	0.47
1:XA:1000:A:H2'	1:XA:1001:G:H8	1.79	0.47
1:XA:41:G:H2'	1:XA:42:G:C8	2.49	0.47
1:XA:429:U:H1'	1:XA:430:A:H5''	1.97	0.47
25:YA:1062:G:H8	25:YA:1062:G:O5'	1.97	0.47
25:YA:1239:G:H2'	25:YA:1240:U:O4'	2.14	0.47
25:YA:1529:A:N6	25:YA:1542:G:O2'	2.41	0.47
25:YA:2392:A:C8	35:YP:60:MET:HG2	2.50	0.47
25:YA:2469:A:H5'	25:YA:2470:G:OP2	2.15	0.47
29:YF:164:ARG:HG3	29:YF:175:THR:OG1	2.15	0.47
33:YN:30:ILE:HG22	33:YN:34:LEU:HD22	1.96	0.47
1:QA:1163:C:H42	1:QA:1173:G:H1	1.62	0.47
1:QA:1207:G:H2'	1:QA:1208:C:C6	2.49	0.47
1:QA:129(A):G:N2	1:QA:188:U:O2'	2.47	0.47
1:QA:1314:C:P	19:QS:6:LYS:HD2	2.55	0.47
1:QA:1443:G:H5'	1:QA:1446:A:OP2	2.15	0.47
1:QA:1392:G:N2	1:QA:1502:A:H8	2.09	0.47
1:QA:181:G:HO2'	1:QA:182:U:P	2.38	0.47
12:QL:27:LEU:O	12:QL:29:GLY:N	2.47	0.47
13:QM:78:ILE:HG23	13:QM:92:HIS:ND1	2.30	0.47
17:QQ:76:LEU:HD21	17:QQ:79:SER:HB2	1.97	0.47
25:RA:860:U:H5	25:RA:917:A:N1	2.12	0.47
26:RB:83:G:H1	26:RB:93:C:H42	1.62	0.47
39:RT:123:GLN:O	39:RT:125:ARG:N	2.48	0.47
1:XA:1070:U:H2'	1:XA:1071:C:H6	1.79	0.47
1:XA:328:C:H4'	1:XA:329:A:C5'	2.45	0.47
2:XB:93:VAL:HG11	2:XB:97:TRP:CD1	2.50	0.47
10:XJ:47:PHE:HB3	14:XN:34:TYR:CE2	2.50	0.47
9:XI:114:TYR:HD1	10:XJ:60:ARG:HB2	1.79	0.47
11:XK:48:ILE:HG13	11:XK:63:LEU:HB2	1.97	0.47
1:XA:35:G:N3	12:XL:118:SER:OG	2.46	0.47
25:YA:1453:A:O2'	25:YA:1454:U:H2'	2.14	0.47
25:YA:1916:A:H2'	25:YA:1917:U:O4'	2.15	0.47
25:YA:2319:G:N7	38:YS:3:ARG:HB3	2.29	0.47
25:YA:593:G:O3'	54:Y8:61:LEU:HD22	2.14	0.47
27:YD:206:LEU:HA	27:YD:206:LEU:HD23	1.51	0.47
29:YF:182:ASN:HD21	29:YF:185:ASP:CG	2.14	0.47
30:YG:28:VAL:O	30:YG:31:VAL:HG13	2.14	0.47
32:YI:144:VAL:HG22	32:YI:145:VAL:H	1.80	0.47
25:YA:896:A:C8	45:YZ:146:ILE:HD12	2.50	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:QA:1125:U:O4	10:QJ:5:ARG:HD3	2.15	0.47
1:QA:474:G:H2'	1:QA:475:G:H8	1.79	0.47
1:QA:801:U:H2'	1:QA:802:A:H8	1.80	0.47
1:QA:1316:G:H5''	14:QN:17:LYS:HE3	1.96	0.47
47:R1:76:ARG:H	47:R1:76:ARG:HD2	1.80	0.47
25:RA:142:G:H2'	25:RA:143:C:C6	2.49	0.47
25:RA:1654:A:OP2	37:RR:2:ARG:HD2	2.14	0.47
25:RA:649:G:H2'	25:RA:650:C:C6	2.49	0.47
25:RA:753:C:H2'	25:RA:754:C:H6	1.78	0.47
27:RD:118:VAL:HG22	27:RD:119:ALA:N	2.29	0.47
28:RE:37:ARG:HA	28:RE:37:ARG:NE	2.29	0.47
31:RH:152:ARG:HG3	31:RH:153:LYS:CD	2.44	0.47
45:RZ:141:VAL:HA	45:RZ:144:LEU:HD23	1.96	0.47
1:XA:1192:C:OP2	3:XC:4:LYS:NZ	2.41	0.47
17:XQ:67:LYS:O	17:XQ:68:ARG:HB3	2.15	0.47
46:Y0:19:LYS:HA	46:Y0:19:LYS:HD3	1.66	0.47
25:YA:1221:C:H2'	25:YA:1222:C:H6	1.79	0.47
25:YA:1665:A:C2'	25:YA:1666:G:H5'	2.43	0.47
25:YA:922:U:H2'	25:YA:923:C:C6	2.50	0.47
27:YD:237:GLU:O	27:YD:239:ARG:N	2.47	0.47
30:YG:113:ARG:HG2	50:Y4:34:GLU:OE2	2.14	0.47
30:YG:34:LEU:HD22	30:YG:35:GLU:N	2.30	0.47
1:QA:1053:G:N7	1:QA:1199:U:H3'	2.30	0.47
3:QC:82:GLU:O	3:QC:86:VAL:HG13	2.14	0.47
7:QG:18:TYR:HD2	7:QG:59:LEU:HD22	1.79	0.47
2:QB:178:ARG:HH21	8:QH:74:PRO:HG3	1.80	0.47
12:QL:17:LYS:HG3	12:QL:18:VAL:N	2.30	0.47
1:QA:110:C:O2'	16:QP:25:ARG:O	2.32	0.47
19:QS:35:SER:O	19:QS:71:LEU:HD12	2.15	0.47
25:RA:1153:C:H2'	25:RA:1154:G:O4'	2.15	0.47
25:RA:2286:A:H4'	25:RA:2287:A:O4'	2.15	0.47
25:RA:500:G:N2	25:RA:502:A:H3'	2.29	0.47
25:RA:521:G:H2'	25:RA:522:G:H8	1.80	0.47
25:RA:2723:C:OP2	28:RE:109:LYS:NZ	2.47	0.47
25:RA:2679:A:H4'	28:RE:165:VAL:HG11	1.96	0.47
28:RE:95:ILE:HD12	28:RE:95:ILE:H	1.80	0.47
38:RS:56:LEU:O	38:RS:58:LEU:N	2.48	0.47
44:RY:76:CYS:HB2	44:RY:101:LYS:HG3	1.96	0.47
25:RA:498:G:N3	44:RY:47:LYS:NZ	2.62	0.47
1:XA:1118:C:P	9:XI:104:ARG:HH11	2.37	0.47
1:XA:1315:U:H2'	1:XA:1316:G:O4'	2.14	0.47
1:XA:1348:U:H3	1:XA:1374:A:H2	1.57	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:XB:18:GLY:H	2:XB:42:ILE:HG22	1.80	0.47
5:XE:89:ILE:HG12	5:XE:91:LEU:HD13	1.97	0.47
49:Y3:23:LEU:HD13	49:Y3:50:VAL:HG11	1.96	0.47
25:YA:99:U:O2'	25:YA:101:G:OP2	2.28	0.47
25:YA:1728:G:H5'	25:YA:1729:A:OP2	2.14	0.47
25:YA:2636:U:H2'	25:YA:2637:U:H6	1.79	0.47
25:YA:307:G:H21	25:YA:330:A:N6	2.13	0.47
28:YE:116:VAL:HG11	28:YE:138:PRO:HB3	1.97	0.47
29:YF:140:LEU:HD12	29:YF:140:LEU:HA	1.77	0.47
29:YF:9:ILE:HG23	29:YF:20:LEU:O	2.15	0.47
30:YG:114:ILE:HD13	30:YG:140:ILE:HG21	1.96	0.47
31:YH:122:THR:HG22	31:YH:134:SER:HB2	1.96	0.47
25:YA:1614:A:H61	42:YW:88:ARG:H	1.61	0.47
1:QA:1001:G:H2'	1:QA:1002:G:O4'	2.15	0.47
1:QA:299:G:H2'	1:QA:300:A:C8	2.50	0.47
1:QA:456:C:H2'	1:QA:457:C:C6	2.50	0.47
1:QA:1179:A:O3'	9:QI:103:THR:HG23	2.14	0.47
11:QK:16:SER:OG	11:QK:106:LYS:NZ	2.48	0.47
13:QM:65:LYS:HB3	50:R4:50:VAL:HG21	1.96	0.47
25:RA:1248:G:C5	40:RU:3:ARG:HB2	2.50	0.47
25:RA:49:A:H61	25:RA:177:G:H2'	1.79	0.47
25:RA:1851:U:H2'	25:RA:1852:C:O4'	2.15	0.47
25:RA:702:G:C2	25:RA:731:C:C2	3.03	0.47
27:RD:12:SER:O	27:RD:16:MET:HB2	2.14	0.47
27:RD:211:ARG:HD2	27:RD:214:TRP:CZ3	2.50	0.47
28:RE:21:VAL:HB	28:RE:22:PRO:HB3	1.96	0.47
29:RF:133:ASN:HA	29:RF:162:LEU:HD22	1.96	0.47
31:RH:27:LYS:HA	31:RH:32:GLU:HA	1.96	0.47
39:RT:16:ARG:HE	39:RT:19:LEU:HD21	1.80	0.47
1:XA:1057:G:H2'	1:XA:1058:G:O4'	2.15	0.47
1:XA:1152:A:H2'	1:XA:1153:C:H6	1.79	0.47
1:XA:1225:A:N3	1:XA:1225:A:H2'	2.29	0.47
1:XA:1227:A:OP2	13:XM:111:LYS:HE3	2.15	0.47
1:XA:1366:C:H2'	1:XA:1367:C:H6	1.80	0.47
1:XA:767:A:H2'	1:XA:768:A:O4'	2.15	0.47
25:YA:1586:A:H3'	25:YA:1587:A:H8	1.80	0.47
25:YA:1658:C:H2'	25:YA:1659:U:C6	2.50	0.47
25:YA:2461:C:H2'	25:YA:2462:U:C6	2.49	0.47
25:YA:478:A:C6	25:YA:480:A:C6	3.03	0.47
25:YA:957:A:N1	25:YA:2458:G:H4'	2.29	0.47
29:YF:129:PHE:HA	29:YF:142:TRP:NE1	2.29	0.47
31:YH:4:ILE:HB	31:YH:6:ARG:CG	2.43	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
31:YH:4:ILE:HG13	31:YH:6:ARG:CZ	2.45	0.47
1:QA:1126:U:OP2	1:QA:1281:U:H1'	2.15	0.47
1:QA:527:G:O2'	1:QA:535:A:N1	2.33	0.47
1:QA:553:A:O2'	12:QL:29:GLY:O	2.33	0.47
2:QB:32:ILE:HD13	2:QB:40:HIS:HB3	1.96	0.47
2:QB:8:LYS:H	2:QB:8:LYS:HD3	1.79	0.47
17:QQ:74:LEU:HB3	17:QQ:75:ARG:H	1.63	0.47
25:RA:1542:G:H5''	25:RA:1543:A:OP2	2.15	0.47
25:RA:1946:U:H2'	25:RA:1947:C:C6	2.50	0.47
25:RA:226:G:O2'	25:RA:227:A:O5'	2.33	0.47
25:RA:2329:G:H2'	25:RA:2330:G:C8	2.49	0.47
25:RA:2867:G:OP2	39:RT:119:LYS:NZ	2.27	0.47
27:RD:61:LEU:HA	27:RD:61:LEU:HD12	1.77	0.47
29:RF:62:ARG:HB3	29:RF:62:ARG:CZ	2.45	0.47
32:RI:9:LEU:O	32:RI:10:GLU:HG3	2.15	0.47
38:RS:48:LEU:HD23	38:RS:82:ILE:HD11	1.96	0.47
41:RV:24:LYS:HG3	41:RV:92:THR:HG23	1.97	0.47
1:XA:791:G:C6	1:XA:792:A:C2	3.03	0.47
1:XA:910:C:P	12:XL:97:ARG:HH22	2.38	0.47
25:YA:1204:A:O2'	25:YA:1205:U:O5'	2.33	0.47
25:YA:1289:C:H2'	25:YA:1290:C:H6	1.79	0.47
25:YA:2439:A:H5'	25:YA:2439:A:C8	2.50	0.47
35:YP:64:LYS:HB2	54:Y8:25:MET:HG3	1.96	0.47
44:YY:73:ARG:HB3	44:YY:73:ARG:HE	1.47	0.47
1:QA:1502:A:H2	1:QA:1505:G:N1	2.07	0.46
20:QT:89:ARG:NH2	20:QT:105:SER:O	2.36	0.46
20:QT:33:ILE:HD13	20:QT:62:LEU:HB3	1.96	0.46
47:R1:89:GLU:HA	47:R1:93:GLU:HB2	1.96	0.46
54:R8:29:LYS:HD3	54:R8:44:LYS:CB	2.45	0.46
25:RA:1025:G:C4	25:RA:1135:C:H1'	2.50	0.46
25:RA:1678:G:N2	25:RA:1989:G:N2	2.63	0.46
25:RA:1843:C:H2'	25:RA:1844:C:H6	1.80	0.46
25:RA:1991:U:H2'	25:RA:1992:G:H5''	1.97	0.46
25:RA:2439:A:P	25:RA:2439:A:H3'	2.56	0.46
25:RA:2303:G:O2'	30:RG:132:ASN:HB2	2.15	0.46
39:RT:20:PRO:HD2	39:RT:86:ILE:HG23	1.97	0.46
42:RW:23:LEU:O	42:RW:27:LYS:HD2	2.14	0.46
1:XA:1126:U:H1'	1:XA:1280:A:C5	2.50	0.46
1:XA:244:U:H4'	1:XA:245:C:O5'	2.15	0.46
4:XD:63:LYS:HD2	4:XD:198:VAL:HG22	1.97	0.46
19:XS:33:THR:OG1	19:XS:34:TRP:N	2.49	0.46
19:XS:41:VAL:HA	19:XS:44:MET:HG3	1.97	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
22:XV:3:G:O2'	22:XV:4:G:P	2.72	0.46
50:Y4:38:LYS:HD3	50:Y4:42:PHE:HE1	1.80	0.46
51:Y5:33:CYS:SG	51:Y5:34:PRO:HD2	2.55	0.46
25:YA:1029:A:N1	25:YA:2465:C:O2'	2.46	0.46
25:YA:2593:U:H2'	25:YA:2594:C:C6	2.50	0.46
25:YA:602:G:O2'	25:YA:655:A:N6	2.48	0.46
25:YA:890:A:O2'	25:YA:892:G:H8	1.98	0.46
27:YD:17:THR:CG2	27:YD:205:VAL:H	2.28	0.46
29:YF:108:LYS:HB3	29:YF:108:LYS:NZ	2.31	0.46
31:YH:154:PRO:HD3	31:YH:162:ILE:H	1.79	0.46
32:YI:68:LEU:HA	32:YI:71:ILE:HG22	1.97	0.46
33:YN:114:ARG:O	33:YN:115:ARG:HB3	2.14	0.46
35:YP:88:LEU:HB2	35:YP:91:PHE:HE2	1.80	0.46
35:YP:96:THR:O	35:YP:99:LEU:HB3	2.15	0.46
1:QA:1152:A:H2'	1:QA:1153:C:C6	2.50	0.46
1:QA:1494:G:O6	58:QA:1666:PAR:H42	2.15	0.46
1:QA:244:U:H4'	1:QA:245:C:O5'	2.14	0.46
5:QE:9:LYS:HB3	5:QE:112:LEU:HD11	1.98	0.46
16:QP:3:LYS:O	16:QP:21:VAL:HA	2.15	0.46
19:QS:15:LEU:H	19:QS:15:LEU:HD23	1.79	0.46
25:RA:1668:A:H4'	25:RA:1669:A:O5'	2.15	0.46
25:RA:1771:C:H1'	25:RA:1786:A:H8	1.77	0.46
25:RA:2011:U:OP2	42:RW:16:LYS:NZ	2.46	0.46
25:RA:620:G:H4'	25:RA:621:A:C5'	2.45	0.46
25:RA:1657:C:OP2	28:RE:136:ARG:HD3	2.14	0.46
28:RE:186:GLY:O	28:RE:188:VAL:N	2.48	0.46
31:RH:153:LYS:HB3	31:RH:162:ILE:H	1.80	0.46
40:RU:8:VAL:HG23	40:RU:11:ARG:HH21	1.80	0.46
1:XA:1262:C:H2'	1:XA:1263:C:H6	1.77	0.46
2:XB:201:ILE:HG21	2:XB:214:ILE:HG21	1.95	0.46
13:XM:12:ASN:HD22	13:XM:12:ASN:N	2.13	0.46
17:XQ:63:ARG:HG2	17:XQ:64:PRO:HD2	1.97	0.46
19:XS:41:VAL:HG23	19:XS:67:VAL:HG13	1.98	0.46
50:Y4:2:LYS:HD2	50:Y4:2:LYS:HA	1.67	0.46
25:YA:234:C:H2'	25:YA:235:U:C6	2.51	0.46
25:YA:415:A:H2'	25:YA:416:C:H6	1.81	0.46
26:YB:16:G:N2	26:YB:69:G:H1'	2.29	0.46
28:YE:150:VAL:HG13	28:YE:154:LYS:HG3	1.96	0.46
28:YE:176:ILE:HB	28:YE:181:LEU:HB2	1.97	0.46
30:YG:11:TYR:HA	30:YG:15:VAL:HB	1.95	0.46
35:YP:19:VAL:HG13	35:YP:21:ARG:N	2.20	0.46
38:YS:52:SER:HB2	38:YS:55:ALA:H	1.79	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
44:YY:87:LYS:HD3	44:YY:92:ASN:HB3	1.98	0.46
1:QA:352:C:O2'	1:QA:354:G:OP1	2.22	0.46
2:QB:166:ASP:OD1	2:QB:169:LYS:HB2	2.15	0.46
1:QA:545:C:OP1	4:QD:61:LYS:NZ	2.49	0.46
7:QG:78:ARG:HG3	7:QG:79:ARG:N	2.29	0.46
25:RA:2100:G:H1	25:RA:2189:U:H3	1.63	0.46
25:RA:2336:A:H61	46:R0:43:THR:CG2	2.28	0.46
25:RA:2632:A:O2'	25:RA:2811:G:O2'	2.18	0.46
25:RA:2790:A:C2	25:RA:2791:C:H2'	2.50	0.46
25:RA:333:G:H5''	25:RA:334:C:OP2	2.15	0.46
27:RD:70:TRP:CD2	27:RD:150:LYS:HD2	2.49	0.46
30:RG:22:ARG:HH22	30:RG:175:LEU:HD21	1.79	0.46
25:RA:662:G:H5'	35:RP:15:ARG:HA	1.96	0.46
35:RP:83:VAL:HG12	35:RP:114:ILE:HA	1.98	0.46
34:RO:76:ALA:HB3	39:RT:75:ILE:HB	1.97	0.46
43:RX:49:VAL:HG13	43:RX:83:VAL:HG13	1.96	0.46
44:RY:89:PHE:O	44:RY:90:LEU:HD13	2.15	0.46
3:XC:14:ILE:HG12	3:XC:15:THR:N	2.30	0.46
7:XG:74:GLU:HG2	7:XG:91:VAL:HG22	1.98	0.46
9:XI:18:PHE:HB2	9:XI:62:TYR:HB3	1.97	0.46
9:XI:83:ARG:O	9:XI:86:VAL:HG12	2.15	0.46
25:YA:1102:C:H2'	25:YA:1103:A:H5''	1.97	0.46
25:YA:1550:C:H2'	25:YA:1551:C:H6	1.80	0.46
25:YA:1771:C:C1'	25:YA:1786:A:C8	2.97	0.46
25:YA:2059:A:H5'	25:YA:2060:A:OP2	2.16	0.46
27:YD:94:LEU:HD22	27:YD:95:LEU:N	2.31	0.46
29:YF:127:GLU:OE2	29:YF:128:ALA:N	2.47	0.46
32:YI:131:LYS:HB3	32:YI:132:PRO:HA	1.98	0.46
35:YP:121:LYS:HE2	35:YP:121:LYS:HB2	1.75	0.46
35:YP:29:LYS:HD2	35:YP:30:THR:HG23	1.97	0.46
1:QA:1258:G:H2'	1:QA:1259:C:C6	2.50	0.46
6:QF:10:LEU:N	6:QF:59:TYR:O	2.46	0.46
25:RA:519:U:H2'	25:RA:520:G:H8	1.81	0.46
26:RB:89(A):A:C5	26:RB:90:C:H1'	2.50	0.46
27:RD:43:ARG:HH11	27:RD:44:ASN:CG	2.16	0.46
25:RA:1754:C:P	39:RT:96:ARG:HH12	2.33	0.46
25:RA:581:C:OP1	40:RU:33:ARG:HG3	2.15	0.46
43:RX:55:ASN:HB2	43:RX:80:ILE:HG23	1.97	0.46
1:XA:1306:A:H61	1:XA:1331:G:H1'	1.80	0.46
1:XA:1443:G:H5'	1:XA:1446:A:OP2	2.15	0.46
1:XA:191(D):U:H2'	1:XA:191(E):G:H8	1.80	0.46
1:XA:791:G:C2'	1:XA:792:A:H5'	2.45	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:XD:30:LYS:C	4:XD:32:ALA:H	2.18	0.46
7:XG:115:ARG:HB2	7:XG:118:VAL:HG22	1.97	0.46
1:XA:134:A:H61	16:XP:25:ARG:NH1	2.14	0.46
46:Y0:17:GLN:O	46:Y0:19:LYS:HE3	2.14	0.46
25:YA:1265:A:H3'	51:Y5:19:ARG:NH1	2.31	0.46
25:YA:1396:U:O2	25:YA:1396:U:H2'	2.15	0.46
25:YA:1794:U:H2'	25:YA:1795:C:H6	1.80	0.46
25:YA:2356:C:H2'	25:YA:2357:U:O4'	2.16	0.46
25:YA:2655:G:O2'	25:YA:2656:U:P	2.73	0.46
27:YD:25:THR:CG2	27:YD:82:ILE:H	2.27	0.46
38:YS:27:SER:HA	38:YS:88:ASP:HB2	1.96	0.46
1:QA:1191:A:O5'	1:QA:1191:A:H8	1.98	0.46
1:QA:1310:G:OP1	13:QM:77:ASN:ND2	2.49	0.46
52:R6:13:CYS:HB2	52:R6:22:ALA:HB3	1.98	0.46
25:RA:1078:U:O2'	25:RA:1079:C:OP2	2.30	0.46
25:RA:2107:C:N4	25:RA:2182:G:H1	2.11	0.46
25:RA:273:G:H1	25:RA:364:C:H42	1.63	0.46
25:RA:345:A:O2'	25:RA:346:A:N7	2.40	0.46
25:RA:864:G:C6	25:RA:865:C:N4	2.84	0.46
26:RB:88:C:H2'	26:RB:89:G:O4'	2.14	0.46
32:RI:104:GLN:C	32:RI:105:HIS:HD1	2.18	0.46
32:RI:88:ILE:HG12	32:RI:122:GLU:H	1.80	0.46
35:RP:124:LYS:HA	35:RP:143:GLY:O	2.16	0.46
38:RS:61:ASN:O	38:RS:65:VAL:HG23	2.14	0.46
38:RS:78:LEU:HD11	38:RS:107:GLU:O	2.15	0.46
25:RA:25:U:H5'	42:RW:79:GLY:HA2	1.98	0.46
2:XB:163:PHE:CD2	2:XB:185:ILE:HG13	2.50	0.46
3:XC:178:LEU:HD13	3:XC:178:LEU:HA	1.84	0.46
10:XJ:62:HIS:H	10:XJ:62:HIS:CD2	2.33	0.46
19:XS:41:VAL:HB	19:XS:42:PRO:HA	1.96	0.46
47:Y1:96:LYS:H	47:Y1:97:LEU:HD12	1.81	0.46
49:Y3:8:LEU:HD22	49:Y3:31:LEU:HD22	1.96	0.46
25:YA:1153:C:H5'	40:YU:76:TYR:HE2	1.81	0.46
25:YA:224:G:O6	25:YA:419:C:O2'	2.33	0.46
25:YA:2545:G:H2'	25:YA:2546:U:O4'	2.16	0.46
25:YA:27:G:H22	25:YA:512:G:H2'	1.79	0.46
44:YY:94:LYS:HD2	44:YY:101:LYS:HZ3	1.81	0.46
1:QA:1169:A:H2'	1:QA:1170:A:C8	2.51	0.46
1:QA:801:U:H2'	1:QA:802:A:C8	2.50	0.46
12:QL:54:LYS:N	12:QL:54:LYS:HD2	2.31	0.46
19:QS:63:THR:HG23	19:QS:65:ASN:OD1	2.16	0.46
22:QV:40:C:H2'	22:QV:41:C:H6	1.79	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
54:R8:39:LYS:O	54:R8:43:GLN:HB2	2.15	0.46
25:RA:1061:U:H3'	25:RA:1062:G:H5''	1.96	0.46
25:RA:1274:A:N3	25:RA:1297:C:H1'	2.30	0.46
25:RA:265:A:N6	25:RA:428:A:C8	2.84	0.46
25:RA:270(R):G:H2'	25:RA:270(S):G:C8	2.50	0.46
25:RA:511:U:O2'	25:RA:1215:G:N2	2.43	0.46
30:RG:98:ARG:O	30:RG:101:ILE:HG13	2.16	0.46
32:RI:29:TYR:CD2	32:RI:30:LEU:HD23	2.51	0.46
32:RI:40:THR:O	32:RI:44:LEU:N	2.44	0.46
25:RA:1649:G:O2'	37:RR:107:ASP:OD1	2.23	0.46
42:RW:86:LEU:O	42:RW:94:ASP:N	2.44	0.46
1:XA:485:G:O2'	1:XA:486:U:O5'	2.31	0.46
1:XA:981:U:H5	1:XA:982:U:HO2'	1.61	0.46
3:XC:78:GLY:HA3	3:XC:83:ARG:HB3	1.98	0.46
12:XL:62:SER:O	12:XL:64:TYR:N	2.48	0.46
25:YA:2392:A:H2'	25:YA:2393:A:O4'	2.16	0.46
27:YD:118:VAL:HG22	27:YD:119:ALA:N	2.31	0.46
27:YD:35:LYS:HB3	27:YD:63:ARG:HA	1.98	0.46
25:YA:2469:A:O2'	36:YQ:56:ARG:NE	2.48	0.46
40:YU:75:ASN:HB3	40:YU:78:THR:H	1.81	0.46
1:QA:859:A:H2'	1:QA:860:A:O4'	2.15	0.46
2:QB:165:VAL:HG23	2:QB:166:ASP:H	1.81	0.46
4:QD:75:PHE:HE1	4:QD:97:LEU:HD11	1.81	0.46
10:QJ:84:GLN:HG3	10:QJ:84:GLN:H	1.49	0.46
14:QN:32:SER:O	14:QN:32:SER:OG	2.26	0.46
20:QT:29:LYS:O	20:QT:33:ILE:HG12	2.16	0.46
52:R6:33:LYS:HG3	52:R6:34:LEU:HD13	1.98	0.46
54:R8:50:LEU:C	54:R8:53:PRO:HD2	2.36	0.46
25:RA:2848:G:O2'	25:RA:2849:U:OP2	2.26	0.46
29:RF:126:VAL:HG11	29:RF:142:TRP:HH2	1.80	0.46
25:RA:955:C:OP2	36:RQ:14:ARG:HD2	2.16	0.46
38:RS:24:LEU:HB2	38:RS:85:VAL:HG12	1.96	0.46
38:RS:83:LYS:O	38:RS:109:GLY:HA3	2.15	0.46
44:RY:17:SER:OG	44:RY:71:LYS:HD2	2.16	0.46
1:XA:1285:A:H4'	1:XA:1286:A:O5'	2.16	0.46
1:XA:221:C:H2'	1:XA:222:U:C6	2.51	0.46
9:XI:46:ALA:HA	9:XI:78:LYS:HB2	1.98	0.46
13:XM:36:LYS:HD3	13:XM:36:LYS:C	2.36	0.46
15:XO:56:LEU:O	15:XO:60:VAL:HG23	2.16	0.46
16:XP:1:MET:O	16:XP:3:LYS:HG3	2.16	0.46
20:XT:87:LYS:HD2	20:XT:87:LYS:HA	1.74	0.46
47:Y1:80:LEU:HB2	47:Y1:81:LYS:H	1.61	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:2364:C:H2'	25:YA:2365:G:O4'	2.16	0.46
25:YA:658:C:H2'	25:YA:659:C:C6	2.50	0.46
27:YD:35:LYS:HE3	27:YD:63:ARG:C	2.36	0.46
30:YG:34:LEU:HD12	30:YG:100:TRP:CH2	2.50	0.46
31:YH:167:GLU:HA	31:YH:168:PRO:HD3	1.79	0.46
32:YI:88:ILE:HG12	32:YI:122:GLU:N	2.31	0.46
36:YQ:136:ALA:O	36:YQ:138:ASP:N	2.40	0.46
1:QA:1275:A:H2'	1:QA:1276:G:O4'	2.16	0.46
1:QA:1346:A:O2'	1:QA:1347:G:O4'	2.34	0.46
1:QA:1391:U:H2'	1:QA:1392:G:C8	2.51	0.46
1:QA:37:U:O2'	1:QA:500:G:H4'	2.15	0.46
1:QA:932:C:H4'	7:QG:4:ARG:NH2	2.31	0.46
4:QD:103:ASN:OD1	4:QD:114:ARG:NE	2.49	0.46
25:RA:140:A:C8	25:RA:1408:C:O2'	2.63	0.46
25:RA:569:U:C4	25:RA:570:G:C6	3.04	0.46
28:RE:63:LEU:HD12	28:RE:64:LYS:N	2.30	0.46
31:RH:115:VAL:HG11	31:RH:148:ILE:HD11	1.97	0.46
31:RH:87:LEU:HA	31:RH:163:TYR:O	2.16	0.46
31:RH:85:LYS:HA	31:RH:85:LYS:HD2	1.85	0.46
34:RO:31:LYS:HB3	34:RO:32:TYR:CD1	2.51	0.46
36:RQ:29:PHE:N	36:RQ:105:GLU:OE2	2.40	0.46
45:RZ:23:LYS:HB3	45:RZ:38:TYR:CD1	2.51	0.46
1:XA:272:C:H2'	1:XA:273:A:C8	2.51	0.46
2:XB:204:ASN:HD22	2:XB:205:ASP:N	2.13	0.46
2:XB:70:PHE:O	2:XB:93:VAL:N	2.34	0.46
1:XA:1055:A:O2'	3:XC:161:GLU:OE2	2.25	0.46
18:XR:32:ARG:HA	18:XR:69:THR:HG21	1.97	0.46
20:XT:26:ASN:O	20:XT:30:LYS:HB2	2.16	0.46
25:YA:1482:U:H5'	25:YA:1483:G:OP2	2.15	0.46
25:YA:2346:A:H5''	25:YA:2383:G:H1'	1.98	0.46
25:YA:270(W):G:H2'	25:YA:270(X):G:O4'	2.16	0.46
25:YA:528:A:C2'	25:YA:529:A:H5'	2.46	0.46
25:YA:969:U:O3'	49:Y3:14:GLY:HA2	2.16	0.46
28:YE:116:VAL:O	28:YE:117:MET:HB3	2.16	0.46
28:YE:36:ARG:NH2	28:YE:88:GLY:HA2	2.29	0.46
31:YH:103:LEU:HD23	31:YH:115:VAL:HB	1.97	0.46
32:YI:3:VAL:O	32:YI:18:VAL:HA	2.15	0.46
1:QA:1126:U:H1'	1:QA:1280:A:N7	2.31	0.46
1:QA:1301:U:O2	1:QA:1301:U:H2'	2.14	0.46
1:QA:1446:A:HO2'	1:QA:1447:G:P	2.39	0.46
1:QA:438:G:H4'	4:QD:123:HIS:CG	2.50	0.46
1:QA:658:G:OP1	15:QO:8:LYS:NZ	2.43	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:QA:784:C:H4'	25:RA:1837:C:OP1	2.16	0.46
13:QM:84:ILE:HD12	13:QM:84:ILE:HA	1.75	0.46
55:R9:8:LYS:O	55:R9:34:GLN:NE2	2.49	0.46
25:RA:1048:A:C5	25:RA:1111:A:H2	2.34	0.46
25:RA:1754:C:H5''	39:RT:113:LYS:HE3	1.97	0.46
25:RA:291:C:H42	25:RA:349:G:H1	1.63	0.46
25:RA:587:C:H4'	25:RA:588:U:O5'	2.16	0.46
25:RA:878:A:N6	25:RA:899:A:O2'	2.48	0.46
27:RD:68:LYS:HD2	27:RD:70:TRP:CZ2	2.51	0.46
31:RH:103:LEU:HD13	31:RH:131:VAL:HG11	1.97	0.46
31:RH:170:ARG:HB3	31:RH:171:LEU:H	1.52	0.46
35:RP:101:VAL:HG23	35:RP:107:LYS:H	1.81	0.46
36:RQ:81:VAL:C	36:RQ:82:ARG:HG2	2.37	0.46
37:RR:37:THR:OG1	37:RR:40:LYS:HG3	2.16	0.46
40:RU:69:CYS:HB3	40:RU:106:PHE:HZ	1.81	0.46
2:XB:114:ARG:O	2:XB:118:LEU:HG	2.16	0.46
7:XG:50:ILE:HG21	7:XG:61:VAL:HG21	1.98	0.46
12:XL:92:ASP:O	12:XL:94:PRO:HD3	2.16	0.46
15:XO:6:GLU:CD	15:XO:6:GLU:H	2.15	0.46
22:XV:2:C:C2'	22:XV:3:G:H5'	2.46	0.46
25:YA:1049:C:C2'	25:YA:1050:A:H5''	2.45	0.46
22:XV:76:A:H2'	25:YA:2602:A:N6	2.31	0.46
25:YA:7:G:H2'	25:YA:8:A:O4'	2.16	0.46
28:YE:70:ALA:O	28:YE:72:VAL:N	2.49	0.46
29:YF:129:PHE:O	29:YF:142:TRP:CD1	2.69	0.46
31:YH:106:THR:HG22	31:YH:112:PRO:HB3	1.97	0.46
42:YW:110:LYS:HG3	42:YW:111:HIS:ND1	2.31	0.46
9:QI:45:ALA:O	9:QI:48:GLU:HG2	2.15	0.46
19:QS:32:LYS:HA	19:QS:50:ALA:HB3	1.98	0.46
47:R1:73:LEU:HB3	47:R1:90:ILE:HG23	1.97	0.46
52:R6:44:ARG:O	52:R6:45:LYS:HB2	2.16	0.46
25:RA:2481:G:HO2'	25:RA:2482:G:P	2.39	0.46
25:RA:2537:U:H2'	25:RA:2538:C:C6	2.50	0.46
25:RA:311:A:C6	25:RA:328:U:C4	3.03	0.46
26:RB:13:A:O2'	26:RB:14:U:H3'	2.16	0.46
26:RB:50:G:H5''	38:RS:61:ASN:ND2	2.31	0.46
36:RQ:104:PHE:HE1	36:RQ:125:LEU:HD11	1.81	0.46
37:RR:33:ARG:HG2	37:RR:34:ILE:N	2.30	0.46
39:RT:26:ASP:HB2	39:RT:90:GLN:O	2.16	0.46
41:RV:51:VAL:HG12	41:RV:53:GLU:H	1.80	0.46
45:RZ:157:LEU:HA	45:RZ:158:PRO:HD2	1.70	0.46
5:XE:41:VAL:HG13	5:XE:113:ALA:HB2	1.97	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:XF:48:LEU:HG	6:XF:57:GLN:HA	1.98	0.46
9:XI:18:PHE:HD1	9:XI:62:TYR:HD2	1.62	0.46
25:YA:1417:C:H2'	25:YA:1418:G:O4'	2.16	0.46
25:YA:2689:U:H5'	25:YA:2713:A:C2	2.51	0.46
25:YA:2712:U:O2'	25:YA:2712(A):A:C8	2.61	0.46
25:YA:612:G:H2'	25:YA:613:U:O2	2.16	0.46
28:YE:108:SER:HB3	28:YE:165:VAL:HG21	1.98	0.46
35:YP:135:LEU:HA	35:YP:135:LEU:HD23	1.74	0.46
36:YQ:135:ASP:OD1	36:YQ:135:ASP:N	2.48	0.46
37:YR:51:LEU:HD12	37:YR:70:LEU:HG	1.97	0.46
25:YA:997:G:OP1	40:YU:93:LYS:HD2	2.16	0.46
1:QA:1172:C:H2'	1:QA:1173:G:C8	2.50	0.45
1:QA:1218:C:H2'	1:QA:1219:U:C6	2.52	0.45
1:QA:1227:A:OP1	19:QS:80:TYR:OH	2.12	0.45
1:QA:170:U:O2'	1:QA:171:A:H5'	2.16	0.45
1:QA:518:C:H2'	1:QA:530:G:N3	2.31	0.45
22:QV:3:G:HO2'	22:QV:4:G:H8	1.64	0.45
23:QY:30:C:H2'	23:QY:31:G:H8	1.82	0.45
50:R4:10:VAL:HA	50:R4:11:PRO:HD2	1.75	0.45
25:RA:1043:C:H42	25:RA:1112:G:H1	1.64	0.45
25:RA:1792:G:H2'	25:RA:1793:C:H6	1.81	0.45
25:RA:2419:U:H2'	25:RA:2420:C:H6	1.80	0.45
25:RA:918:A:C5	25:RA:919:G:H1'	2.51	0.45
31:RH:120:GLY:HA3	31:RH:140:LYS:NZ	2.31	0.45
2:XB:217:ARG:HB2	2:XB:217:ARG:HE	1.54	0.45
2:XB:55:PHE:HD1	2:XB:58:ILE:HG13	1.81	0.45
5:XE:99:GLY:N	5:XE:117:ASP:OD2	2.47	0.45
1:XA:1226:C:O2'	13:XM:103:THR:O	2.28	0.45
47:Y1:58:ILE:HD12	47:Y1:58:ILE:N	2.30	0.45
25:YA:1454:U:H5'	37:YR:63:ARG:HE	1.80	0.45
25:YA:1688:U:O2	25:YA:1700:A:H5''	2.16	0.45
25:YA:1930:G:H2'	25:YA:1968:G:C6	2.50	0.45
25:YA:771:G:OP1	53:Y7:14:LYS:HE3	2.15	0.45
27:YD:10:THR:OG1	27:YD:13:ARG:HB2	2.16	0.45
27:YD:137:PRO:O	27:YD:140:THR:HG23	2.16	0.45
29:YF:129:PHE:C	29:YF:131:GLY:H	2.18	0.45
31:YH:86:GLU:O	31:YH:87:LEU:HB2	2.16	0.45
35:YP:138:LEU:C	35:YP:140:ALA:H	2.18	0.45
25:YA:1754:C:P	39:YT:96:ARG:HH12	2.39	0.45
41:YV:19:LYS:HA	41:YV:94:LEU:O	2.15	0.45
25:YA:751:A:C5'	42:YW:90:ARG:HA	2.46	0.45
44:YY:84:ARG:HB3	44:YY:95:LYS:HD3	1.97	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:QA:790:A:C6	1:QA:791:G:C6	3.03	0.45
4:QD:18:LYS:HD3	4:QD:20:TYR:CZ	2.51	0.45
7:QG:45:ASP:O	7:QG:49:ILE:HG12	2.16	0.45
10:QJ:22:LYS:HB3	10:QJ:22:LYS:HE3	1.68	0.45
22:QV:16:C:H2'	22:QV:16:C:O2	2.16	0.45
22:QV:21:A:H61	22:QV:46:G:H2'	1.80	0.45
1:QA:1312:G:H5''	50:R4:67:TYR:OH	2.16	0.45
25:RA:1331:A:O2'	25:RA:1332:G:H8	1.98	0.45
25:RA:2469:A:H2	25:RA:2481:G:N2	2.13	0.45
25:RA:2734:A:H5'	25:RA:2735:G:OP2	2.17	0.45
25:RA:2630:G:N3	25:RA:2894:G:N2	2.63	0.45
25:RA:2683:C:H4'	28:RE:13:ARG:NH2	2.31	0.45
1:XA:498:A:H4'	1:XA:500:G:OP1	2.17	0.45
13:XM:58:GLU:O	13:XM:62:ASN:ND2	2.33	0.45
18:XR:73:ALA:HB3	18:XR:79:LEU:HD12	1.98	0.45
25:YA:1532:C:H2'	25:YA:1533:C:O4'	2.17	0.45
25:YA:858:U:O2	25:YA:2268:A:H2'	2.15	0.45
25:YA:2584:U:H2'	25:YA:2585:U:C6	2.51	0.45
25:YA:2612:C:H2'	25:YA:2613:U:H5'	1.99	0.45
25:YA:2867:G:O2'	25:YA:2868:A:H8	1.98	0.45
25:YA:601:C:O2'	25:YA:605:C:OP1	2.26	0.45
26:YB:33:G:H5'	30:YG:2:PRO:HG3	1.98	0.45
25:YA:1006:C:O2	33:YN:106:MET:HG2	2.15	0.45
37:YR:78:LYS:O	37:YR:83:ILE:HG12	2.16	0.45
44:YY:51:VAL:HG13	44:YY:52:SER:N	2.28	0.45
1:QA:1446:A:H4'	39:RT:125:ARG:HH22	1.81	0.45
1:QA:45:U:H2'	1:QA:46:G:H8	1.79	0.45
6:QF:99:ALA:HB1	18:QR:23:LYS:NZ	2.31	0.45
8:QH:20:TYR:HA	8:QH:65:TYR:CZ	2.51	0.45
12:QL:113:ARG:HH21	12:QL:116:SER:HB2	1.81	0.45
25:RA:1022:G:O2'	25:RA:1023:U:OP2	2.24	0.45
25:RA:2336:A:H61	46:R0:43:THR:HG21	1.81	0.45
25:RA:2410:G:C2	25:RA:2411:A:H1'	2.51	0.45
25:RA:882:G:H1	25:RA:894:C:H42	1.65	0.45
26:RB:48:A:H2'	26:RB:49:C:C6	2.51	0.45
27:RD:118:VAL:HG22	27:RD:119:ALA:H	1.82	0.45
27:RD:85:ASP:HA	27:RD:86:PRO:HD2	1.72	0.45
29:RF:31:HIS:HB2	35:RP:9:ASN:OD1	2.16	0.45
35:RP:77:ARG:HB2	35:RP:78:PRO:HD2	1.99	0.45
35:RP:6:LEU:HB3	35:RP:7:ARG:H	1.55	0.45
35:RP:88:LEU:HD12	35:RP:95:VAL:HG11	1.99	0.45
36:RQ:2:LEU:HD23	36:RQ:2:LEU:H	1.81	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
38:RS:16:ASN:HA	38:RS:19:LYS:HD3	1.98	0.45
45:RZ:53:ILE:HG22	45:RZ:71:VAL:HG22	1.98	0.45
1:XA:1360:A:H2'	1:XA:1361:G:C8	2.51	0.45
1:XA:486:U:H2'	1:XA:487:A:H8	1.79	0.45
1:XA:792:A:H4'	1:XA:793:U:O5'	2.16	0.45
1:XA:960:U:O2	1:XA:960:U:H2'	2.16	0.45
2:XB:140:HIS:HA	2:XB:143:GLU:OE1	2.17	0.45
9:XI:114:TYR:HD2	9:XI:114:TYR:N	2.14	0.45
19:XS:47:HIS:O	19:XS:62:ILE:HG12	2.17	0.45
52:Y6:33:LYS:HE2	52:Y6:33:LYS:HB2	1.76	0.45
25:YA:1404:C:O2'	25:YA:1405:U:H5'	2.16	0.45
25:YA:1530:G:O6	25:YA:1542:G:N2	2.49	0.45
25:YA:1794:U:H2'	25:YA:1795:C:C6	2.51	0.45
25:YA:1820:U:H4'	25:YA:1821:A:OP2	2.16	0.45
25:YA:2275:C:H5'	25:YA:2275:C:H6	1.81	0.45
25:YA:2314:C:H2'	25:YA:2315:G:C8	2.48	0.45
25:YA:2636:U:H2'	25:YA:2637:U:C6	2.52	0.45
29:YF:11:VAL:HA	29:YF:125:LEU:O	2.16	0.45
25:YA:2563:U:H4'	34:YO:28:SER:HA	1.98	0.45
35:YP:27:HIS:N	35:YP:27:HIS:ND1	2.64	0.45
37:YR:109:ALA:HA	37:YR:110:PRO:HD2	1.77	0.45
40:YU:68:ALA:O	40:YU:71:GLN:HB2	2.16	0.45
44:YY:87:LYS:HA	44:YY:92:ASN:HB3	1.98	0.45
1:QA:176:C:H2'	1:QA:177:C:C6	2.52	0.45
3:QC:19:GLU:HA	3:QC:54:ARG:HH12	1.82	0.45
7:QG:20:ASP:OD1	7:QG:21:VAL:N	2.48	0.45
3:QC:23:TYR:CD1	10:QJ:10:GLY:HA2	2.51	0.45
22:QV:53:G:HO2'	22:QV:54:U:H5	1.58	0.45
13:QM:121:LYS:NZ	23:QY:40:G:O2'	2.44	0.45
25:RA:102:G:OP2	48:R2:7:ARG:NH2	2.50	0.45
52:R6:26:ASN:ND2	52:R6:35:GLU:OE2	2.49	0.45
25:RA:1728:G:H3'	25:RA:1729:A:C5'	2.44	0.45
25:RA:1914:C:H2'	25:RA:1915:U:C6	2.52	0.45
25:RA:2309:A:C6	25:RA:2310:A:C6	3.05	0.45
25:RA:2529:G:H5''	25:RA:2530:A:H5''	1.99	0.45
25:RA:264:C:C2'	25:RA:265:A:H5''	2.46	0.45
25:RA:669:G:H2'	25:RA:669:G:N3	2.31	0.45
31:RH:153:LYS:HG3	31:RH:161:GLY:HA2	1.97	0.45
1:XA:1024:G:OP1	1:XA:1024:G:H4'	2.16	0.45
1:XA:525:C:H2'	1:XA:526:C:C6	2.51	0.45
1:XA:539:A:H2'	1:XA:540:G:C8	2.51	0.45
6:XF:100:ASN:O	18:XR:28:GLU:HG2	2.17	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:XA:686:U:HO2'	11:XK:42:TRP:HE1	1.61	0.45
19:XS:63:THR:HG23	19:XS:66:MET:HG2	1.99	0.45
47:Y1:91:LYS:HE3	47:Y1:91:LYS:HA	1.98	0.45
48:Y2:4:SER:OG	48:Y2:5:GLU:OE1	2.23	0.45
30:YG:6:ALA:N	50:Y4:23:GLU:HG2	2.28	0.45
25:YA:1026:U:O2	25:YA:1027:A:H3'	2.16	0.45
25:YA:1055:G:H1	25:YA:1104:C:N4	2.13	0.45
25:YA:1490:A:O2'	27:YD:99:ASP:OD2	2.35	0.45
25:YA:2365:G:H4'	46:Y0:60:PHE:CZ	2.51	0.45
25:YA:242:G:C5'	54:Y8:62:LEU:HD13	2.46	0.45
25:YA:34:C:N4	25:YA:447:A:H61	2.14	0.45
25:YA:653:A:H4'	25:YA:654:A:OP2	2.16	0.45
25:YA:86:C:H4'	25:YA:104:U:H1'	1.98	0.45
25:YA:1826:G:H4'	27:YD:242:ARG:CZ	2.46	0.45
35:YP:106:LEU:HA	35:YP:106:LEU:HD23	1.84	0.45
37:YR:24:GLN:HE21	37:YR:44:LEU:HG	1.81	0.45
1:XA:1446:A:H5'	39:YT:122:ASP:OD1	2.16	0.45
40:YU:66:ASN:O	40:YU:70:ARG:HB2	2.17	0.45
44:YY:56:PRO:O	44:YY:58:GLY:N	2.49	0.45
4:QD:121:VAL:O	4:QD:134:ASP:HA	2.17	0.45
4:QD:15:GLU:HG2	4:QD:63:LYS:HG3	1.97	0.45
7:QG:113:GLU:CG	7:QG:119:ARG:HG2	2.47	0.45
7:QG:49:ILE:O	7:QG:53:LYS:HB3	2.16	0.45
13:QM:89:GLY:O	13:QM:92:HIS:HB2	2.15	0.45
25:RA:1079:C:H2'	25:RA:1080:C:O4'	2.17	0.45
25:RA:2050:C:H2'	25:RA:2051:A:O4'	2.16	0.45
25:RA:2298:A:H2'	25:RA:2299:G:O4'	2.16	0.45
25:RA:565:C:H2'	25:RA:566:U:O4'	2.17	0.45
25:RA:797:C:OP2	29:RF:62:ARG:HB2	2.16	0.45
27:RD:76:PRO:HB2	27:RD:116:GLN:OE1	2.17	0.45
27:RD:121:PRO:HB3	27:RD:135:PHE:CE1	2.52	0.45
27:RD:30:GLU:HG3	27:RD:63:ARG:CZ	2.47	0.45
1:QA:1423:G:OP1	34:RO:49:ARG:NH2	2.50	0.45
37:RR:78:LYS:HE2	37:RR:83:ILE:HD11	1.98	0.45
37:RR:103:ARG:NH1	42:RW:40:ASN:OD1	2.50	0.45
45:RZ:97:GLU:HB3	45:RZ:125:LEU:HD11	1.98	0.45
1:XA:1067:A:N1	1:XA:1108:G:O2'	2.43	0.45
1:XA:1082:G:H2'	1:XA:1083:U:O4'	2.15	0.45
1:XA:1161:C:O2'	1:XA:1162:C:H5'	2.17	0.45
1:XA:129(A):G:O2'	1:XA:189:U:H3'	2.15	0.45
1:XA:191:G:C4	20:XT:105:SER:HB3	2.51	0.45
1:XA:272:C:H2'	1:XA:273:A:H8	1.81	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:XA:597:G:H1	1:XA:643:C:H42	1.64	0.45
1:XA:857:C:H2'	1:XA:858:G:O4'	2.17	0.45
7:XG:45:ASP:O	7:XG:49:ILE:HG12	2.17	0.45
8:XH:86:ILE:HG13	8:XH:133:LEU:HD22	1.98	0.45
15:XO:32:LEU:HD11	15:XO:62:GLN:HG2	1.99	0.45
46:Y0:23:VAL:HA	46:Y0:38:VAL:HA	1.99	0.45
48:Y2:21:LEU:O	48:Y2:25:VAL:HG23	2.17	0.45
49:Y3:31:LEU:O	49:Y3:32:GLN:HB2	2.17	0.45
52:Y6:15:GLU:CD	52:Y6:41:PRO:HB3	2.37	0.45
25:YA:1012:U:O4	33:YN:25:ARG:HA	2.16	0.45
25:YA:609(A):G:H2'	25:YA:610:C:C6	2.51	0.45
26:YB:87:G:N2	26:YB:89(A):A:OP2	2.29	0.45
30:YG:146:TYR:O	30:YG:149:VAL:HG22	2.16	0.45
35:YP:124:LYS:HA	35:YP:143:GLY:O	2.16	0.45
40:YU:58:ARG:HA	40:YU:61:TRP:CE3	2.52	0.45
41:YV:19:LYS:HG3	41:YV:95:LEU:HD23	1.98	0.45
41:YV:36:PRO:HA	41:YV:56:SER:OG	2.17	0.45
44:YY:101:LYS:HG2	44:YY:102:CYS:H	1.81	0.45
1:QA:1313:U:OP1	19:QS:5:LEU:HB2	2.17	0.45
1:QA:1371:G:O3'	9:QL:69:GLY:HA3	2.17	0.45
1:QA:565:U:OP2	1:QA:566:G:O2'	2.27	0.45
1:QA:743:U:H2'	1:QA:744:C:C6	2.52	0.45
4:QD:28:SER:HB3	4:QD:29:PRO:CD	2.42	0.45
4:QD:8:VAL:HG13	4:QD:21:LEU:HD12	1.97	0.45
11:QK:91:ARG:NH1	11:QK:110:ASP:OD1	2.48	0.45
25:RA:1204:A:H1'	25:RA:1206:G:C4	2.51	0.45
25:RA:141:A:C8	25:RA:1408:C:H1'	2.52	0.45
25:RA:1799:G:N2	27:RD:155:LEU:HD12	2.32	0.45
25:RA:2212:A:H1'	25:RA:2215:G:C5	2.51	0.45
25:RA:2415:G:H5'	35:RP:67:MET:H	1.81	0.45
25:RA:2645:G:C3'	25:RA:2646:C:H5'	2.46	0.45
25:RA:483:A:H5''	44:RY:49:VAL:HG13	1.98	0.45
25:RA:643:A:N1	25:RA:2369:A:O2'	2.45	0.45
32:RI:112:LYS:H	32:RI:112:LYS:HG2	1.50	0.45
33:RN:19:GLU:HB2	33:RN:56:ASN:HD22	1.80	0.45
25:RA:1952:A:C5	34:RO:22:ILE:HD12	2.50	0.45
34:RO:48:PRO:O	34:RO:49:ARG:HG2	2.17	0.45
35:RP:18:ARG:HD2	35:RP:27:HIS:HD2	1.81	0.45
1:XA:1034:G:H2'	1:XA:1035:A:C8	2.51	0.45
1:XA:1149:C:H2'	1:XA:1150:U:C6	2.51	0.45
1:XA:1306:A:N6	1:XA:1331:G:H1'	2.31	0.45
1:XA:51:A:N7	1:XA:114:U:O2'	2.45	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:XC:48:TYR:OH	3:XC:122:GLU:OE2	2.22	0.45
16:XP:17:TYR:CE1	16:XP:41:PRO:HG3	2.52	0.45
25:YA:1899:G:H21	25:YA:1902:C:H42	1.64	0.45
25:YA:2836:U:H2'	25:YA:2837:G:C8	2.52	0.45
25:YA:2630:G:O4'	25:YA:2894:G:H1'	2.16	0.45
25:YA:304:G:H2'	25:YA:305:U:C6	2.51	0.45
25:YA:321:G:H5''	29:YF:136:THR:HG23	1.97	0.45
25:YA:860:U:C5	25:YA:917:A:H2	2.34	0.45
25:YA:956:G:H5'	36:YQ:77:LYS:HE2	1.99	0.45
26:YB:15:A:H1'	26:YB:109:G:N9	2.32	0.45
31:YH:150:ALA:O	31:YH:152:ARG:N	2.49	0.45
39:YT:6:LEU:HA	39:YT:9:LEU:HB2	1.99	0.45
1:QA:1024:G:OP1	1:QA:1024:G:H4'	2.17	0.45
1:QA:1322:C:O2	1:QA:1322:C:H2'	2.17	0.45
1:QA:323:U:H2'	1:QA:324:G:O4'	2.16	0.45
2:QB:30:ARG:HH21	2:QB:194:PRO:HG2	1.81	0.45
4:QD:53:ASP:O	4:QD:57:ARG:HD2	2.16	0.45
6:QF:45:LEU:HD12	6:QF:59:TYR:HD1	1.82	0.45
12:QL:102:ARG:HB3	12:QL:102:ARG:HE	1.39	0.45
20:QT:26:ASN:HB2	20:QT:71:THR:HG23	1.97	0.45
52:R6:34:LEU:HD13	52:R6:34:LEU:H	1.81	0.45
25:RA:1059:G:H3'	25:RA:1060:U:H5''	1.99	0.45
25:RA:1945:G:C6	25:RA:1946:U:C4	3.05	0.45
25:RA:2832:U:O2'	25:RA:2833:G:P	2.74	0.45
30:RG:106:LEU:HA	30:RG:110:ALA:HB3	1.98	0.45
30:RG:10:LYS:O	30:RG:14:GLU:HB3	2.17	0.45
32:RI:76:THR:OG1	32:RI:139:GLN:OE1	2.34	0.45
35:RP:64:LYS:HB2	54:R8:25:MET:HG3	1.98	0.45
37:RR:42:LYS:HA	37:RR:45:ARG:HD2	1.98	0.45
38:RS:10:ARG:O	38:RS:14:VAL:HG12	2.17	0.45
1:XA:179:A:H2'	1:XA:180:U:H6	1.82	0.45
1:XA:321:A:C2	1:XA:333:G:C2	3.05	0.45
1:XA:626:U:C2	1:XA:627:G:C8	3.04	0.45
1:XA:922:G:C6	1:XA:923:A:C6	3.05	0.45
7:XG:15:ASP:OD2	7:XG:44:TYR:OH	2.35	0.45
8:XH:75:ARG:HA	8:XH:76:PRO:HD2	1.71	0.45
13:XM:65:LYS:O	13:XM:70:LEU:HD23	2.17	0.45
48:Y2:24:LEU:HD23	48:Y2:24:LEU:HA	1.67	0.45
25:YA:1338:G:O2'	25:YA:1393:A:N1	2.43	0.45
25:YA:1655:A:H3'	25:YA:1656:C:C6	2.52	0.45
25:YA:2468:G:H5''	36:YQ:120:ILE:HD12	1.99	0.45
25:YA:2760:C:C2'	25:YA:2761:G:H5''	2.43	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:2846:G:H2'	25:YA:2847:U:C6	2.51	0.45
25:YA:414:C:O2	25:YA:1864:U:O2'	2.30	0.45
25:YA:646:A:H2'	25:YA:647:G:O4'	2.17	0.45
27:YD:44:ASN:ND2	27:YD:44:ASN:N	2.64	0.45
28:YE:67:PHE:O	28:YE:69:LYS:N	2.49	0.45
1:QA:358:U:H2'	1:QA:359:U:H6	1.81	0.45
1:QA:580:U:H2'	1:QA:581:G:O4'	2.17	0.45
2:QB:76:GLN:O	2:QB:208:ILE:HG12	2.17	0.45
5:QE:97:GLY:N	5:QE:117:ASP:OD2	2.40	0.45
8:QH:104:ARG:O	8:QH:107:LEU:HB2	2.16	0.45
9:QI:126:SER:O	9:QI:128:ARG:N	2.45	0.45
10:QJ:40:LEU:HB2	10:QJ:69:ASN:CB	2.47	0.45
11:QK:41:THR:HG21	11:QK:71:LYS:HB2	1.99	0.45
25:RA:2166:G:N2	25:RA:2168:G:OP1	2.50	0.45
25:RA:219:G:H2'	25:RA:220:G:O4'	2.17	0.45
25:RA:2245:U:C5'	25:RA:2246:G:H5'	2.47	0.45
25:RA:2532:G:H2'	25:RA:2533:A:C8	2.52	0.45
25:RA:828:U:H4'	25:RA:831:G:N1	2.31	0.45
27:RD:105:ILE:HD12	27:RD:105:ILE:HA	1.63	0.45
28:RE:111:ARG:HA	37:RR:1:MET:SD	2.57	0.45
28:RE:46:ALA:HB2	28:RE:82:ARG:HA	1.98	0.45
29:RF:45:ARG:CG	29:RF:45:ARG:HH11	2.29	0.45
34:RO:22:ILE:HG12	34:RO:41:ALA:HA	1.98	0.45
37:RR:29:LEU:HD12	37:RR:29:LEU:HA	1.74	0.45
26:RB:50:G:OP1	38:RS:63:THR:HG23	2.17	0.45
25:RA:137(A):G:H1'	43:RX:41:ASN:ND2	2.32	0.45
45:RZ:181:GLU:HB3	45:RZ:182:LYS:HD3	1.98	0.45
45:RZ:53:ILE:H	45:RZ:71:VAL:CG1	2.30	0.45
1:XA:1191:A:H2'	1:XA:1192:C:C6	2.52	0.45
1:XA:1346:A:OP1	9:XI:120:ARG:NH1	2.40	0.45
1:XA:1493:A:OP1	58:XA:1673:PAR:H51	2.17	0.45
3:XC:153:VAL:HG22	3:XC:198:VAL:HG22	1.98	0.45
4:XD:86:LYS:H	4:XD:86:LYS:HD2	1.82	0.45
17:XQ:43:LEU:HD12	17:XQ:68:ARG:HG2	1.97	0.45
20:XT:33:ILE:HG23	20:XT:63:ILE:HG12	1.99	0.45
47:Y1:79:GLY:N	47:Y1:80:LEU:HD23	2.32	0.45
25:YA:2074:U:H2'	25:YA:2075:U:C6	2.52	0.45
25:YA:2133:G:H1'	25:YA:2158:A:H61	1.82	0.45
25:YA:277:C:H3'	25:YA:278:A:C5'	2.47	0.45
39:YT:102:ILE:HA	39:YT:105:LEU:CD2	2.47	0.45
42:YW:97:LYS:HE2	42:YW:99:ARG:NH2	2.31	0.45
45:YZ:19:ARG:NH1	45:YZ:84:GLU:HB2	2.32	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:QA:103:C:P	20:QT:17:ARG:HH21	2.40	0.45
1:QA:1290:G:C4	1:QA:1291:G:C8	3.05	0.45
1:QA:452:A:C6	1:QA:453:A:C6	3.05	0.45
1:QA:818:G:O2'	1:QA:819:A:H5''	2.17	0.45
2:QB:163:PHE:HA	2:QB:185:ILE:HG13	1.99	0.45
8:QH:6:ILE:O	8:QH:10:LEU:HG	2.17	0.45
47:R1:83:GLU:N	47:R1:83:GLU:OE2	2.49	0.45
25:RA:1005:C:O2'	33:RN:28:THR:HG21	2.17	0.45
25:RA:1203:G:O6	25:RA:1204:A:N6	2.50	0.45
25:RA:1578:U:C2'	25:RA:1579:A:H5'	2.47	0.45
25:RA:2405:G:O2'	25:RA:2406:U:P	2.75	0.45
25:RA:2663:G:C6	25:RA:2664:G:C4	3.05	0.45
25:RA:2712:U:O2'	25:RA:2712(A):A:H8	1.99	0.45
25:RA:805:G:OP2	35:RP:41:ARG:HG2	2.16	0.45
26:RB:48:A:H4'	38:RS:95:HIS:HD2	1.81	0.45
25:RA:2572:A:N7	28:RE:145:LYS:HB2	2.32	0.45
30:RG:102:PHE:O	30:RG:106:LEU:N	2.50	0.45
36:RQ:111:GLU:C	36:RQ:113:GLN:H	2.19	0.45
44:RY:68:HIS:CE1	44:RY:70:SER:HB3	2.52	0.45
45:RZ:118:GLN:O	45:RZ:120:ILE:N	2.46	0.45
1:XA:1015:A:H2'	1:XA:1016:A:H8	1.81	0.45
1:XA:926:G:C6	1:XA:1505:G:C6	3.05	0.45
1:XA:485:G:O2'	1:XA:486:U:P	2.75	0.45
1:XA:986:A:H2'	1:XA:987:G:O4'	2.16	0.45
2:XB:115:LEU:HD13	2:XB:145:LEU:HB3	1.98	0.45
4:XD:50:ARG:HG3	4:XD:50:ARG:H	1.63	0.45
50:Y4:22:ILE:HG22	50:Y4:23:GLU:H	1.82	0.45
50:Y4:16:CYS:HB3	50:Y4:33:VAL:HB	1.98	0.45
25:YA:1349:A:N6	25:YA:1598:C:N4	2.65	0.45
25:YA:2283:C:H2'	25:YA:2284:C:O4'	2.16	0.45
25:YA:396:G:H1'	47:Y1:42:GLN:HB3	1.99	0.45
25:YA:606:U:H4'	25:YA:658:C:H4'	1.99	0.45
25:YA:971:C:H2'	25:YA:972:G:O4'	2.17	0.45
25:YA:994:C:OP1	40:YU:53:ARG:NH2	2.50	0.45
27:YD:39:LYS:HB2	27:YD:62:TYR:HB2	1.98	0.45
35:YP:126:VAL:HG12	35:YP:147:LEU:HD22	1.99	0.45
43:YX:60:ARG:HH22	53:Y7:47:ARG:NH1	2.14	0.45
45:YZ:80:ARG:NH2	45:YZ:82:ARG:HH22	2.12	0.45
1:QA:1326:C:H2'	1:QA:1327:C:H6	1.82	0.45
1:QA:1360:A:H8	1:QA:1360:A:OP1	2.00	0.45
1:QA:474:G:H5'	16:QP:81:ARG:HG3	1.99	0.45
1:QA:7:G:H2'	5:QE:119:LEU:HD22	1.99	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:QB:51:LEU:HD22	2:QB:55:PHE:HE2	1.82	0.45
25:RA:1246:A:OP1	29:RF:38:ARG:NH1	2.46	0.45
25:RA:2376:A:H2'	25:RA:2377:A:O4'	2.17	0.45
25:RA:2068:U:N3	25:RA:2430:A:C2	2.75	0.45
25:RA:2747:G:O6	25:RA:2755:C:H5''	2.17	0.45
25:RA:608:A:OP1	29:RF:100:THR:OG1	2.33	0.45
26:RB:78:A:H2'	26:RB:79:C:O4'	2.17	0.45
28:RE:107:THR:O	28:RE:190:GLY:HA2	2.17	0.45
1:XA:102:G:C6	1:XA:103:C:C4	3.05	0.45
1:XA:1225:A:H5''	1:XA:1226:C:OP2	2.17	0.45
1:XA:827:U:C5	1:XA:872:A:N1	2.85	0.45
1:XA:950:U:H2'	1:XA:951:G:H8	1.82	0.45
9:XI:25:LYS:HE3	9:XI:25:LYS:HB2	1.72	0.45
9:XI:111:ARG:HH22	10:XJ:62:HIS:CE1	2.35	0.45
11:XK:28:THR:OG1	11:XK:90:GLY:HA3	2.17	0.45
19:XS:24:ALA:O	19:XS:25:LYS:HB3	2.17	0.45
19:XS:66:MET:HB2	19:XS:74:PHE:CZ	2.52	0.45
13:XM:65:LYS:HB3	50:Y4:50:VAL:HG21	1.99	0.45
25:YA:1021:A:H62	25:YA:1141:U:H3	1.65	0.45
25:YA:1204:A:H2	25:YA:1241:A:C2	2.35	0.45
25:YA:1862:G:O2'	25:YA:1863:G:H5'	2.17	0.45
25:YA:2067:G:O2'	25:YA:2069:G:H5''	2.17	0.45
25:YA:2355:C:O3'	46:Y0:24:LYS:HD2	2.17	0.45
25:YA:2674:G:H2'	25:YA:2675:A:C8	2.52	0.45
25:YA:459:U:H2'	25:YA:460:A:C8	2.52	0.45
28:YE:167:VAL:HG21	28:YE:187:ALA:CB	2.47	0.45
31:YH:12:PRO:O	31:YH:13:LYS:HB2	2.17	0.45
31:YH:52:VAL:HG21	31:YH:68:THR:HG22	1.99	0.45
25:YA:1006:C:H5'	33:YN:28:THR:HG23	1.98	0.45
38:YS:88:ASP:HB3	38:YS:89:ARG:H	1.47	0.45
1:QA:1070:U:H2'	1:QA:1071:C:H6	1.82	0.44
1:QA:1159:U:O2'	1:QA:1160:G:N7	2.51	0.44
1:QA:407:G:H2'	1:QA:408:A:C8	2.51	0.44
1:QA:560:U:H5'	1:QA:566:G:N2	2.31	0.44
13:QM:92:HIS:CD2	13:QM:110:ARG:HH21	2.35	0.44
25:RA:2494:G:OP1	46:R0:3:HIS:HA	2.17	0.44
48:R2:41:ILE:HD11	48:R2:44:LEU:HB2	1.99	0.44
25:RA:1049:C:H2'	25:RA:1050:A:H5''	1.98	0.44
25:RA:1142(A):A:H4'	33:RN:25:ARG:HH22	1.81	0.44
25:RA:1428:C:N4	25:RA:1570:A:OP2	2.38	0.44
25:RA:2321:G:N3	25:RA:2321:G:H2'	2.32	0.44
29:RF:161:GLU:OE2	29:RF:164:ARG:NH1	2.51	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
31:RH:52:VAL:HG21	31:RH:69:ARG:HA	1.98	0.44
32:RI:14:ASP:N	32:RI:14:ASP:OD2	2.50	0.44
34:RO:111:PHE:HB3	34:RO:114:ILE:HG13	1.99	0.44
34:RO:87:ILE:HD12	34:RO:91:LEU:HD12	1.99	0.44
37:RR:33:ARG:HH22	51:R5:55:ARG:HG2	1.81	0.44
1:XA:253:U:H2'	1:XA:254:G:C8	2.52	0.44
1:XA:484:G:H4'	1:XA:485:G:O5'	2.16	0.44
1:XA:606:G:H1	1:XA:631:G:H5''	1.81	0.44
4:XD:25:ARG:NH1	4:XD:30:LYS:HG3	2.32	0.44
8:XH:51:VAL:HG11	8:XH:60:ARG:HG3	1.99	0.44
10:XJ:16:LEU:HD11	10:XJ:70:ARG:HB2	1.99	0.44
48:Y2:41:ILE:HD11	48:Y2:44:LEU:CG	2.47	0.44
31:YH:3:ARG:HA	31:YH:3:ARG:NE	2.33	0.44
25:YA:1187:G:H5''	41:YV:81:TYR:CE2	2.52	0.44
1:QA:1318:A:H4'	19:QS:11:VAL:CG1	2.48	0.44
1:QA:133:U:OP1	20:QT:74:LYS:NZ	2.40	0.44
1:QA:179:A:H2'	1:QA:180:U:H6	1.82	0.44
1:QA:487:A:H2'	1:QA:488:C:O4'	2.17	0.44
1:QA:975:A:N6	1:QA:1367:C:O4'	2.50	0.44
6:QF:41:GLU:HB3	6:QF:62:TRP:HB3	2.00	0.44
8:QH:6:ILE:HB	8:QH:85:ARG:HH11	1.82	0.44
10:QJ:33:GLN:O	10:QJ:75:ILE:HG12	2.17	0.44
19:QS:66:MET:HB2	19:QS:74:PHE:CZ	2.51	0.44
52:R6:32:ASN:N	52:R6:32:ASN:OD1	2.49	0.44
25:RA:2262:U:OP1	46:R0:19:LYS:NZ	2.42	0.44
25:RA:2648:C:H2'	25:RA:2649:U:H6	1.82	0.44
25:RA:31:C:O2'	25:RA:1238:G:H5'	2.16	0.44
25:RA:616:A:C4	29:RF:180:GLY:HA2	2.52	0.44
31:RH:109:PHE:CZ	31:RH:152:ARG:HG2	2.52	0.44
25:RA:1138:G:N2	33:RN:106:MET:HE3	2.14	0.44
37:RR:28:LEU:HD12	37:RR:48:VAL:HG11	1.99	0.44
40:RU:65:ILE:HG12	40:RU:96:ALA:CB	2.47	0.44
44:RY:42:VAL:HG12	44:RY:65:ALA:HB3	1.99	0.44
1:XA:1322:C:H6	1:XA:1322:C:OP1	2.00	0.44
1:XA:1363:A:H4'	1:XA:1364:U:H2'	1.98	0.44
2:XB:12:GLU:C	2:XB:14:GLY:H	2.21	0.44
2:XB:33:TYR:HB2	2:XB:43:ASP:HB2	1.99	0.44
5:XE:110:LEU:HD13	5:XE:118:ILE:HD13	1.98	0.44
25:YA:2309:A:C6	25:YA:2310:A:C2	3.05	0.44
25:YA:643:A:N1	25:YA:2369:A:O2'	2.44	0.44
25:YA:862:G:H2'	25:YA:863:A:O4'	2.17	0.44
32:YI:120:ILE:HD11	32:YI:126:TYR:CZ	2.52	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
34:YO:17:ARG:NH2	34:YO:47:ILE:HD13	2.33	0.44
34:YO:86:ILE:HG22	34:YO:94:ARG:HD3	2.00	0.44
42:YW:33:ARG:NH2	42:YW:52:GLU:OE1	2.50	0.44
43:YX:35:THR:O	43:YX:39:ILE:HG13	2.16	0.44
45:YZ:82:ARG:HG3	45:YZ:83:PRO:CD	2.47	0.44
1:QA:1101:A:H4'	1:QA:1102:A:O5'	2.18	0.44
1:QA:1326:C:H2'	1:QA:1327:C:C6	2.52	0.44
1:QA:1388:C:H2'	1:QA:1389:C:C6	2.52	0.44
1:QA:1399:C:C2	1:QA:1502:A:N6	2.86	0.44
1:QA:377:G:H1	1:QA:386:C:H42	1.65	0.44
1:QA:390:C:H2'	1:QA:391:G:C8	2.53	0.44
1:QA:509:A:C8	1:QA:509:A:H3'	2.52	0.44
4:QD:158:ILE:HA	4:QD:158:ILE:HD13	1.82	0.44
6:QF:23:LYS:O	6:QF:27:GLN:HG2	2.17	0.44
19:QS:10:PHE:HB2	19:QS:39:THR:H	1.82	0.44
25:RA:1669:A:OP2	25:RA:1670:C:OP2	2.35	0.44
25:RA:1771:C:C1'	25:RA:1786:A:H8	2.31	0.44
25:RA:2292:C:OP2	38:RS:17:ARG:NH2	2.49	0.44
25:RA:745:G:C2'	25:RA:746:A:H5'	2.48	0.44
28:RE:23:VAL:HG12	28:RE:184:VAL:O	2.17	0.44
32:RI:101:LEU:HD22	32:RI:107:VAL:HB	1.98	0.44
33:RN:114:ARG:O	33:RN:115:ARG:HB3	2.17	0.44
45:RZ:103:ARG:HD3	45:RZ:136:PHE:CD1	2.53	0.44
1:XA:1128:C:H5'	9:XI:16:ARG:NH2	2.27	0.44
1:XA:741:G:H2'	1:XA:742:G:O4'	2.17	0.44
7:XG:138:LYS:HE2	7:XG:142:GLU:OE2	2.17	0.44
8:XH:83:ILE:HB	8:XH:137:VAL:HG13	1.99	0.44
8:XH:65:TYR:HA	8:XH:79:VAL:HG23	1.98	0.44
9:XI:95:LYS:HZ3	9:XI:96:LEU:HD13	1.83	0.44
12:XL:45:PRO:HG3	12:XL:53:ARG:HD3	1.98	0.44
10:XJ:61:GLU:OE1	14:XN:58:LYS:HE2	2.17	0.44
21:XU:5:ASP:HB3	21:XU:8:THR:OG1	2.17	0.44
47:Y1:53:VAL:HB	47:Y1:58:ILE:HD13	1.98	0.44
19:XS:42:PRO:HD3	50:Y4:63:TYR:CE2	2.52	0.44
25:YA:1109:C:O2'	25:YA:1110:G:OP1	2.26	0.44
25:YA:1164:G:H2'	25:YA:1165:U:C6	2.52	0.44
25:YA:1289:C:H2'	25:YA:1290:C:C6	2.53	0.44
25:YA:2282:G:H4'	25:YA:2389:G:O2'	2.18	0.44
25:YA:1638:C:H5''	25:YA:2710:C:O2'	2.17	0.44
25:YA:41:C:H2'	25:YA:43:G:O4'	2.17	0.44
25:YA:531:C:OP1	25:YA:561:G:N1	2.50	0.44
25:YA:99:U:H4'	25:YA:101:G:C5'	2.48	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:YN:62:VAL:HG12	33:YN:66:LYS:HD2	1.98	0.44
25:YA:587:C:O2	35:YP:33:ARG:NH1	2.50	0.44
35:YP:64:LYS:CB	54:Y8:25:MET:HG3	2.48	0.44
40:YU:66:ASN:HB2	40:YU:76:TYR:HB2	1.99	0.44
1:QA:1277:C:O2'	1:QA:1279:A:H8	1.99	0.44
1:QA:1338:G:C6	1:QA:1339:A:C6	3.06	0.44
4:QD:166:LYS:HG3	4:QD:178:VAL:HG11	1.99	0.44
5:QE:47:LYS:HB2	5:QE:47:LYS:HE2	1.82	0.44
48:R2:49:LYS:O	48:R2:53:LEU:HB2	2.18	0.44
25:RA:989:G:N7	49:R3:13:ILE:HD12	2.32	0.44
19:QS:70:LYS:HE2	50:R4:68:ARG:HH21	1.82	0.44
25:RA:250:G:C6	25:RA:251:A:C6	3.05	0.44
25:RA:2610:C:H4'	25:RA:2611:U:OP2	2.16	0.44
25:RA:2758:A:H2'	25:RA:2759:G:O4'	2.18	0.44
25:RA:372:G:HO2'	25:RA:400:G:H1	1.65	0.44
25:RA:602:G:O2'	25:RA:604:G:O2'	2.26	0.44
27:RD:70:TRP:HZ3	27:RD:146:GLU:OE2	2.01	0.44
30:RG:51:ARG:O	30:RG:53:LEU:N	2.48	0.44
32:RI:93:THR:H	32:RI:96:ASP:HB2	1.83	0.44
33:RN:116:LEU:HA	33:RN:116:LEU:HD23	1.78	0.44
36:RQ:12:GLN:HE21	36:RQ:72:LYS:HD3	1.82	0.44
1:XA:109:A:C6	1:XA:326:G:C6	3.05	0.44
1:XA:1239:A:H62	1:XA:1299:A:H62	1.65	0.44
1:XA:337:C:H2'	1:XA:338:A:C8	2.52	0.44
1:XA:542:G:H5'	4:XD:41:GLY:HA3	1.98	0.44
7:XG:87:VAL:HG11	7:XG:155:ARG:HA	1.99	0.44
1:XA:1117:G:H5"	9:XI:104:ARG:NH1	2.32	0.44
13:XM:115:LYS:HE3	13:XM:115:LYS:HB2	1.75	0.44
18:XR:52:PRO:HB2	18:XR:54:ARG:HG2	2.00	0.44
1:XA:735:C:H5'	18:XR:71:LYS:HD3	2.00	0.44
19:XS:81:ARG:HB2	19:XS:81:ARG:HE	1.36	0.44
20:XT:87:LYS:O	20:XT:91:LEU:HG	2.18	0.44
25:YA:1204:A:C2	25:YA:1241:A:C2	3.05	0.44
25:YA:1371:G:HO2'	25:YA:1372:U:H5	1.63	0.44
25:YA:1930:G:O2'	25:YA:1931:U:P	2.75	0.44
25:YA:2175:C:H2'	25:YA:2176:A:O4'	2.17	0.44
25:YA:2563:U:H1'	25:YA:2566:A:N6	2.33	0.44
25:YA:2867:G:O2'	25:YA:2868:A:P	2.76	0.44
31:YH:124:GLU:HB3	31:YH:132:ARG:HG3	1.99	0.44
39:YT:61:PHE:CE2	39:YT:76:PHE:HB2	2.53	0.44
40:YU:104:GLN:OE1	40:YU:105:VAL:HG23	2.18	0.44
41:YV:99:ILE:H	41:YV:99:ILE:HD13	1.82	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:QA:827:U:C5	1:QA:870:U:C4	3.05	0.44
3:QC:70:VAL:HG21	3:QC:76:VAL:HG11	2.00	0.44
4:QD:150:GLU:OE1	4:QD:150:GLU:N	2.51	0.44
12:QL:70:ILE:HD13	12:QL:77:LEU:HD12	1.99	0.44
22:QV:9:G:N2	22:QV:26:G:H1'	2.33	0.44
51:R5:46:CYS:HA	51:R5:47:PRO:HD2	1.63	0.44
52:R6:40:CYS:HA	52:R6:41:PRO:HD2	1.85	0.44
25:RA:1728:G:C6	25:RA:1730:U:OP2	2.70	0.44
25:RA:774:A:H2	25:RA:787:U:O2'	1.99	0.44
27:RD:49:ILE:CD1	27:RD:52:ARG:HA	2.47	0.44
30:RG:37:VAL:O	30:RG:94:LEU:HG	2.17	0.44
31:RH:4:ILE:O	31:RH:6:ARG:N	2.51	0.44
38:RS:11:LYS:HG3	38:RS:91:PRO:HD3	1.98	0.44
1:XA:148:G:H2'	1:XA:149:A:C8	2.51	0.44
1:XA:376:G:H5''	16:XP:5:ARG:HB2	1.99	0.44
1:XA:765:G:N2	1:XA:813:U:OP2	2.50	0.44
1:XA:421:U:H3	3:XC:127:ARG:HH21	1.63	0.44
22:XV:19:G:H5'	22:XV:20:U:C5	2.52	0.44
48:Y2:17:SER:CB	48:Y2:67:LYS:HE3	2.47	0.44
52:Y6:34:LEU:HD13	52:Y6:34:LEU:H	1.82	0.44
52:Y6:7:ILE:HD12	52:Y6:7:ILE:HA	1.85	0.44
25:YA:1085:A:HO2'	25:YA:1086:A:P	2.37	0.44
25:YA:1469:A:H2'	25:YA:1470:G:C8	2.53	0.44
25:YA:1535:U:OP2	25:YA:1537:C:N4	2.51	0.44
25:YA:479:A:N3	25:YA:481:G:H5''	2.32	0.44
29:YF:63:LYS:HE3	29:YF:65:TRP:O	2.18	0.44
30:YG:114:ILE:HB	30:YG:117:PHE:HB2	1.99	0.44
32:YI:110:ASP:HB3	32:YI:112:LYS:N	2.33	0.44
33:YN:134:ARG:O	33:YN:136:GLU:N	2.50	0.44
25:YA:911:A:H2'	36:YQ:9:TYR:OH	2.18	0.44
39:YT:42:ILE:HG21	39:YT:84:GLN:NE2	2.32	0.44
41:YV:15:GLU:HG3	41:YV:16:PRO:HD2	1.99	0.44
44:YY:51:VAL:O	44:YY:56:PRO:HA	2.18	0.44
1:QA:1347:G:O2'	1:QA:1348:U:P	2.76	0.44
1:QA:164:U:H2'	1:QA:165:C:C6	2.53	0.44
1:QA:652:U:O2'	1:QA:653:A:O5'	2.35	0.44
2:QB:228:GLY:O	2:QB:230:VAL:N	2.50	0.44
2:QB:71:VAL:HA	2:QB:93:VAL:HB	2.00	0.44
11:QK:92:GLU:HB3	11:QK:96:ARG:NH1	2.33	0.44
12:QL:109:GLY:HA3	12:QL:121:GLY:O	2.17	0.44
15:QO:50:HIS:O	15:QO:53:HIS:HB3	2.17	0.44
25:RA:1862:G:O2'	25:RA:1863:G:H5'	2.18	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:2300:G:H2'	25:RA:2301:C:C6	2.53	0.44
25:RA:2656:U:H3	25:RA:2665:A:H2	1.65	0.44
25:RA:495:G:N3	42:RW:61:ASN:ND2	2.65	0.44
25:RA:70:G:H21	25:RA:71:A:H62	1.65	0.44
25:RA:754:C:H2'	25:RA:755:C:H6	1.83	0.44
25:RA:899:A:OP2	25:RA:899:A:H8	2.00	0.44
25:RA:934:G:H2'	25:RA:935:C:C6	2.53	0.44
25:RA:953:A:OP2	36:RQ:16:ARG:HD3	2.17	0.44
30:RG:171:ALA:O	30:RG:175:LEU:HG	2.18	0.44
30:RG:57:ALA:HB1	30:RG:68:PRO:HG2	1.99	0.44
31:RH:28:GLY:HA3	31:RH:79:VAL:HB	2.00	0.44
1:XA:1388:C:H2'	1:XA:1389:C:C6	2.52	0.44
1:XA:458:C:H2'	1:XA:464:G:H8	1.83	0.44
1:XA:690:G:H22	11:XK:55:LYS:HZ2	1.65	0.44
15:XO:32:LEU:O	15:XO:36:ILE:HG13	2.18	0.44
15:XO:82:ILE:O	15:XO:86:GLY:N	2.51	0.44
22:XV:61:C:H2'	22:XV:62:C:C6	2.51	0.44
46:Y0:43:THR:HG23	46:Y0:43:THR:O	2.17	0.44
25:YA:1283:G:N2	25:YA:1285:G:H3'	2.32	0.44
25:YA:1537:C:H2'	25:YA:1538:G:C8	2.53	0.44
25:YA:2335:A:O2'	25:YA:2336:A:H2'	2.17	0.44
25:YA:2360:A:H2'	25:YA:2361:A:O4'	2.18	0.44
25:YA:71:A:H2	43:YX:31:HIS:NE2	2.13	0.44
25:YA:77:C:O3'	48:Y2:14:ARG:NH2	2.51	0.44
27:YD:85:ASP:HB2	27:YD:92:ILE:HD13	1.99	0.44
29:YF:184:TYR:CE2	29:YF:188:ARG:HD2	2.52	0.44
29:YF:47:GLY:HA3	29:YF:95:ARG:O	2.18	0.44
35:YP:62:LEU:HB2	54:Y8:30:ARG:HH11	1.83	0.44
1:QA:255:G:H2'	1:QA:256:U:C6	2.53	0.44
1:QA:530:G:HO2'	1:QA:531:U:P	2.40	0.44
1:QA:769:G:H4'	1:QA:1513:A:H4'	1.99	0.44
10:QJ:47:PHE:HE1	10:QJ:63:PHE:HB2	1.83	0.44
12:QL:71:PRO:HG3	12:QL:99:HIS:HD2	1.82	0.44
15:QO:39:LEU:HD23	15:QO:39:LEU:HA	1.68	0.44
16:QP:23:ASP:O	16:QP:26:ARG:HB2	2.17	0.44
1:QA:636:U:H5'	17:QQ:2:PRO:HG3	1.98	0.44
47:R1:49:VAL:HG11	47:R1:70:VAL:HG11	1.98	0.44
55:R9:24:TYR:CE2	55:R9:35:ARG:HG3	2.53	0.44
25:RA:1338:G:N3	25:RA:1393:A:H2	2.16	0.44
25:RA:1588:C:H2'	25:RA:1589:C:C6	2.53	0.44
25:RA:2127:G:N2	25:RA:2173:A:H1'	2.33	0.44
25:RA:2323:G:H2'	25:RA:2324:C:O4'	2.18	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:2377:A:H2'	25:RA:2378:A:C8	2.53	0.44
25:RA:724:U:H2'	25:RA:725:G:O4'	2.17	0.44
27:RD:34:VAL:HG22	27:RD:35:LYS:HG3	2.00	0.44
29:RF:9:ILE:HA	29:RF:10:PRO:HD3	1.89	0.44
30:RG:95:ARG:O	30:RG:99:MET:HG2	2.18	0.44
34:RO:106:LEU:HD23	34:RO:106:LEU:HA	1.81	0.44
35:RP:140:ALA:O	35:RP:141:ALA:HB2	2.17	0.44
39:RT:107:ASP:O	39:RT:111:ARG:NH1	2.51	0.44
41:RV:16:PRO:HB3	41:RV:97:LYS:O	2.17	0.44
41:RV:35:LEU:CD2	41:RV:57:VAL:HG22	2.47	0.44
45:RZ:29:TYR:CE2	45:RZ:87:ASP:HB3	2.53	0.44
1:XA:1103:C:H2'	1:XA:1104:G:O4'	2.17	0.44
1:XA:680:C:H2'	1:XA:681:C:C6	2.51	0.44
3:XC:47:LEU:HA	3:XC:47:LEU:HD12	1.83	0.44
12:XL:42:THR:HA	12:XL:53:ARG:O	2.18	0.44
15:XO:77:ARG:HA	15:XO:80:ALA:HB3	1.99	0.44
16:XP:18:ARG:NH1	16:XP:32:TYR:OH	2.50	0.44
25:YA:2336:A:H61	46:Y0:43:THR:HG21	1.82	0.44
50:Y4:48:ARG:CZ	50:Y4:51:ASP:HA	2.47	0.44
25:YA:2056:G:H1	51:Y5:4:HIS:CD2	2.36	0.44
25:YA:1509:C:H2'	25:YA:1511:A:C8	2.53	0.44
25:YA:2119:A:C2	25:YA:2171:A:H1'	2.52	0.44
25:YA:2392:A:H8	35:YP:60:MET:HG2	1.83	0.44
25:YA:839:U:H2'	25:YA:840:C:C6	2.53	0.44
27:YD:61:LEU:HA	27:YD:61:LEU:HD13	1.91	0.44
30:YG:98:ARG:O	30:YG:101:ILE:HG13	2.17	0.44
39:YT:48:ILE:H	39:YT:48:ILE:HD12	1.83	0.44
25:YA:535:C:O3'	40:YU:53:ARG:NH1	2.51	0.44
43:YX:70:LEU:H	43:YX:70:LEU:HD23	1.83	0.44
45:YZ:52:SER:O	45:YZ:54:HIS:N	2.50	0.44
2:QB:178:ARG:NH2	8:QH:74:PRO:HG3	2.33	0.44
10:QJ:51:ARG:HH22	14:QN:58:LYS:HZ1	1.66	0.44
25:RA:443:A:H1'	25:RA:1201:C:O4'	2.18	0.44
25:RA:1771:C:O2'	25:RA:1786:A:C8	2.67	0.44
25:RA:234:C:H2'	25:RA:235:U:C6	2.53	0.44
25:RA:2784:C:H2'	25:RA:2785:C:C6	2.53	0.44
25:RA:587:C:OP2	35:RP:21:ARG:NH2	2.51	0.44
27:RD:65:ILE:H	27:RD:65:ILE:HD13	1.82	0.44
30:RG:95:ARG:C	30:RG:99:MET:HG2	2.38	0.44
31:RH:123:PHE:O	31:RH:125:VAL:HG23	2.18	0.44
37:RR:54:LEU:HD23	37:RR:66:VAL:HG23	1.98	0.44
41:RV:49:THR:HB	41:RV:50:PRO:HD2	1.99	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
43:RX:57:LEU:HD11	43:RX:78:LYS:HD2	1.99	0.44
43:RX:87:GLN:O	43:RX:88:LYS:HG3	2.18	0.44
45:RZ:148:ASP:OD1	45:RZ:149:SER:N	2.50	0.44
1:XA:110:C:H2'	1:XA:111:G:O4'	2.18	0.44
1:XA:1129:C:C4'	1:XA:1130:A:H5'	2.44	0.44
1:XA:1320:C:OP1	19:XS:70:LYS:HE3	2.17	0.44
1:XA:883:C:O2'	1:XA:884:U:H5'	2.18	0.44
1:XA:865:A:H2	1:XA:918:A:H4'	1.82	0.44
3:XC:82:GLU:O	3:XC:86:VAL:HG13	2.17	0.44
5:XE:9:LYS:HE3	5:XE:9:LYS:HB2	1.89	0.44
6:XF:33:TYR:HB2	6:XF:75:LEU:HD12	1.99	0.44
11:XK:19:ALA:HB2	11:XK:32:ILE:HG22	2.00	0.44
13:XM:23:TYR:HE1	13:XM:70:LEU:HD12	1.83	0.44
1:XA:974:A:OP2	14:XN:41:ARG:NH1	2.51	0.44
15:XO:26:GLU:HG2	15:XO:26:GLU:H	1.54	0.44
15:XO:39:LEU:HD13	15:XO:56:LEU:HB2	2.00	0.44
22:XV:23:C:H2'	22:XV:24:U:H6	1.83	0.44
48:Y2:31:GLU:HB2	48:Y2:53:LEU:HD11	2.00	0.44
50:Y4:35:VAL:C	50:Y4:37:SER:H	2.20	0.44
54:Y8:49:VAL:HG23	54:Y8:53:PRO:HB3	2.00	0.44
25:YA:2051:A:H5'	25:YA:2578:G:O4'	2.17	0.44
25:YA:2097:C:H2'	25:YA:2098:U:O4'	2.18	0.44
25:YA:2872:G:O2'	25:YA:2873:A:H5'	2.17	0.44
25:YA:828:U:H4'	25:YA:831:G:N1	2.33	0.44
28:YE:37:ARG:O	28:YE:45:THR:HA	2.18	0.44
25:YA:674:G:C1'	29:YF:74:ARG:HD3	2.41	0.44
30:YG:10:LYS:HE2	30:YG:175:LEU:O	2.18	0.44
30:YG:47:LYS:HB2	30:YG:47:LYS:HE3	1.73	0.44
45:YZ:166:SER:HB2	45:YZ:167:PRO:C	2.38	0.44
1:QA:1252:A:H2'	1:QA:1253:G:O4'	2.18	0.44
1:QA:1371:G:C6	1:QA:1372:U:C4	3.05	0.44
1:QA:464:G:O6	1:QA:466:C:H5'	2.18	0.44
1:QA:936:C:H2'	1:QA:937:A:H8	1.82	0.44
7:QG:113:GLU:HG2	7:QG:113:GLU:H	1.39	0.44
1:QA:1330:U:OP1	13:QM:25:ILE:O	2.35	0.44
51:R5:16:ARG:HD2	51:R5:20:ARG:NH1	2.33	0.44
52:R6:41:PRO:HD2	52:R6:46:HIS:H	1.83	0.44
25:RA:996:A:N6	25:RA:1160:G:C6	2.86	0.44
25:RA:1282:U:H2'	25:RA:1283:G:O4'	2.18	0.44
25:RA:1728:G:H5'	25:RA:1729:A:OP2	2.17	0.44
25:RA:1729:A:H2'	25:RA:1730:U:H5''	2.00	0.44
25:RA:1962:C:O2'	25:RA:1964:G:OP2	2.36	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:2126:A:H1'	25:RA:2127:G:OP2	2.18	0.44
25:RA:2331:G:O2'	46:R0:43:THR:HG22	2.18	0.44
25:RA:945:A:C4	25:RA:2448:A:C2	3.05	0.44
25:RA:1816:G:C8	27:RD:62:TYR:CZ	3.05	0.44
25:RA:2620:C:O2'	28:RE:157:ALA:O	2.29	0.44
25:RA:2635:C:H5''	28:RE:78:LEU:HA	2.00	0.44
29:RF:117:ARG:HH12	35:RP:1:MET:N	2.16	0.44
37:RR:27:SER:HB3	37:RR:34:ILE:HD11	1.99	0.44
38:RS:19:LYS:O	38:RS:20:ARG:HB3	2.17	0.44
43:RX:67:GLY:O	43:RX:69:TYR:N	2.43	0.44
44:RY:81:LYS:HB2	44:RY:96:ILE:CG2	2.48	0.44
1:XA:292:G:N7	1:XA:293:G:H1'	2.33	0.44
1:XA:755:G:OP2	15:XO:65:ARG:HG2	2.18	0.44
1:XA:975:A:C8	1:XA:975:A:H5'	2.48	0.44
3:XC:72:LYS:HB3	3:XC:75:VAL:HG23	2.00	0.44
12:XL:39:VAL:HG12	12:XL:41:ARG:HG3	2.00	0.44
16:XP:39:TYR:CZ	16:XP:41:PRO:HB3	2.53	0.44
47:Y1:70:VAL:O	47:Y1:73:LEU:HB2	2.18	0.44
52:Y6:41:PRO:HD2	52:Y6:46:HIS:H	1.81	0.44
25:YA:138:G:H2'	25:YA:139:G:C8	2.52	0.44
25:YA:1790:C:H2'	25:YA:1791:A:C4	2.52	0.44
25:YA:636:G:OP1	35:YP:132:LYS:HB2	2.18	0.44
25:YA:855:G:C6	25:YA:856:C:C4	3.06	0.44
28:YE:105:THR:OG1	28:YE:199:ARG:NH1	2.50	0.44
32:YI:130:TYR:N	32:YI:136:VAL:O	2.51	0.44
25:YA:1754:C:H5'	39:YT:101:PHE:CE2	2.52	0.44
45:YZ:19:ARG:HD3	45:YZ:25:PRO:HD2	1.99	0.44
45:YZ:52:SER:OG	45:YZ:52:SER:O	2.30	0.44
1:QA:1181:G:C5	1:QA:1182:G:N2	2.86	0.43
1:QA:963:G:H1	1:QA:972:C:N4	2.15	0.43
1:QA:967:C:H2'	1:QA:968:A:C8	2.53	0.43
7:QG:116:ALA:HA	7:QG:119:ARG:HE	1.83	0.43
20:QT:16:HIS:O	20:QT:19:SER:HB3	2.17	0.43
22:QV:2:C:C2'	22:QV:3:G:H5'	2.48	0.43
25:RA:1022:G:C6	25:RA:1140:C:C4	3.06	0.43
25:RA:1205:U:C4	29:RF:171:PRO:HA	2.52	0.43
25:RA:1651:G:H2'	25:RA:1652:A:O4'	2.18	0.43
25:RA:2134:A:N7	25:RA:2156:G:N2	2.65	0.43
25:RA:2346:A:H5''	25:RA:2383:G:H1'	2.00	0.43
25:RA:754:C:H2'	25:RA:755:C:C6	2.53	0.43
25:RA:879:G:C2	25:RA:880:G:H1'	2.53	0.43
26:RB:14:U:H4'	26:RB:70:C:O2	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:RD:145:VAL:HG11	27:RD:175:LEU:HD11	2.00	0.43
25:RA:1655:A:H4'	28:RE:115:GLY:N	2.33	0.43
32:RI:62:LYS:HA	32:RI:133:HIS:NE2	2.33	0.43
34:RO:22:ILE:HA	34:RO:22:ILE:HD13	1.77	0.43
35:RP:37:GLY:O	35:RP:40:SER:OG	2.26	0.43
36:RQ:136:ALA:O	36:RQ:138:ASP:N	2.46	0.43
38:RS:29:PHE:HD2	38:RS:92:TYR:HH	1.65	0.43
44:RY:42:VAL:O	44:RY:65:ALA:N	2.45	0.43
25:RA:896:A:C2	45:RZ:146:ILE:HD11	2.52	0.43
2:XB:80:ILE:HG21	2:XB:212:GLN:HA	1.99	0.43
3:XC:108:ASN:HB3	3:XC:111:LEU:HD12	2.00	0.43
12:XL:24:VAL:O	12:XL:26:ALA:N	2.47	0.43
12:XL:78:GLN:HB3	12:XL:79:GLU:H	1.67	0.43
1:XA:667:G:H4'	15:XO:51:HIS:ND1	2.33	0.43
16:XP:4:ILE:HB	16:XP:66:PRO:HB3	2.00	0.43
25:YA:1449:A:H5'	25:YA:1449(A):G:OP2	2.18	0.43
25:YA:1803:A:H4'	27:YD:259:THR:HG23	2.00	0.43
30:YG:67:LYS:O	30:YG:67:LYS:HD2	2.17	0.43
35:YP:126:VAL:HG12	35:YP:147:LEU:CD2	2.48	0.43
1:QA:1412:C:H2'	1:QA:1413:A:C8	2.53	0.43
1:QA:954:G:H2'	1:QA:955:U:O4'	2.19	0.43
1:QA:980:C:H5'	1:QA:981:U:C5	2.52	0.43
3:QC:81:GLY:O	3:QC:85:ARG:HB2	2.18	0.43
4:QD:133:VAL:HG12	4:QD:135:LEU:H	1.83	0.43
5:QE:100:VAL:HG22	5:QE:118:ILE:HG22	1.99	0.43
9:QI:16:ARG:O	9:QI:63:ILE:HA	2.17	0.43
52:R6:28:ARG:HG3	52:R6:31:PRO:HD2	2.00	0.43
25:RA:1028:A:H61	25:RA:1125:G:H2'	1.83	0.43
25:RA:1359:A:OP2	25:RA:1371:G:N1	2.47	0.43
25:RA:1430:C:H2'	25:RA:1431:U:C6	2.53	0.43
25:RA:1819:A:H4'	25:RA:1820:U:O5'	2.18	0.43
25:RA:185:U:H2'	25:RA:186:G:O4'	2.18	0.43
25:RA:1638:C:O3'	25:RA:2709:G:N2	2.51	0.43
25:RA:2808:U:H5''	25:RA:2891:G:O6	2.18	0.43
25:RA:540:G:H5'	25:RA:541:C:OP2	2.18	0.43
25:RA:673:C:H5''	29:RF:81:PRO:HD2	2.00	0.43
28:RE:143:ASN:HD22	28:RE:147:PRO:HD3	1.83	0.43
45:RZ:102:LEU:HB3	45:RZ:104:PHE:CE1	2.52	0.43
1:XA:1239:A:O2'	1:XA:1298:C:N4	2.51	0.43
1:XA:210:U:O2'	1:XA:216:G:N7	2.43	0.43
1:XA:719:C:H1'	18:XR:49:LYS:HB3	1.99	0.43
4:XD:100:ARG:NH1	4:XD:137:SER:HB3	2.33	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:XD:153:ARG:NH1	4:XD:181:MET:HB2	2.32	0.43
47:Y1:94:LEU:HD23	47:Y1:94:LEU:HA	1.81	0.43
35:YP:61:ARG:NH1	54:Y8:56:GLU:OE2	2.49	0.43
55:Y9:1:MET:O	55:Y9:34:GLN:HG2	2.18	0.43
25:YA:1263:U:H1'	51:Y5:10:LYS:HG3	1.98	0.43
25:YA:330:A:O2'	25:YA:331:A:H8	2.01	0.43
25:YA:729:G:OP2	27:YD:13:ARG:NH1	2.50	0.43
25:YA:892:G:N2	25:YA:893:C:C2	2.86	0.43
29:YF:66:PRO:O	29:YF:68:LYS:N	2.51	0.43
31:YH:4:ILE:H	31:YH:4:ILE:HG12	1.59	0.43
31:YH:67:LEU:O	31:YH:71:LEU:HB2	2.17	0.43
25:YA:389:G:H22	35:YP:72:PRO:CG	2.30	0.43
1:QA:1004:A:H2	1:QA:1024:G:C8	2.36	0.43
2:QB:74:LYS:O	2:QB:78:GLN:HG3	2.18	0.43
4:QD:155:LEU:O	4:QD:159:ARG:HG2	2.18	0.43
7:QG:9:VAL:HG13	7:QG:94:ARG:NH2	2.27	0.43
1:QA:878:G:H5'	8:QH:89:PRO:HG2	2.00	0.43
10:QJ:54:PHE:HB3	10:QJ:55:LYS:H	1.69	0.43
10:QJ:51:ARG:NE	10:QJ:60:ARG:O	2.45	0.43
11:QK:19:ALA:HB2	11:QK:32:ILE:HG22	2.00	0.43
25:RA:1392:A:N6	25:RA:1393:A:N6	2.66	0.43
25:RA:1459:G:H2'	25:RA:1460:A:H5''	1.99	0.43
25:RA:412:A:N7	25:RA:2411:A:H2	2.16	0.43
25:RA:725:G:O5'	25:RA:725:G:H8	2.01	0.43
25:RA:910:A:N7	36:RQ:13:GLN:HG3	2.32	0.43
39:RT:19:LEU:HA	39:RT:20:PRO:HD3	1.86	0.43
44:RY:97:ARG:HE	44:RY:98:VAL:HB	1.83	0.43
1:XA:1079:G:C6	1:XA:1080:A:N6	2.86	0.43
1:XA:1497:G:C2'	1:XA:1498:U:H5'	2.49	0.43
1:XA:352:C:O2'	1:XA:354:G:OP1	2.26	0.43
1:XA:421:U:H5''	1:XA:422:C:OP2	2.19	0.43
9:XI:118:LYS:O	9:XI:119:ALA:HB3	2.18	0.43
10:XJ:32:ALA:H	10:XJ:78:ASN:ND2	2.16	0.43
1:XA:267:C:OP2	17:XQ:67:LYS:HD2	2.18	0.43
1:XA:1222:G:H5''	19:XS:78:ARG:NH1	2.33	0.43
47:Y1:25:LYS:C	47:Y1:27:GLU:H	2.22	0.43
25:YA:1543:A:C2	25:YA:1545:A:C4	3.06	0.43
25:YA:2271:G:OP1	46:Y0:18:ALA:HB1	2.19	0.43
25:YA:270(B):A:H61	25:YA:270(Y):G:H1'	1.83	0.43
25:YA:2845:G:O2'	25:YA:2846:G:H5'	2.18	0.43
25:YA:898:C:C2'	25:YA:899:A:H5'	2.48	0.43
28:YE:188:VAL:HG13	28:YE:188:VAL:O	2.19	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
32:YI:88:ILE:HG12	32:YI:122:GLU:H	1.83	0.43
33:YN:112:LEU:HG	33:YN:112:LEU:O	2.17	0.43
37:YR:38:VAL:HG22	37:YR:112:ALA:HB2	2.00	0.43
37:YR:34:ILE:HD13	37:YR:34:ILE:HA	1.71	0.43
39:YT:35:LYS:H	39:YT:35:LYS:HD2	1.83	0.43
41:YV:52:VAL:O	41:YV:54:GLY:N	2.51	0.43
43:YX:72:LYS:HG2	43:YX:73:ARG:O	2.18	0.43
1:QA:129(A):G:C6	1:QA:191(A):G:H1'	2.53	0.43
1:QA:54:C:N4	1:QA:353:A:OP2	2.48	0.43
1:QA:368:U:OP1	32:YI:91:SER:OG	2.37	0.43
1:QA:581:G:OP1	15:QO:61:GLY:HA3	2.19	0.43
1:QA:859:A:H2	8:QH:19:VAL:HG11	1.83	0.43
1:QA:936:C:H2'	1:QA:937:A:C8	2.53	0.43
1:QA:947:G:H2'	1:QA:948:C:O4'	2.19	0.43
1:QA:986:A:N3	19:QS:52:TYR:OH	2.45	0.43
2:QB:167:PRO:HG3	2:QB:188:ALA:HB2	2.00	0.43
8:QH:13:ILE:O	8:QH:17:THR:HG23	2.19	0.43
11:QK:38:ASN:HA	11:QK:39:PRO:HD3	1.88	0.43
16:QP:20:VAL:HG21	16:QP:32:TYR:CE1	2.54	0.43
17:QQ:60:ILE:HB	17:QQ:74:LEU:HD23	2.00	0.43
25:RA:458:G:O2'	53:R7:39:ARG:HD3	2.19	0.43
25:RA:1021:A:C8	25:RA:1022:G:H5''	2.53	0.43
25:RA:1766:U:H2'	25:RA:1767:C:C6	2.53	0.43
25:RA:2308:G:HO2'	25:RA:2310:A:H2	1.65	0.43
25:RA:2646:C:H2'	25:RA:2647:U:O4'	2.18	0.43
25:RA:292:C:C2	25:RA:349:G:N2	2.86	0.43
25:RA:588:U:O4	25:RA:670:A:H1'	2.18	0.43
26:RB:73:A:C4	26:RB:104:A:C2	3.07	0.43
28:RE:119:ARG:HD3	28:RE:160:TYR:HB2	2.00	0.43
33:RN:33:LEU:HA	33:RN:38:HIS:CE1	2.54	0.43
1:XA:1451:A:H2'	1:XA:1451:A:N3	2.33	0.43
1:XA:181:G:O2'	1:XA:182:U:H6	2.01	0.43
1:XA:191:G:C2	1:XA:192:U:C2	3.07	0.43
1:XA:381:C:H2'	1:XA:382:A:O4'	2.19	0.43
1:XA:874:G:C6	1:XA:875:C:C4	3.07	0.43
1:XA:865:A:C2	1:XA:918:A:H4'	2.53	0.43
10:XJ:54:PHE:CZ	10:XJ:55:LYS:HE3	2.54	0.43
12:XL:62:SER:C	12:XL:64:TYR:H	2.21	0.43
12:XL:58:VAL:O	12:XL:65:GLU:HA	2.18	0.43
15:XO:25:THR:HG21	15:XO:70:LEU:HB2	2.00	0.43
16:XP:45:THR:HG22	16:XP:47:ASP:N	2.26	0.43
17:XQ:62:SER:HB3	17:XQ:72:ARG:HE	1.84	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:XT:98:PRO:C	20:XT:100:ILE:H	2.21	0.43
25:YA:1268:A:H2'	25:YA:1269:A:O4'	2.19	0.43
25:YA:1796:U:H2'	25:YA:1797:C:H6	1.79	0.43
25:YA:2467:C:C2'	25:YA:2468:G:H5'	2.48	0.43
25:YA:2480:C:H2'	25:YA:2481:G:H5'	1.99	0.43
25:YA:654(A):G:N2	25:YA:654(U):A:H1'	2.32	0.43
25:YA:847:U:C5	25:YA:933:A:N1	2.87	0.43
27:YD:92:ILE:HD12	27:YD:104:TYR:CD2	2.54	0.43
28:YE:87:GLU:O	28:YE:89:ASP:N	2.50	0.43
1:QA:1036:G:C8	1:QA:1037:C:C4	3.07	0.43
5:QE:18:ARG:HE	5:QE:18:ARG:HB3	1.52	0.43
15:QO:17:ARG:HD3	15:QO:26:GLU:HG3	1.99	0.43
25:RA:13:A:H61	25:RA:525:U:H3'	1.83	0.43
25:RA:1952:A:OP1	34:RO:42:SER:OG	2.28	0.43
25:RA:265:A:H2'	25:RA:266:G:O4'	2.18	0.43
25:RA:28:A:C2	25:RA:513:A:C8	3.06	0.43
25:RA:706:A:H2'	25:RA:707:G:O4'	2.19	0.43
25:RA:774:A:C2	25:RA:787:U:O2'	2.72	0.43
25:RA:996:A:H4'	40:RU:92:ARG:NE	2.24	0.43
26:RB:15:A:H3'	26:RB:16:G:H5'	1.99	0.43
28:RE:36:ARG:HH21	28:RE:88:GLY:HA2	1.84	0.43
44:RY:47:LYS:O	44:RY:49:VAL:N	2.51	0.43
44:RY:46:LYS:HB2	44:RY:61:ILE:HG22	2.00	0.43
1:XA:975:A:N6	1:XA:1367:C:O4'	2.52	0.43
1:XA:1446:A:O2'	1:XA:1447:G:P	2.76	0.43
1:XA:464:G:C6	1:XA:466:C:H5'	2.53	0.43
1:XA:923:A:OP1	5:XE:21:ALA:HB2	2.18	0.43
1:XA:9:G:H5''	5:XE:126:ARG:HE	1.84	0.43
2:XB:100:GLY:N	2:XB:176:GLU:OE2	2.47	0.43
2:XB:215:LEU:HA	2:XB:215:LEU:HD22	1.73	0.43
12:XL:110:VAL:CG2	12:XL:120:TYR:HB3	2.48	0.43
13:XM:14:ARG:H	13:XM:44:ARG:CD	2.25	0.43
14:XN:29:ARG:HD3	14:XN:40:CYS:HB2	1.99	0.43
48:Y2:15:LYS:H	48:Y2:67:LYS:CE	2.32	0.43
49:Y3:51:ALA:HA	49:Y3:54:VAL:HG12	2.00	0.43
50:Y4:43:TYR:CD2	50:Y4:43:TYR:C	2.92	0.43
53:Y7:47:ARG:HB2	53:Y7:48:LYS:H	1.59	0.43
25:YA:1021:A:C8	25:YA:1022:G:H5''	2.46	0.43
25:YA:1430:C:H2'	25:YA:1431:U:H6	1.82	0.43
25:YA:1512:G:H2'	25:YA:1513:C:C6	2.54	0.43
25:YA:1534:G:N3	25:YA:1534:G:H2'	2.34	0.43
25:YA:1742:C:H5'	25:YA:1743:G:OP2	2.19	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
29:YF:33:LEU:HD12	29:YF:33:LEU:HA	1.86	0.43
29:YF:64:ILE:HG23	29:YF:65:TRP:CD1	2.53	0.43
34:YO:64:ARG:HG2	34:YO:79:PHE:CD1	2.53	0.43
34:YO:88:ASN:OD1	34:YO:90:GLN:HB2	2.19	0.43
34:YO:88:ASN:ND2	34:YO:92:GLU:HB2	2.23	0.43
25:YA:956:G:C5'	36:YQ:77:LYS:HE2	2.49	0.43
45:YZ:5:LEU:HB3	45:YZ:59:LEU:HA	2.00	0.43
1:QA:1450:U:O2'	1:QA:1451:A:N7	2.52	0.43
1:QA:707:C:H2'	1:QA:708:C:C6	2.53	0.43
1:QA:741:G:H2'	1:QA:742:G:O4'	2.19	0.43
2:QB:217:ARG:HE	2:QB:217:ARG:HB2	1.29	0.43
18:QR:37:VAL:HG22	18:QR:78:LEU:HB3	2.01	0.43
25:RA:1401:G:H2'	25:RA:1402:C:O4'	2.18	0.43
25:RA:1778:U:H2'	25:RA:1784:A:N6	2.33	0.43
25:RA:2459:A:C5	25:RA:2460:U:C5	3.07	0.43
25:RA:286:C:H2'	25:RA:287:C:C6	2.54	0.43
25:RA:83:G:O2'	25:RA:84:A:H8	2.01	0.43
28:RE:179:GLU:HB3	28:RE:181:LEU:HD22	1.99	0.43
33:RN:58:ASP:HB3	33:RN:95:PRO:HB3	2.00	0.43
35:RP:90:ARG:HB3	35:RP:91:PHE:H	1.68	0.43
38:RS:12:PHE:HD2	38:RS:12:PHE:HA	1.72	0.43
39:RT:1:MET:O	39:RT:3:ARG:HG2	2.19	0.43
2:XB:37:ASN:C	2:XB:39:ILE:H	2.20	0.43
10:XJ:44:VAL:HG13	10:XJ:66:ARG:HG2	1.99	0.43
14:XN:27:CYS:SG	14:XN:29:ARG:HB2	2.58	0.43
1:XA:254:G:OP1	17:XQ:67:LYS:O	2.37	0.43
25:YA:1207:C:H2'	25:YA:1208:C:H6	1.83	0.43
25:YA:2238:G:H2'	25:YA:2238:G:N3	2.31	0.43
25:YA:71:A:H5''	25:YA:72:U:H3'	2.01	0.43
25:YA:825:C:O2	35:YP:55:ARG:NH2	2.51	0.43
35:YP:126:VAL:HG22	35:YP:145:PRO:HG2	2.00	0.43
35:YP:83:VAL:O	35:YP:114:ILE:HA	2.19	0.43
37:YR:33:ARG:HH21	51:Y5:55:ARG:HG2	1.82	0.43
38:YS:39:ILE:HD12	38:YS:85:VAL:HG11	2.00	0.43
41:YV:55:ALA:HB2	41:YV:101:GLY:HA2	2.00	0.43
43:YX:53:LYS:H	43:YX:82:GLN:HB3	1.83	0.43
44:YY:87:LYS:HB2	44:YY:87:LYS:NZ	2.33	0.43
1:QA:1018:C:H2'	1:QA:1019:C:C6	2.53	0.43
1:QA:176:C:OP1	20:QT:29:LYS:NZ	2.46	0.43
1:QA:587:G:N2	1:QA:754:C:OP2	2.52	0.43
2:QB:8:LYS:HE3	2:QB:11:LEU:HB3	2.01	0.43
3:QC:11:ARG:HB3	3:QC:15:THR:HB	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:QD:135:LEU:HA	4:QD:135:LEU:HD13	1.86	0.43
9:QI:116:LYS:HE2	9:QI:122:ALA:HB2	2.01	0.43
13:QM:44:ARG:HB2	13:QM:47:ASP:OD2	2.19	0.43
25:RA:1027:A:N6	25:RA:1126:A:C4	2.87	0.43
25:RA:1291:C:H5'	25:RA:1536:A:H5'	1.99	0.43
25:RA:1348:G:C2'	25:RA:1349:A:H5''	2.48	0.43
25:RA:2187:G:C6	25:RA:2188:C:C4	3.06	0.43
25:RA:2303:G:O2'	25:RA:2304:G:H5'	2.19	0.43
25:RA:2419:U:H2'	25:RA:2420:C:C6	2.54	0.43
25:RA:2482:G:O6	36:RQ:124:LYS:NZ	2.52	0.43
25:RA:2702:U:O2	25:RA:2702:U:H2'	2.18	0.43
25:RA:270(R):G:H2'	25:RA:270(S):G:H8	1.84	0.43
25:RA:322:A:H5'	25:RA:340:A:H1'	2.00	0.43
25:RA:485:C:H2'	25:RA:486:C:H6	1.84	0.43
25:RA:654(A):G:OP2	25:RA:654(A):G:H3'	2.18	0.43
25:RA:676:A:H8	25:RA:2069:G:N2	2.03	0.43
25:RA:953:A:C2	25:RA:954:G:C8	3.06	0.43
42:RW:20:VAL:HG22	42:RW:47:VAL:HG21	2.00	0.43
25:RA:748:G:C8	42:RW:89:ALA:HB1	2.54	0.43
44:RY:55:TYR:CD2	44:RY:55:TYR:N	2.87	0.43
1:XA:1072:G:H2'	1:XA:1073:U:C6	2.54	0.43
1:XA:1124:G:H3'	1:XA:1145:C:H41	1.84	0.43
1:XA:1273:G:H3'	1:XA:1274:G:H8	1.82	0.43
1:XA:536:C:H2'	1:XA:537:G:C8	2.54	0.43
9:XI:8:GLY:HA2	9:XI:79:LEU:HD12	2.01	0.43
48:Y2:47:ASN:HB2	48:Y2:48:HIS:H	1.50	0.43
19:XS:42:PRO:HB3	50:Y4:60:GLN:OE1	2.18	0.43
25:YA:2780:G:OP2	33:YN:118:LYS:HE2	2.19	0.43
25:YA:345:A:N3	25:YA:347:A:N6	2.66	0.43
25:YA:657:U:H2'	25:YA:658:C:C6	2.54	0.43
27:YD:132:PRO:HG3	27:YD:190:TYR:CE1	2.54	0.43
28:YE:119:ARG:HG2	28:YE:160:TYR:HB2	2.00	0.43
35:YP:113:LYS:HG2	35:YP:115:LEU:HD23	2.01	0.43
35:YP:30:THR:O	35:YP:33:ARG:HB2	2.18	0.43
37:YR:70:LEU:HA	37:YR:70:LEU:HD23	1.84	0.43
25:YA:1216:G:P	40:YU:12:ARG:HH21	2.39	0.43
44:YY:67:LEU:HA	44:YY:67:LEU:HD12	1.78	0.43
44:YY:80:GLY:O	44:YY:81:LYS:HG3	2.18	0.43
45:YZ:52:SER:C	45:YZ:54:HIS:H	2.22	0.43
36:YQ:20:ALA:HB3	45:YZ:79:ARG:CZ	2.49	0.43
1:QA:148:G:H2'	1:QA:149:A:C8	2.54	0.43
17:QQ:63:ARG:HG2	17:QQ:64:PRO:HD2	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
54:R8:58:ILE:HA	54:R8:61:LEU:HD21	2.01	0.43
25:RA:105:C:H6	25:RA:105:C:O5'	2.02	0.43
25:RA:1240:U:HO2'	25:RA:1241:A:P	2.42	0.43
25:RA:1337:G:OP2	43:RX:73:ARG:NH2	2.51	0.43
25:RA:1464:C:O2'	25:RA:1528:A:H8	1.94	0.43
25:RA:2154:G:H2'	25:RA:2155:G:H8	1.83	0.43
25:RA:2319:G:H4'	25:RA:2320:A:OP1	2.18	0.43
25:RA:2698:U:H2'	25:RA:2699:C:C6	2.53	0.43
25:RA:2836:U:C4	25:RA:2883:A:N6	2.87	0.43
25:RA:395:U:H2'	25:RA:396:G:N7	2.34	0.43
29:RF:23:ASP:OD1	29:RF:23:ASP:N	2.48	0.43
34:RO:104:ARG:HD3	39:RT:36:GLU:OE2	2.19	0.43
35:RP:18:ARG:HD2	35:RP:27:HIS:CD2	2.54	0.43
35:RP:65:ARG:O	35:RP:68:GLN:NE2	2.50	0.43
40:RU:69:CYS:HB3	40:RU:106:PHE:CZ	2.53	0.43
45:RZ:111:VAL:O	45:RZ:113:ALA:N	2.51	0.43
1:XA:960:U:H1'	1:XA:1223:C:H5'	2.00	0.43
1:XA:131:C:H2'	1:XA:132:C:C6	2.53	0.43
1:XA:731:G:H5'	1:XA:766:A:H4'	2.00	0.43
2:XB:172:ILE:O	2:XB:175:ARG:HB3	2.18	0.43
2:XB:7:VAL:HG21	2:XB:217:ARG:NH1	2.34	0.43
7:XG:140:ASP:HA	7:XG:143:ARG:NH1	2.34	0.43
12:XL:59:ARG:NH1	12:XL:65:GLU:OE2	2.51	0.43
13:XM:4:ILE:HG22	13:XM:5:ALA:N	2.34	0.43
14:XN:6:LEU:HD23	14:XN:23:ARG:HH22	1.83	0.43
1:XA:1318:A:O2'	19:XS:37:ARG:HD3	2.18	0.43
48:Y2:17:SER:HB3	48:Y2:67:LYS:HE3	2.00	0.43
25:YA:1105:U:H2'	25:YA:1106:G:H8	1.83	0.43
25:YA:1198:U:H2'	25:YA:1199:U:C6	2.54	0.43
25:YA:1930:G:O2'	25:YA:1931:U:O2	2.35	0.43
26:YB:66:A:H61	26:YB:107:U:H2'	1.84	0.43
28:YE:4:ILE:HD12	28:YE:28:ALA:HB1	2.01	0.43
30:YG:145:THR:O	30:YG:147:ASP:N	2.44	0.43
35:YP:15:ARG:O	35:YP:17:LYS:HG3	2.19	0.43
35:YP:62:LEU:HB2	54:Y8:30:ARG:NH1	2.34	0.43
45:YZ:70:LEU:HA	45:YZ:70:LEU:HD23	1.91	0.43
1:QA:1297:C:HO2'	1:QA:1298:C:P	2.36	0.43
1:QA:255:G:H2'	1:QA:256:U:H6	1.84	0.43
1:QA:868:C:H2'	1:QA:869:G:O4'	2.18	0.43
6:QF:99:ALA:HB1	18:QR:23:LYS:HZ2	1.83	0.43
1:QA:1371:G:OP1	9:QI:12:GLU:HB2	2.19	0.43
10:QJ:76:ASN:HA	10:QJ:77:PRO:HD2	1.85	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:QA:502:G:OP1	12:QL:118:SER:HB2	2.18	0.43
15:QO:48:LYS:HA	15:QO:48:LYS:HD3	1.76	0.43
18:QR:29:PHE:CD2	18:QR:29:PHE:N	2.87	0.43
18:QR:53:ARG:HH21	18:QR:60:ALA:N	2.17	0.43
20:QT:84:LEU:HA	20:QT:84:LEU:HD23	1.86	0.43
25:RA:94:G:N2	48:R2:47:ASN:HD22	2.15	0.43
25:RA:2038:G:H2'	25:RA:2039:C:O4'	2.18	0.43
25:RA:207:A:H2'	25:RA:208:C:O4'	2.19	0.43
25:RA:2245:U:H5''	25:RA:2246:G:H5'	2.01	0.43
25:RA:2767:C:H2'	25:RA:2768:C:C6	2.54	0.43
25:RA:531:C:H4'	25:RA:532:A:H5''	2.01	0.43
25:RA:589:C:H2'	25:RA:590:A:C8	2.53	0.43
25:RA:656:G:H2'	25:RA:657:U:O4'	2.19	0.43
25:RA:709:U:H2'	25:RA:710:G:C8	2.53	0.43
25:RA:911:A:H2'	36:RQ:9:TYR:OH	2.18	0.43
27:RD:35:LYS:HE3	27:RD:64:ILE:C	2.39	0.43
28:RE:116:VAL:HG11	28:RE:138:PRO:HB3	2.01	0.43
29:RF:34:TRP:CE3	29:RF:35:GLU:HG2	2.54	0.43
29:RF:9:ILE:HG23	29:RF:20:LEU:O	2.18	0.43
32:RI:124:GLY:O	32:RI:142:VAL:HG23	2.18	0.43
33:RN:61:ARG:HA	33:RN:61:ARG:HE	1.82	0.43
36:RQ:104:PHE:CE1	36:RQ:125:LEU:HD11	2.54	0.43
36:RQ:20:ALA:HA	36:RQ:98:LYS:HB3	2.00	0.43
38:RS:88:ASP:CG	38:RS:89:ARG:H	2.21	0.43
26:RB:37:C:O2	38:RS:95:HIS:NE2	2.51	0.43
44:RY:54:LYS:HB3	44:RY:55:TYR:CD2	2.53	0.43
45:RZ:48:PHE:CE2	45:RZ:52:SER:HA	2.54	0.43
1:XA:1000:A:H2'	1:XA:1001:G:C8	2.54	0.43
1:XA:1314:C:H2'	1:XA:1315:U:C6	2.54	0.43
1:XA:1404:C:H2'	1:XA:1405:G:C8	2.54	0.43
1:XA:191(D):U:H2'	1:XA:191(E):G:C8	2.54	0.43
1:XA:347:G:H1'	1:XA:348:G:H5''	2.00	0.43
1:XA:837:G:H1	1:XA:849:C:H42	1.66	0.43
1:XA:872:A:C5	1:XA:874:G:C8	3.06	0.43
1:XA:900:A:H2'	1:XA:901:A:C8	2.53	0.43
2:XB:212:GLN:NE2	2:XB:216:SER:HB2	2.34	0.43
3:XC:149:ALA:HA	3:XC:201:TYR:O	2.18	0.43
49:Y3:7:LYS:HE2	49:Y3:32:GLN:O	2.19	0.43
50:Y4:6:HIS:HA	50:Y4:7:PRO:HD2	1.82	0.43
51:Y5:58:LEU:HD13	51:Y5:60:VAL:HB	2.01	0.43
51:Y5:58:LEU:HB2	51:Y5:60:VAL:H	1.83	0.43
52:Y6:28:ARG:HH21	52:Y6:30:THR:HG23	1.84	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:944:G:H5''	25:YA:945:A:O5'	2.19	0.43
26:YB:32:C:C2	26:YB:51:G:N2	2.87	0.43
28:YE:14:ILE:HG23	28:YE:15:PHE:N	2.34	0.43
45:YZ:141:VAL:CG2	45:YZ:144:LEU:HB2	2.46	0.43
1:QA:1130:A:O2'	9:QI:3:GLN:NE2	2.34	0.43
1:QA:1227:A:O3'	13:QM:115:LYS:HE3	2.19	0.43
1:QA:347:G:O2'	1:QA:348:G:OP2	2.30	0.43
1:QA:358:U:H2'	1:QA:359:U:C6	2.54	0.43
1:QA:853:G:H2'	1:QA:854:G:H8	1.84	0.43
8:QH:101:PRO:HG2	8:QH:133:LEU:HD11	2.01	0.43
8:QH:25:ASP:OD1	8:QH:25:ASP:N	2.50	0.43
9:QI:112:LYS:HD3	9:QI:113:LYS:O	2.18	0.43
17:QQ:45:HIS:NE2	17:QQ:47:PRO:HG3	2.34	0.43
52:R6:7:ILE:HG13	52:R6:8:LYS:H	1.84	0.43
25:RA:1265:A:H3'	51:R5:19:ARG:NH1	2.34	0.43
25:RA:1319:G:C6	25:RA:1320:C:N4	2.87	0.43
25:RA:1599:C:OP2	43:RX:36:LYS:HD2	2.19	0.43
25:RA:1930:G:O2'	25:RA:1931:U:P	2.76	0.43
25:RA:2037:G:H2'	25:RA:2038:G:C8	2.54	0.43
25:RA:2630:G:O4'	25:RA:2894:G:H1'	2.18	0.43
25:RA:508:G:O2'	25:RA:509:C:OP2	2.36	0.43
25:RA:99:U:H4'	25:RA:101:G:O5'	2.19	0.43
28:RE:117:MET:HB2	28:RE:122:PHE:O	2.18	0.43
28:RE:48:GLN:OE1	28:RE:64:LYS:NZ	2.52	0.43
31:RH:124:GLU:HB3	31:RH:132:ARG:CG	2.48	0.43
33:RN:89:LYS:O	33:RN:93:THR:HG22	2.19	0.43
25:RA:1665:A:H4'	34:RO:67:LYS:HB2	2.01	0.43
36:RQ:116:GLU:O	36:RQ:120:ILE:HG12	2.18	0.43
37:RR:113:LEU:HD12	37:RR:113:LEU:HA	1.88	0.43
38:RS:93:LYS:HB2	38:RS:93:LYS:HE3	1.65	0.43
39:RT:107:ASP:O	39:RT:110:ILE:HG22	2.19	0.43
45:RZ:181:GLU:HB3	45:RZ:182:LYS:H	1.61	0.43
45:RZ:69:THR:HG22	45:RZ:90:VAL:HA	2.00	0.43
1:XA:1118:C:OP1	9:XI:9:ARG:HD3	2.18	0.43
1:XA:1346:A:H1'	1:XA:1348:U:C5	2.54	0.43
1:XA:1466:C:H2'	1:XA:1467:G:O4'	2.19	0.43
1:XA:224:C:H2'	1:XA:225:C:C6	2.53	0.43
1:XA:228:A:H2'	1:XA:229:U:O4'	2.19	0.43
4:XD:196:LEU:O	4:XD:198:VAL:N	2.51	0.43
5:XE:42:GLY:CA	5:XE:66:MET:HG2	2.48	0.43
5:XE:69:VAL:O	5:XE:71:LEU:N	2.51	0.43
8:XH:13:ILE:O	8:XH:17:THR:HG23	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:XL:28:LYS:HB3	12:XL:30:ALA:HB2	2.01	0.43
52:Y6:41:PRO:HG2	52:Y6:45:LYS:N	2.29	0.43
25:YA:1243:G:O2'	35:YP:7:ARG:NH2	2.42	0.43
25:YA:2056:G:C2	25:YA:2057:A:C8	3.07	0.43
25:YA:2250:G:C4	36:YQ:82:ARG:HG3	2.53	0.43
25:YA:2747:G:O6	25:YA:2755:C:H5''	2.18	0.43
25:YA:900:A:H5'	25:YA:901:A:OP2	2.19	0.43
26:YB:65:C:H41	26:YB:108:C:H2'	1.84	0.43
28:YE:201:THR:HG22	28:YE:203:LYS:H	1.83	0.43
28:YE:36:ARG:HH21	28:YE:88:GLY:CA	2.32	0.43
36:YQ:45:GLN:H	36:YQ:45:GLN:CD	2.22	0.43
38:YS:83:LYS:HZ1	38:YS:109:GLY:HA2	1.83	0.43
41:YV:64:HIS:ND1	41:YV:92:THR:HG22	2.34	0.43
1:QA:1067:A:H4'	1:QA:1068:G:O5'	2.19	0.42
1:QA:224:C:H2'	1:QA:225:C:H6	1.82	0.42
1:QA:440:A:H8	1:QA:440:A:OP2	2.01	0.42
1:QA:664:G:H2'	1:QA:666:G:OP1	2.20	0.42
1:QA:854:G:C2	1:QA:855:G:C8	3.07	0.42
2:QB:21:ARG:HG3	2:QB:38:GLY:O	2.19	0.42
6:QF:62:TRP:CH2	6:QF:64:GLN:HB2	2.54	0.42
7:QG:102:ARG:HG2	7:QG:106:GLN:OE1	2.20	0.42
9:QL:17:VAL:HG11	9:QL:81:ILE:HD13	2.00	0.42
9:QL:95:LYS:HZ1	9:QL:96:LEU:HD13	1.84	0.42
15:QO:25:THR:HG21	15:QO:70:LEU:HB2	2.00	0.42
46:R0:51:VAL:N	46:R0:62:LEU:HD12	2.33	0.42
52:R6:8:LYS:O	52:R6:27:LYS:HA	2.18	0.42
25:RA:1021:A:H3'	25:RA:1021:A:C8	2.54	0.42
25:RA:1152:C:H2'	25:RA:1153:C:H6	1.84	0.42
25:RA:1198:U:H2'	25:RA:1199:U:H6	1.83	0.42
25:RA:1381:G:H1'	25:RA:1571:A:N1	2.34	0.42
25:RA:1506:C:H3'	25:RA:1507:A:H5''	2.01	0.42
25:RA:2027:G:H2'	25:RA:2028:U:O4'	2.19	0.42
25:RA:2688:U:C5	25:RA:2720:U:OP2	2.72	0.42
27:RD:169:GLU:N	27:RD:172:TYR:O	2.51	0.42
29:RF:28:ILE:HG13	29:RF:28:ILE:H	1.68	0.42
31:RH:90:LYS:HE2	31:RH:90:LYS:HB3	1.91	0.42
32:RI:31:LEU:HD11	32:RI:38:LEU:HG	2.00	0.42
32:RI:64:GLU:O	32:RI:67:ARG:NH2	2.51	0.42
36:RQ:78:PRO:O	36:RQ:79:LEU:HB3	2.19	0.42
45:RZ:115:GLY:HA2	45:RZ:175:VAL:O	2.19	0.42
1:XA:1352:C:OP1	21:XU:3:LYS:NZ	2.37	0.42
1:XA:1392:G:N2	1:XA:1502:A:H8	2.16	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:XA:411:A:C6	1:XA:429:U:C4	3.07	0.42
1:XA:652:U:C4	1:XA:752:G:N3	2.87	0.42
1:XA:791:G:H2'	1:XA:792:A:H5'	2.01	0.42
5:XE:131:ILE:HD13	5:XE:131:ILE:HA	1.84	0.42
6:XF:30:LEU:HB3	6:XF:35:ALA:HB3	2.01	0.42
10:XJ:6:ILE:HG22	10:XJ:98:ILE:HG23	2.01	0.42
50:Y4:14:ILE:HG13	50:Y4:31:ILE:HB	1.99	0.42
25:YA:2068:U:N3	25:YA:2430:A:H2	2.15	0.42
25:YA:2716:U:O2'	25:YA:2717:G:H5'	2.18	0.42
25:YA:2850:A:C2	25:YA:2851:A:C4	3.06	0.42
25:YA:476:G:H4'	25:YA:502:A:N1	2.34	0.42
28:YE:111:ARG:HD2	28:YE:160:TYR:CE1	2.54	0.42
35:YP:125:VAL:CG1	35:YP:138:LEU:HD21	2.49	0.42
1:XA:345:C:OP2	39:YT:41:ARG:HD2	2.19	0.42
25:YA:1335:U:OP2	43:YX:65:ARG:NH2	2.51	0.42
45:YZ:6:LYS:HB2	45:YZ:6:LYS:HE3	1.88	0.42
1:QA:1226:C:H4'	19:QS:80:TYR:CZ	2.54	0.42
1:QA:296:U:H2'	1:QA:297:G:C8	2.55	0.42
1:QA:539:A:H2'	1:QA:540:G:H8	1.84	0.42
1:QA:56:U:H2'	1:QA:57:G:C8	2.55	0.42
2:QB:44:LEU:HD12	2:QB:44:LEU:H	1.83	0.42
4:QD:108:LEU:HD21	4:QD:183:GLY:HA3	2.01	0.42
8:QH:105:ARG:HD3	8:QH:105:ARG:HA	1.78	0.42
1:QA:942:G:N2	9:QI:124:GLN:OE1	2.47	0.42
1:QA:35:G:N3	12:QL:118:SER:OG	2.52	0.42
12:QL:85:ILE:HD12	12:QL:85:ILE:HA	1.75	0.42
14:QN:47:LEU:HA	14:QN:47:LEU:HD23	1.74	0.42
17:QQ:29:HIS:CG	17:QQ:30:PRO:HD2	2.54	0.42
22:QV:19:G:H4'	22:QV:20:U:OP2	2.19	0.42
22:QV:0:C:O2'	46:R0:6:GLY:O	2.32	0.42
25:RA:1510:A:H2'	25:RA:1510:A:N3	2.33	0.42
25:RA:1843:C:H2'	25:RA:1844:C:C6	2.55	0.42
25:RA:2247:A:H2'	25:RA:2248:C:C6	2.54	0.42
25:RA:286:C:H2'	25:RA:287:C:H6	1.84	0.42
30:RG:97:ASP:HA	30:RG:100:TRP:HD1	1.84	0.42
33:RN:96:GLU:HB2	33:RN:122:VAL:HG12	2.00	0.42
33:RN:30:ILE:HG23	33:RN:52:VAL:HG11	1.99	0.42
25:RA:1278:A:OP1	37:RR:36:THR:HG22	2.18	0.42
1:XA:1095:U:OP1	1:XA:1108:G:N2	2.49	0.42
1:XA:436:C:H2'	1:XA:437:U:O4'	2.19	0.42
2:XB:68:ILE:HB	2:XB:70:PHE:HE1	1.84	0.42
4:XD:112:VAL:N	4:XD:116:GLN:OE1	2.38	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:XH:104:ARG:HD2	8:XH:138:TRP:CD2	2.53	0.42
1:XA:255:G:H1'	17:XQ:16:GLN:OE1	2.19	0.42
25:YA:1385:G:H4'	25:YA:1386:C:OP1	2.19	0.42
26:YB:80:U:H2'	26:YB:81:G:H21	1.83	0.42
25:YA:2683:C:H4'	28:YE:13:ARG:NH2	2.34	0.42
28:YE:201:THR:HG22	28:YE:203:LYS:N	2.34	0.42
30:YG:31:VAL:HA	30:YG:32:PRO:HD3	1.83	0.42
31:YH:126:PRO:HB2	31:YH:127:GLU:H	1.58	0.42
25:YA:2749:A:H4'	31:YH:62:LYS:HB3	2.00	0.42
33:YN:134:ARG:H	33:YN:135:PRO:HD3	1.83	0.42
39:YT:80:SER:HA	39:YT:81:PRO:HD3	1.89	0.42
45:YZ:157:LEU:HD22	45:YZ:161:VAL:HB	2.01	0.42
45:YZ:8:TYR:HA	45:YZ:62:PRO:HD3	2.00	0.42
1:QA:1213:A:N1	1:QA:1215:G:H1'	2.34	0.42
1:QA:384:G:H2'	1:QA:385:C:C6	2.55	0.42
1:QA:929:G:C6	1:QA:930:C:C4	3.08	0.42
9:QI:48:GLU:N	9:QI:49:PRO:HD2	2.35	0.42
17:QQ:10:VAL:HG13	17:QQ:19:VAL:HB	2.01	0.42
19:QS:41:VAL:HG12	19:QS:44:MET:HB2	2.02	0.42
20:QT:87:LYS:HD2	20:QT:87:LYS:HA	1.68	0.42
52:R6:35:GLU:HG2	52:R6:35:GLU:H	1.72	0.42
25:RA:1728:G:N1	25:RA:1730:U:OP2	2.53	0.42
25:RA:2296:U:OP2	38:RS:6:ALA:HB2	2.20	0.42
25:RA:705:A:H2'	25:RA:706:A:O4'	2.19	0.42
26:RB:104:A:H2'	26:RB:105:G:O4'	2.19	0.42
27:RD:245:PRO:HA	27:RD:246:PRO:HD3	1.95	0.42
27:RD:72:LYS:NZ	27:RD:99:ASP:OD1	2.43	0.42
32:RI:68:LEU:HA	32:RI:71:ILE:HG22	2.00	0.42
40:RU:75:ASN:HB2	40:RU:78:THR:H	1.84	0.42
41:RV:64:HIS:CG	41:RV:92:THR:HG22	2.52	0.42
1:XA:254:G:O2'	17:XQ:15:MET:HB3	2.19	0.42
1:XA:530:G:H4'	1:XA:531:U:OP2	2.20	0.42
1:XA:742:G:OP2	15:XO:35:ARG:NH2	2.44	0.42
5:XE:79:GLU:H	5:XE:79:GLU:HG3	1.45	0.42
7:XG:38:LEU:O	7:XG:38:LEU:HD12	2.20	0.42
12:XL:44:THR:HA	12:XL:45:PRO:HD3	1.69	0.42
13:XM:7:VAL:O	13:XM:9:ILE:HG23	2.19	0.42
1:XA:280:C:O2	17:XQ:38:ARG:HG3	2.19	0.42
18:XR:56:THR:HB	18:XR:58:LEU:HD12	2.02	0.42
47:Y1:58:ILE:HG23	47:Y1:87:PRO:HG3	2.02	0.42
49:Y3:4:LEU:HD22	49:Y3:56:VAL:HG12	2.01	0.42
50:Y4:60:GLN:O	50:Y4:63:TYR:HB3	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
53:Y7:25:PRO:HA	53:Y7:28:ARG:CZ	2.49	0.42
25:YA:1301:A:H2'	25:YA:1301:A:N3	2.35	0.42
25:YA:1416:G:H2'	25:YA:1417:C:C6	2.54	0.42
31:YH:159:GLU:O	31:YH:160:LYS:HG2	2.19	0.42
39:YT:45:PHE:CE1	39:YT:65:LYS:HE3	2.55	0.42
42:YW:86:LEU:HD22	42:YW:96:ILE:HD12	2.01	0.42
1:QA:1068:G:N3	1:QA:1191:A:H2	2.16	0.42
1:QA:1221:G:OP1	1:QA:1320:C:N4	2.52	0.42
1:QA:1478:C:H2'	1:QA:1479:C:H6	1.84	0.42
1:QA:151:A:H2'	1:QA:152:A:O4'	2.19	0.42
1:QA:540:G:H2'	1:QA:541:G:O4'	2.19	0.42
1:QA:583:A:H2'	1:QA:584:G:O4'	2.19	0.42
3:QC:112:SER:O	3:QC:116:VAL:HG23	2.20	0.42
3:QC:148:GLY:HA3	3:QC:172:ARG:O	2.19	0.42
4:QD:192:GLU:HG3	4:QD:192:GLU:H	1.56	0.42
5:QE:79:GLU:HB3	5:QE:92:LYS:HA	2.02	0.42
13:QM:4:ILE:H	13:QM:9:ILE:HG22	1.84	0.42
19:QS:10:PHE:CG	19:QS:11:VAL:N	2.88	0.42
51:R5:56:LYS:HB3	51:R5:56:LYS:HE3	1.79	0.42
52:R6:11:LEU:HD13	52:R6:11:LEU:HA	1.81	0.42
52:R6:17:LYS:HB3	52:R6:44:ARG:NH2	2.30	0.42
25:RA:1174:A:N3	25:RA:1174:A:H2'	2.33	0.42
25:RA:1260:G:C6	25:RA:1261:C:C4	3.08	0.42
25:RA:1872:A:H5'	25:RA:1878:G:OP2	2.20	0.42
25:RA:2359:C:H2'	25:RA:2360:A:O4'	2.19	0.42
25:RA:676:A:H1'	25:RA:2443:C:H1'	2.01	0.42
25:RA:815:C:H2'	25:RA:816:C:H6	1.84	0.42
27:RD:96:HIS:NE2	27:RD:102:LYS:HE2	2.34	0.42
31:RH:153:LYS:HD2	31:RH:153:LYS:N	2.33	0.42
25:RA:2378:A:OP1	38:RS:111:GLU:HG2	2.19	0.42
45:RZ:169:GLU:O	45:RZ:171:ILE:HG23	2.19	0.42
1:XA:313:A:H2'	1:XA:314:C:C6	2.54	0.42
7:XG:89:MET:CE	7:XG:156:TRP:H	2.32	0.42
46:Y0:53:MET:CB	46:Y0:59:LEU:HD23	2.50	0.42
52:Y6:15:GLU:HG2	52:Y6:49:HIS:NE2	2.34	0.42
54:Y8:52:LYS:N	54:Y8:53:PRO:HD2	2.33	0.42
25:YA:1025:G:C4	25:YA:1135:C:H1'	2.53	0.42
25:YA:1914:C:H2'	25:YA:1915:U:O4'	2.19	0.42
25:YA:2275:C:C6	25:YA:2275:C:H5'	2.55	0.42
25:YA:2524:G:H2'	25:YA:2741:A:H2	1.84	0.42
27:YD:36:PRO:CB	27:YD:61:LEU:HB3	2.50	0.42
27:YD:35:LYS:HE3	27:YD:64:ILE:N	2.35	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:2729:G:H1'	28:YE:187:ALA:HB2	2.00	0.42
28:YE:57:LYS:HD2	28:YE:57:LYS:HA	1.87	0.42
30:YG:103:LEU:HD23	30:YG:103:LEU:HA	1.83	0.42
30:YG:16:ARG:N	30:YG:17:PRO:HD2	2.34	0.42
31:YH:126:PRO:HG2	31:YH:128:PRO:HA	2.00	0.42
31:YH:153:LYS:HB3	31:YH:154:PRO:CD	2.49	0.42
33:YN:96:GLU:HG2	33:YN:97:ARG:H	1.84	0.42
35:YP:39:LYS:HG3	35:YP:45:LEU:CD2	2.45	0.42
36:YQ:76:LYS:HG3	36:YQ:77:LYS:N	2.35	0.42
36:YQ:39:PRO:HA	36:YQ:97:VAL:O	2.20	0.42
38:YS:60:GLY:O	38:YS:61:ASN:HB3	2.17	0.42
39:YT:58:ASN:C	39:YT:58:ASN:HD22	2.23	0.42
1:QA:1131:G:H2'	1:QA:1132:C:H6	1.83	0.42
1:QA:134:A:H61	16:QP:25:ARG:NH1	2.17	0.42
1:QA:280:C:H3'	1:QA:281:G:H5'	2.00	0.42
1:QA:369:C:OP2	1:QA:388:G:N1	2.50	0.42
1:QA:701:C:H1'	1:QA:703:G:C6	2.54	0.42
1:QA:791:G:C2'	1:QA:792:A:H5'	2.50	0.42
2:QB:69:LEU:O	2:QB:162:ILE:HA	2.19	0.42
3:QC:59:ARG:HH12	3:QC:97:LYS:HE3	1.84	0.42
6:QF:22:GLU:O	6:QF:26:ILE:HG13	2.19	0.42
14:QN:41:ARG:NH2	14:QN:42:ILE:HD11	2.35	0.42
22:QV:39:C:H2'	22:QV:40:C:C6	2.54	0.42
48:R2:70:GLN:O	48:R2:71:ASN:HB2	2.19	0.42
42:RW:34:ASN:ND2	51:R5:39:MET:HG3	2.34	0.42
54:R8:4:MET:SD	54:R8:61:LEU:HD12	2.60	0.42
54:R8:59:LYS:NZ	54:R8:59:LYS:HB2	2.35	0.42
25:RA:1021:A:H3'	25:RA:1021:A:H8	1.84	0.42
25:RA:1419:A:H2'	25:RA:1421:G:N7	2.34	0.42
25:RA:205:G:O2'	25:RA:206:U:OP2	2.38	0.42
25:RA:2298:A:C2	25:RA:2299:G:H1'	2.53	0.42
25:RA:652:C:N4	25:RA:653:A:N1	2.68	0.42
26:RB:13:A:O2'	26:RB:15:A:O5'	2.37	0.42
27:RD:123:ALA:HA	27:RD:124:PRO:HD2	1.77	0.42
28:RE:9:VAL:HG23	28:RE:26:ILE:HA	2.00	0.42
30:RG:159:VAL:HG21	30:RG:173:LEU:HD11	2.00	0.42
31:RH:6:ARG:HG3	31:RH:7:LEU:HG	2.01	0.42
1:XA:1108:G:H5'	3:XC:176:HIS:ND1	2.34	0.42
1:XA:1233:G:H2'	1:XA:1234:C:H6	1.84	0.42
1:XA:1250:A:N1	1:XA:1353:G:N2	2.64	0.42
1:XA:1453:G:H8	20:XT:39:LYS:CE	2.31	0.42
1:XA:1112:C:N3	3:XC:178:LEU:HB2	2.35	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:XD:120:LEU:HD23	4:XD:120:LEU:HA	1.89	0.42
9:XI:32:ASP:OD1	9:XI:33:PHE:N	2.53	0.42
18:XR:43:PHE:CE2	18:XR:58:LEU:HD11	2.54	0.42
20:XT:50:GLU:HG3	20:XT:51:GLU:N	2.33	0.42
49:Y3:8:LEU:HB3	49:Y3:31:LEU:HA	2.01	0.42
25:YA:2281:C:O2'	25:YA:2282:G:H5'	2.20	0.42
25:YA:263:C:H2'	25:YA:264:C:O4'	2.18	0.42
25:YA:2649:U:H2'	25:YA:2650:U:C6	2.55	0.42
27:YD:25:THR:HG22	27:YD:82:ILE:H	1.84	0.42
25:YA:1823:G:P	27:YD:54:ARG:HH21	2.39	0.42
29:YF:45:ARG:HH11	29:YF:45:ARG:CG	2.33	0.42
30:YG:64:THR:CG2	30:YG:66:GLN:H	2.28	0.42
35:YP:1:MET:HB3	35:YP:2:LYS:H	1.61	0.42
38:YS:81:GLY:O	38:YS:83:LYS:N	2.53	0.42
25:RA:2585:U:C5	56:Z6:76:PPU:O2'	2.70	0.42
1:QA:97:U:H2'	1:QA:99:C:C6	2.55	0.42
1:QA:1104:G:O5'	2:QB:111:ARG:HD2	2.20	0.42
2:QB:92:TYR:CD1	2:QB:151:GLY:HA3	2.55	0.42
4:QD:63:LYS:HE3	4:QD:63:LYS:HB2	1.77	0.42
7:QG:70:LYS:HA	7:QG:71:PRO:HD2	1.89	0.42
15:QO:43:LEU:HD23	15:QO:43:LEU:HA	1.74	0.42
15:QO:87:ILE:HG22	15:QO:88:ARG:N	2.35	0.42
1:QA:332:G:OP2	20:QT:10:LEU:HD23	2.19	0.42
52:R6:45:LYS:HD3	52:R6:45:LYS:HA	1.75	0.42
25:RA:2014:A:H2'	25:RA:2015:A:C8	2.54	0.42
25:RA:830:G:N2	25:RA:2445:G:O2'	2.53	0.42
25:RA:253:C:H2'	25:RA:254:G:O4'	2.20	0.42
25:RA:35:G:H2'	25:RA:36:G:O4'	2.19	0.42
25:RA:524:U:H2'	25:RA:525:U:C6	2.55	0.42
25:RA:607:U:N3	25:RA:621:A:C2	2.79	0.42
29:RF:182:ASN:O	29:RF:186:ILE:HG12	2.20	0.42
37:RR:63:ARG:HA	37:RR:80:PHE:CZ	2.54	0.42
38:RS:39:ILE:HD11	38:RS:73:LEU:HD11	2.00	0.42
40:RU:83:LEU:HD12	40:RU:113:ALA:HB2	2.01	0.42
1:XA:1347:G:O2'	1:XA:1348:U:P	2.77	0.42
1:XA:16:A:N1	1:XA:919:A:H2	2.18	0.42
1:XA:376:G:H5''	16:XP:5:ARG:HD2	2.01	0.42
1:XA:560:U:O2'	1:XA:561:U:OP2	2.30	0.42
1:XA:918:A:H2'	1:XA:919:A:C8	2.55	0.42
1:XA:950:U:H2'	1:XA:951:G:C8	2.55	0.42
1:XA:963:G:N2	1:XA:972:C:C2	2.83	0.42
2:XB:113:HIS:O	2:XB:116:GLU:HB2	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:XB:7:VAL:HG11	2:XB:217:ARG:CZ	2.49	0.42
3:XC:85:ARG:HD2	3:XC:85:ARG:HA	1.83	0.42
6:XF:95:GLU:HA	6:XF:96:PRO:HD3	1.87	0.42
9:XI:91:ASP:C	9:XI:93:ARG:H	2.21	0.42
1:XA:501:C:P	12:XL:117:ARG:HH22	2.42	0.42
13:XM:121:LYS:HA	13:XM:121:LYS:HD3	1.90	0.42
46:Y0:27:GLU:HB2	46:Y0:69:PHE:CD1	2.53	0.42
48:Y2:8:LYS:HB2	48:Y2:8:LYS:HE3	1.83	0.42
25:YA:1221:C:H2'	25:YA:1222:C:C6	2.55	0.42
27:YD:25:THR:HG21	27:YD:81:ALA:HA	2.02	0.42
32:YI:67:ARG:NH2	32:YI:68:LEU:HB2	2.33	0.42
33:YN:46:VAL:HG13	33:YN:48:MET:HG3	2.02	0.42
34:YO:21:CYS:O	34:YO:22:ILE:HD13	2.20	0.42
38:YS:106:ARG:HA	38:YS:110:LEU:CD2	2.47	0.42
1:QA:1034:G:N2	1:QA:1035:A:C6	2.88	0.42
1:QA:1120:G:H2'	1:QA:1121:U:C6	2.54	0.42
1:QA:298:A:H2'	1:QA:299:G:O4'	2.19	0.42
1:QA:313:A:H2'	1:QA:314:C:C6	2.55	0.42
1:QA:727:G:N1	1:QA:731:G:C6	2.88	0.42
2:QB:60:ASP:O	2:QB:64:ARG:HG2	2.19	0.42
11:QK:41:THR:HG22	11:QK:42:TRP:N	2.34	0.42
11:QK:48:ILE:HG23	11:QK:63:LEU:HD22	2.01	0.42
15:QO:2:PRO:HB2	15:QO:3:ILE:H	1.56	0.42
50:R4:14:ILE:HG22	50:R4:24:THR:HG22	2.01	0.42
25:RA:1005:C:C2	25:RA:1143:A:C5	3.08	0.42
25:RA:150:C:H2'	25:RA:151:C:H6	1.85	0.42
25:RA:1931:U:H5	25:RA:1969:A:N7	2.17	0.42
25:RA:2102:U:H2'	25:RA:2103:C:C6	2.54	0.42
25:RA:270(R):G:OP1	32:RI:42:SER:OG	2.35	0.42
25:RA:2729:G:H2'	25:RA:2730:C:C6	2.55	0.42
27:RD:33:LEU:HB3	27:RD:34:VAL:H	1.64	0.42
28:RE:34:VAL:HG23	28:RE:64:LYS:HZ2	1.84	0.42
28:RE:78:LEU:HG	28:RE:79:ARG:NE	2.35	0.42
30:RG:151:ALA:HB3	30:RG:153:ARG:NH1	2.35	0.42
30:RG:173:LEU:O	30:RG:178:PHE:HB2	2.20	0.42
31:RH:164:TYR:O	31:RH:166:GLY:N	2.52	0.42
31:RH:16:SER:OG	31:RH:26:VAL:O	2.30	0.42
32:RI:113:ARG:HG3	32:RI:131:LYS:HZ3	1.83	0.42
33:RN:35:ARG:HB2	33:RN:42:TRP:CZ3	2.54	0.42
38:RS:14:VAL:HG11	38:RS:90:GLY:O	2.19	0.42
39:RT:26:ASP:HB3	39:RT:92:GLY:N	2.18	0.42
43:RX:44:GLU:O	43:RX:48:LYS:N	2.52	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
44:RY:50:ARG:H	44:RY:50:ARG:HG2	1.67	0.42
45:RZ:103:ARG:HD3	45:RZ:136:PHE:CG	2.54	0.42
1:XA:1148:U:H2'	1:XA:1149:C:O4'	2.19	0.42
1:XA:1206:G:C6	1:XA:1207:G:C5	3.07	0.42
1:XA:1223:C:P	19:XS:78:ARG:NH1	2.92	0.42
1:XA:1302:U:O2	1:XA:1302:U:H2'	2.19	0.42
1:XA:1431:C:H2'	1:XA:1432:G:O4'	2.20	0.42
1:XA:123:C:OP1	1:XA:312:C:H5'	2.19	0.42
1:XA:431:A:H2'	1:XA:432:A:O4'	2.20	0.42
1:XA:735:C:H2'	1:XA:736:C:H6	1.83	0.42
1:XA:942:G:C2	1:XA:1342:C:C2	3.07	0.42
2:XB:19:HIS:CE1	2:XB:206:ASP:HB2	2.54	0.42
3:XC:91:LEU:O	3:XC:95:THR:OG1	2.19	0.42
8:XH:121:ASP:N	8:XH:121:ASP:OD1	2.46	0.42
1:XA:963:G:N2	10:XJ:55:LYS:HE2	2.34	0.42
13:XM:40:ASN:ND2	13:XM:43:THR:HG23	2.34	0.42
1:XA:1296:C:OP1	13:XM:44:ARG:NH2	2.53	0.42
46:Y0:41:ARG:HA	46:Y0:41:ARG:NE	2.33	0.42
52:Y6:14:THR:HG21	52:Y6:19:ARG:HH21	1.85	0.42
25:YA:2370:G:H21	52:Y6:45:LYS:CE	2.33	0.42
54:Y8:60:LEU:C	54:Y8:63:PRO:HD2	2.40	0.42
25:YA:1188:U:O2'	25:YA:1189:A:H5'	2.20	0.42
25:YA:1250:G:OP2	35:YP:21:ARG:HD3	2.20	0.42
25:YA:582:G:H2'	25:YA:583:G:C8	2.55	0.42
25:YA:1792:G:P	27:YD:206:LEU:HB2	2.60	0.42
33:YN:137:LYS:HD2	33:YN:137:LYS:HA	1.77	0.42
35:YP:36:LYS:HB3	35:YP:40:SER:CB	2.49	0.42
38:YS:83:LYS:NZ	38:YS:109:GLY:HA2	2.33	0.42
39:YT:26:ASP:HB2	39:YT:91:ARG:HA	2.00	0.42
40:YU:109:LEU:HD23	40:YU:109:LEU:HA	1.89	0.42
41:YV:65:GLY:O	41:YV:90:PRO:HA	2.20	0.42
1:QA:1367:C:H5'	10:QJ:60:ARG:NH2	2.35	0.42
1:QA:175:C:H2'	1:QA:176:C:C6	2.55	0.42
1:QA:7:G:H21	5:QE:121:LYS:HG2	1.85	0.42
2:QB:130:ARG:HA	2:QB:131:PRO:HD3	1.81	0.42
2:QB:27:LYS:HD2	2:QB:193:ASP:CB	2.46	0.42
4:QD:11:LEU:HD22	4:QD:66:ARG:HD3	2.02	0.42
7:QG:13:GLN:O	7:QG:24:THR:HG21	2.20	0.42
51:R5:56:LYS:H	51:R5:56:LYS:CD	2.31	0.42
52:R6:28:ARG:HB3	52:R6:30:THR:H	1.84	0.42
25:RA:1157:G:C6	25:RA:1158:C:C4	3.08	0.42
25:RA:1417:C:H2'	25:RA:1418:G:O4'	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:2032:G:H21	28:RE:146:THR:CG2	2.32	0.42
25:RA:2506:U:O2	25:RA:2506:U:H2'	2.20	0.42
25:RA:646:A:H2'	25:RA:647:G:O4'	2.19	0.42
25:RA:817:C:O2'	25:RA:839:U:H5''	2.19	0.42
25:RA:861:A:C2	25:RA:917:A:C5	3.08	0.42
29:RF:78:ILE:H	29:RF:78:ILE:HG13	1.66	0.42
29:RF:93:LYS:HB3	29:RF:94:PRO:HD2	2.01	0.42
30:RG:116:ASP:OD1	30:RG:116:ASP:N	2.53	0.42
33:RN:10:GLU:HA	33:RN:11:PRO:HD3	1.65	0.42
25:RA:831:G:N2	35:RP:53:GLY:O	2.53	0.42
42:RW:75:TYR:CZ	42:RW:104:THR:HG21	2.54	0.42
45:RZ:94:GLU:HB2	45:RZ:130:PRO:CD	2.42	0.42
1:XA:1084:G:C5	1:XA:1085:U:C4	3.08	0.42
1:XA:1410:G:H2'	1:XA:1411:C:H6	1.85	0.42
1:XA:1492:A:OP1	12:XL:47:LYS:N	2.53	0.42
1:XA:1497:G:H2'	1:XA:1498:U:H5'	2.02	0.42
1:XA:102:G:O2'	1:XA:151:A:N3	2.45	0.42
1:XA:187:C:H2'	1:XA:188:U:O4'	2.20	0.42
1:XA:654:G:H2'	1:XA:655:A:O4'	2.20	0.42
2:XB:223:ILE:HA	2:XB:226:ARG:HB3	2.02	0.42
3:XC:32:LEU:HD22	3:XC:59:ARG:NH1	2.34	0.42
7:XG:15:ASP:O	7:XG:19:GLY:HA2	2.20	0.42
9:XI:125:TYR:HD2	9:XI:126:SER:H	1.68	0.42
19:XS:78:ARG:H	19:XS:78:ARG:HG2	1.56	0.42
25:YA:76:C:H1'	48:Y2:62:THR:HG21	2.00	0.42
50:Y4:68:ARG:HB2	50:Y4:69:LYS:H	1.51	0.42
25:YA:1190:G:H5'	35:YP:32:THR:HA	2.01	0.42
25:YA:1859:A:N6	25:YA:1883:G:O2'	2.52	0.42
25:YA:2688:U:C5	25:YA:2720:U:OP2	2.72	0.42
25:YA:2784:C:O2'	28:YE:37:ARG:NH1	2.52	0.42
25:YA:565:C:H2'	25:YA:566:U:O4'	2.19	0.42
27:YD:89:SER:O	27:YD:198:ASN:ND2	2.52	0.42
38:YS:38:GLN:HG3	38:YS:47:THR:HG21	2.02	0.42
43:YX:84:ALA:HB1	43:YX:85:PRO:HD2	2.02	0.42
1:QA:1267:C:C5	1:QA:1268:A:C5	3.08	0.42
1:QA:224:C:H2'	1:QA:225:C:C6	2.55	0.42
1:QA:440:A:C6	1:QA:494:U:C2	3.08	0.42
2:QB:88:ALA:HB2	2:QB:219:VAL:HG13	2.02	0.42
2:QB:230:VAL:HB	2:QB:231:GLU:H	1.60	0.42
3:QC:36:ASP:HA	3:QC:39:ILE:HD12	2.02	0.42
4:QD:165:MET:SD	4:QD:168:ARG:HD2	2.60	0.42
8:QH:54:ASP:O	8:QH:56:LYS:HG3	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:QR:53:ARG:HE	18:QR:59:SER:C	2.22	0.42
47:R1:90:ILE:O	47:R1:94:LEU:HB2	2.20	0.42
25:RA:1043:C:HO2'	25:RA:1048:A:HO2'	1.63	0.42
25:RA:1512:G:C2	25:RA:1513:C:C2	3.08	0.42
25:RA:1659:U:C4	25:RA:1660:C:C5	3.07	0.42
25:RA:196:A:H2'	25:RA:196:A:N3	2.35	0.42
25:RA:2308:G:N1	25:RA:2311:A:C2	2.85	0.42
25:RA:2729:G:H1'	28:RE:187:ALA:HB2	2.01	0.42
25:RA:508:G:O2'	25:RA:509:C:P	2.78	0.42
28:RE:188:VAL:HG23	28:RE:189:PRO:HD2	2.01	0.42
29:RF:181:LEU:HD22	29:RF:181:LEU:HA	1.79	0.42
35:RP:20:GLY:HA2	35:RP:27:HIS:O	2.19	0.42
25:RA:2415:G:C5'	35:RP:67:MET:H	2.33	0.42
39:RT:51:ARG:HG3	39:RT:98:LYS:HG3	2.02	0.42
44:RY:39:VAL:HB	44:RY:40:GLU:H	1.57	0.42
1:XA:1002:G:H1	1:XA:1038:C:N4	2.07	0.42
1:XA:1127:G:N1	1:XA:1145:C:C2	2.87	0.42
1:XA:1233:G:C4	1:XA:1234:C:C5	3.08	0.42
1:XA:1442:G:C5	1:XA:1446:A:C6	3.08	0.42
1:XA:284:G:H2'	1:XA:285:G:C8	2.55	0.42
1:XA:401:C:H2'	1:XA:402:G:C8	2.54	0.42
9:XI:4:TYR:CE1	9:XI:88:TYR:HB2	2.55	0.42
11:XK:109:VAL:HG11	18:XR:84:LYS:HD3	2.02	0.42
20:XT:39:LYS:H	20:XT:39:LYS:HG3	1.63	0.42
50:Y4:16:CYS:SG	50:Y4:36:CYS:HB3	2.59	0.42
50:Y4:39:CYS:O	50:Y4:40:HIS:HB2	2.20	0.42
54:Y8:44:LYS:N	54:Y8:44:LYS:HD2	2.34	0.42
25:YA:1374:G:H2'	25:YA:1375:C:O4'	2.20	0.42
25:YA:141:A:H8	25:YA:1408:C:H1'	1.85	0.42
25:YA:1499:C:H2'	25:YA:1500:G:H8	1.84	0.42
25:YA:1510:A:O2'	25:YA:1511:A:N7	2.47	0.42
25:YA:70:G:H21	25:YA:71:A:N6	2.17	0.42
27:YD:34:VAL:HG22	27:YD:35:LYS:HG3	2.00	0.42
31:YH:30:LYS:HE2	31:YH:81:GLU:H	1.85	0.42
32:YI:133:HIS:HB2	32:YI:134:PRO:CD	2.50	0.42
32:YI:37:VAL:HG12	32:YI:38:LEU:H	1.84	0.42
35:YP:29:LYS:HD2	35:YP:30:THR:CG2	2.50	0.42
43:YX:26:TYR:HB3	43:YX:92:LEU:HD12	2.02	0.42
45:YZ:150:LEU:HD22	45:YZ:171:ILE:HB	2.02	0.42
1:QA:1068:G:N3	1:QA:1191:A:C2	2.88	0.42
1:QA:1206:G:C6	1:QA:1207:G:C5	3.08	0.42
1:QA:1226:C:H4'	19:QS:80:TYR:OH	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:QA:1238:A:H62	1:QA:1299:A:H61	1.68	0.42
1:QA:925:G:N2	1:QA:1503:A:OP1	2.53	0.42
3:QC:56:ASP:O	3:QC:66:VAL:HA	2.20	0.42
4:QD:171:GLY:HA2	4:QD:172:PRO:HD3	1.87	0.42
8:QH:51:VAL:HG21	8:QH:60:ARG:HG2	2.02	0.42
8:QH:59:LEU:O	8:QH:61:VAL:HG23	2.20	0.42
10:QJ:81:THR:C	10:QJ:83:GLU:H	2.23	0.42
14:QN:23:ARG:NH1	14:QN:30:ALA:HB2	2.35	0.42
22:QV:64:G:H2'	22:QV:65:C:C6	2.55	0.42
30:RG:6:ALA:N	50:R4:23:GLU:HG2	2.31	0.42
50:R4:55:ARG:O	50:R4:59:PHE:HB3	2.20	0.42
25:RA:1178:C:HO2'	25:RA:1179:C:P	2.43	0.42
25:RA:1766:U:H2'	25:RA:1767:C:H6	1.84	0.42
25:RA:829:A:N7	25:RA:2248:C:H5'	2.34	0.42
25:RA:2562:U:O2'	34:RO:23:ARG:NH1	2.40	0.42
25:RA:389:G:H22	35:RP:72:PRO:CD	2.32	0.42
25:RA:521:G:H2'	25:RA:522:G:C8	2.55	0.42
25:RA:898:C:C2'	25:RA:899:A:H5'	2.48	0.42
25:RA:847:U:C5	25:RA:933:A:N1	2.88	0.42
27:RD:35:LYS:HB3	27:RD:36:PRO:HA	2.01	0.42
29:RF:184:TYR:O	29:RF:188:ARG:HG3	2.19	0.42
31:RH:125:VAL:HA	31:RH:126:PRO:HA	1.90	0.42
35:RP:100:LEU:HD22	35:RP:100:LEU:HA	1.77	0.42
38:RS:108:GLY:O	38:RS:110:LEU:HG	2.20	0.42
1:XA:1170:A:H2'	1:XA:1171:G:O4'	2.20	0.42
1:XA:1241:G:H2'	1:XA:1242:C:H6	1.85	0.42
1:XA:9:G:C6	1:XA:26:A:N6	2.88	0.42
1:XA:345:C:H1'	1:XA:346:G:OP2	2.19	0.42
13:XM:3:ARG:HG3	13:XM:9:ILE:HG21	2.02	0.42
13:XM:16:ASP:HB3	13:XM:41:PRO:HB3	2.01	0.42
22:XV:16:C:H2'	22:XV:16:C:O2	2.19	0.42
46:Y0:53:MET:HB3	46:Y0:59:LEU:HD23	2.01	0.42
50:Y4:37:SER:HB3	50:Y4:42:PHE:HB3	2.00	0.42
51:Y5:31:VAL:HG13	51:Y5:42:PRO:HG3	2.01	0.42
51:Y5:56:LYS:CD	51:Y5:56:LYS:H	2.29	0.42
54:Y8:26:LYS:HB3	54:Y8:44:LYS:HG3	2.01	0.42
25:YA:142:G:H1'	43:YX:37:THR:CG2	2.45	0.42
25:YA:2712:U:OP1	25:YA:2714:G:H4'	2.20	0.42
25:YA:2845:G:H2'	25:YA:2846:G:C8	2.55	0.42
25:YA:415:A:H2'	25:YA:416:C:C6	2.55	0.42
25:YA:67:U:N3	25:YA:74:A:H2	1.95	0.42
27:YD:221:VAL:HG22	27:YD:226:MET:CE	2.49	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:YE:167:VAL:HG21	28:YE:187:ALA:HB1	2.01	0.42
30:YG:86:MET:HA	30:YG:87:PRO:HD2	1.95	0.42
35:YP:82:GLY:HA3	35:YP:115:LEU:HD21	2.01	0.42
38:YS:30:ARG:NH2	38:YS:92:TYR:CD1	2.87	0.42
44:YY:51:VAL:HG23	44:YY:57:GLN:N	2.35	0.42
44:YY:96:ILE:HG13	44:YY:98:VAL:H	1.85	0.42
45:YZ:1:MET:HG2	45:YZ:2:GLU:H	1.85	0.42
1:QA:186(D):C:H2'	1:QA:186(E):C:C6	2.55	0.41
1:QA:381:C:H2'	1:QA:382:A:O4'	2.20	0.41
1:QA:9:G:C6	1:QA:26:A:N6	2.88	0.41
3:QC:134:ILE:HD11	3:QC:153:VAL:HG21	2.02	0.41
8:QH:54:ASP:N	8:QH:54:ASP:OD1	2.53	0.41
19:QS:50:ALA:HB1	19:QS:57:HIS:HB3	2.02	0.41
47:R1:85:LEU:HA	47:R1:87:PRO:HD2	2.01	0.41
49:R3:35:ARG:HB3	49:R3:37:LEU:HD21	2.01	0.41
49:R3:7:LYS:HA	49:R3:33:GLN:O	2.20	0.41
25:RA:127:A:H5'	25:RA:128:C:C6	2.55	0.41
25:RA:2168:G:N3	25:RA:2168:G:H2'	2.35	0.41
25:RA:2199:A:H3'	25:RA:2205:C:C6	2.55	0.41
25:RA:527:C:H4'	25:RA:528:A:H5'	2.01	0.41
25:RA:646:A:N3	25:RA:646:A:H5'	2.35	0.41
25:RA:868:U:H2'	25:RA:869:G:O4'	2.20	0.41
25:RA:95:G:H4'	48:R2:46:GLN:HB3	2.01	0.41
26:RB:49:C:H2'	26:RB:50:G:C8	2.55	0.41
27:RD:101:GLU:OE1	27:RD:103:ARG:NH1	2.53	0.41
27:RD:43:ARG:HB2	27:RD:54:ARG:HB2	2.02	0.41
29:RF:129:PHE:O	29:RF:130:ALA:HB3	2.20	0.41
30:RG:47:LYS:HD3	30:RG:81:LYS:CB	2.49	0.41
31:RH:105:LEU:HD22	31:RH:113:VAL:HB	2.01	0.41
38:RS:78:LEU:HD23	38:RS:78:LEU:HA	1.86	0.41
40:RU:58:ARG:NH1	40:RU:93:LYS:HE2	2.35	0.41
1:XA:1000:A:O5'	1:XA:1000:A:H8	2.03	0.41
1:XA:1469:G:H2'	1:XA:1470:G:C8	2.55	0.41
1:XA:164:U:H2'	1:XA:165:C:C6	2.54	0.41
1:XA:280:C:H4'	1:XA:281:G:OP2	2.20	0.41
1:XA:539:A:OP2	12:XL:115:LYS:HE3	2.20	0.41
1:XA:818:G:C3'	1:XA:819:A:H5'	2.50	0.41
10:XJ:3:LYS:HB2	10:XJ:75:ILE:O	2.19	0.41
13:XM:20:THR:O	13:XM:22:ILE:N	2.51	0.41
25:YA:1169:G:H1	25:YA:1180:C:H42	1.68	0.41
25:YA:1192:G:C2'	25:YA:1193:G:H5'	2.50	0.41
25:YA:565:C:H4'	25:YA:1253:A:C6	2.55	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:1400:G:H2'	25:YA:1401:G:C8	2.55	0.41
25:YA:1469:A:H2'	25:YA:1470:G:H8	1.84	0.41
25:YA:1709:U:H2'	25:YA:1710:C:C6	2.55	0.41
25:YA:234:C:H2'	25:YA:235:U:H6	1.84	0.41
25:YA:556:G:H2'	25:YA:557:U:C6	2.55	0.41
27:YD:105:ILE:HD12	27:YD:105:ILE:HA	1.55	0.41
27:YD:232:PRO:HB3	27:YD:244:ARG:CZ	2.50	0.41
32:YI:98:ALA:HB2	32:YI:111:PRO:HB3	2.01	0.41
33:YN:35:ARG:HB2	33:YN:42:TRP:CZ3	2.55	0.41
33:YN:59:LYS:HE3	33:YN:61:ARG:HH22	1.85	0.41
25:YA:661:C:H5''	35:YP:15:ARG:HH21	1.85	0.41
36:YQ:85:LYS:O	36:YQ:86:GLY:C	2.58	0.41
38:YS:51:ALA:HB1	38:YS:69:VAL:HG23	2.02	0.41
1:QA:1004:A:H1'	1:QA:1036:G:N2	2.34	0.41
1:QA:1346:A:O2'	1:QA:1347:G:P	2.78	0.41
1:QA:51:A:C6	1:QA:353:A:C2	3.08	0.41
1:QA:940:C:H2'	1:QA:941:G:H8	1.83	0.41
8:QH:38:ILE:HD12	8:QH:118:VAL:HG12	2.02	0.41
8:QH:12:ARG:NH1	8:QH:27:PRO:HD2	2.35	0.41
9:QI:111:ARG:HG2	9:QI:112:LYS:N	2.35	0.41
12:QL:27:LEU:HG	12:QL:62:SER:HB3	2.01	0.41
12:QL:38:THR:HG21	12:QL:65:GLU:OE2	2.19	0.41
13:QM:40:ASN:HA	13:QM:41:PRO:HD3	1.89	0.41
15:QO:31:LEU:O	15:QO:35:ARG:HG3	2.20	0.41
18:QR:56:THR:HB	18:QR:58:LEU:CD1	2.50	0.41
53:R7:47:ARG:HB2	53:R7:48:LYS:H	1.68	0.41
35:RP:63:PRO:HA	54:R8:13:ARG:HB3	2.02	0.41
25:RA:1288:U:C2	25:RA:1327:C:C2	3.08	0.41
25:RA:1931:U:C5	25:RA:1969:A:N7	2.87	0.41
25:RA:2238:G:H2'	25:RA:2238:G:N3	2.35	0.41
25:RA:2320:A:H2'	25:RA:2320:A:N3	2.35	0.41
25:RA:239:U:H2'	25:RA:240:G:O4'	2.20	0.41
25:RA:250:G:H2'	25:RA:251:A:C8	2.55	0.41
25:RA:2851:A:N6	25:RA:2852:G:C6	2.89	0.41
25:RA:649:G:C5	25:RA:650:C:C4	3.08	0.41
25:RA:814:C:H2'	25:RA:815:C:C6	2.55	0.41
28:RE:76:ARG:HD2	28:RE:76:ARG:N	2.35	0.41
29:RF:113:ALA:HB1	29:RF:186:ILE:HG21	2.02	0.41
29:RF:46:ARG:HH11	29:RF:46:ARG:HG2	1.84	0.41
31:RH:4:ILE:HB	31:RH:6:ARG:HG2	2.02	0.41
31:RH:10:PRO:HD2	31:RH:50:VAL:O	2.20	0.41
34:RO:7:TYR:CE1	34:RO:20:MET:HB2	2.55	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
37:RR:109:ALA:HA	37:RR:110:PRO:HD2	1.95	0.41
26:RB:103:U:O2'	45:RZ:72:ARG:HD3	2.20	0.41
1:XA:1194:U:H2'	1:XA:1195:C:C6	2.55	0.41
1:XA:477:G:H2'	1:XA:478:A:C8	2.55	0.41
1:XA:567:G:H2'	1:XA:568:G:O4'	2.19	0.41
4:XD:127:THR:HA	4:XD:132:ARG:HA	2.03	0.41
8:XH:104:ARG:HD2	8:XH:138:TRP:CG	2.56	0.41
9:XI:40:LEU:O	9:XI:42:ARG:N	2.48	0.41
20:XT:53:LEU:HD12	20:XT:100:ILE:HG23	2.02	0.41
46:Y0:36:ILE:HD11	46:Y0:39:ARG:HG2	2.02	0.41
49:Y3:35:ARG:HB3	49:Y3:37:LEU:HD21	2.01	0.41
50:Y4:24:THR:OG1	50:Y4:25:TYR:N	2.53	0.41
25:YA:1089:G:H21	25:YA:1102:C:H42	1.68	0.41
25:YA:1124:C:H2'	25:YA:1125:G:O4'	2.20	0.41
25:YA:2293:C:OP1	38:YS:89:ARG:NH1	2.53	0.41
25:YA:251:A:H8	25:YA:251:A:O5'	2.03	0.41
25:YA:2693:A:H2'	25:YA:2694:G:H8	1.85	0.41
25:YA:2867:G:O2'	25:YA:2868:A:C8	2.72	0.41
25:YA:729:G:H2'	25:YA:1775:U:H1'	2.02	0.41
26:YB:116:G:H4'	38:YS:54:LEU:HD13	2.03	0.41
27:YD:245:PRO:HA	27:YD:246:PRO:HD3	1.87	0.41
28:YE:144:ARG:HB3	28:YE:145:LYS:H	1.45	0.41
28:YE:181:LEU:HA	28:YE:181:LEU:HD13	1.85	0.41
37:YR:2:ARG:HG2	37:YR:5:LYS:NZ	2.35	0.41
37:YR:3:HIS:O	37:YR:5:LYS:N	2.53	0.41
40:YU:30:LYS:HA	40:YU:30:LYS:HD3	1.90	0.41
1:QA:701:C:O2	1:QA:703:G:N1	2.53	0.41
2:QB:208:ILE:HA	2:QB:211:ILE:HD12	2.02	0.41
2:QB:219:VAL:O	2:QB:223:ILE:HG13	2.19	0.41
4:QD:169:LYS:HE2	4:QD:169:LYS:HB3	1.88	0.41
5:QE:127:ASN:HA	5:QE:128:PRO:HD3	1.89	0.41
11:QK:120:ARG:HA	11:QK:121:PRO:HD3	1.87	0.41
14:QN:29:ARG:HG2	14:QN:31:ARG:O	2.20	0.41
14:QN:4:LYS:O	14:QN:7:ILE:HG12	2.20	0.41
16:QP:53:VAL:O	16:QP:57:ARG:HG2	2.21	0.41
20:QT:64:ASP:CG	20:QT:81:LYS:HZ2	2.23	0.41
21:QU:2:GLY:O	21:QU:5:ASP:N	2.47	0.41
54:R8:23:VAL:CG1	54:R8:46:ARG:HD3	2.49	0.41
25:RA:1653:G:H4'	25:RA:1654:A:O5'	2.20	0.41
25:RA:194:G:C2	25:RA:202:U:H1'	2.55	0.41
25:RA:2108:C:H2'	25:RA:2109:U:C6	2.55	0.41
25:RA:2626:C:H2'	25:RA:2627:G:C8	2.55	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:2756:U:H4'	25:RA:2757:A:OP1	2.20	0.41
25:RA:2770:G:H5''	25:RA:2771:C:OP2	2.19	0.41
25:RA:952:G:C6	25:RA:966:G:C6	3.08	0.41
25:RA:1818:U:H2'	27:RD:157:ARG:HG3	2.01	0.41
29:RF:177:ALA:HB1	29:RF:178:PRO:HD2	2.03	0.41
34:RO:73:ASP:OD2	39:RT:32:TYR:OH	2.28	0.41
25:RA:2394:C:OP1	35:RP:63:PRO:HD2	2.20	0.41
36:RQ:18:LYS:HB3	36:RQ:19:GLY:H	1.50	0.41
36:RQ:58:PHE:HD1	36:RQ:61:GLY:HA3	1.85	0.41
43:RX:40:LYS:C	43:RX:42:ALA:H	2.23	0.41
44:RY:88:LYS:HA	44:RY:88:LYS:NZ	2.35	0.41
9:XI:46:ALA:HB2	9:XI:74:ILE:HG23	2.02	0.41
11:XK:88:GLY:C	11:XK:90:GLY:H	2.23	0.41
16:XP:60:LEU:HD23	16:XP:60:LEU:HA	1.80	0.41
16:XP:56:ALA:HB1	16:XP:74:LEU:HD13	2.02	0.41
18:XR:38:GLU:O	18:XR:42:ARG:NH1	2.54	0.41
19:XS:40:ILE:CG1	19:XS:41:VAL:HG13	2.47	0.41
22:XV:5:G:H1	22:XV:67:C:H42	1.67	0.41
47:Y1:76:ARG:H	47:Y1:76:ARG:HD2	1.84	0.41
47:Y1:89:GLU:HA	47:Y1:93:GLU:HB2	2.02	0.41
25:YA:1107:G:H2'	25:YA:1108:U:H6	1.85	0.41
25:YA:2639:A:H1'	25:YA:2778:A:C2	2.56	0.41
25:YA:385:C:O2	35:YP:71:VAL:HG21	2.20	0.41
25:YA:630:G:OP2	54:Y8:15:LYS:NZ	2.53	0.41
25:YA:685:A:H1'	25:YA:688:U:O4	2.20	0.41
26:YB:2:C:H2'	26:YB:3:C:C6	2.55	0.41
29:YF:117:ARG:HD2	29:YF:120:GLU:OE2	2.20	0.41
30:YG:165:THR:OG1	30:YG:168:GLU:HG3	2.21	0.41
33:YN:18:ALA:HB3	33:YN:55:VAL:O	2.19	0.41
33:YN:65:LYS:O	33:YN:69:GLN:HG2	2.19	0.41
33:YN:7:LYS:H	33:YN:7:LYS:HD2	1.84	0.41
36:YQ:54:MET:HB3	36:YQ:64:ILE:HD13	2.01	0.41
40:YU:69:CYS:HB3	40:YU:106:PHE:CZ	2.56	0.41
41:YV:22:VAL:HG12	41:YV:23:GLU:H	1.85	0.41
44:YY:84:ARG:O	44:YY:95:LYS:HD3	2.20	0.41
1:QA:1004:A:H1'	1:QA:1036:G:C2	2.56	0.41
1:QA:1084:G:OP1	1:QA:1086:U:C2	2.74	0.41
1:QA:1516:G:N1	1:QA:1519:A:OP2	2.52	0.41
1:QA:947:G:O3'	13:QM:109:THR:OG1	2.36	0.41
8:QH:20:TYR:CE2	8:QH:75:ARG:HD2	2.55	0.41
8:QH:36:LEU:HD12	8:QH:59:LEU:HD13	2.02	0.41
17:QQ:83:ASP:O	17:QQ:87:LYS:HG2	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
46:R0:23:VAL:HA	46:R0:38:VAL:HG22	2.00	0.41
53:R7:1:MET:SD	53:R7:3:ARG:NH2	2.93	0.41
25:RA:769:G:H5'	25:RA:1379:A:N6	2.36	0.41
25:RA:1449:A:H5'	25:RA:1449(A):G:OP2	2.21	0.41
25:RA:2282:G:H4'	25:RA:2389:G:O2'	2.20	0.41
25:RA:2570:G:H2'	25:RA:2571:C:O4'	2.20	0.41
25:RA:2637:U:C4	25:RA:2638:G:C6	3.08	0.41
25:RA:322:A:C5	25:RA:340:A:C2	3.07	0.41
27:RD:35:LYS:HE3	27:RD:63:ARG:C	2.41	0.41
29:RF:178:PRO:HB2	29:RF:201:VAL:CG1	2.50	0.41
26:RB:42:C:O2'	30:RG:67:LYS:O	2.23	0.41
30:RG:6:ALA:HB3	30:RG:104:GLU:OE2	2.20	0.41
36:RQ:17:LEU:HD21	36:RQ:41:TRP:HD1	1.84	0.41
36:RQ:68:ILE:HD13	36:RQ:103:MET:HG2	2.02	0.41
41:RV:76:LYS:HB2	41:RV:81:TYR:HB3	2.01	0.41
45:RZ:109:ALA:O	45:RZ:112:ARG:HB2	2.20	0.41
1:XA:1190:G:OP1	3:XC:4:LYS:HA	2.20	0.41
1:XA:1216:G:H5''	14:XN:5:ALA:HB2	2.02	0.41
1:XA:790:A:N1	1:XA:1497:G:H5''	2.35	0.41
1:XA:373:A:H2'	1:XA:374:A:H8	1.86	0.41
1:XA:376:G:OP1	16:XP:5:ARG:HB2	2.20	0.41
1:XA:453:A:C6	1:XA:454:C:C4	3.09	0.41
1:XA:690:G:H22	11:XK:55:LYS:HZ1	1.66	0.41
9:XI:125:TYR:HD2	9:XI:126:SER:N	2.18	0.41
11:XK:18:ARG:HA	11:XK:81:ASP:H	1.86	0.41
12:XL:102:ARG:HB3	12:XL:102:ARG:HE	1.71	0.41
1:XA:1492:A:OP1	12:XL:47:LYS:HB3	2.20	0.41
13:XM:12:ASN:N	13:XM:45:VAL:HG13	2.35	0.41
16:XP:17:TYR:HE1	16:XP:41:PRO:HG3	1.85	0.41
16:XP:23:ASP:O	16:XP:26:ARG:HB2	2.20	0.41
53:Y7:47:ARG:HE	53:Y7:47:ARG:HB2	1.58	0.41
25:YA:1101:U:H2'	25:YA:1102:C:C6	2.56	0.41
25:YA:174:C:H2'	25:YA:175:G:O4'	2.21	0.41
25:YA:2197:U:H1'	25:YA:2198:A:C8	2.56	0.41
25:YA:2210:G:H2'	25:YA:2210:G:N3	2.35	0.41
25:YA:2392:A:H2	25:YA:2424:C:N4	2.10	0.41
25:YA:2836:U:C4	25:YA:2883:A:N6	2.89	0.41
25:YA:572:A:H5''	25:YA:573:G:OP2	2.20	0.41
25:YA:593:G:O2'	54:Y8:61:LEU:HD13	2.20	0.41
26:YB:41:U:O4	30:YG:70:VAL:HG23	2.20	0.41
31:YH:19:VAL:HG22	31:YH:24:VAL:HG12	2.03	0.41
32:YI:21:VAL:HG22	32:YI:22:LYS:H	1.85	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
36:YQ:19:GLY:O	36:YQ:21:THR:OG1	2.23	0.41
25:YA:2275:C:O2	36:YQ:83:MET:HG3	2.19	0.41
38:YS:107:GLU:N	38:YS:110:LEU:HD11	2.35	0.41
41:YV:38:LEU:O	41:YV:51:VAL:HA	2.20	0.41
41:YV:72:VAL:HG13	41:YV:85:LYS:HG2	2.01	0.41
1:QA:1227:A:OP2	13:QM:111:LYS:HE3	2.20	0.41
1:QA:1327:C:H2'	1:QA:1328:C:C6	2.55	0.41
1:QA:1402:C:H2'	1:QA:1403:C:O4'	2.21	0.41
1:QA:347:G:O2'	1:QA:348:G:H5''	2.21	0.41
4:QD:122:ARG:HD3	4:QD:122:ARG:O	2.20	0.41
4:QD:38:TYR:HB2	4:QD:44:GLY:O	2.21	0.41
5:QE:110:LEU:HD13	5:QE:118:ILE:HG12	2.01	0.41
1:QA:1148:U:OP1	9:QI:7:THR:HG21	2.20	0.41
10:QJ:79:ARG:HA	10:QJ:79:ARG:HD3	1.78	0.41
13:QM:91:ARG:HB2	13:QM:98:VAL:HG13	2.03	0.41
16:QP:20:VAL:HG21	16:QP:32:TYR:CD1	2.56	0.41
1:QA:585:G:O3'	17:QQ:34:LYS:NZ	2.52	0.41
25:RA:30:G:O2'	25:RA:1214:A:N3	2.49	0.41
25:RA:1469:A:H2'	25:RA:1470:G:O4'	2.19	0.41
25:RA:1784:A:H4'	25:RA:1785:A:O5'	2.21	0.41
25:RA:265:A:O2'	25:RA:266:G:H4'	2.20	0.41
25:RA:831:G:O2'	35:RP:38:GLN:NE2	2.53	0.41
29:RF:33:LEU:HA	29:RF:33:LEU:HD12	1.83	0.41
35:RP:81:GLN:HG2	35:RP:106:LEU:HD23	2.02	0.41
36:RQ:40:ALA:O	36:RQ:42:ILE:HD12	2.21	0.41
37:RR:22:ARG:HA	37:RR:47:PHE:HE2	1.86	0.41
38:RS:14:VAL:HG21	38:RS:89:ARG:HG2	2.02	0.41
44:RY:54:LYS:HB3	44:RY:55:TYR:CE2	2.55	0.41
44:RY:84:ARG:HD3	44:RY:86:ARG:NH1	2.35	0.41
45:RZ:93:ASP:N	45:RZ:93:ASP:OD1	2.53	0.41
45:RZ:99:TYR:HB3	45:RZ:123:ASP:HB2	2.03	0.41
1:XA:1446:A:HO2'	1:XA:1447:G:P	2.44	0.41
3:XC:150:LYS:HE3	3:XC:167:TRP:HE1	1.84	0.41
12:XL:62:SER:HB2	12:XL:64:TYR:CD1	2.56	0.41
17:XQ:59:ILE:HB	17:XQ:71:PHE:HB3	2.03	0.41
25:YA:517:C:OP1	51:Y5:16:ARG:NH2	2.53	0.41
25:YA:117:G:C6	25:YA:119:A:C6	3.08	0.41
25:YA:1209:G:H21	25:YA:1210:A:H62	1.68	0.41
25:YA:2286:A:H2'	52:Y6:31:PRO:HG2	2.02	0.41
25:YA:2306:C:H2'	25:YA:2307:G:N2	2.33	0.41
25:YA:2334:G:C2	38:YS:12:PHE:CE2	3.08	0.41
25:YA:2528:U:H2'	25:YA:2530:A:O5'	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:2862:G:H2'	25:YA:2863:C:C6	2.56	0.41
25:YA:2811:G:H1	25:YA:2889:C:H42	1.69	0.41
25:YA:783:A:C8	25:YA:783:A:H3'	2.55	0.41
28:YE:86:PRO:HB2	28:YE:87:GLU:H	1.66	0.41
29:YF:125:LEU:HA	29:YF:194:MET:O	2.20	0.41
29:YF:107:LYS:CD	29:YF:207:GLY:H	2.30	0.41
30:YG:166:ASP:N	30:YG:166:ASP:OD1	2.54	0.41
44:YY:63:LYS:HD2	44:YY:63:LYS:HA	1.86	0.41
1:QA:1223:C:OP1	19:QS:78:ARG:NH1	2.51	0.41
1:QA:730:G:C5	1:QA:731:G:H1'	2.55	0.41
1:QA:758:G:H5'	1:QA:880:C:H1'	2.02	0.41
2:QB:120:ALA:C	2:QB:122:PHE:H	2.23	0.41
2:QB:184:VAL:N	2:QB:198:ASP:OD1	2.44	0.41
3:QC:42:LEU:HA	3:QC:42:LEU:HD12	1.79	0.41
11:QK:99:GLN:HG2	11:QK:105:VAL:HG21	2.03	0.41
1:QA:1216:G:H5''	14:QN:5:ALA:HB2	2.02	0.41
1:QA:1220:G:N2	19:QS:54:GLY:O	2.52	0.41
20:QT:89:ARG:HH21	20:QT:104:LEU:HG	1.85	0.41
52:R6:13:CYS:O	52:R6:21:TYR:HA	2.20	0.41
25:RA:1786:A:C4	25:RA:1938:A:C6	3.08	0.41
25:RA:1956:U:H1'	25:RA:2552:U:OP1	2.20	0.41
25:RA:2740:A:C6	25:RA:2764:A:C8	3.08	0.41
25:RA:900:A:H3'	25:RA:901:A:C8	2.46	0.41
25:RA:975:G:C2	25:RA:990:A:C8	3.09	0.41
29:RF:29:ASN:O	29:RF:112:MET:HE1	2.20	0.41
29:RF:164:ARG:HG3	29:RF:175:THR:OG1	2.20	0.41
30:RG:124:SER:HB2	30:RG:131:TYR:CE1	2.56	0.41
30:RG:27:ASN:HB3	30:RG:30:GLU:HG3	2.01	0.41
33:RN:71:ILE:HG21	33:RN:84:LYS:HB3	2.02	0.41
43:RX:51:VAL:HG13	43:RX:81:VAL:HG23	2.03	0.41
2:XB:80:ILE:HD11	2:XB:208:ILE:HG12	2.02	0.41
6:XF:46:ARG:HB3	6:XF:60:PHE:CE1	2.55	0.41
10:XJ:3:LYS:HD2	10:XJ:77:PRO:HD3	2.01	0.41
16:XP:8:ARG:C	16:XP:9:PHE:HD2	2.24	0.41
18:XR:85:LEU:HD23	18:XR:88:LYS:HD2	2.03	0.41
46:Y0:72:ARG:HB2	46:Y0:75:LEU:HB2	2.03	0.41
50:Y4:48:ARG:NH1	50:Y4:52:THR:H	2.19	0.41
25:YA:1087:G:C5	25:YA:1089:G:H1'	2.56	0.41
25:YA:1411:C:H5'	25:YA:1412:A:OP2	2.20	0.41
25:YA:248:G:H5'	25:YA:250:G:N7	2.36	0.41
25:YA:792:G:H5''	25:YA:793:A:H5'	2.01	0.41
25:YA:2061:G:OP1	29:YF:68:LYS:NZ	2.54	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:YN:29:LYS:H	33:YN:29:LYS:HG2	1.53	0.41
35:YP:101:VAL:C	35:YP:103:ALA:H	2.23	0.41
38:YS:88:ASP:O	38:YS:89:ARG:HB3	2.21	0.41
25:YA:583:G:OP2	40:YU:10:ARG:HD2	2.21	0.41
1:QA:266:G:H5'	1:QA:268:C:H41	1.85	0.41
1:QA:484:G:H5'	1:QA:486:U:O4'	2.21	0.41
1:QA:751:U:H2'	1:QA:752:G:O4'	2.20	0.41
1:QA:882:C:O2'	1:QA:883:C:H5'	2.21	0.41
2:QB:210:SER:O	2:QB:214:ILE:HG12	2.21	0.41
3:QC:122:GLU:HA	3:QC:125:GLU:OE1	2.21	0.41
22:QV:18:G:N2	22:QV:57:A:H2'	2.36	0.41
25:RA:1652:A:N7	25:RA:1653:G:C6	2.89	0.41
25:RA:1752:C:H2'	25:RA:1753:G:C8	2.56	0.41
25:RA:1891:G:H2'	25:RA:1892:C:O4'	2.21	0.41
25:RA:301:G:H1	25:RA:316:C:N4	2.18	0.41
25:RA:612:G:H2'	25:RA:613:U:O2	2.21	0.41
25:RA:676:A:H2	25:RA:802:A:H61	1.65	0.41
27:RD:127:VAL:HA	27:RD:193:VAL:HG22	2.02	0.41
28:RE:35:GLN:HB3	28:RE:48:GLN:HB2	2.02	0.41
28:RE:92:THR:HB	28:RE:93:VAL:H	1.54	0.41
33:RN:47:ALA:HB2	33:RN:112:LEU:HD11	2.02	0.41
37:RR:10:LEU:O	37:RR:12:ARG:HG3	2.21	0.41
37:RR:70:LEU:C	37:RR:72:ASP:H	2.21	0.41
26:RB:74:U:H1'	45:RZ:34:ASN:HD21	1.86	0.41
1:XA:1226:C:H4'	1:XA:1227:A:OP1	2.20	0.41
1:XA:1308:U:OP1	13:XM:98:VAL:HG23	2.21	0.41
1:XA:186(C):G:C6	1:XA:191(E):G:C6	3.09	0.41
1:XA:221:C:H2'	1:XA:222:U:H6	1.84	0.41
1:XA:241:C:C2	1:XA:286:G:C2	3.09	0.41
1:XA:528:C:H41	12:XL:49:ASN:CG	2.24	0.41
1:XA:694:A:H2'	1:XA:695:A:O4'	2.21	0.41
1:XA:779:C:H2'	1:XA:780:A:O4'	2.20	0.41
8:XH:44:PHE:HE2	8:XH:109:ILE:CG2	2.34	0.41
1:XA:963:G:H21	10:XJ:55:LYS:HD3	1.84	0.41
11:XK:48:ILE:HD13	11:XK:48:ILE:HA	1.83	0.41
25:YA:2421:G:OP1	52:Y6:6:ARG:NH2	2.54	0.41
25:YA:1021:A:C3'	25:YA:1021:A:C8	3.04	0.41
25:YA:1085:A:O2'	25:YA:1086:A:P	2.78	0.41
25:YA:1317:A:H2'	25:YA:1318:C:C6	2.55	0.41
25:YA:1342:A:OP1	43:YX:36:LYS:NZ	2.54	0.41
25:YA:1878:G:H2'	25:YA:1879:C:H6	1.84	0.41
25:YA:1919:A:H5''	25:YA:1920:C:OP2	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:2134:A:OP2	25:YA:2157:G:N2	2.53	0.41
25:YA:2663:G:C6	25:YA:2664:G:C4	3.09	0.41
25:YA:2713:A:H3'	25:YA:2714:G:H5''	2.02	0.41
25:YA:273(F):C:H2'	25:YA:274:G:H5''	2.03	0.41
25:YA:820:A:H2'	25:YA:821:A:O4'	2.20	0.41
32:YI:115:ALA:HB3	32:YI:128:LEU:HD12	2.02	0.41
32:YI:23:PRO:O	32:YI:27:ARG:HG2	2.21	0.41
36:YQ:16:ARG:HB3	36:YQ:17:LEU:H	1.76	0.41
40:YU:98:LEU:HD23	40:YU:99:ALA:N	2.36	0.41
41:YV:72:VAL:CG1	41:YV:85:LYS:HG2	2.50	0.41
1:QA:1263:C:H42	1:QA:1272:G:H1	1.69	0.41
1:QA:148:G:H2'	1:QA:149:A:H8	1.85	0.41
1:QA:15:G:H2'	1:QA:16:A:O4'	2.21	0.41
1:QA:514:C:H2'	1:QA:515:G:H8	1.86	0.41
1:QA:573:A:N3	1:QA:883:C:O2'	2.53	0.41
1:QA:967:C:H2'	1:QA:968:A:N7	2.36	0.41
1:QA:978:A:H5''	1:QA:979:C:OP2	2.20	0.41
2:QB:104:ASN:OD1	2:QB:107:THR:OG1	2.30	0.41
2:QB:47:THR:HA	2:QB:202:PRO:HG2	2.00	0.41
7:QG:45:ASP:O	7:QG:48:LYS:HB3	2.21	0.41
15:QO:4:THR:HB	15:QO:6:GLU:CD	2.41	0.41
19:QS:36:ARG:HA	19:QS:71:LEU:HB2	2.02	0.41
47:R1:58:ILE:CD1	47:R1:86:SER:HB2	2.50	0.41
25:RA:1068:G:O2'	25:RA:1096:A:N3	2.54	0.41
25:RA:150:C:H2'	25:RA:151:C:C6	2.55	0.41
25:RA:749:C:O2	25:RA:1618:A:H2'	2.20	0.41
25:RA:2133:G:H2'	25:RA:2157:G:N2	2.36	0.41
25:RA:2774:C:H2'	25:RA:2775:A:O4'	2.20	0.41
27:RD:150:LYS:N	27:RD:150:LYS:HD3	2.36	0.41
31:RH:152:ARG:HE	31:RH:153:LYS:HZ3	1.69	0.41
32:RI:14:ASP:O	32:RI:16:GLY:N	2.54	0.41
33:RN:57:ALA:O	33:RN:60:ILE:HD11	2.21	0.41
33:RN:73:THR:HB	33:RN:82:LEU:HD11	2.02	0.41
39:RT:91:ARG:HB2	39:RT:121:ILE:HG13	2.03	0.41
1:XA:1152:A:H2'	1:XA:1153:C:C6	2.55	0.41
1:XA:1199:U:H4'	10:XJ:54:PHE:CZ	2.56	0.41
1:XA:192:U:H2'	1:XA:193:C:C6	2.56	0.41
1:XA:44:G:C2	1:XA:45:U:H1'	2.56	0.41
1:XA:651:C:H2'	1:XA:652:U:C6	2.56	0.41
2:XB:118:LEU:CB	2:XB:142:LEU:HD12	2.50	0.41
3:XC:119:ARG:HH21	3:XC:140:ARG:CZ	2.34	0.41
10:XJ:76:ASN:HA	10:XJ:77:PRO:HD2	1.96	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:XL:68:ALA:HB2	12:XL:85:ILE:HD11	2.03	0.41
12:XL:70:ILE:HA	12:XL:71:PRO:HD3	1.81	0.41
14:XN:51:GLY:O	14:XN:53:LEU:N	2.53	0.41
17:XQ:62:SER:CB	17:XQ:72:ARG:HE	2.33	0.41
22:XV:1:G:H2'	22:XV:2:C:H6	1.86	0.41
54:Y8:37:SER:O	54:Y8:40:GLU:HB3	2.21	0.41
55:Y9:2:LYS:HA	55:Y9:2:LYS:HD2	1.86	0.41
25:YA:1107:G:H2'	25:YA:1108:U:C6	2.56	0.41
25:YA:1126:A:OP1	25:YA:1126:A:H8	2.03	0.41
25:YA:1265:A:H8	25:YA:1265:A:OP1	2.04	0.41
25:YA:2292:C:OP2	38:YS:17:ARG:NH2	2.47	0.41
25:YA:414:C:H1'	25:YA:1864:U:O2'	2.21	0.41
27:YD:102:LYS:C	27:YD:103:ARG:HG2	2.40	0.41
27:YD:3:VAL:HG13	27:YD:17:THR:HG23	2.03	0.41
27:YD:36:PRO:HB3	27:YD:61:LEU:HB3	2.03	0.41
28:YE:64:LYS:C	28:YE:66:HIS:H	2.24	0.41
29:YF:9:ILE:HD11	29:YF:125:LEU:HG	2.03	0.41
30:YG:103:LEU:O	30:YG:107:LEU:HG	2.21	0.41
30:YG:124:SER:HB2	30:YG:131:TYR:CE1	2.56	0.41
32:YI:57:ARG:O	32:YI:61:ARG:HG2	2.20	0.41
33:YN:7:LYS:H	33:YN:7:LYS:NZ	2.18	0.41
40:YU:8:VAL:O	40:YU:12:ARG:HG3	2.20	0.41
45:YZ:136:PHE:C	45:YZ:137:ILE:HG12	2.41	0.41
1:QA:1336:C:O2'	1:QA:1337:G:P	2.78	0.41
4:QD:173:TRP:CD1	4:QD:174:LEU:HG	2.56	0.41
5:QE:12:LEU:O	5:QE:13:ILE:HD12	2.21	0.41
8:QH:41:ARG:NH2	8:QH:123:GLU:OE2	2.54	0.41
9:QI:40:LEU:HD11	9:QI:70:LYS:HG2	2.02	0.41
12:QL:103:GLY:N	12:QL:107:ALA:O	2.49	0.41
1:QA:452:A:P	16:QP:43:LYS:HZ1	2.44	0.41
36:RQ:79:LEU:HD12	46:R0:5:LYS:HD3	2.02	0.41
50:R4:39:CYS:HB2	50:R4:41:PRO:HD2	2.02	0.41
25:RA:1007:C:OP1	33:RN:35:ARG:NH1	2.53	0.41
25:RA:1085:A:HO2'	25:RA:1086:A:P	2.44	0.41
25:RA:815:C:C2	25:RA:1193:G:C2	3.09	0.41
25:RA:2262:U:H4'	25:RA:2328:A:H2	1.84	0.41
25:RA:2758:A:C2	25:RA:2759:G:H1'	2.56	0.41
25:RA:2777:G:OP2	25:RA:2781:A:O2'	2.34	0.41
25:RA:815:C:H2'	25:RA:816:C:C6	2.55	0.41
26:RB:29:A:H2'	26:RB:30:C:C6	2.55	0.41
27:RD:111:LEU:HA	27:RD:111:LEU:HD23	1.78	0.41
27:RD:226:MET:HB3	27:RD:230:ASP:HB2	2.03	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:784:A:O4'	27:RD:227:ASN:ND2	2.53	0.41
27:RD:257:LEU:HA	27:RD:257:LEU:HD23	1.90	0.41
31:RH:33:LEU:HD11	31:RH:136:ILE:O	2.20	0.41
32:RI:144:VAL:O	32:RI:145:VAL:HG12	2.21	0.41
33:RN:57:ALA:C	33:RN:60:ILE:HD11	2.40	0.41
34:RO:26:LYS:HB2	34:RO:30:ALA:HB2	2.02	0.41
36:RQ:66:ILE:HG13	36:RQ:67:ARG:N	2.36	0.41
40:RU:61:TRP:O	40:RU:65:ILE:HG13	2.21	0.41
1:XA:1112:C:C2	3:XC:178:LEU:HB2	2.55	0.41
1:XA:1128:C:H42	1:XA:1144:G:H1	1.69	0.41
1:XA:1213:A:C5	1:XA:1215:G:C4	3.09	0.41
1:XA:1336:C:O2	1:XA:1336:C:H2'	2.20	0.41
1:XA:302:G:C6	1:XA:303:A:C5	3.09	0.41
1:XA:375:U:C2	1:XA:376:G:C8	3.09	0.41
1:XA:438:G:H4'	4:XD:123:HIS:NE2	2.36	0.41
1:XA:418:C:H1'	1:XA:540:G:O2'	2.21	0.41
1:XA:622:A:C8	1:XA:623:C:C6	3.09	0.41
1:XA:626:U:N3	1:XA:627:G:N7	2.69	0.41
4:XD:52:SER:O	4:XD:55:ALA:HB3	2.21	0.41
5:XE:68:GLU:HG3	5:XE:68:GLU:O	2.21	0.41
9:XI:79:LEU:O	9:XI:83:ARG:HG2	2.19	0.41
10:XJ:54:PHE:CD2	10:XJ:55:LYS:HG3	2.56	0.41
20:XT:11:SER:HA	20:XT:13:LEU:HD12	2.01	0.41
25:YA:1094:U:O2	25:YA:1096:A:H5'	2.21	0.41
25:YA:1048:A:C5	25:YA:1111:A:H2	2.39	0.41
25:YA:1032:A:H2	25:YA:1122:G:H22	1.68	0.41
25:YA:1682:G:H2'	25:YA:1683:C:C6	2.55	0.41
25:YA:2688:U:O2	25:YA:2719:G:C6	2.74	0.41
25:YA:2783:G:H2'	25:YA:2784:C:C6	2.56	0.41
25:YA:620:G:H4'	25:YA:621:A:C5'	2.36	0.41
25:YA:724:U:H2'	25:YA:725:G:O4'	2.21	0.41
26:YB:20:C:H2'	26:YB:21:G:O4'	2.21	0.41
27:YD:130:ALA:C	27:YD:131:LEU:HD12	2.42	0.41
28:YE:41:LYS:HA	28:YE:41:LYS:HE2	2.02	0.41
33:YN:96:GLU:O	33:YN:100:GLU:HG3	2.20	0.41
45:YZ:182:LYS:CB	45:YZ:183:LEU:HA	2.51	0.41
1:QA:565:U:H5''	1:QA:566:G:C2'	2.51	0.41
10:QJ:31:GLY:HA3	10:QJ:78:ASN:CG	2.41	0.41
11:QK:25:TYR:CZ	11:QK:87:THR:HB	2.55	0.41
52:R6:24:GLU:HB3	52:R6:25:LYS:H	1.74	0.41
25:RA:1364:G:C8	47:R1:2:SER:N	2.89	0.41
25:RA:2120:G:H2'	25:RA:2121:G:H8	1.85	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:RA:2477:C:H2'	55:R9:1:MET:HG3	2.02	0.41
25:RA:734:A:O2'	25:RA:1635:G:H5'	2.21	0.41
30:RG:131:TYR:O	30:RG:159:VAL:HG13	2.21	0.41
30:RG:47:LYS:HE3	30:RG:47:LYS:HB2	1.81	0.41
32:RI:12:LEU:HG	32:RI:19:VAL:HG11	2.03	0.41
33:RN:9:VAL:HG21	33:RN:48:MET:HB3	2.02	0.41
38:RS:62:LYS:HB3	38:RS:97:ARG:CD	2.44	0.41
45:RZ:74:VAL:HG22	45:RZ:86:VAL:HG22	2.03	0.41
1:XA:1004:A:H1'	1:XA:1036:G:H22	1.86	0.41
1:XA:652:U:H1'	1:XA:653:A:C2	2.56	0.41
1:XA:659:U:H2'	1:XA:660:G:C8	2.55	0.41
2:XB:126:GLU:O	2:XB:129:GLU:HB2	2.20	0.41
3:XC:138:VAL:HG13	3:XC:149:ALA:HB3	2.02	0.41
4:XD:131:ARG:HG2	4:XD:131:ARG:H	1.67	0.41
4:XD:186:LEU:HD23	4:XD:186:LEU:HA	1.95	0.41
5:XE:82:VAL:HB	5:XE:138:ALA:HB2	2.03	0.41
5:XE:69:VAL:HA	5:XE:70:PRO:HD2	1.76	0.41
8:XH:12:ARG:HD3	8:XH:26:VAL:HB	2.03	0.41
19:XS:36:ARG:HA	19:XS:71:LEU:HB2	2.02	0.41
47:Y1:83:GLU:C	47:Y1:85:LEU:H	2.24	0.41
52:Y6:36:LEU:HD13	52:Y6:50:ARG:CZ	2.51	0.41
25:YA:1683:C:H2'	25:YA:1684:C:C6	2.56	0.41
25:YA:213:A:H2'	25:YA:214:G:O4'	2.21	0.41
25:YA:2772:C:H5'	28:YE:168:MET:SD	2.60	0.41
25:YA:2845:G:H2'	25:YA:2846:G:H8	1.85	0.41
25:YA:568:U:H5'	25:YA:945:A:N1	2.36	0.41
25:YA:649:G:C5	25:YA:650:C:C4	3.08	0.41
27:YD:145:VAL:HG11	27:YD:175:LEU:HD11	2.02	0.41
28:YE:32:PRO:HA	28:YE:90:THR:HA	2.03	0.41
29:YF:28:ILE:H	29:YF:28:ILE:HG13	1.68	0.41
29:YF:64:ILE:HA	29:YF:64:ILE:HD12	1.80	0.41
29:YF:67:GLN:HG3	29:YF:67:GLN:O	2.21	0.41
35:YP:106:LEU:O	35:YP:107:LYS:HB2	2.20	0.41
36:YQ:80:GLU:HB2	36:YQ:81:VAL:H	1.69	0.41
37:YR:44:LEU:HD22	37:YR:48:VAL:HG23	2.02	0.41
40:YU:17:ILE:HG23	40:YU:39:LEU:HD12	2.02	0.41
40:YU:92:ARG:HD2	40:YU:95:LEU:HD12	2.02	0.41
40:YU:92:ARG:NH2	41:YV:11:GLN:H	2.18	0.41
43:YX:31:HIS:HB3	43:YX:34:ALA:HB2	2.03	0.41
45:YZ:8:TYR:HD1	45:YZ:38:TYR:CZ	2.39	0.41
1:QA:1098:C:H2'	1:QA:1099:G:O4'	2.21	0.41
1:QA:1225:A:N3	1:QA:1225:A:H2'	2.36	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:QA:438:G:H4'	4:QD:123:HIS:CD2	2.56	0.41
1:QA:593:G:H1	1:QA:646:U:H3	1.67	0.41
1:QA:598:U:H4'	8:QH:94:TYR:CD2	2.56	0.41
3:QC:83:ARG:O	3:QC:86:VAL:HG22	2.21	0.41
5:QE:147:ASP:O	5:QE:151:LEU:HG	2.21	0.41
6:QF:35:ALA:HA	6:QF:67:MET:HB3	2.02	0.41
8:QH:44:PHE:HD1	8:QH:80:ILE:HG12	1.86	0.41
22:QV:76:A:H2'	25:RA:2602:A:H61	1.83	0.41
50:R4:23:GLU:HG3	50:R4:25:TYR:HE2	1.85	0.41
25:RA:244:A:H2'	25:RA:245:G:O4'	2.21	0.41
25:RA:2712:U:OP1	25:RA:2714:G:H4'	2.21	0.41
25:RA:2820:A:O5'	37:RR:4:LEU:HD23	2.21	0.41
25:RA:392:C:H5''	25:RA:409:C:H5''	2.02	0.41
25:RA:65:C:O2'	25:RA:456:C:N3	2.43	0.41
25:RA:587:C:N3	35:RP:33:ARG:NH1	2.65	0.41
25:RA:626:U:H5''	25:RA:627:A:C5'	2.51	0.41
25:RA:705:A:H1'	27:RD:9:TYR:CE1	2.56	0.41
25:RA:77:C:O3'	48:R2:14:ARG:NH2	2.48	0.41
26:RB:110:G:H2'	26:RB:111:U:O4'	2.21	0.41
27:RD:34:VAL:C	27:RD:35:LYS:HG3	2.40	0.41
28:RE:184:VAL:HB	28:RE:185:LYS:H	1.64	0.41
25:RA:2198:A:C2	32:RI:29:TYR:HB2	2.56	0.41
35:RP:62:LEU:N	35:RP:62:LEU:HD13	2.36	0.41
25:RA:389:G:H22	35:RP:72:PRO:HD3	1.86	0.41
38:RS:83:LYS:C	38:RS:109:GLY:HA3	2.42	0.41
1:XA:1107:C:C4	1:XA:1108:G:C8	3.09	0.41
2:XB:166:ASP:HB3	2:XB:169:LYS:HB2	2.02	0.41
3:XC:42:LEU:HD12	3:XC:42:LEU:HA	1.87	0.41
4:XD:64:LEU:HD13	4:XD:198:VAL:HG11	2.02	0.41
6:XF:25:ILE:HD13	6:XF:28:ARG:NH1	2.35	0.41
10:XJ:6:ILE:O	10:XJ:71:LEU:HD12	2.21	0.41
11:XK:19:ALA:CB	11:XK:32:ILE:HG22	2.50	0.41
22:XV:53:G:O2'	22:XV:54:U:O5'	2.39	0.41
25:YA:1588:C:H2'	25:YA:1589:C:H6	1.86	0.41
25:YA:173:G:H2'	25:YA:174:C:C6	2.56	0.41
25:YA:1931:U:C5	25:YA:1969:A:N7	2.89	0.41
25:YA:297:C:H5''	44:YY:85:VAL:CG2	2.51	0.41
25:YA:566:U:OP1	35:YP:29:LYS:NZ	2.50	0.41
25:YA:69:C:H2'	25:YA:70:G:C8	2.55	0.41
25:YA:747:U:OP2	51:Y5:3:LYS:HD2	2.21	0.41
27:YD:201:HIS:O	27:YD:204:ILE:HG12	2.21	0.41
27:YD:35:LYS:HZ1	27:YD:65:ILE:HA	1.86	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:YE:95:ILE:H	28:YE:95:ILE:CD1	2.31	0.41
34:YO:4:PRO:O	34:YO:5:GLN:CB	2.69	0.41
1:QA:1034:G:H2'	1:QA:1035:A:C8	2.55	0.40
1:QA:126:G:H2'	1:QA:127:G:O4'	2.21	0.40
7:QG:54:THR:O	7:QG:56:GLN:N	2.52	0.40
7:QG:93:PRO:O	7:QG:96:GLN:HB2	2.21	0.40
1:QA:1329:A:H5'	13:QM:29:ARG:NE	2.36	0.40
21:QU:10:ARG:HA	21:QU:13:ILE:HB	2.02	0.40
46:R0:72:ARG:HB2	46:R0:75:LEU:HB2	2.03	0.40
50:R4:13:ARG:O	50:R4:30:GLU:HA	2.21	0.40
53:R7:31:LEU:HA	53:R7:31:LEU:HD23	1.86	0.40
25:RA:1364:G:N7	47:R1:2:SER:N	2.69	0.40
25:RA:2469:A:H5''	25:RA:2470:G:C8	2.56	0.40
25:RA:13:A:N1	25:RA:525:U:H2'	2.37	0.40
25:RA:634:C:H2'	25:RA:635:C:C6	2.56	0.40
25:RA:2788:C:OP1	28:RE:61:ARG:NH1	2.54	0.40
31:RH:103:LEU:HG	31:RH:105:LEU:HD12	2.02	0.40
31:RH:107:VAL:HB	31:RH:153:LYS:HE3	2.03	0.40
32:RI:120:ILE:HD11	32:RI:126:TYR:OH	2.20	0.40
39:RT:109:GLU:O	39:RT:113:LYS:HB2	2.21	0.40
43:RX:67:GLY:C	43:RX:69:TYR:H	2.23	0.40
1:XA:1363:A:H1'	1:XA:1365:G:N7	2.36	0.40
1:XA:22:G:H4'	1:XA:885:G:C8	2.56	0.40
1:XA:965:A:H4'	1:XA:966:G:OP1	2.20	0.40
5:XE:51:VAL:HB	5:XE:52:PRO:HD3	2.03	0.40
7:XG:89:MET:HE3	7:XG:155:ARG:HB2	2.03	0.40
8:XH:6:ILE:HB	8:XH:85:ARG:NH1	2.36	0.40
9:XI:95:LYS:NZ	9:XI:96:LEU:HD13	2.36	0.40
20:XT:43:LEU:HA	20:XT:43:LEU:HD23	1.88	0.40
50:Y4:43:TYR:O	50:Y4:46:GLN:HA	2.20	0.40
50:Y4:48:ARG:HH12	50:Y4:52:THR:H	1.69	0.40
25:YA:1331:A:C6	25:YA:1333:C:C2	3.09	0.40
25:YA:2108:C:H2'	25:YA:2109:U:C6	2.56	0.40
25:YA:270:A:H1'	25:YA:370:G:C2	2.56	0.40
25:YA:270(X):G:C6	25:YA:270(Y):G:N1	2.89	0.40
25:YA:654:A:O2'	25:YA:654(A):G:OP2	2.36	0.40
25:YA:654:A:HO2'	25:YA:654(A):G:P	2.44	0.40
25:YA:659:C:H2'	25:YA:660:G:H8	1.85	0.40
30:YG:18:GLU:OE1	30:YG:22:ARG:NH1	2.49	0.40
30:YG:61:ALA:HA	30:YG:64:THR:HG22	2.02	0.40
31:YH:125:VAL:HG22	31:YH:131:VAL:HG13	2.02	0.40
35:YP:29:LYS:HB3	35:YP:30:THR:H	1.59	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:18:C:O3'	40:YU:23:GLY:HA2	2.21	0.40
40:YU:96:ALA:HA	40:YU:98:LEU:HD23	2.03	0.40
1:QA:115:G:H4'	1:QA:116:A:O5'	2.20	0.40
1:QA:955:U:H2'	1:QA:956:U:O4'	2.21	0.40
3:QC:71:ALA:HB2	3:QC:109:PRO:HB3	2.04	0.40
10:QJ:4:ILE:HA	10:QJ:100:THR:HG22	2.02	0.40
19:QS:5:LEU:HD12	19:QS:5:LEU:HA	1.93	0.40
22:QV:43:A:H2'	22:QV:44:A:C8	2.57	0.40
25:RA:1285:G:N1	25:RA:1329:U:OP1	2.50	0.40
25:RA:1504:C:H5'	25:RA:1505:C:OP2	2.21	0.40
25:RA:155:C:H5'	25:RA:161:U:OP2	2.22	0.40
25:RA:2086:U:H2'	25:RA:2087:G:C8	2.56	0.40
25:RA:2779:U:H2'	25:RA:2779:U:H6	1.75	0.40
25:RA:315:G:H2'	25:RA:316:C:C6	2.57	0.40
25:RA:778:G:H5'	27:RD:48:ARG:NH1	2.35	0.40
28:RE:197:ILE:HD11	28:RE:199:ARG:CZ	2.50	0.40
28:RE:55:ASN:ND2	28:RE:75:VAL:HG22	2.35	0.40
29:RF:107:LYS:HE3	29:RF:206:ILE:HD12	2.03	0.40
31:RH:30:LYS:HD2	31:RH:81:GLU:H	1.85	0.40
31:RH:98:LEU:HB2	31:RH:125:VAL:HB	2.03	0.40
34:RO:63:VAL:HB	34:RO:106:LEU:HD11	2.02	0.40
36:RQ:58:PHE:CD1	36:RQ:61:GLY:HA3	2.56	0.40
40:RU:83:LEU:HG	40:RU:88:ILE:HB	2.03	0.40
1:XA:1164:G:H2'	1:XA:1165:C:H6	1.87	0.40
1:XA:1216:G:OP1	14:YN:2:ALA:HA	2.21	0.40
1:XA:652:U:H1'	1:XA:653:A:H2	1.86	0.40
1:XA:982:U:H4'	1:XA:983:A:O5'	2.21	0.40
2:XB:120:ALA:C	2:XB:122:PHE:H	2.25	0.40
2:XB:19:HIS:NE2	2:XB:206:ASP:HB2	2.36	0.40
3:XC:188:LEU:HD13	3:XC:188:LEU:HA	1.90	0.40
4:XD:165:MET:O	4:XD:167:GLY:N	2.54	0.40
5:XE:34:VAL:HG11	5:XE:63:ARG:HG2	2.02	0.40
11:XK:38:ASN:HA	11:XK:39:PRO:HD3	1.75	0.40
52:Y6:13:CYS:HB2	52:Y6:22:ALA:HB3	2.03	0.40
25:YA:1076:C:H2'	25:YA:1077:A:H5''	2.03	0.40
25:YA:1087:G:C4	25:YA:1089:G:H1'	2.56	0.40
25:YA:1209:G:N2	25:YA:1210:A:H62	2.19	0.40
25:YA:1550:C:H2'	25:YA:1551:C:C6	2.55	0.40
25:YA:2884:U:C2	51:Y5:51:TYR:HE1	2.39	0.40
25:YA:549:G:H2'	25:YA:550:G:O4'	2.21	0.40
25:YA:593:G:C4'	54:Y8:4:MET:HE1	2.51	0.40
25:YA:857:C:H1'	46:Y0:26:TYR:CE2	2.56	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:YD:62:TYR:HA	27:YD:87:ASN:OD1	2.21	0.40
28:YE:49:LEU:HD12	28:YE:49:LEU:HA	1.71	0.40
30:YG:7:LEU:HD12	30:YG:104:GLU:HA	2.04	0.40
26:YB:41:U:H5	30:YG:70:VAL:O	2.04	0.40
31:YH:109:PHE:HZ	31:YH:152:ARG:HG2	1.86	0.40
32:YI:52:ARG:O	32:YI:56:LYS:HB3	2.21	0.40
33:YN:65:LYS:HG2	33:YN:65:LYS:H	1.60	0.40
38:YS:69:VAL:HA	38:YS:72:ALA:HB3	2.03	0.40
3:QC:43:LEU:HD22	3:QC:47:LEU:HD22	2.02	0.40
6:QF:33:TYR:CE1	6:QF:78:GLU:HG2	2.56	0.40
6:QF:30:LEU:HD23	6:QF:75:LEU:HD11	2.02	0.40
47:R1:95:LEU:HA	47:R1:95:LEU:HD23	1.94	0.40
35:RP:62:LEU:O	54:R8:13:ARG:HB2	2.22	0.40
54:R8:49:VAL:HG23	54:R8:53:PRO:HB3	2.04	0.40
25:RA:221:A:C4	25:RA:266:G:N7	2.89	0.40
25:RA:2233:U:H2'	25:RA:2234:G:C8	2.56	0.40
25:RA:2716:U:O2'	25:RA:2717:G:H5'	2.21	0.40
25:RA:439:G:H2'	25:RA:440:G:C8	2.56	0.40
25:RA:485:C:H2'	25:RA:486:C:C6	2.56	0.40
25:RA:579:G:H2'	25:RA:580:C:C6	2.56	0.40
26:RB:15:A:H1'	26:RB:109:G:C8	2.56	0.40
27:RD:96:HIS:CD2	27:RD:102:LYS:HG2	2.56	0.40
27:RD:44:ASN:HB2	27:RD:49:ILE:HA	2.02	0.40
27:RD:35:LYS:HB3	27:RD:63:ARG:HA	2.04	0.40
28:RE:26:ILE:O	28:RE:26:ILE:HG12	2.18	0.40
28:RE:36:ARG:HB3	28:RE:36:ARG:HH11	1.87	0.40
30:RG:117:PHE:HE1	30:RG:120:LEU:HD23	1.87	0.40
32:RI:30:LEU:HD22	32:RI:35:LEU:HD11	2.02	0.40
35:RP:114:ILE:HD11	35:RP:130:PHE:CD1	2.57	0.40
39:RT:51:ARG:CG	39:RT:98:LYS:HG3	2.52	0.40
44:RY:11:ASP:O	44:RY:26:LYS:HG3	2.21	0.40
45:RZ:48:PHE:HE2	45:RZ:71:VAL:HG21	1.87	0.40
1:XA:1032(B):G:H2'	1:XA:1033:G:H8	1.86	0.40
1:XA:1508:G:H2'	1:XA:1509:C:C6	2.56	0.40
1:XA:97:U:H2'	1:XA:99:C:C6	2.56	0.40
9:XI:75:ASP:HA	9:XI:78:LYS:HB3	2.04	0.40
11:XK:18:ARG:HB3	11:XK:33:THR:OG1	2.21	0.40
12:XL:38:THR:CG2	12:XL:57:LYS:HB3	2.49	0.40
12:XL:90:VAL:O	12:XL:92:ASP:N	2.54	0.40
1:XA:1314:C:OP2	19:XS:4:SER:OG	2.37	0.40
52:Y6:11:LEU:HD13	52:Y6:11:LEU:HA	1.86	0.40
25:YA:1071:G:H8	25:YA:1071:G:O5'	2.03	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:YA:1093:G:H5'	31:YH:170:ARG:HH12	1.86	0.40
25:YA:1790:C:H2'	25:YA:1791:A:C5	2.56	0.40
25:YA:1906:G:OP2	25:YA:1930:G:H5''	2.21	0.40
25:YA:1991:U:H2'	25:YA:1992:G:H5''	2.03	0.40
25:YA:2168:G:H2'	25:YA:2168:G:N3	2.36	0.40
25:YA:2477:C:O5'	25:YA:2477:C:H6	2.04	0.40
25:YA:2607:G:H2'	25:YA:2608:G:O4'	2.20	0.40
25:YA:2660:A:C2	25:YA:2661:G:H1'	2.56	0.40
25:YA:2722:G:H2'	25:YA:2723:C:C6	2.56	0.40
25:YA:468:G:C6	25:YA:469:G:C4	3.09	0.40
25:YA:849:A:N1	49:Y3:25:ALA:HB2	2.36	0.40
25:YA:2635:C:H5'	28:YE:77:ILE:HD13	2.04	0.40
29:YF:168:ARG:HG3	29:YF:175:THR:HG21	2.02	0.40
29:YF:198:ALA:HA	29:YF:201:VAL:HG12	2.03	0.40
32:YI:56:LYS:HG3	32:YI:57:ARG:N	2.34	0.40
45:YZ:106:GLY:O	45:YZ:141:VAL:HG13	2.20	0.40
1:QA:1006:C:H2'	1:QA:1007:C:C6	2.57	0.40
1:QA:1129:C:C4'	1:QA:1130:A:H5'	2.52	0.40
1:QA:1157:A:H1'	1:QA:1158:C:C4	2.56	0.40
1:QA:1347:G:N2	1:QA:1374:A:OP2	2.47	0.40
3:QC:7:PRO:O	3:QC:11:ARG:NH1	2.54	0.40
13:QM:4:ILE:H	13:QM:9:ILE:CG2	2.35	0.40
16:QP:34:GLU:OE2	16:QP:55:ARG:NH1	2.53	0.40
1:QA:186:C:H5'	20:QT:78:ALA:HB1	2.03	0.40
20:QT:86:ARG:O	20:QT:90:GLN:HG3	2.21	0.40
46:R0:12:ASN:HB3	46:R0:13:GLY:H	1.67	0.40
25:RA:242:G:C5'	54:R8:62:LEU:HD13	2.49	0.40
25:RA:1011:G:C2	25:RA:1013:C:C2	3.09	0.40
25:RA:1047:G:H2'	25:RA:1110:G:H1	1.86	0.40
25:RA:1179:C:H2'	25:RA:1180:C:O4'	2.21	0.40
25:RA:2173:A:C2	25:RA:2174:C:H1'	2.56	0.40
25:RA:2567:G:H2'	25:RA:2568:C:C6	2.55	0.40
25:RA:2593:U:H2'	25:RA:2594:C:H6	1.86	0.40
25:RA:795:C:H2'	25:RA:796:C:H6	1.85	0.40
27:RD:209:ALA:O	27:RD:212:SER:HB2	2.22	0.40
29:RF:29:ASN:HB3	29:RF:32:LEU:HD23	2.04	0.40
31:RH:167:GLU:HA	31:RH:168:PRO:HD3	1.90	0.40
33:RN:17:ASP:O	33:RN:19:GLU:N	2.54	0.40
34:RO:66:LYS:HA	34:RO:79:PHE:O	2.21	0.40
36:RQ:72:LYS:HB3	36:RQ:94:VAL:O	2.21	0.40
40:RU:66:ASN:CG	40:RU:70:ARG:HH21	2.21	0.40
44:RY:67:LEU:HA	44:RY:67:LEU:HD12	1.93	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:XA:114:U:H2'	1:XA:115:G:C8	2.57	0.40
1:XA:41:G:H2'	1:XA:42:G:H8	1.86	0.40
1:XA:951:G:OP2	13:XM:102:ARG:NH2	2.54	0.40
3:XC:20:SER:HB2	3:XC:40:ARG:NH2	2.29	0.40
4:XD:108:LEU:HB3	4:XD:110:PHE:CD1	2.57	0.40
5:XE:89:ILE:HG12	5:XE:91:LEU:CD1	2.52	0.40
19:XS:15:LEU:HA	19:XS:18:LYS:HB3	2.04	0.40
49:Y3:12:PRO:O	49:Y3:14:GLY:N	2.55	0.40
49:Y3:52:HIS:CD2	49:Y3:53:LEU:HG	2.57	0.40
50:Y4:14:ILE:HG23	50:Y4:14:ILE:O	2.21	0.40
52:Y6:28:ARG:HB3	52:Y6:30:THR:C	2.41	0.40
25:YA:1429:G:H2'	25:YA:1430:C:C6	2.57	0.40
25:YA:1698:A:H4'	25:YA:1699:G:OP1	2.22	0.40
25:YA:1759:A:H1'	25:YA:2711:A:C2	2.57	0.40
25:YA:661:C:H5''	35:YP:15:ARG:NH2	2.37	0.40
25:YA:699:A:H2'	25:YA:700:G:O4'	2.22	0.40
26:YB:66:A:O2'	26:YB:67:G:P	2.80	0.40
25:YA:1800:C:OP2	27:YD:183:ARG:NH1	2.54	0.40
27:YD:237:GLU:O	27:YD:238:GLY:C	2.59	0.40
31:YH:46:GLU:OE1	31:YH:51:ARG:NH1	2.54	0.40
40:YU:17:ILE:HA	40:YU:17:ILE:HD13	1.92	0.40
40:YU:19:LYS:O	40:YU:22:LYS:HB2	2.22	0.40
25:YA:65:C:H5'	43:YX:71:GLY:HA3	2.03	0.40
44:YY:89:PHE:C	44:YY:90:LEU:HD13	2.42	0.40
45:YZ:136:PHE:CD1	45:YZ:138:GLU:HG3	2.56	0.40
45:YZ:140:ASP:N	45:YZ:140:ASP:OD2	2.51	0.40
1:QA:1169:A:C6	1:QA:1170:A:C6	3.09	0.40
1:QA:1312:G:H2'	1:QA:1313:U:H6	1.87	0.40
1:QA:186(C):G:C6	1:QA:191(E):G:C6	3.10	0.40
1:QA:514:C:H2'	1:QA:515:G:C8	2.57	0.40
1:QA:557:G:C6	1:QA:558:G:C6	3.09	0.40
4:QD:176:LEU:HD12	4:QD:182:LYS:O	2.21	0.40
5:QE:50:GLU:HG3	5:QE:52:PRO:HD2	2.04	0.40
7:QG:117:ALA:HA	7:QG:120:ILE:HG12	2.03	0.40
10:QJ:61:GLU:OE1	14:QN:58:LYS:HE2	2.21	0.40
22:QV:4:G:H2'	22:QV:5:G:O4'	2.21	0.40
25:RA:123:G:O3'	25:RA:1376:C:H4'	2.22	0.40
25:RA:1638:C:H5''	25:RA:2710:C:O2'	2.21	0.40
25:RA:2302:G:C6	25:RA:2303:G:N7	2.90	0.40
25:RA:826:U:H4'	35:RP:55:ARG:HB3	2.03	0.40
27:RD:132:PRO:HG3	27:RD:190:TYR:CE1	2.56	0.40
33:RN:108:PRO:O	33:RN:113:GLY:HA3	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:RP:25:SER:OG	35:RP:26:GLY:O	2.38	0.40
37:RR:116:LEU:HD23	37:RR:116:LEU:HA	1.83	0.40
38:RS:69:VAL:HG13	38:RS:101:LEU:HD22	2.03	0.40
38:RS:23:ARG:HB2	38:RS:86:ALA:HB2	2.03	0.40
39:RT:120:ARG:HA	39:RT:123:GLN:NE2	2.37	0.40
42:RW:73:ALA:HB3	42:RW:106:ILE:HG23	2.02	0.40
1:XA:1239:A:H62	1:XA:1299:A:N6	2.19	0.40
1:XA:233:C:H2'	1:XA:234:C:H6	1.86	0.40
3:XC:56:ASP:HB2	3:XC:67:THR:HB	2.03	0.40
5:XE:12:LEU:HB3	5:XE:31:LEU:CB	2.52	0.40
9:XI:5:TYR:HA	9:XI:17:VAL:O	2.21	0.40
10:XJ:77:PRO:O	10:XJ:79:ARG:NH1	2.54	0.40
25:YA:1321:A:H2'	25:YA:1322:A:O4'	2.21	0.40
25:YA:1406:U:H2'	25:YA:1407:C:C6	2.57	0.40
25:YA:141:A:H1'	25:YA:1408:C:O4'	2.21	0.40
25:YA:1547:C:O2'	25:YA:1548:C:H5'	2.21	0.40
25:YA:1931:U:H5	25:YA:1969:A:N7	2.20	0.40
25:YA:2025:C:H2'	25:YA:2026:C:C6	2.55	0.40
25:YA:226:G:O2'	25:YA:227:A:P	2.79	0.40
25:YA:305:U:H2'	25:YA:306:U:C6	2.56	0.40
25:YA:607:U:N3	25:YA:621:A:C2	2.82	0.40
25:YA:638:G:H2'	25:YA:639:U:C6	2.56	0.40
25:YA:69:C:H2'	25:YA:70:G:H8	1.86	0.40
25:YA:747:U:O2	25:YA:2014:A:H1'	2.21	0.40
25:YA:888:C:C3'	25:YA:889:C:H4'	2.48	0.40
29:YF:122:LYS:HD3	29:YF:122:LYS:HA	1.86	0.40
29:YF:125:LEU:HD21	29:YF:199:TRP:CE3	2.57	0.40
32:YI:110:ASP:HB2	32:YI:130:TYR:HE1	1.87	0.40
32:YI:90:GLY:O	32:YI:121:LYS:HE2	2.21	0.40
40:YU:61:TRP:O	40:YU:65:ILE:HG13	2.22	0.40
41:YV:21:ARG:HD2	41:YV:91:TYR:CE1	2.56	0.40
41:YV:3:ALA:HA	41:YV:40:LEU:O	2.21	0.40
45:YZ:28:MET:O	45:YZ:34:ASN:HA	2.22	0.40

All (2) 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	Distance(Å)	Clash(Å)
25:RA:1593:G:O2'	26:RB:54:G:OP1[1.655]	2.12	0.08
32:RI:91:SER:OG	1:XA:368:U:OP1[4.555]	2.15	0.05

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	QB	235/256 (92%)	175 (74%)	43 (18%)	17 (7%)	2	4
2	XB	235/256 (92%)	178 (76%)	42 (18%)	15 (6%)	2	5
3	QC	203/239 (85%)	163 (80%)	34 (17%)	6 (3%)	7	26
3	XC	203/239 (85%)	171 (84%)	29 (14%)	3 (2%)	15	50
4	QD	206/209 (99%)	175 (85%)	25 (12%)	6 (3%)	7	27
4	XD	206/209 (99%)	177 (86%)	24 (12%)	5 (2%)	9	34
5	QE	149/162 (92%)	136 (91%)	8 (5%)	5 (3%)	6	22
5	XE	149/162 (92%)	133 (89%)	13 (9%)	3 (2%)	11	40
6	QF	99/101 (98%)	95 (96%)	4 (4%)	0	100	100
6	XF	99/101 (98%)	94 (95%)	5 (5%)	0	100	100
7	QG	153/156 (98%)	135 (88%)	16 (10%)	2 (1%)	18	54
7	XG	153/156 (98%)	138 (90%)	13 (8%)	2 (1%)	18	54
8	QH	136/138 (99%)	121 (89%)	14 (10%)	1 (1%)	30	72
8	XH	136/138 (99%)	120 (88%)	12 (9%)	4 (3%)	7	27
9	QI	125/128 (98%)	103 (82%)	17 (14%)	5 (4%)	5	16
9	XI	125/128 (98%)	97 (78%)	24 (19%)	4 (3%)	6	24
10	QJ	97/105 (92%)	75 (77%)	19 (20%)	3 (3%)	7	25
10	XJ	97/105 (92%)	78 (80%)	14 (14%)	5 (5%)	3	9
11	QK	117/129 (91%)	100 (86%)	14 (12%)	3 (3%)	8	31
11	XK	117/129 (91%)	100 (86%)	15 (13%)	2 (2%)	14	45
12	QL	123/132 (93%)	98 (80%)	18 (15%)	7 (6%)	3	7
12	XL	123/132 (93%)	98 (80%)	15 (12%)	10 (8%)	1	3
13	QM	119/126 (94%)	95 (80%)	15 (13%)	9 (8%)	2	3
13	XM	119/126 (94%)	94 (79%)	16 (13%)	9 (8%)	2	3
14	QN	58/61 (95%)	48 (83%)	6 (10%)	4 (7%)	2	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	XN	58/61 (95%)	46 (79%)	6 (10%)	6 (10%)	1	2
15	QO	86/89 (97%)	80 (93%)	5 (6%)	1 (1%)	19	57
15	XO	86/89 (97%)	80 (93%)	4 (5%)	2 (2%)	10	35
16	QP	82/88 (93%)	73 (89%)	8 (10%)	1 (1%)	19	57
16	XP	82/88 (93%)	71 (87%)	10 (12%)	1 (1%)	19	57
17	QQ	98/105 (93%)	91 (93%)	5 (5%)	2 (2%)	11	40
17	XQ	98/105 (93%)	88 (90%)	10 (10%)	0	100	100
18	QR	68/88 (77%)	56 (82%)	9 (13%)	3 (4%)	4	14
18	XR	68/88 (77%)	61 (90%)	6 (9%)	1 (2%)	15	50
19	QS	82/93 (88%)	56 (68%)	15 (18%)	11 (13%)	0	1
19	XS	82/93 (88%)	54 (66%)	17 (21%)	11 (13%)	0	1
20	QT	97/106 (92%)	76 (78%)	15 (16%)	6 (6%)	2	6
20	XT	97/106 (92%)	75 (77%)	16 (16%)	6 (6%)	2	6
21	QU	23/27 (85%)	19 (83%)	3 (13%)	1 (4%)	4	14
21	XU	23/27 (85%)	18 (78%)	4 (17%)	1 (4%)	4	14
27	RD	270/276 (98%)	226 (84%)	32 (12%)	12 (4%)	4	14
27	YD	270/276 (98%)	227 (84%)	34 (13%)	9 (3%)	6	23
28	RE	203/206 (98%)	147 (72%)	36 (18%)	20 (10%)	1	2
28	YE	203/206 (98%)	142 (70%)	41 (20%)	20 (10%)	1	2
29	RF	200/210 (95%)	167 (84%)	20 (10%)	13 (6%)	2	5
29	YF	200/210 (95%)	167 (84%)	25 (12%)	8 (4%)	5	16
30	RG	179/182 (98%)	139 (78%)	26 (14%)	14 (8%)	1	3
30	YG	179/182 (98%)	142 (79%)	25 (14%)	12 (7%)	2	4
31	RH	168/180 (93%)	114 (68%)	33 (20%)	21 (12%)	1	1
31	YH	168/180 (93%)	121 (72%)	23 (14%)	24 (14%)	0	1
32	RI	144/148 (97%)	101 (70%)	30 (21%)	13 (9%)	1	2
32	YI	144/148 (97%)	104 (72%)	23 (16%)	17 (12%)	1	1
33	RN	136/140 (97%)	104 (76%)	20 (15%)	12 (9%)	1	3
33	YN	136/140 (97%)	106 (78%)	16 (12%)	14 (10%)	1	2
34	RO	120/122 (98%)	109 (91%)	9 (8%)	2 (2%)	14	45
34	YO	120/122 (98%)	108 (90%)	10 (8%)	2 (2%)	14	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	RP	148/150 (99%)	106 (72%)	28 (19%)	14 (10%)	1	2
35	YP	148/150 (99%)	108 (73%)	23 (16%)	17 (12%)	1	1
36	RQ	139/141 (99%)	99 (71%)	22 (16%)	18 (13%)	0	1
36	YQ	139/141 (99%)	98 (70%)	22 (16%)	19 (14%)	0	1
37	RR	116/118 (98%)	106 (91%)	5 (4%)	5 (4%)	4	14
37	YR	116/118 (98%)	99 (85%)	11 (10%)	6 (5%)	3	9
38	RS	109/112 (97%)	76 (70%)	22 (20%)	11 (10%)	1	2
38	YS	109/112 (97%)	78 (72%)	18 (16%)	13 (12%)	1	1
39	RT	135/146 (92%)	106 (78%)	17 (13%)	12 (9%)	1	2
39	YT	135/146 (92%)	108 (80%)	17 (13%)	10 (7%)	2	4
40	RU	115/118 (98%)	102 (89%)	9 (8%)	4 (4%)	6	21
40	YU	115/118 (98%)	101 (88%)	10 (9%)	4 (4%)	6	21
41	RV	99/101 (98%)	82 (83%)	11 (11%)	6 (6%)	2	6
41	YV	99/101 (98%)	79 (80%)	12 (12%)	8 (8%)	1	3
42	RW	111/113 (98%)	99 (89%)	8 (7%)	4 (4%)	5	20
42	YW	111/113 (98%)	100 (90%)	9 (8%)	2 (2%)	13	43
43	RX	90/96 (94%)	77 (86%)	11 (12%)	2 (2%)	10	37
43	YX	90/96 (94%)	82 (91%)	6 (7%)	2 (2%)	10	37
44	RY	100/110 (91%)	71 (71%)	13 (13%)	16 (16%)	0	0
44	YY	100/110 (91%)	70 (70%)	18 (18%)	12 (12%)	1	1
45	RZ	181/206 (88%)	124 (68%)	32 (18%)	25 (14%)	0	1
45	YZ	181/206 (88%)	124 (68%)	40 (22%)	17 (9%)	1	2
46	R0	80/85 (94%)	65 (81%)	14 (18%)	1 (1%)	18	54
46	Y0	80/85 (94%)	73 (91%)	7 (9%)	0	100	100
47	R1	95/98 (97%)	75 (79%)	11 (12%)	9 (10%)	1	2
47	Y1	95/98 (97%)	72 (76%)	17 (18%)	6 (6%)	2	5
48	R2	67/72 (93%)	53 (79%)	9 (13%)	5 (8%)	2	3
48	Y2	67/72 (93%)	55 (82%)	6 (9%)	6 (9%)	1	2
49	R3	57/60 (95%)	52 (91%)	3 (5%)	2 (4%)	6	21
49	Y3	57/60 (95%)	52 (91%)	4 (7%)	1 (2%)	13	43
50	R4	69/71 (97%)	35 (51%)	18 (26%)	16 (23%)	0	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	Y4	69/71 (97%)	35 (51%)	15 (22%)	19 (28%)	0	0
51	R5	57/60 (95%)	44 (77%)	11 (19%)	2 (4%)	6	21
51	Y5	57/60 (95%)	46 (81%)	9 (16%)	2 (4%)	6	21
52	R6	47/54 (87%)	23 (49%)	13 (28%)	11 (23%)	0	0
52	Y6	47/54 (87%)	22 (47%)	17 (36%)	8 (17%)	0	0
53	R7	47/49 (96%)	45 (96%)	1 (2%)	1 (2%)	11	39
53	Y7	47/49 (96%)	43 (92%)	3 (6%)	1 (2%)	11	39
54	R8	62/65 (95%)	51 (82%)	6 (10%)	5 (8%)	1	3
54	Y8	62/65 (95%)	48 (77%)	10 (16%)	4 (6%)	2	5
55	R9	35/37 (95%)	35 (100%)	0	0	100	100
55	Y9	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
All	All	11470/12128 (95%)	9215 (80%)	1533 (13%)	722 (6%)	2	5

All (722) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	QB	236	TYR
3	QC	12	LEU
3	QC	190	ARG
4	QD	28	SER
13	QM	67	GLU
13	QM	106	ASN
13	QM	118	ALA
14	QN	16	PHE
19	QS	12	ASP
19	QS	45	VAL
20	QT	49	ALA
27	RD	26	LYS
27	RD	122	ASP
27	RD	242	ARG
28	RE	22	PRO
28	RE	53	PRO
28	RE	63	LEU
28	RE	68	ALA
28	RE	71	GLY
28	RE	93	VAL
31	RH	12	PRO
31	RH	86	GLU

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Mol	Chain	Res	Type
31	RH	126	PRO
31	RH	127	GLU
31	RH	154	PRO
31	RH	168	PRO
31	RH	169	VAL
32	RI	115	ALA
32	RI	133	HIS
33	RN	9	VAL
33	RN	22	THR
33	RN	96	GLU
33	RN	131	GLN
34	RO	5	GLN
35	RP	6	LEU
35	RP	10	PRO
35	RP	15	ARG
35	RP	65	ARG
35	RP	95	VAL
35	RP	141	ALA
35	RP	148	LEU
36	RQ	22	LYS
36	RQ	66	ILE
36	RQ	78	PRO
36	RQ	90	VAL
36	RQ	139	GLU
37	RR	3	HIS
37	RR	4	LEU
38	RS	57	LYS
38	RS	88	ASP
38	RS	89	ARG
39	RT	2	ASN
39	RT	3	ARG
39	RT	106	SER
39	RT	112	ARG
39	RT	124	ASP
40	RU	91	ASP
41	RV	48	GLY
41	RV	50	PRO
41	RV	100	ARG
42	RW	111	HIS
44	RY	3	VAL
44	RY	50	ARG
44	RY	57	GLN

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Mol	Chain	Res	Type
44	RY	77	PRO
44	RY	78	ALA
45	RZ	13	GLU
48	R2	47	ASN
48	R2	48	HIS
48	R2	70	GLN
48	R2	71	ASN
50	R4	16	CYS
50	R4	18	CYS
50	R4	40	HIS
50	R4	43	TYR
50	R4	49	PHE
50	R4	50	VAL
50	R4	53	GLU
51	R5	4	HIS
51	R5	47	PRO
52	R6	15	GLU
54	R8	34	TRP
54	R8	52	LYS
54	R8	62	LEU
2	XB	230	VAL
2	XB	236	TYR
3	XC	12	LEU
3	XC	79	ARG
4	XD	154	ASN
11	XK	91	ARG
12	XL	48	PRO
12	XL	64	TYR
13	XM	67	GLU
13	XM	106	ASN
13	XM	118	ALA
14	XN	14	PRO
14	XN	16	PHE
14	XN	52	GLN
19	XS	3	ARG
19	XS	12	ASP
20	XT	48	LYS
20	XT	96	GLY
27	YD	26	LYS
27	YD	28	GLU
27	YD	122	ASP
27	YD	123	ALA

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Mol	Chain	Res	Type
28	YE	2	LYS
28	YE	19	ARG
28	YE	22	PRO
28	YE	53	PRO
28	YE	63	LEU
28	YE	71	GLY
29	YF	73	ALA
29	YF	134	GLY
30	YG	96	ARG
31	YH	3	ARG
31	YH	12	PRO
31	YH	13	LYS
31	YH	86	GLU
31	YH	126	PRO
31	YH	127	GLU
31	YH	128	PRO
31	YH	168	PRO
31	YH	169	VAL
32	YI	133	HIS
32	YI	145	VAL
33	YN	9	VAL
33	YN	22	THR
33	YN	36	GLY
35	YP	6	LEU
35	YP	10	PRO
35	YP	14	LYS
35	YP	15	ARG
35	YP	25	SER
35	YP	27	HIS
35	YP	95	VAL
35	YP	106	LEU
35	YP	148	LEU
36	YQ	18	LYS
36	YQ	22	LYS
36	YQ	25	ASP
36	YQ	79	LEU
36	YQ	86	GLY
36	YQ	90	VAL
36	YQ	134	ARG
37	YR	3	HIS
38	YS	82	ILE
38	YS	88	ASP

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Mol	Chain	Res	Type
38	YS	107	GLU
39	YT	2	ASN
39	YT	123	GLN
39	YT	124	ASP
40	YU	90	VAL
40	YU	91	ASP
40	YU	93	LYS
41	YV	45	THR
43	YX	68	ARG
44	YY	50	ARG
44	YY	57	GLN
44	YY	77	PRO
44	YY	78	ALA
45	YZ	6	LYS
45	YZ	53	ILE
45	YZ	146	ILE
45	YZ	152	ALA
45	YZ	159	PRO
47	Y1	30	VAL
47	Y1	84	GLY
47	Y1	91	LYS
47	Y1	95	LEU
48	Y2	16	LEU
48	Y2	43	GLN
48	Y2	47	ASN
48	Y2	48	HIS
50	Y4	24	THR
50	Y4	40	HIS
50	Y4	49	PHE
51	Y5	4	HIS
52	Y6	15	GLU
53	Y7	48	LYS
54	Y8	52	LYS
54	Y8	62	LEU
2	QB	15	VAL
2	QB	96	ARG
2	QB	229	VAL
2	QB	230	VAL
2	QB	237	ALA
3	QC	79	ARG
4	QD	51	PRO
4	QD	154	ASN

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Mol	Chain	Res	Type
5	QE	115	VAL
8	QH	129	VAL
9	QI	41	VAL
9	QI	117	HIS
11	QK	101	SER
12	QL	47	LYS
12	QL	91	LYS
13	QM	12	ASN
14	QN	12	ARG
17	QQ	74	LEU
17	QQ	81	ARG
19	QS	3	ARG
19	QS	11	VAL
19	QS	26	GLY
19	QS	31	ILE
19	QS	41	VAL
27	RD	32	SER
28	RE	50	GLY
28	RE	60	ASN
28	RE	66	HIS
28	RE	72	VAL
28	RE	90	THR
28	RE	92	THR
28	RE	187	ALA
29	RF	17	ARG
29	RF	67	GLN
29	RF	73	ALA
29	RF	89	VAL
29	RF	134	GLY
29	RF	198	ALA
30	RG	4	ASP
30	RG	5	VAL
30	RG	14	GLU
30	RG	96	ARG
30	RG	137	GLU
30	RG	146	TYR
31	RH	8	PRO
31	RH	128	PRO
31	RH	137	ASP
31	RH	153	LYS
31	RH	155	SER
32	RI	10	GLU

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Mol	Chain	Res	Type
32	RI	11	ASN
32	RI	102	SER
32	RI	117	GLU
32	RI	145	VAL
35	RP	11	GLY
35	RP	90	ARG
35	RP	103	ALA
35	RP	106	LEU
36	RQ	6	ARG
36	RQ	25	ASP
36	RQ	27	VAL
36	RQ	133	ARG
37	RR	107	ASP
38	RS	4	LEU
38	RS	107	GLU
39	RT	37	GLY
40	RU	90	VAL
41	RV	49	THR
41	RV	79	VAL
43	RX	41	ASN
44	RY	45	VAL
44	RY	48	ALA
44	RY	63	LYS
45	RZ	6	LYS
45	RZ	53	ILE
45	RZ	92	SER
45	RZ	111	VAL
45	RZ	112	ARG
45	RZ	153	SER
45	RZ	177	PRO
45	RZ	179	ASP
47	R1	30	VAL
47	R1	80	LEU
47	R1	84	GLY
47	R1	91	LYS
47	R1	95	LEU
48	R2	43	GLN
49	R3	26	LEU
50	R4	24	THR
50	R4	30	GLU
50	R4	51	ASP
50	R4	66	SER

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Mol	Chain	Res	Type
52	R6	7	ILE
52	R6	45	LYS
2	XB	15	VAL
4	XD	30	LYS
4	XD	166	LYS
5	XE	115	VAL
7	XG	55	GLY
8	XH	50	ARG
9	XI	41	VAL
9	XI	127	LYS
10	XJ	30	SER
10	XJ	86	MET
12	XL	63	GLY
12	XL	91	LYS
12	XL	115	LYS
13	XM	6	GLY
13	XM	21	TYR
19	XS	41	VAL
19	XS	45	VAL
20	XT	99	LEU
27	YD	238	GLY
27	YD	242	ARG
28	YE	7	VAL
28	YE	204	ALA
29	YF	128	ALA
29	YF	132	VAL
29	YF	181	LEU
30	YG	4	ASP
30	YG	36	LYS
31	YH	27	LYS
31	YH	50	VAL
31	YH	85	LYS
31	YH	152	ARG
31	YH	155	SER
33	YN	23	LEU
33	YN	96	GLU
34	YO	5	GLN
35	YP	66	GLY
35	YP	93	GLY
35	YP	141	ALA
36	YQ	6	ARG
36	YQ	60	ARG

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Mol	Chain	Res	Type
36	YQ	137	TYR
37	YR	4	LEU
37	YR	45	ARG
37	YR	107	ASP
38	YS	12	PHE
38	YS	57	LYS
38	YS	109	GLY
39	YT	13	ARG
39	YT	39	ARG
39	YT	106	SER
41	YV	31	ALA
41	YV	48	GLY
41	YV	79	VAL
42	YW	111	HIS
44	YY	58	GLY
44	YY	102	CYS
45	YZ	13	GLU
45	YZ	81	ARG
48	Y2	70	GLN
48	Y2	71	ASN
50	Y4	5	ILE
50	Y4	18	CYS
50	Y4	22	ILE
50	Y4	37	SER
50	Y4	43	TYR
50	Y4	50	VAL
52	Y6	7	ILE
52	Y6	16	CYS
52	Y6	33	LYS
2	QB	26	PRO
2	QB	87	ARG
2	QB	204	ASN
2	QB	207	ALA
3	QC	4	LYS
3	QC	51	GLY
4	QD	155	LEU
5	QE	77	PRO
10	QJ	30	SER
11	QK	103	LEU
11	QK	125	PHE
12	QL	28	LYS
13	QM	120	LYS

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Mol	Chain	Res	Type
14	QN	14	PRO
15	QO	23	GLY
19	QS	9	VAL
19	QS	14	HIS
19	QS	28	LYS
20	QT	96	GLY
27	RD	46	GLN
27	RD	239	ARG
28	RE	79	ARG
28	RE	204	ALA
29	RF	133	ASN
30	RG	32	PRO
30	RG	116	ASP
31	RH	5	GLY
31	RH	27	LYS
31	RH	55	PRO
31	RH	87	LEU
31	RH	138	LYS
32	RI	15	VAL
32	RI	118	LYS
33	RN	8	GLN
33	RN	23	LEU
33	RN	95	PRO
33	RN	130	HIS
34	RO	97	ARG
35	RP	29	LYS
35	RP	67	MET
36	RQ	11	LYS
36	RQ	19	GLY
36	RQ	137	TYR
37	RR	74	LYS
38	RS	12	PHE
38	RS	61	ASN
39	RT	12	SER
39	RT	97	ALA
40	RU	117	GLN
43	RX	67	GLY
44	RY	58	GLY
45	RZ	7	ALA
45	RZ	66	SER
45	RZ	116	VAL
45	RZ	119	GLU

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Mol	Chain	Res	Type
45	RZ	152	ALA
47	R1	76	ARG
49	R3	27	GLY
52	R6	33	LYS
52	R6	35	GLU
52	R6	49	HIS
54	R8	31	HIS
54	R8	51	ALA
2	XB	13	ALA
2	XB	22	LYS
2	XB	24	TRP
2	XB	135	GLN
2	XB	207	ALA
4	XD	73	ARG
4	XD	155	LEU
7	XG	7	ALA
8	XH	2	LEU
9	XI	56	LEU
9	XI	95	LYS
10	XJ	59	SER
11	XK	103	LEU
13	XM	4	ILE
13	XM	12	ASN
13	XM	42	ALA
19	XS	27	GLU
19	XS	28	LYS
27	YD	32	SER
28	YE	20	ALA
28	YE	50	GLY
28	YE	79	ARG
28	YE	90	THR
28	YE	92	THR
28	YE	117	MET
28	YE	184	VAL
29	YF	198	ALA
31	YH	8	PRO
31	YH	10	PRO
31	YH	87	LEU
31	YH	137	ASP
31	YH	138	LYS
31	YH	153	LYS
31	YH	154	PRO

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Mol	Chain	Res	Type
32	YI	11	ASN
32	YI	12	LEU
32	YI	72	LEU
32	YI	113	ARG
32	YI	122	GLU
33	YN	7	LYS
33	YN	131	GLN
35	YP	16	ARG
35	YP	29	LYS
35	YP	65	ARG
36	YQ	19	GLY
36	YQ	105	GLU
36	YQ	133	ARG
37	YR	86	ARG
38	YS	4	LEU
38	YS	11	LYS
39	YT	97	ALA
41	YV	49	THR
41	YV	53	GLU
41	YV	100	ARG
44	YY	42	VAL
44	YY	63	LYS
45	YZ	59	LEU
45	YZ	92	SER
45	YZ	166	SER
49	Y3	3	ARG
50	Y4	9	LEU
50	Y4	23	GLU
50	Y4	30	GLU
50	Y4	34	GLU
50	Y4	66	SER
51	Y5	47	PRO
52	Y6	19	ARG
52	Y6	49	HIS
54	Y8	30	ARG
54	Y8	34	TRP
2	QB	22	LYS
2	QB	126	GLU
2	QB	209	ARG
4	QD	171	GLY
9	QI	56	LEU
12	QL	27	LEU

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Mol	Chain	Res	Type
12	QL	48	PRO
13	QM	6	GLY
13	QM	13	LYS
18	QR	20	ALA
18	QR	54	ARG
20	QT	71	THR
21	QU	9	ARG
27	RD	3	VAL
27	RD	123	ALA
27	RD	237	GLU
28	RE	78	LEU
29	RF	66	PRO
29	RF	197	ASP
30	RG	36	LYS
30	RG	86	MET
31	RH	92	ILE
32	RI	122	GLU
35	RP	21	ARG
36	RQ	21	THR
36	RQ	28	ALA
36	RQ	86	GLY
36	RQ	104	PHE
36	RQ	105	GLU
37	RR	71	GLN
38	RS	109	GLY
39	RT	38	ASN
39	RT	39	ARG
40	RU	98	LEU
42	RW	18	ARG
42	RW	63	ASP
42	RW	68	ARG
44	RY	4	LYS
44	RY	53	PRO
44	RY	99	CYS
45	RZ	108	PRO
45	RZ	165	VAL
52	R6	16	CYS
53	R7	48	LYS
2	XB	19	HIS
2	XB	101	MET
2	XB	155	LEU
5	XE	70	PRO

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Mol	Chain	Res	Type
8	XH	129	VAL
12	XL	19	ARG
12	XL	28	LYS
14	XN	15	LYS
14	XN	32	SER
15	XO	88	ARG
18	XR	20	ALA
19	XS	9	VAL
20	XT	84	LEU
20	XT	98	PRO
21	XU	9	ARG
30	YG	14	GLU
30	YG	82	LEU
30	YG	86	MET
30	YG	116	ASP
31	YH	83	TYR
32	YI	10	GLU
32	YI	87	LYS
32	YI	114	LEU
33	YN	11	PRO
33	YN	28	THR
33	YN	47	ALA
36	YQ	104	PHE
36	YQ	140	ALA
38	YS	89	ARG
38	YS	96	GLY
39	YT	17	THR
43	YX	40	LYS
44	YY	51	VAL
44	YY	53	PRO
45	YZ	160	GLY
50	Y4	16	CYS
50	Y4	25	TYR
50	Y4	54	GLY
50	Y4	60	GLN
52	Y6	35	GLU
2	QB	234	PRO
4	QD	42	GLN
5	QE	70	PRO
5	QE	96	PRO
7	QG	7	ALA
9	QI	121	ARG

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Mol	Chain	Res	Type
12	QL	19	ARG
12	QL	121	GLY
13	QM	4	ILE
18	QR	26	LEU
20	QT	73	HIS
20	QT	97	ALA
27	RD	238	GLY
28	RE	54	GLN
29	RF	8	GLN
30	RG	82	LEU
31	RH	21	PRO
31	RH	83	TYR
32	RI	12	LEU
32	RI	30	LEU
33	RN	18	ALA
33	RN	57	ALA
33	RN	135	PRO
38	RS	97	ARG
38	RS	110	LEU
39	RT	40	THR
44	RY	5	MET
44	RY	39	VAL
44	RY	41	GLY
44	RY	62	GLU
45	RZ	12	GLY
45	RZ	51	ALA
45	RZ	61	LEU
45	RZ	158	PRO
45	RZ	181	GLU
46	R0	18	ALA
47	R1	74	VAL
47	R1	82	LEU
50	R4	5	ILE
50	R4	23	GLU
50	R4	28	LYS
50	R4	68	ARG
52	R6	9	LEU
52	R6	19	ARG
2	XB	121	LEU
3	XC	181	ASN
10	XJ	27	ALA
12	XL	27	LEU

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Mol	Chain	Res	Type
12	XL	65	GLU
13	XM	101	GLN
15	XO	23	GLY
20	XT	97	ALA
27	YD	3	VAL
27	YD	46	GLN
28	YE	68	ALA
28	YE	82	ARG
28	YE	86	PRO
30	YG	5	VAL
30	YG	53	LEU
30	YG	117	PHE
31	YH	151	ILE
32	YI	18	VAL
32	YI	71	ILE
32	YI	117	GLU
32	YI	118	LYS
33	YN	95	PRO
33	YN	127	ASP
33	YN	134	ARG
33	YN	135	PRO
36	YQ	11	LYS
36	YQ	27	VAL
38	YS	94	TYR
38	YS	110	LEU
39	YT	86	ILE
40	YU	117	GLN
41	YV	50	PRO
44	YY	39	VAL
45	YZ	51	ALA
45	YZ	61	LEU
45	YZ	62	PRO
45	YZ	168	GLU
45	YZ	181	GLU
47	Y1	74	VAL
50	Y4	14	ILE
52	Y6	21	TYR
2	QB	155	LEU
10	QJ	82	ILE
13	QM	10	PRO
14	QN	15	LYS
20	QT	98	PRO

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Mol	Chain	Res	Type
27	RD	125	ILE
28	RE	82	ARG
29	RF	130	ALA
30	RG	52	ILE
30	RG	88	ILE
30	RG	117	PHE
38	RS	82	ILE
45	RZ	62	PRO
45	RZ	166	SER
47	R1	55	GLY
50	R4	11	PRO
52	R6	21	TYR
52	R6	34	LEU
2	XB	26	PRO
2	XB	126	GLU
2	XB	237	ALA
10	XJ	91	PRO
14	XN	60	SER
19	XS	7	LYS
28	YE	72	VAL
29	YF	58	ALA
34	YO	97	ARG
35	YP	7	ARG
36	YQ	62	GLY
36	YQ	81	VAL
44	YY	3	VAL
47	Y1	55	GLY
2	QB	5	ILE
16	QP	46	PRO
28	RE	21	VAL
28	RE	86	PRO
29	RF	25	PRO
31	RH	166	GLY
5	XE	74	GLY
12	XL	18	VAL
32	YI	15	VAL
3	QC	81	GLY
5	QE	74	GLY
19	QS	46	GLY
27	RD	35	LYS
32	RI	13	GLY
19	XS	26	GLY

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Mol	Chain	Res	Type
19	XS	46	GLY
29	YF	66	PRO
32	YI	16	GLY
39	YT	37	GLY
45	YZ	101	PRO
7	QG	50	ILE
9	QI	89	ASN
10	QJ	37	PRO
33	RN	134	ARG
36	RQ	81	VAL
39	RT	86	ILE
8	XH	51	VAL
16	XP	46	PRO
19	XS	31	ILE
28	YE	21	VAL
32	YI	13	GLY
42	YW	14	PRO
29	RF	132	VAL
41	RV	54	GLY
45	RZ	94	GLU
30	YG	52	ILE
30	YG	88	ILE
31	YH	7	LEU
35	YP	24	GLY
37	YR	117	VAL
2	QB	227	GLY
45	RZ	106	GLY
38	YS	60	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	QB	205/220 (93%)	172 (84%)	33 (16%)	3	9
2	XB	205/220 (93%)	180 (88%)	25 (12%)	7	20
3	QC	159/188 (85%)	145 (91%)	14 (9%)	14	40
3	XC	159/188 (85%)	146 (92%)	13 (8%)	17	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	QD	180/181 (99%)	157 (87%)	23 (13%)	6	18
4	XD	180/181 (99%)	154 (86%)	26 (14%)	5	13
5	QE	116/123 (94%)	104 (90%)	12 (10%)	10	30
5	XE	116/123 (94%)	104 (90%)	12 (10%)	10	30
6	QF	90/90 (100%)	78 (87%)	12 (13%)	6	16
6	XF	90/90 (100%)	82 (91%)	8 (9%)	14	39
7	QG	126/127 (99%)	114 (90%)	12 (10%)	12	35
7	XG	126/127 (99%)	114 (90%)	12 (10%)	12	35
8	QH	119/119 (100%)	109 (92%)	10 (8%)	16	42
8	XH	119/119 (100%)	106 (89%)	13 (11%)	9	26
9	QI	98/99 (99%)	81 (83%)	17 (17%)	3	8
9	XI	98/99 (99%)	80 (82%)	18 (18%)	2	6
10	QJ	89/92 (97%)	77 (86%)	12 (14%)	6	15
10	XJ	89/92 (97%)	74 (83%)	15 (17%)	3	8
11	QK	90/99 (91%)	81 (90%)	9 (10%)	11	32
11	XK	90/99 (91%)	81 (90%)	9 (10%)	11	32
12	QL	104/109 (95%)	87 (84%)	17 (16%)	3	9
12	XL	104/109 (95%)	93 (89%)	11 (11%)	10	28
13	QM	97/101 (96%)	73 (75%)	24 (25%)	1	2
13	XM	97/101 (96%)	78 (80%)	19 (20%)	2	5
14	QN	49/50 (98%)	40 (82%)	9 (18%)	2	6
14	XN	49/50 (98%)	42 (86%)	7 (14%)	5	13
15	QO	79/80 (99%)	72 (91%)	7 (9%)	14	39
15	XO	79/80 (99%)	69 (87%)	10 (13%)	6	18
16	QP	72/74 (97%)	63 (88%)	9 (12%)	7	19
16	XP	72/74 (97%)	64 (89%)	8 (11%)	9	25
17	QQ	95/97 (98%)	87 (92%)	8 (8%)	16	42
17	XQ	95/97 (98%)	89 (94%)	6 (6%)	25	60
18	QR	61/77 (79%)	50 (82%)	11 (18%)	2	6
18	XR	61/77 (79%)	52 (85%)	9 (15%)	4	12
19	QS	73/80 (91%)	59 (81%)	14 (19%)	2	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	XS	73/80 (91%)	57 (78%)	16 (22%)	1	4
20	QT	76/82 (93%)	67 (88%)	9 (12%)	8	22
20	XT	76/82 (93%)	66 (87%)	10 (13%)	6	16
21	QU	20/22 (91%)	20 (100%)	0	100	100
21	XU	20/22 (91%)	19 (95%)	1 (5%)	34	72
27	RD	214/218 (98%)	175 (82%)	39 (18%)	2	6
27	YD	214/218 (98%)	181 (85%)	33 (15%)	4	11
28	RE	165/166 (99%)	126 (76%)	39 (24%)	1	2
28	YE	165/166 (99%)	137 (83%)	28 (17%)	3	8
29	RF	161/166 (97%)	132 (82%)	29 (18%)	2	6
29	YF	161/166 (97%)	137 (85%)	24 (15%)	4	12
30	RG	155/156 (99%)	134 (86%)	21 (14%)	6	15
30	YG	155/156 (99%)	133 (86%)	22 (14%)	5	13
31	RH	142/148 (96%)	121 (85%)	21 (15%)	4	12
31	YH	142/148 (96%)	115 (81%)	27 (19%)	2	6
32	RI	122/124 (98%)	99 (81%)	23 (19%)	2	6
32	YI	122/124 (98%)	92 (75%)	30 (25%)	1	2
33	RN	117/119 (98%)	97 (83%)	20 (17%)	3	8
33	YN	117/119 (98%)	96 (82%)	21 (18%)	2	7
34	RO	100/100 (100%)	90 (90%)	10 (10%)	11	32
34	YO	100/100 (100%)	89 (89%)	11 (11%)	9	26
35	RP	116/116 (100%)	85 (73%)	31 (27%)	1	2
35	YP	116/116 (100%)	82 (71%)	34 (29%)	0	1
36	RQ	111/111 (100%)	95 (86%)	16 (14%)	5	13
36	YQ	111/111 (100%)	92 (83%)	19 (17%)	3	8
37	RR	101/101 (100%)	83 (82%)	18 (18%)	2	7
37	YR	101/101 (100%)	80 (79%)	21 (21%)	2	4
38	RS	87/88 (99%)	69 (79%)	18 (21%)	2	4
38	YS	87/88 (99%)	68 (78%)	19 (22%)	1	4
39	RT	120/127 (94%)	102 (85%)	18 (15%)	4	12
39	YT	120/127 (94%)	98 (82%)	22 (18%)	2	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	RU	93/94 (99%)	78 (84%)	15 (16%)	3	9
40	YU	93/94 (99%)	77 (83%)	16 (17%)	3	8
41	RV	82/82 (100%)	66 (80%)	16 (20%)	2	5
41	YV	82/82 (100%)	67 (82%)	15 (18%)	2	6
42	RW	92/92 (100%)	73 (79%)	19 (21%)	2	4
42	YW	92/92 (100%)	76 (83%)	16 (17%)	3	8
43	RX	74/78 (95%)	64 (86%)	10 (14%)	6	15
43	YX	74/78 (95%)	60 (81%)	14 (19%)	2	6
44	RY	85/91 (93%)	63 (74%)	22 (26%)	1	2
44	YY	85/91 (93%)	64 (75%)	21 (25%)	1	2
45	RZ	162/179 (90%)	133 (82%)	29 (18%)	2	7
45	YZ	162/179 (90%)	130 (80%)	32 (20%)	2	5
46	R0	65/67 (97%)	60 (92%)	5 (8%)	18	47
46	Y0	65/67 (97%)	59 (91%)	6 (9%)	13	37
47	R1	82/83 (99%)	73 (89%)	9 (11%)	9	26
47	Y1	82/83 (99%)	70 (85%)	12 (15%)	5	12
48	R2	64/67 (96%)	57 (89%)	7 (11%)	9	26
48	Y2	64/67 (96%)	47 (73%)	17 (27%)	1	2
49	R3	51/52 (98%)	45 (88%)	6 (12%)	8	22
49	Y3	51/52 (98%)	43 (84%)	8 (16%)	4	10
50	R4	63/63 (100%)	45 (71%)	18 (29%)	0	1
50	Y4	63/63 (100%)	43 (68%)	20 (32%)	0	1
51	R5	51/52 (98%)	37 (72%)	14 (28%)	0	1
51	Y5	51/52 (98%)	37 (72%)	14 (28%)	0	1
52	R6	48/52 (92%)	35 (73%)	13 (27%)	1	2
52	Y6	48/52 (92%)	38 (79%)	10 (21%)	2	4
53	R7	42/42 (100%)	34 (81%)	8 (19%)	2	6
53	Y7	42/42 (100%)	35 (83%)	7 (17%)	3	8
54	R8	54/55 (98%)	44 (82%)	10 (18%)	2	6
54	Y8	54/55 (98%)	41 (76%)	13 (24%)	1	2
55	R9	34/34 (100%)	32 (94%)	2 (6%)	28	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	Y9	34/34 (100%)	32 (94%)	2 (6%)	28	63
All	All	9702/10066 (96%)	8152 (84%)	1550 (16%)	3	9

All (1550) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	QB	5	ILE
2	QB	6	THR
2	QB	7	VAL
2	QB	8	LYS
2	QB	15	VAL
2	QB	23	ARG
2	QB	24	TRP
2	QB	32	ILE
2	QB	33	TYR
2	QB	53	ARG
2	QB	60	ASP
2	QB	67	THR
2	QB	82	ARG
2	QB	87	ARG
2	QB	92	TYR
2	QB	94	ASN
2	QB	101	MET
2	QB	109	SER
2	QB	119	GLU
2	QB	121	LEU
2	QB	150	SER
2	QB	155	LEU
2	QB	158	LEU
2	QB	163	PHE
2	QB	165	VAL
2	QB	168	THR
2	QB	172	ILE
2	QB	175	ARG
2	QB	187	LEU
2	QB	196	LEU
2	QB	204	ASN
2	QB	215	LEU
2	QB	217	ARG
3	QC	3	ASN
3	QC	5	ILE
3	QC	12	LEU

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Mol	Chain	Res	Type
3	QC	16	ARG
3	QC	21	ARG
3	QC	45	LYS
3	QC	52	LEU
3	QC	76	VAL
3	QC	94	LEU
3	QC	127	ARG
3	QC	131	ARG
3	QC	154	SER
3	QC	165	THR
3	QC	206	GLU
4	QD	3	ARG
4	QD	14	ARG
4	QD	22	LYS
4	QD	26	CYS
4	QD	30	LYS
4	QD	33	MET
4	QD	50	ARG
4	QD	58	LEU
4	QD	73	ARG
4	QD	76	ARG
4	QD	86	LYS
4	QD	94	LEU
4	QD	96	LEU
4	QD	122	ARG
4	QD	127	THR
4	QD	131	ARG
4	QD	135	LEU
4	QD	154	ASN
4	QD	175	SER
4	QD	187	ARG
4	QD	190	ASP
4	QD	191	ARG
4	QD	192	GLU
5	QE	10	MET
5	QE	12	LEU
5	QE	31	LEU
5	QE	34	VAL
5	QE	41	VAL
5	QE	51	VAL
5	QE	68	GLU
5	QE	79	GLU

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Mol	Chain	Res	Type
5	QE	81	GLU
5	QE	98	THR
5	QE	101	ILE
5	QE	153	LYS
6	QF	16	GLN
6	QF	21	LEU
6	QF	23	LYS
6	QF	43	LEU
6	QF	45	LEU
6	QF	47	ARG
6	QF	55	ASP
6	QF	69	GLU
6	QF	70	ASP
6	QF	72	VAL
6	QF	75	LEU
6	QF	98	LEU
7	QG	8	GLU
7	QG	54	THR
7	QG	80	VAL
7	QG	92	SER
7	QG	94	ARG
7	QG	104	LEU
7	QG	113	GLU
7	QG	114	ARG
7	QG	135	VAL
7	QG	136	LYS
7	QG	137	LYS
7	QG	155	ARG
8	QH	1	MET
8	QH	24	THR
8	QH	25	ASP
8	QH	26	VAL
8	QH	41	ARG
8	QH	99	GLU
8	QH	109	ILE
8	QH	112	LEU
8	QH	125	ARG
8	QH	129	VAL
9	QI	9	ARG
9	QI	10	ARG
9	QI	11	LYS
9	QI	23	ASN

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Mol	Chain	Res	Type
9	QI	47	LEU
9	QI	56	LEU
9	QI	64	THR
9	QI	65	VAL
9	QI	75	ASP
9	QI	95	LYS
9	QI	104	ARG
9	QI	105	ASP
9	QI	113	LYS
9	QI	114	TYR
9	QI	121	ARG
9	QI	125	TYR
9	QI	128	ARG
10	QJ	22	LYS
10	QJ	47	PHE
10	QJ	54	PHE
10	QJ	57	LYS
10	QJ	58	ASP
10	QJ	62	HIS
10	QJ	73	ASP
10	QJ	74	ILE
10	QJ	80	LYS
10	QJ	84	GLN
10	QJ	92	THR
10	QJ	96	ILE
11	QK	26	ASN
11	QK	29	ILE
11	QK	32	ILE
11	QK	34	ASP
11	QK	63	LEU
11	QK	92	GLU
11	QK	103	LEU
11	QK	109	VAL
11	QK	127	LYS
12	QL	17	LYS
12	QL	18	VAL
12	QL	20	LYS
12	QL	27	LEU
12	QL	33	ARG
12	QL	38	THR
12	QL	42	THR
12	QL	50	SER

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Mol	Chain	Res	Type
12	QL	54	LYS
12	QL	59	ARG
12	QL	60	LEU
12	QL	73	GLU
12	QL	83	VAL
12	QL	85	ILE
12	QL	89	ARG
12	QL	102	ARG
12	QL	113	ARG
13	QM	8	GLU
13	QM	11	ARG
13	QM	13	LYS
13	QM	17	VAL
13	QM	19	LEU
13	QM	45	VAL
13	QM	47	ASP
13	QM	48	LEU
13	QM	56	LEU
13	QM	57	ARG
13	QM	64	TRP
13	QM	66	LEU
13	QM	70	LEU
13	QM	77	ASN
13	QM	84	ILE
13	QM	88	ARG
13	QM	90	LEU
13	QM	98	VAL
13	QM	108	ARG
13	QM	111	LYS
13	QM	114	ARG
13	QM	115	LYS
13	QM	117	VAL
13	QM	122	LYS
14	QN	6	LEU
14	QN	12	ARG
14	QN	13	THR
14	QN	18	VAL
14	QN	33	VAL
14	QN	43	CYS
14	QN	44	LEU
14	QN	46	GLU
14	QN	57	ARG

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Mol	Chain	Res	Type
15	QO	3	ILE
15	QO	4	THR
15	QO	26	GLU
15	QO	31	LEU
15	QO	39	LEU
15	QO	64	ARG
15	QO	84	LYS
16	QP	2	VAL
16	QP	20	VAL
16	QP	26	ARG
16	QP	28	ARG
16	QP	33	ILE
16	QP	53	VAL
16	QP	67	THR
16	QP	69	THR
16	QP	71	ARG
17	QQ	37	LYS
17	QQ	38	ARG
17	QQ	52	LYS
17	QQ	59	ILE
17	QQ	62	SER
17	QQ	68	ARG
17	QQ	74	LEU
17	QQ	101	ARG
18	QR	26	LEU
18	QR	29	PHE
18	QR	31	LEU
18	QR	32	ARG
18	QR	36	ASN
18	QR	46	GLU
18	QR	54	ARG
18	QR	76	LEU
18	QR	82	THR
18	QR	83	GLU
18	QR	86	VAL
19	QS	5	LEU
19	QS	10	PHE
19	QS	12	ASP
19	QS	21	GLU
19	QS	28	LYS
19	QS	29	ARG
19	QS	30	LEU

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Mol	Chain	Res	Type
19	QS	37	ARG
19	QS	43	GLU
19	QS	44	MET
19	QS	63	THR
19	QS	67	VAL
19	QS	77	THR
19	QS	83	HIS
20	QT	17	ARG
20	QT	24	LEU
20	QT	45	GLN
20	QT	72	LEU
20	QT	73	HIS
20	QT	75	ASN
20	QT	80	ARG
20	QT	84	LEU
20	QT	93	GLU
27	RD	10	THR
27	RD	17	THR
27	RD	25	THR
27	RD	40	THR
27	RD	43	ARG
27	RD	44	ASN
27	RD	46	GLN
27	RD	49	ILE
27	RD	61	LEU
27	RD	65	ILE
27	RD	69	ARG
27	RD	71	ASP
27	RD	73	VAL
27	RD	83	GLU
27	RD	87	ASN
27	RD	88	ARG
27	RD	95	LEU
27	RD	103	ARG
27	RD	105	ILE
27	RD	106	ILE
27	RD	111	LEU
27	RD	134	ARG
27	RD	150	LYS
27	RD	155	LEU
27	RD	157	ARG
27	RD	173	VAL

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Mol	Chain	Res	Type
27	RD	192	THR
27	RD	211	ARG
27	RD	212	SER
27	RD	221	VAL
27	RD	229	VAL
27	RD	237	GLU
27	RD	242	ARG
27	RD	257	LEU
27	RD	259	THR
27	RD	261	LYS
27	RD	268	ARG
27	RD	271	ILE
27	RD	273	ARG
28	RE	2	LYS
28	RE	4	ILE
28	RE	7	VAL
28	RE	12	THR
28	RE	13	ARG
28	RE	16	ARG
28	RE	26	ILE
28	RE	27	LEU
28	RE	33	VAL
28	RE	34	VAL
28	RE	38	THR
28	RE	41	LYS
28	RE	42	ASP
28	RE	47	VAL
28	RE	49	LEU
28	RE	52	LEU
28	RE	54	GLN
28	RE	63	LEU
28	RE	77	ILE
28	RE	79	ARG
28	RE	80	GLU
28	RE	82	ARG
28	RE	92	THR
28	RE	101	ARG
28	RE	113	PHE
28	RE	116	VAL
28	RE	119	ARG
28	RE	127	ASP
28	RE	144	ARG

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Mol	Chain	Res	Type
28	RE	146	THR
28	RE	167	VAL
28	RE	175	VAL
28	RE	179	GLU
28	RE	181	LEU
28	RE	184	VAL
28	RE	197	ILE
28	RE	200	GLU
28	RE	202	LYS
28	RE	203	LYS
29	RF	9	ILE
29	RF	13	SER
29	RF	24	LEU
29	RF	28	ILE
29	RF	32	LEU
29	RF	33	LEU
29	RF	45	ARG
29	RF	57	VAL
29	RF	65	TRP
29	RF	68	LYS
29	RF	70	THR
29	RF	74	ARG
29	RF	77	ASP
29	RF	78	ILE
29	RF	84	VAL
29	RF	104	LYS
29	RF	107	LYS
29	RF	117	ARG
29	RF	127	GLU
29	RF	149	ASP
29	RF	158	THR
29	RF	161	GLU
29	RF	165	ARG
29	RF	174	VAL
29	RF	176	LEU
29	RF	181	LEU
29	RF	192	LEU
29	RF	194	MET
29	RF	197	ASP
30	RG	7	LEU
30	RG	10	LYS
30	RG	20	ILE

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Mol	Chain	Res	Type
30	RG	26	GLN
30	RG	33	ARG
30	RG	34	LEU
30	RG	43	LEU
30	RG	53	LEU
30	RG	54	GLU
30	RG	67	LYS
30	RG	71	THR
30	RG	88	ILE
30	RG	94	LEU
30	RG	98	ARG
30	RG	116	ASP
30	RG	118	ARG
30	RG	133	LEU
30	RG	147	ASP
30	RG	159	VAL
30	RG	167	GLU
30	RG	174	GLU
31	RH	3	ARG
31	RH	4	ILE
31	RH	7	LEU
31	RH	9	ILE
31	RH	27	LYS
31	RH	42	ARG
31	RH	43	VAL
31	RH	51	ARG
31	RH	59	ARG
31	RH	64	LEU
31	RH	77	LYS
31	RH	81	GLU
31	RH	88	LEU
31	RH	89	ILE
31	RH	105	LEU
31	RH	107	VAL
31	RH	132	ARG
31	RH	152	ARG
31	RH	153	LYS
31	RH	158	HIS
31	RH	169	VAL
32	RI	1	MET
32	RI	2	LYS
32	RI	9	LEU

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Mol	Chain	Res	Type
32	RI	10	GLU
32	RI	27	ARG
32	RI	31	LEU
32	RI	33	ARG
32	RI	38	LEU
32	RI	44	LEU
32	RI	56	LYS
32	RI	57	ARG
32	RI	70	GLU
32	RI	81	VAL
32	RI	92	VAL
32	RI	101	LEU
32	RI	113	ARG
32	RI	128	LEU
32	RI	129	THR
32	RI	130	TYR
32	RI	131	LYS
32	RI	135	GLU
32	RI	142	VAL
32	RI	145	VAL
33	RN	1	MET
33	RN	2	LYS
33	RN	5	VAL
33	RN	7	LYS
33	RN	12	ARG
33	RN	32	THR
33	RN	34	LEU
33	RN	43	THR
33	RN	48	MET
33	RN	60	ILE
33	RN	61	ARG
33	RN	62	VAL
33	RN	87	LEU
33	RN	90	MET
33	RN	96	GLU
33	RN	98	VAL
33	RN	109	LYS
33	RN	120	LEU
33	RN	127	ASP
33	RN	136	GLU
34	RO	3	GLN
34	RO	9	GLU

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Mol	Chain	Res	Type
34	RO	19	ILE
34	RO	24	VAL
34	RO	31	LYS
34	RO	49	ARG
34	RO	53	LYS
34	RO	69	ILE
34	RO	91	LEU
34	RO	102	VAL
35	RP	5	ASP
35	RP	6	LEU
35	RP	9	ASN
35	RP	14	LYS
35	RP	15	ARG
35	RP	16	ARG
35	RP	19	VAL
35	RP	21	ARG
35	RP	30	THR
35	RP	36	LYS
35	RP	41	ARG
35	RP	45	LEU
35	RP	50	ARG
35	RP	56	SER
35	RP	61	ARG
35	RP	62	LEU
35	RP	64	LYS
35	RP	70	GLN
35	RP	71	VAL
35	RP	75	ILE
35	RP	81	GLN
35	RP	88	LEU
35	RP	91	PHE
35	RP	100	LEU
35	RP	105	LEU
35	RP	107	LYS
35	RP	112	LEU
35	RP	133	SER
35	RP	138	LEU
35	RP	144	GLU
35	RP	146	VAL
36	RQ	17	LEU
36	RQ	26	TYR
36	RQ	27	VAL

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Mol	Chain	Res	Type
36	RQ	35	VAL
36	RQ	45	GLN
36	RQ	54	MET
36	RQ	60	ARG
36	RQ	79	LEU
36	RQ	81	VAL
36	RQ	82	ARG
36	RQ	83	MET
36	RQ	85	LYS
36	RQ	96	VAL
36	RQ	112	GLU
36	RQ	135	ASP
36	RQ	139	GLU
37	RR	1	MET
37	RR	6	SER
37	RR	9	LYS
37	RR	18	LEU
37	RR	29	LEU
37	RR	35	THR
37	RR	44	LEU
37	RR	63	ARG
37	RR	71	GLN
37	RR	75	LEU
37	RR	79	LEU
37	RR	91	GLN
37	RR	95	THR
37	RR	100	LEU
37	RR	104	ARG
37	RR	105	ARG
37	RR	117	VAL
37	RR	118	GLU
38	RS	3	ARG
38	RS	4	LEU
38	RS	12	PHE
38	RS	17	ARG
38	RS	20	ARG
38	RS	27	SER
38	RS	39	ILE
38	RS	44	LYS
38	RS	50	SER
38	RS	54	LEU
38	RS	56	LEU

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Mol	Chain	Res	Type
38	RS	57	LYS
38	RS	58	LEU
38	RS	59	LYS
38	RS	98	VAL
38	RS	101	LEU
38	RS	103	GLU
38	RS	106	ARG
39	RT	18	ASP
39	RT	27	THR
39	RT	30	VAL
39	RT	41	ARG
39	RT	42	ILE
39	RT	50	ILE
39	RT	51	ARG
39	RT	62	THR
39	RT	65	LYS
39	RT	74	ARG
39	RT	88	ILE
39	RT	89	VAL
39	RT	99	LEU
39	RT	105	LEU
39	RT	107	ASP
39	RT	112	ARG
39	RT	125	ARG
39	RT	128	GLU
40	RU	52	ARG
40	RU	55	ARG
40	RU	59	ARG
40	RU	60	LEU
40	RU	64	ARG
40	RU	69	CYS
40	RU	74	LEU
40	RU	90	VAL
40	RU	92	ARG
40	RU	94	ASN
40	RU	98	LEU
40	RU	108	GLU
40	RU	111	GLU
40	RU	114	LYS
40	RU	117	GLN
41	RV	13	ARG
41	RV	19	LYS

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Mol	Chain	Res	Type
41	RV	21	ARG
41	RV	22	VAL
41	RV	24	LYS
41	RV	35	LEU
41	RV	37	VAL
41	RV	45	THR
41	RV	47	VAL
41	RV	57	VAL
41	RV	61	VAL
41	RV	62	LEU
41	RV	64	HIS
41	RV	78	LYS
41	RV	79	VAL
41	RV	99	ILE
42	RW	11	ARG
42	RW	16	LYS
42	RW	18	ARG
42	RW	19	LEU
42	RW	20	VAL
42	RW	23	LEU
42	RW	27	LYS
42	RW	30	GLU
42	RW	40	ASN
42	RW	51	LEU
42	RW	60	ASN
42	RW	63	ASP
42	RW	67	ASP
42	RW	76	VAL
42	RW	82	LEU
42	RW	92	ARG
42	RW	100	THR
42	RW	106	ILE
42	RW	107	LEU
43	RX	12	VAL
43	RX	23	GLU
43	RX	27	THR
43	RX	30	VAL
43	RX	35	THR
43	RX	49	VAL
43	RX	65	ARG
43	RX	70	LEU
43	RX	80	ILE

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Mol	Chain	Res	Type
43	RX	81	VAL
44	RY	2	ARG
44	RY	13	VAL
44	RY	14	LEU
44	RY	27	VAL
44	RY	34	LYS
44	RY	37	VAL
44	RY	38	ILE
44	RY	43	ASN
44	RY	45	VAL
44	RY	55	TYR
44	RY	57	GLN
44	RY	61	ILE
44	RY	67	LEU
44	RY	70	SER
44	RY	75	ILE
44	RY	76	CYS
44	RY	87	LYS
44	RY	90	LEU
44	RY	95	LYS
44	RY	96	ILE
44	RY	97	ARG
44	RY	102	CYS
45	RZ	2	GLU
45	RZ	5	LEU
45	RZ	19	ARG
45	RZ	20	ARG
45	RZ	52	SER
45	RZ	53	ILE
45	RZ	60	GLU
45	RZ	70	LEU
45	RZ	71	VAL
45	RZ	81	ARG
45	RZ	87	ASP
45	RZ	91	LEU
45	RZ	92	SER
45	RZ	93	ASP
45	RZ	94	GLU
45	RZ	112	ARG
45	RZ	117	LEU
45	RZ	121	HIS
45	RZ	128	VAL

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Mol	Chain	Res	Type
45	RZ	131	ARG
45	RZ	142	SER
45	RZ	145	GLU
45	RZ	150	LEU
45	RZ	151	HIS
45	RZ	163	LEU
45	RZ	168	GLU
45	RZ	174	VAL
45	RZ	182	LYS
45	RZ	183	LEU
46	R0	7	LEU
46	R0	10	THR
46	R0	36	ILE
46	R0	53	MET
46	R0	74	ARG
47	R1	21	ARG
47	R1	41	ARG
47	R1	51	VAL
47	R1	62	VAL
47	R1	78	LYS
47	R1	80	LEU
47	R1	90	ILE
47	R1	91	LYS
47	R1	92	LYS
48	R2	17	SER
48	R2	24	LEU
48	R2	27	GLU
48	R2	32	LEU
48	R2	50	ILE
48	R2	53	LEU
48	R2	62	THR
49	R3	6	VAL
49	R3	8	LEU
49	R3	18	ASP
49	R3	32	GLN
49	R3	40	THR
49	R3	56	VAL
50	R4	13	ARG
50	R4	15	ILE
50	R4	23	GLU
50	R4	33	VAL
50	R4	34	GLU

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Mol	Chain	Res	Type
50	R4	37	SER
50	R4	42	PHE
50	R4	48	ARG
50	R4	49	PHE
50	R4	50	VAL
50	R4	52	THR
50	R4	57	GLU
50	R4	61	ARG
50	R4	62	ARG
50	R4	63	TYR
50	R4	66	SER
50	R4	67	TYR
50	R4	68	ARG
51	R5	4	HIS
51	R5	6	VAL
51	R5	11	THR
51	R5	21	SER
51	R5	23	HIS
51	R5	25	LEU
51	R5	29	THR
51	R5	36	CYS
51	R5	40	LYS
51	R5	51	TYR
51	R5	52	TYR
51	R5	56	LYS
51	R5	58	LEU
51	R5	60	VAL
52	R6	6	ARG
52	R6	8	LYS
52	R6	9	LEU
52	R6	10	LEU
52	R6	11	LEU
52	R6	17	LYS
52	R6	19	ARG
52	R6	23	THR
52	R6	27	LYS
52	R6	30	THR
52	R6	34	LEU
52	R6	37	ARG
52	R6	44	ARG
53	R7	1	MET
53	R7	2	LYS

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Mol	Chain	Res	Type
53	R7	4	THR
53	R7	9	ARG
53	R7	10	ARG
53	R7	14	LYS
53	R7	43	THR
53	R7	46	VAL
54	R8	14	VAL
54	R8	15	LYS
54	R8	34	TRP
54	R8	35	GLN
54	R8	44	LYS
54	R8	47	LYS
54	R8	49	VAL
54	R8	52	LYS
54	R8	64	TYR
54	R8	65	GLU
55	R9	1	MET
55	R9	29	ASN
2	XB	5	ILE
2	XB	7	VAL
2	XB	8	LYS
2	XB	15	VAL
2	XB	23	ARG
2	XB	24	TRP
2	XB	33	TYR
2	XB	36	ARG
2	XB	67	THR
2	XB	71	VAL
2	XB	82	ARG
2	XB	92	TYR
2	XB	113	HIS
2	XB	145	LEU
2	XB	155	LEU
2	XB	163	PHE
2	XB	172	ILE
2	XB	175	ARG
2	XB	178	ARG
2	XB	187	LEU
2	XB	195	ASP
2	XB	196	LEU
2	XB	204	ASN
2	XB	215	LEU

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Mol	Chain	Res	Type
2	XB	235	SER
3	XC	3	ASN
3	XC	5	ILE
3	XC	12	LEU
3	XC	21	ARG
3	XC	45	LYS
3	XC	47	LEU
3	XC	56	ASP
3	XC	94	LEU
3	XC	95	THR
3	XC	131	ARG
3	XC	178	LEU
3	XC	184	TYR
3	XC	192	THR
4	XD	3	ARG
4	XD	9	CYS
4	XD	15	GLU
4	XD	19	LEU
4	XD	30	LYS
4	XD	33	MET
4	XD	50	ARG
4	XD	53	ASP
4	XD	58	LEU
4	XD	73	ARG
4	XD	76	ARG
4	XD	84	LYS
4	XD	86	LYS
4	XD	96	LEU
4	XD	108	LEU
4	XD	122	ARG
4	XD	127	THR
4	XD	131	ARG
4	XD	137	SER
4	XD	150	GLU
4	XD	154	ASN
4	XD	175	SER
4	XD	187	ARG
4	XD	190	ASP
4	XD	193	ASP
4	XD	208	SER
5	XE	6	PHE
5	XE	7	GLU

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Mol	Chain	Res	Type
5	XE	10	MET
5	XE	11	ILE
5	XE	18	ARG
5	XE	31	LEU
5	XE	41	VAL
5	XE	73	ASN
5	XE	79	GLU
5	XE	101	ILE
5	XE	147	ASP
5	XE	153	LYS
6	XF	21	LEU
6	XF	23	LYS
6	XF	36	ARG
6	XF	71	ARG
6	XF	74	ASP
6	XF	91	VAL
6	XF	92	LYS
6	XF	98	LEU
7	XG	5	ARG
7	XG	8	GLU
7	XG	35	LYS
7	XG	54	THR
7	XG	63	LYS
7	XG	78	ARG
7	XG	104	LEU
7	XG	113	GLU
7	XG	114	ARG
7	XG	136	LYS
7	XG	137	LYS
7	XG	155	ARG
8	XH	1	MET
8	XH	12	ARG
8	XH	19	VAL
8	XH	24	THR
8	XH	26	VAL
8	XH	41	ARG
8	XH	54	ASP
8	XH	63	LEU
8	XH	80	ILE
8	XH	85	ARG
8	XH	109	ILE
8	XH	112	LEU

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Mol	Chain	Res	Type
8	XH	137	VAL
9	XI	9	ARG
9	XI	38	GLN
9	XI	44	VAL
9	XI	56	LEU
9	XI	65	VAL
9	XI	95	LYS
9	XI	96	LEU
9	XI	102	LEU
9	XI	104	ARG
9	XI	105	ASP
9	XI	108	VAL
9	XI	111	ARG
9	XI	112	LYS
9	XI	114	TYR
9	XI	121	ARG
9	XI	124	GLN
9	XI	125	TYR
9	XI	128	ARG
10	XJ	3	LYS
10	XJ	17	ASP
10	XJ	22	LYS
10	XJ	45	ARG
10	XJ	47	PHE
10	XJ	49	VAL
10	XJ	54	PHE
10	XJ	57	LYS
10	XJ	62	HIS
10	XJ	70	ARG
10	XJ	74	ILE
10	XJ	80	LYS
10	XJ	84	GLN
10	XJ	96	ILE
10	XJ	98	ILE
11	XK	26	ASN
11	XK	29	ILE
11	XK	31	THR
11	XK	32	ILE
11	XK	36	ASP
11	XK	57	THR
11	XK	96	ARG
11	XK	114	VAL

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Mol	Chain	Res	Type
11	XK	116	HIS
12	XL	17	LYS
12	XL	18	VAL
12	XL	20	LYS
12	XL	27	LEU
12	XL	33	ARG
12	XL	59	ARG
12	XL	62	SER
12	XL	81	SER
12	XL	89	ARG
12	XL	91	LYS
12	XL	126	LYS
13	XM	3	ARG
13	XM	13	LYS
13	XM	17	VAL
13	XM	19	LEU
13	XM	32	GLU
13	XM	45	VAL
13	XM	48	LEU
13	XM	56	LEU
13	XM	64	TRP
13	XM	66	LEU
13	XM	70	LEU
13	XM	84	ILE
13	XM	88	ARG
13	XM	98	VAL
13	XM	108	ARG
13	XM	114	ARG
13	XM	115	LYS
13	XM	117	VAL
13	XM	122	LYS
14	XN	6	LEU
14	XN	12	ARG
14	XN	32	SER
14	XN	33	VAL
14	XN	40	CYS
14	XN	41	ARG
14	XN	44	LEU
15	XO	3	ILE
15	XO	8	LYS
15	XO	24	SER
15	XO	26	GLU

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Mol	Chain	Res	Type
15	XO	39	LEU
15	XO	62	GLN
15	XO	64	ARG
15	XO	66	LEU
15	XO	82	ILE
15	XO	87	ILE
16	XP	2	VAL
16	XP	11	SER
16	XP	20	VAL
16	XP	28	ARG
16	XP	32	TYR
16	XP	67	THR
16	XP	69	THR
16	XP	72	ARG
17	XQ	52	LYS
17	XQ	59	ILE
17	XQ	62	SER
17	XQ	68	ARG
17	XQ	74	LEU
17	XQ	101	ARG
18	XR	26	LEU
18	XR	29	PHE
18	XR	36	ASN
18	XR	41	LYS
18	XR	46	GLU
18	XR	54	ARG
18	XR	76	LEU
18	XR	82	THR
18	XR	86	VAL
19	XS	5	LEU
19	XS	10	PHE
19	XS	11	VAL
19	XS	12	ASP
19	XS	13	ASP
19	XS	21	GLU
19	XS	28	LYS
19	XS	29	ARG
19	XS	30	LEU
19	XS	31	ILE
19	XS	37	ARG
19	XS	44	MET
19	XS	63	THR

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Mol	Chain	Res	Type
19	XS	78	ARG
19	XS	81	ARG
19	XS	83	HIS
20	XT	10	LEU
20	XT	13	LEU
20	XT	24	LEU
20	XT	37	SER
20	XT	41	ILE
20	XT	45	GLN
20	XT	50	GLU
20	XT	73	HIS
20	XT	84	LEU
20	XT	93	GLU
21	XU	6	ARG
27	YD	5	LYS
27	YD	17	THR
27	YD	27	THR
27	YD	28	GLU
27	YD	30	GLU
27	YD	38	LYS
27	YD	43	ARG
27	YD	44	ASN
27	YD	49	ILE
27	YD	65	ILE
27	YD	73	VAL
27	YD	88	ARG
27	YD	94	LEU
27	YD	95	LEU
27	YD	103	ARG
27	YD	105	ILE
27	YD	106	ILE
27	YD	111	LEU
27	YD	112	GLN
27	YD	141	VAL
27	YD	192	THR
27	YD	200	ASP
27	YD	202	LYS
27	YD	212	SER
27	YD	217	ARG
27	YD	218	ARG
27	YD	221	VAL
27	YD	229	VAL

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Mol	Chain	Res	Type
27	YD	237	GLU
27	YD	242	ARG
27	YD	257	LEU
27	YD	259	THR
27	YD	273	ARG
28	YE	4	ILE
28	YE	12	THR
28	YE	13	ARG
28	YE	16	ARG
28	YE	17	ASP
28	YE	26	ILE
28	YE	27	LEU
28	YE	41	LYS
28	YE	42	ASP
28	YE	49	LEU
28	YE	77	ILE
28	YE	79	ARG
28	YE	82	ARG
28	YE	92	THR
28	YE	113	PHE
28	YE	116	VAL
28	YE	117	MET
28	YE	119	ARG
28	YE	127	ASP
28	YE	128	SER
28	YE	144	ARG
28	YE	146	THR
28	YE	154	LYS
28	YE	175	VAL
28	YE	197	ILE
28	YE	200	GLU
28	YE	202	LYS
28	YE	203	LYS
29	YF	9	ILE
29	YF	32	LEU
29	YF	33	LEU
29	YF	38	ARG
29	YF	45	ARG
29	YF	65	TRP
29	YF	70	THR
29	YF	78	ILE
29	YF	105	VAL

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Mol	Chain	Res	Type
29	YF	106	ARG
29	YF	107	LYS
29	YF	117	ARG
29	YF	127	GLU
29	YF	161	GLU
29	YF	164	ARG
29	YF	165	ARG
29	YF	170	LEU
29	YF	174	VAL
29	YF	176	LEU
29	YF	181	LEU
29	YF	183	VAL
29	YF	196	LEU
29	YF	197	ASP
29	YF	206	ILE
30	YG	3	LEU
30	YG	7	LEU
30	YG	22	ARG
30	YG	31	VAL
30	YG	34	LEU
30	YG	43	LEU
30	YG	45	GLU
30	YG	58	GLN
30	YG	63	ILE
30	YG	66	GLN
30	YG	67	LYS
30	YG	80	PHE
30	YG	82	LEU
30	YG	84	LYS
30	YG	88	ILE
30	YG	90	LEU
30	YG	94	LEU
30	YG	116	ASP
30	YG	118	ARG
30	YG	145	THR
30	YG	147	ASP
30	YG	167	GLU
31	YH	3	ARG
31	YH	4	ILE
31	YH	6	ARG
31	YH	9	ILE
31	YH	27	LYS

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Mol	Chain	Res	Type
31	YH	32	GLU
31	YH	37	VAL
31	YH	40	GLU
31	YH	41	MET
31	YH	53	GLU
31	YH	59	ARG
31	YH	77	LYS
31	YH	88	LEU
31	YH	89	ILE
31	YH	103	LEU
31	YH	105	LEU
31	YH	122	THR
31	YH	129	THR
31	YH	132	ARG
31	YH	136	ILE
31	YH	139	GLN
31	YH	143	GLN
31	YH	149	ARG
31	YH	152	ARG
31	YH	153	LYS
31	YH	155	SER
31	YH	169	VAL
32	YI	1	MET
32	YI	2	LYS
32	YI	9	LEU
32	YI	10	GLU
32	YI	20	ASP
32	YI	27	ARG
32	YI	33	ARG
32	YI	35	LEU
32	YI	38	LEU
32	YI	40	THR
32	YI	56	LYS
32	YI	67	ARG
32	YI	70	GLU
32	YI	85	GLU
32	YI	86	THR
32	YI	87	LYS
32	YI	88	ILE
32	YI	92	VAL
32	YI	101	LEU
32	YI	110	ASP

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Mol	Chain	Res	Type
32	YI	112	LYS
32	YI	113	ARG
32	YI	130	TYR
32	YI	131	LYS
32	YI	135	GLU
32	YI	136	VAL
32	YI	138	ILE
32	YI	139	GLN
32	YI	140	LEU
32	YI	142	VAL
33	YN	2	LYS
33	YN	5	VAL
33	YN	7	LYS
33	YN	32	THR
33	YN	34	LEU
33	YN	43	THR
33	YN	48	MET
33	YN	60	ILE
33	YN	61	ARG
33	YN	62	VAL
33	YN	65	LYS
33	YN	67	LEU
33	YN	73	THR
33	YN	90	MET
33	YN	96	GLU
33	YN	99	LEU
33	YN	109	LYS
33	YN	112	LEU
33	YN	116	LEU
33	YN	120	LEU
33	YN	136	GLU
34	YO	9	GLU
34	YO	19	ILE
34	YO	20	MET
34	YO	23	ARG
34	YO	24	VAL
34	YO	31	LYS
34	YO	47	ILE
34	YO	49	ARG
34	YO	53	LYS
34	YO	66	LYS
34	YO	91	LEU

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Mol	Chain	Res	Type
35	YP	6	LEU
35	YP	7	ARG
35	YP	9	ASN
35	YP	14	LYS
35	YP	16	ARG
35	YP	19	VAL
35	YP	21	ARG
35	YP	27	HIS
35	YP	29	LYS
35	YP	32	THR
35	YP	36	LYS
35	YP	45	LEU
35	YP	49	ARG
35	YP	50	ARG
35	YP	61	ARG
35	YP	64	LYS
35	YP	65	ARG
35	YP	71	VAL
35	YP	75	ILE
35	YP	88	LEU
35	YP	91	PHE
35	YP	94	GLU
35	YP	98	GLU
35	YP	100	LEU
35	YP	101	VAL
35	YP	112	LEU
35	YP	115	LEU
35	YP	117	GLU
35	YP	123	LEU
35	YP	135	LEU
35	YP	144	GLU
35	YP	146	VAL
35	YP	147	LEU
35	YP	149	GLU
36	YQ	5	ARG
36	YQ	10	ARG
36	YQ	25	ASP
36	YQ	45	GLN
36	YQ	55	VAL
36	YQ	59	ARG
36	YQ	71	ASP
36	YQ	75	THR

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Mol	Chain	Res	Type
36	YQ	76	LYS
36	YQ	79	LEU
36	YQ	81	VAL
36	YQ	82	ARG
36	YQ	83	MET
36	YQ	87	LYS
36	YQ	103	MET
36	YQ	112	GLU
36	YQ	132	VAL
36	YQ	135	ASP
36	YQ	139	GLU
37	YR	1	MET
37	YR	18	LEU
37	YR	28	LEU
37	YR	29	LEU
37	YR	34	ILE
37	YR	36	THR
37	YR	40	LYS
37	YR	44	LEU
37	YR	51	LEU
37	YR	54	LEU
37	YR	57	ARG
37	YR	63	ARG
37	YR	65	LEU
37	YR	79	LEU
37	YR	83	ILE
37	YR	91	GLN
37	YR	95	THR
37	YR	100	LEU
37	YR	102	GLU
37	YR	104	ARG
37	YR	105	ARG
38	YS	10	ARG
38	YS	12	PHE
38	YS	14	VAL
38	YS	15	ARG
38	YS	20	ARG
38	YS	25	ARG
38	YS	27	SER
38	YS	44	LYS
38	YS	54	LEU
38	YS	56	LEU

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Mol	Chain	Res	Type
38	YS	58	LEU
38	YS	69	VAL
38	YS	78	LEU
38	YS	83	LYS
38	YS	85	VAL
38	YS	89	ARG
38	YS	103	GLU
38	YS	106	ARG
38	YS	111	GLU
39	YT	17	THR
39	YT	23	ARG
39	YT	27	THR
39	YT	28	VAL
39	YT	40	THR
39	YT	41	ARG
39	YT	42	ILE
39	YT	51	ARG
39	YT	58	ASN
39	YT	65	LYS
39	YT	66	VAL
39	YT	74	ARG
39	YT	86	ILE
39	YT	87	ASP
39	YT	88	ILE
39	YT	89	VAL
39	YT	110	ILE
39	YT	112	ARG
39	YT	115	ARG
39	YT	125	ARG
39	YT	128	GLU
39	YT	134	GLU
40	YU	5	LYS
40	YU	11	ARG
40	YU	27	LEU
40	YU	51	LYS
40	YU	52	ARG
40	YU	60	LEU
40	YU	64	ARG
40	YU	70	ARG
40	YU	74	LEU
40	YU	88	ILE
40	YU	91	ASP

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Mol	Chain	Res	Type
40	YU	98	LEU
40	YU	104	GLN
40	YU	111	GLU
40	YU	112	ARG
40	YU	114	LYS
41	YV	7	THR
41	YV	10	LYS
41	YV	13	ARG
41	YV	19	LYS
41	YV	35	LEU
41	YV	39	LEU
41	YV	40	LEU
41	YV	45	THR
41	YV	61	VAL
41	YV	66	ARG
41	YV	72	VAL
41	YV	73	SER
41	YV	78	LYS
41	YV	79	VAL
41	YV	99	ILE
42	YW	11	ARG
42	YW	16	LYS
42	YW	23	LEU
42	YW	37	ARG
42	YW	40	ASN
42	YW	51	LEU
42	YW	67	ASP
42	YW	69	LEU
42	YW	76	VAL
42	YW	88	ARG
42	YW	92	ARG
42	YW	95	ILE
42	YW	96	ILE
42	YW	100	THR
42	YW	106	ILE
42	YW	107	LEU
43	YX	6	ASP
43	YX	12	VAL
43	YX	15	GLU
43	YX	27	THR
43	YX	36	LYS
43	YX	43	VAL

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Mol	Chain	Res	Type
43	YX	49	VAL
43	YX	57	LEU
43	YX	59	VAL
43	YX	63	LYS
43	YX	65	ARG
43	YX	66	LEU
43	YX	80	ILE
43	YX	88	LYS
44	YY	14	LEU
44	YY	26	LYS
44	YY	27	VAL
44	YY	28	LYS
44	YY	29	GLU
44	YY	34	LYS
44	YY	38	ILE
44	YY	44	ILE
44	YY	57	GLN
44	YY	61	ILE
44	YY	64	GLU
44	YY	67	LEU
44	YY	71	LYS
44	YY	73	ARG
44	YY	75	ILE
44	YY	86	ARG
44	YY	87	LYS
44	YY	89	PHE
44	YY	90	LEU
44	YY	95	LYS
44	YY	97	ARG
45	YZ	2	GLU
45	YZ	4	ARG
45	YZ	5	LEU
45	YZ	8	TYR
45	YZ	10	ARG
45	YZ	18	LEU
45	YZ	19	ARG
45	YZ	20	ARG
45	YZ	31	ARG
45	YZ	41	LEU
45	YZ	53	ILE
45	YZ	74	VAL
45	YZ	76	LEU

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Mol	Chain	Res	Type
45	YZ	81	ARG
45	YZ	93	ASP
45	YZ	94	GLU
45	YZ	95	PRO
45	YZ	112	ARG
45	YZ	122	ARG
45	YZ	129	SER
45	YZ	133	ILE
45	YZ	137	ILE
45	YZ	140	ASP
45	YZ	141	VAL
45	YZ	144	LEU
45	YZ	150	LEU
45	YZ	151	HIS
45	YZ	153	SER
45	YZ	156	LYS
45	YZ	163	LEU
45	YZ	166	SER
45	YZ	180	VAL
46	Y0	9	SER
46	Y0	11	ARG
46	Y0	36	ILE
46	Y0	55	ARG
46	Y0	64	ASP
46	Y0	74	ARG
47	Y1	30	VAL
47	Y1	46	LEU
47	Y1	50	ARG
47	Y1	51	VAL
47	Y1	56	GLN
47	Y1	62	VAL
47	Y1	78	LYS
47	Y1	80	LEU
47	Y1	82	LEU
47	Y1	83	GLU
47	Y1	91	LYS
47	Y1	92	LYS
48	Y2	4	SER
48	Y2	7	ARG
48	Y2	9	GLN
48	Y2	16	LEU
48	Y2	23	LYS

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Mol	Chain	Res	Type
48	Y2	24	LEU
48	Y2	27	GLU
48	Y2	32	LEU
48	Y2	34	GLU
48	Y2	41	ILE
48	Y2	47	ASN
48	Y2	50	ILE
48	Y2	51	ARG
48	Y2	52	ASP
48	Y2	53	LEU
48	Y2	64	LEU
48	Y2	65	ASN
49	Y3	6	VAL
49	Y3	8	LEU
49	Y3	23	LEU
49	Y3	30	ARG
49	Y3	31	LEU
49	Y3	36	VAL
49	Y3	37	LEU
49	Y3	56	VAL
50	Y4	6	HIS
50	Y4	10	VAL
50	Y4	15	ILE
50	Y4	16	CYS
50	Y4	22	ILE
50	Y4	27	THR
50	Y4	34	GLU
50	Y4	39	CYS
50	Y4	42	PHE
50	Y4	43	TYR
50	Y4	48	ARG
50	Y4	49	PHE
50	Y4	53	GLU
50	Y4	57	GLU
50	Y4	58	ARG
50	Y4	61	ARG
50	Y4	63	TYR
50	Y4	67	TYR
50	Y4	68	ARG
50	Y4	71	ARG
51	Y5	3	LYS
51	Y5	4	HIS

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Mol	Chain	Res	Type
51	Y5	6	VAL
51	Y5	11	THR
51	Y5	29	THR
51	Y5	36	CYS
51	Y5	37	LYS
51	Y5	40	LYS
51	Y5	48	GLU
51	Y5	49	CYS
51	Y5	51	TYR
51	Y5	52	TYR
51	Y5	56	LYS
51	Y5	58	LEU
52	Y6	6	ARG
52	Y6	8	LYS
52	Y6	11	LEU
52	Y6	19	ARG
52	Y6	23	THR
52	Y6	30	THR
52	Y6	33	LYS
52	Y6	34	LEU
52	Y6	37	ARG
52	Y6	44	ARG
53	Y7	1	MET
53	Y7	4	THR
53	Y7	8	ASN
53	Y7	9	ARG
53	Y7	10	ARG
53	Y7	14	LYS
53	Y7	47	ARG
54	Y8	13	ARG
54	Y8	14	VAL
54	Y8	15	LYS
54	Y8	29	LYS
54	Y8	30	ARG
54	Y8	34	TRP
54	Y8	43	GLN
54	Y8	44	LYS
54	Y8	47	LYS
54	Y8	56	GLU
54	Y8	58	ILE
54	Y8	64	TYR
54	Y8	65	GLU

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Mol	Chain	Res	Type
55	Y9	1	MET
55	Y9	17	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
2	QB	19	HIS
2	QB	204	ASN
2	QB	212	GLN
4	QD	43	HIS
10	QJ	13	HIS
10	QJ	78	ASN
13	QM	92	HIS
19	QS	47	HIS
20	QT	45	GLN
28	RE	55	ASN
38	RS	34	HIS
45	RZ	54	HIS
45	RZ	73	GLN
50	R4	47	GLN
55	R9	29	ASN
55	R9	32	HIS
2	XB	19	HIS
2	XB	204	ASN
2	XB	212	GLN
10	XJ	78	ASN
11	XK	26	ASN
39	YT	58	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	QA	1499/1522 (98%)	304 (20%)	48 (3%)
1	XA	1498/1522 (98%)	311 (20%)	50 (3%)
22	QV	76/77 (98%)	21 (27%)	1 (1%)
22	XV	76/77 (98%)	17 (22%)	1 (1%)
23	QY	14/17 (82%)	5 (35%)	1 (7%)
23	XY	14/17 (82%)	6 (42%)	1 (7%)
24	QX	7/25 (28%)	3 (42%)	2 (28%)
24	XX	7/25 (28%)	1 (14%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	RA	2879/2916 (98%)	659 (22%)	74 (2%)
25	YA	2880/2916 (98%)	623 (21%)	75 (2%)
26	RB	119/122 (97%)	29 (24%)	2 (1%)
26	YB	119/122 (97%)	29 (24%)	3 (2%)
56	Z6	1/3 (33%)	0	0
56	Z8	1/3 (33%)	0	0
All	All	9190/9364 (98%)	2008 (21%)	258 (2%)

All (2008) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	QA	6	G
1	QA	29	G
1	QA	32	A
1	QA	39	G
1	QA	47	C
1	QA	48	C
1	QA	50	A
1	QA	51	A
1	QA	64	G
1	QA	65	U
1	QA	66	G
1	QA	76	G
1	QA	79	G
1	QA	80	G
1	QA	90	C
1	QA	91	C
1	QA	95	G
1	QA	101	A
1	QA	108	G
1	QA	116	A
1	QA	120	A
1	QA	121	C
1	QA	144	G
1	QA	146	G
1	QA	147	G
1	QA	163	C
1	QA	169	C
1	QA	171	A
1	QA	172	A
1	QA	173	U
1	QA	174	C

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Mol	Chain	Res	Type
1	QA	182	U
1	QA	190	G
1	QA	191(A)	G
1	QA	195	A
1	QA	197	A
1	QA	209	U
1	QA	210	U
1	QA	216	G
1	QA	244	U
1	QA	245	C
1	QA	247	G
1	QA	251	G
1	QA	267	C
1	QA	270	A
1	QA	281	G
1	QA	289	G
1	QA	298	A
1	QA	316	G
1	QA	321	A
1	QA	328	C
1	QA	329	A
1	QA	332	G
1	QA	344	A
1	QA	346	G
1	QA	347	G
1	QA	351	G
1	QA	352	C
1	QA	353	A
1	QA	354	G
1	QA	356	A
1	QA	367	U
1	QA	372	C
1	QA	388	G
1	QA	389	A
1	QA	390	C
1	QA	397	A
1	QA	398	C
1	QA	406	G
1	QA	411	A
1	QA	412	A
1	QA	413	G
1	QA	414	A

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Mol	Chain	Res	Type
1	QA	421	U
1	QA	422	C
1	QA	423	G
1	QA	424	G
1	QA	429	U
1	QA	430	A
1	QA	442	C
1	QA	465	A
1	QA	466	C
1	QA	467	G
1	QA	482	A
1	QA	485	G
1	QA	486	U
1	QA	495	A
1	QA	496	A
1	QA	497	U
1	QA	498	A
1	QA	505	G
1	QA	509	A
1	QA	510	A
1	QA	511	C
1	QA	518	C
1	QA	521	G
1	QA	527	G
1	QA	531	U
1	QA	532	A
1	QA	533	A
1	QA	534	U
1	QA	544	G
1	QA	545	C
1	QA	547	A
1	QA	559	A
1	QA	561	U
1	QA	562	C
1	QA	566	G
1	QA	568	G
1	QA	572	A
1	QA	573	A
1	QA	576	G
1	QA	577	G
1	QA	595	G
1	QA	596	C

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Mol	Chain	Res	Type
1	QA	618	C
1	QA	623	C
1	QA	630	G
1	QA	631	G
1	QA	653	A
1	QA	665	A
1	QA	686	U
1	QA	687	A
1	QA	688	G
1	QA	701	C
1	QA	702	A
1	QA	703	G
1	QA	704	A
1	QA	723	U
1	QA	731	G
1	QA	748	C
1	QA	754	C
1	QA	755	G
1	QA	760	G
1	QA	776	G
1	QA	777	A
1	QA	786	G
1	QA	792	A
1	QA	793	U
1	QA	794	A
1	QA	796	C
1	QA	802	A
1	QA	813	U
1	QA	817	C
1	QA	819	A
1	QA	821	G
1	QA	828	A
1	QA	841	U
1	QA	843	U
1	QA	848	C
1	QA	859	A
1	QA	870	U
1	QA	871	U
1	QA	872	A
1	QA	873	A
1	QA	885	G
1	QA	902	G

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Mol	Chain	Res	Type
1	QA	914	A
1	QA	923	A
1	QA	927	G
1	QA	934	C
1	QA	935	A
1	QA	939	G
1	QA	960	U
1	QA	961	U
1	QA	966	G
1	QA	968	A
1	QA	969	A
1	QA	971	G
1	QA	972	C
1	QA	974	A
1	QA	975	A
1	QA	976	G
1	QA	977	A
1	QA	978	A
1	QA	980	C
1	QA	982	U
1	QA	983	A
1	QA	991	U
1	QA	992	U
1	QA	993	G
1	QA	994	A
1	QA	1001	G
1	QA	1004	A
1	QA	1006	C
1	QA	1008	C
1	QA	1009	G
1	QA	1021	G
1	QA	1024	G
1	QA	1025	U
1	QA	1026	G
1	QA	1028	C
1	QA	1029	G
1	QA	1032(A)	G
1	QA	1036	G
1	QA	1040	U
1	QA	1054	C
1	QA	1055	A
1	QA	1064	G

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Mol	Chain	Res	Type
1	QA	1065	U
1	QA	1066	C
1	QA	1067	A
1	QA	1081	G
1	QA	1094	G
1	QA	1095	U
1	QA	1101	A
1	QA	1124	G
1	QA	1125	U
1	QA	1126	U
1	QA	1127	G
1	QA	1130	A
1	QA	1131	G
1	QA	1136	U
1	QA	1137	C
1	QA	1138	G
1	QA	1139	G
1	QA	1145	C
1	QA	1146	A
1	QA	1157	A
1	QA	1158	C
1	QA	1159	U
1	QA	1160	G
1	QA	1163	C
1	QA	1171	G
1	QA	1180	A
1	QA	1181	G
1	QA	1182	G
1	QA	1183	A
1	QA	1185	G
1	QA	1187	G
1	QA	1193	G
1	QA	1196	U
1	QA	1197	G
1	QA	1200	C
1	QA	1201	A
1	QA	1202	G
1	QA	1204	A
1	QA	1212	U
1	QA	1213	A
1	QA	1225	A
1	QA	1238	A

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Mol	Chain	Res	Type
1	QA	1241	G
1	QA	1256	A
1	QA	1257	U
1	QA	1258	G
1	QA	1260	C
1	QA	1272	G
1	QA	1273	G
1	QA	1280	A
1	QA	1281	U
1	QA	1282	C
1	QA	1286	A
1	QA	1287	A
1	QA	1296	C
1	QA	1297	C
1	QA	1298	C
1	QA	1299	A
1	QA	1300	G
1	QA	1301	U
1	QA	1302	U
1	QA	1303	C
1	QA	1305	G
1	QA	1319	A
1	QA	1320	C
1	QA	1321	C
1	QA	1322	C
1	QA	1323	G
1	QA	1331	G
1	QA	1334	G
1	QA	1335	C
1	QA	1336	C
1	QA	1337	G
1	QA	1338	G
1	QA	1346	A
1	QA	1347	G
1	QA	1348	U
1	QA	1353	G
1	QA	1358	U
1	QA	1359	C
1	QA	1362(A)	C
1	QA	1370	G
1	QA	1387	G
1	QA	1397	C

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Mol	Chain	Res	Type
1	QA	1398	A
1	QA	1406	U
1	QA	1419	G
1	QA	1442	G
1	QA	1443	G
1	QA	1446	A
1	QA	1447	G
1	QA	1452	C
1	QA	1453	G
1	QA	1454	G
1	QA	1492	A
1	QA	1499	A
1	QA	1503	A
1	QA	1504	G
1	QA	1506	U
1	QA	1507	A
1	QA	1517	G
1	QA	1519	A
1	QA	1520	G
1	QA	1529	G
1	QA	1530	G
22	QV	3	G
22	QV	4	G
22	QV	7	U
22	QV	8	G
22	QV	15	C
22	QV	17	U
22	QV	18	G
22	QV	19	G
22	QV	21	A
22	QV	22	G
22	QV	25	C
22	QV	31	G
22	QV	47	U
22	QV	48	C
22	QV	52	G
22	QV	53	G
22	QV	54	U
22	QV	64	G
22	QV	67	C
22	QV	75	C
22	QV	76	A

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Mol	Chain	Res	Type
23	QY	31	G
23	QY	32	U
23	QY	33	U
23	QY	36	G
23	QY	42	G
24	QX	4	C
24	QX	7	U
24	QX	8	A
25	RA	9	U
25	RA	11	G
25	RA	14	A
25	RA	15	G
25	RA	28	A
25	RA	32	C
25	RA	34	C
25	RA	46	C
25	RA	49	A
25	RA	51	G
25	RA	55	G
25	RA	71	A
25	RA	72	U
25	RA	74	A
25	RA	75	G
25	RA	83	G
25	RA	84	A
25	RA	95	G
25	RA	96	G
25	RA	101	G
25	RA	102	G
25	RA	103	A
25	RA	118	A
25	RA	119	A
25	RA	120	U
25	RA	123	G
25	RA	138	G
25	RA	161	U
25	RA	177	G
25	RA	178	G
25	RA	181	A
25	RA	196	A
25	RA	199	A
25	RA	205	G

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Mol	Chain	Res	Type
25	RA	206	U
25	RA	214	G
25	RA	215	G
25	RA	216	A
25	RA	221	A
25	RA	222	A
25	RA	223	A
25	RA	228	A
25	RA	229	A
25	RA	230	U
25	RA	232	G
25	RA	233	A
25	RA	243	U
25	RA	248	G
25	RA	249	C
25	RA	252	G
25	RA	265	A
25	RA	266	G
25	RA	269	U
25	RA	270(E)	G
25	RA	270(L)	U
25	RA	270(M)	U
25	RA	270(N)	G
25	RA	270(P)	C
25	RA	271(B)	G
25	RA	271(C)	U
25	RA	271	G
25	RA	273(F)	C
25	RA	275	G
25	RA	276	A
25	RA	277	C
25	RA	278	A
25	RA	279	C
25	RA	299	A
25	RA	305	U
25	RA	311	A
25	RA	312	G
25	RA	323	G
25	RA	327	G
25	RA	329	G
25	RA	330	A
25	RA	333	G

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Mol	Chain	Res	Type
25	RA	342	G
25	RA	343	C
25	RA	346	A
25	RA	352	G
25	RA	363(F)	A
25	RA	364	C
25	RA	371	A
25	RA	372	G
25	RA	373	U
25	RA	386	G
25	RA	396	G
25	RA	399	G
25	RA	405	U
25	RA	411	G
25	RA	412	A
25	RA	421	U
25	RA	428	A
25	RA	429	A
25	RA	434	U
25	RA	444	C
25	RA	448	U
25	RA	454	A
25	RA	455	C
25	RA	456	C
25	RA	457	A
25	RA	470	A
25	RA	481	G
25	RA	504	U
25	RA	505	A
25	RA	509	C
25	RA	512	G
25	RA	513	A
25	RA	519	U
25	RA	527	C
25	RA	528	A
25	RA	529	A
25	RA	531	C
25	RA	532	A
25	RA	533	G
25	RA	537	C
25	RA	539	G
25	RA	540	G

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Mol	Chain	Res	Type
25	RA	544	C
25	RA	546	C
25	RA	550	G
25	RA	554	U
25	RA	556	G
25	RA	563	G
25	RA	573	G
25	RA	574	C
25	RA	575	A
25	RA	586	A
25	RA	588	U
25	RA	603	A
25	RA	607	U
25	RA	609(A)	G
25	RA	614	U
25	RA	615	G
25	RA	616	A
25	RA	617	G
25	RA	621	A
25	RA	626	U
25	RA	627	A
25	RA	631	A
25	RA	634	C
25	RA	637	A
25	RA	638	G
25	RA	645	C
25	RA	646	A
25	RA	650	C
25	RA	651	G
25	RA	652	C
25	RA	654	A
25	RA	654(A)	G
25	RA	654(B)	C
25	RA	657	U
25	RA	658	C
25	RA	659	C
25	RA	668	G
25	RA	669	G
25	RA	686	G
25	RA	702	G
25	RA	708	C
25	RA	717	G

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Mol	Chain	Res	Type
25	RA	722	A
25	RA	726	G
25	RA	730	C
25	RA	752	A
25	RA	753	C
25	RA	775	G
25	RA	776	G
25	RA	782	A
25	RA	784	A
25	RA	785	G
25	RA	789	A
25	RA	790	C
25	RA	792	G
25	RA	793	A
25	RA	794	G
25	RA	805	G
25	RA	812	C
25	RA	819	A
25	RA	827	U
25	RA	828	U
25	RA	846	C
25	RA	847	U
25	RA	856	C
25	RA	857	C
25	RA	859	G
25	RA	860	U
25	RA	869	G
25	RA	870	A
25	RA	871	U
25	RA	872	A
25	RA	880	G
25	RA	881	G
25	RA	882	G
25	RA	884	C
25	RA	885	C
25	RA	886	C
25	RA	888	C
25	RA	889	C
25	RA	893	C
25	RA	896	A
25	RA	897	C
25	RA	899	A

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Mol	Chain	Res	Type
25	RA	900	A
25	RA	901	A
25	RA	904	C
25	RA	907	U
25	RA	910	A
25	RA	917	A
25	RA	932	G
25	RA	933	A
25	RA	938	G
25	RA	941	A
25	RA	945	A
25	RA	946	G
25	RA	961	C
25	RA	974	G
25	RA	974(A)	C
25	RA	975	G
25	RA	983	A
25	RA	991	C
25	RA	996	A
25	RA	1003	G
25	RA	1005	C
25	RA	1011	G
25	RA	1012	U
25	RA	1013	C
25	RA	1015	G
25	RA	1016	G
25	RA	1017	G
25	RA	1022	G
25	RA	1023	U
25	RA	1025	G
25	RA	1026	U
25	RA	1027	A
25	RA	1033	U
25	RA	1044	G
25	RA	1045	A
25	RA	1046	A
25	RA	1050	A
25	RA	1053	C
25	RA	1054	A
25	RA	1055	G
25	RA	1057	A
25	RA	1059	G

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Mol	Chain	Res	Type
25	RA	1060	U
25	RA	1061	U
25	RA	1066	U
25	RA	1067	A
25	RA	1068	G
25	RA	1069	A
25	RA	1070	A
25	RA	1071	G
25	RA	1076	C
25	RA	1077	A
25	RA	1078	U
25	RA	1079	C
25	RA	1082	U
25	RA	1083	U
25	RA	1084	A
25	RA	1085	A
25	RA	1086	A
25	RA	1087	G
25	RA	1088	A
25	RA	1091	G
25	RA	1093	G
25	RA	1095	A
25	RA	1096	A
25	RA	1099	G
25	RA	1104	C
25	RA	1105	U
25	RA	1110	G
25	RA	1111	A
25	RA	1112	G
25	RA	1130	U
25	RA	1131	G
25	RA	1135	C
25	RA	1136	G
25	RA	1137	G
25	RA	1140	C
25	RA	1142	U
25	RA	1142(A)	A
25	RA	1149	G
25	RA	1155	A
25	RA	1170	G
25	RA	1173	G
25	RA	1174	A

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Mol	Chain	Res	Type
25	RA	1175	U
25	RA	1176	G
25	RA	1178	C
25	RA	1179	C
25	RA	1180	C
25	RA	1191	G
25	RA	1195	G
25	RA	1204	A
25	RA	1205	U
25	RA	1206	G
25	RA	1210	A
25	RA	1211	U
25	RA	1212	G
25	RA	1220	A
25	RA	1221	C
25	RA	1229(A)	G
25	RA	1238	G
25	RA	1241	A
25	RA	1248	G
25	RA	1250	G
25	RA	1252	G
25	RA	1253	A
25	RA	1256	G
25	RA	1265	A
25	RA	1269	A
25	RA	1271	G
25	RA	1272	A
25	RA	1287	A
25	RA	1300	U
25	RA	1301	A
25	RA	1303	G
25	RA	1304	C
25	RA	1312	U
25	RA	1313	U
25	RA	1314	C
25	RA	1321	A
25	RA	1328	G
25	RA	1329	U
25	RA	1349	A
25	RA	1352	U
25	RA	1356	G
25	RA	1365	A

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Mol	Chain	Res	Type
25	RA	1368	G
25	RA	1370	C
25	RA	1372	U
25	RA	1378	A
25	RA	1379	A
25	RA	1380	G
25	RA	1384	A
25	RA	1385	G
25	RA	1386	C
25	RA	1388	G
25	RA	1390	U
25	RA	1395	A
25	RA	1407	C
25	RA	1411	C
25	RA	1416	G
25	RA	1419	A
25	RA	1420	U
25	RA	1421	G
25	RA	1428	C
25	RA	1444(A)	A
25	RA	1445	C
25	RA	1448	G
25	RA	1449	A
25	RA	1449(A)	G
25	RA	1455	G
25	RA	1458	C
25	RA	1460	A
25	RA	1461	G
25	RA	1464	C
25	RA	1467	C
25	RA	1471	A
25	RA	1476	C
25	RA	1482	U
25	RA	1483	G
25	RA	1485	G
25	RA	1486	A
25	RA	1493	C
25	RA	1495	A
25	RA	1496	A
25	RA	1497	U
25	RA	1505	C
25	RA	1506	C

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Mol	Chain	Res	Type
25	RA	1507	A
25	RA	1508	A
25	RA	1510	A
25	RA	1514	U
25	RA	1515	C
25	RA	1519	G
25	RA	1520	U
25	RA	1522	G
25	RA	1534	G
25	RA	1535	U
25	RA	1536	A
25	RA	1537	C
25	RA	1538	G
25	RA	1543	A
25	RA	1544	C
25	RA	1545	A
25	RA	1554	A
25	RA	1558	A
25	RA	1559	G
25	RA	1566	A
25	RA	1569	A
25	RA	1578	U
25	RA	1579	A
25	RA	1581	G
25	RA	1585	C
25	RA	1586	A
25	RA	1598	C
25	RA	1608	A
25	RA	1609	A
25	RA	1610	A
25	RA	1616	A
25	RA	1617	C
25	RA	1618	A
25	RA	1647	G
25	RA	1648	C
25	RA	1654	A
25	RA	1667	G
25	RA	1674	G
25	RA	1675	C
25	RA	1688	U
25	RA	1694	C
25	RA	1695	G

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Mol	Chain	Res	Type
25	RA	1725	G
25	RA	1726	G
25	RA	1729	A
25	RA	1730	U
25	RA	1731	G
25	RA	1732	A
25	RA	1733	G
25	RA	1742	C
25	RA	1756	G
25	RA	1758	G
25	RA	1763	G
25	RA	1764	G
25	RA	1773	A
25	RA	1780	A
25	RA	1782	C
25	RA	1791	A
25	RA	1799	G
25	RA	1800	C
25	RA	1801	G
25	RA	1806	C
25	RA	1816	G
25	RA	1820	U
25	RA	1829	A
25	RA	1835	G
25	RA	1839	G
25	RA	1845	G
25	RA	1847	A
25	RA	1848	A
25	RA	1849	G
25	RA	1858	G
25	RA	1869	G
25	RA	1872	A
25	RA	1878	G
25	RA	1882	C
25	RA	1888	G
25	RA	1889	A
25	RA	1899	G
25	RA	1906	G
25	RA	1913	A
25	RA	1930	G
25	RA	1931	U
25	RA	1934	C

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Mol	Chain	Res	Type
25	RA	1937	A
25	RA	1938	A
25	RA	1939	U
25	RA	1955	U
25	RA	1963	U
25	RA	1964	G
25	RA	1967	C
25	RA	1968	G
25	RA	1969	A
25	RA	1970	A
25	RA	1971	A
25	RA	1972	A
25	RA	1981	A
25	RA	1982	C
25	RA	1991	U
25	RA	1992	G
25	RA	1993	U
25	RA	2020	A
25	RA	2023	G
25	RA	2031	A
25	RA	2033	A
25	RA	2043	C
25	RA	2055	C
25	RA	2056	G
25	RA	2059	A
25	RA	2060	A
25	RA	2061	G
25	RA	2062	A
25	RA	2063	C
25	RA	2069	G
25	RA	2093	G
25	RA	2099	U
25	RA	2100	G
25	RA	2107	C
25	RA	2111	C
25	RA	2113	U
25	RA	2114	A
25	RA	2115	G
25	RA	2116	G
25	RA	2117	A
25	RA	2118	U
25	RA	2126	A

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Mol	Chain	Res	Type
25	RA	2127	G
25	RA	2128	C
25	RA	2131	G
25	RA	2132	U
25	RA	2133	G
25	RA	2136	C
25	RA	2146	C
25	RA	2148	G
25	RA	2157	G
25	RA	2158	A
25	RA	2166	G
25	RA	2168	G
25	RA	2169	A
25	RA	2171	A
25	RA	2173	A
25	RA	2176	A
25	RA	2190	G
25	RA	2192	G
25	RA	2198	A
25	RA	2210	G
25	RA	2211	G
25	RA	2212	A
25	RA	2213	U
25	RA	2215	G
25	RA	2225	A
25	RA	2239	G
25	RA	2243	U
25	RA	2245	U
25	RA	2267	A
25	RA	2274	A
25	RA	2275	C
25	RA	2280	G
25	RA	2283	C
25	RA	2287	A
25	RA	2299	G
25	RA	2300	G
25	RA	2307	G
25	RA	2308	G
25	RA	2312	U
25	RA	2319	G
25	RA	2320	A
25	RA	2325	G

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Mol	Chain	Res	Type
25	RA	2327	A
25	RA	2334	G
25	RA	2336	A
25	RA	2342	C
25	RA	2346	A
25	RA	2347	C
25	RA	2350	C
25	RA	2383	G
25	RA	2385	C
25	RA	2391	G
25	RA	2392	A
25	RA	2394	C
25	RA	2402	C
25	RA	2403	C
25	RA	2406	U
25	RA	2410	G
25	RA	2411	A
25	RA	2423	U
25	RA	2425	A
25	RA	2429	G
25	RA	2430	A
25	RA	2431	U
25	RA	2434	A
25	RA	2435	A
25	RA	2439	A
25	RA	2440	C
25	RA	2441	C
25	RA	2448	A
25	RA	2469	A
25	RA	2470	G
25	RA	2474	C
25	RA	2475	C
25	RA	2476	A
25	RA	2482	G
25	RA	2483	C
25	RA	2484	G
25	RA	2487	G
25	RA	2491	U
25	RA	2492	U
25	RA	2494	G
25	RA	2502	G
25	RA	2505	G

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Mol	Chain	Res	Type
25	RA	2506	U
25	RA	2507	C
25	RA	2519	U
25	RA	2529	G
25	RA	2542	A
25	RA	2543	G
25	RA	2554	U
25	RA	2557	G
25	RA	2558	C
25	RA	2564	A
25	RA	2566	A
25	RA	2567	G
25	RA	2569	G
25	RA	2573	C
25	RA	2585	U
25	RA	2602	A
25	RA	2609	U
25	RA	2611	U
25	RA	2612	C
25	RA	2613	U
25	RA	2614	A
25	RA	2623	G
25	RA	2629	A
25	RA	2641	G
25	RA	2646	C
25	RA	2655	G
25	RA	2656	U
25	RA	2665	A
25	RA	2673	G
25	RA	2689	U
25	RA	2690	C
25	RA	2702	U
25	RA	2703	C
25	RA	2707	G
25	RA	2712	U
25	RA	2712(A)	A
25	RA	2713	A
25	RA	2714	G
25	RA	2726	U
25	RA	2732	G
25	RA	2733	A
25	RA	2734	A

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Mol	Chain	Res	Type
25	RA	2739	U
25	RA	2748	A
25	RA	2752	C
25	RA	2757	A
25	RA	2758	A
25	RA	2761	G
25	RA	2764	A
25	RA	2765	A
25	RA	2766	G
25	RA	2770	G
25	RA	2777	G
25	RA	2778	A
25	RA	2779	U
25	RA	2780	G
25	RA	2790	A
25	RA	2791	C
25	RA	2797	U
25	RA	2799	A
25	RA	2807	G
25	RA	2812	G
25	RA	2813	A
25	RA	2818	G
25	RA	2820	A
25	RA	2821	A
25	RA	2823	A
25	RA	2830	G
25	RA	2833	G
25	RA	2834	G
25	RA	2835	A
25	RA	2849	U
25	RA	2867	G
25	RA	2868	A
25	RA	2872	G
25	RA	2880	C
25	RA	2891	G
25	RA	2892	A
25	RA	2894	G
26	RB	8	U
26	RB	9	G
26	RB	13	A
26	RB	15	A
26	RB	16	G

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Mol	Chain	Res	Type
26	RB	19	G
26	RB	20	C
26	RB	22	U
26	RB	24	G
26	RB	25	A
26	RB	26	A
26	RB	27	C
26	RB	32	C
26	RB	41	U
26	RB	42	C
26	RB	44	G
26	RB	45	A
26	RB	47	C
26	RB	52	A
26	RB	53	A
26	RB	56	G
26	RB	67	G
26	RB	73	A
26	RB	81	G
26	RB	82	G
26	RB	89	G
26	RB	97	G
26	RB	105	G
26	RB	109	G
1	XA	7	G
1	XA	9	G
1	XA	12	U
1	XA	26	A
1	XA	32	A
1	XA	39	G
1	XA	48	C
1	XA	51	A
1	XA	61	G
1	XA	64	G
1	XA	65	U
1	XA	66	G
1	XA	76	G
1	XA	78	G
1	XA	79	G
1	XA	81	G
1	XA	89	U
1	XA	90	C

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Mol	Chain	Res	Type
1	XA	91	C
1	XA	92	G
1	XA	95	G
1	XA	101	A
1	XA	108	G
1	XA	116	A
1	XA	121	C
1	XA	129(A)	G
1	XA	130	A
1	XA	144	G
1	XA	146	G
1	XA	147	G
1	XA	163	C
1	XA	172	A
1	XA	173	U
1	XA	174	C
1	XA	182	U
1	XA	189	U
1	XA	190	G
1	XA	191(A)	G
1	XA	195	A
1	XA	197	A
1	XA	201	C
1	XA	209	U
1	XA	216	G
1	XA	243	A
1	XA	244	U
1	XA	245	C
1	XA	247	G
1	XA	251	G
1	XA	262	A
1	XA	267	C
1	XA	271	C
1	XA	281	G
1	XA	289	G
1	XA	316	G
1	XA	317	G
1	XA	321	A
1	XA	328	C
1	XA	329	A
1	XA	332	G
1	XA	343	U

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Mol	Chain	Res	Type
1	XA	345	C
1	XA	346	G
1	XA	347	G
1	XA	348	G
1	XA	352	C
1	XA	353	A
1	XA	354	G
1	XA	355	C
1	XA	356	A
1	XA	367	U
1	XA	372	C
1	XA	373	A
1	XA	384	G
1	XA	388	G
1	XA	389	A
1	XA	390	C
1	XA	397	A
1	XA	398	C
1	XA	406	G
1	XA	411	A
1	XA	412	A
1	XA	413	G
1	XA	414	A
1	XA	422	C
1	XA	423	G
1	XA	424	G
1	XA	429	U
1	XA	430	A
1	XA	436	C
1	XA	438	G
1	XA	439	A
1	XA	465	A
1	XA	466	C
1	XA	467	G
1	XA	482	A
1	XA	485	G
1	XA	486	U
1	XA	487	A
1	XA	496	A
1	XA	497	U
1	XA	505	G
1	XA	509	A

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Mol	Chain	Res	Type
1	XA	510	A
1	XA	511	C
1	XA	518	C
1	XA	527	G
1	XA	531	U
1	XA	532	A
1	XA	533	A
1	XA	536	C
1	XA	545	C
1	XA	547	A
1	XA	548	G
1	XA	559	A
1	XA	561	U
1	XA	562	C
1	XA	564	C
1	XA	568	G
1	XA	572	A
1	XA	573	A
1	XA	576	G
1	XA	577	G
1	XA	579	G
1	XA	596	C
1	XA	607	A
1	XA	617	G
1	XA	630	G
1	XA	631	G
1	XA	633	G
1	XA	649	G
1	XA	653	A
1	XA	661	G
1	XA	665	A
1	XA	666	G
1	XA	688	G
1	XA	701	C
1	XA	702	A
1	XA	704	A
1	XA	723	U
1	XA	724	G
1	XA	731	G
1	XA	749	C
1	XA	752	G
1	XA	753	A

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Mol	Chain	Res	Type
1	XA	754	C
1	XA	755	G
1	XA	759	A
1	XA	774	G
1	XA	777	A
1	XA	792	A
1	XA	793	U
1	XA	794	A
1	XA	813	U
1	XA	816	A
1	XA	817	C
1	XA	818	G
1	XA	819	A
1	XA	821	G
1	XA	828	A
1	XA	836	G
1	XA	841	U
1	XA	843	U
1	XA	848	C
1	XA	859	A
1	XA	871	U
1	XA	872	A
1	XA	902	G
1	XA	914	A
1	XA	916	G
1	XA	920	U
1	XA	922	G
1	XA	926	G
1	XA	927	G
1	XA	934	C
1	XA	935	A
1	XA	940	C
1	XA	960	U
1	XA	961	U
1	XA	966	G
1	XA	968	A
1	XA	969	A
1	XA	972	C
1	XA	974	A
1	XA	975	A
1	XA	976	G
1	XA	977	A

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Mol	Chain	Res	Type
1	XA	983	A
1	XA	991	U
1	XA	992	U
1	XA	993	G
1	XA	994	A
1	XA	1001	G
1	XA	1004	A
1	XA	1005	A
1	XA	1006	C
1	XA	1008	C
1	XA	1009	G
1	XA	1021	G
1	XA	1024	G
1	XA	1025	U
1	XA	1028	C
1	XA	1029	G
1	XA	1032(A)	G
1	XA	1036	G
1	XA	1039	C
1	XA	1040	U
1	XA	1042	G
1	XA	1054	C
1	XA	1055	A
1	XA	1066	C
1	XA	1081	G
1	XA	1094	G
1	XA	1095	U
1	XA	1101	A
1	XA	1124	G
1	XA	1125	U
1	XA	1126	U
1	XA	1127	G
1	XA	1130	A
1	XA	1131	G
1	XA	1136	U
1	XA	1137	C
1	XA	1138	G
1	XA	1139	G
1	XA	1145	C
1	XA	1146	A
1	XA	1151	A
1	XA	1152	A

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Mol	Chain	Res	Type
1	XA	1157	A
1	XA	1158	C
1	XA	1159	U
1	XA	1160	G
1	XA	1162	C
1	XA	1163	C
1	XA	1171	G
1	XA	1176	A
1	XA	1177	G
1	XA	1181	G
1	XA	1182	G
1	XA	1183	A
1	XA	1184	G
1	XA	1187	G
1	XA	1188	A
1	XA	1189	C
1	XA	1190	G
1	XA	1196	U
1	XA	1200	C
1	XA	1201	A
1	XA	1202	G
1	XA	1212	U
1	XA	1214	C
1	XA	1225	A
1	XA	1230	C
1	XA	1238	A
1	XA	1240	U
1	XA	1241	G
1	XA	1256	A
1	XA	1257	U
1	XA	1258	G
1	XA	1263	C
1	XA	1267	C
1	XA	1270	C
1	XA	1272	G
1	XA	1280	A
1	XA	1281	U
1	XA	1282	C
1	XA	1286	A
1	XA	1287	A
1	XA	1298	C
1	XA	1299	A

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Mol	Chain	Res	Type
1	XA	1300	G
1	XA	1301	U
1	XA	1302	U
1	XA	1303	C
1	XA	1305	G
1	XA	1320	C
1	XA	1321	C
1	XA	1322	C
1	XA	1323	G
1	XA	1331	G
1	XA	1334	G
1	XA	1336	C
1	XA	1337	G
1	XA	1338	G
1	XA	1347	G
1	XA	1348	U
1	XA	1353	G
1	XA	1362(A)	C
1	XA	1364	U
1	XA	1397	C
1	XA	1400	C
1	XA	1419	G
1	XA	1442	G
1	XA	1446	A
1	XA	1447	G
1	XA	1452	C
1	XA	1453	G
1	XA	1454	G
1	XA	1487	G
1	XA	1492	A
1	XA	1499	A
1	XA	1502	A
1	XA	1503	A
1	XA	1504	G
1	XA	1506	U
1	XA	1517	G
1	XA	1519	A
1	XA	1520	G
1	XA	1525	G
1	XA	1529	G
1	XA	1530	G
22	XV	3	G

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Mol	Chain	Res	Type
22	XV	4	G
22	XV	8	G
22	XV	12	C
22	XV	15	C
22	XV	17	U
22	XV	18	G
22	XV	19	G
22	XV	21	A
22	XV	22	G
22	XV	47	U
22	XV	48	C
22	XV	49	G
22	XV	52	G
22	XV	54	U
22	XV	67	C
22	XV	76	A
24	XX	7	U
23	XY	31	G
23	XY	32	U
23	XY	33	U
23	XY	34	C
23	XY	40	G
23	XY	42	G
25	YA	9	U
25	YA	15	G
25	YA	27	G
25	YA	34	C
25	YA	35	G
25	YA	46	C
25	YA	55	G
25	YA	71	A
25	YA	74	A
25	YA	75	G
25	YA	96	G
25	YA	99	U
25	YA	101	G
25	YA	102	G
25	YA	103	A
25	YA	118	A
25	YA	119	A
25	YA	120	U
25	YA	125	G

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Mol	Chain	Res	Type
25	YA	138	G
25	YA	155	C
25	YA	161	U
25	YA	162	U
25	YA	177	G
25	YA	188	G
25	YA	196	A
25	YA	214	G
25	YA	215	G
25	YA	216	A
25	YA	221	A
25	YA	222	A
25	YA	223	A
25	YA	227	A
25	YA	229	A
25	YA	230	U
25	YA	232	G
25	YA	242	G
25	YA	243	U
25	YA	248	G
25	YA	252	G
25	YA	261	G
25	YA	264	C
25	YA	265	A
25	YA	266	G
25	YA	269	U
25	YA	270(L)	U
25	YA	270(M)	U
25	YA	270(N)	G
25	YA	270(P)	C
25	YA	271(A)	C
25	YA	271(B)	G
25	YA	271(C)	U
25	YA	271	G
25	YA	274	G
25	YA	275	G
25	YA	276	A
25	YA	278	A
25	YA	279	C
25	YA	299	A
25	YA	311	A
25	YA	316	C

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Mol	Chain	Res	Type
25	YA	323	G
25	YA	324	A
25	YA	329	G
25	YA	330	A
25	YA	332	A
25	YA	342	G
25	YA	352	G
25	YA	363	G
25	YA	364	C
25	YA	371	A
25	YA	372	G
25	YA	373	U
25	YA	380	U
25	YA	386	G
25	YA	387	U
25	YA	396	G
25	YA	405	U
25	YA	406	G
25	YA	411	G
25	YA	412	A
25	YA	428	A
25	YA	441	U
25	YA	443	A
25	YA	444	C
25	YA	448	U
25	YA	455	C
25	YA	457	A
25	YA	470	A
25	YA	481	G
25	YA	496	G
25	YA	503	A
25	YA	504	U
25	YA	505	A
25	YA	509	C
25	YA	512	G
25	YA	518	G
25	YA	531	C
25	YA	532	A
25	YA	533	G
25	YA	537	C
25	YA	539	G
25	YA	540	G

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Mol	Chain	Res	Type
25	YA	546	C
25	YA	547	A
25	YA	549	G
25	YA	562	U
25	YA	563	G
25	YA	573	G
25	YA	574	C
25	YA	575	A
25	YA	586	A
25	YA	588	U
25	YA	603	A
25	YA	607	U
25	YA	613	U
25	YA	614	U
25	YA	615	G
25	YA	616	A
25	YA	617	G
25	YA	621	A
25	YA	622	G
25	YA	624	C
25	YA	626	U
25	YA	627	A
25	YA	634	C
25	YA	637	A
25	YA	638	G
25	YA	645	C
25	YA	646	A
25	YA	650	C
25	YA	651	G
25	YA	654	A
25	YA	654(A)	G
25	YA	654(B)	C
25	YA	654(T)	C
25	YA	657	U
25	YA	664	C
25	YA	670	A
25	YA	686	G
25	YA	702	G
25	YA	717	G
25	YA	722	A
25	YA	730	C
25	YA	734	A

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Mol	Chain	Res	Type
25	YA	747	U
25	YA	750	A
25	YA	752	A
25	YA	753	C
25	YA	764	A
25	YA	765	G
25	YA	776	G
25	YA	782	A
25	YA	784	A
25	YA	785	G
25	YA	790	C
25	YA	792	G
25	YA	793	A
25	YA	805	G
25	YA	806	C
25	YA	812	C
25	YA	819	A
25	YA	827	U
25	YA	828	U
25	YA	831	G
25	YA	846	C
25	YA	847	U
25	YA	856	C
25	YA	857	C
25	YA	859	G
25	YA	860	U
25	YA	866	A
25	YA	881	G
25	YA	882	G
25	YA	884	C
25	YA	885	C
25	YA	886	C
25	YA	888	C
25	YA	889	C
25	YA	890	A
25	YA	896	A
25	YA	899	A
25	YA	900	A
25	YA	901	A
25	YA	902	C
25	YA	904	C
25	YA	907	U

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Mol	Chain	Res	Type
25	YA	910	A
25	YA	915	C
25	YA	917	A
25	YA	932	G
25	YA	938	G
25	YA	941	A
25	YA	945	A
25	YA	946	G
25	YA	959	A
25	YA	961	C
25	YA	974	G
25	YA	974(A)	C
25	YA	975	G
25	YA	980	A
25	YA	983	A
25	YA	990	A
25	YA	991	C
25	YA	996	A
25	YA	1003	G
25	YA	1005	C
25	YA	1011	G
25	YA	1012	U
25	YA	1013	C
25	YA	1022	G
25	YA	1023	U
25	YA	1025	G
25	YA	1026	U
25	YA	1027	A
25	YA	1033	U
25	YA	1045	A
25	YA	1046	A
25	YA	1050	A
25	YA	1054	A
25	YA	1055	G
25	YA	1059	G
25	YA	1060	U
25	YA	1061	U
25	YA	1066	U
25	YA	1067	A
25	YA	1068	G
25	YA	1071	G
25	YA	1076	C

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Mol	Chain	Res	Type
25	YA	1077	A
25	YA	1078	U
25	YA	1079	C
25	YA	1082	U
25	YA	1083	U
25	YA	1084	A
25	YA	1085	A
25	YA	1086	A
25	YA	1088	A
25	YA	1089	G
25	YA	1090	U
25	YA	1095	A
25	YA	1096	A
25	YA	1097	U
25	YA	1099	G
25	YA	1103	A
25	YA	1104	C
25	YA	1105	U
25	YA	1110	G
25	YA	1111	A
25	YA	1122	G
25	YA	1128	A
25	YA	1130	U
25	YA	1131	G
25	YA	1135	C
25	YA	1136	G
25	YA	1139	G
25	YA	1142	U
25	YA	1142(A)	A
25	YA	1148	A
25	YA	1169	G
25	YA	1170	G
25	YA	1173	G
25	YA	1174	A
25	YA	1175	U
25	YA	1176	G
25	YA	1178	C
25	YA	1179	C
25	YA	1180	C
25	YA	1195	G
25	YA	1204	A
25	YA	1205	U

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Mol	Chain	Res	Type
25	YA	1211	U
25	YA	1220	A
25	YA	1221	C
25	YA	1228	G
25	YA	1238	G
25	YA	1241	A
25	YA	1250	G
25	YA	1253	A
25	YA	1256	G
25	YA	1265	A
25	YA	1271	G
25	YA	1272	A
25	YA	1273	U
25	YA	1284	A
25	YA	1300	U
25	YA	1301	A
25	YA	1321	A
25	YA	1329	U
25	YA	1345	C
25	YA	1349	A
25	YA	1352	U
25	YA	1365	A
25	YA	1368	G
25	YA	1379	A
25	YA	1384	A
25	YA	1385	G
25	YA	1386	C
25	YA	1388	G
25	YA	1389	G
25	YA	1390	U
25	YA	1391	U
25	YA	1395	A
25	YA	1407	C
25	YA	1411	C
25	YA	1416	G
25	YA	1417	C
25	YA	1419	A
25	YA	1420	U
25	YA	1421	G
25	YA	1428	C
25	YA	1444(A)	A
25	YA	1445	C

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Mol	Chain	Res	Type
25	YA	1449	A
25	YA	1449(A)	G
25	YA	1453	A
25	YA	1455	G
25	YA	1458	C
25	YA	1460	A
25	YA	1461	G
25	YA	1467	C
25	YA	1471	A
25	YA	1482	U
25	YA	1483	G
25	YA	1485	G
25	YA	1486	A
25	YA	1487	G
25	YA	1493	C
25	YA	1495	A
25	YA	1497	U
25	YA	1505	C
25	YA	1506	C
25	YA	1507	A
25	YA	1508	A
25	YA	1510	A
25	YA	1511	A
25	YA	1514	U
25	YA	1519	G
25	YA	1520	U
25	YA	1522	G
25	YA	1534	G
25	YA	1535	U
25	YA	1536	A
25	YA	1537	C
25	YA	1543	A
25	YA	1544	C
25	YA	1545	A
25	YA	1547	C
25	YA	1554	A
25	YA	1558	A
25	YA	1559	G
25	YA	1566	A
25	YA	1569	A
25	YA	1578	U
25	YA	1579	A

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Mol	Chain	Res	Type
25	YA	1581	G
25	YA	1585	C
25	YA	1586	A
25	YA	1591	G
25	YA	1593	G
25	YA	1598	C
25	YA	1608	A
25	YA	1609	A
25	YA	1610	A
25	YA	1616	A
25	YA	1617	C
25	YA	1618	A
25	YA	1634	A
25	YA	1640	C
25	YA	1648	C
25	YA	1654	A
25	YA	1668	A
25	YA	1674	G
25	YA	1678	G
25	YA	1681	G
25	YA	1688	U
25	YA	1695	G
25	YA	1697	G
25	YA	1699	G
25	YA	1700	A
25	YA	1701	A
25	YA	1725	G
25	YA	1729	A
25	YA	1730	U
25	YA	1731	G
25	YA	1732	A
25	YA	1733	G
25	YA	1742	C
25	YA	1743	G
25	YA	1750	G
25	YA	1753	G
25	YA	1754	C
25	YA	1756	G
25	YA	1762	A
25	YA	1763	G
25	YA	1764	G
25	YA	1773	A

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Mol	Chain	Res	Type
25	YA	1780	A
25	YA	1786	A
25	YA	1791	A
25	YA	1799	G
25	YA	1800	C
25	YA	1801	G
25	YA	1811	G
25	YA	1816	G
25	YA	1820	U
25	YA	1829	A
25	YA	1835	G
25	YA	1836	C
25	YA	1847	A
25	YA	1848	A
25	YA	1849	G
25	YA	1858	G
25	YA	1869	G
25	YA	1870	C
25	YA	1872	A
25	YA	1878	G
25	YA	1882	C
25	YA	1889	A
25	YA	1896	G
25	YA	1899	G
25	YA	1906	G
25	YA	1919	A
25	YA	1924	C
25	YA	1930	G
25	YA	1931	U
25	YA	1937	A
25	YA	1938	A
25	YA	1939	U
25	YA	1955	U
25	YA	1956	U
25	YA	1960	A
25	YA	1963	U
25	YA	1965	C
25	YA	1967	C
25	YA	1969	A
25	YA	1970	A
25	YA	1971	A
25	YA	1972	A

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Mol	Chain	Res	Type
25	YA	1982	C
25	YA	1987	G
25	YA	1991	U
25	YA	1992	G
25	YA	1993	U
25	YA	2020	A
25	YA	2021	C
25	YA	2023	G
25	YA	2031	A
25	YA	2032	G
25	YA	2033	A
25	YA	2034	U
25	YA	2043	C
25	YA	2055	C
25	YA	2056	G
25	YA	2059	A
25	YA	2060	A
25	YA	2061	G
25	YA	2062	A
25	YA	2069	G
25	YA	2089	U
25	YA	2093	G
25	YA	2099	U
25	YA	2100	G
25	YA	2111	C
25	YA	2112	G
25	YA	2113	U
25	YA	2114	A
25	YA	2115	G
25	YA	2116	G
25	YA	2117	A
25	YA	2119	A
25	YA	2120	G
25	YA	2126	A
25	YA	2127	G
25	YA	2128	C
25	YA	2131	G
25	YA	2132	U
25	YA	2133	G
25	YA	2136	C
25	YA	2146	C
25	YA	2148	G

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Mol	Chain	Res	Type
25	YA	2158	A
25	YA	2166	G
25	YA	2167	U
25	YA	2168	G
25	YA	2169	A
25	YA	2173	A
25	YA	2176	A
25	YA	2178	C
25	YA	2181	G
25	YA	2190	G
25	YA	2192	G
25	YA	2194	G
25	YA	2198	A
25	YA	2210	G
25	YA	2211	G
25	YA	2212	A
25	YA	2215	G
25	YA	2225	A
25	YA	2238	G
25	YA	2239	G
25	YA	2246	G
25	YA	2268	A
25	YA	2273	A
25	YA	2275	C
25	YA	2283	C
25	YA	2287	A
25	YA	2288	A
25	YA	2302	G
25	YA	2307	G
25	YA	2308	G
25	YA	2311	A
25	YA	2319	G
25	YA	2320	A
25	YA	2325	G
25	YA	2334	G
25	YA	2346	A
25	YA	2347	C
25	YA	2350	C
25	YA	2377	A
25	YA	2379	G
25	YA	2382	G
25	YA	2383	G

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Mol	Chain	Res	Type
25	YA	2385	C
25	YA	2395	C
25	YA	2402	C
25	YA	2403	C
25	YA	2405	G
25	YA	2406	U
25	YA	2410	G
25	YA	2423	U
25	YA	2425	A
25	YA	2429	G
25	YA	2430	A
25	YA	2435	A
25	YA	2439	A
25	YA	2440	C
25	YA	2441	C
25	YA	2448	A
25	YA	2450	A
25	YA	2468	G
25	YA	2469	A
25	YA	2470	G
25	YA	2471	C
25	YA	2475	C
25	YA	2476	A
25	YA	2480	C
25	YA	2482	G
25	YA	2484	G
25	YA	2494	G
25	YA	2498	C
25	YA	2502	G
25	YA	2505	G
25	YA	2518	A
25	YA	2529	G
25	YA	2542	A
25	YA	2543	G
25	YA	2554	U
25	YA	2558	C
25	YA	2566	A
25	YA	2567	G
25	YA	2573	C
25	YA	2585	U
25	YA	2602	A
25	YA	2609	U

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Mol	Chain	Res	Type
25	YA	2610	C
25	YA	2611	U
25	YA	2612	C
25	YA	2613	U
25	YA	2629	A
25	YA	2632	A
25	YA	2655	G
25	YA	2656	U
25	YA	2665	A
25	YA	2673	G
25	YA	2675	A
25	YA	2682	U
25	YA	2689	U
25	YA	2690	C
25	YA	2691	C
25	YA	2702	U
25	YA	2707	G
25	YA	2712	U
25	YA	2712(A)	A
25	YA	2713	A
25	YA	2714	G
25	YA	2726	U
25	YA	2733	A
25	YA	2734	A
25	YA	2744	G
25	YA	2752	C
25	YA	2757	A
25	YA	2758	A
25	YA	2761	G
25	YA	2765	A
25	YA	2766	G
25	YA	2770	G
25	YA	2777	G
25	YA	2778	A
25	YA	2779	U
25	YA	2780	G
25	YA	2785	C
25	YA	2789	C
25	YA	2790	A
25	YA	2791	C
25	YA	2797	U
25	YA	2807	G

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Mol	Chain	Res	Type
25	YA	2808	U
25	YA	2818	G
25	YA	2820	A
25	YA	2821	A
25	YA	2830	G
25	YA	2833	G
25	YA	2834	G
25	YA	2835	A
25	YA	2847	U
25	YA	2867	G
25	YA	2868	A
25	YA	2872	G
25	YA	2873	A
25	YA	2880	C
25	YA	2892	A
25	YA	2894	G
26	YB	2	C
26	YB	8	U
26	YB	9	G
26	YB	13	A
26	YB	15	A
26	YB	19	G
26	YB	21	G
26	YB	24	G
26	YB	25	A
26	YB	26	A
26	YB	27	C
26	YB	31	C
26	YB	32	C
26	YB	40	U
26	YB	41	U
26	YB	42	C
26	YB	44	G
26	YB	45	A
26	YB	47	C
26	YB	52	A
26	YB	53	A
26	YB	56	G
26	YB	67	G
26	YB	72	G
26	YB	73	A
26	YB	81	G

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Mol	Chain	Res	Type
26	YB	89	G
26	YB	108	C
26	YB	109	G

All (258) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	QA	5	U
1	QA	31	G
1	QA	64	G
1	QA	115	G
1	QA	119	A
1	QA	181	G
1	QA	243	A
1	QA	244	U
1	QA	250	A
1	QA	266	G
1	QA	315	A
1	QA	328	C
1	QA	388	G
1	QA	410	G
1	QA	412	A
1	QA	429	U
1	QA	481	G
1	QA	484	G
1	QA	485	G
1	QA	509	A
1	QA	530	G
1	QA	533	A
1	QA	560	U
1	QA	687	A
1	QA	701	C
1	QA	703	G
1	QA	753	A
1	QA	792	A
1	QA	793	U
1	QA	812	C
1	QA	913	A
1	QA	934	C
1	QA	960	U
1	QA	992	U
1	QA	1025	U

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Mol	Chain	Res	Type
1	QA	1027	C
1	QA	1065	U
1	QA	1200	C
1	QA	1201	A
1	QA	1285	A
1	QA	1297	C
1	QA	1336	C
1	QA	1346	A
1	QA	1347	G
1	QA	1446	A
1	QA	1498	U
1	QA	1503	A
1	QA	1528	U
22	QV	53	G
23	QY	30	C
24	QX	3	G
24	QX	6	C
25	RA	27	G
25	RA	71	A
25	RA	74	A
25	RA	83	G
25	RA	99	U
25	RA	102	G
25	RA	195	A
25	RA	205	G
25	RA	221	A
25	RA	222	A
25	RA	227	A
25	RA	229	A
25	RA	242	G
25	RA	271(B)	G
25	RA	271(C)	U
25	RA	277	C
25	RA	345	A
25	RA	372	G
25	RA	404	C
25	RA	503	A
25	RA	508	G
25	RA	512	G
25	RA	587	C
25	RA	637	A
25	RA	669	G

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Mol	Chain	Res	Type
25	RA	752	A
25	RA	774	A
25	RA	846	C
25	RA	856	C
25	RA	859	G
25	RA	974(A)	C
25	RA	1012	U
25	RA	1022	G
25	RA	1026	U
25	RA	1045	A
25	RA	1078	U
25	RA	1085	A
25	RA	1130	U
25	RA	1178	C
25	RA	1204	A
25	RA	1210	A
25	RA	1240	U
25	RA	1312	U
25	RA	1427	A
25	RA	1558	A
25	RA	1608	A
25	RA	1653	G
25	RA	1667	G
25	RA	1694	C
25	RA	1799	G
25	RA	1819	A
25	RA	1847	A
25	RA	1929	G
25	RA	1930	G
25	RA	1936	A
25	RA	1980	G
25	RA	1992	G
25	RA	2060	A
25	RA	2126	A
25	RA	2198	A
25	RA	2238	G
25	RA	2405	G
25	RA	2439	A
25	RA	2481	G
25	RA	2506	U
25	RA	2518	A
25	RA	2566	A

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Mol	Chain	Res	Type
25	RA	2610	C
25	RA	2689	U
25	RA	2712	U
25	RA	2726	U
25	RA	2776	A
25	RA	2832	U
25	RA	2867	G
26	RB	24	G
26	RB	66	A
1	XA	31	G
1	XA	60	A
1	XA	64	G
1	XA	78	G
1	XA	89	U
1	XA	115	G
1	XA	181	G
1	XA	243	A
1	XA	244	U
1	XA	250	A
1	XA	266	G
1	XA	315	A
1	XA	328	C
1	XA	345	C
1	XA	388	G
1	XA	410	G
1	XA	412	A
1	XA	428	G
1	XA	429	U
1	XA	481	G
1	XA	484	G
1	XA	485	G
1	XA	509	A
1	XA	530	G
1	XA	560	U
1	XA	687	A
1	XA	701	C
1	XA	703	G
1	XA	753	A
1	XA	758	G
1	XA	793	U
1	XA	812	C
1	XA	819	A

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Mol	Chain	Res	Type
1	XA	913	A
1	XA	960	U
1	XA	965	A
1	XA	991	U
1	XA	992	U
1	XA	1027	C
1	XA	1065	U
1	XA	1094	G
1	XA	1200	C
1	XA	1285	A
1	XA	1297	C
1	XA	1298	C
1	XA	1336	C
1	XA	1347	G
1	XA	1446	A
1	XA	1498	U
1	XA	1503	A
22	XV	53	G
23	XY	30	C
25	YA	71	A
25	YA	74	A
25	YA	99	U
25	YA	102	G
25	YA	195	A
25	YA	196	A
25	YA	199	A
25	YA	221	A
25	YA	222	A
25	YA	229	A
25	YA	242	G
25	YA	271(B)	G
25	YA	278	A
25	YA	372	G
25	YA	404	C
25	YA	503	A
25	YA	508	G
25	YA	562	U
25	YA	587	C
25	YA	637	A
25	YA	653	A
25	YA	654	A
25	YA	669	G

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Mol	Chain	Res	Type
25	YA	752	A
25	YA	764	A
25	YA	846	C
25	YA	856	C
25	YA	859	G
25	YA	974	G
25	YA	974(A)	C
25	YA	1022	G
25	YA	1026	U
25	YA	1045	A
25	YA	1078	U
25	YA	1085	A
25	YA	1109	C
25	YA	1130	U
25	YA	1141	U
25	YA	1178	C
25	YA	1204	A
25	YA	1210	A
25	YA	1379	A
25	YA	1427	A
25	YA	1558	A
25	YA	1608	A
25	YA	1609	A
25	YA	1617	C
25	YA	1653	G
25	YA	1694	C
25	YA	1698	A
25	YA	1799	G
25	YA	1819	A
25	YA	1847	A
25	YA	1929	G
25	YA	1930	G
25	YA	1939	U
25	YA	1955	U
25	YA	1992	G
25	YA	2126	A
25	YA	2238	G
25	YA	2288	A
25	YA	2382	G
25	YA	2405	G
25	YA	2439	A
25	YA	2481	G

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Mol	Chain	Res	Type
25	YA	2566	A
25	YA	2610	C
25	YA	2655	G
25	YA	2681	C
25	YA	2689	U
25	YA	2712	U
25	YA	2756	U
25	YA	2776	A
25	YA	2832	U
25	YA	2867	G
26	YB	24	G
26	YB	66	A
26	YB	108	C

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

4 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	$\# Z > 2$
23	1MG	QY	37	23	24,26,27	2.85	5 (20%)	34,39,42	4.28	7 (20%)
23	1MG	XY	37	23	24,26,27	2.77	6 (25%)	34,39,42	4.58	7 (20%)
56	PPU	Z6	76	25,56	38,40,41	2.43	9 (23%)	54,57,60	2.62	14 (25%)
56	PPU	Z8	76	25,56	38,40,41	2.42	9 (23%)	54,57,60	2.61	14 (25%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	1MG	QY	37	23	-	0/8/25/26	0/3/3/3
23	1MG	XY	37	23	-	0/8/25/26	0/3/3/3
56	PPU	Z6	76	25,56	-	0/26/43/44	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
56	PPU	Z8	76	25,56	-	0/26/43/44	0/4/4/4

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	Z6	76	PPU	O-C	9.27	1.41	1.23
56	Z8	76	PPU	O-C	9.19	1.41	1.23
23	QY	37	1MG	C4-N3	8.17	1.49	1.35
23	XY	37	1MG	C4-N3	7.80	1.48	1.35
23	XY	37	1MG	C2-N2	6.61	1.48	1.33
23	QY	37	1MG	C2-N2	6.44	1.47	1.33
23	QY	37	1MG	C2-N1	6.16	1.46	1.37
23	XY	37	1MG	C2-N1	5.70	1.45	1.37
56	Z6	76	PPU	C9-N6	-5.45	1.31	1.45
56	Z8	76	PPU	C9-N6	-5.44	1.32	1.45
56	Z6	76	PPU	C-N3'	5.38	1.46	1.34
56	Z8	76	PPU	C-N3'	5.37	1.46	1.34
56	Z8	76	PPU	C10-N6	-5.11	1.32	1.45
56	Z6	76	PPU	C10-N6	-5.11	1.32	1.45
23	XY	37	1MG	P-OP1	4.83	1.52	1.46
23	QY	37	1MG	P-OP1	4.81	1.52	1.46
23	QY	37	1MG	C5-N7	-3.92	1.33	1.38
23	XY	37	1MG	C5-N7	-3.39	1.34	1.38
56	Z6	76	PPU	C4-N9	-3.17	1.33	1.37
56	Z8	76	PPU	C4-N9	-3.15	1.33	1.37
56	Z8	76	PPU	C8-N9	-3.04	1.32	1.36
56	Z6	76	PPU	C8-N9	-2.98	1.32	1.36
56	Z6	76	PPU	O4'-C1'	2.96	1.44	1.41
56	Z8	76	PPU	O4'-C1'	2.91	1.44	1.41
56	Z8	76	PPU	C6-C5	-2.56	1.40	1.44
56	Z6	76	PPU	C6-C5	-2.56	1.40	1.44
23	XY	37	1MG	O5'-C5'	-2.14	1.41	1.44
56	Z8	76	PPU	C5-N7	-2.01	1.32	1.39
56	Z6	76	PPU	C5-N7	-2.01	1.32	1.39

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	XY	37	1MG	C6-C5-N7	-21.95	133.07	134.24
23	QY	37	1MG	C6-C5-N7	-19.88	133.18	134.24
23	XY	37	1MG	C6-N1-C2	11.39	123.83	120.71
23	QY	37	1MG	C6-N1-C2	11.17	123.77	120.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	Z8	76	PPU	N3-C2-N1	-8.55	121.37	128.89
56	Z6	76	PPU	N3-C2-N1	-8.50	121.41	128.89
56	Z6	76	PPU	C3'-N3'-C	-8.16	110.19	123.19
56	Z8	76	PPU	C3'-N3'-C	-8.15	110.22	123.19
56	Z6	76	PPU	C5-C4-N3	-6.40	119.74	125.98
56	Z8	76	PPU	C5-C4-N3	-6.29	119.85	125.98
56	Z8	76	PPU	C2'-C1'-N9	-5.46	98.49	113.35
56	Z6	76	PPU	C2'-C1'-N9	-5.44	98.53	113.35
56	Z8	76	PPU	C2'-C3'-N3'	5.17	125.08	113.08
56	Z6	76	PPU	C2'-C3'-N3'	5.17	125.08	113.08
23	QY	37	1MG	C5-C4-N3	-4.93	120.39	126.07
56	Z6	76	PPU	C2-N1-C6	4.71	121.72	111.52
56	Z8	76	PPU	C2-N1-C6	4.71	121.72	111.52
23	QY	37	1MG	C2-N3-C4	4.55	120.76	115.30
23	XY	37	1MG	C2-N3-C4	4.47	120.66	115.30
23	XY	37	1MG	N3-C4-N9	4.44	133.42	126.91
23	XY	37	1MG	C5-C4-N3	-4.41	120.99	126.07
23	QY	37	1MG	N3-C4-N9	4.33	133.25	126.91
23	QY	37	1MG	N2-C2-N1	4.08	123.99	118.45
56	Z6	76	PPU	C4'-O4'-C1'	-3.99	105.33	109.72
56	Z8	76	PPU	C4'-O4'-C1'	-3.94	105.39	109.72
56	Z6	76	PPU	N3-C4-N9	3.90	132.08	125.39
56	Z8	76	PPU	N3-C4-N9	3.87	132.03	125.39
23	XY	37	1MG	N2-C2-N1	3.70	123.47	118.45
56	Z6	76	PPU	C4-C5-N7	-3.64	105.89	109.41
56	Z8	76	PPU	C4-C5-N7	-3.56	105.97	109.41
23	XY	37	1MG	N3-C2-N1	-3.56	117.42	123.84
23	QY	37	1MG	N3-C2-N1	-3.29	117.90	123.84
56	Z6	76	PPU	CM-OC-CZ	-3.19	110.12	117.54
56	Z8	76	PPU	CM-OC-CZ	-3.14	110.23	117.54
56	Z6	76	PPU	C4'-C3'-N3'	-2.68	107.92	113.56
56	Z6	76	PPU	O4'-C1'-N9	-2.65	102.32	108.10
56	Z8	76	PPU	O4'-C1'-N9	-2.65	102.34	108.10
56	Z6	76	PPU	C2-N3-C4	2.64	120.87	113.27
56	Z8	76	PPU	C4'-C3'-N3'	-2.64	108.01	113.56
56	Z8	76	PPU	C2-N3-C4	2.63	120.83	113.27
56	Z6	76	PPU	CA-C-N3'	2.07	121.75	115.94
56	Z8	76	PPU	CA-C-N3'	2.04	121.69	115.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 683 ligands modelled in this entry, 681 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	PAR	QA	1666	-	45,45,45	1.32	7 (15%)	67,67,67	1.40	8 (11%)
58	PAR	XA	1673	-	45,45,45	1.36	6 (13%)	67,67,67	1.33	5 (7%)

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	PAR	QA	1666	-	-	0/18/94/94	0/4/4/4
58	PAR	XA	1673	-	-	0/18/94/94	0/4/4/4

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	QA	1666	PAR	C52-C42	3.22	1.58	1.52
58	XA	1673	PAR	C52-C42	3.08	1.58	1.52
58	QA	1666	PAR	C64-C54	2.92	1.59	1.51
58	XA	1673	PAR	O54-C14	2.89	1.49	1.41
58	QA	1666	PAR	O54-C14	2.88	1.49	1.41
58	XA	1673	PAR	C11-C21	2.78	1.57	1.52
58	XA	1673	PAR	C64-C54	2.77	1.58	1.51
58	XA	1673	PAR	O51-C11	2.65	1.48	1.41
58	QA	1666	PAR	O51-C11	2.30	1.47	1.41
58	XA	1673	PAR	C14-C24	2.24	1.56	1.52
58	QA	1666	PAR	C11-C21	2.20	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	QA	1666	PAR	C14-C24	2.05	1.56	1.52
58	QA	1666	PAR	C31-C21	2.03	1.56	1.53

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	QA	1666	PAR	O52-C13-C23	4.72	115.92	107.50
58	XA	1673	PAR	C14-O54-C54	4.35	122.16	113.73
58	XA	1673	PAR	O52-C13-C23	4.24	115.07	107.50
58	XA	1673	PAR	O33-C14-C24	4.17	116.32	108.08
58	QA	1666	PAR	C14-O54-C54	3.87	121.21	113.73
58	QA	1666	PAR	O33-C14-C24	3.35	114.69	108.08
58	QA	1666	PAR	O11-C42-C52	3.15	115.44	107.42
58	QA	1666	PAR	O11-C42-C32	-3.04	101.70	108.97
58	QA	1666	PAR	O54-C54-C64	2.93	111.54	105.97
58	XA	1673	PAR	O54-C54-C64	2.81	111.32	105.97
58	XA	1673	PAR	C11-O51-C51	2.60	118.76	113.73
58	QA	1666	PAR	C22-C32-C42	2.16	114.70	109.37
58	QA	1666	PAR	O54-C54-C44	-2.12	105.79	109.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	QA	1500/1522 (98%)	0.28	40 (2%) 52 62	14, 55, 134, 294	0
1	XA	1500/1522 (98%)	0.24	26 (1%) 67 78	7, 42, 133, 270	0
2	QB	237/256 (92%)	2.28	105 (44%) 1 0	42, 98, 171, 216	0
2	XB	237/256 (92%)	1.71	77 (32%) 1 1	27, 78, 141, 206	0
3	QC	205/239 (85%)	2.09	88 (42%) 1 0	37, 91, 139, 193	0
3	XC	205/239 (85%)	1.05	40 (19%) 2 2	11, 53, 103, 148	0
4	QD	208/209 (99%)	1.18	49 (23%) 1 2	23, 54, 106, 136	0
4	XD	208/209 (99%)	1.37	50 (24%) 1 2	17, 51, 103, 175	0
5	QE	151/162 (93%)	0.73	16 (10%) 7 9	29, 65, 114, 172	0
5	XE	151/162 (93%)	0.63	13 (8%) 11 14	15, 43, 86, 138	0
6	QF	101/101 (100%)	0.26	4 (3%) 36 45	13, 48, 78, 119	0
6	XF	101/101 (100%)	0.28	5 (4%) 28 35	13, 46, 76, 153	0
7	QG	155/156 (99%)	1.61	52 (33%) 1 1	23, 73, 121, 172	0
7	XG	155/156 (99%)	1.44	36 (23%) 1 2	18, 62, 109, 143	0
8	QH	138/138 (100%)	0.58	13 (9%) 9 11	30, 67, 99, 116	0
8	XH	138/138 (100%)	0.29	6 (4%) 34 42	13, 48, 84, 127	0
9	QI	127/128 (99%)	2.48	78 (61%) 0 0	33, 89, 129, 180	0
9	XI	127/128 (99%)	1.84	51 (40%) 1 0	19, 69, 124, 167	0
10	QJ	99/105 (94%)	3.16	64 (64%) 0 0	27, 98, 176, 200	0
10	XJ	99/105 (94%)	2.14	48 (48%) 1 0	5, 72, 131, 162	0
11	QK	119/129 (92%)	2.18	50 (42%) 1 0	22, 55, 110, 180	0
11	XK	119/129 (92%)	1.76	33 (27%) 1 1	16, 43, 106, 177	0
12	QL	125/132 (94%)	2.26	57 (45%) 1 0	14, 47, 100, 195	0
12	XL	125/132 (94%)	0.76	13 (10%) 7 9	7, 30, 103, 185	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
13	QM	121/126 (96%)	2.04	41 (33%)	1 1	27, 84, 121, 226	0
13	XM	121/126 (96%)	1.12	24 (19%)	2 2	24, 57, 113, 211	0
14	QN	60/61 (98%)	2.98	41 (68%)	0 0	38, 80, 105, 122	0
14	XN	60/61 (98%)	1.28	16 (26%)	1 1	22, 43, 76, 100	0
15	QO	88/89 (98%)	0.39	4 (4%)	32 40	15, 52, 101, 137	0
15	XO	88/89 (98%)	0.59	10 (11%)	6 7	10, 42, 80, 97	0
16	QP	84/88 (95%)	0.32	1 (1%)	75 84	26, 50, 96, 135	0
16	XP	84/88 (95%)	0.63	11 (13%)	4 6	25, 57, 102, 179	0
17	QQ	100/105 (95%)	1.04	16 (16%)	3 4	27, 56, 100, 119	0
17	XQ	100/105 (95%)	1.22	27 (27%)	1 1	23, 55, 94, 109	0
18	QR	70/88 (79%)	0.43	5 (7%)	16 20	18, 55, 97, 111	0
18	XR	70/88 (79%)	1.23	16 (22%)	1 2	16, 50, 102, 113	0
19	QS	84/93 (90%)	2.22	40 (47%)	1 0	50, 96, 144, 180	0
19	XS	84/93 (90%)	1.28	21 (25%)	1 1	20, 65, 113, 176	0
20	QT	99/106 (93%)	1.66	37 (37%)	1 0	20, 59, 117, 189	0
20	XT	99/106 (93%)	1.97	47 (47%)	1 0	30, 68, 122, 151	0
21	QU	25/27 (92%)	1.54	6 (24%)	1 2	30, 73, 126, 140	0
21	XU	25/27 (92%)	1.09	5 (20%)	2 2	31, 45, 98, 136	0
22	QV	77/77 (100%)	0.43	4 (5%)	26 33	13, 59, 116, 149	0
22	XV	77/77 (100%)	0.32	3 (3%)	37 46	3, 42, 86, 154	0
23	QY	15/17 (88%)	2.94	10 (66%)	0 0	54, 89, 150, 155	0
23	XY	15/17 (88%)	2.12	6 (40%)	1 0	24, 66, 120, 138	0
24	QX	8/25 (32%)	0.66	0	100 100	30, 49, 70, 98	0
24	XX	8/25 (32%)	0.47	0	100 100	15, 25, 40, 55	0
25	RA	2882/2916 (98%)	0.42	155 (5%)	25 32	1, 31, 175, 318	0
25	YA	2883/2916 (98%)	0.35	121 (4%)	35 43	0, 21, 170, 311	0
26	RB	120/122 (98%)	0.01	1 (0%)	83 90	29, 55, 88, 110	0
26	YB	120/122 (98%)	0.04	0	100 100	14, 37, 58, 106	0
27	RD	272/276 (98%)	0.34	12 (4%)	33 41	0, 24, 63, 135	0
27	YD	272/276 (98%)	0.13	7 (2%)	53 64	0, 14, 46, 168	0
28	RE	205/206 (99%)	0.76	24 (11%)	5 7	1, 36, 109, 193	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	YE	205/206 (99%)	0.91	34 (16%) 2 3	0, 32, 113, 183	0
29	RF	202/210 (96%)	0.93	35 (17%) 2 3	2, 41, 94, 154	0
29	YF	202/210 (96%)	0.13	6 (2%) 48 58	0, 27, 83, 144	0
30	RG	181/182 (99%)	1.92	75 (41%) 1 0	26, 79, 130, 185	0
30	YG	181/182 (99%)	0.89	28 (15%) 3 4	14, 43, 93, 158	0
31	RH	170/180 (94%)	3.97	117 (68%) 0 0	42, 117, 172, 219	0
31	YH	170/180 (94%)	0.52	14 (8%) 12 15	12, 50, 96, 160	0
32	RI	146/148 (98%)	2.16	67 (45%) 1 0	22, 74, 128, 179	0
32	YI	146/148 (98%)	1.13	27 (18%) 2 3	16, 74, 128, 161	0
33	RN	138/140 (98%)	1.67	37 (26%) 1 1	16, 43, 86, 151	0
33	YN	138/140 (98%)	0.81	13 (9%) 9 11	10, 35, 87, 139	0
34	RO	122/122 (100%)	0.83	14 (11%) 5 7	10, 34, 75, 103	0
34	YO	122/122 (100%)	0.63	9 (7%) 14 18	1, 25, 48, 76	0
35	RP	150/150 (100%)	2.09	49 (32%) 1 1	3, 48, 112, 222	0
35	YP	150/150 (100%)	0.97	23 (15%) 3 4	2, 32, 95, 190	0
36	RQ	141/141 (100%)	1.86	49 (34%) 1 1	4, 47, 104, 139	0
36	YQ	141/141 (100%)	1.11	22 (15%) 3 4	1, 27, 82, 153	0
37	RR	118/118 (100%)	0.23	5 (4%) 35 43	3, 30, 55, 88	0
37	YR	118/118 (100%)	1.27	29 (24%) 1 2	6, 31, 58, 113	0
38	RS	111/112 (99%)	1.07	23 (20%) 1 2	23, 58, 109, 127	0
38	YS	111/112 (99%)	0.84	15 (13%) 4 5	13, 40, 93, 150	0
39	RT	137/146 (93%)	1.52	40 (29%) 1 1	16, 42, 124, 206	0
39	YT	137/146 (93%)	1.10	21 (15%) 3 4	9, 35, 131, 196	0
40	RU	117/118 (99%)	0.81	14 (11%) 5 7	6, 34, 96, 165	0
40	YU	117/118 (99%)	0.40	9 (7%) 13 17	2, 21, 85, 144	0
41	RV	101/101 (100%)	1.60	32 (31%) 1 1	7, 53, 108, 198	0
41	YV	101/101 (100%)	1.27	28 (27%) 1 1	0, 46, 93, 208	0
42	RW	113/113 (100%)	0.42	5 (4%) 33 41	3, 25, 69, 172	0
42	YW	113/113 (100%)	0.77	7 (6%) 20 25	1, 25, 79, 174	0
43	RX	92/96 (95%)	0.64	9 (9%) 8 11	0, 33, 64, 106	0
43	YX	92/96 (95%)	0.14	3 (3%) 44 54	0, 22, 59, 109	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	RY	102/110 (92%)	2.53	51 (50%) 0 0	10, 65, 132, 205	0
44	YY	102/110 (92%)	0.81	13 (12%) 4 6	8, 46, 109, 201	0
45	RZ	183/206 (88%)	2.30	88 (48%) 1 0	28, 81, 152, 203	0
45	YZ	183/206 (88%)	1.37	45 (24%) 1 2	16, 59, 135, 195	0
46	R0	82/85 (96%)	1.16	16 (19%) 2 2	13, 36, 60, 83	0
46	Y0	82/85 (96%)	0.46	3 (3%) 39 48	2, 22, 41, 74	0
47	R1	97/98 (98%)	1.42	13 (13%) 4 5	5, 33, 134, 196	0
47	Y1	97/98 (98%)	0.63	8 (8%) 12 15	1, 29, 123, 178	0
48	R2	69/72 (95%)	0.91	7 (10%) 7 10	15, 51, 121, 133	0
48	Y2	69/72 (95%)	0.25	4 (5%) 22 28	8, 32, 85, 167	0
49	R3	59/60 (98%)	1.37	12 (20%) 1 2	15, 41, 78, 134	0
49	Y3	59/60 (98%)	0.59	4 (6%) 17 22	10, 30, 81, 142	0
50	R4	71/71 (100%)	3.41	40 (56%) 0 0	59, 140, 202, 292	0
50	Y4	71/71 (100%)	2.05	23 (32%) 1 1	39, 97, 174, 227	0
51	R5	59/60 (98%)	1.06	13 (22%) 1 2	2, 33, 145, 188	0
51	Y5	59/60 (98%)	2.15	22 (37%) 1 0	1, 39, 172, 198	0
52	R6	49/54 (90%)	9.60	48 (97%) 0 0	68, 125, 194, 221	0
52	Y6	49/54 (90%)	7.84	49 (100%) 0 0	70, 113, 183, 206	0
53	R7	49/49 (100%)	1.02	8 (16%) 2 3	2, 12, 67, 170	0
53	Y7	49/49 (100%)	0.15	2 (4%) 35 44	0, 7, 50, 140	0
54	R8	64/65 (98%)	1.53	14 (21%) 1 2	8, 31, 93, 151	0
54	Y8	64/65 (98%)	1.24	12 (18%) 2 2	0, 25, 81, 172	0
55	R9	37/37 (100%)	9.00	36 (97%) 0 0	55, 105, 158, 176	0
55	Y9	37/37 (100%)	7.42	37 (100%) 0 0	47, 87, 153, 202	0
56	Z6	3/3 (100%)	3.28	1 (33%) 1 1	21, 21, 24, 28	0
56	Z8	3/3 (100%)	2.80	1 (33%) 1 1	5, 5, 14, 15	0
All	All	20877/21492 (97%)	0.91	3154 (15%) 3 4	0, 43, 135, 318	0

All (3154) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
35	RP	150	ALA	31.3
52	R6	13	CYS	30.8

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Mol	Chain	Res	Type	RSRZ
52	R6	6	ARG	28.7
52	Y6	42	TRP	28.3
13	QM	7	VAL	24.6
52	R6	5	VAL	23.5
47	R1	98	LEU	22.6
52	R6	14	THR	22.2
11	QK	129	SER	21.8
55	Y9	1	MET	20.5
35	RP	149	GLU	20.2
55	R9	14	CYS	19.5
31	RH	43	VAL	19.3
52	R6	7	ILE	19.0
45	YZ	113	ALA	18.7
55	R9	11	CYS	18.5
52	Y6	43	CYS	18.4
52	R6	29	ASN	18.3
11	QK	128	ALA	17.5
12	XL	129	ALA	17.3
52	R6	52	VAL	16.9
11	XK	129	SER	16.6
7	QG	82	GLY	16.6
41	YV	36	PRO	16.1
55	R9	13	LYS	16.1
55	R9	15	LYS	16.0
55	Y9	12	ASP	16.0
52	R6	50	ARG	15.9
55	Y9	27	CYS	15.7
55	R9	26	ILE	15.6
50	R4	49	PHE	15.3
42	YW	113	LYS	15.3
55	Y9	29	ASN	15.2
51	Y5	54	GLY	15.2
55	R9	1	MET	15.1
52	Y6	20	ASN	15.0
42	YW	111	HIS	14.7
12	QL	128	ALA	14.5
13	QM	6	GLY	14.4
52	R6	12	GLU	14.4
55	R9	16	VAL	14.4
41	RV	36	PRO	14.3
50	R4	39	CYS	14.1
35	YP	149	GLU	14.1

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Mol	Chain	Res	Type	RSRZ
52	Y6	26	ASN	14.0
52	Y6	18	ARG	14.0
25	RA	1095	A	14.0
31	RH	49	VAL	14.0
55	R9	12	ASP	13.9
25	YA	2112	G	13.8
2	QB	234	PRO	13.6
2	QB	231	GLU	13.5
55	Y9	28	GLU	13.5
12	QL	129	ALA	13.3
52	R6	42	TRP	13.3
2	XB	125	PRO	13.2
52	Y6	34	LEU	13.1
55	R9	27	CYS	13.1
50	R4	71	ARG	12.9
52	R6	34	LEU	12.8
28	RE	204	ALA	12.7
51	Y5	55	ARG	12.6
45	YZ	166	SER	12.3
13	XM	7	VAL	12.3
25	YA	2804	C	12.3
50	R4	69	LYS	12.1
52	R6	53	LYS	11.9
25	RA	2797	U	11.8
55	Y9	7	VAL	11.7
2	QB	165	VAL	11.6
52	R6	9	LEU	11.6
51	Y5	60	VAL	11.6
35	RP	108	LYS	11.6
47	R1	96	LYS	11.5
2	QB	240	GLN	11.5
12	XL	128	ALA	11.5
7	QG	81	GLY	11.4
11	QK	11	LYS	11.3
13	QM	122	LYS	11.3
25	YA	2116	G	11.3
52	R6	11	LEU	11.3
45	RZ	162	GLU	11.3
55	Y9	32	HIS	11.2
52	R6	30	THR	11.2
19	QS	85	LYS	11.2
54	R8	65	GLU	11.1

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Mol	Chain	Res	Type	RSRZ
50	R4	68	ARG	11.0
52	Y6	44	ARG	11.0
50	Y4	68	ARG	11.0
12	QL	28	LYS	10.8
31	RH	105	LEU	10.8
32	RI	12	LEU	10.8
49	R3	60	GLU	10.7
55	R9	25	VAL	10.7
55	Y9	10	ILE	10.7
51	Y5	58	LEU	10.7
31	RH	45	VAL	10.6
10	QJ	47	PHE	10.6
50	Y4	67	TYR	10.5
52	Y6	12	GLU	10.4
20	QT	99	LEU	10.3
52	R6	20	ASN	10.3
52	Y6	6	ARG	10.3
25	YA	2145	C	10.2
22	XV	0	C	10.1
10	QJ	88	LEU	10.1
4	XD	167	GLY	10.1
53	R7	49	ARG	10.1
25	YA	2164	C	10.1
31	RH	18	GLU	10.1
50	Y4	69	LYS	10.1
13	XM	122	LYS	10.1
55	R9	24	TYR	10.0
55	R9	30	PRO	10.0
32	YI	117	GLU	10.0
47	R1	97	LEU	10.0
31	RH	89	ILE	9.9
55	R9	10	ILE	9.9
50	Y4	40	HIS	9.9
52	R6	23	THR	9.9
49	Y3	60	GLU	9.8
52	R6	21	TYR	9.8
28	RE	205	ALA	9.7
35	RP	13	ASN	9.7
25	RA	2798	C	9.6
31	RH	123	PHE	9.6
7	XG	85	TYR	9.6
36	RQ	104	PHE	9.6

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Mol	Chain	Res	Type	RSRZ
55	Y9	34	GLN	9.6
10	QJ	85	LEU	9.5
2	QB	131	PRO	9.5
13	XM	121	LYS	9.5
53	R7	48	LYS	9.5
12	QL	127	GLU	9.5
13	QM	8	GLU	9.5
55	R9	19	ARG	9.4
52	Y6	29	ASN	9.4
55	Y9	25	VAL	9.4
25	RA	1093	G	9.4
55	R9	17	ILE	9.4
51	Y5	59	GLU	9.4
25	RA	1092	C	9.3
2	QB	238	LEU	9.3
54	R8	64	TYR	9.2
52	R6	51	GLU	9.2
31	RH	109	PHE	9.2
1	QA	1029	G	9.2
44	RY	58	GLY	9.1
39	YT	1	MET	9.1
23	QY	31	G	9.1
7	XG	156	TRP	9.1
45	YZ	167	PRO	9.0
25	YA	2117	A	9.0
45	RZ	155	LEU	9.0
10	QJ	34	VAL	9.0
11	QK	127	LYS	9.0
45	RZ	163	LEU	9.0
25	RA	1096	A	8.9
31	RH	47	GLU	8.9
52	Y6	48	VAL	8.9
45	RZ	159	PRO	8.9
2	QB	230	VAL	8.9
50	R4	70	GLY	8.9
52	R6	25	LYS	8.9
40	YU	117	GLN	8.9
55	R9	34	GLN	8.9
44	RY	52	SER	8.8
52	R6	49	HIS	8.8
36	YQ	91	GLU	8.8
33	RN	9	VAL	8.8

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Mol	Chain	Res	Type	RSRZ
52	R6	22	ALA	8.8
31	RH	103	LEU	8.8
55	R9	9	ARG	8.8
50	R4	40	HIS	8.8
19	QS	15	LEU	8.7
2	XB	127	ILE	8.7
55	Y9	13	LYS	8.7
7	QG	32	ARG	8.7
20	XT	72	LEU	8.7
52	R6	26	ASN	8.7
52	Y6	23	THR	8.6
35	RP	79	ARG	8.5
14	QN	39	LEU	8.5
28	YE	69	LYS	8.5
25	YA	277	C	8.5
10	QJ	4	ILE	8.5
44	RY	63	LYS	8.5
52	Y6	13	CYS	8.5
55	R9	22	ARG	8.4
55	R9	32	HIS	8.4
12	QL	64	TYR	8.4
50	Y4	39	CYS	8.4
30	YG	80	PHE	8.4
52	Y6	33	LYS	8.4
52	Y6	14	THR	8.4
55	R9	33	LYS	8.3
22	QV	0	C	8.3
28	YE	68	ALA	8.3
45	RZ	96	VAL	8.3
42	YW	112	GLY	8.2
3	XC	79	ARG	8.2
31	RH	169	VAL	8.2
3	QC	78	GLY	8.2
35	RP	148	LEU	8.2
52	R6	24	GLU	8.2
50	R4	67	TYR	8.2
1	QA	1032	A	8.2
51	Y5	57	VAL	8.2
52	Y6	32	ASN	8.2
2	QB	4	GLU	8.2
13	XM	6	GLY	8.2
2	QB	70	PHE	8.2

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Mol	Chain	Res	Type	RSRZ
53	Y7	49	ARG	8.2
55	R9	37	GLY	8.2
2	QB	233	SER	8.2
52	Y6	8	LYS	8.1
12	XL	127	GLU	8.1
33	RN	10	GLU	8.1
32	RI	59	ALA	8.1
10	XJ	47	PHE	8.1
52	Y6	16	CYS	8.1
25	RA	2164	C	8.1
52	R6	33	LYS	8.1
2	QB	133	LYS	8.1
56	Z6	76	PPU	8.1
52	Y6	52	VAL	8.0
41	RV	45	THR	8.0
25	RA	229	A	8.0
2	XB	233	SER	8.0
45	RZ	153	SER	8.0
28	YE	205	ALA	8.0
55	R9	28	GLU	8.0
19	XS	11	VAL	8.0
2	QB	130	ARG	7.9
28	RE	79	ARG	7.9
52	Y6	19	ARG	7.9
36	YQ	90	VAL	7.9
14	QN	25	VAL	7.9
46	R0	2	ALA	7.9
2	XB	133	LYS	7.9
4	QD	49	ARG	7.9
55	R9	36	GLN	7.9
11	XK	11	LYS	7.9
31	RH	33	LEU	7.8
31	RH	113	VAL	7.8
25	RA	1177	A	7.8
52	Y6	36	LEU	7.8
54	Y8	64	TYR	7.8
31	RH	125	VAL	7.8
52	Y6	9	LEU	7.7
31	RH	95	ARG	7.7
55	Y9	30	PRO	7.7
31	YH	152	ARG	7.7
25	YA	2174	C	7.7

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Mol	Chain	Res	Type	RSRZ
47	R1	95	LEU	7.7
51	R5	2	ALA	7.7
4	XD	168	ARG	7.7
55	Y9	26	ILE	7.7
27	YD	26	LYS	7.7
39	YT	135	ALA	7.6
52	Y6	53	LYS	7.6
7	XG	78	ARG	7.6
52	R6	27	LYS	7.6
2	QB	15	VAL	7.6
55	Y9	35	ARG	7.6
52	Y6	5	VAL	7.6
47	Y1	97	LEU	7.6
55	Y9	24	TYR	7.6
44	RY	55	TYR	7.5
14	QN	37	PHE	7.5
7	XG	5	ARG	7.5
35	RP	98	GLU	7.5
35	RP	109	GLY	7.5
25	RA	1094	U	7.5
55	Y9	6	SER	7.5
31	RH	48	GLY	7.4
25	YA	2161	C	7.4
45	RZ	113	ALA	7.4
44	RY	62	GLU	7.3
1	QA	1451	A	7.3
25	YA	1536	A	7.3
25	YA	2165	G	7.3
30	RG	178	PHE	7.3
11	XK	12	ARG	7.3
44	RY	50	ARG	7.3
3	QC	177	THR	7.3
52	Y6	30	THR	7.3
1	XA	1451	A	7.3
52	R6	43	CYS	7.3
44	RY	5	MET	7.3
31	RH	96	ALA	7.3
7	XG	81	GLY	7.3
25	RA	1176	G	7.3
52	Y6	7	ILE	7.3
45	RZ	160	GLY	7.2
25	YA	2173	A	7.2

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Mol	Chain	Res	Type	RSRZ
10	XJ	59	SER	7.2
25	YA	2119	A	7.2
2	QB	163	PHE	7.2
32	RI	11	ASN	7.2
36	RQ	66	ILE	7.2
31	RH	121	ILE	7.2
31	RH	32	GLU	7.2
38	YS	2	ALA	7.2
55	R9	29	ASN	7.2
2	XB	229	VAL	7.2
31	RH	17	VAL	7.2
10	QJ	46	ARG	7.1
30	RG	80	PHE	7.1
52	R6	36	LEU	7.1
2	QB	239	VAL	7.1
50	Y4	56	VAL	7.1
25	RA	2799	A	7.1
2	QB	152	PHE	7.1
25	RA	1088	A	7.0
10	XJ	5	ARG	7.0
45	RZ	69	THR	7.0
36	YQ	140	ALA	7.0
35	RP	76	LYS	7.0
52	Y6	22	ALA	7.0
31	RH	50	VAL	7.0
31	RH	87	LEU	7.0
10	QJ	100	THR	7.0
32	RI	9	LEU	7.0
25	YA	2125	G	7.0
31	RH	152	ARG	7.0
9	QI	110	GLU	7.0
32	YI	118	LYS	7.0
25	YA	2162	G	7.0
35	YP	150	ALA	7.0
50	R4	51	ASP	7.0
52	R6	19	ARG	6.9
39	RT	112	ARG	6.9
31	RH	97	ARG	6.9
2	QB	229	VAL	6.9
25	YA	2133	G	6.9
2	QB	236	TYR	6.8
52	R6	32	ASN	6.8

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Mol	Chain	Res	Type	RSRZ
2	QB	68	ILE	6.8
31	RH	106	THR	6.8
30	RG	115	ARG	6.8
51	R5	53	ALA	6.8
50	Y4	66	SER	6.8
9	QI	27	THR	6.8
12	QL	27	LEU	6.8
56	Z8	76	PPU	6.8
1	QA	1453	G	6.8
25	YA	2805	G	6.8
30	YG	116	ASP	6.8
31	RH	27	LYS	6.8
52	R6	10	LEU	6.8
7	QG	156	TRP	6.7
45	RZ	169	GLU	6.7
45	RZ	57	ILE	6.7
32	RI	1	MET	6.7
55	Y9	36	GLN	6.7
52	Y6	17	LYS	6.7
25	YA	2118	U	6.7
2	XB	130	ARG	6.7
7	XG	154	TYR	6.7
10	QJ	5	ARG	6.7
28	RE	54	GLN	6.7
32	RI	15	VAL	6.7
12	QL	60	LEU	6.7
25	YA	2132	U	6.7
32	YI	79	ILE	6.7
55	R9	20	HIS	6.6
47	Y1	96	LYS	6.6
33	RN	135	PRO	6.6
2	XB	123	ALA	6.6
3	QC	79	ARG	6.6
31	RH	115	VAL	6.6
3	QC	193	TYR	6.6
50	Y4	70	GLY	6.6
52	Y6	37	ARG	6.6
25	RA	2145	C	6.5
33	RN	138	LEU	6.5
39	YT	106	SER	6.5
2	XB	96	ARG	6.5
7	QG	154	TYR	6.5

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Mol	Chain	Res	Type	RSRZ
35	RP	16	ARG	6.5
40	RU	90	VAL	6.5
50	R4	55	ARG	6.5
10	XJ	6	ILE	6.5
45	RZ	93	ASP	6.5
7	XG	79	ARG	6.5
7	QG	79	ARG	6.5
7	XG	84	ASN	6.5
25	RA	2159	G	6.5
2	XB	217	ARG	6.5
44	RY	43	ASN	6.4
13	QM	61	GLU	6.4
14	QN	36	PHE	6.4
25	YA	2175	C	6.4
11	QK	99	GLN	6.4
41	YV	45	THR	6.4
25	RA	1089	G	6.4
55	Y9	16	VAL	6.4
1	XA	87	A	6.3
52	Y6	47	THR	6.3
32	RI	3	VAL	6.3
54	R8	34	TRP	6.3
32	YI	113	ARG	6.3
45	RZ	114	GLY	6.3
9	QI	53	VAL	6.3
30	RG	118	ARG	6.3
51	R5	60	VAL	6.3
52	R6	48	VAL	6.3
14	QN	55	GLY	6.3
28	YE	204	ALA	6.3
2	QB	80	ILE	6.3
11	QK	12	ARG	6.3
7	QG	86	GLN	6.3
52	Y6	51	GLU	6.3
55	Y9	23	VAL	6.3
13	QM	121	LYS	6.2
52	Y6	21	TYR	6.2
13	QM	97	PRO	6.2
28	YE	72	VAL	6.2
31	RH	88	LEU	6.2
12	QL	19	ARG	6.2
31	RH	114	VAL	6.2

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Mol	Chain	Res	Type	RSRZ
3	QC	6	HIS	6.2
19	QS	50	ALA	6.2
25	RA	1103	A	6.2
31	RH	94	TYR	6.2
30	RG	39	ILE	6.2
50	R4	22	ILE	6.2
55	R9	23	VAL	6.2
45	RZ	149	SER	6.2
10	QJ	62	HIS	6.2
2	QB	215	LEU	6.1
54	Y8	65	GLU	6.1
25	RA	1064	C	6.1
20	XT	9	ASN	6.1
31	RH	31	GLY	6.1
25	RA	1536	A	6.1
25	RA	1063	G	6.1
3	QC	135	LYS	6.1
39	RT	106	SER	6.1
11	XK	127	LYS	6.1
30	YG	182	LYS	6.1
13	QM	120	LYS	6.1
18	QR	88	LYS	6.1
25	RA	887	A	6.1
31	RH	107	VAL	6.1
32	RI	54	GLN	6.1
9	XI	46	ALA	6.1
11	QK	31	THR	6.1
44	RY	79	CYS	6.1
31	RH	155	SER	6.1
39	YT	133	GLU	6.0
31	RH	24	VAL	6.0
36	RQ	1	MET	6.0
10	QJ	6	ILE	6.0
31	RH	42	ARG	6.0
55	R9	2	LYS	6.0
36	YQ	141	GLN	6.0
31	RH	46	GLU	6.0
31	RH	133	VAL	6.0
44	RY	46	LYS	6.0
36	RQ	32	TYR	6.0
53	R7	46	VAL	6.0
3	XC	78	GLY	6.0

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Mol	Chain	Res	Type	RSRZ
25	YA	276	A	6.0
53	Y7	48	LYS	6.0
19	QS	41	VAL	6.0
13	XM	100	GLY	6.0
13	QM	3	ARG	6.0
2	QB	155	LEU	5.9
31	RH	30	LYS	5.9
35	RP	71	VAL	5.9
2	QB	232	PRO	5.9
10	QJ	98	ILE	5.9
2	QB	79	ASP	5.9
31	RH	141	VAL	5.9
40	YU	118	GLY	5.9
7	QG	16	LEU	5.9
25	RA	277	C	5.9
25	RA	2174	C	5.9
45	RZ	121	HIS	5.9
14	QN	35	ARG	5.9
32	RI	85	GLU	5.9
25	RA	1068	G	5.9
13	QM	103	THR	5.9
35	YP	13	ASN	5.9
2	XB	234	PRO	5.9
25	RA	1098	A	5.9
25	YA	1058	G	5.8
31	RH	148	ILE	5.8
44	RY	61	ILE	5.8
30	RG	139	LEU	5.8
14	QN	34	TYR	5.8
52	Y6	49	HIS	5.8
32	YI	116	LEU	5.8
11	XK	81	ASP	5.8
7	QG	78	ARG	5.8
3	QC	87	LEU	5.8
4	QD	84	LYS	5.8
41	RV	1	MET	5.8
7	XG	80	VAL	5.8
25	YA	897	C	5.8
55	Y9	14	CYS	5.8
10	XJ	101	VAL	5.8
25	RA	2173	A	5.8
31	RH	144	VAL	5.8

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Mol	Chain	Res	Type	RSRZ
29	RF	8	GLN	5.8
44	YY	50	ARG	5.8
47	R1	92	LYS	5.8
50	R4	23	GLU	5.8
52	Y6	41	PRO	5.7
13	QM	102	ARG	5.7
2	XB	76	GLN	5.7
2	QB	149	LEU	5.7
9	XI	102	LEU	5.7
14	QN	13	THR	5.7
13	QM	2	ALA	5.7
36	YQ	87	LYS	5.7
3	QC	149	ALA	5.7
13	QM	85	GLY	5.7
31	RH	13	LYS	5.7
31	RH	25	LYS	5.7
10	XJ	4	ILE	5.7
3	QC	167	TRP	5.7
21	QU	10	ARG	5.7
25	YA	2129	C	5.7
10	QJ	55	LYS	5.7
25	RA	2125	G	5.7
31	RH	145	ALA	5.7
20	XT	27	LYS	5.7
44	RY	102	CYS	5.7
31	RH	132	ARG	5.7
45	RZ	125	LEU	5.7
52	Y6	11	LEU	5.6
7	XG	32	ARG	5.6
31	RH	170	ARG	5.6
44	RY	44	ILE	5.6
51	R5	55	ARG	5.6
52	Y6	50	ARG	5.6
50	R4	47	GLN	5.6
31	RH	19	VAL	5.6
55	Y9	9	ARG	5.6
11	QK	95	ILE	5.6
32	RI	17	GLN	5.6
45	RZ	171	ILE	5.6
8	XH	1	MET	5.6
25	YA	2135	A	5.6
32	RI	10	GLU	5.6

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Mol	Chain	Res	Type	RSRZ
36	RQ	80	GLU	5.6
55	R9	35	ARG	5.6
10	QJ	72	VAL	5.6
31	RH	44	VAL	5.6
25	YA	2111	C	5.6
52	Y6	35	GLU	5.6
55	R9	4	ARG	5.6
31	RH	29	PRO	5.6
10	QJ	71	LEU	5.6
48	R2	43	GLN	5.6
42	RW	113	LYS	5.6
2	QB	187	LEU	5.6
32	YI	84	GLY	5.6
3	QC	152	ILE	5.6
13	QM	5	ALA	5.6
3	QC	101	LEU	5.6
45	RZ	70	LEU	5.5
47	Y1	92	LYS	5.5
20	QT	42	GLN	5.5
36	RQ	133	ARG	5.5
25	RA	2147	G	5.5
36	RQ	141	GLN	5.5
2	QB	211	ILE	5.5
30	RG	157	ILE	5.5
31	RH	15	VAL	5.5
9	QI	119	ALA	5.5
51	Y5	52	TYR	5.5
3	QC	179	ARG	5.5
25	RA	2116	G	5.5
13	XM	94	ARG	5.5
36	RQ	91	GLU	5.5
39	YT	2	ASN	5.5
31	RH	157	TYR	5.5
36	YQ	80	GLU	5.4
50	R4	25	TYR	5.4
10	QJ	33	GLN	5.4
45	RZ	161	VAL	5.4
45	RZ	152	ALA	5.4
2	QB	75	LYS	5.4
32	RI	4	ILE	5.4
2	XB	227	GLY	5.4
10	QJ	64	GLU	5.4

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Mol	Chain	Res	Type	RSRZ
31	RH	102	ALA	5.4
32	RI	83	ALA	5.4
9	XI	49	PRO	5.4
2	XB	231	GLU	5.4
4	XD	50	ARG	5.4
50	Y4	51	ASP	5.4
55	R9	5	ALA	5.4
55	Y9	11	CYS	5.4
44	RY	49	VAL	5.4
25	RA	1070	A	5.4
41	RV	34	GLU	5.4
3	QC	204	LEU	5.4
7	QG	83	ALA	5.3
2	XB	240	GLN	5.3
25	YA	2167	U	5.3
23	QY	42	G	5.3
45	RZ	156	LYS	5.3
12	QL	62	SER	5.3
35	RP	106	LEU	5.3
9	XI	17	VAL	5.3
10	QJ	59	SER	5.3
20	XT	70	SER	5.3
31	RH	81	GLU	5.3
28	RE	21	VAL	5.3
45	RZ	167	PRO	5.3
25	YA	2803	C	5.3
21	QU	15	ARG	5.3
44	RY	86	ARG	5.3
40	RU	91	ASP	5.3
38	YS	109	GLY	5.3
4	XD	209	ARG	5.3
10	QJ	28	ARG	5.3
1	QA	1026	G	5.3
36	YQ	104	PHE	5.3
9	QI	106	ALA	5.3
36	RQ	90	VAL	5.3
7	QG	5	ARG	5.3
10	QJ	70	ARG	5.2
4	XD	169	LYS	5.2
25	YA	2795	G	5.2
25	YA	1177	A	5.2
10	QJ	76	ASN	5.2

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Mol	Chain	Res	Type	RSRZ
7	QG	76	ARG	5.2
52	R6	39	TYR	5.2
14	QN	61	TRP	5.2
25	YA	2126	A	5.2
13	XM	118	ALA	5.2
41	YV	101	GLY	5.2
31	RH	111	HIS	5.2
3	QC	180	ALA	5.2
51	Y5	2	ALA	5.2
50	Y4	37	SER	5.2
51	R5	54	GLY	5.2
55	Y9	3	VAL	5.2
2	XB	131	PRO	5.2
35	RP	110	TYR	5.2
39	YT	136	GLN	5.2
9	XI	59	PHE	5.2
25	RA	1099	G	5.1
25	YA	2166	G	5.1
31	RH	161	GLY	5.1
31	RH	104	GLU	5.1
13	QM	101	GLN	5.1
4	QD	209	ARG	5.1
45	RZ	122	ARG	5.1
9	XI	94	ALA	5.1
25	YA	1059	G	5.1
10	QJ	83	GLU	5.1
29	RF	196	LEU	5.1
29	RF	128	ALA	5.1
1	XA	88	C	5.1
32	RI	86	THR	5.1
25	YA	1176	G	5.1
54	R8	63	PRO	5.1
18	XR	88	LYS	5.1
2	XB	188	ALA	5.0
11	QK	49	GLY	5.0
25	YA	654	A	5.0
31	RH	117	PRO	5.0
45	RZ	183	LEU	5.0
12	XL	126	LYS	5.0
52	R6	17	LYS	5.0
28	RE	72	VAL	5.0
25	YA	2159	G	5.0

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Mol	Chain	Res	Type	RSRZ
10	XJ	98	ILE	5.0
25	RA	2161	C	5.0
4	QD	50	ARG	5.0
50	Y4	18	CYS	5.0
25	YA	2123	G	5.0
32	RI	5	LEU	5.0
12	QL	18	VAL	5.0
49	Y3	59	VAL	5.0
19	QS	71	LEU	5.0
25	RA	1059	G	5.0
41	YV	37	VAL	5.0
14	XN	2	ALA	5.0
52	Y6	25	LYS	5.0
2	QB	6	THR	5.0
45	YZ	163	LEU	5.0
27	RD	26	LYS	5.0
51	Y5	51	TYR	5.0
37	YR	48	VAL	5.0
44	RY	64	GLU	4.9
1	QA	1257	U	4.9
25	YA	2158	A	4.9
38	RS	20	ARG	4.9
31	RH	11	VAL	4.9
12	XL	28	LYS	4.9
19	XS	85	LYS	4.9
33	RN	12	ARG	4.9
28	YE	88	GLY	4.9
10	QJ	63	PHE	4.9
55	Y9	33	LYS	4.9
9	QI	109	VAL	4.9
25	YA	2114	A	4.9
31	YH	125	VAL	4.9
2	XB	122	PHE	4.9
10	XJ	64	GLU	4.9
41	RV	37	VAL	4.9
3	QC	178	LEU	4.9
7	QG	42	ILE	4.9
9	QI	75	ASP	4.9
11	XK	69	ALA	4.9
32	RI	13	GLY	4.9
39	RT	94	ALA	4.9
25	RA	2160	G	4.9

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Mol	Chain	Res	Type	RSRZ
25	YA	2131	G	4.9
33	YN	134	ARG	4.9
2	XB	15	VAL	4.9
52	R6	31	PRO	4.9
18	QR	84	LYS	4.9
45	YZ	155	LEU	4.9
52	R6	37	ARG	4.9
55	Y9	4	ARG	4.9
2	QB	90	MET	4.9
25	YA	2122	U	4.9
31	RH	154	PRO	4.9
32	YI	128	LEU	4.9
9	XI	77	ILE	4.9
45	RZ	124	ILE	4.9
9	QI	43	ALA	4.9
39	RT	1	MET	4.8
25	YA	229	A	4.8
30	RG	64	THR	4.8
7	QG	149	ARG	4.8
31	RH	82	GLY	4.8
32	RI	20	ASP	4.8
36	RQ	109	VAL	4.8
45	RZ	131	ARG	4.8
38	YS	44	LYS	4.8
25	YA	2146	C	4.8
9	QI	47	LEU	4.8
50	R4	9	LEU	4.8
52	R6	47	THR	4.8
2	QB	207	ALA	4.8
25	YA	2144	U	4.8
7	QG	12	LEU	4.8
30	RG	91	ARG	4.8
52	R6	28	ARG	4.8
31	RH	164	TYR	4.8
55	Y9	17	ILE	4.8
2	QB	94	ASN	4.8
28	YE	79	ARG	4.8
2	QB	235	SER	4.8
36	RQ	19	GLY	4.8
10	XJ	21	GLN	4.8
11	QK	32	ILE	4.8
42	RW	92	ARG	4.8

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Mol	Chain	Res	Type	RSRZ
25	RA	2144	U	4.8
31	RH	14	GLY	4.8
44	RY	59	GLY	4.8
30	RG	138	GLN	4.8
50	R4	48	ARG	4.8
13	QM	106	ASN	4.8
25	YA	2130	U	4.8
2	QB	71	VAL	4.7
7	QG	28	ASN	4.7
25	YA	2127	G	4.7
40	RU	118	GLY	4.7
2	XB	129	GLU	4.7
20	XT	17	ARG	4.7
20	XT	25	ARG	4.7
50	Y4	5	ILE	4.7
12	QL	63	GLY	4.7
11	QK	89	ALA	4.7
32	RI	146	ALA	4.7
25	RA	1097	U	4.7
37	YR	72	ASP	4.7
3	QC	30	ARG	4.7
7	QG	41	ARG	4.7
40	RU	117	GLN	4.7
3	XC	167	TRP	4.7
55	Y9	15	LYS	4.7
41	YV	98	GLU	4.7
35	YP	139	LYS	4.7
9	XI	81	ILE	4.7
32	RI	61	ARG	4.7
44	YY	53	PRO	4.7
52	R6	41	PRO	4.7
17	XQ	101	ARG	4.7
50	R4	61	ARG	4.7
3	XC	80	GLY	4.7
28	YE	21	VAL	4.7
20	XT	55	ILE	4.7
10	XJ	72	VAL	4.7
2	QB	92	TYR	4.7
27	YD	262	ARG	4.6
28	YE	187	ALA	4.6
55	Y9	5	ALA	4.6
48	Y2	43	GLN	4.6

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Mol	Chain	Res	Type	RSRZ
38	RS	24	LEU	4.6
33	YN	130	HIS	4.6
2	QB	186	ALA	4.6
25	YA	2121	G	4.6
31	RH	131	VAL	4.6
14	QN	12	ARG	4.6
27	YD	35	LYS	4.6
31	RH	41	MET	4.6
21	XU	26	LYS	4.6
25	RA	2148	G	4.6
31	RH	85	LYS	4.6
44	RY	45	VAL	4.6
29	RF	172	TRP	4.6
54	R8	61	LEU	4.6
20	XT	73	HIS	4.6
25	RA	1100	C	4.6
45	RZ	55	HIS	4.6
25	YA	2170	A	4.6
25	YA	2794	C	4.6
10	QJ	101	VAL	4.6
32	RI	144	VAL	4.6
52	Y6	39	TYR	4.6
2	QB	134	GLU	4.6
25	RA	2129	C	4.6
28	YE	182	LEU	4.6
1	QA	81	G	4.6
4	XD	207	TYR	4.6
33	RN	130	HIS	4.6
35	RP	105	LEU	4.5
27	RD	34	VAL	4.5
2	XB	135	GLN	4.5
9	QI	117	HIS	4.5
3	QC	198	VAL	4.5
31	YH	3	ARG	4.5
4	QD	161	ASN	4.5
39	RT	2	ASN	4.5
10	XJ	95	GLU	4.5
2	QB	83	MET	4.5
10	QJ	65	LEU	4.5
25	RA	2154	G	4.5
33	RN	98	VAL	4.5
52	Y6	27	LYS	4.5

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Mol	Chain	Res	Type	RSRZ
31	RH	119	GLU	4.5
20	XT	28	ALA	4.5
2	XB	230	VAL	4.5
1	XA	208	U	4.5
25	RA	888	C	4.5
3	XC	201	TYR	4.5
30	RG	137	GLU	4.5
2	QB	82	ARG	4.5
20	XT	63	ILE	4.5
30	RG	114	ILE	4.5
41	YV	99	ILE	4.5
50	R4	58	ARG	4.5
50	Y4	52	THR	4.5
20	XT	69	GLY	4.5
52	R6	35	GLU	4.5
25	YA	2141	G	4.5
36	YQ	1	MET	4.5
3	QC	148	GLY	4.5
30	RG	85	GLY	4.5
45	YZ	169	GLU	4.5
50	R4	34	GLU	4.5
9	QI	10	ARG	4.5
2	XB	214	ILE	4.5
20	QT	100	ILE	4.5
25	RA	2175	C	4.5
9	QI	115	GLY	4.5
28	RE	1	MET	4.5
2	QB	217	ARG	4.5
25	RA	889	C	4.5
27	RD	35	LYS	4.5
50	R4	1	MET	4.5
30	RG	2	PRO	4.5
23	XY	31	G	4.4
23	XY	42	G	4.4
35	YP	16	ARG	4.4
12	QL	55	VAL	4.4
1	QA	1450	U	4.4
25	RA	2127	G	4.4
40	RU	88	ILE	4.4
41	YV	48	GLY	4.4
31	RH	84	SER	4.4
32	YI	144	VAL	4.4

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Mol	Chain	Res	Type	RSRZ
1	QA	88	C	4.4
25	RA	2139	C	4.4
42	YW	92	ARG	4.4
25	RA	1058	G	4.4
25	RA	1057	A	4.4
32	RI	35	LEU	4.4
3	XC	5	ILE	4.4
32	YI	120	ILE	4.4
14	QN	38	GLY	4.4
3	QC	147	LYS	4.4
9	XI	106	ALA	4.4
38	RS	57	LYS	4.4
30	RG	54	GLU	4.4
9	QI	111	ARG	4.4
33	RN	8	GLN	4.4
1	QA	1531	A	4.4
23	QY	28	C	4.4
25	RA	1075	C	4.4
25	YA	645	C	4.4
3	QC	160	ALA	4.4
23	XY	32	U	4.4
50	R4	60	GLN	4.4
44	YY	63	LYS	4.4
30	YG	48	GLU	4.4
2	XB	165	VAL	4.4
40	RU	92	ARG	4.4
20	XT	24	LEU	4.4
25	RA	1083	U	4.4
41	RV	44	LYS	4.4
10	QJ	38	ILE	4.4
19	QS	80	TYR	4.4
45	RZ	2	GLU	4.4
25	YA	2124	G	4.4
28	RE	104	VAL	4.4
37	YR	41	ALA	4.4
42	RW	112	GLY	4.4
2	QB	5	ILE	4.3
4	QD	24	GLU	4.3
30	RG	72	ARG	4.3
45	RZ	126	VAL	4.3
35	RP	127	ALA	4.3
47	Y1	98	LEU	4.3

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Mol	Chain	Res	Type	RSRZ
38	YS	43	GLU	4.3
25	RA	1091	G	4.3
4	XD	3	ARG	4.3
14	QN	57	ARG	4.3
52	R6	44	ARG	4.3
30	RG	155	MET	4.3
14	QN	53	LEU	4.3
28	YE	56	PRO	4.3
25	RA	1082	U	4.3
1	XA	81	G	4.3
25	YA	2793	G	4.3
3	XC	62	ASP	4.3
33	RN	133	GLN	4.3
30	RG	152	LEU	4.3
31	RH	10	PRO	4.3
36	YQ	24	GLY	4.3
4	QD	47	ARG	4.3
44	RY	33	LYS	4.3
53	R7	47	ARG	4.3
19	XS	10	PHE	4.3
1	QA	1027	C	4.3
55	R9	7	VAL	4.3
9	QI	20	ARG	4.3
55	Y9	22	ARG	4.3
25	YA	1061	U	4.3
32	RI	43	ASN	4.3
25	YA	1096	A	4.3
9	QI	17	VAL	4.3
28	RE	76	ARG	4.3
31	RH	76	VAL	4.3
35	YP	90	ARG	4.3
50	R4	50	VAL	4.3
52	R6	18	ARG	4.3
11	XK	15	ALA	4.3
2	QB	208	ILE	4.3
45	YZ	146	ILE	4.3
25	RA	1062	G	4.3
25	RA	2162	G	4.3
21	QU	14	TRP	4.3
25	RA	1067	A	4.3
51	Y5	46	CYS	4.3
52	R6	16	CYS	4.3

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Mol	Chain	Res	Type	RSRZ
11	QK	25	TYR	4.3
10	XJ	34	VAL	4.3
2	QB	77	ALA	4.3
2	XB	222	ILE	4.3
48	R2	15	LYS	4.3
25	RA	2119	A	4.3
17	XQ	91	ARG	4.3
44	YY	49	VAL	4.2
41	YV	38	LEU	4.2
10	QJ	99	LYS	4.2
32	YI	145	VAL	4.2
19	XS	44	MET	4.2
10	QJ	45	ARG	4.2
54	Y8	48	PHE	4.2
7	QG	84	ASN	4.2
3	XC	82	GLU	4.2
10	XJ	65	LEU	4.2
35	RP	88	LEU	4.2
25	RA	2121	G	4.2
33	RN	72	TYR	4.2
8	QH	83	ILE	4.2
30	RG	17	PRO	4.2
2	XB	4	GLU	4.2
12	QL	69	TYR	4.2
45	RZ	133	ILE	4.2
7	QG	146	GLU	4.2
36	RQ	24	GLY	4.2
9	QI	19	LEU	4.2
7	XG	155	ARG	4.2
19	QS	64	GLU	4.2
31	RH	162	ILE	4.2
51	Y5	53	ALA	4.2
9	XI	19	LEU	4.2
25	RA	1026	U	4.2
37	YR	69	ASP	4.2
25	YA	2107	C	4.2
12	XL	26	ALA	4.2
17	XQ	97	SER	4.2
50	R4	66	SER	4.2
9	QI	33	PHE	4.2
12	QL	32	PHE	4.2
33	RN	134	ARG	4.2

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Mol	Chain	Res	Type	RSRZ
31	RH	9	ILE	4.1
35	YP	118	GLY	4.1
45	YZ	110	GLY	4.1
51	Y5	56	LYS	4.1
30	RG	82	LEU	4.1
6	XF	55	ASP	4.1
25	RA	1061	U	4.1
39	RT	115	ARG	4.1
27	YD	33	LEU	4.1
32	RI	6	LEU	4.1
25	YA	2178	C	4.1
23	QY	32	U	4.1
30	YG	26	GLN	4.1
21	XU	25	LYS	4.1
29	RF	193	VAL	4.1
14	QN	59	ALA	4.1
45	YZ	144	LEU	4.1
41	RV	53	GLU	4.1
45	YZ	162	GLU	4.1
50	R4	65	ASP	4.1
28	YE	71	GLY	4.1
36	RQ	64	ILE	4.1
9	XI	41	VAL	4.1
25	RA	2110	G	4.1
45	RZ	99	TYR	4.1
45	YZ	165	VAL	4.1
52	Y6	46	HIS	4.1
44	RY	2	ARG	4.1
39	YT	137	LYS	4.1
45	YZ	133	ILE	4.1
30	RG	86	MET	4.1
4	XD	76	ARG	4.1
9	XI	126	SER	4.1
10	XJ	46	ARG	4.1
25	YA	2160	G	4.1
3	QC	157	ILE	4.1
44	RY	3	VAL	4.1
20	QT	104	LEU	4.1
47	Y1	95	LEU	4.1
45	RZ	50	GLN	4.1
3	QC	146	ALA	4.1
17	XQ	86	GLU	4.1

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Mol	Chain	Res	Type	RSRZ
32	YI	107	VAL	4.1
29	RF	161	GLU	4.0
10	QJ	36	GLY	4.0
25	YA	2140	C	4.0
1	QA	210	U	4.0
9	QI	44	VAL	4.0
18	XR	31	LEU	4.0
4	XD	4	TYR	4.0
25	RA	2155	G	4.0
2	QB	19	HIS	4.0
35	RP	15	ARG	4.0
1	QA	1030	C	4.0
17	QQ	21	VAL	4.0
20	QT	41	ILE	4.0
20	QT	45	GLN	4.0
25	YA	2136	C	4.0
41	RV	101	GLY	4.0
45	RZ	68	PRO	4.0
36	RQ	63	LYS	4.0
3	QC	124	ILE	4.0
11	XK	30	VAL	4.0
33	YN	62	VAL	4.0
45	RZ	165	VAL	4.0
40	YU	91	ASP	4.0
4	QD	164	ALA	4.0
12	XL	29	GLY	4.0
31	RH	135	GLY	4.0
45	YZ	159	PRO	4.0
1	QA	89	U	4.0
2	QB	76	GLN	4.0
25	YA	2147	G	4.0
10	QJ	61	GLU	4.0
19	QS	49	ILE	4.0
31	RH	98	LEU	4.0
30	RG	35	GLU	4.0
31	RH	35	VAL	4.0
3	QC	15	THR	4.0
9	QI	36	TYR	4.0
9	QI	105	ASP	4.0
7	QG	35	LYS	4.0
10	QJ	29	ARG	4.0
41	YV	42	GLY	4.0

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Mol	Chain	Res	Type	RSRZ
25	RA	2146	C	4.0
52	Y6	40	CYS	4.0
2	QB	214	ILE	4.0
3	QC	10	PHE	4.0
4	XD	170	VAL	4.0
13	QM	4	ILE	4.0
30	RG	160	VAL	4.0
45	YZ	96	VAL	4.0
5	QE	24	ARG	4.0
9	XI	95	LYS	4.0
50	Y4	55	ARG	4.0
7	QG	34	GLY	4.0
44	RY	41	GLY	4.0
10	XJ	77	PRO	4.0
2	QB	11	LEU	4.0
12	QL	37	CYS	4.0
3	QC	134	ILE	4.0
31	RH	136	ILE	4.0
14	QN	56	VAL	4.0
44	RY	42	VAL	4.0
54	R8	29	LYS	4.0
3	QC	63	ASN	4.0
34	YO	122	LEU	4.0
41	YV	35	LEU	4.0
3	QC	13	GLY	4.0
23	XY	28	C	3.9
41	YV	53	GLU	3.9
31	RH	90	LYS	3.9
25	RA	1084	A	3.9
45	RZ	128	VAL	3.9
31	RH	159	GLU	3.9
11	XK	43	SER	3.9
7	XG	8	GLU	3.9
30	RG	182	LYS	3.9
31	RH	108	GLY	3.9
32	RI	41	GLU	3.9
25	RA	1066	U	3.9
38	YS	41	ASP	3.9
20	XT	23	ARG	3.9
54	Y8	35	GLN	3.9
2	XB	10	LEU	3.9
9	QI	59	PHE	3.9

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Mol	Chain	Res	Type	RSRZ
10	QJ	27	ALA	3.9
30	RG	53	LEU	3.9
25	YA	2163	C	3.9
2	XB	236	TYR	3.9
29	RF	7	TYR	3.9
31	RH	158	HIS	3.9
44	RY	31	LEU	3.9
28	YE	73	GLU	3.9
38	RS	35	ILE	3.9
9	XI	51	ARG	3.9
45	RZ	58	VAL	3.9
20	XT	21	LYS	3.9
45	RZ	151	HIS	3.9
32	RI	44	LEU	3.9
11	XK	56	GLY	3.9
32	RI	16	GLY	3.9
35	RP	114	ILE	3.9
7	QG	36	LYS	3.9
25	RA	2138	C	3.9
30	RG	108	ASN	3.9
1	XA	1453	G	3.9
25	YA	2168	G	3.9
44	YY	99	CYS	3.9
55	Y9	20	HIS	3.9
9	QI	9	ARG	3.9
31	RH	21	PRO	3.9
25	YA	887	A	3.9
39	YT	35	LYS	3.9
3	QC	172	ARG	3.9
9	QI	42	ARG	3.9
19	QS	81	ARG	3.9
1	QA	1032(B)	G	3.9
2	XB	68	ILE	3.9
11	XK	29	ILE	3.9
12	QL	100	ILE	3.9
7	QG	33	ASP	3.9
39	YT	11	GLU	3.9
11	QK	50	TYR	3.8
15	XO	88	ARG	3.8
30	RG	60	LEU	3.8
30	RG	146	TYR	3.8
36	YQ	19	GLY	3.8

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Mol	Chain	Res	Type	RSRZ
14	QN	7	ILE	3.8
3	QC	138	VAL	3.8
31	RH	37	VAL	3.8
30	YG	82	LEU	3.8
7	XG	43	PHE	3.8
2	QB	222	ILE	3.8
9	QI	81	ILE	3.8
45	YZ	142	SER	3.8
9	XI	7	THR	3.8
12	XL	19	ARG	3.8
7	QG	38	LEU	3.8
30	RG	135	LEU	3.8
4	QD	145	GLU	3.8
12	QL	68	ALA	3.8
48	R2	72	ALA	3.8
3	QC	11	ARG	3.8
32	RI	113	ARG	3.8
25	RA	2136	C	3.8
25	YA	2150	U	3.8
35	RP	57	THR	3.8
25	RA	1173	G	3.8
11	XK	42	TRP	3.8
18	XR	22	VAL	3.8
30	YG	139	LEU	3.8
3	QC	166	GLU	3.8
45	YZ	114	GLY	3.8
19	QS	70	LYS	3.8
25	YA	889	C	3.8
50	Y4	49	PHE	3.8
3	QC	174	PRO	3.8
2	QB	97	TRP	3.8
25	YA	2169	A	3.8
4	XD	5	ILE	3.8
23	QY	30	C	3.8
32	RI	117	GLU	3.8
54	Y8	61	LEU	3.8
2	QB	78	GLN	3.8
25	RA	2156	G	3.8
2	XB	232	PRO	3.8
10	QJ	25	GLU	3.8
54	R8	24	ALA	3.8
3	QC	173	VAL	3.8

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Mol	Chain	Res	Type	RSRZ
2	QB	212	GLN	3.8
3	QC	88	ARG	3.8
4	QD	118	ARG	3.8
18	XR	42	ARG	3.8
19	QS	47	HIS	3.8
20	XT	16	HIS	3.8
14	XN	17	LYS	3.7
31	RH	83	TYR	3.7
52	R6	8	LYS	3.7
1	QA	1032(A)	G	3.7
33	YN	57	ALA	3.7
2	XB	228	GLY	3.7
9	QI	28	VAL	3.7
10	XJ	85	LEU	3.7
13	QM	96	LEU	3.7
25	RA	2142	C	3.7
50	R4	44	THR	3.7
3	QC	7	PRO	3.7
4	XD	96	LEU	3.7
19	QS	11	VAL	3.7
19	QS	84	GLY	3.7
25	RA	2126	A	3.7
19	QS	10	PHE	3.7
20	QT	54	LYS	3.7
25	RA	101	G	3.7
14	QN	49	HIS	3.7
25	RA	1065	U	3.7
3	QC	62	ASP	3.7
30	RG	116	ASP	3.7
14	XN	30	ALA	3.7
32	RI	116	LEU	3.7
49	R3	25	ALA	3.7
19	XS	41	VAL	3.7
36	RQ	106	VAL	3.7
2	XB	105	PHE	3.7
9	XI	101	PHE	3.7
34	RO	45	GLU	3.7
34	YO	108	GLU	3.7
45	RZ	60	GLU	3.7
25	RA	1071	G	3.7
36	RQ	6	ARG	3.7
42	YW	68	ARG	3.7

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Mol	Chain	Res	Type	RSRZ
32	YI	12	LEU	3.7
38	RS	32	LEU	3.7
31	RH	12	PRO	3.7
45	YZ	161	VAL	3.7
13	QM	69	GLU	3.7
10	XJ	8	LEU	3.7
33	RN	26	LEU	3.7
9	QI	76	ALA	3.7
25	RA	2133	G	3.7
49	R3	2	PRO	3.7
10	QJ	89	ASP	3.7
29	RF	9	ILE	3.7
3	QC	23	TYR	3.7
20	QT	72	LEU	3.7
2	QB	161	ALA	3.7
4	QD	3	ARG	3.7
16	XP	35	LYS	3.7
9	XI	75	ASP	3.7
29	RF	116	ASP	3.7
1	XA	162	A	3.7
13	QM	65	LYS	3.7
31	RH	101	ARG	3.7
33	RN	85	ILE	3.7
20	XT	99	LEU	3.7
25	YA	2120	G	3.7
2	XB	132	LYS	3.7
55	Y9	8	LYS	3.7
4	QD	117	ALA	3.6
12	QL	31	PRO	3.6
17	XQ	11	VAL	3.6
37	YR	47	PHE	3.7
45	YZ	164	ALA	3.6
1	XA	91	C	3.6
9	QI	50	LEU	3.6
9	QI	102	LEU	3.6
20	XT	18	GLN	3.6
41	RV	96	ILE	3.6
25	RA	645	C	3.6
35	RP	1	MET	3.6
2	QB	81	VAL	3.6
9	QI	123	PRO	3.6
31	RH	55	PRO	3.6

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Mol	Chain	Res	Type	RSRZ
45	RZ	95	PRO	3.6
13	XM	8	GLU	3.6
14	QN	44	LEU	3.6
35	YP	148	LEU	3.6
25	YA	2108	C	3.6
32	RI	8	PRO	3.6
51	R5	57	VAL	3.6
20	QT	30	LYS	3.6
31	RH	153	LYS	3.6
9	XI	24	GLY	3.6
2	XB	11	LEU	3.6
3	QC	127	ARG	3.6
36	RQ	68	ILE	3.6
13	XM	96	LEU	3.6
1	QA	208	U	3.6
1	XA	210	U	3.6
25	RA	2795	G	3.6
35	RP	91	PHE	3.6
41	RV	74	LYS	3.6
3	XC	193	TYR	3.6
14	XN	34	TYR	3.6
35	RP	77	ARG	3.6
35	RP	111	ARG	3.6
7	QG	75	VAL	3.6
25	RA	890	A	3.6
9	QI	70	LYS	3.6
55	R9	3	VAL	3.6
14	QN	2	ALA	3.6
11	QK	98	LEU	3.6
11	XK	36	ASP	3.6
2	QB	96	ARG	3.6
25	YA	888	C	3.6
2	QB	164	VAL	3.6
14	QN	17	LYS	3.6
28	RE	69	LYS	3.6
29	RF	6	VAL	3.6
31	RH	134	SER	3.6
2	QB	88	ALA	3.6
10	QJ	32	ALA	3.6
2	QB	69	LEU	3.6
45	YZ	120	ILE	3.6
25	RA	1060	U	3.5

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Mol	Chain	Res	Type	RSRZ
15	XO	86	GLY	3.5
12	QL	39	VAL	3.5
36	YQ	81	VAL	3.5
41	RV	98	GLU	3.5
44	RY	30	VAL	3.5
30	RG	158	ALA	3.5
3	QC	39	ILE	3.5
32	RI	79	ILE	3.5
52	R6	46	HIS	3.5
7	QG	37	ASN	3.5
10	XJ	69	ASN	3.5
2	XB	121	LEU	3.5
9	QI	52	ALA	3.5
39	RT	99	LEU	3.5
3	QC	164	ARG	3.5
7	QG	27	ILE	3.5
11	QK	51	LYS	3.5
25	RA	2143	C	3.5
44	RY	89	PHE	3.5
50	R4	42	PHE	3.5
31	RH	86	GLU	3.5
51	Y5	49	CYS	3.5
7	XG	59	LEU	3.5
7	QG	152	ALA	3.5
11	QK	71	LYS	3.5
32	YI	121	LYS	3.5
1	XA	1001	G	3.5
25	RA	2120	G	3.5
25	RA	2793	G	3.5
25	YA	2110	G	3.5
1	QA	90	C	3.5
41	RV	15	GLU	3.5
3	XC	63	ASN	3.5
3	QC	132	ARG	3.5
4	QD	157	LEU	3.5
17	QQ	84	LEU	3.5
19	XS	67	VAL	3.5
32	RI	18	VAL	3.5
32	RI	19	VAL	3.5
37	YR	68	ARG	3.5
52	Y6	38	LYS	3.5
45	YZ	157	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
52	R6	40	CYS	3.5
10	QJ	74	ILE	3.5
31	RH	20	ALA	3.5
41	YV	4	ILE	3.5
10	XJ	62	HIS	3.5
28	YE	67	PHE	3.5
19	XS	84	GLY	3.5
25	RA	898	C	3.5
35	YP	15	ARG	3.5
43	RX	68	ARG	3.5
12	QL	101	VAL	3.5
31	YH	155	SER	3.5
36	RQ	34	LEU	3.5
42	RW	67	ASP	3.5
11	QK	21	ILE	3.5
9	QI	124	GLN	3.5
10	QJ	8	LEU	3.5
37	YR	113	LEU	3.5
50	R4	56	VAL	3.5
1	QA	1028(A)	C	3.5
35	RP	81	GLN	3.5
47	R1	26	ARG	3.5
55	Y9	18	ARG	3.5
3	XC	98	ASN	3.5
13	QM	19	LEU	3.5
39	YT	6	LEU	3.5
17	XQ	23	VAL	3.5
35	RP	83	VAL	3.5
45	RZ	127	LYS	3.5
14	QN	23	ARG	3.5
14	QN	26	ARG	3.5
25	RA	1087	G	3.5
30	RG	48	GLU	3.4
39	RT	104	ASN	3.4
17	XQ	84	LEU	3.4
41	RV	40	LEU	3.4
44	RY	29	GLU	3.4
50	Y4	71	ARG	3.4
9	QI	69	GLY	3.4
38	RS	60	GLY	3.4
50	R4	6	HIS	3.4
10	XJ	97	GLU	3.4

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Mol	Chain	Res	Type	RSRZ
4	XD	120	LEU	3.4
10	QJ	86	MET	3.4
3	QC	104	GLN	3.4
3	QC	190	ARG	3.4
4	XD	70	ILE	3.4
7	QG	85	TYR	3.4
11	XK	99	GLN	3.4
25	RA	2801	A	3.4
32	YI	146	ALA	3.4
25	YA	1060	U	3.4
31	RH	26	VAL	3.4
41	RV	33	VAL	3.4
19	XS	39	THR	3.4
28	RE	77	ILE	3.4
39	RT	60	THR	3.4
4	QD	86	LYS	3.4
13	XM	120	LYS	3.4
38	RS	33	LYS	3.4
10	XJ	71	LEU	3.4
45	YZ	82	ARG	3.4
33	RN	46	VAL	3.4
4	QD	158	ILE	3.4
19	XS	38	SER	3.4
21	QU	2	GLY	3.4
30	RG	52	ILE	3.4
32	RI	120	ILE	3.4
45	RZ	78	LYS	3.4
7	QG	2	ALA	3.4
12	QL	56	ALA	3.4
25	RA	2135	A	3.4
25	YA	275	G	3.4
9	QI	113	LYS	3.4
20	XT	74	LYS	3.4
46	R0	40	GLN	3.4
4	QD	179	GLU	3.4
19	QS	51	VAL	3.4
47	Y1	93	GLU	3.4
9	QI	88	TYR	3.4
10	XJ	45	ARG	3.4
12	QL	59	ARG	3.4
45	RZ	102	LEU	3.4
11	QK	13	GLN	3.4

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Mol	Chain	Res	Type	RSRZ
52	Y6	15	GLU	3.4
3	XC	76	VAL	3.4
2	XB	208	ILE	3.4
3	XC	39	ILE	3.4
13	XM	119	GLY	3.4
31	RH	142	GLY	3.4
3	QC	29	TYR	3.4
14	QN	54	PRO	3.4
38	RS	55	ALA	3.4
45	YZ	112	ARG	3.4
20	XT	20	LEU	3.4
25	RA	2140	C	3.4
35	RP	100	LEU	3.4
3	XC	166	GLU	3.4
29	RF	23	ASP	3.4
29	YF	133	ASN	3.4
34	YO	112	MET	3.4
3	QC	205	GLY	3.4
41	YV	5	VAL	3.4
4	XD	49	ARG	3.4
51	Y5	37	LYS	3.4
7	XG	153	HIS	3.4
23	QY	40	G	3.4
44	RY	53	PRO	3.4
12	QL	77	LEU	3.4
20	XT	62	LEU	3.4
38	RS	58	LEU	3.4
5	XE	155	GLU	3.4
38	RS	64	GLU	3.4
52	Y6	24	GLU	3.4
22	QV	47	U	3.4
36	RQ	65	PHE	3.3
32	YI	126	TYR	3.3
25	RA	899	A	3.3
13	QM	88	ARG	3.3
13	QM	98	VAL	3.3
34	RO	47	ILE	3.3
41	YV	51	VAL	3.3
52	Y6	31	PRO	3.3
30	YG	118	ARG	3.3
38	RS	109	GLY	3.3
40	YU	97	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
3	QC	202	ILE	3.3
22	XV	20	U	3.3
25	YA	2151	G	3.3
31	RH	124	GLU	3.3
45	RZ	38	TYR	3.3
9	XI	61	ALA	3.3
5	XE	135	THR	3.3
50	R4	52	THR	3.3
55	Y9	37	GLY	3.3
20	QT	55	ILE	3.3
23	XY	41	A	3.3
25	RA	1077	A	3.3
9	QI	101	PHE	3.3
30	RG	23	PHE	3.3
33	RN	137	LYS	3.3
55	Y9	2	LYS	3.3
13	QM	92	HIS	3.3
3	XC	165	THR	3.3
32	RI	40	THR	3.3
37	RR	69	ASP	3.3
25	RA	2132	U	3.3
30	RG	84	LYS	3.3
31	RH	149	ARG	3.3
2	XB	16	HIS	3.3
11	QK	92	GLU	3.3
12	QL	61	THR	3.3
2	QB	101	MET	3.3
4	XD	178	VAL	3.3
10	QJ	96	ILE	3.3
30	YG	52	ILE	3.3
36	RQ	103	MET	3.3
3	QC	139	GLN	3.3
14	QN	47	LEU	3.3
21	QU	6	ARG	3.3
29	RF	176	LEU	3.3
44	YY	55	TYR	3.3
11	XK	128	ALA	3.3
31	RH	150	ALA	3.3
44	RY	65	ALA	3.3
55	R9	21	GLY	3.3
34	RO	18	LYS	3.3
36	YQ	112	GLU	3.3

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Mol	Chain	Res	Type	RSRZ
17	QQ	36	ILE	3.3
3	QC	76	VAL	3.3
20	XT	42	GLN	3.3
25	RA	34	C	3.3
43	YX	92	LEU	3.3
45	YZ	5	LEU	3.3
31	RH	39	PRO	3.3
31	YH	18	GLU	3.3
50	R4	38	LYS	3.3
2	QB	206	ASP	3.3
25	RA	2790	A	3.3
20	QT	25	ARG	3.3
31	RH	79	VAL	3.3
34	RO	1	MET	3.3
43	RX	89	ILE	3.3
49	R3	58	VAL	3.3
12	QL	126	LYS	3.3
19	QS	35	SER	3.3
25	RA	2128	C	3.3
51	Y5	48	GLU	3.3
1	XA	631	G	3.2
54	Y8	63	PRO	3.2
2	XB	75	LYS	3.2
9	QI	23	ASN	3.2
17	QQ	7	THR	3.2
18	XR	44	LEU	3.2
28	YE	92	THR	3.2
30	RG	176	LEU	3.2
1	QA	1129	C	3.2
19	XS	12	ASP	3.2
45	RZ	80	ARG	3.2
4	XD	146	ILE	3.2
11	XK	82	VAL	3.2
30	RG	33	ARG	3.2
10	QJ	12	ASP	3.2
31	RH	163	TYR	3.2
2	XB	201	ILE	3.2
13	XM	4	ILE	3.2
13	QM	90	LEU	3.2
38	YS	24	LEU	3.2
25	RA	2792	G	3.2
34	RO	97	ARG	3.2

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Mol	Chain	Res	Type	RSRZ
2	XB	139	LYS	3.2
10	QJ	80	LYS	3.2
32	RI	56	LYS	3.2
12	QL	98	TYR	3.2
3	QC	60	ALA	3.2
9	QI	46	ALA	3.2
13	XM	2	ALA	3.2
44	RY	16	ALA	3.2
2	QB	185	ILE	3.2
2	XB	211	ILE	3.2
31	RH	4	ILE	3.2
3	QC	153	VAL	3.2
9	XI	79	LEU	3.2
32	RI	123	LEU	3.2
5	XE	154	GLY	3.2
25	YA	2139	C	3.2
39	YT	104	ASN	3.2
7	QG	6	ARG	3.2
35	YP	61	ARG	3.2
32	RI	93	THR	3.2
11	QK	75	TYR	3.2
19	QS	61	TYR	3.2
25	RA	2165	G	3.2
54	Y8	34	TRP	3.2
2	QB	122	PHE	3.2
30	YG	178	PHE	3.2
30	RG	144	ILE	3.2
12	XL	27	LEU	3.2
41	RV	71	LEU	3.2
52	Y6	10	LEU	3.2
4	QD	122	ARG	3.2
4	XD	118	ARG	3.2
10	QJ	49	VAL	3.2
19	QS	36	ARG	3.2
31	RH	23	ARG	3.2
37	YR	45	ARG	3.2
25	YA	2105	C	3.2
14	QN	46	GLU	3.2
28	YE	87	GLU	3.2
28	YE	66	HIS	3.2
31	RH	112	PRO	3.2
35	RP	78	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
7	QG	26	PHE	3.2
2	XB	156	LYS	3.2
9	QI	11	LYS	3.2
7	XG	38	LEU	3.2
32	RI	38	LEU	3.2
39	RT	111	ARG	3.2
1	QA	1031	G	3.2
16	XP	1	MET	3.2
32	YI	15	VAL	3.2
10	QJ	87	THR	3.2
10	XJ	48	THR	3.2
14	QN	22	THR	3.2
19	QS	12	ASP	3.2
25	RA	2179	C	3.2
36	RQ	121	ALA	3.2
42	RW	93	ALA	3.2
43	YX	65	ARG	3.2
36	YQ	79	LEU	3.2
45	RZ	150	LEU	3.2
25	YA	2799	A	3.2
30	YG	164	GLU	3.2
38	RS	43	GLU	3.2
45	RZ	132	ASN	3.2
1	QA	1124	G	3.2
10	XJ	22	LYS	3.2
7	XG	62	PHE	3.2
14	XN	37	PHE	3.2
19	XS	74	PHE	3.2
30	RG	117	PHE	3.2
17	XQ	90	ILE	3.2
25	YA	2402	C	3.2
35	RP	112	LEU	3.2
45	YZ	59	LEU	3.2
17	QQ	24	GLU	3.1
17	XQ	85	VAL	3.1
5	QE	20	GLN	3.1
4	XD	47	ARG	3.1
2	QB	105	PHE	3.1
1	QA	1001	G	3.1
6	XF	101	ALA	3.1
19	QS	31	ILE	3.1
41	YV	96	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
44	RY	38	ILE	3.1
4	XD	181	MET	3.1
25	RA	1178	C	3.1
32	RI	21	VAL	3.1
46	R0	53	MET	3.1
10	XJ	60	ARG	3.1
19	XS	13	ASP	3.1
29	YF	17	ARG	3.1
39	YT	3	ARG	3.1
19	QS	69	HIS	3.1
31	RH	38	SER	3.1
2	QB	72	GLY	3.1
2	XB	33	TYR	3.1
2	XB	187	LEU	3.1
4	XD	78	LEU	3.1
9	XI	114	TYR	3.1
25	YA	1095	A	3.1
36	RQ	105	GLU	3.1
7	XG	42	ILE	3.1
9	QI	61	ALA	3.1
12	QL	23	LYS	3.1
32	RI	95	LYS	3.1
45	YZ	182	LYS	3.1
1	QA	1202	G	3.1
2	QB	93	VAL	3.1
7	QG	105	VAL	3.1
9	XI	28	VAL	3.1
25	RA	2190	G	3.1
28	YE	7	VAL	3.1
8	QH	104	ARG	3.1
2	XB	19	HIS	3.1
37	YR	102	GLU	3.1
9	QI	92	TYR	3.1
30	RG	43	LEU	3.1
19	QS	62	ILE	3.1
20	XT	106	ALA	3.1
2	QB	21	ARG	3.1
41	YV	57	VAL	3.1
44	RY	57	GLN	3.1
44	YY	2	ARG	3.1
1	XA	1450	U	3.1
25	YA	1082	U	3.1

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Mol	Chain	Res	Type	RSRZ
25	YA	2106	G	3.1
33	RN	91	LEU	3.1
39	RT	114	LEU	3.1
11	QK	65	ALA	3.1
3	QC	64	VAL	3.1
10	XJ	49	VAL	3.1
40	YU	90	VAL	3.1
1	XA	1531	A	3.1
14	QN	58	LYS	3.1
36	RQ	112	GLU	3.1
51	R5	49	CYS	3.1
13	QM	89	GLY	3.1
40	RU	40	PHE	3.1
27	RD	33	LEU	3.1
1	XA	90	C	3.1
4	XD	73	ARG	3.1
25	RA	1109	C	3.1
32	RI	145	VAL	3.1
45	RZ	175	VAL	3.1
33	RN	90	MET	3.1
19	QS	65	ASN	3.1
37	YR	21	TYR	3.1
7	XG	83	ALA	3.1
10	QJ	84	GLN	3.1
20	XT	67	ALA	3.1
28	RE	187	ALA	3.1
39	RT	35	LYS	3.1
10	QJ	67	THR	3.1
11	XK	14	VAL	3.1
41	RV	5	VAL	3.1
2	QB	114	ARG	3.1
37	YR	18	LEU	3.1
12	QL	17	LYS	3.1
15	XO	87	ILE	3.1
2	QB	86	GLU	3.1
4	QD	156	GLU	3.1
35	YP	92	GLU	3.1
44	RY	39	VAL	3.1
32	RI	2	LYS	3.0
37	YR	44	LEU	3.0
44	RY	34	LYS	3.0
25	YA	2807	G	3.0

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Mol	Chain	Res	Type	RSRZ
2	XB	134	GLU	3.0
11	XK	92	GLU	3.0
44	RY	75	ILE	3.0
9	QI	114	TYR	3.0
31	RH	168	PRO	3.0
4	QD	102	ASP	3.0
17	XQ	7	THR	3.0
29	RF	114	VAL	3.0
41	YV	58	VAL	3.0
36	RQ	15	GLY	3.0
11	XK	98	LEU	3.0
19	XS	71	LEU	3.0
48	R2	71	ASN	3.0
25	RA	1102	C	3.0
25	YA	2798	C	3.0
55	R9	6	SER	3.0
4	XD	68	TYR	3.0
25	YA	2792	G	3.0
19	QS	66	MET	3.0
2	QB	55	PHE	3.0
20	QT	53	LEU	3.0
30	RG	62	LEU	3.0
32	YI	122	GLU	3.0
37	YR	20	LEU	3.0
40	RU	108	GLU	3.0
45	RZ	91	LEU	3.0
11	QK	29	ILE	3.0
9	QI	127	LYS	3.0
3	QC	131	ARG	3.0
5	QE	107	ARG	3.0
5	XE	133	TYR	3.0
25	RA	2188	C	3.0
9	XI	8	GLY	3.0
49	R3	59	VAL	3.0
10	QJ	73	ASP	3.0
28	YE	18	ASP	3.0
27	YD	27	THR	3.0
33	RN	48	MET	3.0
29	RF	148	LEU	3.0
33	RN	99	LEU	3.0
34	RO	99	PHE	3.0
41	YV	39	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
48	R2	44	LEU	3.0
4	XD	153	ARG	3.0
55	R9	18	ARG	3.0
2	XB	148	TYR	3.0
31	YH	39	PRO	3.0
9	XI	44	VAL	3.0
11	XK	17	GLY	3.0
15	QO	7	GLU	3.0
30	RG	44	GLY	3.0
36	RQ	102	VAL	3.0
39	RT	21	GLU	3.0
9	QI	37	PHE	3.0
10	XJ	86	MET	3.0
30	RG	180	PHE	3.0
7	XG	60	LYS	3.0
18	XR	47	THR	3.0
52	Y6	45	LYS	3.0
30	YG	137	GLU	3.0
3	QC	196	LEU	3.0
4	XD	139	ARG	3.0
9	QI	66	ARG	3.0
39	YT	134	GLU	3.0
45	YZ	168	GLU	3.0
11	XK	19	ALA	3.0
14	QN	15	LYS	3.0
31	YH	154	PRO	3.0
54	Y8	53	PRO	3.0
9	XI	105	ASP	3.0
35	RP	101	VAL	3.0
9	XI	96	LEU	3.0
10	XJ	9	ARG	3.0
37	RR	68	ARG	3.0
41	RV	100	ARG	3.0
3	QC	206	GLU	3.0
9	QI	77	ILE	3.0
14	QN	42	ILE	3.0
31	RH	122	THR	3.0
10	XJ	7	LYS	3.0
25	RA	2109	U	3.0
10	XJ	10	GLY	3.0
35	RP	118	GLY	3.0
12	QL	48	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
44	RY	48	ALA	3.0
12	QL	86	ARG	3.0
30	RG	90	LEU	3.0
50	Y4	47	GLN	3.0
19	XS	27	GLU	3.0
10	QJ	3	LYS	3.0
12	QL	85	ILE	3.0
25	YA	2188	C	2.9
2	XB	95	GLN	2.9
4	XD	104	VAL	2.9
8	QH	129	VAL	2.9
11	QK	19	ALA	2.9
35	RP	61	ARG	2.9
51	R5	51	TYR	2.9
17	XQ	71	PHE	2.9
54	Y8	23	VAL	2.9
10	XJ	57	LYS	2.9
29	RF	120	GLU	2.9
44	YY	62	GLU	2.9
3	XC	8	ILE	2.9
16	XP	33	ILE	2.9
10	XJ	70	ARG	2.9
11	XK	18	ARG	2.9
1	QA	1028(B)	C	2.9
6	QF	55	ASP	2.9
11	QK	69	ALA	2.9
37	YR	114	VAL	2.9
39	RT	49	VAL	2.9
39	RT	101	PHE	2.9
10	XJ	74	ILE	2.9
7	QG	24	THR	2.9
18	XR	87	ARG	2.9
4	QD	21	LEU	2.9
20	XT	14	LYS	2.9
11	XK	80	VAL	2.9
13	QM	87	TYR	2.9
25	RA	2211	G	2.9
31	YH	113	VAL	2.9
32	RI	46	ALA	2.9
44	RY	35	TYR	2.9
2	QB	111	ARG	2.9
10	QJ	75	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
11	QK	126	ARG	2.9
19	QS	57	HIS	2.9
39	RT	110	ILE	2.9
20	QT	29	LYS	2.9
44	RY	26	LYS	2.9
25	RA	2189	U	2.9
9	XI	47	LEU	2.9
30	RG	4	ASP	2.9
32	RI	7	GLU	2.9
39	RT	6	LEU	2.9
39	YT	109	GLU	2.9
45	RZ	130	PRO	2.9
45	YZ	177	PRO	2.9
5	XE	132	ALA	2.9
9	QI	14	VAL	2.9
9	XI	82	ALA	2.9
12	QL	66	VAL	2.9
1	QA	1373	G	2.9
2	QB	153	ARG	2.9
2	QB	201	ILE	2.9
5	QE	13	ILE	2.9
10	QJ	66	ARG	2.9
32	RI	88	ILE	2.9
31	RH	167	GLU	2.9
2	XB	6	THR	2.9
18	XR	82	THR	2.9
25	YA	2172	U	2.9
3	QC	103	VAL	2.9
3	QC	200	ALA	2.9
9	QI	13	ALA	2.9
19	QS	75	ALA	2.9
36	RQ	87	LYS	2.9
39	YT	33	LYS	2.9
43	YX	68	ARG	2.9
50	Y4	61	ARG	2.9
12	QL	70	ILE	2.9
18	QR	46	GLU	2.9
25	RA	2157	G	2.9
2	XB	215	LEU	2.9
10	QJ	90	LEU	2.9
4	QD	4	TYR	2.9
9	QI	65	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
14	XN	35	ARG	2.9
20	XT	22	ARG	2.9
41	YV	55	ALA	2.9
50	R4	10	VAL	2.9
55	R9	31	LYS	2.9
4	XD	80	GLU	2.9
30	RG	58	GLN	2.9
2	XB	27	LYS	2.9
2	XB	163	PHE	2.9
3	QC	17	ASP	2.9
28	RE	78	LEU	2.9
5	QE	9	LYS	2.9
14	QN	60	SER	2.9
45	RZ	154	ASP	2.9
7	QG	88	PRO	2.9
11	XK	25	TYR	2.9
25	RA	1074	G	2.9
25	RA	2123	G	2.9
33	YN	9	VAL	2.9
9	QI	63	ILE	2.9
2	XB	61	LEU	2.9
3	XC	26	LYS	2.9
9	XI	50	LEU	2.9
29	RF	181	LEU	2.9
32	YI	140	LEU	2.9
39	RT	78	LEU	2.9
41	RV	95	LEU	2.9
20	XT	83	ARG	2.9
46	R0	45	PHE	2.9
2	QB	150	SER	2.9
5	QE	115	VAL	2.8
16	XP	32	TYR	2.8
31	RH	116	GLU	2.8
32	RI	36	ALA	2.8
39	RT	135	ALA	2.8
25	YA	2128	C	2.8
2	XB	5	ILE	2.8
32	RI	58	LEU	2.8
3	QC	171	GLY	2.8
9	QI	21	PRO	2.8
9	QI	26	VAL	2.8
30	YG	50	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
37	YR	112	ALA	2.8
34	RO	22	ILE	2.8
25	RA	2794	C	2.8
11	XK	103	LEU	2.8
33	RN	116	LEU	2.8
45	RZ	5	LEU	2.8
45	RZ	18	LEU	2.8
13	QM	64	TRP	2.8
39	RT	22	PHE	2.8
25	RA	2141	G	2.8
38	YS	107	GLU	2.8
1	QA	1000	A	2.8
3	XC	153	VAL	2.8
9	QI	116	LYS	2.8
12	XL	18	VAL	2.8
28	RE	116	VAL	2.8
28	YE	3	GLY	2.8
29	RF	207	GLY	2.8
39	RT	33	LYS	2.8
39	YT	30	VAL	2.8
44	RY	88	LYS	2.8
51	Y5	40	LYS	2.8
54	R8	23	VAL	2.8
14	QN	21	TYR	2.8
32	RI	55	ALA	2.8
3	XC	164	ARG	2.8
8	QH	86	ILE	2.8
31	RH	3	ARG	2.8
32	RI	97	ILE	2.8
37	YR	33	ARG	2.8
39	RT	39	ARG	2.8
39	YT	111	ARG	2.8
43	RX	60	ARG	2.8
3	XC	178	LEU	2.8
25	RA	2178	C	2.8
1	QA	1131	G	2.8
2	QB	237	ALA	2.8
10	QJ	21	GLN	2.8
11	QK	94	ALA	2.8
36	YQ	59	ARG	2.8
44	RY	78	ALA	2.8
50	R4	43	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
53	R7	45	ALA	2.8
40	RU	17	ILE	2.8
2	XB	126	GLU	2.8
18	XR	83	GLU	2.8
29	YF	27	GLU	2.8
43	RX	92	LEU	2.8
30	YG	84	LYS	2.8
20	XT	19	SER	2.8
25	YA	2179	C	2.8
45	RZ	129	SER	2.8
7	XG	41	ARG	2.8
9	QI	121	ARG	2.8
10	XJ	94	VAL	2.8
17	XQ	75	ARG	2.8
28	RE	196	VAL	2.8
30	RG	149	VAL	2.8
36	RQ	35	VAL	2.8
9	XI	52	ALA	2.8
39	YT	130	ALA	2.8
14	QN	8	GLU	2.8
4	XD	202	LEU	2.8
25	RA	2124	G	2.8
11	QK	90	GLY	2.8
13	QM	95	GLY	2.8
7	XG	77	SER	2.8
13	XM	91	ARG	2.8
18	XR	54	ARG	2.8
34	RO	17	ARG	2.8
30	RG	41	GLN	2.8
36	RQ	81	VAL	2.8
45	YZ	174	VAL	2.8
12	QL	47	LYS	2.8
25	RA	1104	C	2.8
28	RE	176	ILE	2.8
41	YV	97	LYS	2.8
52	R6	38	LYS	2.8
55	Y9	31	LYS	2.8
2	QB	154	LEU	2.8
10	QJ	60	ARG	2.8
20	QT	101	GLY	2.8
23	QY	41	A	2.8
20	XT	45	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
34	RO	98	VAL	2.8
36	RQ	132	VAL	2.8
38	YS	11	LYS	2.8
50	Y4	34	GLU	2.8
19	XS	76	PRO	2.8
11	XK	21	ILE	2.8
12	QL	105	TYR	2.8
27	RD	153	ALA	2.8
28	YE	26	ILE	2.8
25	RA	1076	C	2.8
39	RT	40	THR	2.8
13	QM	114	ARG	2.8
20	XT	80	ARG	2.8
29	RF	133	ASN	2.8
32	RI	84	GLY	2.8
10	XJ	33	GLN	2.8
45	RZ	71	VAL	2.8
47	R1	70	VAL	2.8
11	XK	108	ILE	2.8
33	RN	30	ILE	2.8
2	QB	144	ARG	2.7
2	XB	209	ARG	2.7
30	RG	136	ARG	2.7
25	RA	886	C	2.7
1	QA	1348	U	2.7
28	RE	7	VAL	2.7
32	YI	143	SER	2.7
41	RV	58	VAL	2.7
11	QK	83	ILE	2.7
14	XN	14	PRO	2.7
13	QM	66	LEU	2.7
13	XM	3	ARG	2.7
20	QT	91	LEU	2.7
36	YQ	47	ILE	2.7
21	XU	15	ARG	2.7
30	YG	72	ARG	2.7
45	YZ	150	LEU	2.7
11	QK	70	LYS	2.7
4	QD	167	GLY	2.7
17	QQ	54	GLY	2.7
3	QC	192	THR	2.7
19	QS	79	THR	2.7

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Mol	Chain	Res	Type	RSRZ
25	RA	2166	G	2.7
25	YA	2181	G	2.7
44	YY	29	GLU	2.7
51	Y5	50	GLY	2.7
9	QI	108	VAL	2.7
11	QK	30	VAL	2.7
7	QG	4	ARG	2.7
9	XI	10	ARG	2.7
12	QL	46	LYS	2.7
14	QN	41	ARG	2.7
14	XN	44	LEU	2.7
20	XT	79	ARG	2.7
35	YP	79	ARG	2.7
38	YS	59	LYS	2.7
9	QI	62	TYR	2.7
41	RV	94	LEU	2.7
14	QN	10	ALA	2.7
4	XD	93	PHE	2.7
5	QE	155	GLU	2.7
20	XT	101	GLY	2.7
30	RG	89	GLY	2.7
39	YT	21	GLU	2.7
45	RZ	48	PHE	2.7
45	YZ	121	HIS	2.7
25	RA	2149	G	2.7
2	XB	136	VAL	2.7
9	QI	71	SER	2.7
28	RE	14	ILE	2.7
30	RG	63	ILE	2.7
31	YH	89	ILE	2.7
2	XB	128	GLU	2.7
9	QI	4	TYR	2.7
20	QT	56	MET	2.7
36	RQ	29	PHE	2.7
25	RA	1069	A	2.7
25	YA	2062	A	2.7
17	XQ	20	THR	2.7
32	RI	121	LYS	2.7
36	RQ	5	ARG	2.7
4	QD	112	VAL	2.7
2	XB	238	LEU	2.7
3	XC	42	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
4	QD	152	SER	2.7
30	RG	159	VAL	2.7
45	RZ	37	VAL	2.7
5	QE	12	LEU	2.7
12	QL	93	LEU	2.7
38	RS	82	ILE	2.7
41	YV	71	LEU	2.7
1	XA	1026	G	2.7
20	XT	59	ALA	2.7
33	RN	57	ALA	2.7
44	YY	69	ALA	2.7
17	XQ	83	ASP	2.7
25	RA	1053	C	2.7
35	RP	128	HIS	2.7
14	QN	31	ARG	2.7
1	XA	1000	A	2.7
1	XA	1032	A	2.7
25	RA	1510	A	2.7
25	RA	2170	A	2.7
25	YA	899	A	2.7
50	R4	24	THR	2.7
3	QC	91	LEU	2.7
4	QD	135	LEU	2.7
4	XD	126	ILE	2.7
7	QG	101	LEU	2.7
14	XN	32	SER	2.7
22	XV	47	U	2.7
41	YV	95	LEU	2.7
28	YE	74	PRO	2.7
4	XD	48	ALA	2.7
4	XD	115	ARG	2.7
16	XP	48	TRP	2.7
20	QT	35	THR	2.7
19	QS	38	SER	2.7
30	RG	103	LEU	2.7
25	RA	2897	U	2.7
10	XJ	63	PHE	2.7
32	RI	118	LYS	2.7
38	YS	83	LYS	2.7
20	XT	76	ALA	2.7
20	QT	9	ASN	2.7
9	XI	108	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
20	QT	39	LYS	2.7
25	YA	1173	G	2.7
30	YG	74	LYS	2.7
35	RP	19	VAL	2.7
44	YY	81	LYS	2.7
51	R5	37	LYS	2.7
3	QC	170	GLN	2.7
39	RT	76	PHE	2.7
54	R8	48	PHE	2.7
4	XD	164	ALA	2.7
25	YA	2176	A	2.7
30	YG	49	ASP	2.7
18	XR	40	LEU	2.6
1	QA	1240	U	2.6
4	XD	75	PHE	2.6
10	XJ	66	ARG	2.6
12	XL	89	ARG	2.6
25	YA	1076	C	2.6
42	YW	37	ARG	2.6
20	QT	46	GLU	2.6
48	R2	52	ASP	2.6
7	QG	31	MET	2.6
31	RH	140	LYS	2.6
39	RT	98	LYS	2.6
29	RF	192	LEU	2.6
30	RG	94	LEU	2.6
46	R0	37	LEU	2.6
7	XG	13	GLN	2.6
30	RG	26	GLN	2.6
39	RT	83	ILE	2.6
10	QJ	48	THR	2.6
11	QK	43	SER	2.6
12	QL	106	ASP	2.6
32	RI	64	GLU	2.6
36	YQ	48	GLU	2.6
29	RF	113	ALA	2.6
8	XH	63	LEU	2.6
9	QI	83	ARG	2.6
12	QL	29	GLY	2.6
13	QM	119	GLY	2.6
25	RA	276	A	2.6
30	RG	111	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
37	YR	75	LEU	2.6
3	QC	84	ILE	2.6
31	YH	169	VAL	2.6
30	RG	102	PHE	2.6
40	RU	89	GLU	2.6
2	QB	107	THR	2.6
8	QH	24	THR	2.6
19	QS	77	THR	2.6
45	YZ	127	LYS	2.6
12	QL	51	ALA	2.6
38	RS	36	TYR	2.6
3	QC	194	GLY	2.6
3	XC	87	LEU	2.6
14	QN	6	LEU	2.6
32	RI	34	GLY	2.6
49	R3	26	LEU	2.6
2	QB	84	GLU	2.6
4	XD	163	GLU	2.6
12	QL	83	VAL	2.6
25	YA	2157	G	2.6
3	QC	201	TYR	2.6
9	QI	128	ARG	2.6
20	QT	57	ARG	2.6
30	RG	96	ARG	2.6
35	RP	102	ARG	2.6
45	RZ	172	ALA	2.6
9	XI	115	GLY	2.6
46	Y0	70	GLN	2.6
2	QB	57	PHE	2.6
45	YZ	124	ILE	2.6
51	Y5	45	VAL	2.6
25	YA	2180	U	2.6
31	RH	51	ARG	2.6
9	QI	84	ALA	2.6
12	QL	21	LYS	2.6
20	QT	38	LYS	2.6
45	RZ	98	MET	2.6
46	Y0	3	HIS	2.6
54	R8	25	MET	2.6
39	RT	11	GLU	2.6
3	QC	203	PHE	2.6
7	XG	21	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
9	XI	37	PHE	2.6
45	RZ	86	VAL	2.6
4	QD	73	ARG	2.6
25	RA	1079	C	2.6
45	YZ	122	ARG	2.6
30	YG	87	PRO	2.6
7	QG	151	TYR	2.6
41	RV	27	ALA	2.6
8	XH	2	LEU	2.6
17	QQ	80	GLY	2.6
21	QU	16	GLY	2.6
25	RA	654	A	2.6
25	YA	1057	A	2.6
41	YV	1	MET	2.6
50	R4	32	TYR	2.6
29	RF	131	GLY	2.6
45	RZ	117	LEU	2.6
1	QA	1033	G	2.6
32	YI	92	VAL	2.6
39	RT	28	VAL	2.6
4	QD	166	LYS	2.6
12	QL	57	LYS	2.6
28	YE	89	ASP	2.6
37	YR	49	ASP	2.6
25	YA	2113	U	2.6
39	RT	77	PRO	2.6
10	QJ	10	GLY	2.6
44	RY	20	TYR	2.6
19	XS	40	ILE	2.6
27	RD	64	ILE	2.6
27	RD	262	ARG	2.6
30	RG	141	PHE	2.6
32	YI	109	ILE	2.6
2	QB	112	VAL	2.6
11	QK	84	VAL	2.6
25	RA	274	G	2.5
1	XA	1025	U	2.5
13	XM	10	PRO	2.5
44	RY	56	PRO	2.5
51	Y5	27	PRO	2.5
33	RN	47	ALA	2.5
10	QJ	9	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
20	XT	8	ARG	2.5
28	YE	77	ILE	2.5
27	YD	34	VAL	2.5
33	YN	68	GLU	2.5
43	RX	43	VAL	2.5
44	RY	11	ASP	2.5
2	QB	89	GLY	2.5
9	XI	98	PRO	2.5
3	QC	33	LEU	2.5
5	QE	10	MET	2.5
6	XF	54	LYS	2.5
7	QG	153	HIS	2.5
11	QK	42	TRP	2.5
19	XS	16	LEU	2.5
29	RF	199	TRP	2.5
33	RN	101	HIS	2.5
51	R5	3	LYS	2.5
30	RG	113	ARG	2.5
3	QC	77	ILE	2.5
9	QI	74	ILE	2.5
25	YA	1075	C	2.5
2	XB	38	GLY	2.5
10	QJ	14	LYS	2.5
19	QS	32	LYS	2.5
31	RH	110	SER	2.5
38	YS	108	GLY	2.5
23	QY	33	U	2.5
25	RA	1090	U	2.5
5	XE	64	ARG	2.5
11	QK	54	ARG	2.5
11	QK	91	ARG	2.5
45	RZ	54	HIS	2.5
49	R3	29	ARG	2.5
12	XL	64	TYR	2.5
19	QS	34	TRP	2.5
36	YQ	32	TYR	2.5
36	YQ	83	MET	2.5
50	Y4	32	TYR	2.5
4	QD	150	GLU	2.5
20	QT	50	GLU	2.5
7	XG	30	ILE	2.5
20	QT	26	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
25	YA	2115	G	2.5
7	QG	9	VAL	2.5
45	RZ	87	ASP	2.5
13	XM	31	LYS	2.5
2	QB	14	GLY	2.5
3	QC	162	GLN	2.5
2	XB	124	SER	2.5
2	XB	213	LEU	2.5
17	QQ	6	LEU	2.5
36	RQ	10	ARG	2.5
39	RT	29	ARG	2.5
46	R0	62	LEU	2.5
5	XE	81	GLU	2.5
8	QH	9	MET	2.5
9	QI	125	TYR	2.5
30	RG	25	TYR	2.5
7	XG	26	PHE	2.5
17	QQ	71	PHE	2.5
4	QD	146	ILE	2.5
9	QI	78	LYS	2.5
9	XI	63	ILE	2.5
17	QQ	60	ILE	2.5
36	RQ	21	THR	2.5
20	XT	29	LYS	2.5
30	RG	74	LYS	2.5
4	XD	140	VAL	2.5
11	QK	67	ASP	2.5
12	QL	24	VAL	2.5
25	RA	2894	G	2.5
28	YE	37	ARG	2.5
28	YE	76	ARG	2.5
41	RV	48	GLY	2.5
4	XD	11	LEU	2.5
46	R0	21	LEU	2.5
25	RA	1078	U	2.5
33	RN	100	GLU	2.5
39	RT	46	GLU	2.5
2	XB	218	ALA	2.5
8	QH	58	TYR	2.5
35	RP	129	ALA	2.5
4	XD	110	PHE	2.5
29	RF	202	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
33	RN	93	THR	2.5
3	XC	173	VAL	2.5
4	QD	17	VAL	2.5
15	XO	79	ARG	2.5
17	QQ	11	VAL	2.5
34	YO	45	GLU	2.5
51	R5	59	GLU	2.5
1	XA	102	G	2.5
10	QJ	68	HIS	2.5
14	QN	9	LYS	2.5
20	QT	34	LYS	2.5
37	YR	50	HIS	2.5
50	R4	36	CYS	2.5
2	XB	34	ALA	2.5
3	QC	89	GLU	2.5
19	QS	27	GLU	2.5
4	XD	174	LEU	2.5
9	XI	56	LEU	2.5
9	XI	116	LYS	2.5
20	XT	53	LEU	2.5
29	RF	140	LEU	2.5
30	RG	34	LEU	2.5
30	RG	107	LEU	2.5
31	YH	103	LEU	2.5
41	YV	16	PRO	2.5
14	QN	29	ARG	2.5
53	R7	41	ARG	2.5
9	QI	73	GLN	2.5
9	QI	22	GLY	2.5
25	RA	2153	G	2.5
11	QK	80	VAL	2.5
28	RE	198	VAL	2.5
41	RV	28	GLU	2.5
45	RZ	100	VAL	2.5
4	QD	162	LEU	2.5
11	QK	103	LEU	2.5
18	QR	76	LEU	2.5
25	YA	2171	A	2.5
32	YI	91	SER	2.5
35	YP	65	ARG	2.4
3	XC	90	GLU	2.4
11	QK	48	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
13	QM	84	ILE	2.4
15	XO	82	ILE	2.4
33	YN	133	GLN	2.4
31	RH	160	LYS	2.4
32	YI	141	LYS	2.4
33	YN	50	ASP	2.4
36	RQ	33	GLY	2.4
7	QG	87	VAL	2.4
16	XP	59	TRP	2.4
37	YR	35	THR	2.4
45	RZ	24	LEU	2.4
25	RA	1534	G	2.4
9	QI	120	ARG	2.4
8	QH	44	PHE	2.4
22	QV	20	U	2.4
25	RA	896	A	2.4
25	RA	2062	A	2.4
39	RT	20	PRO	2.4
45	RZ	31	ARG	2.4
52	Y6	28	ARG	2.4
2	QB	33	TYR	2.4
3	QC	28	GLN	2.4
3	QC	169	ALA	2.4
4	QD	201	GLN	2.4
7	QG	73	MET	2.4
47	R1	93	GLU	2.4
4	XD	102	ASP	2.4
31	RH	151	ILE	2.4
43	RX	6	ASP	2.4
45	RZ	137	ILE	2.4
44	RY	27	VAL	2.4
35	RP	45	LEU	2.4
45	RZ	170	THR	2.4
8	XH	23	SER	2.4
25	YA	1092	C	2.4
41	YV	100	ARG	2.4
14	QN	14	PRO	2.4
30	RG	179	PRO	2.4
44	RY	47	LYS	2.4
45	YZ	6	LYS	2.4
38	RS	29	PHE	2.4
48	Y2	11	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
20	XT	66	ALA	2.4
25	RA	2112	G	2.4
37	YR	34	ILE	2.4
13	QM	60	VAL	2.4
32	RI	37	VAL	2.4
34	YO	98	VAL	2.4
3	QC	26	LYS	2.4
54	R8	36	LYS	2.4
35	RP	94	GLU	2.4
45	RZ	119	GLU	2.4
7	XG	11	GLN	2.4
9	QI	3	GLN	2.4
25	RA	1072	C	2.4
25	YA	886	C	2.4
7	XG	82	GLY	2.4
7	QG	155	ARG	2.4
12	QL	84	LEU	2.4
15	XO	34	LEU	2.4
20	QT	43	LEU	2.4
25	YA	1534	G	2.4
30	RG	37	VAL	2.4
37	YR	100	LEU	2.4
42	YW	110	LYS	2.4
44	RY	101	LYS	2.4
46	R0	41	ARG	2.4
51	Y5	3	LYS	2.4
41	RV	32	THR	2.4
4	XD	185	PHE	2.4
43	RX	28	PHE	2.4
23	QY	29	U	2.4
25	RA	1101	U	2.4
36	RQ	99	PRO	2.4
3	XC	168	ALA	2.4
20	QT	44	ALA	2.4
2	XB	226	ARG	2.4
4	QD	115	ARG	2.4
21	XU	6	ARG	2.4
55	Y9	19	ARG	2.4
4	XD	15	GLU	2.4
9	QI	41	VAL	2.4
13	QM	81	LEU	2.4
10	QJ	97	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
25	YA	2211	G	2.4
45	YZ	66	SER	2.4
11	QK	108	ILE	2.4
37	YR	19	ALA	2.4
39	YT	94	ALA	2.4
49	R3	4	LEU	2.4
49	R3	38	GLU	2.4
7	QG	80	VAL	2.4
35	YP	19	VAL	2.4
45	RZ	56	VAL	2.4
7	QG	97	GLN	2.4
2	QB	210	SER	2.4
17	QQ	4	LYS	2.4
20	XT	71	THR	2.4
30	YG	136	ARG	2.4
35	RP	65	ARG	2.4
39	RT	52	ILE	2.4
9	QI	45	ALA	2.4
54	Y8	40	GLU	2.4
7	XG	124	LEU	2.4
28	RE	195	LEU	2.4
28	YE	78	LEU	2.4
35	RP	80	TYR	2.4
36	RQ	17	LEU	2.4
40	RU	83	LEU	2.4
17	QQ	19	VAL	2.4
20	XT	75	ASN	2.4
31	RH	52	VAL	2.4
34	YO	43	VAL	2.4
12	QL	20	LYS	2.4
51	R5	40	LYS	2.4
1	QA	1028	C	2.4
4	QD	2	GLY	2.4
5	XE	23	GLY	2.4
9	QI	126	SER	2.4
41	RV	73	SER	2.4
4	QD	5	ILE	2.4
4	QD	7	PRO	2.4
5	QE	118	ILE	2.4
7	XG	120	ILE	2.4
16	XP	4	ILE	2.4
19	QS	40	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
20	QT	93	GLU	2.4
2	QB	118	LEU	2.3
2	QB	218	ALA	2.4
25	RA	1847	A	2.4
25	YA	1508	A	2.4
30	YG	86	MET	2.4
3	XC	94	LEU	2.3
3	XC	184	TYR	2.3
19	QS	30	LEU	2.3
36	RQ	125	LEU	2.3
2	XB	147	LYS	2.3
29	RF	126	VAL	2.3
41	RV	14	VAL	2.3
50	R4	33	VAL	2.3
3	QC	136	GLN	2.3
19	QS	37	ARG	2.3
7	XG	34	GLY	2.3
33	RN	125	GLY	2.3
45	RZ	92	SER	2.3
10	XJ	100	THR	2.3
25	RA	2896	C	2.3
25	YA	898	C	2.3
33	RN	23	LEU	2.3
35	YP	108	LYS	2.3
16	XP	53	VAL	2.3
17	XQ	93	GLN	2.3
46	R0	38	VAL	2.3
3	QC	158	GLY	2.3
18	XR	43	PHE	2.3
28	RE	200	GLU	2.3
1	XA	78	G	2.3
34	RO	42	SER	2.3
3	QC	8	ILE	2.3
7	XG	27	ILE	2.3
11	QK	57	THR	2.3
20	QT	48	LYS	2.3
36	RQ	25	ASP	2.3
41	RV	4	ILE	2.3
45	RZ	6	LYS	2.3
1	QA	82	U	2.3
20	XT	13	LEU	2.3
4	XD	32	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
36	RQ	117	ALA	2.3
49	R3	21	ALA	2.3
4	QD	27	TYR	2.3
9	QI	87	GLN	2.3
9	XI	53	VAL	2.3
9	XI	93	ARG	2.3
12	QL	96	VAL	2.3
32	RI	81	VAL	2.3
38	YS	20	ARG	2.3
38	YS	46	VAL	2.3
17	QQ	78	GLU	2.3
30	YG	79	ASN	2.3
25	RA	2176	A	2.3
46	R0	52	GLY	2.3
54	Y8	15	LYS	2.3
13	QM	9	ILE	2.3
30	YG	140	ILE	2.3
32	RI	14	ASP	2.3
4	QD	120	LEU	2.3
33	RN	86	PRO	2.3
34	RO	122	LEU	2.3
44	RY	66	PRO	2.3
51	Y5	28	PRO	2.3
13	XM	103	THR	2.3
2	QB	95	GLN	2.3
13	QM	108	ARG	2.3
14	XN	57	ARG	2.3
17	XQ	81	ARG	2.3
36	RQ	136	ALA	2.3
46	R0	11	ARG	2.3
32	RI	25	TYR	2.3
29	RF	89	VAL	2.3
15	XO	84	LYS	2.3
30	RG	36	LYS	2.3
2	XB	41	ILE	2.3
2	XB	42	ILE	2.3
8	QH	35	ILE	2.3
8	QH	80	ILE	2.3
34	YO	17	ARG	2.3
35	YP	106	LEU	2.3
47	Y1	26	ARG	2.3
16	QP	48	TRP	2.3

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Mol	Chain	Res	Type	RSRZ
2	QB	66	GLY	2.3
3	QC	66	VAL	2.3
13	XM	87	TYR	2.3
25	YA	2833	G	2.3
54	R8	20	GLY	2.3
28	YE	51	PHE	2.3
48	Y2	71	ASN	2.3
25	RA	2137	C	2.3
9	QI	56	LEU	2.3
9	XI	85	LEU	2.3
11	QK	44	SER	2.3
20	XT	100	ILE	2.3
33	YN	61	ARG	2.3
37	RR	51	LEU	2.3
39	RT	86	ILE	2.3
50	Y4	65	ASP	2.3
1	QA	994	A	2.3
3	QC	82	GLU	2.3
4	XD	182	LYS	2.3
6	XF	57	GLN	2.3
25	RA	6	A	2.3
12	QL	114	LYS	2.3
32	RI	45	LYS	2.3
45	RZ	51	ALA	2.3
28	RE	88	GLY	2.3
31	YH	107	VAL	2.3
33	YN	54	VAL	2.3
35	RP	95	VAL	2.3
31	RH	147	ASN	2.3
38	RS	61	ASN	2.3
11	XK	91	ARG	2.3
4	QD	11	LEU	2.3
17	QQ	53	LEU	2.3
34	RO	56	ASP	2.3
25	RA	884	C	2.3
25	RA	2163	C	2.3
33	RN	68	GLU	2.3
4	XD	29	PRO	2.3
39	RT	24	PRO	2.3
1	XA	1257	U	2.3
7	QG	39	ALA	2.3
21	XU	16	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
2	QB	197	VAL	2.3
2	XB	71	VAL	2.3
3	QC	151	VAL	2.3
30	RG	92	VAL	2.3
37	YR	73	VAL	2.3
35	RP	90	ARG	2.3
47	R1	21	ARG	2.3
20	XT	68	LYS	2.3
50	Y4	38	LYS	2.3
38	YS	48	LEU	2.3
38	RS	31	SER	2.3
19	XS	2	PRO	2.3
2	QB	228	GLY	2.3
9	XI	39	GLY	2.3
20	QT	106	ALA	2.3
22	QV	53	G	2.3
25	RA	271(C)	U	2.3
25	YA	2148	G	2.3
25	YA	2149	G	2.3
40	RU	43	GLY	2.3
9	QI	5	TYR	2.3
9	XI	26	VAL	2.3
30	RG	181	ARG	2.3
33	RN	117	PHE	2.3
36	RQ	137	TYR	2.3
45	RZ	104	PHE	2.3
35	RP	107	LYS	2.2
35	YP	121	LYS	2.2
4	QD	80	GLU	2.2
32	RI	122	GLU	2.2
3	QC	182	ILE	2.2
4	QD	67	ILE	2.2
11	XK	95	ILE	2.2
17	XQ	6	LEU	2.2
19	QS	56	GLN	2.2
32	RI	77	LEU	2.2
45	RZ	166	SER	2.2
1	XA	89	U	2.2
2	QB	227	GLY	2.2
13	QM	10	PRO	2.2
11	QK	106	LYS	2.2
18	QR	87	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
20	QT	49	ALA	2.2
20	XT	32	ALA	2.2
43	RX	65	ARG	2.2
4	QD	20	TYR	2.2
25	RA	2791	C	2.2
47	R1	71	TYR	2.2
25	YA	1093	G	2.2
4	QD	160	GLN	2.2
12	QL	92	ASP	2.2
14	XN	53	LEU	2.2
37	YR	28	LEU	2.2
10	XJ	50	ILE	2.2
7	QG	77	SER	2.2
37	YR	14	SER	2.2
2	QB	132	LYS	2.2
3	QC	159	GLY	2.2
5	QE	22	GLY	2.2
17	XQ	87	LYS	2.2
19	QS	82	GLY	2.2
30	RG	83	ARG	2.2
47	R1	22	GLY	2.2
3	XC	100	ALA	2.2
4	XD	72	GLU	2.2
9	XI	119	ALA	2.2
28	RE	188	VAL	2.2
28	YE	198	VAL	2.2
41	YV	34	GLU	2.2
2	QB	67	THR	2.2
1	XA	103	C	2.2
25	YA	1585	C	2.2
29	YF	8	GLN	2.2
35	RP	99	LEU	2.2
49	Y3	4	LEU	2.2
2	QB	162	ILE	2.2
5	QE	131	ILE	2.2
13	XM	115	LYS	2.2
12	QL	72	GLY	2.2
14	QN	32	SER	2.2
25	YA	2152	G	2.2
27	RD	36	PRO	2.2
34	RO	9	GLU	2.2
45	RZ	97	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
45	YZ	178	GLU	2.2
1	XA	209	U	2.2
11	QK	109	VAL	2.2
43	RX	5	TYR	2.2
7	XG	86	GLN	2.2
36	YQ	17	LEU	2.2
39	YT	38	ASN	2.2
3	QC	4	LYS	2.2
41	YV	40	LEU	2.2
44	RY	28	LYS	2.2
17	XQ	36	ILE	2.2
25	YA	2143	C	2.2
30	RG	51	ARG	2.2
30	RG	88	ILE	2.2
14	XN	49	HIS	2.2
9	XI	86	VAL	2.2
11	XK	68	ALA	2.2
45	RZ	44	PHE	2.2
30	YG	146	TYR	2.2
40	RU	16	LYS	2.2
44	YY	34	LYS	2.2
3	QC	12	LEU	2.2
39	RT	19	LEU	2.2
45	YZ	125	LEU	2.2
2	QB	87	ARG	2.2
2	QB	226	ARG	2.2
4	XD	127	THR	2.2
19	QS	33	THR	2.2
3	XC	152	ILE	2.2
31	YH	60	ARG	2.2
14	XN	61	TRP	2.2
36	RQ	47	ILE	2.2
54	R8	41	ILE	2.2
35	RP	74	GLU	2.2
52	R6	15	GLU	2.2
44	YY	52	SER	2.2
29	RF	194	MET	2.2
29	YF	66	PRO	2.2
45	RZ	158	PRO	2.2
2	QB	156	LYS	2.2
12	QL	91	LYS	2.2
37	RR	47	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
35	YP	71	VAL	2.2
47	Y1	32	LYS	2.2
25	YA	2801	A	2.2
30	YG	34	LEU	2.2
36	RQ	74	TYR	2.2
54	R8	35	GLN	2.2
2	XB	137	ARG	2.2
2	XB	144	ARG	2.2
30	YG	83	ARG	2.2
41	RV	35	LEU	2.2
2	QB	223	ILE	2.2
10	XJ	23	ILE	2.2
3	XC	150	LYS	2.2
17	XQ	12	SER	2.2
20	QT	37	SER	2.2
44	RY	4	LYS	2.2
3	XC	10	PHE	2.2
5	QE	45	PHE	2.2
30	YG	141	PHE	2.2
4	QD	66	ARG	2.2
7	QG	108	ALA	2.2
11	QK	23	ALA	2.2
15	QO	79	ARG	2.2
31	RH	99	VAL	2.2
33	YN	52	VAL	2.2
50	Y4	60	GLN	2.2
38	RS	110	LEU	2.2
50	R4	18	CYS	2.2
10	QJ	58	ASP	2.2
45	RZ	168	GLU	2.2
3	XC	77	ILE	2.2
17	XQ	59	ILE	2.2
25	RA	529	A	2.2
45	YZ	160	GLY	2.2
4	XD	89	THR	2.2
8	XH	3	THR	2.2
29	RF	175	THR	2.2
33	RN	73	THR	2.2
32	RI	62	LYS	2.2
33	YN	7	LYS	2.2
35	RP	35	HIS	2.2
4	XD	152	SER	2.2

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Mol	Chain	Res	Type	RSRZ
31	RH	16	SER	2.2
2	QB	91	PRO	2.2
9	QI	18	PHE	2.2
12	QL	33	ARG	2.2
13	QM	110	ARG	2.2
45	RZ	28	MET	2.2
48	R2	7	ARG	2.2
5	XE	50	GLU	2.2
25	RA	546	C	2.2
26	RB	88	C	2.2
20	QT	33	ILE	2.2
40	YU	88	ILE	2.2
45	RZ	53	ILE	2.2
25	RA	2311	A	2.1
7	XG	106	GLN	2.1
10	QJ	54	PHE	2.1
15	XO	63	ARG	2.1
28	YE	54	GLN	2.1
37	RR	8	ARG	2.1
39	RT	129	ARG	2.1
46	R0	82	ARG	2.1
9	QI	49	PRO	2.1
9	XI	123	PRO	2.1
6	QF	9	VAL	2.1
7	XG	16	LEU	2.1
8	QH	93	VAL	2.1
8	XH	93	VAL	2.1
17	XQ	5	VAL	2.1
20	QT	20	LEU	2.1
45	RZ	59	LEU	2.1
49	Y3	58	VAL	2.1
7	XG	18	TYR	2.1
31	RH	100	GLY	2.1
45	YZ	99	TYR	2.1
36	YQ	66	ILE	2.1
39	RT	42	ILE	2.1
3	XC	15	THR	2.1
25	RA	2111	C	2.1
17	XQ	92	ARG	2.1
49	R3	30	ARG	2.1
15	XO	62	GLN	2.1
46	Y0	68	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
10	QJ	37	PRO	2.1
15	QO	84	LYS	2.1
28	YE	152	LYS	2.1
32	RI	80	PRO	2.1
50	R4	11	PRO	2.1
2	QB	219	VAL	2.1
15	XO	81	LEU	2.1
11	QK	72	ALA	2.1
19	QS	9	VAL	2.1
20	QT	88	VAL	2.1
29	RF	156	LEU	2.1
37	YR	51	LEU	2.1
54	Y8	50	LEU	2.1
40	YU	68	ALA	2.1
17	XQ	88	TYR	2.1
38	RS	108	GLY	2.1
45	RZ	8	TYR	2.1
3	XC	14	ILE	2.1
32	RI	103	ARG	2.1
12	QL	99	HIS	2.1
3	QC	165	THR	2.1
30	YG	14	GLU	2.1
1	QA	1116	C	2.1
11	XK	16	SER	2.1
36	RQ	69	PHE	2.1
10	QJ	40	LEU	2.1
33	RN	13	TRP	2.1
32	RI	92	VAL	2.1
44	RY	13	VAL	2.1
45	RZ	74	VAL	2.1
45	YZ	175	VAL	2.1
11	QK	68	ALA	2.1
12	QL	88	GLY	2.1
33	RN	92	ALA	2.1
38	YS	60	GLY	2.1
2	XB	114	ARG	2.1
2	XB	185	ILE	2.1
3	XC	30	ARG	2.1
3	XC	84	ILE	2.1
5	QE	133	TYR	2.1
7	QG	10	ARG	2.1
28	YE	60	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
29	RF	206	ILE	2.1
35	RP	18	ARG	2.1
36	YQ	5	ARG	2.1
41	RV	99	ILE	2.1
9	XI	78	LYS	2.1
19	XS	17	GLU	2.1
10	XJ	68	HIS	2.1
14	QN	4	LYS	2.1
47	R1	72	GLU	2.1
29	RF	129	PHE	2.1
29	RF	139	PHE	2.1
40	RU	71	GLN	2.1
50	R4	46	GLN	2.1
10	XJ	35	SER	2.1
25	RA	275	G	2.1
25	RA	508	G	2.1
25	YA	654(S)	G	2.1
35	YP	30	THR	2.1
18	XR	80	PRO	2.1
31	RH	118	PRO	2.1
37	YR	70	LEU	2.1
23	QY	39	C	2.1
33	RN	14	VAL	2.1
4	QD	131	ARG	2.1
5	XE	21	ALA	2.1
10	QJ	20	ALA	2.1
15	QO	88	ARG	2.1
20	QT	40	ALA	2.1
27	RD	2	ALA	2.1
30	RG	46	ALA	2.1
41	RV	26	ASP	2.1
45	RZ	112	ARG	2.1
9	XI	125	TYR	2.1
10	XJ	96	ILE	2.1
12	QL	119	LYS	2.1
13	QM	78	ILE	2.1
17	XQ	96	GLU	2.1
32	YI	4	ILE	2.1
50	R4	8	LYS	2.1
45	YZ	118	GLN	2.1
8	QH	31	PHE	2.1
2	QB	216	SER	2.1

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Mol	Chain	Res	Type	RSRZ
3	QC	175	LEU	2.1
33	RN	33	LEU	2.1
3	XC	2	GLY	2.1
4	QD	69	GLY	2.1
4	QD	168	ARG	2.1
9	XI	120	ARG	2.1
10	QJ	44	VAL	2.1
10	XJ	24	VAL	2.1
10	XJ	93	GLY	2.1
11	XK	84	VAL	2.1
17	QQ	81	ARG	2.1
36	RQ	100	GLY	2.1
25	RA	1667	G	2.1
27	RD	30	GLU	2.1
36	RQ	8	LYS	2.1
41	RV	31	ALA	2.1
28	YE	14	ILE	2.1
20	XT	26	ASN	2.1
51	R5	46	CYS	2.1
25	YA	890	A	2.1
25	YA	1847	A	2.1
45	RZ	88	PHE	2.1
2	XB	149	LEU	2.1
2	XB	221	LEU	2.1
19	XS	30	LEU	2.1
40	YU	98	LEU	2.1
2	XB	167	PRO	2.1
4	XD	172	PRO	2.1
9	QI	104	ARG	2.1
11	QK	56	GLY	2.1
16	XP	67	THR	2.1
20	XT	65	LYS	2.1
32	YI	52	ARG	2.1
34	YO	97	ARG	2.1
47	R1	69	LYS	2.1
16	XP	21	VAL	2.1
33	RN	122	VAL	2.1
33	YN	10	GLU	2.1
39	RT	89	VAL	2.1
45	YZ	60	GLU	2.1
14	XN	59	ALA	2.1
30	RG	57	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
2	QB	41	ILE	2.1
11	QK	20	TYR	2.1
11	XK	48	ILE	2.1
32	YI	88	ILE	2.1
7	QG	13	GLN	2.1
1	XA	150	C	2.1
1	XA	345	C	2.1
23	XY	39	C	2.1
2	QB	106	LYS	2.1
3	QC	42	LEU	2.1
3	XC	11	ARG	2.1
3	XC	83	ARG	2.1
5	QE	25	ARG	2.1
5	XE	91	LEU	2.1
18	XR	41	LYS	2.1
20	QT	21	LYS	2.1
12	QL	50	SER	2.1
27	YD	111	LEU	2.1
25	RA	1085	A	2.1
34	YO	120	GLU	2.1
45	YZ	43	GLU	2.1
51	Y5	35	GLU	2.1
17	XQ	10	VAL	2.1
29	RF	163	VAL	2.1
20	XT	38	LYS	2.1
36	RQ	89	ASN	2.1
41	RV	75	PHE	2.1
48	Y2	15	LYS	2.1
10	XJ	28	ARG	2.1
25	RA	2108	C	2.1
25	RA	2474	C	2.1
34	RO	117	LEU	2.1
36	RQ	38	GLU	2.1
1	QA	965	A	2.0
4	QD	178	VAL	2.0
14	XN	25	VAL	2.0
16	XP	22	THR	2.0
38	RS	85	VAL	2.0
46	R0	63	VAL	2.0
27	RD	126	GLN	2.0
36	RQ	140	ALA	2.0
10	XJ	3	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
46	R0	5	LYS	2.0
45	YZ	80	ARG	2.0
35	YP	119	GLU	2.0
35	YP	144	GLU	2.0
46	R0	68	GLU	2.0
3	QC	81	GLY	2.0
11	QK	37	GLY	2.0
35	RP	147	LEU	2.0
35	YP	147	LEU	2.0
38	RS	56	LEU	2.0
5	XE	90	VAL	2.0
6	QF	89	MET	2.0
14	XN	56	VAL	2.0
28	YE	59	VAL	2.0
30	RG	142	PRO	2.0
1	QA	1034	G	2.0
3	XC	180	ALA	2.0
6	XF	53	ALA	2.0
25	RA	1056	G	2.0
25	RA	2152	G	2.0
25	YA	1066	U	2.0
32	RI	109	ILE	2.0
9	QI	107	ARG	2.0
13	QM	67	GLU	2.0
36	YQ	41	TRP	2.0
2	QB	158	LEU	2.0
5	XE	139	LEU	2.0
9	XI	117	HIS	2.0
13	XM	19	LEU	2.0
18	XR	79	LEU	2.0
32	YI	123	LEU	2.0
35	RP	104	GLY	2.0
55	Y9	21	GLY	2.0
41	YV	56	SER	2.0
2	XB	212	GLN	2.0
3	QC	130	VAL	2.0
10	XJ	73	ASP	2.0
19	XS	9	VAL	2.0
20	XT	64	ASP	2.0
49	R3	39	ASP	2.0
53	R7	1	MET	2.0
2	XB	58	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	QA	1112	C	2.0
2	QB	13	ALA	2.0
2	QB	32	ILE	2.0
10	QJ	23	ILE	2.0
28	RE	19	ARG	2.0
25	YA	2797	U	2.0
27	RD	27	THR	2.0
45	RZ	72	ARG	2.0
45	RZ	120	ILE	2.0
46	R0	39	ARG	2.0
53	R7	23	ARG	2.0
29	YF	128	ALA	2.0
40	YU	86	ALA	2.0
45	YZ	7	ALA	2.0
44	RY	60	PHE	2.0
1	QA	1035	A	2.0
8	QH	2	LEU	2.0
12	QL	52	LEU	2.0
17	XQ	89	LEU	2.0
29	RF	162	LEU	2.0
30	YG	53	LEU	2.0
37	YR	10	LEU	2.0
38	RS	52	SER	2.0
4	QD	8	VAL	2.0
5	QE	82	VAL	2.0
6	QF	47	ARG	2.0
9	XI	66	ARG	2.0
13	XM	97	PRO	2.0
13	XM	102	ARG	2.0
19	QS	59	PRO	2.0
29	RF	191	ARG	2.0
39	RT	3	ARG	2.0
45	RZ	81	ARG	2.0
18	XR	46	GLU	2.0
35	YP	98	GLU	2.0
12	XL	44	THR	2.0
25	RA	1535	U	2.0
25	YA	2109	U	2.0
38	RS	37	ALA	2.0
1	QA	934	C	2.0
7	QG	148	ASN	2.0
13	XM	56	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
31	YH	161	GLY	2.0
35	RP	27	HIS	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
23	1MG	XY	37	24/25	0.20	-	30,30,30,30	0
23	1MG	QY	37	24/25	0.18	-	53,53,53,53	0
56	PPU	Z6	76	37/38	0.30	-	27,27,27,27	0
56	PPU	Z8	76	37/38	0.27	-	14,14,14,14	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
57	MG	YA	3222	1/1	0.13	-	27,27,27,27	0
57	MG	XA	1659	1/1	0.13	-	43,43,43,43	0
57	MG	RA	3090	1/1	0.18	-	8,8,8,8	0
57	MG	QA	1665	1/1	0.20	-	31,31,31,31	0
57	MG	RA	3016	1/1	0.28	-	1,1,1,1	0
57	MG	YA	3140	1/1	0.27	-	2,2,2,2	0
57	MG	XA	1646	1/1	0.25	-	30,30,30,30	0
57	MG	YA	3258	1/1	0.13	-	2,2,2,2	0
57	MG	RA	3238	1/1	0.24	-	14,14,14,14	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3043	1/1	0.27	-	1,1,1,1	0
57	MG	XA	1672	1/1	0.12	-	27,27,27,27	0
57	MG	RA	3013	1/1	0.23	-	11,11,11,11	0
57	MG	RA	3177	1/1	0.39	-	24,24,24,24	0
57	MG	XA	1628	1/1	0.07	-	1,1,1,1	0
57	MG	QA	1629	1/1	0.21	-	30,30,30,30	0
57	MG	R5	101	1/1	0.14	-	21,21,21,21	0
57	MG	RA	3185	1/1	0.11	-	16,16,16,16	0
57	MG	RA	3029	1/1	0.37	-	3,3,3,3	0
57	MG	YA	3078	1/1	0.15	-	14,14,14,14	0
57	MG	RA	3190	1/1	0.30	-	27,27,27,27	0
57	MG	RA	3006	1/1	0.45	-	17,17,17,17	0
57	MG	QA	1640	1/1	0.26	-	24,24,24,24	0
57	MG	YA	3237	1/1	0.23	-	25,25,25,25	0
57	MG	RA	3214	1/1	0.21	-	13,13,13,13	0
57	MG	YA	3104	1/1	0.18	-	3,3,3,3	0
57	MG	RA	3231	1/1	0.37	-	1,1,1,1	0
57	MG	RA	3225	1/1	0.18	-	40,40,40,40	0
57	MG	RA	3157	1/1	0.25	-	25,25,25,25	0
57	MG	XA	1667	1/1	0.32	-	29,29,29,29	0
57	MG	YA	3130	1/1	0.23	-	20,20,20,20	0
57	MG	XA	1624	1/1	0.12	-	16,16,16,16	0
57	MG	YA	3037	1/1	0.24	-	0,0,0,0	0
57	MG	RA	3115	1/1	0.21	-	5,5,5,5	0
59	ZN	QD	301	1/1	0.21	-	58,58,58,58	0
57	MG	RA	3168	1/1	0.20	-	19,19,19,19	0
57	MG	QA	1602	1/1	0.25	-	22,22,22,22	0
57	MG	YA	3223	1/1	0.22	-	20,20,20,20	0
57	MG	YA	3097	1/1	0.21	-	14,14,14,14	0
57	MG	XA	1621	1/1	0.31	-	23,23,23,23	0
57	MG	YA	3191	1/1	0.19	-	14,14,14,14	0
57	MG	YA	3189	1/1	0.07	-	1,1,1,1	0
57	MG	QA	1647	1/1	0.10	-	32,32,32,32	0
57	MG	YA	3117	1/1	0.36	-	24,24,24,24	0
57	MG	YA	3158	1/1	0.30	-	14,14,14,14	0
57	MG	RA	3181	1/1	0.22	-	29,29,29,29	0
57	MG	RA	3164	1/1	0.26	-	20,20,20,20	0
57	MG	YA	3066	1/1	0.35	-	12,12,12,12	0
57	MG	RA	3008	1/1	0.21	-	30,30,30,30	0
57	MG	QA	1660	1/1	0.13	-	38,38,38,38	0
57	MG	RA	3187	1/1	0.44	-	66,66,66,66	0
57	MG	YA	3086	1/1	0.20	-	10,10,10,10	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3085	1/1	0.26	-	9,9,9,9	0
57	MG	YA	3177	1/1	0.18	-	12,12,12,12	0
57	MG	YA	3260	1/1	0.28	-	13,13,13,13	0
57	MG	YA	3067	1/1	0.24	-	2,2,2,2	0
57	MG	QA	1613	1/1	0.18	-	37,37,37,37	0
57	MG	YA	3199	1/1	0.27	-	11,11,11,11	0
57	MG	XA	1632	1/1	0.19	-	21,21,21,21	0
57	MG	YA	3045	1/1	0.17	-	1,1,1,1	0
57	MG	XA	1604	1/1	0.28	-	19,19,19,19	0
57	MG	RA	3171	1/1	0.31	-	33,33,33,33	0
57	MG	QA	1632	1/1	0.21	-	88,88,88,88	0
57	MG	YA	3233	1/1	0.12	-	6,6,6,6	0
57	MG	YA	3262	1/1	0.20	-	4,4,4,4	0
57	MG	YA	3141	1/1	0.06	-	17,17,17,17	0
57	MG	YA	3122	1/1	0.15	-	3,3,3,3	0
57	MG	RA	3100	1/1	0.14	-	6,6,6,6	0
57	MG	YA	3042	1/1	0.17	-	4,4,4,4	0
57	MG	QA	1624	1/1	0.13	-	30,30,30,30	0
57	MG	XA	1617	1/1	0.15	-	8,8,8,8	0
57	MG	YA	3149	1/1	0.19	-	9,9,9,9	0
57	MG	RA	3179	1/1	0.11	-	2,2,2,2	0
57	MG	XA	1661	1/1	0.11	-	23,23,23,23	0
57	MG	RA	3007	1/1	0.32	-	5,5,5,5	0
57	MG	RA	3026	1/1	0.16	-	3,3,3,3	0
57	MG	RA	3047	1/1	0.30	-	12,12,12,12	0
57	MG	YA	3029	1/1	0.24	-	1,1,1,1	0
57	MG	QA	1601	1/1	0.30	-	34,34,34,34	0
57	MG	RA	3162	1/1	0.10	-	2,2,2,2	0
57	MG	RA	3205	1/1	0.27	-	5,5,5,5	0
57	MG	YA	3175	1/1	0.19	-	23,23,23,23	0
57	MG	XA	1613	1/1	0.08	-	6,6,6,6	0
57	MG	RA	3148	1/1	0.20	-	15,15,15,15	0
57	MG	RA	3237	1/1	0.43	-	28,28,28,28	0
57	MG	YA	3015	1/1	0.29	-	15,15,15,15	0
57	MG	YA	3203	1/1	0.12	-	25,25,25,25	0
57	MG	YA	3006	1/1	0.35	-	0,0,0,0	0
57	MG	QA	1623	1/1	0.27	-	19,19,19,19	0
57	MG	YA	3077	1/1	0.27	-	6,6,6,6	0
57	MG	YA	3080	1/1	0.31	-	1,1,1,1	0
57	MG	XA	1652	1/1	0.10	-	47,47,47,47	0
57	MG	RB	201	1/1	0.19	-	41,41,41,41	0
57	MG	QX	101	1/1	0.25	-	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3121	1/1	0.11	-	27,27,27,27	0
57	MG	RA	3025	1/1	0.31	-	12,12,12,12	0
57	MG	RA	3022	1/1	0.21	-	3,3,3,3	0
57	MG	YA	3190	1/1	0.16	-	0,0,0,0	0
57	MG	YA	3224	1/1	0.08	-	14,14,14,14	0
57	MG	YA	3102	1/1	0.24	-	44,44,44,44	0
57	MG	YA	3137	1/1	0.16	-	1,1,1,1	0
57	MG	YA	3081	1/1	0.17	-	10,10,10,10	0
57	MG	YA	3106	1/1	0.25	-	12,12,12,12	0
57	MG	YA	3236	1/1	0.13	-	24,24,24,24	0
57	MG	YA	3027	1/1	0.27	-	9,9,9,9	0
57	MG	YA	3064	1/1	0.18	-	6,6,6,6	0
57	MG	QA	1650	1/1	0.25	-	20,20,20,20	0
57	MG	QA	1642	1/1	0.18	-	43,43,43,43	0
57	MG	RA	3110	1/1	0.21	-	2,2,2,2	0
57	MG	RA	3004	1/1	0.38	-	14,14,14,14	0
57	MG	YA	3075	1/1	0.34	-	24,24,24,24	0
57	MG	RA	3132	1/1	0.30	-	24,24,24,24	0
57	MG	RA	3155	1/1	0.13	-	10,10,10,10	0
57	MG	YA	3251	1/1	0.36	-	38,38,38,38	0
57	MG	RP	201	1/1	0.66	-	144,144,144,144	0
57	MG	XA	1645	1/1	0.18	-	15,15,15,15	0
57	MG	YA	3031	1/1	0.34	-	1,1,1,1	0
57	MG	YA	3092	1/1	0.24	-	3,3,3,3	0
57	MG	YA	3115	1/1	0.26	-	18,18,18,18	0
57	MG	RA	3119	1/1	0.15	-	30,30,30,30	0
57	MG	RA	3070	1/1	0.31	-	13,13,13,13	0
57	MG	RA	3009	1/1	0.06	-	0,0,0,0	0
57	MG	YA	3052	1/1	0.27	-	1,1,1,1	0
57	MG	YA	3094	1/1	0.19	-	4,4,4,4	0
57	MG	XA	1625	1/1	0.10	-	6,6,6,6	0
57	MG	YA	3206	1/1	0.22	-	14,14,14,14	0
57	MG	RA	3056	1/1	0.24	-	1,1,1,1	0
57	MG	RA	3043	1/1	0.21	-	7,7,7,7	0
57	MG	YA	3185	1/1	0.14	-	8,8,8,8	0
59	ZN	QN	101	1/1	0.07	-	95,95,95,95	0
57	MG	RA	3044	1/1	0.24	-	18,18,18,18	0
57	MG	YA	3079	1/1	0.16	-	2,2,2,2	0
57	MG	YA	3169	1/1	0.25	-	12,12,12,12	0
57	MG	YA	3187	1/1	0.14	-	25,25,25,25	0
57	MG	RA	3127	1/1	0.21	-	12,12,12,12	0
57	MG	RA	3151	1/1	0.08	-	0,0,0,0	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3228	1/1	0.12	-	11,11,11,11	0
57	MG	YA	3201	1/1	0.14	-	2,2,2,2	0
57	MG	YA	3022	1/1	0.26	-	1,1,1,1	0
57	MG	YA	3051	1/1	0.32	-	15,15,15,15	0
57	MG	YA	3170	1/1	0.08	-	15,15,15,15	0
57	MG	YA	3263	1/1	0.41	-	16,16,16,16	0
57	MG	YA	3167	1/1	0.16	-	1,1,1,1	0
57	MG	YA	3020	1/1	0.28	-	10,10,10,10	0
57	MG	RA	3161	1/1	0.15	-	17,17,17,17	0
57	MG	YA	3230	1/1	0.17	-	18,18,18,18	0
57	MG	RA	3023	1/1	0.21	-	5,5,5,5	0
57	MG	YA	3113	1/1	0.17	-	11,11,11,11	0
57	MG	RA	3034	1/1	0.32	-	17,17,17,17	0
57	MG	RA	3173	1/1	0.14	-	1,1,1,1	0
57	MG	YA	3196	1/1	0.23	-	54,54,54,54	0
57	MG	RF	301	1/1	0.13	-	24,24,24,24	0
57	MG	RA	3037	1/1	0.27	-	11,11,11,11	0
57	MG	QA	1655	1/1	0.14	-	38,38,38,38	0
57	MG	RA	3059	1/1	0.16	-	4,4,4,4	0
57	MG	YA	3114	1/1	0.26	-	13,13,13,13	0
57	MG	RA	3194	1/1	0.18	-	13,13,13,13	0
57	MG	RA	3241	1/1	0.23	-	13,13,13,13	0
57	MG	YA	3159	1/1	0.13	-	16,16,16,16	0
57	MG	YA	3068	1/1	0.27	-	12,12,12,12	0
57	MG	YA	3161	1/1	0.19	-	34,34,34,34	0
57	MG	YA	3036	1/1	0.17	-	4,4,4,4	0
57	MG	RA	3180	1/1	0.13	-	18,18,18,18	0
57	MG	YA	3157	1/1	0.22	-	23,23,23,23	0
57	MG	YA	3209	1/1	0.14	-	11,11,11,11	0
57	MG	RA	3153	1/1	0.24	-	29,29,29,29	0
57	MG	RA	3189	1/1	0.24	-	46,46,46,46	0
57	MG	XA	1631	1/1	0.24	-	33,33,33,33	0
57	MG	QA	1618	1/1	0.10	-	13,13,13,13	0
57	MG	QA	1606	1/1	0.19	-	11,11,11,11	0
57	MG	RA	3204	1/1	0.24	-	33,33,33,33	0
57	MG	RA	3144	1/1	0.26	-	8,8,8,8	0
57	MG	RA	3239	1/1	0.43	-	28,28,28,28	0
57	MG	YA	3200	1/1	0.29	-	12,12,12,12	0
57	MG	YA	3057	1/1	0.26	-	1,1,1,1	0
57	MG	YA	3146	1/1	0.33	-	37,37,37,37	0
57	MG	RA	3108	1/1	0.17	-	8,8,8,8	0
57	MG	QA	1615	1/1	0.16	-	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	RA	3137	1/1	0.29	-	7,7,7,7	0
57	MG	RA	3213	1/1	0.34	-	17,17,17,17	0
57	MG	QA	1661	1/1	0.25	-	138,138,138,138	0
57	MG	YA	3134	1/1	0.23	-	19,19,19,19	0
57	MG	YA	3181	1/1	0.29	-	36,36,36,36	0
57	MG	RA	3230	1/1	0.33	-	7,7,7,7	0
57	MG	YA	3072	1/1	0.20	-	9,9,9,9	0
57	MG	RA	3084	1/1	0.12	-	7,7,7,7	0
57	MG	RA	3209	1/1	0.32	-	47,47,47,47	0
57	MG	QA	1653	1/1	0.10	-	88,88,88,88	0
57	MG	YA	3136	1/1	0.24	-	14,14,14,14	0
57	MG	QA	1643	1/1	0.08	-	21,21,21,21	0
57	MG	RA	3126	1/1	0.32	-	33,33,33,33	0
57	MG	YA	3247	1/1	0.32	-	16,16,16,16	0
57	MG	RA	3048	1/1	0.18	-	1,1,1,1	0
57	MG	RA	3114	1/1	0.25	-	19,19,19,19	0
57	MG	XA	1663	1/1	0.14	-	38,38,38,38	0
57	MG	RA	3077	1/1	0.30	-	13,13,13,13	0
57	MG	YA	3088	1/1	0.32	-	5,5,5,5	0
57	MG	XA	1651	1/1	0.10	-	95,95,95,95	0
57	MG	YA	3172	1/1	0.20	-	25,25,25,25	0
57	MG	RA	3058	1/1	0.18	-	34,34,34,34	0
57	MG	YA	3160	1/1	0.07	-	18,18,18,18	0
57	MG	QA	1657	1/1	0.16	-	37,37,37,37	0
57	MG	RA	3075	1/1	0.11	-	6,6,6,6	0
57	MG	RA	3089	1/1	0.21	-	2,2,2,2	0
57	MG	RA	3196	1/1	0.15	-	42,42,42,42	0
57	MG	YA	3061	1/1	0.19	-	17,17,17,17	0
57	MG	RA	3166	1/1	0.29	-	28,28,28,28	0
57	MG	YA	3244	1/1	0.20	-	30,30,30,30	0
57	MG	QA	1636	1/1	0.19	-	39,39,39,39	0
57	MG	RA	3207	1/1	0.15	-	60,60,60,60	0
57	MG	XA	1648	1/1	0.11	-	14,14,14,14	0
57	MG	XA	1649	1/1	0.19	-	8,8,8,8	0
57	MG	XA	1668	1/1	0.21	-	15,15,15,15	0
57	MG	RA	3152	1/1	0.20	-	11,11,11,11	0
57	MG	RA	3019	1/1	0.32	-	13,13,13,13	0
57	MG	XA	1629	1/1	0.30	-	32,32,32,32	0
57	MG	YA	3019	1/1	0.39	-	8,8,8,8	0
57	MG	QA	1614	1/1	0.15	-	20,20,20,20	0
57	MG	QA	1627	1/1	0.27	-	22,22,22,22	0
57	MG	YA	3239	1/1	0.34	-	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	RA	3210	1/1	0.13	-	18,18,18,18	0
57	MG	XA	1658	1/1	0.21	-	12,12,12,12	0
57	MG	RA	3242	1/1	0.35	-	31,31,31,31	0
57	MG	YA	3120	1/1	0.26	-	21,21,21,21	0
57	MG	RA	3216	1/1	0.19	-	33,33,33,33	0
57	MG	RA	3057	1/1	0.23	-	6,6,6,6	0
57	MG	RA	3039	1/1	0.20	-	10,10,10,10	0
57	MG	RA	3046	1/1	0.18	-	8,8,8,8	0
57	MG	YA	3002	1/1	0.30	-	1,1,1,1	0
57	MG	YA	3016	1/1	0.16	-	0,0,0,0	0
57	MG	RA	3097	1/1	0.28	-	4,4,4,4	0
57	MG	YA	3093	1/1	0.17	-	9,9,9,9	0
57	MG	YA	3214	1/1	0.20	-	25,25,25,25	0
57	MG	YA	3264	1/1	0.15	-	7,7,7,7	0
57	MG	XA	1642	1/1	0.12	-	7,7,7,7	0
57	MG	RA	3091	1/1	0.32	-	23,23,23,23	0
57	MG	YA	3162	1/1	0.13	-	16,16,16,16	0
57	MG	RA	3086	1/1	0.34	-	13,13,13,13	0
57	MG	YA	3105	1/1	0.09	-	24,24,24,24	0
57	MG	XA	1623	1/1	0.12	-	13,13,13,13	0
57	MG	YA	3220	1/1	0.21	-	32,32,32,32	0
57	MG	YA	3046	1/1	0.32	-	20,20,20,20	0
57	MG	YA	3245	1/1	0.42	-	28,28,28,28	0
57	MG	QA	1648	1/1	0.08	-	34,34,34,34	0
57	MG	XA	1647	1/1	0.23	-	23,23,23,23	0
57	MG	RA	3176	1/1	0.23	-	10,10,10,10	0
57	MG	RA	3182	1/1	0.11	-	6,6,6,6	0
57	MG	RA	3139	1/1	0.29	-	59,59,59,59	0
57	MG	RA	3113	1/1	0.14	-	29,29,29,29	0
57	MG	YA	3217	1/1	0.10	-	9,9,9,9	0
57	MG	RA	3104	1/1	0.13	-	9,9,9,9	0
57	MG	QA	1619	1/1	0.14	-	1,1,1,1	0
57	MG	RA	3067	1/1	0.21	-	3,3,3,3	0
57	MG	QA	1605	1/1	0.38	-	23,23,23,23	0
57	MG	XA	1641	1/1	0.12	-	33,33,33,33	0
57	MG	YB	203	1/1	0.16	-	18,18,18,18	0
57	MG	QA	1641	1/1	0.15	-	22,22,22,22	0
57	MG	YA	3065	1/1	0.22	-	0,0,0,0	0
57	MG	RA	3051	1/1	0.22	-	4,4,4,4	0
57	MG	YA	3099	1/1	0.24	-	9,9,9,9	0
57	MG	YA	3050	1/1	0.26	-	2,2,2,2	0
57	MG	YA	3213	1/1	0.12	-	6,6,6,6	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	RA	3116	1/1	0.18	-	0,0,0,0	0
57	MG	QA	1620	1/1	0.10	-	16,16,16,16	0
57	MG	YA	3127	1/1	0.15	-	26,26,26,26	0
57	MG	YA	3184	1/1	0.17	-	26,26,26,26	0
57	MG	YA	3176	1/1	0.13	-	2,2,2,2	0
57	MG	RA	3234	1/1	0.23	-	10,10,10,10	0
57	MG	RA	3032	1/1	0.33	-	27,27,27,27	0
57	MG	XA	1618	1/1	0.20	-	11,11,11,11	0
57	MG	RA	3228	1/1	0.14	-	43,43,43,43	0
57	MG	XA	1601	1/1	0.25	-	7,7,7,7	0
57	MG	YA	3259	1/1	0.43	-	13,13,13,13	0
57	MG	YA	3178	1/1	0.13	-	29,29,29,29	0
59	ZN	XD	301	1/1	0.26	-	39,39,39,39	0
57	MG	YA	3261	1/1	0.34	-	19,19,19,19	0
57	MG	R8	101	1/1	0.16	-	25,25,25,25	0
57	MG	RA	3011	1/1	0.47	-	36,36,36,36	0
57	MG	QH	201	1/1	0.18	-	74,74,74,74	0
57	MG	YA	3188	1/1	0.24	-	33,33,33,33	0
57	MG	YA	3155	1/1	0.19	-	50,50,50,50	0
57	MG	RA	3229	1/1	0.10	-	26,26,26,26	0
57	MG	XA	1640	1/1	0.20	-	15,15,15,15	0
57	MG	RA	3220	1/1	0.29	-	31,31,31,31	0
57	MG	QA	1611	1/1	0.30	-	12,12,12,12	0
57	MG	QA	1654	1/1	0.14	-	36,36,36,36	0
57	MG	RA	3093	1/1	0.29	-	8,8,8,8	0
57	MG	YA	3192	1/1	0.27	-	19,19,19,19	0
57	MG	YA	3087	1/1	0.26	-	1,1,1,1	0
57	MG	RA	3211	1/1	0.27	-	30,30,30,30	0
57	MG	Y5	101	1/1	0.19	-	12,12,12,12	0
57	MG	RA	3142	1/1	0.16	-	32,32,32,32	0
57	MG	QA	1663	1/1	0.14	-	67,67,67,67	0
57	MG	YA	3059	1/1	0.15	-	19,19,19,19	0
57	MG	XA	1653	1/1	0.14	-	70,70,70,70	0
57	MG	YA	3023	1/1	0.28	-	6,6,6,6	0
57	MG	RA	3178	1/1	0.21	-	26,26,26,26	0
57	MG	YA	3049	1/1	0.29	-	8,8,8,8	0
57	MG	XA	1627	1/1	0.36	-	28,28,28,28	0
57	MG	RA	3001	1/1	0.15	-	4,4,4,4	0
57	MG	RA	3134	1/1	0.23	-	23,23,23,23	0
57	MG	RA	3121	1/1	0.34	-	36,36,36,36	0
57	MG	XA	1620	1/1	0.16	-	10,10,10,10	0
57	MG	YA	3125	1/1	0.16	-	9,9,9,9	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	RA	3170	1/1	0.16	-	33,33,33,33	0
57	MG	YA	3232	1/1	0.24	-	47,47,47,47	0
57	MG	RA	3120	1/1	0.46	-	80,80,80,80	0
57	MG	RA	3215	1/1	0.07	-	24,24,24,24	0
57	MG	RA	3163	1/1	0.25	-	19,19,19,19	0
57	MG	YA	3202	1/1	0.08	-	13,13,13,13	0
57	MG	RA	3235	1/1	0.36	-	28,28,28,28	0
57	MG	YA	3118	1/1	0.33	-	22,22,22,22	0
57	MG	XA	1602	1/1	0.12	-	18,18,18,18	0
57	MG	YA	3144	1/1	0.08	-	11,11,11,11	0
57	MG	YA	3124	1/1	0.24	-	9,9,9,9	0
57	MG	YB	202	1/1	0.26	-	16,16,16,16	0
57	MG	RA	3128	1/1	0.23	-	4,4,4,4	0
57	MG	YA	3084	1/1	0.24	-	2,2,2,2	0
57	MG	YA	3009	1/1	0.35	-	2,2,2,2	0
57	MG	RA	3111	1/1	0.30	-	14,14,14,14	0
57	MG	QA	1626	1/1	0.08	-	21,21,21,21	0
57	MG	XA	1635	1/1	0.24	-	12,12,12,12	0
57	MG	RA	3232	1/1	0.26	-	10,10,10,10	0
57	MG	YA	3165	1/1	0.26	-	40,40,40,40	0
57	MG	YA	3198	1/1	0.39	-	69,69,69,69	0
57	MG	QA	1612	1/1	0.26	-	9,9,9,9	0
57	MG	QA	1651	1/1	0.16	-	18,18,18,18	0
57	MG	XA	1633	1/1	0.26	-	16,16,16,16	0
57	MG	YA	3076	1/1	0.40	-	15,15,15,15	0
57	MG	QA	1604	1/1	0.21	-	4,4,4,4	0
58	PAR	QA	1666	42/42	0.24	-	43,43,43,43	0
57	MG	XA	1638	1/1	0.13	-	20,20,20,20	0
57	MG	R0	101	1/1	0.20	-	15,15,15,15	0
57	MG	RA	3118	1/1	0.09	-	22,22,22,22	0
57	MG	RA	3160	1/1	0.13	-	12,12,12,12	0
57	MG	YA	3234	1/1	0.18	-	25,25,25,25	0
57	MG	YA	3007	1/1	0.18	-	9,9,9,9	0
57	MG	YA	3139	1/1	0.33	-	55,55,55,55	0
57	MG	YA	3110	1/1	0.24	-	14,14,14,14	0
57	MG	YA	3132	1/1	0.25	-	5,5,5,5	0
57	MG	YA	3218	1/1	0.11	-	1,1,1,1	0
57	MG	RA	3027	1/1	0.30	-	1,1,1,1	0
57	MG	RA	3069	1/1	0.10	-	1,1,1,1	0
57	MG	QA	1649	1/1	0.12	-	31,31,31,31	0
57	MG	YA	3255	1/1	0.34	-	20,20,20,20	0
57	MG	RA	3184	1/1	0.14	-	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3186	1/1	0.13	-	15,15,15,15	0
57	MG	QA	1659	1/1	0.17	-	21,21,21,21	0
57	MG	YA	3053	1/1	0.32	-	0,0,0,0	0
57	MG	RA	3106	1/1	0.16	-	4,4,4,4	0
57	MG	QA	1662	1/1	0.12	-	58,58,58,58	0
57	MG	RA	3101	1/1	0.12	-	2,2,2,2	0
57	MG	YA	3101	1/1	0.23	-	3,3,3,3	0
57	MG	QA	1638	1/1	0.19	-	27,27,27,27	0
57	MG	YA	3238	1/1	0.15	-	26,26,26,26	0
57	MG	RA	3005	1/1	0.39	-	9,9,9,9	0
57	MG	QA	1608	1/1	0.09	-	22,22,22,22	0
57	MG	XA	1608	1/1	0.09	-	34,34,34,34	0
57	MG	YA	3147	1/1	0.12	-	2,2,2,2	0
57	MG	RA	3083	1/1	0.23	-	17,17,17,17	0
57	MG	RA	3117	1/1	0.19	-	2,2,2,2	0
57	MG	RA	3159	1/1	0.12	-	24,24,24,24	0
57	MG	XA	1614	1/1	0.11	-	7,7,7,7	0
57	MG	YA	3231	1/1	0.20	-	20,20,20,20	0
57	MG	RA	3092	1/1	0.32	-	17,17,17,17	0
57	MG	XM	201	1/1	0.09	-	58,58,58,58	0
57	MG	YA	3195	1/1	0.09	-	26,26,26,26	0
57	MG	YA	3040	1/1	0.30	-	0,0,0,0	0
57	MG	QA	1634	1/1	0.08	-	35,35,35,35	0
57	MG	YA	3240	1/1	0.18	-	32,32,32,32	0
57	MG	YA	3058	1/1	0.24	-	0,0,0,0	0
57	MG	XA	1607	1/1	0.23	-	22,22,22,22	0
57	MG	RA	3227	1/1	0.27	-	32,32,32,32	0
57	MG	RA	3198	1/1	0.06	-	27,27,27,27	0
57	MG	RA	3017	1/1	0.22	-	0,0,0,0	0
57	MG	RA	3061	1/1	0.27	-	2,2,2,2	0
57	MG	RA	3200	1/1	0.43	-	23,23,23,23	0
57	MG	XA	1609	1/1	0.25	-	14,14,14,14	0
57	MG	YA	3197	1/1	0.19	-	42,42,42,42	0
57	MG	YA	3074	1/1	0.12	-	2,2,2,2	0
57	MG	YA	3111	1/1	0.09	-	8,8,8,8	0
57	MG	RA	3135	1/1	0.26	-	31,31,31,31	0
57	MG	YA	3047	1/1	0.26	-	4,4,4,4	0
57	MG	QA	1631	1/1	0.07	-	39,39,39,39	0
57	MG	RA	3042	1/1	0.35	-	10,10,10,10	0
57	MG	XA	1603	1/1	0.40	-	13,13,13,13	0
57	MG	YA	3225	1/1	0.20	-	3,3,3,3	0
57	MG	RA	3143	1/1	0.18	-	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3249	1/1	0.41	-	42,42,42,42	0
57	MG	RA	3030	1/1	0.30	-	0,0,0,0	0
57	MG	RA	3078	1/1	0.27	-	23,23,23,23	0
57	MG	RA	3071	1/1	0.25	-	22,22,22,22	0
57	MG	XA	1670	1/1	0.14	-	35,35,35,35	0
57	MG	YA	3039	1/1	0.18	-	10,10,10,10	0
57	MG	RA	3219	1/1	0.63	-	159,159,159,159	0
57	MG	YA	3212	1/1	0.12	-	20,20,20,20	0
57	MG	RA	3028	1/1	0.34	-	2,2,2,2	0
57	MG	YA	3210	1/1	0.36	-	26,26,26,26	0
57	MG	XA	1669	1/1	0.12	-	49,49,49,49	0
57	MG	RA	3066	1/1	0.32	-	17,17,17,17	0
57	MG	RA	3169	1/1	0.30	-	30,30,30,30	0
57	MG	YA	3152	1/1	0.27	-	31,31,31,31	0
57	MG	RA	3140	1/1	0.31	-	17,17,17,17	0
57	MG	QA	1622	1/1	0.15	-	40,40,40,40	0
57	MG	RA	3014	1/1	0.24	-	3,3,3,3	0
57	MG	QA	1610	1/1	0.29	-	14,14,14,14	0
57	MG	YA	3103	1/1	0.26	-	8,8,8,8	0
57	MG	XA	1622	1/1	0.20	-	33,33,33,33	0
57	MG	XA	1665	1/1	0.16	-	56,56,56,56	0
57	MG	QA	1656	1/1	0.09	-	89,89,89,89	0
57	MG	YA	3150	1/1	0.17	-	62,62,62,62	0
57	MG	RA	3172	1/1	0.12	-	15,15,15,15	0
57	MG	YA	3250	1/1	0.32	-	22,22,22,22	0
57	MG	RA	3186	1/1	0.07	-	14,14,14,14	0
57	MG	RA	3217	1/1	0.13	-	14,14,14,14	0
57	MG	XA	1634	1/1	0.13	-	6,6,6,6	0
57	MG	RA	3062	1/1	0.26	-	29,29,29,29	0
57	MG	YA	3129	1/1	0.27	-	28,28,28,28	0
57	MG	RA	3174	1/1	0.20	-	25,25,25,25	0
57	MG	QA	1603	1/1	0.25	-	22,22,22,22	0
57	MG	XV	101	1/1	0.16	-	0,0,0,0	0
57	MG	RA	3038	1/1	0.24	-	1,1,1,1	0
57	MG	RA	3076	1/1	0.23	-	0,0,0,0	0
57	MG	RA	3236	1/1	0.17	-	28,28,28,28	0
57	MG	XA	1615	1/1	0.24	-	2,2,2,2	0
57	MG	RA	3146	1/1	0.09	-	27,27,27,27	0
57	MG	YA	3041	1/1	0.23	-	2,2,2,2	0
57	MG	QA	1607	1/1	0.15	-	10,10,10,10	0
57	MG	RA	3109	1/1	0.08	-	3,3,3,3	0
57	MG	XA	1655	1/1	0.18	-	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3243	1/1	0.16	-	21,21,21,21	0
57	MG	YA	3018	1/1	0.30	-	16,16,16,16	0
57	MG	YA	3126	1/1	0.14	-	1,1,1,1	0
57	MG	RA	3199	1/1	0.08	-	10,10,10,10	0
57	MG	RA	3088	1/1	0.29	-	25,25,25,25	0
57	MG	QM	201	1/1	0.12	-	58,58,58,58	0
57	MG	YA	3204	1/1	0.13	-	17,17,17,17	0
57	MG	YA	3268	1/1	0.14	-	17,17,17,17	0
57	MG	YA	3253	1/1	0.29	-	2,2,2,2	0
57	MG	RA	3233	1/1	0.15	-	13,13,13,13	0
57	MG	YA	3119	1/1	0.27	-	23,23,23,23	0
57	MG	YA	3116	1/1	0.15	-	39,39,39,39	0
57	MG	YA	3229	1/1	0.11	-	19,19,19,19	0
57	MG	YE	301	1/1	0.22	-	0,0,0,0	0
57	MG	RA	3154	1/1	0.27	-	26,26,26,26	0
57	MG	YA	3025	1/1	0.13	-	6,6,6,6	0
57	MG	RA	3193	1/1	0.25	-	63,63,63,63	0
57	MG	RA	3049	1/1	0.08	-	1,1,1,1	0
57	MG	RA	3095	1/1	0.26	-	6,6,6,6	0
57	MG	QA	1644	1/1	0.18	-	21,21,21,21	0
57	MG	XA	1644	1/1	0.15	-	23,23,23,23	0
57	MG	XA	1660	1/1	0.08	-	6,6,6,6	0
57	MG	RA	3191	1/1	0.05	-	16,16,16,16	0
57	MG	RA	3158	1/1	0.43	-	40,40,40,40	0
57	MG	RA	3218	1/1	0.23	-	17,17,17,17	0
57	MG	RA	3012	1/1	0.26	-	7,7,7,7	0
57	MG	RA	3222	1/1	0.14	-	36,36,36,36	0
57	MG	QA	1609	1/1	0.15	-	13,13,13,13	0
57	MG	XA	1639	1/1	0.27	-	58,58,58,58	0
57	MG	RA	3188	1/1	0.21	-	29,29,29,29	0
57	MG	RA	3167	1/1	0.17	-	22,22,22,22	0
57	MG	RA	3010	1/1	0.37	-	38,38,38,38	0
57	MG	XA	1616	1/1	0.23	-	6,6,6,6	0
57	MG	YA	3123	1/1	0.24	-	4,4,4,4	0
57	MG	RA	3123	1/1	0.14	-	28,28,28,28	0
57	MG	YA	3246	1/1	0.14	-	26,26,26,26	0
57	MG	RA	3130	1/1	0.40	-	43,43,43,43	0
57	MG	YA	3227	1/1	0.15	-	8,8,8,8	0
57	MG	YA	3069	1/1	0.15	-	6,6,6,6	0
57	MG	YA	3014	1/1	0.27	-	4,4,4,4	0
57	MG	YA	3148	1/1	0.16	-	21,21,21,21	0
57	MG	YA	3142	1/1	0.15	-	8,8,8,8	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YP	201	1/1	0.09	-	96,96,96,96	0
57	MG	RE	302	1/1	0.25	-	5,5,5,5	0
57	MG	RA	3136	1/1	0.17	-	14,14,14,14	0
57	MG	QA	1635	1/1	0.15	-	18,18,18,18	0
59	ZN	XN	101	1/1	0.10	-	42,42,42,42	0
57	MG	YA	3208	1/1	0.09	-	29,29,29,29	0
57	MG	XA	1650	1/1	0.16	-	27,27,27,27	0
57	MG	YA	3012	1/1	0.33	-	2,2,2,2	0
57	MG	YA	3055	1/1	0.27	-	11,11,11,11	0
57	MG	QA	1664	1/1	0.14	-	17,17,17,17	0
58	PAR	XA	1673	42/42	0.23	-	31,31,31,31	0
57	MG	YA	3215	1/1	0.10	-	18,18,18,18	0
57	MG	XA	1612	1/1	0.16	-	3,3,3,3	0
57	MG	XA	1657	1/1	0.21	-	21,21,21,21	0
57	MG	QA	1658	1/1	0.18	-	39,39,39,39	0
57	MG	RA	3156	1/1	0.11	-	31,31,31,31	0
57	MG	RA	3063	1/1	0.36	-	1,1,1,1	0
57	MG	RA	3055	1/1	0.21	-	8,8,8,8	0
57	MG	YA	3151	1/1	0.27	-	30,30,30,30	0
57	MG	RA	3175	1/1	0.09	-	19,19,19,19	0
57	MG	RA	3079	1/1	0.24	-	11,11,11,11	0
57	MG	RA	3060	1/1	0.29	-	0,0,0,0	0
57	MG	RA	3202	1/1	0.21	-	15,15,15,15	0
57	MG	YP	202	1/1	0.14	-	5,5,5,5	0
57	MG	YA	3048	1/1	0.28	-	11,11,11,11	0
57	MG	XA	1666	1/1	0.07	-	13,13,13,13	0
57	MG	YA	3221	1/1	0.14	-	29,29,29,29	0
57	MG	RA	3129	1/1	0.17	-	10,10,10,10	0
57	MG	RA	3192	1/1	0.18	-	68,68,68,68	0
57	MG	RA	3208	1/1	0.17	-	7,7,7,7	0
57	MG	RA	3240	1/1	0.30	-	14,14,14,14	0
57	MG	RA	3081	1/1	0.13	-	10,10,10,10	0
57	MG	RA	3149	1/1	0.27	-	22,22,22,22	0
57	MG	YA	3226	1/1	0.25	-	4,4,4,4	0
57	MG	RA	3036	1/1	0.23	-	2,2,2,2	0
57	MG	RR	201	1/1	0.26	-	20,20,20,20	0
57	MG	QF	201	1/1	0.19	-	54,54,54,54	0
57	MG	YA	3241	1/1	0.09	-	37,37,37,37	0
57	MG	RD	301	1/1	0.24	-	35,35,35,35	0
57	MG	YA	3265	1/1	0.26	-	17,17,17,17	0
57	MG	RA	3201	1/1	0.13	-	17,17,17,17	0
57	MG	XA	1610	1/1	0.14	-	7,7,7,7	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	RA	3183	1/1	0.15	-	1,1,1,1	0
57	MG	RA	3124	1/1	0.39	-	24,24,24,24	0
57	MG	XA	1643	1/1	0.13	-	12,12,12,12	0
57	MG	QA	1621	1/1	0.10	-	30,30,30,30	0
57	MG	YA	3038	1/1	0.20	-	4,4,4,4	0
57	MG	YX	101	1/1	0.18	-	46,46,46,46	0
57	MG	RA	3150	1/1	0.11	-	25,25,25,25	0
57	MG	YA	3082	1/1	0.12	-	0,0,0,0	0
57	MG	RB	202	1/1	0.20	-	46,46,46,46	0
57	MG	YA	3083	1/1	0.19	-	0,0,0,0	0
57	MG	RA	3103	1/1	0.14	-	2,2,2,2	0
57	MG	QA	1617	1/1	0.23	-	31,31,31,31	0
57	MG	YA	3248	1/1	0.30	-	30,30,30,30	0
57	MG	RA	3107	1/1	0.19	-	6,6,6,6	0
57	MG	YA	3242	1/1	0.18	-	33,33,33,33	0
57	MG	XA	1656	1/1	0.33	-	31,31,31,31	0
57	MG	RA	3002	1/1	0.29	-	26,26,26,26	0
57	MG	XA	1619	1/1	0.14	-	7,7,7,7	0
57	MG	QA	1646	1/1	0.11	-	38,38,38,38	0
57	MG	QA	1645	1/1	0.08	-	20,20,20,20	0
57	MG	YA	3095	1/1	0.20	-	5,5,5,5	0
57	MG	YA	3013	1/1	0.25	-	7,7,7,7	0
57	MG	XA	1671	1/1	0.10	-	18,18,18,18	0
57	MG	YA	3219	1/1	0.14	-	31,31,31,31	0
57	MG	YQ	201	1/1	0.29	-	142,142,142,142	0
57	MG	RA	3098	1/1	0.30	-	7,7,7,7	0
57	MG	RA	3096	1/1	0.23	-	18,18,18,18	0
57	MG	YA	3001	1/1	0.31	-	1,1,1,1	0
57	MG	RA	3145	1/1	0.25	-	27,27,27,27	0
57	MG	YA	3021	1/1	0.23	-	1,1,1,1	0
57	MG	YA	3182	1/1	0.27	-	18,18,18,18	0
57	MG	RA	3094	1/1	0.13	-	8,8,8,8	0
57	MG	YA	3128	1/1	0.33	-	3,3,3,3	0
57	MG	YA	3030	1/1	0.39	-	6,6,6,6	0
57	MG	YA	3163	1/1	0.22	-	25,25,25,25	0
57	MG	RA	3015	1/1	0.16	-	5,5,5,5	0
57	MG	RA	3226	1/1	0.18	-	15,15,15,15	0
57	MG	RA	3053	1/1	0.31	-	12,12,12,12	0
57	MG	YA	3235	1/1	0.26	-	30,30,30,30	0
57	MG	RA	3040	1/1	0.23	-	15,15,15,15	0
57	MG	YA	3254	1/1	0.18	-	18,18,18,18	0
57	MG	YA	3008	1/1	0.29	-	2,2,2,2	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3207	1/1	0.23	-	46,46,46,46	0
57	MG	YA	3173	1/1	0.22	-	49,49,49,49	0
57	MG	RA	3087	1/1	0.19	-	25,25,25,25	0
57	MG	YA	3010	1/1	0.24	-	1,1,1,1	0
57	MG	RU	201	1/1	0.20	-	117,117,117,117	0
57	MG	YA	3063	1/1	0.30	-	3,3,3,3	0
57	MG	RA	3080	1/1	0.19	-	17,17,17,17	0
57	MG	RA	3045	1/1	0.28	-	6,6,6,6	0
57	MG	QV	101	1/1	0.26	-	9,9,9,9	0
57	MG	RA	3102	1/1	0.23	-	28,28,28,28	0
57	MG	RA	3073	1/1	0.12	-	10,10,10,10	0
57	MG	YA	3211	1/1	0.07	-	0,0,0,0	0
57	MG	YA	3033	1/1	0.27	-	9,9,9,9	0
57	MG	YA	3143	1/1	0.18	-	33,33,33,33	0
57	MG	XA	1626	1/1	0.16	-	9,9,9,9	0
57	MG	YA	3266	1/1	0.29	-	51,51,51,51	0
57	MG	RA	3122	1/1	0.22	-	32,32,32,32	0
57	MG	YA	3005	1/1	0.17	-	6,6,6,6	0
57	MG	QA	1639	1/1	0.16	-	25,25,25,25	0
57	MG	YA	3193	1/1	0.25	-	18,18,18,18	0
57	MG	RA	3147	1/1	0.13	-	14,14,14,14	0
57	MG	XA	1637	1/1	0.15	-	20,20,20,20	0
57	MG	YA	3107	1/1	0.28	-	2,2,2,2	0
57	MG	YA	3003	1/1	0.22	-	1,1,1,1	0
57	MG	YA	3138	1/1	0.18	-	0,0,0,0	0
57	MG	RA	3035	1/1	0.27	-	0,0,0,0	0
57	MG	YA	3252	1/1	0.41	-	17,17,17,17	0
57	MG	YA	3056	1/1	0.19	-	1,1,1,1	0
57	MG	YA	3098	1/1	0.28	-	2,2,2,2	0
57	MG	YA	3062	1/1	0.21	-	7,7,7,7	0
57	MG	YA	3135	1/1	0.13	-	3,3,3,3	0
57	MG	RA	3033	1/1	0.36	-	3,3,3,3	0
57	MG	RA	3131	1/1	0.10	-	13,13,13,13	0
57	MG	YA	3156	1/1	0.25	-	13,13,13,13	0
57	MG	YA	3011	1/1	0.28	-	14,14,14,14	0
57	MG	YA	3133	1/1	0.10	-	26,26,26,26	0
57	MG	RA	3085	1/1	0.25	-	6,6,6,6	0
57	MG	YA	3054	1/1	0.20	-	48,48,48,48	0
57	MG	YA	3194	1/1	0.11	-	17,17,17,17	0
57	MG	RA	3031	1/1	0.20	-	3,3,3,3	0
57	MG	YA	3183	1/1	0.23	-	13,13,13,13	0
57	MG	YA	3090	1/1	0.42	-	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	QA	1633	1/1	0.31	-	35,35,35,35	0
57	MG	YA	3112	1/1	0.10	-	11,11,11,11	0
57	MG	YA	3179	1/1	0.40	-	35,35,35,35	0
57	MG	YA	3032	1/1	0.33	-	4,4,4,4	0
57	MG	YA	3089	1/1	0.24	-	16,16,16,16	0
57	MG	RA	3068	1/1	0.20	-	16,16,16,16	0
57	MG	YA	3171	1/1	0.46	-	29,29,29,29	0
57	MG	RA	3195	1/1	0.13	-	1,1,1,1	0
57	MG	RA	3221	1/1	0.22	-	39,39,39,39	0
57	MG	RA	3141	1/1	0.10	-	15,15,15,15	0
57	MG	RA	3020	1/1	0.25	-	8,8,8,8	0
57	MG	YA	3109	1/1	0.08	-	5,5,5,5	0
57	MG	XA	1611	1/1	0.23	-	7,7,7,7	0
57	MG	RA	3024	1/1	0.28	-	7,7,7,7	0
57	MG	YA	3108	1/1	0.29	-	12,12,12,12	0
57	MG	QA	1652	1/1	0.19	-	32,32,32,32	0
57	MG	YA	3164	1/1	0.14	-	45,45,45,45	0
57	MG	RA	3065	1/1	0.28	-	9,9,9,9	0
57	MG	RE	301	1/1	0.15	-	1,1,1,1	0
57	MG	RA	3072	1/1	0.21	-	3,3,3,3	0
57	MG	RA	3224	1/1	0.27	-	18,18,18,18	0
57	MG	XA	1630	1/1	0.12	-	13,13,13,13	0
57	MG	YA	3091	1/1	0.21	-	29,29,29,29	0
57	MG	YA	3071	1/1	0.14	-	0,0,0,0	0
57	MG	YA	3257	1/1	0.40	-	3,3,3,3	0
57	MG	YA	3073	1/1	0.28	-	8,8,8,8	0
57	MG	YA	3154	1/1	0.10	-	3,3,3,3	0
57	MG	YA	3153	1/1	0.12	-	13,13,13,13	0
57	MG	YA	3180	1/1	0.26	-	41,41,41,41	0
57	MG	RA	3197	1/1	0.12	-	9,9,9,9	0
57	MG	YA	3028	1/1	0.17	-	2,2,2,2	0
57	MG	YA	3100	1/1	0.30	-	1,1,1,1	0
57	MG	YA	3267	1/1	0.45	-	24,24,24,24	0
57	MG	YA	3044	1/1	0.20	-	4,4,4,4	0
57	MG	YB	201	1/1	0.23	-	39,39,39,39	0
57	MG	RA	3112	1/1	0.22	-	21,21,21,21	0
57	MG	XA	1605	1/1	0.28	-	17,17,17,17	0
57	MG	QA	1628	1/1	0.33	-	37,37,37,37	0
57	MG	YA	3131	1/1	0.25	-	34,34,34,34	0
57	MG	RA	3052	1/1	0.26	-	7,7,7,7	0
57	MG	RA	3018	1/1	0.19	-	17,17,17,17	0
57	MG	RA	3021	1/1	0.26	-	2,2,2,2	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	RA	3041	1/1	0.21	-	22,22,22,22	0
57	MG	YA	3060	1/1	0.28	-	1,1,1,1	0
57	MG	RA	3165	1/1	0.07	-	14,14,14,14	0
57	MG	YA	3205	1/1	0.17	-	27,27,27,27	0
57	MG	QA	1637	1/1	0.15	-	16,16,16,16	0
57	MG	RA	3125	1/1	0.13	-	13,13,13,13	0
57	MG	YA	3096	1/1	0.23	-	5,5,5,5	0
57	MG	YA	3145	1/1	0.20	-	18,18,18,18	0
57	MG	QA	1630	1/1	0.13	-	48,48,48,48	0
57	MG	RA	3064	1/1	0.31	-	13,13,13,13	0
57	MG	YA	3024	1/1	0.26	-	1,1,1,1	0
57	MG	YA	3174	1/1	0.09	-	7,7,7,7	0
57	MG	XA	1664	1/1	0.09	-	44,44,44,44	0
57	MG	RP	202	1/1	0.18	-	85,85,85,85	0
57	MG	RA	3082	1/1	0.17	-	35,35,35,35	0
57	MG	RA	3099	1/1	0.35	-	12,12,12,12	0
57	MG	XA	1654	1/1	0.06	-	37,37,37,37	0
57	MG	YA	3035	1/1	0.21	-	1,1,1,1	0
57	MG	RA	3050	1/1	0.27	-	30,30,30,30	0
57	MG	QA	1616	1/1	0.15	-	28,28,28,28	0
57	MG	XX	101	1/1	0.22	-	45,45,45,45	0
57	MG	RA	3212	1/1	0.12	-	13,13,13,13	0
57	MG	YA	3256	1/1	0.36	-	3,3,3,3	0
57	MG	RA	3223	1/1	0.26	-	59,59,59,59	0
57	MG	XA	1636	1/1	0.17	-	24,24,24,24	0
57	MG	QA	1625	1/1	0.21	-	70,70,70,70	0
57	MG	YA	3168	1/1	0.20	-	0,0,0,0	0
57	MG	YA	3070	1/1	0.21	-	18,18,18,18	0
57	MG	YA	3216	1/1	0.26	-	30,30,30,30	0
57	MG	RA	3074	1/1	0.20	-	0,0,0,0	0
57	MG	XA	1606	1/1	0.27	-	12,12,12,12	0
57	MG	RA	3138	1/1	0.31	-	6,6,6,6	0
57	MG	RA	3203	1/1	0.12	-	47,47,47,47	0
57	MG	RA	3206	1/1	0.26	-	44,44,44,44	0
57	MG	RA	3133	1/1	0.27	-	6,6,6,6	0
57	MG	YA	3026	1/1	0.32	-	2,2,2,2	0
57	MG	RA	3105	1/1	0.27	-	6,6,6,6	0
57	MG	RA	3003	1/1	0.34	-	4,4,4,4	0
57	MG	XA	1662	1/1	0.27	-	40,40,40,40	0
57	MG	YA	3017	1/1	0.20	-	18,18,18,18	0
57	MG	YA	3034	1/1	0.26	-	13,13,13,13	0
57	MG	YA	3004	1/1	0.23	-	0,0,0,0	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3166	1/1	0.78	-	156,156,156,156	0
57	MG	RA	3054	1/1	0.11	-	2,2,2,2	0

6.5 Other polymers ⓘ

There are no such residues in this entry.