



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 02:35 PM EDT

PDB ID : 6NSH / pdb_00006nsh
Title : Modified ASL proline bound to Thermus thermophilus 70S (near-cognate)
Authors : Hoffer, E.D.; Maehigashi, T.; Subaramanian, S.; Hong, S.; Dunham, C.M.
Deposited on : 2019-01-24
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

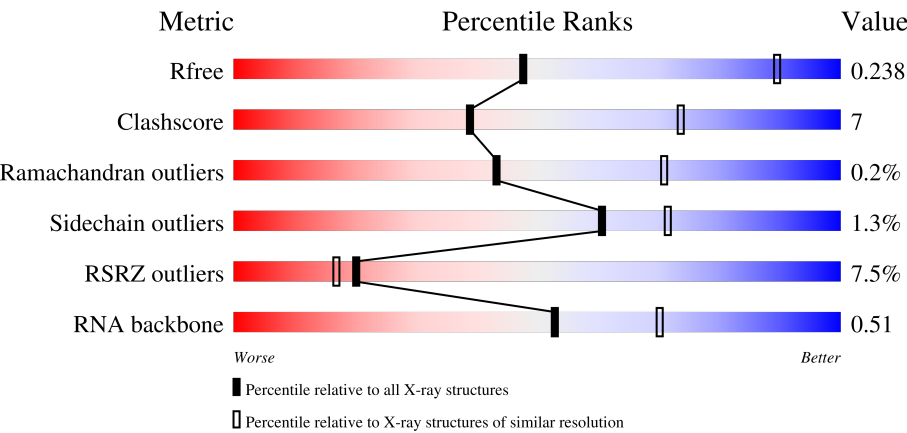
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	180053	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)
RNA backbone	3983	1157 (3.80-3.00)

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

Mol	Chain	Length	Quality of chain
1	RA	2915	3% 62% 30% 8%
1	YA	2915	3% 63% 29% 6%
2	RB	122	2% 64% 25% 10%
2	YB	122	% 67% 23% 8%

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Mol	Chain	Length	Quality of chain
3	RD	276	
3	YD	276	
4	RE	206	
4	YE	206	
5	RF	210	
5	YF	210	
6	RG	182	
6	YG	182	
7	RH	180	
7	YH	180	
8	RI	148	
8	YI	148	
9	RN	140	
9	YN	140	
10	RO	122	
10	YO	122	
11	RP	150	
11	YP	150	
12	RQ	141	
12	YQ	141	
13	RR	118	
13	YR	118	
14	RS	112	
14	YS	112	
15	RT	146	

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Mol	Chain	Length	Quality of chain
15	YT	146	
16	RU	118	
16	YU	118	
17	RV	101	
17	YV	101	
18	RW	113	
18	YW	113	
19	RX	96	
19	YX	96	
20	RY	110	
20	YY	110	
21	RZ	206	
21	YZ	206	
22	R0	85	
22	Y0	85	
23	R1	98	
23	Y1	98	
24	R2	72	
24	Y2	72	
25	R3	60	
25	Y3	60	
26	R4	71	
26	Y4	71	
27	R5	60	
27	Y5	60	

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Mol	Chain	Length	Quality of chain
28	R6	54	
28	Y6	54	
29	R7	49	
29	Y7	49	
30	R8	65	
30	Y8	65	
31	R9	37	
31	Y9	37	
32	QA	1521	
32	XA	1521	
33	QB	256	
33	XB	256	
34	QC	239	
34	XC	239	
35	QD	209	
35	XD	209	
36	QE	162	
36	XE	162	
37	QF	101	
37	XF	101	
38	QG	156	
38	XG	156	
39	QH	138	
39	XH	138	
40	QI	128	

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Mol	Chain	Length	Quality of chain
40	XI	128	
41	QJ	105	
41	XJ	105	
42	QK	129	
42	XK	129	
43	QL	132	
43	XL	132	
44	QM	126	
44	XM	126	
45	QN	61	
45	XN	61	
46	QO	89	
46	XO	89	
47	QP	88	
47	XP	88	
48	QQ	105	
48	XQ	105	
49	QR	88	
49	XR	88	
50	QS	93	
50	XS	93	
51	QT	106	
51	XT	106	
52	QU	27	
52	XU	27	

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Mol	Chain	Length	Quality of chain
53	QV	17	
53	XV	17	
54	QX	19	
54	XX	19	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
55	MG	RA	3246	-	-	-	X
55	MG	RF	301	-	-	-	X
55	MG	YA	3193	-	-	-	X
55	MG	YA	3393	-	-	-	X
57	SF4	XD	301	-	-	X	-

2 Entry composition [i](#)

There are 57 unique types of molecules in this entry. The entry contains 290035 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	RA	2881	Total	C	N	O	P	0	0	0
			62051	27618	11609	19944	2880			
1	YA	2883	Total	C	N	O	P	0	0	0
			62091	27636	11613	19960	2882			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	RD	272	Total	C	N	O	S	0	0	0
			2115	1335	420	357	3			
3	YD	273	Total	C	N	O	S	0	0	0
			2126	1341	424	358	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	RE	204	Total	C	N	O	S	0	0	0
			1563	988	299	270	6			
4	YE	205	Total	C	N	O	S	0	0	0
			1568	991	300	271	6			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	RH	174	Total	C	N	O	S	0	0	0
			1336	848	251	236	1			
7	YH	174	Total	C	N	O	S	0	0	0
			1336	848	251	236	1			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	RN	138	Total	C	N	O	S	0	0	0
			1104	712	206	182	4			
9	YN	140	Total	C	N	O	S	0	0	0
			1121	722	208	187	4			

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	RP	148	Total	C	N	O	S	0	0	0
			1130	704	230	193	3			
11	YP	147	Total	C	N	O	S	0	0	0
			1122	698	229	192	3			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	RR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			
13	YR	117	Total	C	N	O		0	0	0
			960	599	202	159				

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	RS	111	Total	C	N	O	0	0	0
			882	556	176	150			
14	YS	110	Total	C	N	O	0	0	0
			877	553	175	149			

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	RX	92	Total	C	N	O	S	0	0	0
			725	471	131	123				
19	YX	94	Total	C	N	O	S	0	0	0
			742	482	134	125	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	RY	107	Total	C	N	O	S	0	0	0
			818	525	155	132	6			
20	YY	107	Total	C	N	O	S	0	0	0
			818	525	155	132	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	RZ	203	Total	C	N	O	S	0	0	0
			1601	1020	283	295	3			
21	YZ	201	Total	C	N	O	S	0	0	0
			1587	1012	281	291	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	R0	76	Total	C	N	O	S	0	0	0
			603	372	128	102	1			
22	Y0	75	Total	C	N	O	S	0	0	0
			599	370	127	101	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	R1	97	Total	C	N	O	S	0	0	0
			763	481	150	131	1			
23	Y1	93	Total	C	N	O	S	0	0	0
			729	457	145	126	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	R2	69	Total	C	N	O	S	0	0	0
			581	358	118	104	1			
24	Y2	72	Total	C	N	O	S	0	0	0
			606	375	122	107	2			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	R4	69	Total	C	N	O	S	0	0	0
			565	356	103	101	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	Y4	69	Total	C	N	O	S	0	0	0
			565	356	103	101	5			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	R7	47	Total	C	N	O	S	0	0	0
			409	251	102	54	2			
29	Y7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	R9	36	Total	C	N	O	S	0	0	0
			302	186	67	45	4			
31	Y9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	QA	1511	Total	C	N	O	P	0	0	0
			32469	14453	6011	10495	1510			
32	XA	1511	Total	C	N	O	P	0	0	0
			32471	14454	6014	10493	1510			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	QB	235	Total	C	N	O	S	0	0	0
			1907	1217	342	343	5			
33	XB	236	Total	C	N	O	S	0	0	0
			1915	1223	343	344	5			

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	QH	137	Total	C	N	O	S	0	0	0
			1108	700	214	192	2			
39	XH	137	Total	C	N	O	S	0	0	0
			1108	700	214	192	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
40	QI	127	Total	C	N	O	0	0	0
			1010	639	197	174			
40	XI	126	Total	C	N	O	0	0	0
			998	633	193	172			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	QJ	99	Total	C	N	O	S	0	0	0
			801	504	157	139	1			
41	XJ	96	Total	C	N	O	S	0	0	0
			777	487	153	136	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	QK	116	Total	C	N	O	S	0	0	0
			864	537	164	160	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	XK	116	Total	C	N	O	S	0	0	0
			864	537	164	160	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	QL	125	Total	C	N	O	S	0	0	0
			975	614	196	164	1			
43	XL	122	Total	C	N	O	S	0	0	0
			956	603	193	159	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	QM	120	Total	C	N	O	S	0	0	0
			955	591	197	165	2			
44	XM	119	Total	C	N	O	S	0	0	0
			946	585	195	164	2			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	QO	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			
46	XO	87	Total	C	N	O	S	0	0	0
			729	457	146	124	2			

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	QS	83	Total	C	N	O	S	0	0	0
			665	424	124	115	2			
50	XS	84	Total	C	N	O	S	0	0	0
			674	430	126	116	2			

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

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

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

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

- Molecule 53 is a RNA chain called P-site ASLPro.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	QV	17	Total	C	N	O	P	0	0	0
			365	163	65	120	17			
53	XV	15	Total	C	N	O	P	0	0	0
			322	144	57	106	15			

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	QX	18	Total	C	N	O	P	0	0	0
			389	174	76	121	18			
54	XX	19	Total	C	N	O	P	0	0	0
			412	184	81	128	19			

- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
55	RA	485	Total	Mg	0	0
			485	485		
55	RB	8	Total	Mg	0	0
			8	8		
55	RE	2	Total	Mg	0	0
			2	2		
55	RF	1	Total	Mg	0	0
			1	1		
55	RN	1	Total	Mg	0	0
			1	1		
55	RO	1	Total	Mg	0	0
			1	1		
55	RP	2	Total	Mg	0	0
			2	2		
55	RQ	2	Total	Mg	0	0
			2	2		
55	RT	1	Total	Mg	0	0
			1	1		
55	RX	1	Total	Mg	0	0
			1	1		
55	R0	1	Total	Mg	0	0
			1	1		
55	R1	1	Total	Mg	0	0
			1	1		
55	R5	1	Total	Mg	0	0
			1	1		
55	R8	1	Total	Mg	0	0
			1	1		

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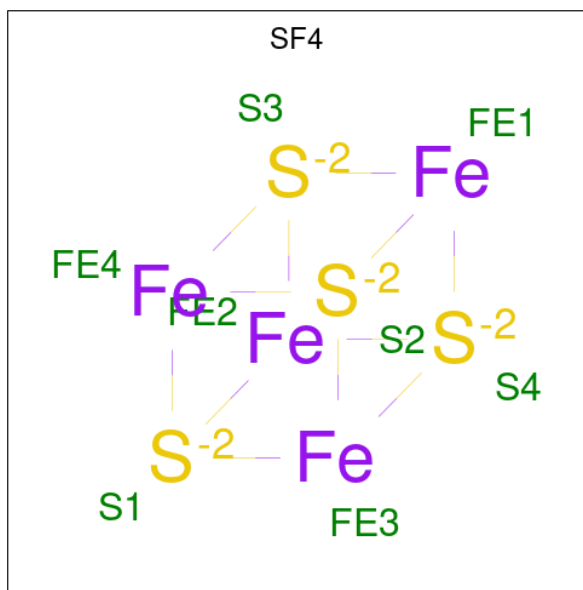
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
55	QA	66	Total 66	Mg 66	0	0
55	QF	1	Total 1	Mg 1	0	0
55	YA	510	Total 510	Mg 510	0	0
55	YB	7	Total 7	Mg 7	0	0
55	YD	1	Total 1	Mg 1	0	0
55	YE	4	Total 4	Mg 4	0	0
55	YO	1	Total 1	Mg 1	0	0
55	YP	2	Total 2	Mg 2	0	0
55	YQ	1	Total 1	Mg 1	0	0
55	YR	1	Total 1	Mg 1	0	0
55	Y0	2	Total 2	Mg 2	0	0
55	Y1	1	Total 1	Mg 1	0	0
55	Y5	1	Total 1	Mg 1	0	0
55	Y7	1	Total 1	Mg 1	0	0
55	Y8	1	Total 1	Mg 1	0	0
55	XA	87	Total 87	Mg 87	0	0
55	XE	1	Total 1	Mg 1	0	0
55	XL	1	Total 1	Mg 1	0	0
55	XQ	1	Total 1	Mg 1	0	0
55	XS	1	Total 1	Mg 1	0	0

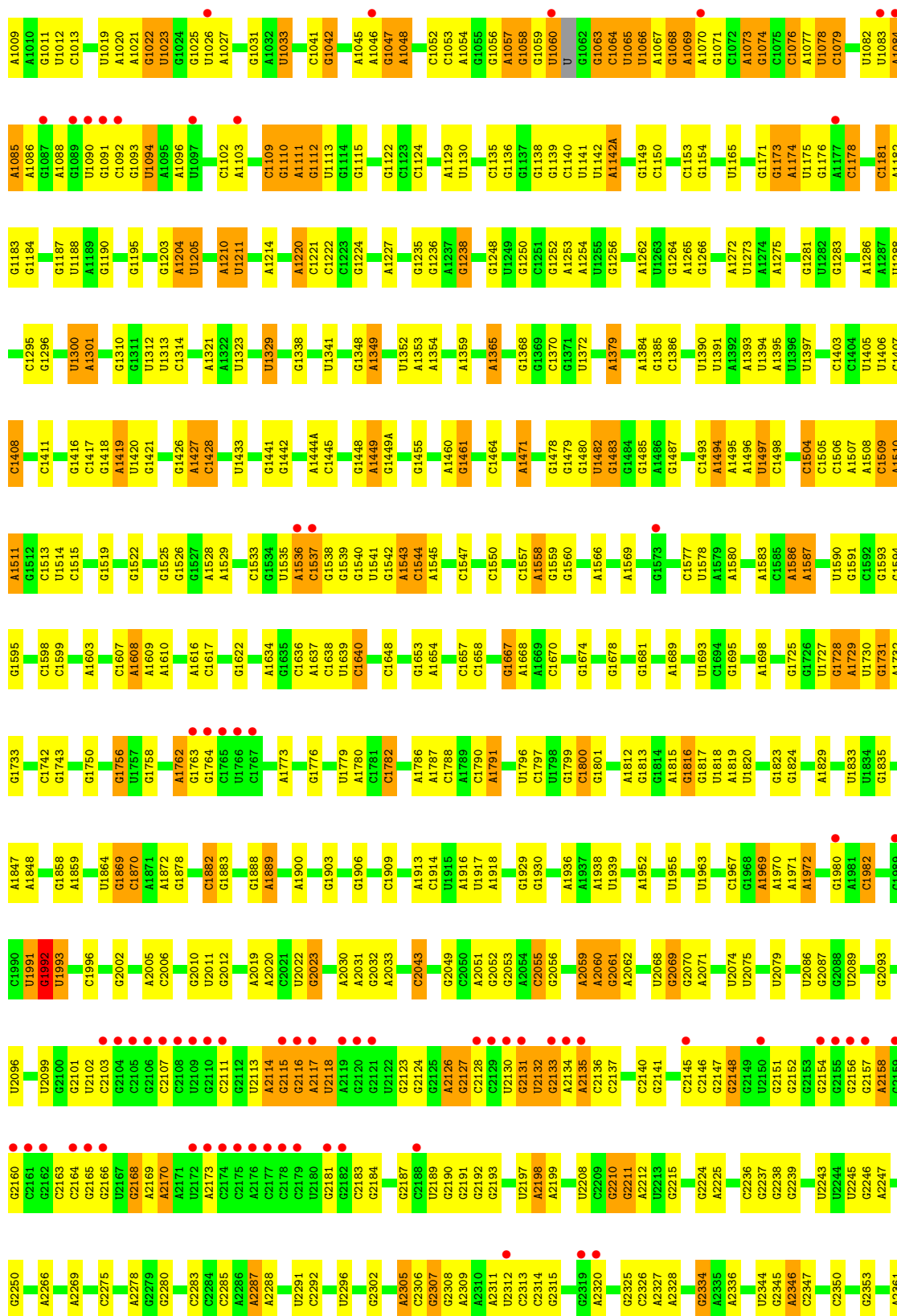
- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

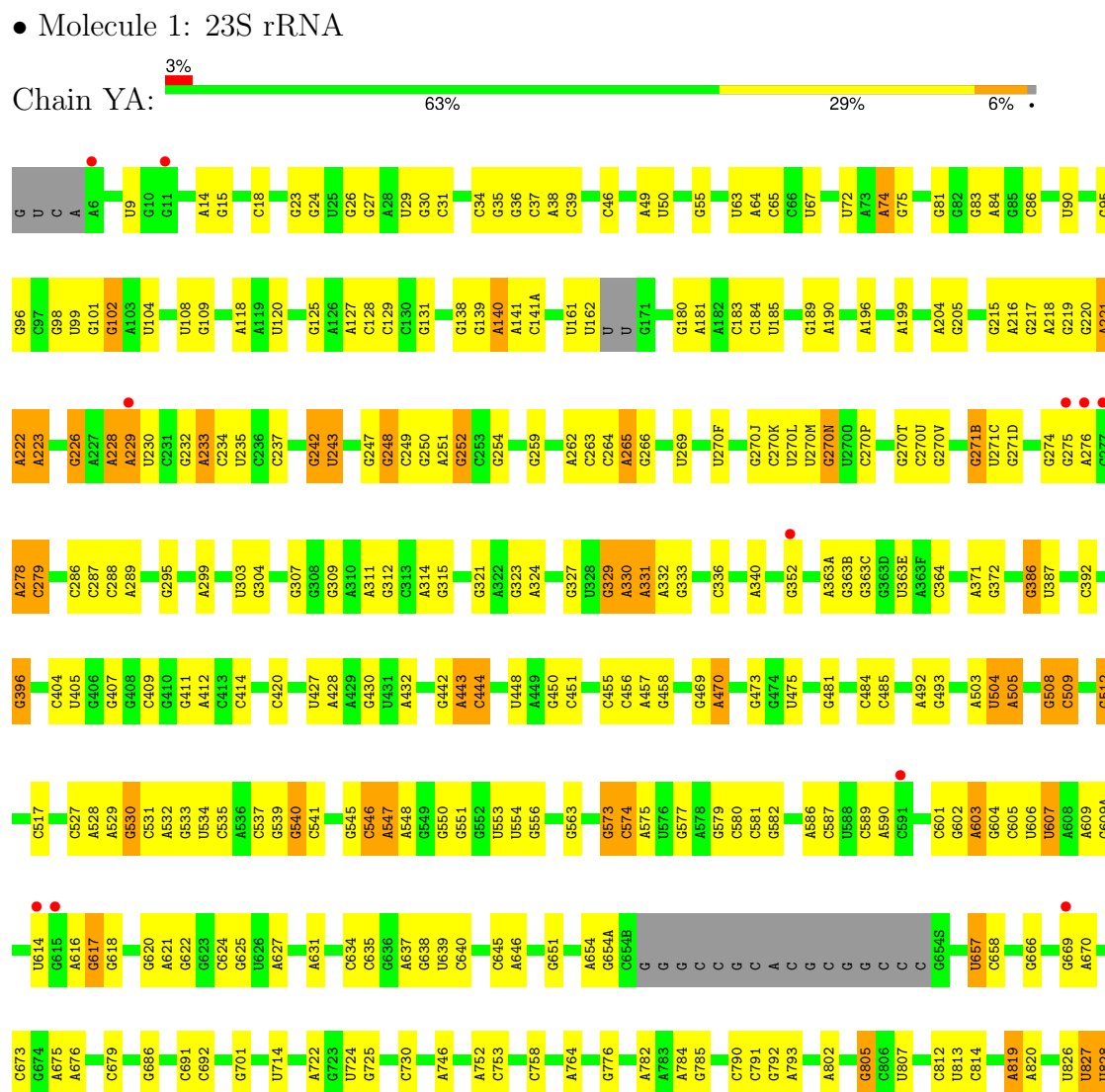
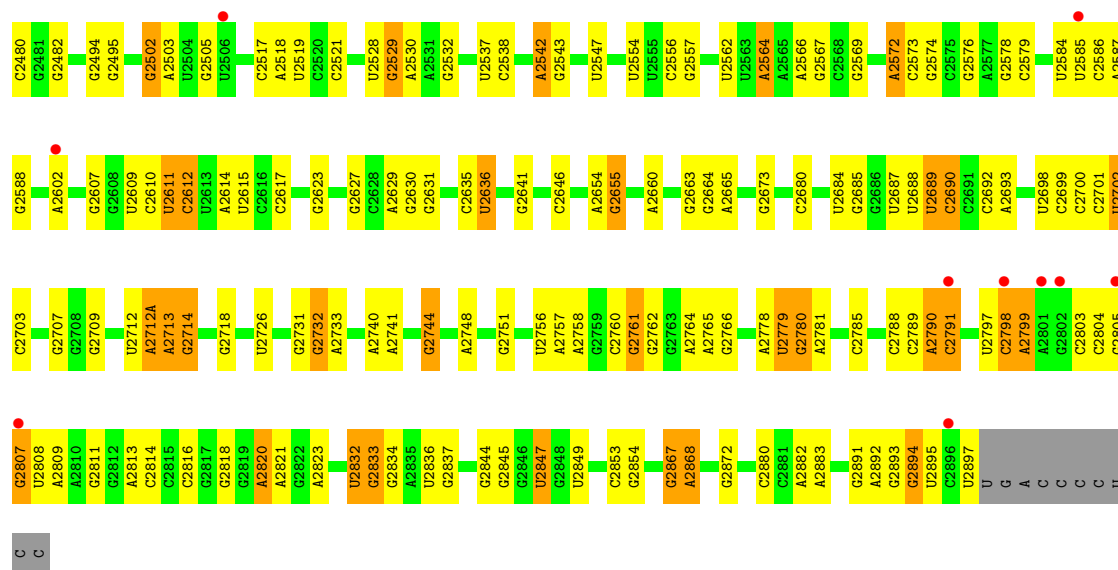
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	RY	1	Total Zn 1 1	0	0
56	R4	1	Total Zn 1 1	0	0
56	R5	1	Total Zn 1 1	0	0
56	R6	1	Total Zn 1 1	0	0
56	R9	1	Total Zn 1 1	0	0
56	QN	1	Total Zn 1 1	0	0
56	YY	1	Total Zn 1 1	0	0
56	Y4	1	Total Zn 1 1	0	0
56	Y5	1	Total Zn 1 1	0	0
56	Y6	1	Total Zn 1 1	0	0
56	Y9	1	Total Zn 1 1	0	0
56	XN	1	Total Zn 1 1	0	0

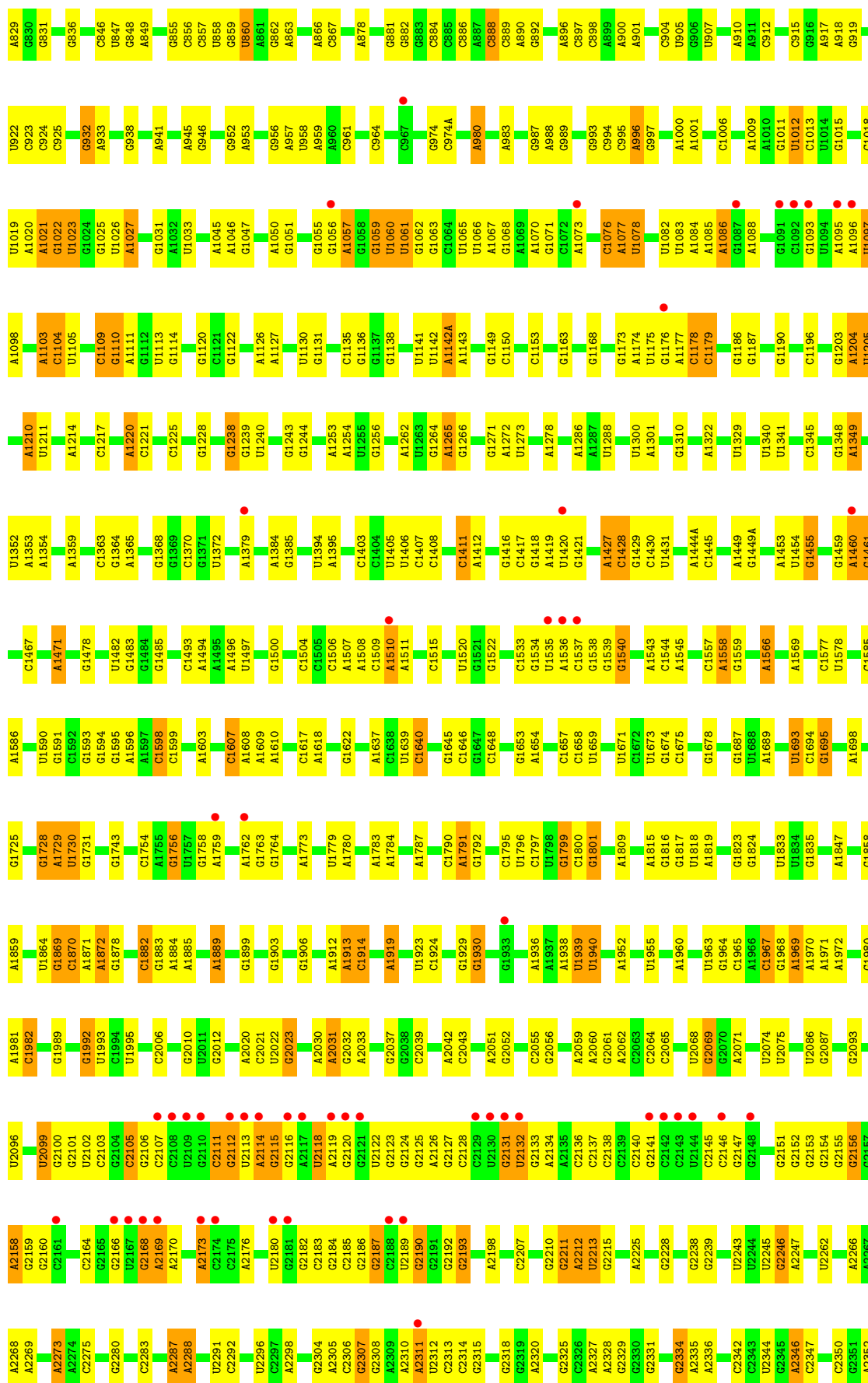
- Molecule 57 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).

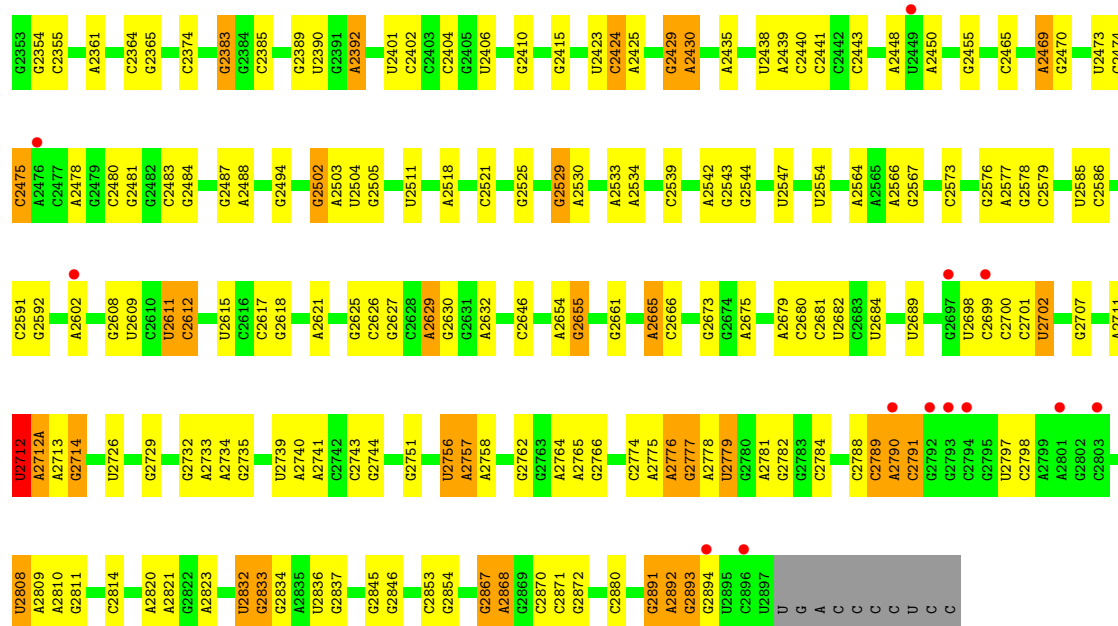


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
57	QD	1	Total 8	Fe 4	S 4	0	0
57	XD	1	Total 8	Fe 4	S 4	0	0

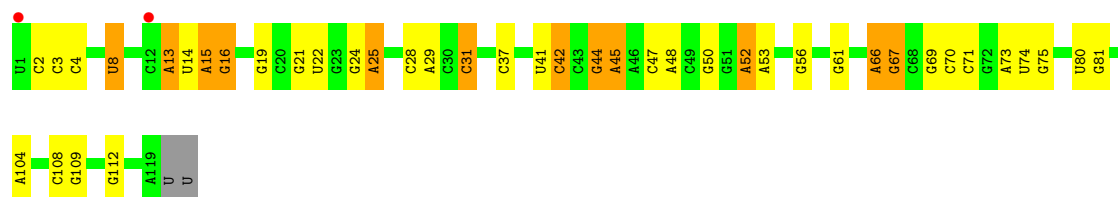




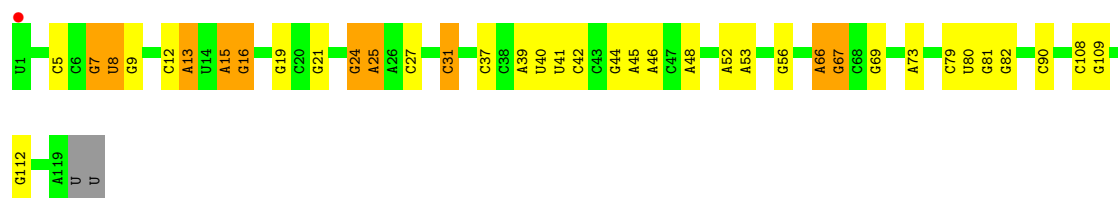




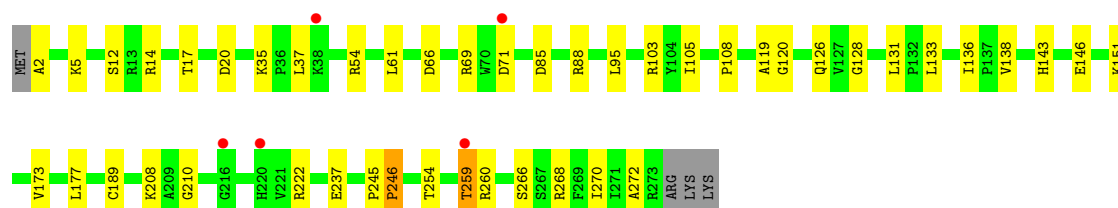
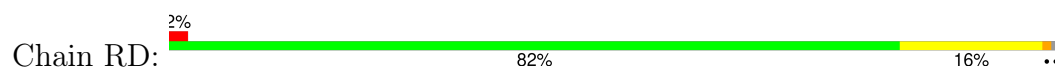
• Molecule 2: 5S rRNA



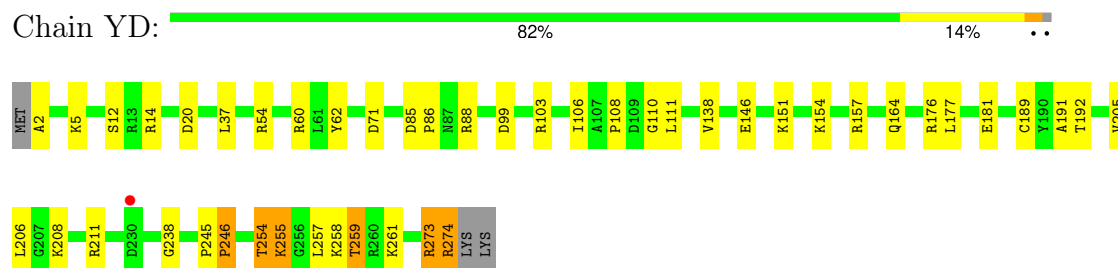
• Molecule 2: 5S rRNA



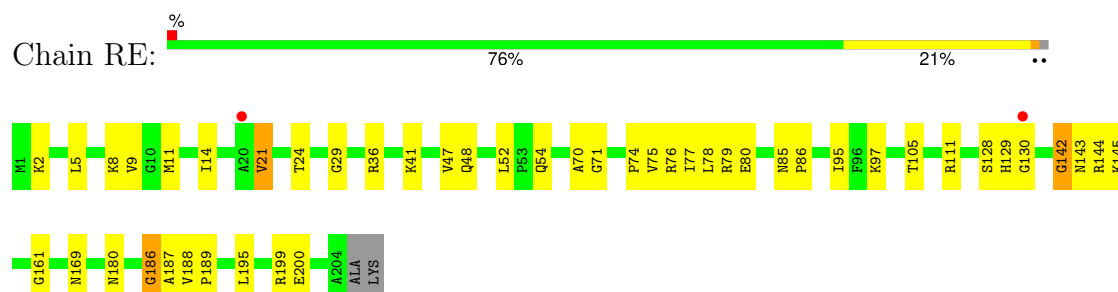
• Molecule 3: 50S ribosomal protein L2



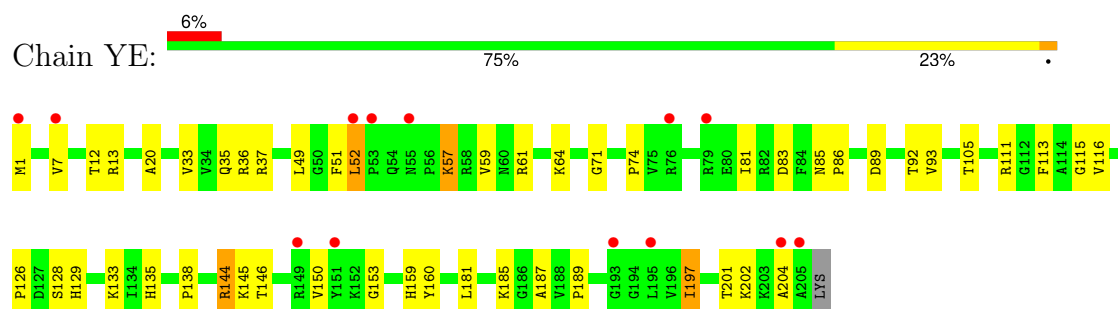
- Molecule 3: 50S ribosomal protein L2



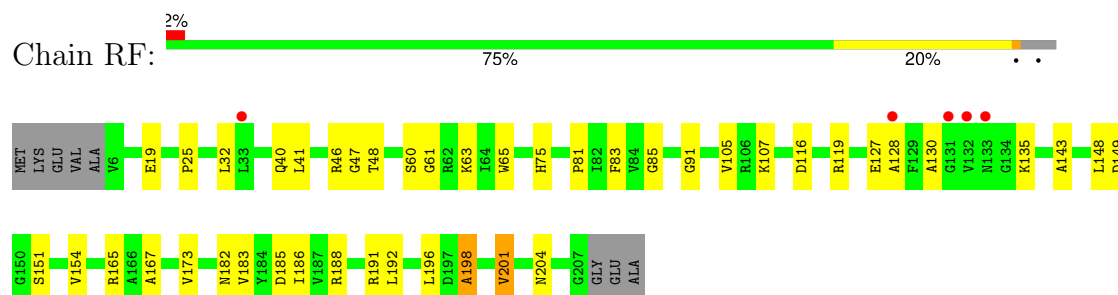
- Molecule 4: 50S ribosomal protein L3



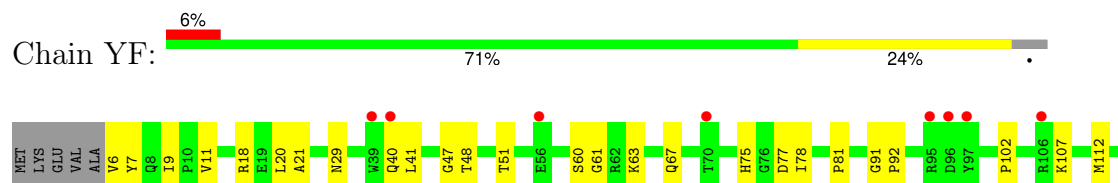
- Molecule 4: 50S ribosomal protein L3



- Molecule 5: 50S ribosomal protein L4

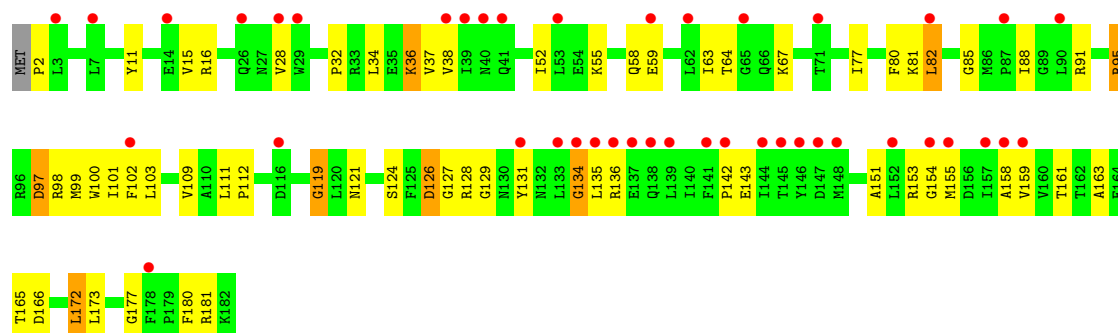


- Molecule 5: 50S ribosomal protein L4

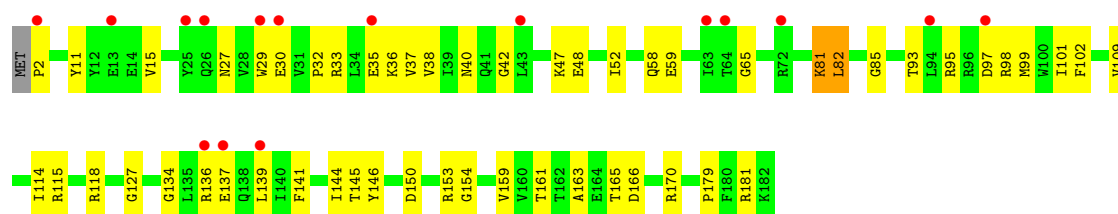




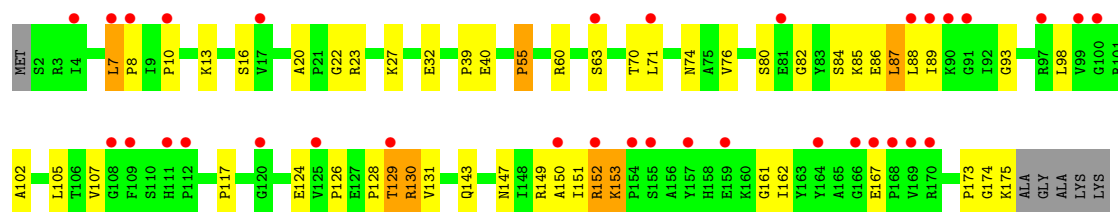
• Molecule 6: 50S ribosomal protein L5



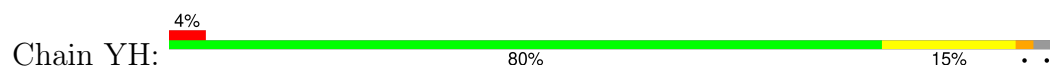
• Molecule 6: 50S ribosomal protein L5



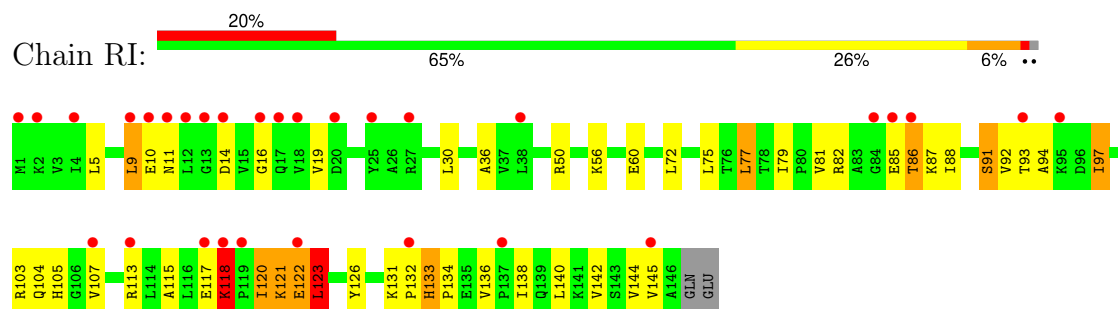
• Molecule 7: 50S ribosomal protein L6



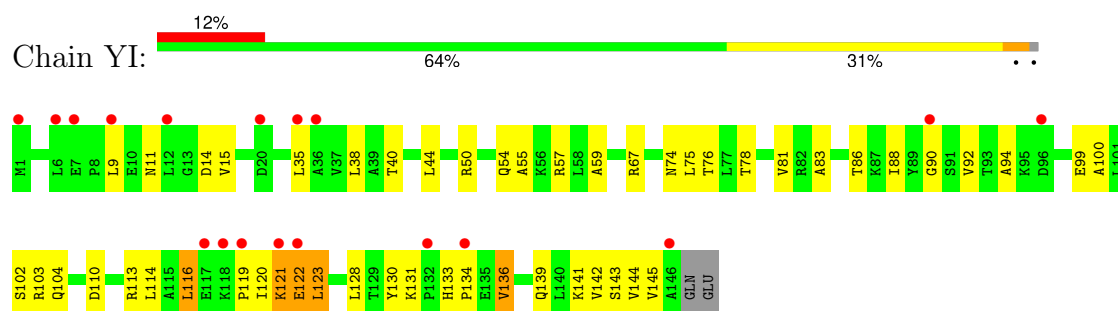
• Molecule 7: 50S ribosomal protein L6



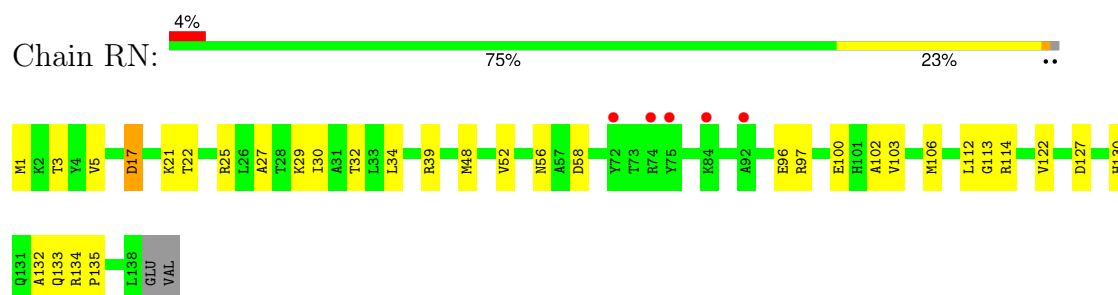
- Molecule 8: 50S ribosomal protein L9



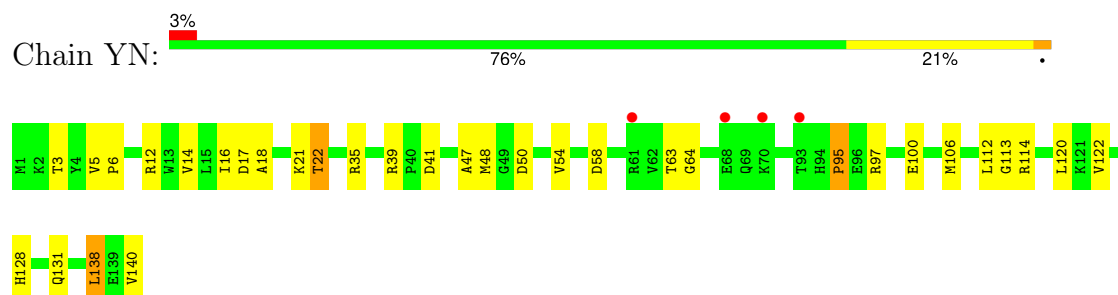
- Molecule 8: 50S ribosomal protein L9



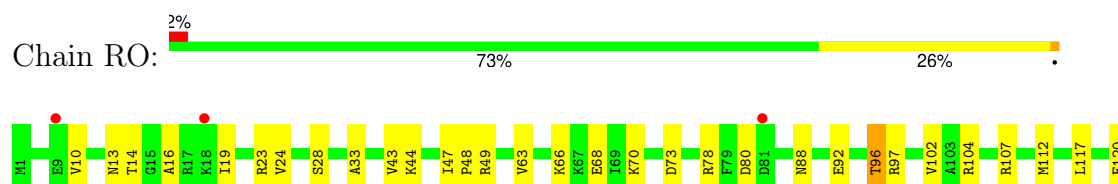
- Molecule 9: 50S ribosomal protein L13



- Molecule 9: 50S ribosomal protein L13

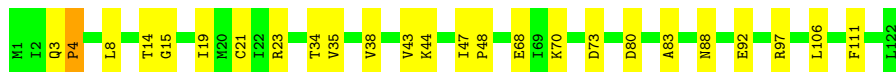


- Molecule 10: 50S ribosomal protein L14



V121
L122

- Molecule 10: 50S ribosomal protein L14

Chain YO:  80% 20% .


- Molecule 11: 50S ribosomal protein L15

Chain RP:  9% 64% 32% . .



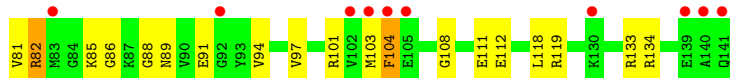
- Molecule 11: 50S ribosomal protein L15

Chain YP:  3% 71% 25% . .

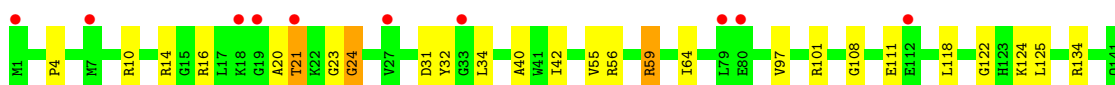


- Molecule 12: 50S ribosomal protein L16

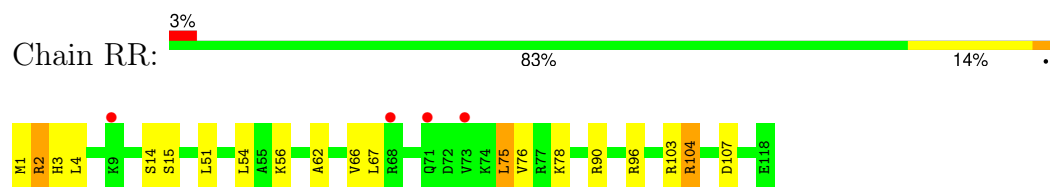
Chain RQ:  15% 62% 33% 5%



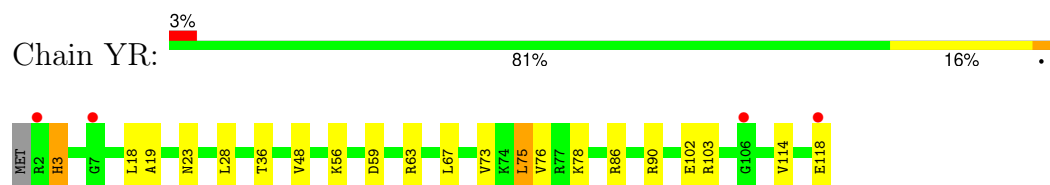
- Molecule 12: 50S ribosomal protein L16

Chain YQ:  7% 82% 16% .


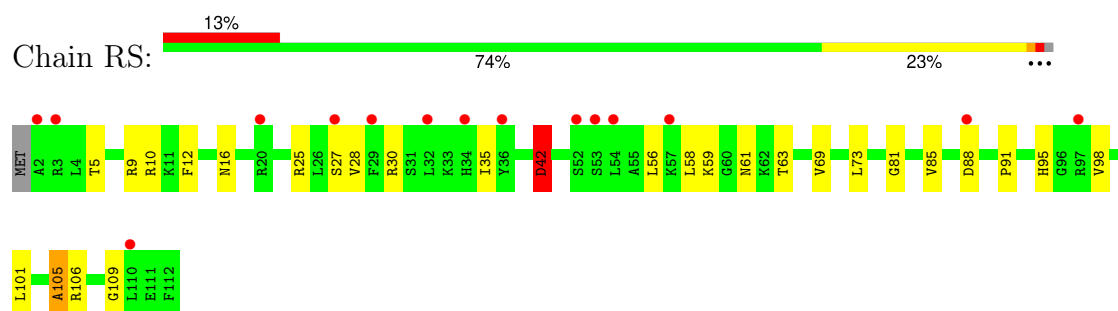
- Molecule 13: 50S ribosomal protein L17



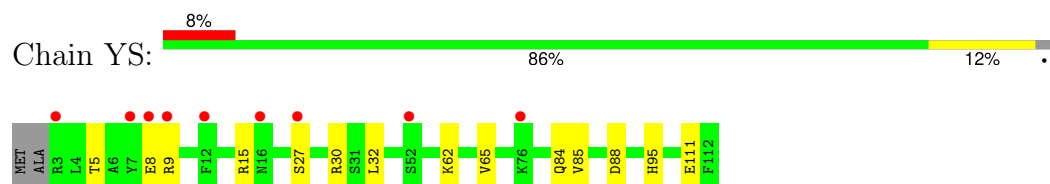
- Molecule 13: 50S ribosomal protein L17



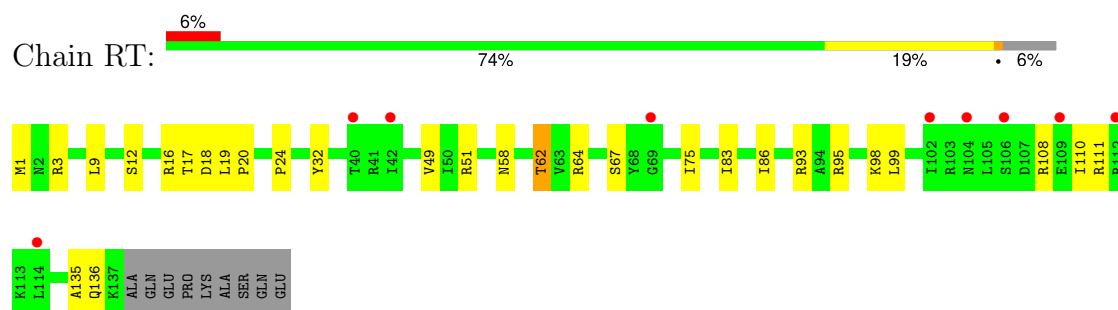
- Molecule 14: 50S ribosomal protein L18



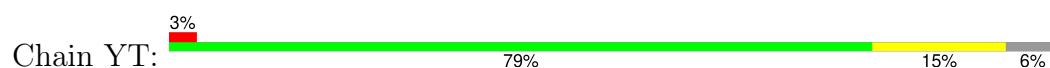
- Molecule 14: 50S ribosomal protein L18



- Molecule 15: 50S ribosomal protein L19

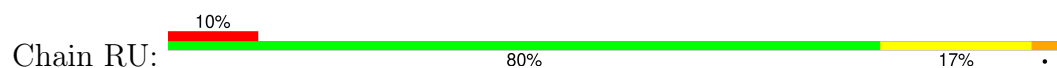


- Molecule 15: 50S ribosomal protein L19

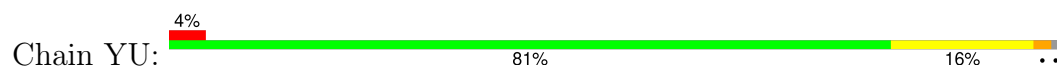




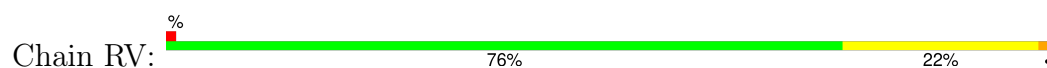
- Molecule 16: 50S ribosomal protein L20



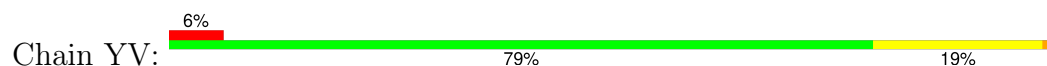
- Molecule 16: 50S ribosomal protein L20



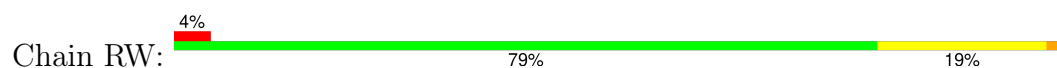
- Molecule 17: 50S ribosomal protein L21



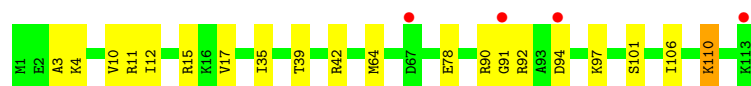
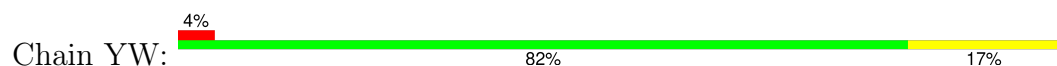
- Molecule 17: 50S ribosomal protein L21



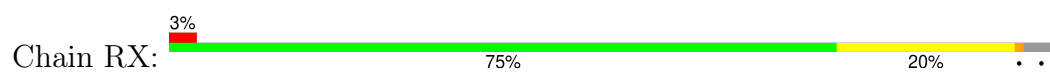
- Molecule 18: 50S ribosomal protein L22



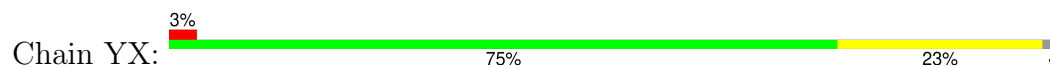
- Molecule 18: 50S ribosomal protein L22



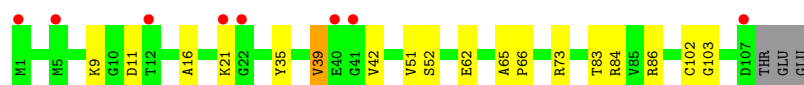
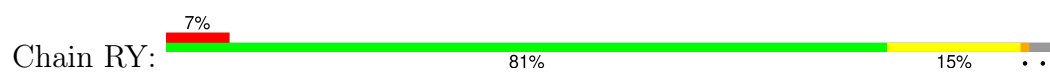
- Molecule 19: 50S ribosomal protein L23



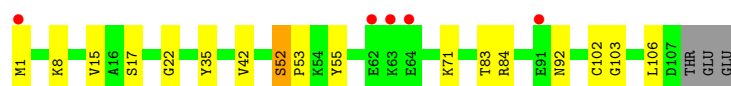
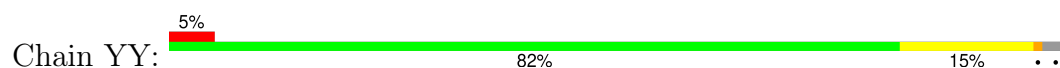
- Molecule 19: 50S ribosomal protein L23



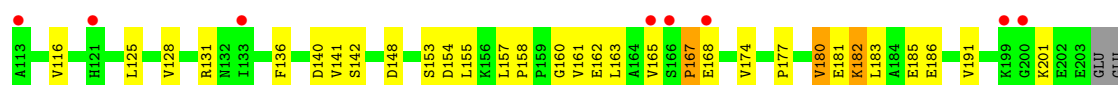
- Molecule 20: 50S ribosomal protein L24



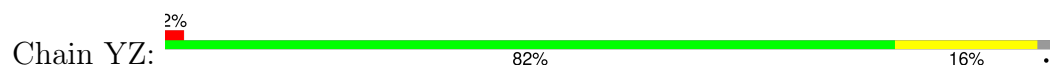
- Molecule 20: 50S ribosomal protein L24

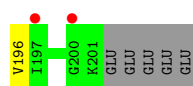


- Molecule 21: 50S ribosomal protein L25

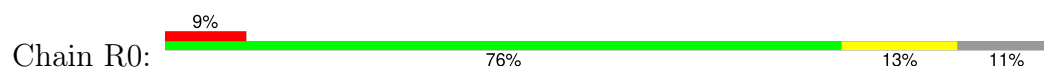


- Molecule 21: 50S ribosomal protein L25

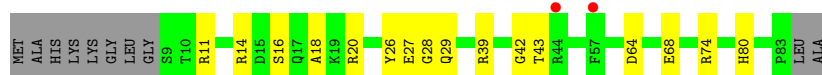




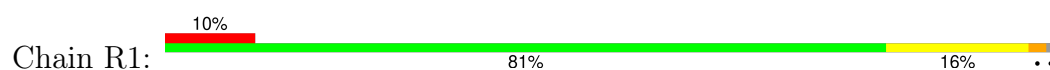
- Molecule 22: 50S ribosomal protein L27



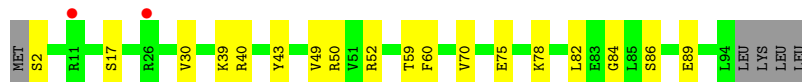
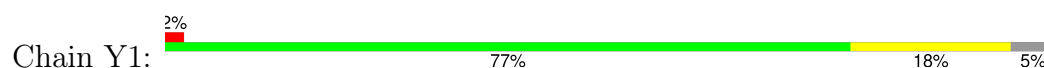
- Molecule 22: 50S ribosomal protein L27



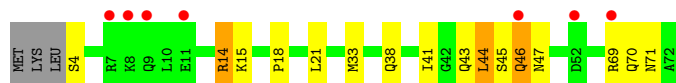
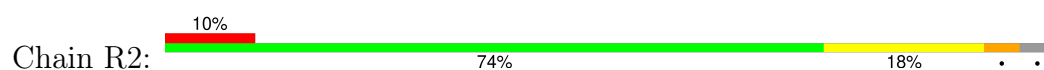
- Molecule 23: 50S ribosomal protein L28



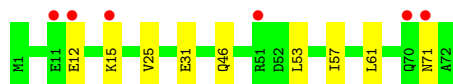
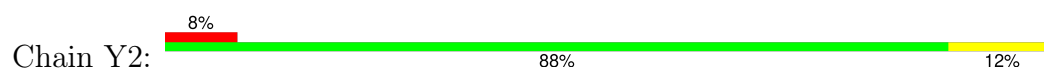
- Molecule 23: 50S ribosomal protein L28



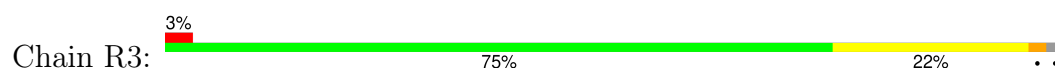
- Molecule 24: 50S ribosomal protein L29



- Molecule 24: 50S ribosomal protein L29



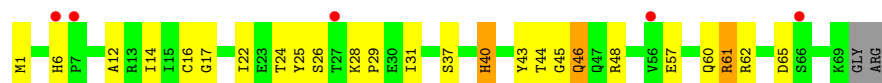
- Molecule 25: 50S ribosomal protein L30



- Molecule 25: 50S ribosomal protein L30



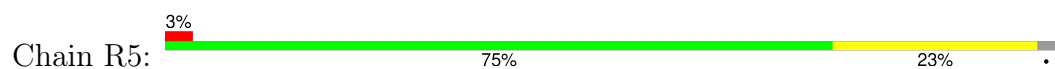
- Molecule 26: 50S ribosomal protein L31



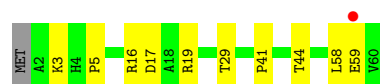
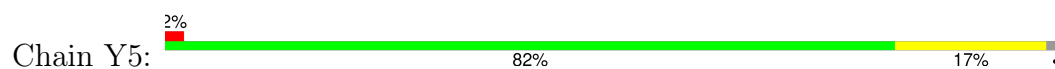
- Molecule 26: 50S ribosomal protein L31



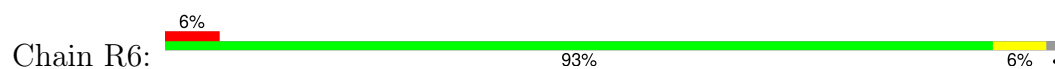
- Molecule 27: 50S ribosomal protein L32



- Molecule 27: 50S ribosomal protein L32



- Molecule 28: 50S ribosomal protein L33



- Molecule 28: 50S ribosomal protein L33

Chain Y6:  87% 11%



- Molecule 29: 50S ribosomal protein L34

Chain R7:  4% 80% 14%



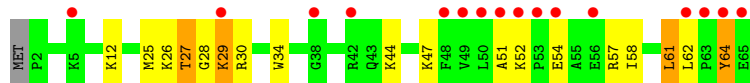
- Molecule 29: 50S ribosomal protein L34

Chain Y7:  2% 82% 16%



- Molecule 30: 50S ribosomal protein L35

Chain R8:  25% 71% 22% 6%



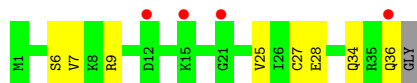
- Molecule 30: 50S ribosomal protein L35

Chain Y8:  5% 69% 25% 5%



- Molecule 31: 50S ribosomal protein L36

Chain R9:  11% 76% 22%

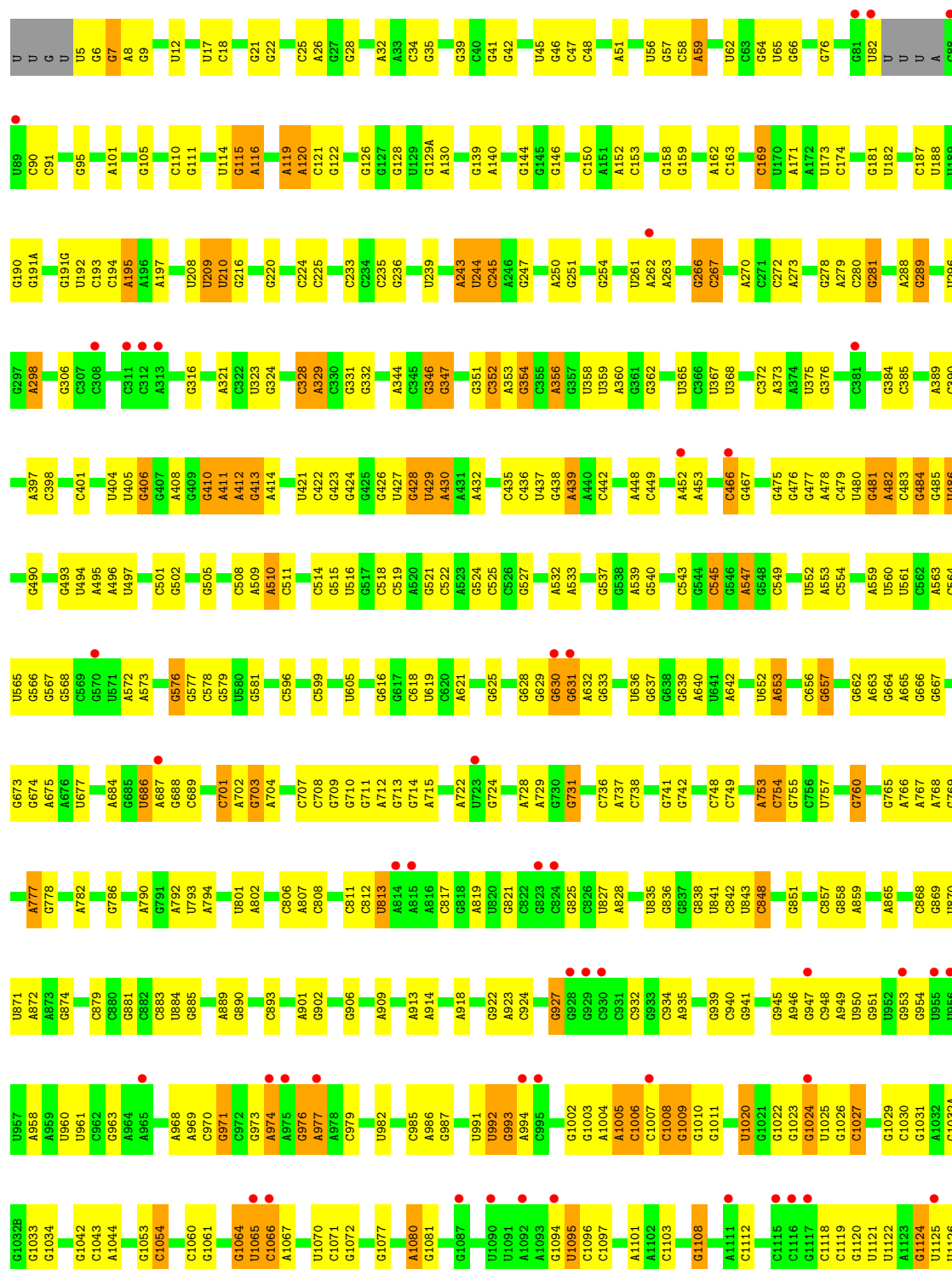


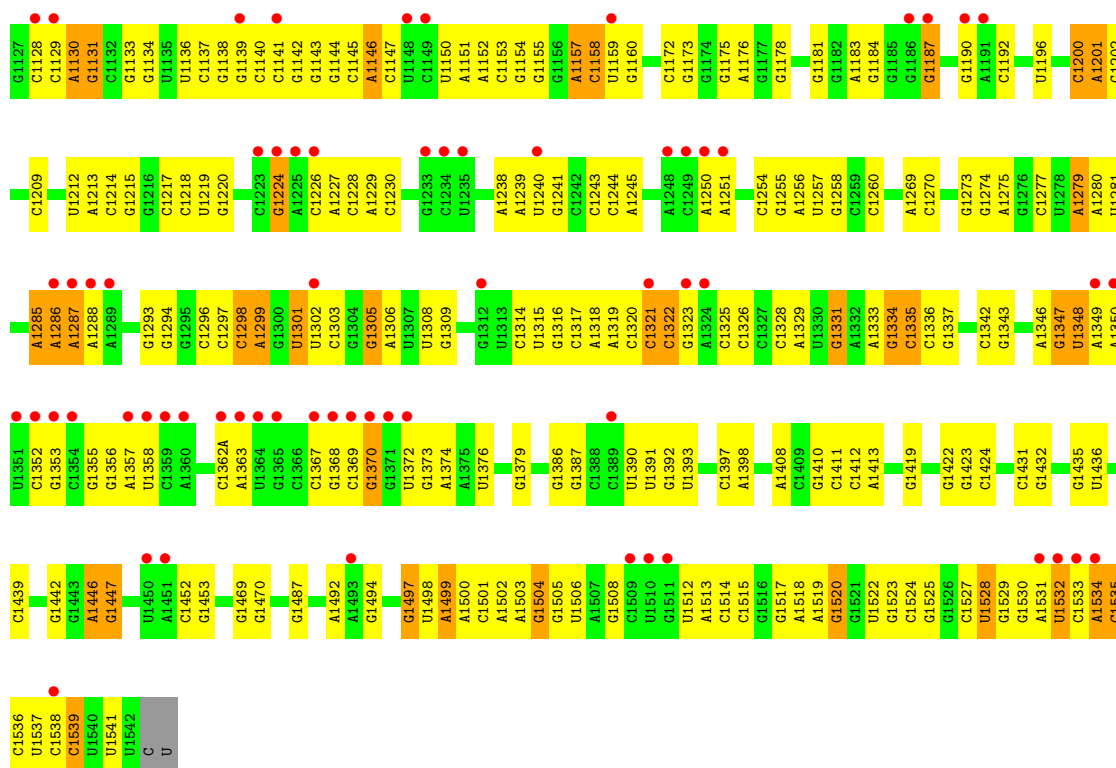
- Molecule 31: 50S ribosomal protein L36

Chain Y9:  8% 68% 32%

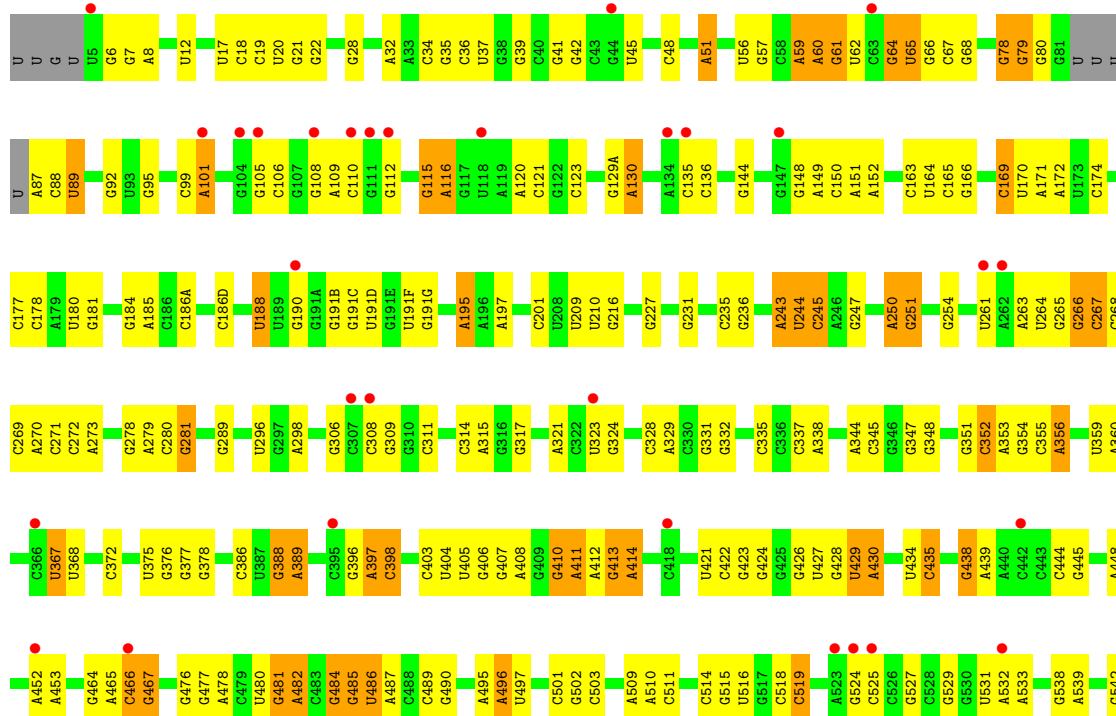


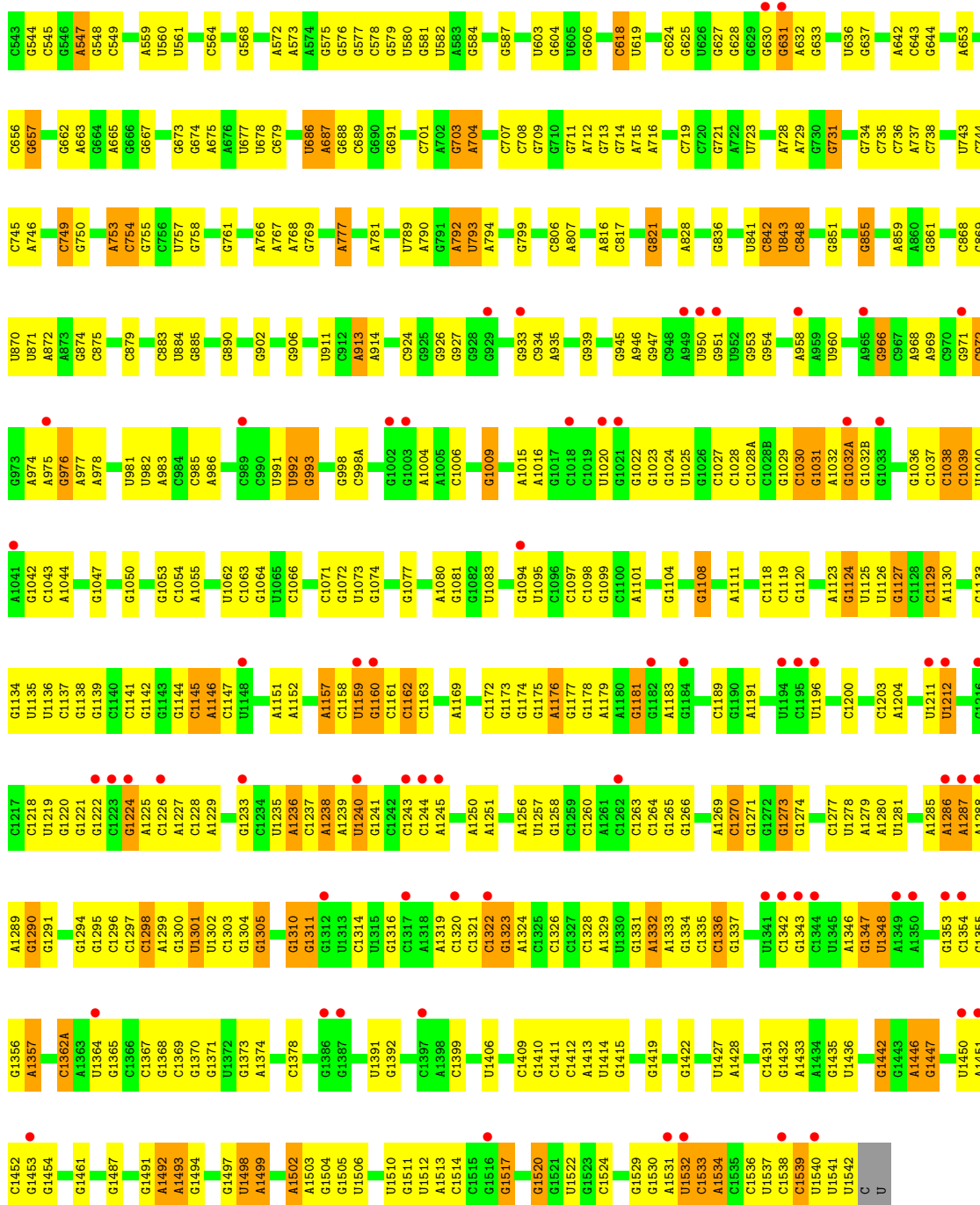
• Molecule 32: 16S rRNA



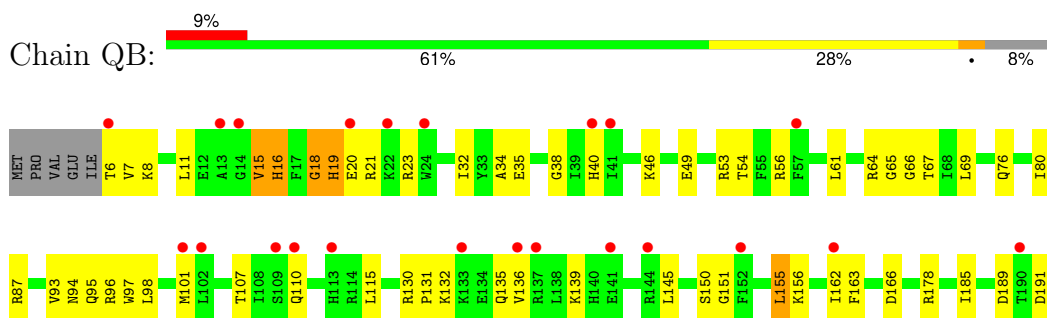


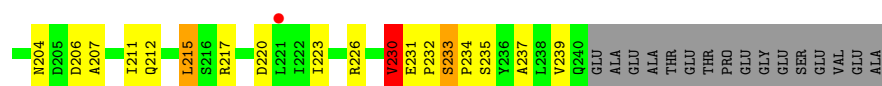
- Molecule 32: 16S rRNA



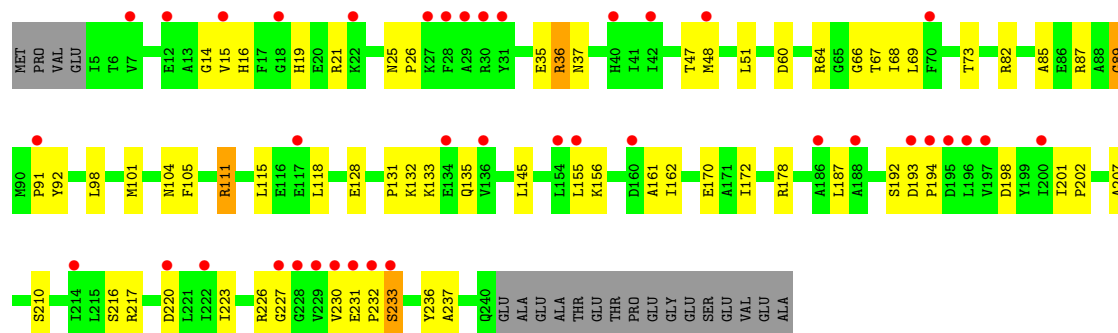


• Molecule 33: 30S ribosomal protein S2

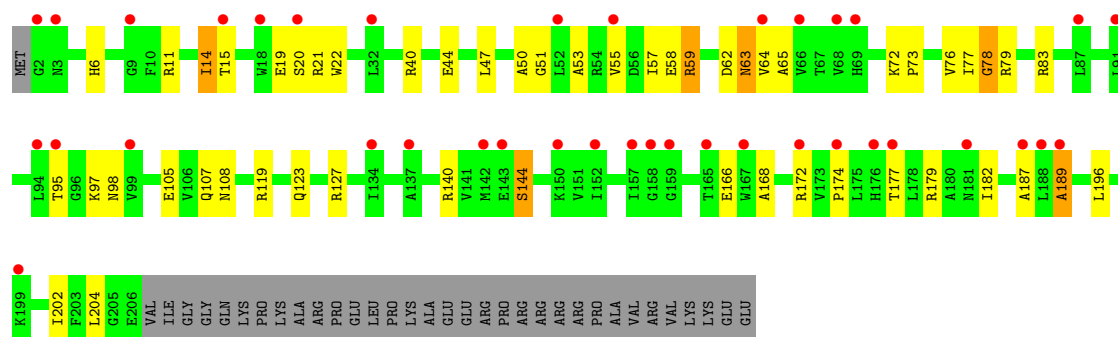




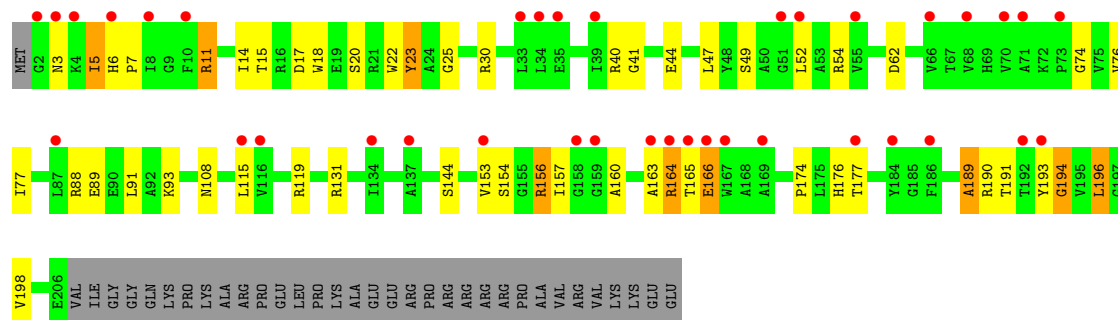
• Molecule 33: 30S ribosomal protein S2



• Molecule 34: 30S ribosomal protein S3

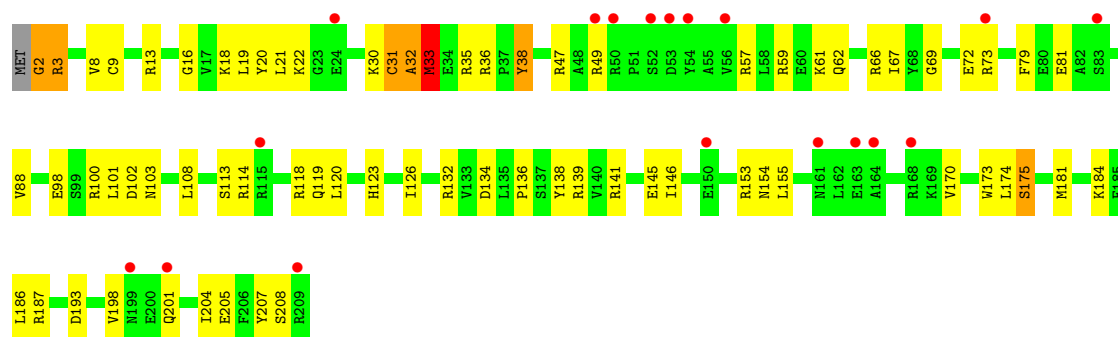


• Molecule 34: 30S ribosomal protein S3



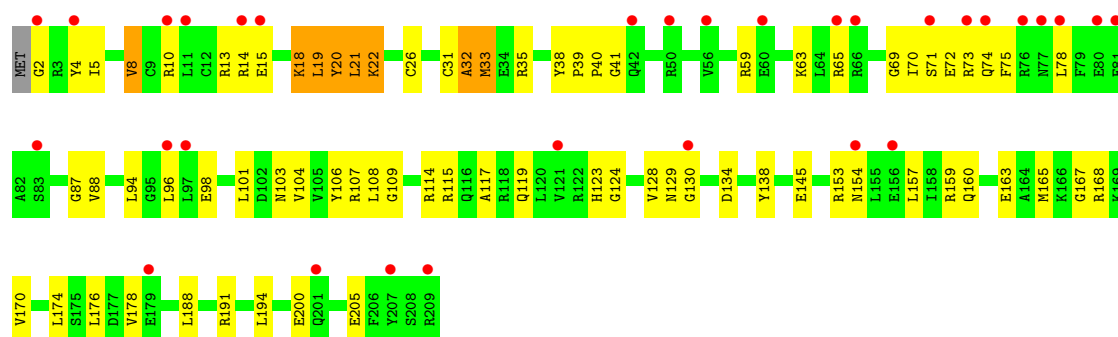
• Molecule 35: 30S ribosomal protein S4





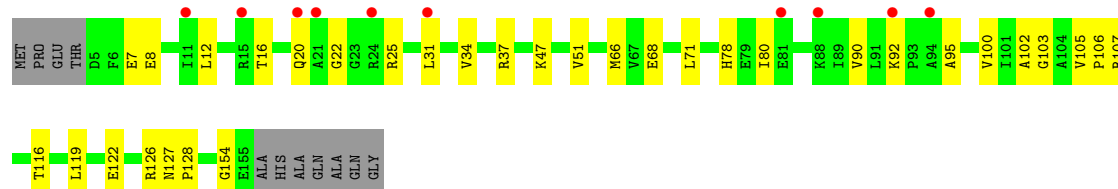
- Molecule 35: 30S ribosomal protein S4

Chain XD: 15% 64% 32%



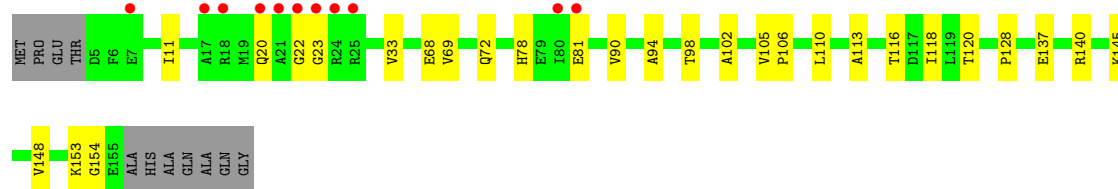
- Molecule 36: 30S ribosomal protein S5

Chain QE: 6% 73% 20% 7%



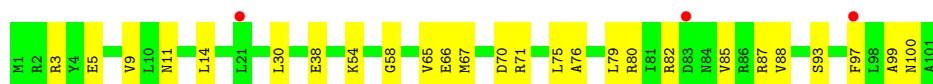
- Molecule 36: 30S ribosomal protein S5

Chain XE: 7% 76% 17% 7%

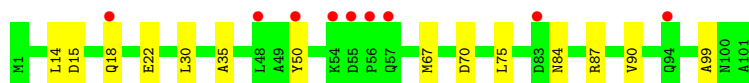
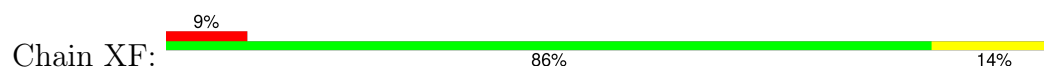


- Molecule 37: 30S ribosomal protein S6

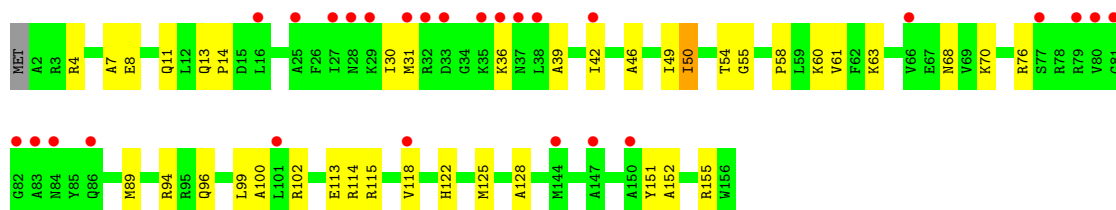
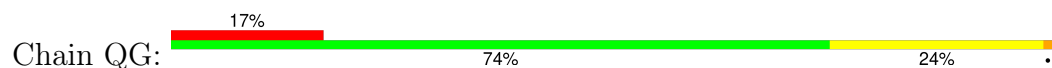
Chain QF: 3% 74% 26%



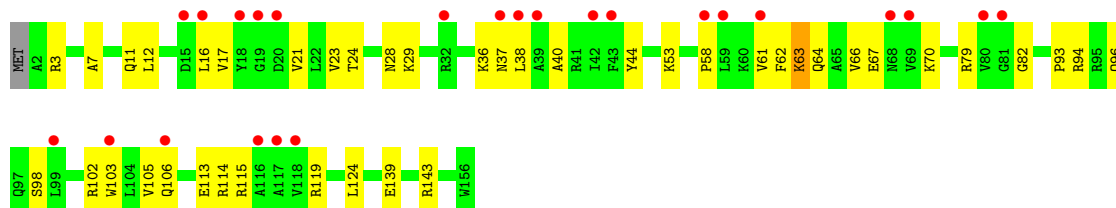
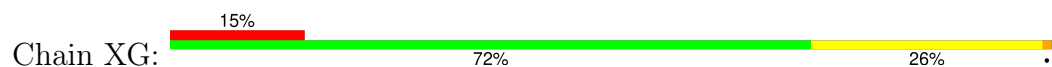
- Molecule 37: 30S ribosomal protein S6



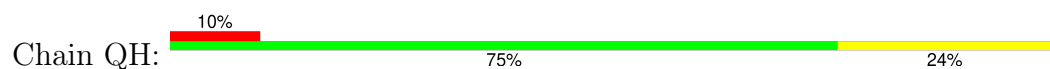
- Molecule 38: 30S ribosomal protein S7



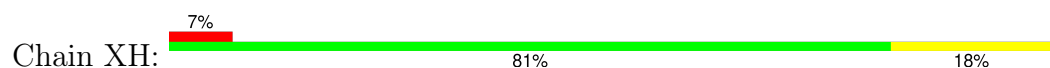
- Molecule 38: 30S ribosomal protein S7

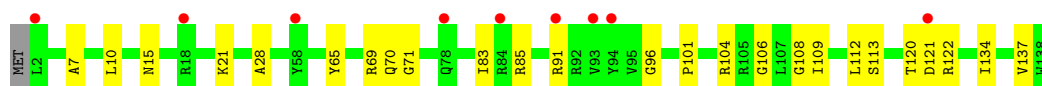


- Molecule 39: 30S ribosomal protein S8



- Molecule 39: 30S ribosomal protein S8

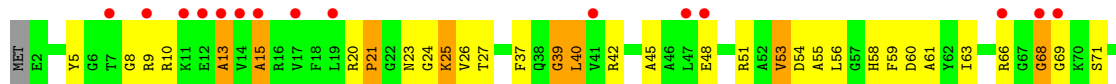




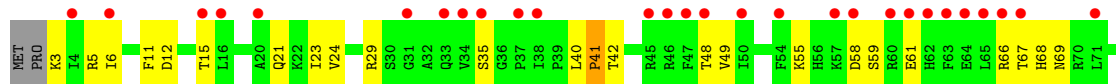
- Molecule 40: 30S ribosomal protein S9



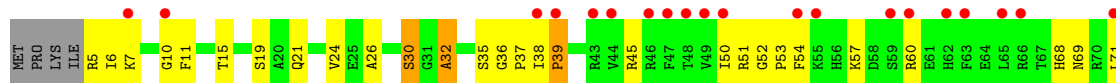
- Molecule 40: 30S ribosomal protein S9



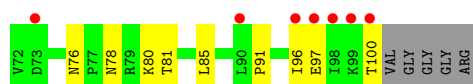
- Molecule 41: 30S ribosomal protein S10

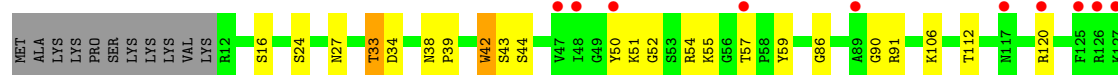
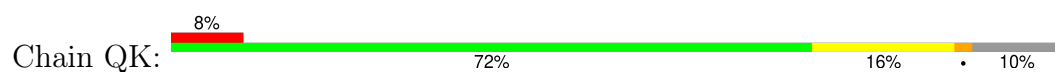


- Molecule 41: 30S ribosomal protein S10



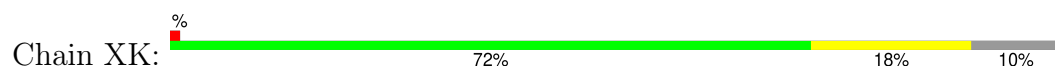
- Molecule 42: 30S ribosomal protein S11





ALA
SER

- Molecule 42: 30S ribosomal protein S11



- Molecule 43: 30S ribosomal protein S12



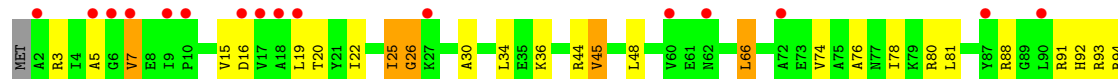
K119, Y120, T122, E127, A128, LYS, THR, ALA, ALA, LYS, LYS

- Molecule 43: 30S ribosomal protein S12



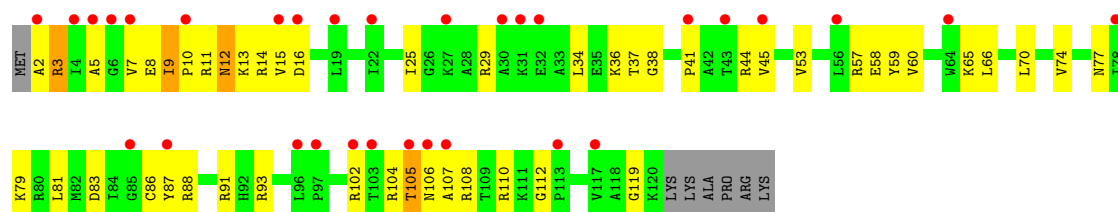
A107, A108, R113, K114, K115, S116, R117, S118, K119, Y120, G121, T122, K126, GLU, ALA, ALA, LYS, THR, ALA, ALA, LYS, LYS

- Molecule 44: 30S ribosomal protein S13

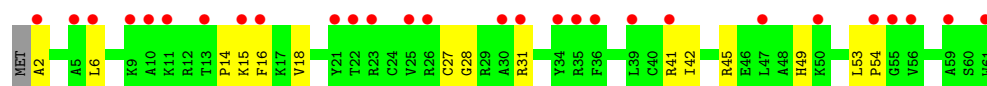
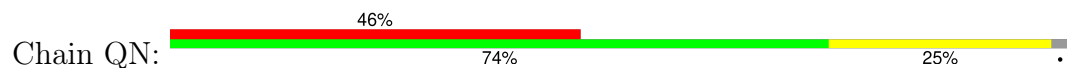


G95, L96, P97, V98, G99, R99, G100, Q101, R102, T103, R104, N105, D106, A107, R108, P113, R114, K115, A118, G119, K120, K121, LYS, ALA, PRO, ARG, LYS

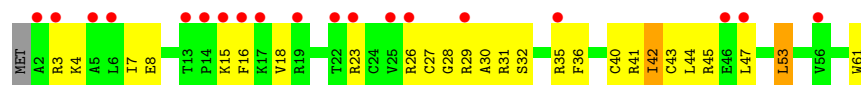
- Molecule 44: 30S ribosomal protein S13



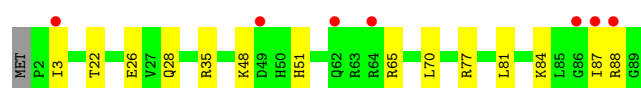
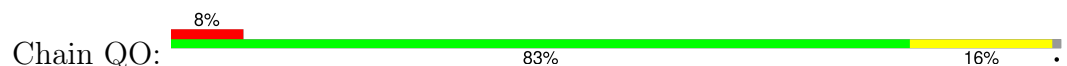
- Molecule 45: 30S ribosomal protein S14 type Z



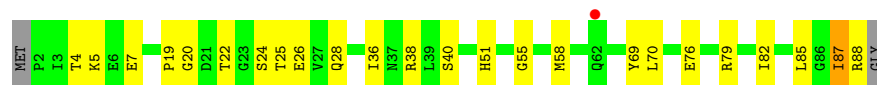
- Molecule 45: 30S ribosomal protein S14 type Z



- Molecule 46: 30S ribosomal protein S15



- Molecule 46: 30S ribosomal protein S15

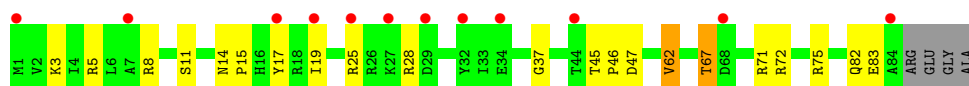


- Molecule 47: 30S ribosomal protein S16

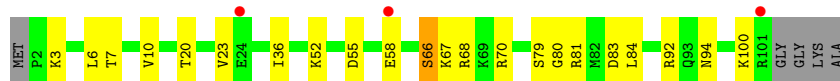
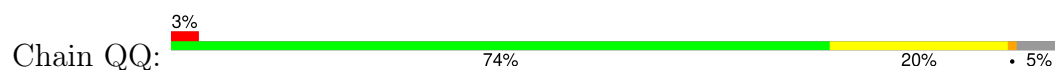


- Molecule 47: 30S ribosomal protein S16





- Molecule 48: 30S ribosomal protein S17



- Molecule 48: 30S ribosomal protein S17



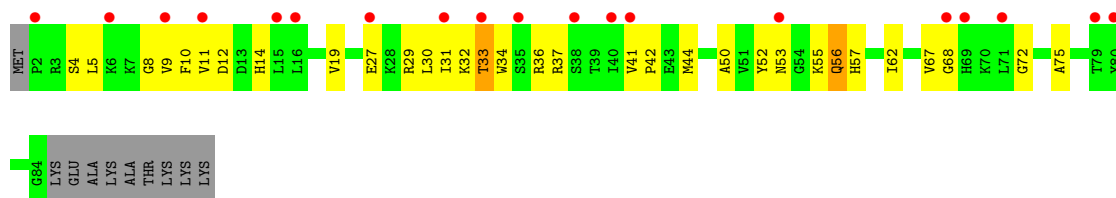
- Molecule 49: 30S ribosomal protein S18



- Molecule 49: 30S ribosomal protein S18

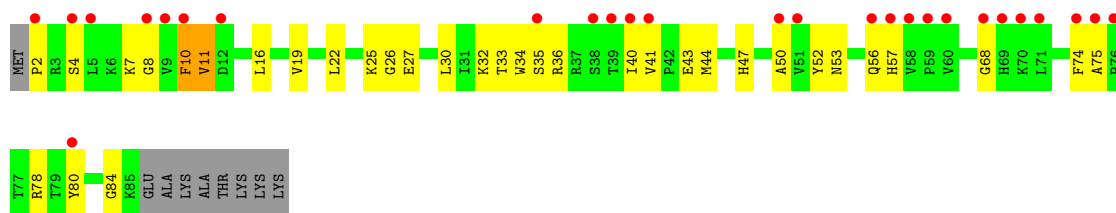


- Molecule 50: 30S ribosomal protein S19

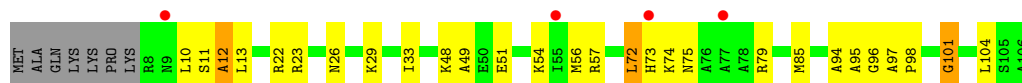


- Molecule 50: 30S ribosomal protein S19

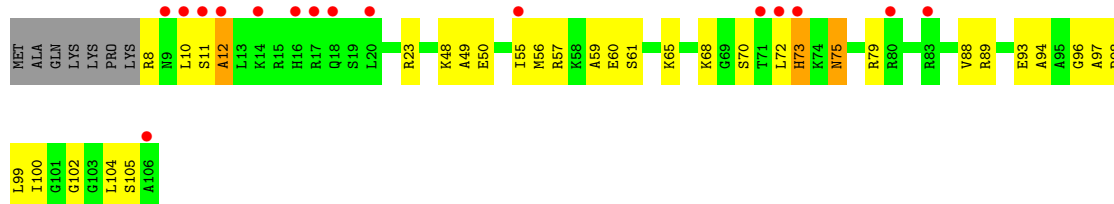




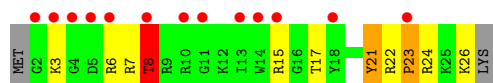
- Molecule 51: 30S ribosomal protein S20



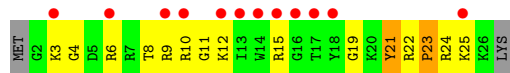
- Molecule 51: 30S ribosomal protein S20



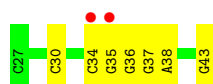
- Molecule 52: 30S ribosomal protein Thx



- Molecule 52: 30S ribosomal protein Thx



- Molecule 53: P-site ASLPro



- Molecule 53: P-site ASLPro

Chain XV:

47%

41%

12%



● Molecule 54: mRNA

Chain QX:

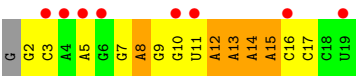
21%

42%

47%

26%

5%



● Molecule 54: mRNA

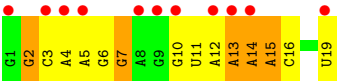
Chain XX:

26%

58%

47%

26%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	210.12Å 451.80Å 622.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	188.68 – 3.40 188.68 – 3.40	Depositor EDS
% Data completeness (in resolution range)	98.8 (188.68-3.40) 98.8 (188.68-3.40)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 3.41Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.198 , 0.237 0.200 , 0.238	Depositor DCC
R_{free} test set	36729 reflections (4.60%)	wwPDB-VP
Wilson B-factor (Å ²)	79.0	Xtriage
Anisotropy	0.210	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 149.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	290035	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.54% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 1MG, MG, SF4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	RA	0.46	0/69498	0.43	1/108491 (0.0%)
1	YA	0.56	0/69543	0.48	3/108563 (0.0%)
2	RB	0.34	0/2878	0.40	0/4490
2	YB	0.48	0/2878	0.47	0/4490
3	RD	0.66	0/2165	0.61	1/2919 (0.0%)
3	YD	0.79	0/2176	0.66	0/2933
4	RE	0.62	0/1596	0.63	0/2153
4	YE	0.75	0/1601	0.78	1/2160 (0.0%)
5	RF	0.59	0/1620	0.60	0/2194
5	YF	0.73	0/1620	0.66	0/2194
6	RG	0.33	0/1499	0.69	0/2016
6	YG	0.43	0/1499	0.67	0/2016
7	RH	0.39	0/1362	0.62	0/1841
7	YH	0.59	0/1362	0.59	0/1841
8	RI	0.56	0/1151	0.88	3/1558 (0.2%)
8	YI	0.46	0/1151	0.71	0/1558
9	RN	0.57	0/1131	0.60	0/1525
9	YN	0.72	0/1148	0.64	0/1547
10	RO	0.66	1/943 (0.1%)	0.57	0/1269
10	YO	0.76	2/943 (0.2%)	0.62	0/1269
11	RP	0.57	0/1147	0.73	0/1525
11	YP	0.74	0/1139	0.74	0/1514
12	RQ	0.55	0/1143	0.75	2/1527 (0.1%)
12	YQ	0.70	0/1143	0.63	0/1527
13	RR	0.62	0/982	0.70	0/1312
13	YR	0.74	0/974	0.74	1/1302 (0.1%)
14	RS	0.41	0/892	0.70	2/1187 (0.2%)
14	YS	0.58	0/887	0.58	0/1180
15	RT	0.56	0/1155	0.67	0/1542
15	YT	0.64	0/1155	0.59	0/1542
16	RU	0.59	0/982	0.63	0/1306
16	YU	0.78	0/982	0.68	0/1306

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	RV	0.49	0/790	0.56	0/1057
17	YV	0.74	0/790	0.67	2/1057 (0.2%)
18	RW	0.63	0/911	0.57	0/1220
18	YW	0.77	0/911	0.66	1/1220 (0.1%)
19	RX	0.57	0/739	0.60	0/993
19	YX	0.71	0/756	0.66	0/1014
20	RY	0.48	0/831	0.52	0/1108
20	YY	0.64	0/831	0.58	2/1108 (0.2%)
21	RZ	0.44	0/1634	0.76	2/2216 (0.1%)
21	YZ	0.54	0/1620	0.59	0/2197
22	R0	0.54	0/611	0.58	0/814
22	Y0	0.72	0/607	0.62	0/809
23	R1	0.60	0/770	0.63	0/1022
23	Y1	0.69	0/736	0.57	0/978
24	R2	0.44	0/583	0.53	0/771
24	Y2	0.62	0/608	0.52	0/803
25	R3	0.53	0/474	0.56	0/635
25	Y3	0.71	0/474	0.70	1/635 (0.2%)
26	R4	0.30	0/578	0.65	0/776
26	Y4	0.34	0/578	0.80	0/776
27	R5	0.67	0/473	0.61	0/639
27	Y5	0.75	0/473	0.70	0/639
28	R6	0.50	0/460	0.53	0/613
28	Y6	0.64	0/460	0.56	0/613
29	R7	0.72	0/417	0.60	0/550
29	Y7	0.88	1/426 (0.2%)	0.63	0/561
30	R8	0.61	0/525	0.77	0/691
30	Y8	0.74	0/525	0.70	0/691
31	R9	0.47	0/305	0.48	0/402
31	Y9	0.67	0/310	0.48	0/407
32	QA	0.34	0/36343	0.39	0/56720
32	XA	0.35	0/36346	0.40	0/56725
33	QB	0.37	0/1942	0.67	2/2619 (0.1%)
33	XB	0.36	0/1950	0.66	0/2630
34	QC	0.30	0/1629	0.63	0/2195
34	XC	0.30	0/1629	0.62	0/2195
35	QD	0.50	0/1733	0.65	0/2318
35	XD	0.46	0/1733	0.67	0/2318
36	QE	0.43	0/1171	0.59	0/1576
36	XE	0.46	0/1171	0.57	0/1576
37	QF	0.43	0/856	0.59	0/1154
37	XF	0.42	0/856	0.52	0/1154
38	QG	0.27	0/1276	0.58	0/1709

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	XG	0.29	0/1276	0.58	0/1709
39	QH	0.46	0/1128	0.58	0/1517
39	XH	0.45	0/1128	0.57	0/1517
40	QI	0.27	0/1029	0.66	0/1379
40	XI	0.29	0/1017	0.63	1/1365 (0.1%)
41	QJ	0.30	0/814	0.65	0/1095
41	XJ	0.30	0/790	0.56	0/1063
42	QK	0.42	0/879	0.53	0/1187
42	XK	0.43	0/879	0.53	0/1187
43	QL	0.53	0/991	0.59	0/1327
43	XL	0.48	0/972	0.69	0/1301
44	QM	0.31	0/965	0.72	2/1292 (0.2%)
44	XM	0.38	0/956	0.75	2/1281 (0.2%)
45	QN	0.37	0/501	0.77	0/664
45	XN	0.33	0/501	0.67	0/664
46	QO	0.41	0/745	0.52	0/992
46	XO	0.45	0/740	0.52	0/987
47	QP	0.47	0/721	0.57	0/970
47	XP	0.41	0/721	0.63	0/970
48	QQ	0.47	0/847	0.54	0/1131
48	XQ	0.44	0/847	0.54	0/1131
49	QR	0.44	0/579	0.56	0/768
49	XR	0.45	0/579	0.56	0/768
50	QS	0.26	0/680	0.60	0/915
50	XS	0.27	0/689	0.72	0/926
51	QT	0.42	0/765	0.57	0/1007
51	XT	0.40	0/765	0.58	0/1007
52	QU	0.27	0/221	0.53	0/288
52	XU	0.31	0/221	0.59	0/288
53	QV	0.34	1/380 (0.3%)	0.25	0/590
53	XV	0.37	1/332 (0.3%)	0.31	0/515
54	QX	0.25	0/436	0.36	0/678
54	XX	0.22	0/462	0.37	0/719
All	All	0.49	6/313742 (0.0%)	0.50	29/468899 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	RD	0	7

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	YD	0	10
4	RE	0	10
4	YE	0	13
5	RF	0	13
5	YF	0	9
6	RG	0	17
6	YG	0	18
7	RH	0	24
7	YH	0	5
8	RI	0	13
8	YI	0	18
9	RN	0	10
9	YN	0	6
10	RO	0	2
10	YO	0	2
11	RP	0	19
11	YP	0	18
12	RQ	0	11
12	YQ	0	8
13	RR	0	6
13	YR	0	5
14	RS	0	8
14	YS	0	2
15	RT	0	6
15	YT	0	4
16	RU	0	3
16	YU	0	5
17	RV	0	8
17	YV	0	4
18	RW	0	5
18	YW	0	5
19	RX	0	5
19	YX	0	4
20	RY	0	5
20	YY	0	2
21	RZ	0	22
21	YZ	0	9
22	R0	0	2
22	Y0	0	3
23	R1	0	6
23	Y1	0	2
24	R2	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
25	R3	0	3
25	Y3	0	1
26	R4	0	10
26	Y4	0	12
27	R5	0	1
27	Y5	0	2
29	R7	0	2
30	R8	0	7
30	Y8	0	4
31	Y9	0	1
33	QB	0	21
33	XB	0	18
34	QC	0	14
34	XC	0	17
35	QD	0	13
35	XD	0	13
36	QE	0	5
36	XE	0	5
37	QF	0	2
37	XF	0	1
38	QG	0	9
38	XG	0	6
39	QH	0	4
39	XH	0	8
40	QI	0	11
40	XI	0	19
41	QJ	0	6
41	XJ	0	9
42	QK	0	4
42	XK	0	5
43	QL	0	8
43	XL	0	12
44	QM	0	17
44	XM	0	14
45	QN	0	6
45	XN	0	5
46	QO	0	2
46	XO	0	3
47	QP	0	6
47	XP	0	7
48	QQ	0	2
48	XQ	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
49	QR	0	4
49	XR	0	4
50	QS	0	11
50	XS	0	14
51	QT	0	13
51	XT	0	13
52	QU	0	3
52	XU	0	5
All	All	0	749

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	RO	14	THR	CA-C	-6.95	1.43	1.52
10	YO	70	LYS	C-N	-6.46	1.24	1.33
29	Y7	23	ARG	C-N	-6.24	1.20	1.33
10	YO	14	THR	CA-C	-5.74	1.44	1.52
53	XV	37	1MG	O3'-P	5.22	1.61	1.56
53	QV	37	1MG	O3'-P	5.05	1.61	1.56

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	XM	12	ASN	N-CA-C	7.38	122.00	112.92
4	YE	144	ARG	N-CA-CB	7.13	116.78	109.51
8	RI	122	GLU	CA-C-N	6.87	131.55	121.31
8	RI	122	GLU	C-N-CA	6.87	131.55	121.31
13	YR	3	HIS	N-CA-C	-6.52	99.07	108.07
12	RQ	52	VAL	N-CA-C	-6.11	104.39	110.62
21	RZ	128	VAL	CA-C-N	5.94	128.65	120.39
21	RZ	128	VAL	C-N-CA	5.94	128.65	120.39
25	Y3	15	TYR	CB-CA-C	5.85	117.12	108.87
8	RI	123	LEU	N-CA-C	5.74	118.38	110.35
1	YA	2712	U	P-O3'-C3'	5.68	126.52	119.70
33	QB	207	ALA	CA-C-N	5.64	129.88	120.62
33	QB	207	ALA	C-N-CA	5.64	129.88	120.62
17	YV	79	VAL	N-CA-C	-5.62	108.37	113.71
1	RA	1992	G	C2'-C3'-O3'	5.57	117.86	109.50
18	YW	17	VAL	N-CA-C	-5.38	107.12	113.42
1	YA	1992	G	C2'-C3'-O3'	5.34	117.51	109.50
44	QM	105	THR	CA-C-N	5.34	131.74	121.54
44	QM	105	THR	C-N-CA	5.34	131.74	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	XM	12	ASN	N-CA-CB	-5.32	102.80	110.56
20	YY	53	PRO	CA-C-N	5.22	131.52	121.54
20	YY	53	PRO	C-N-CA	5.22	131.52	121.54
14	RS	42	ASP	CA-C-N	5.22	131.51	121.54
14	RS	42	ASP	C-N-CA	5.22	131.51	121.54
40	XI	53	VAL	N-CA-C	-5.22	108.75	113.71
3	RD	237	GLU	N-CA-C	-5.21	102.15	109.96
17	YV	79	VAL	CB-CA-C	5.10	115.42	110.63
1	YA	271(B)	G	P-O3'-C3'	5.09	125.81	119.70
12	RQ	50	ALA	N-CA-C	5.05	116.60	111.14

There are no chirality outliers.

All (749) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	QB	15	VAL	Peptide
33	QB	155	LEU	Peptide
33	QB	156	LYS	Peptide
33	QB	16	HIS	Peptide
33	QB	166	ASP	Peptide
33	QB	18	GLY	Peptide
33	QB	19	HIS	Peptide
33	QB	21	ARG	Peptide
33	QB	230	VAL	Peptide
33	QB	232	PRO	Peptide
33	QB	233	SER	Peptide
33	QB	234	PRO	Peptide
33	QB	237	ALA	Peptide
33	QB	239	VAL	Peptide
33	QB	34	ALA	Peptide
33	QB	35	GLU	Peptide
33	QB	38	GLY	Peptide
33	QB	64	ARG	Peptide
33	QB	66	GLY	Peptide
33	QB	95	GLN	Peptide
33	QB	96	ARG	Peptide
34	QC	11	ARG	Peptide
34	QC	14	ILE	Peptide
34	QC	144	SER	Peptide
34	QC	166	GLU	Peptide
34	QC	168	ALA	Peptide
34	QC	187	ALA	Peptide

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Mol	Chain	Res	Type	Group
34	QC	189	ALA	Peptide
34	QC	204	LEU	Peptide
34	QC	44	GLU	Peptide
34	QC	51	GLY	Peptide
34	QC	53	ALA	Peptide
34	QC	59	ARG	Peptide
34	QC	62	ASP	Peptide
34	QC	78	GLY	Peptide
35	QD	146	ILE	Peptide
35	QD	154	ASN	Peptide
35	QD	155	LEU	Peptide
35	QD	175	SER	Peptide
35	QD	198	VAL	Peptide
35	QD	2	GLY	Peptide
35	QD	208	SER	Peptide
35	QD	3	ARG	Peptide
35	QD	38	TYR	Peptide
35	QD	47	ARG	Peptide
35	QD	49	ARG	Peptide
35	QD	69	GLY	Peptide
35	QD	88	VAL	Peptide
36	QE	103	GLY	Peptide
36	QE	154	GLY	Peptide
36	QE	22	GLY	Peptide
36	QE	68	GLU	Peptide
36	QE	95	ALA	Peptide
37	QF	58	GLY	Peptide
37	QF	71	ARG	Peptide
38	QG	11	GLN	Peptide
38	QG	113	GLU	Peptide
38	QG	152	ALA	Peptide
38	QG	30	ILE	Peptide
38	QG	50	ILE	Peptide
38	QG	54	THR	Peptide
38	QG	55	GLY	Peptide
38	QG	7	ALA	Peptide
38	QG	8	GLU	Peptide
39	QH	101	PRO	Peptide
39	QH	137	VAL	Peptide
39	QH	55	GLY	Peptide
39	QH	96	GLY	Peptide
40	QI	100	GLY	Peptide

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Mol	Chain	Res	Type	Group
40	QI	102	LEU	Peptide
40	QI	127	LYS	Peptide
40	QI	28	VAL	Peptide
40	QI	29	ASN	Peptide
40	QI	4	TYR	Peptide
40	QI	42	ARG	Peptide
40	QI	6	GLY	Peptide
40	QI	69	GLY	Peptide
40	QI	92	TYR	Peptide
40	QI	99	LEU	Peptide
41	QJ	35	SER	Peptide
41	QJ	41	PRO	Peptide
41	QJ	5	ARG	Peptide
41	QJ	76	ASN	Peptide
41	QJ	85	LEU	Peptide
41	QJ	90	LEU	Peptide
42	QK	38	ASN	Peptide
42	QK	42	TRP	Peptide
42	QK	90	GLY	Peptide
42	QK	91	ARG	Peptide
43	QL	103	GLY	Peptide
43	QL	104	VAL	Peptide
43	QL	118	SER	Peptide
43	QL	120	TYR	Peptide
43	QL	127	GLU	Peptide
43	QL	17	LYS	Peptide
43	QL	29	GLY	Peptide
43	QL	47	LYS	Peptide
44	QM	104	ARG	Peptide
44	QM	105	THR	Peptide
44	QM	107	ALA	Peptide
44	QM	108	ARG	Peptide
44	QM	113	PRO	Peptide
44	QM	118	ALA	Peptide
44	QM	120	LYS	Peptide
44	QM	25	ILE	Peptide
44	QM	26	GLY	Peptide
44	QM	3	ARG	Peptide
44	QM	36	LYS	Peptide
44	QM	48	LEU	Peptide
44	QM	5	ALA	Peptide
44	QM	66	LEU	Peptide

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Mol	Chain	Res	Type	Group
44	QM	7	VAL	Peptide
44	QM	97	PRO	Peptide
44	QM	99	ARG	Peptide
45	QN	14	PRO	Peptide
45	QN	15	LYS	Peptide
45	QN	16	PHE	Peptide
45	QN	42	ILE	Peptide
45	QN	53	LEU	Peptide
45	QN	54	PRO	Peptide
46	QO	3	ILE	Peptide
46	QO	88	ARG	Peptide
47	QP	2	VAL	Peptide
47	QP	36	ILE	Peptide
47	QP	62	VAL	Peptide
47	QP	77	ALA	Peptide
47	QP	82	GLN	Peptide
47	QP	83	GLU	Peptide
48	QQ	100	LYS	Peptide
48	QQ	66	SER	Peptide
49	QR	21	LYS	Peptide
49	QR	26	LEU	Peptide
49	QR	54	ARG	Peptide
49	QR	87	ARG	Peptide
50	QS	10	PHE	Peptide
50	QS	11	VAL	Peptide
50	QS	27	GLU	Peptide
50	QS	41	VAL	Peptide
50	QS	5	LEU	Peptide
50	QS	56	GLN	Peptide
50	QS	62	ILE	Peptide
50	QS	67	VAL	Peptide
50	QS	68	GLY	Peptide
50	QS	8	GLY	Peptide
50	QS	9	VAL	Peptide
51	QT	101	GLY	Peptide
51	QT	11	SER	Peptide
51	QT	12	ALA	Peptide
51	QT	13	LEU	Peptide
51	QT	48	LYS	Peptide
51	QT	49	ALA	Peptide
51	QT	72	LEU	Peptide
51	QT	73	HIS	Peptide

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Mol	Chain	Res	Type	Group
51	QT	94	ALA	Peptide
51	QT	95	ALA	Peptide
51	QT	96	GLY	Peptide
51	QT	97	ALA	Peptide
51	QT	98	PRO	Peptide
52	QU	21	TYR	Peptide
52	QU	23	PRO	Peptide
52	QU	8	THR	Peptide
22	R0	42	GLY	Peptide
22	R0	43	THR	Peptide
23	R1	53	VAL	Peptide
23	R1	54	ALA	Peptide
23	R1	80	LEU	Peptide
23	R1	85	LEU	Peptide
23	R1	87	PRO	Peptide
23	R1	96	LYS	Peptide
24	R2	14	ARG	Peptide
24	R2	15	LYS	Peptide
24	R2	4	SER	Peptide
24	R2	43	GLN	Peptide
24	R2	44	LEU	Peptide
24	R2	46	GLN	Peptide
24	R2	69	ARG	Peptide
24	R2	70	GLN	Peptide
24	R2	71	ASN	Peptide
25	R3	2	PRO	Peptide
25	R3	36	VAL	Peptide
25	R3	48	GLU	Peptide
26	R4	43	TYR	Peptide
26	R4	44	THR	Peptide
26	R4	45	GLY	Peptide
26	R4	46	GLN	Peptide
26	R4	48	ARG	Peptide
26	R4	57	GLU	Peptide
26	R4	60	GLN	Peptide
26	R4	61	ARG	Peptide
26	R4	62	ARG	Peptide
26	R4	65	ASP	Peptide
27	R5	5	PRO	Peptide
29	R7	46	VAL	Peptide
29	R7	6	GLN	Peptide
30	R8	27	THR	Peptide

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Mol	Chain	Res	Type	Group
30	R8	28	GLY	Peptide
30	R8	29	LYS	Peptide
30	R8	51	ALA	Peptide
30	R8	52	LYS	Peptide
30	R8	62	LEU	Peptide
30	R8	64	TYR	Peptide
3	RD	119	ALA	Peptide
3	RD	120	GLY	Peptide
3	RD	126	GLN	Peptide
3	RD	2	ALA	Peptide
3	RD	246	PRO	Peptide
3	RD	259	THR	Peptide
3	RD	272	ALA	Peptide
4	RE	130	GLY	Peptide
4	RE	142	GLY	Peptide
4	RE	161	GLY	Peptide
4	RE	180	ASN	Peptide
4	RE	186	GLY	Peptide
4	RE	187	ALA	Peptide
4	RE	29	GLY	Peptide
4	RE	70	ALA	Peptide
4	RE	71	GLY	Peptide
4	RE	74	PRO	Peptide
5	RF	127	GLU	Peptide
5	RF	128	ALA	Peptide
5	RF	130	ALA	Peptide
5	RF	135	LYS	Peptide
5	RF	19	GLU	Peptide
5	RF	196	LEU	Peptide
5	RF	198	ALA	Peptide
5	RF	25	PRO	Peptide
5	RF	47	GLY	Peptide
5	RF	65	TRP	Peptide
5	RF	83	PHE	Peptide
5	RF	85	GLY	Peptide
5	RF	91	GLY	Peptide
6	RG	111	LEU	Peptide
6	RG	112	PRO	Peptide
6	RG	119	GLY	Peptide
6	RG	126	ASP	Peptide
6	RG	127	GLY	Peptide
6	RG	128	ARG	Peptide

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Mol	Chain	Res	Type	Group
6	RG	134	GLY	Peptide
6	RG	136	ARG	Peptide
6	RG	159	VAL	Peptide
6	RG	180	PHE	Peptide
6	RG	2	PRO	Peptide
6	RG	36	LYS	Peptide
6	RG	52	ILE	Peptide
6	RG	82	LEU	Peptide
6	RG	85	GLY	Peptide
6	RG	95	ARG	Peptide
6	RG	97	ASP	Peptide
7	RH	10	PRO	Peptide
7	RH	124	GLU	Peptide
7	RH	126	PRO	Peptide
7	RH	128	PRO	Peptide
7	RH	129	THR	Peptide
7	RH	13	LYS	Peptide
7	RH	130	ARG	Peptide
7	RH	150	ALA	Peptide
7	RH	151	ILE	Peptide
7	RH	152	ARG	Peptide
7	RH	153	LYS	Peptide
7	RH	16	SER	Peptide
7	RH	161	GLY	Peptide
7	RH	173	PRO	Peptide
7	RH	174	GLY	Peptide
7	RH	22	GLY	Peptide
7	RH	39	PRO	Peptide
7	RH	55	PRO	Peptide
7	RH	7	LEU	Peptide
7	RH	8	PRO	Peptide
7	RH	82	GLY	Peptide
7	RH	87	LEU	Peptide
7	RH	93	GLY	Peptide
7	RH	98	LEU	Peptide
8	RI	10	GLU	Peptide
8	RI	11	ASN	Peptide
8	RI	122	GLU	Mainchain
8	RI	131	LYS	Peptide
8	RI	132	PRO	Peptide
8	RI	133	HIS	Peptide
8	RI	134	PRO	Peptide

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Mol	Chain	Res	Type	Group
8	RI	14	ASP	Peptide
8	RI	142	VAL	Peptide
8	RI	144	VAL	Peptide
8	RI	145	VAL	Peptide
8	RI	16	GLY	Peptide
8	RI	9	LEU	Peptide
9	RN	113	GLY	Peptide
9	RN	114	ARG	Peptide
9	RN	127	ASP	Peptide
9	RN	130	HIS	Peptide
9	RN	132	ALA	Peptide
9	RN	134	ARG	Peptide
9	RN	17	ASP	Peptide
9	RN	21	LYS	Peptide
9	RN	22	THR	Peptide
9	RN	34	LEU	Peptide
10	RO	28	SER	Peptide
10	RO	96	THR	Peptide
11	RP	106	LEU	Peptide
11	RP	107	LYS	Peptide
11	RP	115	LEU	Peptide
11	RP	117	GLU	Peptide
11	RP	118	GLY	Peptide
11	RP	144	GLU	Peptide
11	RP	147	LEU	Peptide
11	RP	21	ARG	Peptide
11	RP	22	GLY	Peptide
11	RP	28	GLY	Peptide
11	RP	35	HIS	Peptide
11	RP	37	GLY	Peptide
11	RP	43	GLY	Peptide
11	RP	58	THR	Peptide
11	RP	63	PRO	Peptide
11	RP	66	GLY	Peptide
11	RP	67	MET	Peptide
11	RP	72	PRO	Peptide
11	RP	97	PRO	Peptide
12	RQ	1	MET	Peptide
12	RQ	104	PHE	Peptide
12	RQ	108	GLY	Peptide
12	RQ	112	GLU	Peptide
12	RQ	23	GLY	Peptide

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Mol	Chain	Res	Type	Group
12	RQ	24	GLY	Peptide
12	RQ	4	PRO	Peptide
12	RQ	82	ARG	Peptide
12	RQ	88	GLY	Peptide
12	RQ	89	ASN	Peptide
12	RQ	91	GLU	Peptide
13	RR	1	MET	Peptide
13	RR	103	ARG	Peptide
13	RR	104	ARG	Peptide
13	RR	2	ARG	Peptide
13	RR	3	HIS	Peptide
13	RR	75	LEU	Peptide
14	RS	105	ALA	Peptide
14	RS	106	ARG	Peptide
14	RS	109	GLY	Peptide
14	RS	42	ASP	Peptide
14	RS	5	THR	Peptide
14	RS	56	LEU	Peptide
14	RS	61	ASN	Peptide
14	RS	81	GLY	Peptide
15	RT	111	ARG	Peptide
15	RT	135	ALA	Peptide
15	RT	136	GLN	Peptide
15	RT	17	THR	Peptide
15	RT	58	ASN	Peptide
15	RT	93	ARG	Peptide
16	RU	91	ASP	Peptide
16	RU	95	LEU	Peptide
16	RU	96	ALA	Peptide
17	RV	100	ARG	Peptide
17	RV	15	GLU	Peptide
17	RV	23	GLU	Peptide
17	RV	40	LEU	Peptide
17	RV	52	VAL	Peptide
17	RV	54	GLY	Peptide
17	RV	72	VAL	Peptide
17	RV	9	GLY	Peptide
18	RW	110	LYS	Peptide
18	RW	64	MET	Peptide
18	RW	90	ARG	Peptide
18	RW	91	GLY	Peptide
18	RW	92	ARG	Peptide

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Mol	Chain	Res	Type	Group
19	RX	22	ALA	Peptide
19	RX	28	PHE	Peptide
19	RX	70	LEU	Peptide
19	RX	84	ALA	Peptide
19	RX	93	GLU	Peptide
20	RY	39	VAL	Peptide
20	RY	51	VAL	Peptide
20	RY	52	SER	Peptide
20	RY	62	GLU	Peptide
20	RY	9	LYS	Peptide
21	RZ	10	ARG	Peptide
21	RZ	11	GLU	Peptide
21	RZ	12	GLY	Peptide
21	RZ	125	LEU	Peptide
21	RZ	131	ARG	Peptide
21	RZ	136	PHE	Peptide
21	RZ	148	ASP	Peptide
21	RZ	155	LEU	Peptide
21	RZ	160	GLY	Peptide
21	RZ	162	GLU	Peptide
21	RZ	165	VAL	Peptide
21	RZ	167	PRO	Peptide
21	RZ	168	GLU	Peptide
21	RZ	191	VAL	Peptide
21	RZ	37	VAL	Peptide
21	RZ	51	ALA	Peptide
21	RZ	52	SER	Peptide
21	RZ	62	PRO	Peptide
21	RZ	63	ASP	Peptide
21	RZ	95	PRO	Peptide
21	RZ	96	VAL	Peptide
21	RZ	97	GLU	Peptide
33	XB	111	ARG	Peptide
33	XB	128	GLU	Peptide
33	XB	15	VAL	Peptide
33	XB	19	HIS	Peptide
33	XB	194	PRO	Peptide
33	XB	21	ARG	Peptide
33	XB	227	GLY	Peptide
33	XB	230	VAL	Peptide
33	XB	232	PRO	Peptide
33	XB	233	SER	Peptide

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Mol	Chain	Res	Type	Group
33	XB	236	TYR	Peptide
33	XB	237	ALA	Peptide
33	XB	35	GLU	Peptide
33	XB	36	ARG	Peptide
33	XB	60	ASP	Peptide
33	XB	64	ARG	Peptide
33	XB	66	GLY	Peptide
33	XB	89	GLY	Peptide
34	XC	11	ARG	Peptide
34	XC	156	ARG	Peptide
34	XC	163	ALA	Peptide
34	XC	164	ARG	Peptide
34	XC	166	GLU	Peptide
34	XC	189	ALA	Peptide
34	XC	193	TYR	Peptide
34	XC	194	GLY	Peptide
34	XC	196	LEU	Peptide
34	XC	23	TYR	Peptide
34	XC	25	GLY	Peptide
34	XC	41	GLY	Peptide
34	XC	47	LEU	Peptide
34	XC	49	SER	Peptide
34	XC	5	ILE	Peptide
34	XC	62	ASP	Peptide
34	XC	76	VAL	Peptide
35	XD	124	GLY	Peptide
35	XD	130	GLY	Peptide
35	XD	153	ARG	Peptide
35	XD	154	ASN	Peptide
35	XD	157	LEU	Peptide
35	XD	167	GLY	Peptide
35	XD	168	ARG	Peptide
35	XD	170	VAL	Peptide
35	XD	188	LEU	Peptide
35	XD	194	LEU	Peptide
35	XD	69	GLY	Peptide
35	XD	87	GLY	Peptide
35	XD	88	VAL	Peptide
36	XE	153	LYS	Peptide
36	XE	154	GLY	Peptide
36	XE	22	GLY	Peptide
36	XE	68	GLU	Peptide

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Mol	Chain	Res	Type	Group
36	XE	72	GLN	Peptide
37	XF	99	ALA	Peptide
38	XG	113	GLU	Peptide
38	XG	44	TYR	Peptide
38	XG	53	LYS	Peptide
38	XG	63	LYS	Peptide
38	XG	64	GLN	Peptide
38	XG	7	ALA	Peptide
39	XH	101	PRO	Peptide
39	XH	108	GLY	Peptide
39	XH	137	VAL	Peptide
39	XH	28	ALA	Peptide
39	XH	69	ARG	Peptide
39	XH	70	GLN	Peptide
39	XH	71	GLY	Peptide
39	XH	96	GLY	Peptide
40	XI	13	ALA	Peptide
40	XI	15	ALA	Peptide
40	XI	21	PRO	Peptide
40	XI	23	ASN	Peptide
40	XI	24	GLY	Peptide
40	XI	25	LYS	Peptide
40	XI	39	GLY	Peptide
40	XI	40	LEU	Peptide
40	XI	42	ARG	Peptide
40	XI	54	ASP	Peptide
40	XI	56	LEU	Peptide
40	XI	58	HIS	Peptide
40	XI	63	ILE	Peptide
40	XI	66	ARG	Peptide
40	XI	68	GLY	Peptide
40	XI	69	GLY	Peptide
40	XI	89	ASN	Peptide
40	XI	91	ASP	Peptide
40	XI	99	LEU	Peptide
41	XJ	30	SER	Peptide
41	XJ	32	ALA	Peptide
41	XJ	35	SER	Peptide
41	XJ	39	PRO	Peptide
41	XJ	52	GLY	Peptide
41	XJ	54	PHE	Peptide
41	XJ	80	LYS	Peptide

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Mol	Chain	Res	Type	Group
41	XJ	85	LEU	Peptide
41	XJ	91	PRO	Peptide
42	XK	100	ALA	Peptide
42	XK	102	GLY	Peptide
42	XK	13	GLN	Peptide
42	XK	14	VAL	Peptide
42	XK	67	ASP	Peptide
43	XL	102	ARG	Peptide
43	XL	103	GLY	Peptide
43	XL	104	VAL	Peptide
43	XL	118	SER	Peptide
43	XL	120	TYR	Peptide
43	XL	17	LYS	Peptide
43	XL	26	ALA	Peptide
43	XL	27	LEU	Peptide
43	XL	28	LYS	Peptide
43	XL	29	GLY	Peptide
43	XL	37	CYS	Peptide
43	XL	61	THR	Peptide
44	XM	10	PRO	Peptide
44	XM	105	THR	Peptide
44	XM	107	ALA	Peptide
44	XM	11	ARG	Peptide
44	XM	110	ARG	Peptide
44	XM	112	GLY	Peptide
44	XM	119	GLY	Peptide
44	XM	12	ASN	Peptide
44	XM	25	ILE	Peptide
44	XM	37	THR	Peptide
44	XM	38	GLY	Peptide
44	XM	58	GLU	Peptide
44	XM	59	TYR	Peptide
44	XM	66	LEU	Peptide
45	XN	15	LYS	Peptide
45	XN	16	PHE	Peptide
45	XN	3	ARG	Peptide
45	XN	42	ILE	Peptide
45	XN	8	GLU	Peptide
46	XO	19	PRO	Peptide
46	XO	20	GLY	Peptide
46	XO	87	ILE	Peptide
47	XP	15	PRO	Peptide

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Mol	Chain	Res	Type	Group
47	XP	19	ILE	Peptide
47	XP	37	GLY	Peptide
47	XP	46	PRO	Peptide
47	XP	62	VAL	Peptide
47	XP	82	GLN	Peptide
47	XP	83	GLU	Peptide
48	XQ	44	ALA	Peptide
48	XQ	66	SER	Peptide
48	XQ	7	THR	Peptide
48	XQ	79	SER	Peptide
49	XR	21	LYS	Peptide
49	XR	31	LEU	Peptide
49	XR	38	GLU	Peptide
49	XR	55	ARG	Peptide
50	XS	10	PHE	Peptide
50	XS	11	VAL	Peptide
50	XS	22	LEU	Peptide
50	XS	25	LYS	Peptide
50	XS	26	GLY	Peptide
50	XS	27	GLU	Peptide
50	XS	34	TRP	Peptide
50	XS	4	SER	Peptide
50	XS	40	ILE	Peptide
50	XS	47	HIS	Peptide
50	XS	68	GLY	Peptide
50	XS	74	PHE	Peptide
50	XS	8	GLY	Peptide
50	XS	84	GLY	Peptide
51	XT	11	SER	Peptide
51	XT	12	ALA	Peptide
51	XT	48	LYS	Peptide
51	XT	49	ALA	Peptide
51	XT	60	GLU	Peptide
51	XT	72	LEU	Peptide
51	XT	73	HIS	Peptide
51	XT	75	ASN	Peptide
51	XT	8	ARG	Peptide
51	XT	94	ALA	Peptide
51	XT	96	GLY	Peptide
51	XT	97	ALA	Peptide
51	XT	98	PRO	Peptide
52	XU	11	GLY	Peptide

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Mol	Chain	Res	Type	Group
52	XU	19	GLY	Peptide
52	XU	21	TYR	Peptide
52	XU	23	PRO	Peptide
52	XU	25	LYS	Peptide
22	Y0	28	GLY	Peptide
22	Y0	42	GLY	Peptide
22	Y0	43	THR	Peptide
23	Y1	30	VAL	Peptide
23	Y1	84	GLY	Peptide
25	Y3	2	PRO	Peptide
26	Y4	42	PHE	Peptide
26	Y4	43	TYR	Peptide
26	Y4	44	THR	Peptide
26	Y4	45	GLY	Peptide
26	Y4	46	GLN	Peptide
26	Y4	47	GLN	Peptide
26	Y4	48	ARG	Peptide
26	Y4	53	GLU	Peptide
26	Y4	55	ARG	Peptide
26	Y4	56	VAL	Peptide
26	Y4	57	GLU	Peptide
26	Y4	62	ARG	Peptide
27	Y5	5	PRO	Peptide
27	Y5	59	GLU	Peptide
30	Y8	27	THR	Peptide
30	Y8	28	GLY	Peptide
30	Y8	29	LYS	Peptide
30	Y8	35	GLN	Peptide
31	Y9	5	ALA	Peptide
3	YD	106	ILE	Peptide
3	YD	110	GLY	Peptide
3	YD	191	ALA	Peptide
3	YD	192	THR	Peptide
3	YD	2	ALA	Peptide
3	YD	238	GLY	Peptide
3	YD	246	PRO	Peptide
3	YD	254	THR	Peptide
3	YD	255	LYS	Peptide
3	YD	259	THR	Peptide
4	YE	115	GLY	Peptide
4	YE	146	THR	Peptide
4	YE	153	GLY	Peptide

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Mol	Chain	Res	Type	Group
4	YE	185	LYS	Peptide
4	YE	20	ALA	Peptide
4	YE	202	LYS	Peptide
4	YE	204	ALA	Peptide
4	YE	52	LEU	Peptide
4	YE	57	LYS	Peptide
4	YE	71	GLY	Peptide
4	YE	74	PRO	Peptide
4	YE	81	ILE	Peptide
4	YE	89	ASP	Peptide
5	YF	127	GLU	Peptide
5	YF	128	ALA	Peptide
5	YF	132	VAL	Peptide
5	YF	196	LEU	Peptide
5	YF	198	ALA	Peptide
5	YF	47	GLY	Peptide
5	YF	6	VAL	Peptide
5	YF	67	GLN	Peptide
5	YF	91	GLY	Peptide
6	YG	109	VAL	Peptide
6	YG	118	ARG	Peptide
6	YG	127	GLY	Peptide
6	YG	134	GLY	Peptide
6	YG	136	ARG	Peptide
6	YG	145	THR	Peptide
6	YG	150	ASP	Peptide
6	YG	181	ARG	Peptide
6	YG	2	PRO	Peptide
6	YG	32	PRO	Peptide
6	YG	35	GLU	Peptide
6	YG	48	GLU	Peptide
6	YG	52	ILE	Peptide
6	YG	58	GLN	Peptide
6	YG	82	LEU	Peptide
6	YG	85	GLY	Peptide
6	YG	95	ARG	Peptide
6	YG	97	ASP	Peptide
7	YH	12	PRO	Peptide
7	YH	174	GLY	Peptide
7	YH	33	LEU	Peptide
7	YH	58	GLU	Peptide
7	YH	85	LYS	Peptide

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Mol	Chain	Res	Type	Group
8	YI	11	ASN	Peptide
8	YI	116	LEU	Peptide
8	YI	119	PRO	Peptide
8	YI	121	LYS	Peptide
8	YI	122	GLU	Peptide
8	YI	123	LEU	Peptide
8	YI	131	LYS	Peptide
8	YI	133	HIS	Peptide
8	YI	134	PRO	Peptide
8	YI	14	ASP	Peptide
8	YI	142	VAL	Peptide
8	YI	144	VAL	Peptide
8	YI	145	VAL	Peptide
8	YI	35	LEU	Peptide
8	YI	55	ALA	Peptide
8	YI	59	ALA	Peptide
8	YI	75	LEU	Peptide
8	YI	9	LEU	Peptide
9	YN	113	GLY	Peptide
9	YN	114	ARG	Peptide
9	YN	17	ASP	Peptide
9	YN	21	LYS	Peptide
9	YN	22	THR	Peptide
9	YN	95	PRO	Peptide
10	YO	4	PRO	Peptide
10	YO	83	ALA	Peptide
11	YP	102	ARG	Peptide
11	YP	106	LEU	Peptide
11	YP	107	LYS	Peptide
11	YP	108	LYS	Peptide
11	YP	115	LEU	Peptide
11	YP	116	GLY	Peptide
11	YP	18	ARG	Peptide
11	YP	21	ARG	Peptide
11	YP	22	GLY	Peptide
11	YP	28	GLY	Peptide
11	YP	29	LYS	Peptide
11	YP	35	HIS	Peptide
11	YP	37	GLY	Peptide
11	YP	43	GLY	Peptide
11	YP	54	GLY	Peptide
11	YP	91	PHE	Peptide

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Mol	Chain	Res	Type	Group
11	YP	97	PRO	Peptide
11	YP	98	GLU	Peptide
12	YQ	108	GLY	Peptide
12	YQ	20	ALA	Peptide
12	YQ	21	THR	Peptide
12	YQ	23	GLY	Peptide
12	YQ	24	GLY	Peptide
12	YQ	4	PRO	Peptide
12	YQ	40	ALA	Peptide
12	YQ	59	ARG	Peptide
13	YR	102	GLU	Peptide
13	YR	103	ARG	Peptide
13	YR	3	HIS	Peptide
13	YR	73	VAL	Peptide
13	YR	75	LEU	Peptide
14	YS	111	GLU	Peptide
14	YS	84	GLN	Peptide
15	YT	110	ILE	Peptide
15	YT	111	ARG	Peptide
15	YT	27	THR	Peptide
15	YT	38	ASN	Peptide
16	YU	115	ALA	Peptide
16	YU	117	GLN	Peptide
16	YU	91	ASP	Peptide
16	YU	95	LEU	Peptide
16	YU	96	ALA	Peptide
17	YV	42	GLY	Peptide
17	YV	43	GLU	Peptide
17	YV	44	LYS	Peptide
17	YV	54	GLY	Peptide
18	YW	110	LYS	Peptide
18	YW	3	ALA	Peptide
18	YW	64	MET	Peptide
18	YW	90	ARG	Peptide
18	YW	91	GLY	Peptide
19	YX	48	LYS	Peptide
19	YX	68	ARG	Peptide
19	YX	84	ALA	Peptide
19	YX	93	GLU	Peptide
20	YY	106	LEU	Peptide
20	YY	52	SER	Peptide
21	YZ	106	GLY	Peptide

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Mol	Chain	Res	Type	Group
21	YZ	11	GLU	Peptide
21	YZ	136	PHE	Peptide
21	YZ	159	PRO	Peptide
21	YZ	160	GLY	Peptide
21	YZ	188	ALA	Peptide
21	YZ	37	VAL	Peptide
21	YZ	50	GLN	Peptide
21	YZ	51	ALA	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	RA	62051	0	31279	542	1
1	YA	62091	0	31300	505	0
2	RB	2573	0	1306	26	0
2	YB	2573	0	1306	17	0
3	RD	2115	0	2195	31	0
3	YD	2126	0	2208	42	0
4	RE	1563	0	1629	29	0
4	YE	1568	0	1633	31	0
5	RF	1585	0	1632	22	0
5	YF	1585	0	1632	30	0
6	RG	1474	0	1535	38	0
6	YG	1474	0	1535	27	0
7	RH	1336	0	1418	22	0
7	YH	1336	0	1418	23	1
8	RI	1136	0	1223	35	2
8	YI	1136	0	1223	22	0
9	RN	1104	0	1180	17	0
9	YN	1121	0	1195	18	0
10	RO	933	0	996	24	0
10	YO	933	0	996	15	0
11	RP	1130	0	1217	25	0
11	YP	1122	0	1206	23	0
12	RQ	1122	0	1179	51	0
12	YQ	1122	0	1179	16	0
13	RR	968	0	1033	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	YR	960	0	1021	10	0
14	RS	882	0	943	13	0
14	YS	877	0	938	9	0
15	RT	1141	0	1202	17	0
15	YT	1141	0	1202	13	0
16	RU	964	0	1022	20	0
16	YU	964	0	1022	20	0
17	RV	779	0	852	12	0
17	YV	779	0	852	18	0
18	RW	900	0	964	16	1
18	YW	900	0	964	11	0
19	RX	725	0	778	7	0
19	YX	742	0	803	9	0
20	RY	818	0	909	12	0
20	YY	818	0	909	9	2
21	RZ	1601	0	1630	43	0
21	YZ	1587	0	1622	16	0
22	R0	603	0	619	7	0
22	Y0	599	0	617	9	0
23	R1	763	0	848	10	0
23	Y1	729	0	802	12	0
24	R2	581	0	629	9	0
24	Y2	606	0	665	5	1
25	R3	469	0	518	6	0
25	Y3	469	0	518	12	0
26	R4	565	0	557	11	0
26	Y4	565	0	557	15	0
27	R5	459	0	476	11	0
27	Y5	459	0	476	7	0
28	R6	453	0	473	3	0
28	Y6	453	0	473	3	0
29	R7	409	0	454	6	0
29	Y7	418	0	467	4	0
30	R8	517	0	582	14	0
30	Y8	517	0	582	15	0
31	R9	302	0	332	6	0
31	Y9	307	0	335	10	0
32	QA	32469	0	16393	422	0
32	XA	32471	0	16393	441	2
33	QB	1907	0	1958	37	0
33	XB	1915	0	1969	29	0
34	QC	1605	0	1668	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	XC	1605	0	1668	30	0
35	QD	1703	0	1763	68	0
35	XD	1703	0	1764	52	0
36	QE	1155	0	1213	19	0
36	XE	1155	0	1213	11	0
37	QF	843	0	857	17	0
37	XF	843	0	857	15	0
38	QG	1257	0	1296	22	0
38	XG	1257	0	1296	25	0
39	QH	1108	0	1165	17	0
39	XH	1108	0	1165	12	0
40	QI	1010	0	1037	26	0
40	XI	998	0	1024	27	0
41	QJ	801	0	849	21	0
41	XJ	777	0	816	26	0
42	QK	864	0	881	15	0
42	XK	864	0	881	12	0
43	QL	975	0	1062	18	0
43	XL	956	0	1046	18	0
44	QM	955	0	1021	25	0
44	XM	946	0	1008	32	0
45	QN	492	0	529	10	0
45	XN	492	0	529	17	0
46	QO	734	0	771	11	0
46	XO	729	0	768	15	0
47	QP	705	0	725	12	0
47	XP	705	0	725	11	0
48	QQ	834	0	904	16	0
48	XQ	834	0	904	15	0
49	QR	574	0	644	9	0
49	XR	574	0	644	10	0
50	QS	665	0	686	16	0
50	XS	674	0	699	16	0
51	QT	763	0	861	14	0
51	XT	763	0	861	16	0
52	QU	217	0	234	10	0
52	XU	217	0	234	11	0
53	QV	365	0	186	5	0
53	XV	322	0	164	5	0
54	QX	389	0	197	27	0
54	XX	412	0	208	12	0
55	QA	66	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	QF	1	0	0	0	0
55	R0	1	0	0	0	0
55	R1	1	0	0	0	0
55	R5	1	0	0	0	0
55	R8	1	0	0	0	0
55	RA	485	0	0	0	0
55	RB	8	0	0	0	0
55	RE	2	0	0	0	0
55	RF	1	0	0	0	0
55	RN	1	0	0	0	0
55	RO	1	0	0	0	0
55	RP	2	0	0	0	0
55	RQ	2	0	0	0	0
55	RT	1	0	0	0	0
55	RX	1	0	0	0	0
55	XA	87	0	0	0	0
55	XE	1	0	0	0	0
55	XL	1	0	0	0	0
55	XQ	1	0	0	0	0
55	XS	1	0	0	0	0
55	Y0	2	0	0	0	0
55	Y1	1	0	0	0	0
55	Y5	1	0	0	0	0
55	Y7	1	0	0	0	0
55	Y8	1	0	0	0	0
55	YA	510	0	0	0	0
55	YB	7	0	0	0	0
55	YD	1	0	0	0	0
55	YE	4	0	0	0	0
55	YO	1	0	0	0	0
55	YP	2	0	0	0	0
55	YQ	1	0	0	0	0
55	YR	1	0	0	0	0
56	QN	1	0	0	0	0
56	R4	1	0	0	0	0
56	R5	1	0	0	0	0
56	R6	1	0	0	0	0
56	R9	1	0	0	0	0
56	RY	1	0	0	0	0
56	XN	1	0	0	0	0
56	Y4	1	0	0	0	0
56	Y5	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	Y6	1	0	0	0	0
56	Y9	1	0	0	0	0
56	YY	1	0	0	0	0
57	QD	8	0	0	1	0
57	XD	8	0	0	3	0
All	All	290035	0	197002	3194	5

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (3194) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:1535:C:N4	54:QX:9:G:C2	1.91	1.37
32:QA:1535:C:N4	54:QX:9:G:N2	1.78	1.30
17:YV:49:THR:OG1	17:YV:50:PRO:HD2	1.30	1.25
21:RZ:182:LYS:O	21:RZ:186:GLU:HG2	1.39	1.22
32:QA:1535:C:C4	54:QX:9:G:N2	2.07	1.22
17:YV:49:THR:OG1	17:YV:50:PRO:CD	1.88	1.18
32:QA:1534:A:H1'	54:QX:10:G:H22	1.15	1.07
8:RI:120:ILE:HD11	8:RI:126:TYR:CE2	1.89	1.06
32:XA:356:A:H2	32:XA:368:U:O2	1.37	1.05
1:RA:2135:A:H62	1:RA:2156:G:N2	1.55	1.04
1:RA:2135:A:N6	1:RA:2156:G:H21	1.56	1.03
35:XD:20:TYR:HE1	35:XD:106:TYR:OH	1.41	1.02
44:XM:2:ALA:O	44:XM:9:ILE:HD12	1.61	1.01
12:RQ:56:ARG:HD2	21:RZ:180:VAL:HG11	1.37	1.01
17:YV:49:THR:CB	17:YV:50:PRO:CD	2.39	1.00
17:YV:49:THR:CB	17:YV:50:PRO:HD3	1.92	1.00
32:XA:452:A:N6	32:XA:480:U:H3	1.59	1.00
1:YA:1359:A:N6	1:YA:1372:U:H3	1.60	0.99
17:YV:49:THR:HB	17:YV:50:PRO:HD3	1.44	0.97
32:XA:438:G:H21	32:XA:496:A:H62	1.02	0.96
7:YH:3:ARG:HE	7:YH:54:ARG:NH1	1.62	0.96
12:RQ:56:ARG:HD2	21:RZ:180:VAL:CG1	1.97	0.94
8:RI:77:LEU:HD11	8:RI:79:ILE:HD11	1.46	0.93
1:YA:2701:C:H3'	1:YA:2702:U:H5''	1.50	0.93
32:XA:992:U:H3	32:XA:1044:A:H62	0.97	0.92
3:YD:258:LYS:HE2	3:YD:273:ARG:HH12	1.31	0.92
12:RQ:60:ARG:HH11	21:RZ:177:PRO:HG3	1.34	0.91
35:QD:31:CYS:O	35:QD:31:CYS:SG	2.28	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:356:A:C2	32:XA:368:U:O2	2.22	0.91
8:RI:120:ILE:HD11	8:RI:126:TYR:CD2	2.06	0.91
1:YA:2099:U:H3	1:YA:2190:G:H1	0.98	0.91
25:Y3:10:LYS:NZ	25:Y3:15:TYR:OH	2.05	0.90
12:RQ:56:ARG:CD	21:RZ:180:VAL:CG1	2.50	0.89
32:QA:1535:C:C5	54:QX:9:G:N2	2.38	0.89
35:XD:20:TYR:CE1	35:XD:106:TYR:OH	2.26	0.88
12:RQ:60:ARG:NH1	21:RZ:177:PRO:HG3	1.88	0.88
1:YA:1607:C:N4	1:YA:1622:G:OP2	2.07	0.88
32:QA:1534:A:C1'	54:QX:10:G:H22	1.86	0.88
32:QA:429:U:O3'	35:QD:22:LYS:NZ	2.06	0.88
1:RA:2788:C:O2'	1:RA:2809:A:N3	2.07	0.88
1:RA:2245:U:H5'	1:RA:2246:G:H5'	1.55	0.87
35:XD:31:CYS:O	35:XD:31:CYS:SG	2.33	0.87
32:XA:992:U:H3	32:XA:1044:A:N6	1.72	0.86
3:YD:274:ARG:HH11	3:YD:274:ARG:HG3	1.39	0.86
32:XA:438:G:H21	32:XA:496:A:N6	1.73	0.86
35:XD:20:TYR:HE1	35:XD:106:TYR:HH	0.92	0.86
35:XD:21:LEU:HD12	57:XD:301:SF4:S1	2.16	0.85
32:XA:438:G:N2	32:XA:496:A:H62	1.74	0.85
1:RA:2096:U:H3	1:RA:2193:G:H1	1.25	0.84
35:QD:19:LEU:HD22	35:QD:67:ILE:CG1	2.08	0.84
32:QA:410:G:H21	32:QA:432:A:H62	1.23	0.84
32:XA:180:U:H3	32:XA:195:A:H62	1.26	0.84
32:XA:56:U:H2'	32:XA:57:G:H8	1.44	0.82
32:QA:1532:U:C6	54:QX:10:G:O6	2.33	0.81
1:RA:1433:U:H3	1:RA:1560:G:H1	1.27	0.81
32:XA:62:U:H3	32:XA:105:G:H1	1.29	0.81
7:YH:3:ARG:HD2	7:YH:54:ARG:HH12	1.45	0.80
17:YV:49:THR:HG1	17:YV:50:PRO:HD2	1.43	0.80
12:RQ:56:ARG:HD3	21:RZ:180:VAL:HG12	1.62	0.80
7:YH:3:ARG:CD	7:YH:54:ARG:HH12	1.95	0.80
32:QA:150:C:H42	32:QA:171:A:H62	1.28	0.80
1:RA:1069:A:H5'	1:RA:1096:A:H5'	1.63	0.80
32:QA:1539:C:H42	54:QX:5:A:H61	1.30	0.80
32:QA:1534:A:H1'	54:QX:10:G:N2	1.96	0.79
12:RQ:56:ARG:CD	21:RZ:180:VAL:HG11	2.13	0.79
8:RI:77:LEU:HD23	8:RI:140:LEU:CB	2.11	0.79
1:RA:1264:G:OP1	27:R5:19:ARG:NH2	2.15	0.79
1:YA:996:A:OP2	16:YU:92:ARG:NH2	2.16	0.79
7:YH:3:ARG:NE	7:YH:54:ARG:NH1	2.31	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:QX:10:G:H2'	54:QX:11:U:H5	1.48	0.78
1:RA:676:A:H8	1:RA:2069:G:H21	1.31	0.78
1:YA:2096:U:H3	1:YA:2193:G:H1	1.30	0.78
35:QD:19:LEU:HD22	35:QD:67:ILE:HG13	1.66	0.77
1:RA:517:C:OP1	27:R5:16:ARG:NH2	2.16	0.77
1:RA:1607:C:N4	1:RA:1622:G:OP2	2.18	0.77
35:XD:32:ALA:HB3	57:XD:301:SF4:S3	2.25	0.77
1:RA:1479:G:OP2	1:RA:1510:A:N6	2.18	0.77
1:RA:2701:C:H3'	1:RA:2702:U:H5''	1.65	0.76
2:YB:8:U:H3	2:YB:112:G:H1	1.32	0.76
32:XA:686:U:H1'	42:XK:42:TRP:HE1	1.50	0.76
1:RA:1102:C:H2'	1:RA:1103:A:H8	1.49	0.76
1:RA:1094:U:OP1	1:RA:1096:A:N6	2.19	0.76
3:YD:258:LYS:CE	3:YD:273:ARG:HH12	1.98	0.76
32:XA:978:A:OP2	32:XA:1362(A):C:N4	2.20	0.75
32:XA:261:U:OP2	51:XT:79:ARG:NH2	2.19	0.75
1:RA:139:G:N2	1:RA:141:A:C6	2.53	0.75
32:QA:1372:U:H5''	40:QI:71:SER:HB3	1.68	0.75
35:QD:20:TYR:CE2	37:XF:15:ASP:CB	2.70	0.74
12:RQ:62:GLY:HA2	21:RZ:116:VAL:HG21	1.67	0.74
3:YD:274:ARG:HG3	3:YD:274:ARG:NH1	1.97	0.74
1:RA:31:C:O2'	1:RA:1238:G:OP1	2.05	0.74
1:RA:2135:A:H62	1:RA:2156:G:H21	0.81	0.74
1:RA:2882:A:OP1	13:RR:96:ARG:NH1	2.19	0.74
12:RQ:60:ARG:NH1	21:RZ:177:PRO:CG	2.50	0.74
32:QA:1536:C:H42	54:QX:8:A:H61	1.35	0.74
32:XA:180:U:H3	32:XA:195:A:N6	1.85	0.74
35:XD:26:CYS:HA	57:XD:301:SF4:S2	2.27	0.74
32:QA:1373:G:H5'	38:QG:36:LYS:HG2	1.70	0.74
1:YA:1693:U:O2'	3:YD:14:ARG:NH2	2.21	0.74
32:QA:1373:G:H4'	38:QG:31:MET:HE1	1.69	0.74
32:XA:544:G:OP1	35:XD:59:ARG:NH2	2.21	0.73
1:RA:27:G:N2	1:RA:513:A:OP2	2.20	0.73
32:XA:12:U:H3	32:XA:22:G:H1	1.36	0.73
1:RA:299:A:N3	1:RA:319:C:O2'	2.21	0.73
1:YA:265:A:N6	1:YA:427:U:O2'	2.22	0.73
1:RA:2392:A:OP2	1:RA:2422:A:N6	2.22	0.73
1:YA:517:C:OP1	27:Y5:16:ARG:NH2	2.22	0.73
1:YA:1264:G:OP1	27:Y5:19:ARG:NH2	2.18	0.73
32:QA:316:G:OP2	32:QA:351:G:O2'	2.06	0.72
35:QD:16:GLY:C	35:QD:33:MET:HE1	2.14	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:XH:7:ALA:HB2	39:XH:85:ARG:HD3	1.71	0.72
1:RA:1165:U:H3	1:RA:1184:G:H1	1.36	0.72
25:Y3:15:TYR:CE2	25:Y3:53:LEU:HD21	2.23	0.72
35:QD:8:VAL:HG11	35:QD:21:LEU:HB2	1.72	0.72
32:XA:388:G:O2'	32:XA:389:A:OP2	2.06	0.72
1:YA:1359:A:N7	1:YA:1372:U:O4	2.23	0.72
1:RA:301:G:OP2	20:RY:84:ARG:NH2	2.23	0.72
33:QB:185:ILE:HG22	33:QB:199:TYR:HB2	1.72	0.72
1:YA:2304:G:H22	1:YA:2312:U:H3	1.36	0.72
1:YA:2808:U:C2	1:YA:2892:A:N6	2.56	0.71
1:YA:993:G:OP1	16:YU:50:ARG:NH2	2.24	0.71
35:XD:8:VAL:HG12	35:XD:21:LEU:HD13	1.70	0.71
1:YA:2621:A:HO2'	4:YE:159:HIS:HD1	1.38	0.71
1:YA:819:A:OP2	1:YA:1187:G:N2	2.23	0.71
1:YA:2712:U:HO2'	1:YA:2712(A):A:H8	1.38	0.71
54:QX:10:G:H2'	54:QX:11:U:C5	2.26	0.71
7:YH:3:ARG:NE	7:YH:54:ARG:HH12	1.87	0.71
51:QT:54:LYS:HD2	51:QT:57:ARG:HH22	1.56	0.71
32:QA:346:G:H1'	32:QA:347:G:H5'	1.71	0.71
1:YA:24:G:O2'	18:YW:78:GLU:O	2.09	0.71
32:XA:790:A:OP1	53:XV:38:A:O2'	2.09	0.71
32:QA:1009:G:H1	32:QA:1020:U:H3	0.77	0.70
32:QA:1306:A:N6	32:QA:1331:G:O2'	2.24	0.70
1:YA:1823:G:OP1	3:YD:54:ARG:NH1	2.24	0.70
1:RA:572:A:OP2	17:RV:78:LYS:NZ	2.23	0.70
32:QA:954:G:H21	32:QA:1227:A:H62	1.38	0.70
8:RI:120:ILE:CD1	8:RI:126:TYR:CD2	2.73	0.70
40:XI:53:VAL:HG23	40:XI:55:ALA:H	1.55	0.70
1:RA:139:G:N2	1:RA:141:A:N6	2.40	0.70
1:RA:993:G:OP1	16:RU:50:ARG:NH2	2.24	0.70
32:QA:410:G:N2	32:QA:432:A:H62	1.89	0.70
42:QK:86:GLY:H	42:QK:112:THR:HG22	1.57	0.70
32:XA:152:A:H62	32:XA:169:C:N4	1.90	0.70
8:RI:77:LEU:CD2	8:RI:140:LEU:HB2	2.22	0.70
35:QD:19:LEU:CD2	35:QD:67:ILE:CG1	2.70	0.70
32:XA:201:C:H42	32:XA:216:G:H1	1.40	0.70
32:QA:514:C:H2'	32:QA:515:G:H8	1.58	0.69
32:XA:56:U:H2'	32:XA:57:G:C8	2.26	0.69
1:RA:1980:G:O2'	1:RA:1982:C:OP2	2.10	0.69
32:QA:1141:C:H2'	32:QA:1142:G:H8	1.58	0.69
1:YA:2680:C:H5'	4:YE:189:PRO:HA	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:259:G:H21	1:RA:621:A:H8	1.39	0.69
32:XA:972:C:OP2	41:XJ:57:LYS:NZ	2.26	0.69
1:RA:819:A:OP2	1:RA:1187:G:N2	2.26	0.69
32:XA:1157:A:N7	32:XA:1178:G:N2	2.41	0.69
1:RA:300:A:OP1	20:RY:86:ARG:NH2	2.26	0.69
32:QA:490:G:OP2	35:QD:132:ARG:NH2	2.26	0.68
1:YA:676:A:H8	1:YA:2069:G:H21	1.41	0.68
1:YA:1496:A:H8	1:YA:1577:C:HO2'	1.42	0.68
1:YA:2788:C:OP1	4:YE:61:ARG:NH2	2.26	0.68
35:QD:19:LEU:HD22	35:QD:67:ILE:HG12	1.76	0.68
35:QD:32:ALA:O	35:QD:35:ARG:N	2.27	0.68
32:XA:1269:A:OP1	52:XU:24:ARG:NH1	2.27	0.68
32:QA:12:U:H3	32:QA:22:G:H1	1.40	0.68
43:XL:60:LEU:HD12	43:XL:62:SER:H	1.59	0.68
1:RA:141:A:H8	1:RA:1595:G:H21	1.39	0.68
1:YA:2521:C:O2'	1:YA:2564:A:N3	2.26	0.68
1:YA:1566:A:OP1	3:YD:211:ARG:NH1	2.27	0.68
8:RI:77:LEU:HD23	8:RI:140:LEU:HB2	1.75	0.67
32:QA:62:U:H3	32:QA:105:G:H1	1.41	0.67
41:QJ:6:ILE:HA	41:QJ:97:GLU:O	1.93	0.67
1:YA:270(F):U:H3	1:YA:270(T):G:H1	1.43	0.67
31:Y9:27:CYS:SG	31:Y9:28:GLU:N	2.67	0.67
33:XB:69:LEU:HB3	33:XB:162:ILE:HG22	1.76	0.67
1:YA:2777:G:OP2	1:YA:2781:A:O2'	2.11	0.67
21:RZ:182:LYS:C	21:RZ:186:GLU:HG2	2.18	0.67
32:QA:1251:A:N3	32:QA:1369:C:O2'	2.28	0.67
48:QQ:66:SER:O	48:QQ:70:ARG:NH1	2.27	0.67
1:YA:2296:U:OP2	14:YS:9:ARG:NH2	2.26	0.67
32:QA:827:U:O2	32:QA:874:G:N2	2.28	0.67
35:QD:3:ARG:HH21	35:QD:118:ARG:HD3	1.60	0.67
44:QM:91:ARG:HG2	44:QM:98:VAL:HA	1.77	0.67
1:YA:2392:A:H2	1:YA:2424:C:H42	1.43	0.67
2:RB:80:U:H2'	2:RB:81:G:H21	1.60	0.67
8:RI:77:LEU:HD23	8:RI:140:LEU:HB3	1.77	0.67
5:RF:143:ALA:HB1	5:RF:148:LEU:HB2	1.77	0.67
44:XM:3:ARG:H	44:XM:3:ARG:NE	1.93	0.67
41:XJ:6:ILE:HD11	41:XJ:96:ILE:HB	1.76	0.67
8:RI:120:ILE:CD1	8:RI:126:TYR:CE2	2.76	0.67
1:YA:1138:G:H21	9:YN:106:MET:HE3	1.60	0.66
32:XA:1316:G:N2	32:XA:1319:A:OP2	2.26	0.66
1:RA:2867:G:HO2'	1:RA:2868:A:H8	1.42	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:QB:230:VAL:HG12	33:QB:231:GLU:HG3	1.78	0.66
1:YA:226:G:O2'	1:YA:228:A:N6	2.28	0.66
32:QA:1118:C:OP1	40:QI:104:ARG:NH1	2.28	0.66
1:YA:141:A:H8	1:YA:1595:G:H21	1.41	0.66
8:RI:77:LEU:CD1	8:RI:79:ILE:HD11	2.23	0.66
32:QA:547:A:OP1	35:QD:73:ARG:NH1	2.29	0.66
32:QA:1119:C:OP2	40:QI:9:ARG:NH2	2.29	0.66
32:XA:674:G:H2'	32:XA:675:A:H8	1.59	0.66
1:YA:987:G:O2'	1:YA:1000:A:N3	2.28	0.66
15:YT:16:ARG:NH2	15:YT:83:ILE:O	2.28	0.66
32:XA:1251:A:N3	32:XA:1369:C:O2'	2.28	0.66
3:YD:273:ARG:HG3	3:YD:273:ARG:O	1.95	0.66
32:XA:403:C:OP2	35:XD:74:GLN:NE2	2.28	0.66
32:XA:547:A:OP1	35:XD:73:ARG:NH2	2.29	0.66
1:RA:994:C:OP1	16:RU:53:ARG:NH2	2.29	0.66
6:YG:27:ASN:HB3	6:YG:30:GLU:HG3	1.77	0.66
26:Y4:16:CYS:SG	26:Y4:17:GLY:N	2.68	0.66
32:XA:1347:G:N2	32:XA:1374:A:OP2	2.29	0.66
1:RA:2502:G:H5''	1:RA:2503:A:H5''	1.76	0.66
20:RY:102:CYS:SG	20:RY:103:GLY:N	2.69	0.66
32:QA:1023:G:H3'	32:QA:1024:G:H5''	1.78	0.66
1:RA:372:G:N2	1:RA:401:A:OP2	2.28	0.66
1:RA:137(A):G:O6	1:RA:139:G:O2'	2.14	0.65
32:QA:1393:U:HO2'	32:QA:1501:C:HO2'	1.44	0.65
1:RA:2023:G:H5'	1:RA:2617:C:H4'	1.78	0.65
1:YA:220:G:O2'	1:YA:233:A:N3	2.27	0.65
2:RB:74:U:H1'	21:RZ:34:ASN:HD21	1.59	0.65
32:QA:673:G:H2'	32:QA:674:G:C8	2.31	0.65
1:YA:994:C:OP1	16:YU:53:ARG:NH2	2.29	0.65
8:RI:77:LEU:CD2	8:RI:140:LEU:CB	2.74	0.65
38:QG:46:ALA:HA	38:QG:49:ILE:HD12	1.78	0.65
32:XA:1373:G:H5''	38:XG:36:LYS:HE3	1.78	0.65
32:QA:152:A:H62	32:QA:169:C:H42	1.44	0.65
34:QC:172:ARG:HG2	34:QC:174:PRO:HD3	1.80	0.64
1:YA:573:G:O2'	1:YA:574:C:H3'	1.97	0.64
1:RA:2660:A:N7	7:RH:175:LYS:NZ	2.46	0.64
1:YA:1062:G:H2'	1:YA:1063:G:H8	1.62	0.64
1:YA:2133:G:O2'	1:YA:2158:A:N1	2.29	0.64
32:XA:514:C:H2'	32:XA:515:G:H8	1.62	0.64
32:XA:618:C:H5'	32:XA:619:U:H5''	1.78	0.64
48:XQ:66:SER:O	48:XQ:70:ARG:NH1	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:219:G:N3	1:RA:234:C:O2'	2.30	0.64
1:YA:1228:G:OP2	16:YU:16:LYS:NZ	2.30	0.64
32:XA:1304:G:H21	32:XA:1333:A:H62	1.45	0.64
1:RA:1509:C:H3'	1:RA:1510:A:H5''	1.78	0.64
12:RQ:63:LYS:HD3	12:RQ:65:PHE:CE2	2.33	0.64
32:QA:1349:A:H62	32:QA:1373:G:H21	1.43	0.64
1:YA:1645:G:H5''	1:YA:1646:C:H5'	1.79	0.64
1:YA:1980:G:O2'	1:YA:1982:C:OP2	2.14	0.64
1:RA:302:C:OP2	20:RY:73:ARG:NH1	2.31	0.64
4:RE:128:SER:OG	4:RE:129:HIS:N	2.31	0.64
25:Y3:13:ILE:HD13	25:Y3:13:ILE:N	2.12	0.64
41:XJ:57:LYS:HE2	41:XJ:60:ARG:HH12	1.62	0.64
1:RA:1403:C:H5''	1:RA:1471:A:H1'	1.79	0.64
1:RA:2578:G:OP1	1:RA:2614:A:N6	2.31	0.64
15:RT:51:ARG:HG3	15:RT:98:LYS:HE3	1.80	0.64
5:RF:40:GLN:HE22	5:RF:182:ASN:HB2	1.63	0.64
32:QA:1318:A:H1'	50:QS:37:ARG:HH21	1.62	0.64
1:YA:458:G:N2	1:YA:470:A:OP2	2.23	0.64
1:YA:2022:U:O2'	1:YA:2617:C:H5'	1.97	0.64
53:XV:36:G:H1	54:XX:16:C:H42	1.45	0.64
5:YF:63:LYS:NZ	5:YF:75:HIS:O	2.30	0.64
7:YH:3:ARG:HE	7:YH:54:ARG:HH11	1.46	0.64
16:YU:92:ARG:NH1	17:YV:11:GLN:O	2.31	0.64
1:RA:1310:G:OP2	29:R7:9:ARG:NE	2.30	0.63
1:RA:2285:C:OP2	28:R6:6:ARG:NH1	2.30	0.63
34:QC:119:ARG:HD3	34:QC:140:ARG:HH22	1.63	0.63
32:QA:838:G:H1	32:QA:848:C:H42	1.44	0.63
1:YA:2655:G:N2	1:YA:2665:A:OP2	2.31	0.63
32:XA:1239:A:N3	38:XG:115:ARG:NH2	2.45	0.63
32:QA:674:G:H2'	32:QA:675:A:H8	1.62	0.63
34:QC:119:ARG:HE	34:QC:140:ARG:HH12	1.45	0.63
40:QI:9:ARG:H	40:QI:79:LEU:HD23	1.63	0.63
14:YS:27:SER:HA	14:YS:88:ASP:HB3	1.80	0.63
35:XD:104:VAL:HA	35:XD:107:ARG:HB2	1.81	0.63
1:YA:2010:G:H5''	18:YW:42:ARG:HB2	1.80	0.63
1:YA:2483:C:N3	12:YQ:124:LYS:NZ	2.45	0.63
11:YP:63:PRO:HB2	30:Y8:30:ARG:HH21	1.62	0.63
1:RA:94:G:N3	24:R2:47:ASN:ND2	2.47	0.63
32:XA:992:U:O4	32:XA:1044:A:N7	2.32	0.63
40:XI:111:ARG:NH1	40:XI:112:LYS:O	2.31	0.63
26:R4:61:ARG:HH21	50:QS:42:PRO:HD3	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1995:U:O2	10:YO:3:GLN:NE2	2.31	0.63
1:RA:1078:U:H4'	1:RA:1079:C:H5''	1.81	0.63
16:RU:92:ARG:HD2	17:RV:11:GLN:HB2	1.81	0.63
1:YA:1196:C:HO2'	1:YA:1228:G:HO2'	1.47	0.63
1:RA:2022:U:O2'	1:RA:2617:C:H5'	1.98	0.63
1:RA:2684:U:O2'	10:RO:68:GLU:OE1	2.16	0.63
32:QA:686:U:H1'	42:QK:42:TRP:HE1	1.64	0.63
1:YA:1109:C:O2'	1:YA:1110:G:OP1	2.16	0.63
1:YA:1939:U:H3'	1:YA:1940:U:H5'	1.81	0.63
3:YD:258:LYS:NZ	3:YD:273:ARG:NH1	2.47	0.63
32:XA:1009:G:H1	32:XA:1020:U:H3	1.47	0.63
35:QD:98:GLU:OE2	35:QD:103:ASN:ND2	2.32	0.62
1:YA:2213:U:H1'	23:Y1:52:ARG:HH22	1.64	0.62
7:YH:3:ARG:HH11	7:YH:3:ARG:CG	2.12	0.62
9:RN:133:GLN:HG2	9:RN:135:PRO:HD3	1.80	0.62
32:QA:130:A:HO2'	32:QA:263:A:HO2'	1.46	0.62
20:YY:102:CYS:SG	20:YY:103:GLY:N	2.71	0.62
32:XA:689:C:OP1	42:XK:27:ASN:ND2	2.31	0.62
32:XA:1540:U:O2	54:XX:2:G:N2	2.32	0.62
1:RA:2353:G:O2'	22:R0:35:ASN:ND2	2.33	0.62
6:RG:16:ARG:HH21	6:RG:28:VAL:HG22	1.64	0.62
32:QA:278:G:N7	48:QQ:92:ARG:NH1	2.47	0.62
48:QQ:7:THR:HG22	48:QQ:58:GLU:HG2	1.81	0.62
49:QR:53:ARG:HH21	49:QR:59:SER:HA	1.64	0.62
1:YA:2315:G:OP1	6:YG:36:LYS:NZ	2.31	0.62
1:RA:300:A:OP2	20:RY:84:ARG:NH1	2.32	0.62
12:RQ:56:ARG:HD3	21:RZ:180:VAL:CG1	2.20	0.62
32:QA:412:A:N7	35:QD:35:ARG:NH1	2.48	0.62
16:YU:50:ARG:O	16:YU:54:LYS:NZ	2.31	0.62
41:XJ:57:LYS:O	41:XJ:60:ARG:NH1	2.32	0.62
1:RA:830:G:N2	1:RA:2445:G:O2'	2.32	0.62
32:XA:789:U:H4'	54:XX:14:A:H2	1.63	0.62
16:RU:92:ARG:NH1	17:RV:11:GLN:O	2.32	0.62
6:YG:101:ILE:HD11	26:Y4:25:TYR:H	1.63	0.62
1:RA:65:C:O2'	1:RA:456:C:N3	2.32	0.62
31:R9:27:CYS:SG	31:R9:28:GLU:N	2.73	0.62
1:YA:602:G:HO2'	1:YA:604:G:HO2'	1.35	0.62
3:YD:274:ARG:HH11	3:YD:274:ARG:CG	2.13	0.62
5:YF:167:ALA:HB1	5:YF:173:VAL:HG11	1.81	0.62
1:RA:1011:G:OP1	16:RU:66:ASN:ND2	2.33	0.62
6:RG:161:THR:HG22	6:RG:163:ALA:H	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:XL:27:LEU:O	43:XL:33:ARG:NH2	2.33	0.62
32:QA:1112:C:H42	34:QC:177:THR:HA	1.65	0.61
1:YA:2312:U:O2	6:YG:40:ASN:ND2	2.33	0.61
32:XA:152:A:H62	32:XA:169:C:H42	1.47	0.61
34:XC:189:ALA:HB3	34:XC:196:LEU:HB2	1.82	0.61
1:RA:270(L):U:H2'	8:RI:50:ARG:HH12	1.63	0.61
8:RI:86:THR:O	8:RI:87:LYS:HG2	2.00	0.61
32:QA:765:G:N2	32:QA:813:U:OP2	2.26	0.61
33:QB:53:ARG:HA	33:QB:56:ARG:HH21	1.64	0.61
1:YA:259:G:H21	1:YA:621:A:H8	1.46	0.61
13:YR:75:LEU:HA	13:YR:78:LYS:HB3	1.81	0.61
44:XM:8:GLU:O	44:XM:9:ILE:C	2.43	0.61
1:RA:1693:U:O2'	3:RD:14:ARG:NH2	2.34	0.61
5:RF:167:ALA:HB1	5:RF:173:VAL:HG11	1.82	0.61
9:RN:97:ARG:HA	9:RN:100:GLU:HB2	1.82	0.61
14:RS:25:ARG:NH1	14:RS:42:ASP:OD2	2.32	0.61
32:QA:1147:C:O2	40:QI:16:ARG:NH2	2.33	0.61
1:YA:620:G:H4'	1:YA:621:A:H5'	1.83	0.61
1:YA:793:A:OP2	1:YA:2071:A:O2'	2.18	0.61
1:RA:39:C:O2	5:RF:46:ARG:NH2	2.33	0.61
6:RG:38:VAL:HB	6:RG:158:ALA:HB3	1.82	0.61
6:YG:146:TYR:HE2	44:XM:8:GLU:HB3	1.64	0.61
32:XA:51:A:N1	32:XA:314:C:O2'	2.32	0.61
32:XA:1073:U:O2'	33:XB:104:ASN:OD1	2.17	0.61
40:QI:71:SER:HA	40:QI:74:ILE:HD12	1.81	0.61
1:YA:2107:C:O2	1:YA:2182:G:N2	2.33	0.61
1:YA:2168:G:N2	1:YA:2170:A:N7	2.48	0.61
32:XA:64:G:H5''	32:XA:65:U:H5'	1.81	0.61
32:XA:954:G:H21	32:XA:1227:A:H62	1.48	0.61
32:XA:1289:A:OP1	52:XU:9:ARG:NH2	2.33	0.61
15:RT:108:ARG:N	32:QA:1432:G:OP1	2.32	0.61
51:QT:51:GLU:HA	51:QT:54:LYS:HG2	1.80	0.61
4:YE:128:SER:OG	4:YE:129:HIS:N	2.33	0.61
40:XI:21:PRO:HA	40:XI:59:PHE:HA	1.80	0.61
32:QA:427:U:OP1	35:QD:13:ARG:NH1	2.34	0.61
32:QA:1446:A:O2'	32:QA:1447:G:O5'	2.18	0.61
1:YA:1689:A:H62	1:YA:1698:A:H2	1.47	0.61
32:XA:707:C:OP1	42:XK:85:ARG:NH1	2.33	0.61
32:XA:1071:C:H2'	32:XA:1072:G:H8	1.66	0.61
1:RA:517:C:O2'	18:RW:18:ARG:NH2	2.34	0.61
1:RA:1728:G:H3'	1:RA:1729:A:H5''	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:2052:G:H4'	4:RE:143:ASN:H	1.65	0.61
32:QA:664:G:H22	32:QA:741:G:H1	1.49	0.61
32:XA:1286:A:H2'	32:XA:1287:A:H4'	1.83	0.61
35:XD:18:LYS:HG3	35:XD:18:LYS:O	1.99	0.61
6:RG:82:LEU:HD21	6:RG:88:ILE:HG21	1.83	0.61
32:QA:642:A:N3	39:QH:113:SER:OG	2.34	0.61
51:XT:56:MET:HE1	51:XT:88:VAL:HG21	1.82	0.61
1:RA:2118:U:O2	1:RA:2148:G:O2'	2.18	0.61
32:QA:483:C:OP2	32:QA:484:G:O2'	2.17	0.61
32:QA:1124:G:H3'	32:QA:1145:C:N4	2.15	0.61
33:QB:67:THR:HG21	33:QB:155:LEU:HG	1.82	0.61
1:YA:577:G:O2'	1:YA:1254:A:OP1	2.19	0.61
32:XA:578:C:O2'	32:XA:728:A:N3	2.33	0.61
32:XA:1356:G:H2'	32:XA:1357:A:C8	2.36	0.61
21:RZ:10:ARG:NH1	21:RZ:26:GLY:O	2.34	0.60
39:QH:12:ARG:HD2	39:QH:26:VAL:HG12	1.83	0.60
32:XA:243:A:H4'	32:XA:244:U:O5'	1.99	0.60
1:RA:1689:A:H62	1:RA:1698:A:H2	1.47	0.60
37:QF:3:ARG:NH1	37:QF:38:GLU:OE2	2.33	0.60
1:YA:958:U:OP2	12:YQ:14:ARG:NH1	2.34	0.60
7:YH:3:ARG:HG2	7:YH:3:ARG:NH1	2.16	0.60
1:RA:2079:U:OP1	23:R1:21:ARG:NH1	2.30	0.60
1:RA:2468:G:OP1	12:RQ:119:ARG:NH2	2.35	0.60
7:RH:143:GLN:O	7:RH:147:ASN:ND2	2.33	0.60
32:QA:262:A:H5'	51:QT:74:LYS:HG3	1.84	0.60
1:YA:574:C:N3	4:YE:145:LYS:NZ	2.42	0.60
2:RB:22:U:H3	2:RB:61:G:H1	1.47	0.60
2:YB:37:C:O2	14:YS:95:HIS:NE2	2.33	0.60
32:XA:352:C:O2	32:XA:355:C:N4	2.32	0.60
32:XA:1356:G:H2'	32:XA:1357:A:H8	1.66	0.60
1:RA:1066:U:O2'	1:RA:1068:G:OP2	2.19	0.60
1:RA:1667:G:O2'	1:RA:1991:U:O4	2.19	0.60
35:QD:20:TYR:CE2	37:XF:15:ASP:HB3	2.35	0.60
32:XA:662:G:O2'	32:XA:836:G:OP1	2.19	0.60
34:XC:11:ARG:NH2	34:XC:177:THR:O	2.34	0.60
8:RI:107:VAL:O	8:RI:107:VAL:HG12	2.01	0.60
35:QD:153:ARG:HH11	35:QD:181:MET:HE3	1.66	0.60
26:Y4:27:THR:HG23	26:Y4:28:LYS:HG3	1.84	0.60
32:XA:150:C:H42	32:XA:171:A:H62	1.49	0.60
32:XA:933:G:O6	38:XG:3:ARG:NH2	2.34	0.60
1:RA:2612:C:OP2	27:R5:2:ALA:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:YF:116:ASP:OD2	11:YP:1:MET:N	2.35	0.60
33:XB:231:GLU:HG3	33:XB:233:SER:H	1.66	0.60
1:RA:2588:G:O6	1:RA:2607:G:C6	2.54	0.60
26:R4:16:CYS:SG	26:R4:17:GLY:N	2.75	0.60
1:YA:1728:G:N2	1:YA:1730:U:OP1	2.35	0.60
32:XA:1147:C:HO2'	40:XI:5:TYR:HH	1.48	0.60
1:RA:2438:U:O3'	1:RA:2439:A:H3'	2.02	0.60
32:QA:578:C:O2'	32:QA:728:A:N3	2.33	0.60
1:YA:1403:C:H5''	1:YA:1471:A:H1'	1.82	0.60
32:XA:152:A:N6	32:XA:169:C:H42	2.00	0.60
44:XM:86:CYS:SG	44:XM:87:TYR:N	2.75	0.60
1:RA:1348:G:H2'	1:RA:1349:A:H5''	1.84	0.60
11:RP:58:THR:O	11:RP:61:ARG:NH2	2.29	0.60
32:XA:1305:G:N2	32:XA:1332:A:OP2	2.24	0.60
40:XI:45:ALA:HA	40:XI:48:GLU:HG2	1.84	0.60
1:RA:223:A:O2'	1:RA:420:C:O2	2.19	0.59
1:RA:1262:A:OP2	18:RW:97:LYS:NZ	2.35	0.59
1:RA:1426:G:OP2	1:RA:1427:A:O2'	2.18	0.59
1:RA:2392:A:H2	1:RA:2424:C:H42	1.50	0.59
2:RB:8:U:H3	2:RB:112:G:H1	1.50	0.59
1:YA:2808:U:O2	1:YA:2892:A:C6	2.54	0.59
30:Y8:6:THR:OG1	30:Y8:8:LYS:NZ	2.35	0.59
1:RA:1815:A:OP2	3:RD:54:ARG:NH2	2.35	0.59
32:QA:1532:U:C5	54:QX:10:G:O6	2.54	0.59
1:YA:1203:G:H3'	1:YA:1204:A:H5''	1.83	0.59
1:YA:1454:U:H5'	13:YR:63:ARG:NH2	2.16	0.59
32:XA:587:G:N2	32:XA:754:C:OP2	2.34	0.59
2:RB:37:C:O2	14:RS:95:HIS:NE2	2.35	0.59
32:QA:150:C:N4	32:QA:171:A:H62	2.00	0.59
32:QA:1002:G:H2'	32:QA:1003:G:H8	1.67	0.59
1:YA:675:A:N3	1:YA:2443:C:O2'	2.29	0.59
41:XJ:78:ASN:HB2	41:XJ:81:THR:HG23	1.83	0.59
32:QA:448:A:H62	32:QA:486:U:H3	1.51	0.59
54:QX:2:G:N7	54:QX:3:C:N4	2.50	0.59
1:YA:442:G:H1'	5:YF:48:THR:HG21	1.84	0.59
1:YA:2334:G:O6	22:Y0:74:ARG:NH2	2.35	0.59
32:XA:266:G:O2'	32:XA:267:C:OP2	2.18	0.59
32:XA:486:U:H2'	32:XA:487:A:H8	1.67	0.59
32:XA:542:G:H5'	35:XD:41:GLY:HA3	1.83	0.59
1:RA:2588:G:O6	1:RA:2607:G:N1	2.36	0.59
1:RA:65:C:H1'	1:RA:456:C:H42	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:956:G:OP2	12:RQ:14:ARG:NH2	2.35	0.59
31:R9:25:VAL:HB	31:R9:34:GLN:HB2	1.83	0.59
32:QA:662:G:O2'	32:QA:836:G:OP1	2.21	0.59
1:YA:848:G:H2'	1:YA:849:A:C8	2.37	0.59
1:YA:2245:U:H5'	1:YA:2246:G:H5'	1.84	0.59
6:YG:161:THR:HG22	6:YG:163:ALA:H	1.67	0.59
32:XA:59:A:H3'	32:XA:331:G:H22	1.68	0.59
1:RA:996:A:OP2	16:RU:92:ARG:NH2	2.36	0.59
1:RA:1586:A:H3'	1:RA:1587:A:H8	1.67	0.59
15:RT:16:ARG:NH2	15:RT:83:ILE:O	2.36	0.59
41:QJ:3:LYS:N	41:QJ:74:ILE:O	2.36	0.59
54:QX:2:G:C8	54:QX:3:C:H5	2.20	0.59
1:YA:504:U:H5''	1:YA:505:A:H5'	1.85	0.59
9:YN:14:VAL:HG13	9:YN:138:LEU:HB2	1.85	0.59
11:RP:4:SER:O	11:RP:7:ARG:NH2	2.36	0.59
32:QA:1230:C:H5'	53:QV:30:C:H5''	1.84	0.59
1:YA:890:A:H2'	1:YA:892:G:H8	1.68	0.59
21:YZ:180:VAL:O	21:YZ:183:LEU:HB2	2.03	0.59
32:XA:643:C:H2'	32:XA:644:G:H8	1.68	0.59
1:RA:139:G:N3	1:RA:141:A:N1	2.50	0.59
1:RA:1816:G:O6	3:RD:35:LYS:NZ	2.35	0.59
12:RQ:75:THR:HG21	12:RQ:85:LYS:HE3	1.85	0.59
32:QA:1286:A:H2'	32:QA:1287:A:H4'	1.84	0.59
32:QA:1502:A:H2	32:QA:1505:G:H1	1.50	0.59
33:QB:54:THR:HG22	33:QB:199:TYR:HB3	1.84	0.59
33:QB:69:LEU:HB3	33:QB:162:ILE:HG22	1.83	0.59
41:QJ:77:PRO:O	41:QJ:79:ARG:NH1	2.35	0.59
3:YD:85:ASP:OD2	3:YD:88:ARG:NH1	2.35	0.59
19:YX:72:LYS:NZ	19:YX:75:ASP:OD1	2.35	0.59
32:QA:1535:C:H41	54:QX:9:G:N2	1.68	0.59
48:QQ:83:ASP:N	48:QQ:83:ASP:OD1	2.35	0.59
1:YA:84:A:OP2	20:YY:8:LYS:NZ	2.34	0.59
4:YE:7:VAL:HG13	4:YE:51:PHE:HE2	1.67	0.59
8:YI:94:ALA:HB1	8:YI:114:LEU:HD23	1.84	0.59
1:RA:1171:G:N7	1:RA:1174:A:N6	2.50	0.58
1:RA:2126:A:N6	1:RA:2163:C:O2'	2.36	0.58
41:QJ:29:ARG:NH1	32:XA:1163:C:OP1	2.35	0.58
32:XA:191(F):U:H2'	32:XA:191(G):G:H8	1.68	0.58
32:XA:1047:G:H5''	45:YN:4:LYS:HD3	1.85	0.58
47:XP:45:THR:HG22	47:XP:47:ASP:H	1.68	0.58
32:QA:28:G:O2'	32:QA:296:U:OP1	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:QC:182:ILE:HA	34:QC:202:ILE:O	2.03	0.58
1:YA:1815:A:OP2	3:YD:54:ARG:NH2	2.36	0.58
1:YA:2701:C:H3'	1:YA:2702:U:C5'	2.29	0.58
1:YA:2867:G:O2'	1:YA:2868:A:H8	1.86	0.58
32:XA:430:A:OP2	35:XD:8:VAL:HG23	2.02	0.58
33:XB:82:ARG:NH1	33:XB:92:TYR:OH	2.36	0.58
1:RA:546:C:H3'	1:RA:547:A:H8	1.69	0.58
1:RA:627:A:N7	11:RP:84:ASN:ND2	2.46	0.58
26:R4:28:LYS:HB2	26:R4:31:ILE:HD11	1.84	0.58
39:QH:10:LEU:HD22	39:QH:83:ILE:HD11	1.85	0.58
40:QI:96:LEU:O	40:QI:100:GLY:N	2.36	0.58
1:YA:2621:A:O2'	4:YE:159:HIS:ND1	2.33	0.58
32:XA:642:A:N3	39:XH:113:SER:OG	2.34	0.58
32:QA:656:C:O2'	46:QO:28:GLN:OE1	2.18	0.58
34:QC:14:ILE:HG13	34:QC:15:THR:HB	1.85	0.58
1:YA:2791:C:H5	1:YA:2893:G:H3'	1.68	0.58
32:XA:388:G:HO2'	32:XA:389:A:P	2.24	0.58
32:XA:1229:A:O2'	53:XV:30:C:OP1	2.20	0.58
1:RA:675:A:N3	1:RA:2443:C:O2'	2.34	0.58
12:RQ:59:ARG:HG3	21:RZ:180:VAL:HG23	1.84	0.58
32:QA:684:A:O2'	42:QK:39:PRO:O	2.20	0.58
37:QF:100:ASN:ND2	49:QR:23:LYS:O	2.33	0.58
1:YA:219:G:N3	1:YA:234:C:O2'	2.34	0.58
6:YG:47:LYS:HD3	6:YG:81:LYS:HD3	1.86	0.58
32:XA:1191:A:OP2	34:XC:3:ASN:ND2	2.36	0.58
32:XA:1227:A:OP1	50:XS:80:TYR:OH	2.21	0.58
1:RA:1059:G:OP2	1:RA:1060:U:H3'	2.03	0.58
1:RA:2779:U:O2'	1:RA:2781:A:N7	2.35	0.58
11:RP:49:ARG:HH11	30:R8:58:ILE:HG22	1.68	0.58
32:QA:970:C:N4	40:QI:128:ARG:O	2.37	0.58
32:QA:1080:A:H5'	36:QE:16:THR:HG21	1.86	0.58
39:QH:7:ALA:HB2	39:QH:85:ARG:HD3	1.86	0.58
32:XA:376:G:H5''	47:XP:5:ARG:HB2	1.86	0.58
1:RA:1019:U:H3	1:RA:1142(A):A:H62	1.51	0.58
33:QB:19:HIS:HB3	33:QB:20:GLU:HG2	1.85	0.58
33:QB:223:ILE:HA	33:QB:226:ARG:HB3	1.86	0.58
1:YA:2791:C:OP1	1:YA:2893:G:N2	2.37	0.58
32:XA:946:A:O2'	32:XA:1333:A:N3	2.32	0.58
1:RA:1969:A:O2'	1:RA:1972:A:N3	2.29	0.58
32:QA:742:G:OP2	46:QO:35:ARG:NH2	2.37	0.58
32:QA:835:U:H3	32:QA:851:G:H1	1.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:XI:112:LYS:NZ	40:XI:113:LYS:O	2.37	0.58
1:RA:2588:G:C6	1:RA:2607:G:C2	2.92	0.58
34:QC:77:ILE:HG23	34:QC:79:ARG:H	1.69	0.58
1:YA:2680:C:OP2	4:YE:111:ARG:NH2	2.33	0.58
32:XA:673:G:H2'	32:XA:674:G:C8	2.38	0.58
32:XA:1095:U:OP1	32:XA:1108:G:N2	2.27	0.58
1:RA:24:G:O2'	18:RW:78:GLU:O	2.20	0.58
10:RO:48:PRO:HB3	32:QA:1422:G:H5''	1.85	0.58
10:RO:80:ASP:OD2	15:RT:64:ARG:NH2	2.37	0.58
32:QA:401:C:O2'	32:QA:621:A:N3	2.33	0.58
1:YA:919:G:N2	1:YA:2269:A:OP2	2.34	0.58
1:YA:1824:G:N3	3:YD:254:THR:OG1	2.37	0.58
32:XA:359:U:H2'	32:XA:360:A:H8	1.69	0.58
32:XA:842:C:O2'	32:XA:848:C:N4	2.37	0.58
32:XA:1298:C:H2'	38:XG:114:ARG:HH12	1.69	0.58
1:RA:503:A:H4'	1:RA:504:U:H5'	1.85	0.57
32:QA:1009:G:O6	32:QA:1020:U:O4	2.22	0.57
32:QA:1119:C:H2'	32:QA:1120:G:H8	1.69	0.57
32:QA:1321:C:O2	50:QS:36:ARG:NH1	2.37	0.57
1:YA:2711:A:H5''	1:YA:2712:U:H5'	1.86	0.57
11:YP:65:ARG:NH1	30:Y8:25:MET:SD	2.77	0.57
32:XA:250:A:H4'	32:XA:251:G:O5'	2.03	0.57
34:XC:20:SER:OG	34:XC:22:TRP:NE1	2.37	0.57
40:XI:10:ARG:NH2	40:XI:103:THR:O	2.37	0.57
49:XR:32:ARG:HA	49:XR:69:THR:HG21	1.86	0.57
32:QA:191(G):G:O2'	51:QT:101:GLY:O	2.22	0.57
35:QD:108:LEU:HD23	35:QD:170:VAL:HG21	1.85	0.57
9:YN:39:ARG:NH2	9:YN:41:ASP:OD2	2.37	0.57
10:YO:88:ASN:HD21	10:YO:92:GLU:HB2	1.69	0.57
21:YZ:10:ARG:HH21	21:YZ:26:GLY:H	1.52	0.57
21:YZ:157:LEU:HD23	21:YZ:161:VAL:HG12	1.86	0.57
32:XA:1236:A:OP1	52:XU:3:LYS:NZ	2.36	0.57
1:RA:200:U:O2	1:RA:386:G:N2	2.38	0.57
1:RA:1047:G:N3	1:RA:1111:A:N6	2.52	0.57
27:R5:16:ARG:NH1	27:R5:17:ASP:OD1	2.35	0.57
32:QA:152:A:H62	32:QA:169:C:N4	2.02	0.57
32:QA:769:G:H4'	32:QA:1513:A:H4'	1.85	0.57
1:YA:2808:U:C2	1:YA:2892:A:C6	2.93	0.57
16:YU:92:ARG:HD2	17:YV:11:GLN:HB2	1.85	0.57
32:XA:405:U:O4	35:XD:2:GLY:N	2.37	0.57
32:XA:1273:G:H3'	32:XA:1274:G:H8	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:XG:139:GLU:O	38:XG:143:ARG:N	2.37	0.57
4:RE:77:ILE:HD13	4:RE:195:LEU:HD13	1.85	0.57
5:RF:198:ALA:HA	5:RF:201:VAL:H	1.69	0.57
12:RQ:62:GLY:HA2	21:RZ:116:VAL:CG2	2.33	0.57
21:RZ:19:ARG:NH1	21:RZ:84:GLU:O	2.36	0.57
36:QE:100:VAL:O	36:QE:107:ARG:NH2	2.35	0.57
50:QS:19:VAL:HG21	50:QS:44:MET:HG3	1.86	0.57
54:QX:2:G:C8	54:QX:3:C:C5	2.93	0.57
1:YA:140:A:H8	1:YA:1408:C:HO2'	1.53	0.57
5:YF:143:ALA:HB1	5:YF:148:LEU:HB2	1.86	0.57
32:XA:407:G:H5''	35:XD:115:ARG:HB3	1.86	0.57
1:RA:221:A:H4'	1:RA:222:A:O5'	2.04	0.57
12:RQ:71:ASP:OD1	12:RQ:71:ASP:N	2.38	0.57
1:YA:2776:A:OP1	1:YA:2776:A:H3'	2.05	0.57
6:YG:29:TRP:O	6:YG:33:ARG:NH1	2.37	0.57
7:YH:164:TYR:HB2	7:YH:167:GLU:HB2	1.86	0.57
32:XA:1111:A:N6	34:XC:176:HIS:O	2.37	0.57
32:XA:1243:C:OP2	52:XU:10:ARG:NH2	2.38	0.57
32:XA:1499:A:H1'	32:XA:1520:G:H5'	1.86	0.57
44:XM:83:ASP:OD1	44:XM:93:ARG:NH2	2.38	0.57
1:RA:918:A:N3	2:RB:80:U:O2'	2.35	0.57
1:RA:1275:A:N1	1:RA:1295:C:O2'	2.32	0.57
1:YA:2701:C:C3'	1:YA:2702:U:H5''	2.30	0.57
1:YA:2832:U:H4'	1:YA:2833:G:H5''	1.87	0.57
2:YB:48:A:H4'	14:YS:95:HIS:HD2	1.70	0.57
12:YQ:34:LEU:HB2	12:YQ:118:LEU:HD22	1.85	0.57
18:YW:92:ARG:NH1	18:YW:94:ASP:OD1	2.38	0.57
32:XA:1498:U:OP2	54:XX:16:C:O2'	2.22	0.57
1:RA:392:C:H5''	1:RA:409:C:H5''	1.87	0.57
9:YN:58:ASP:OD1	9:YN:58:ASP:N	2.35	0.57
15:YT:18:ASP:N	15:YT:18:ASP:OD1	2.37	0.57
32:XA:769:G:H4'	32:XA:1513:A:H4'	1.85	0.57
1:RA:1889:A:N3	1:RA:2086:U:O2'	2.38	0.57
1:RA:2006:C:O2'	1:RA:2823:A:N3	2.36	0.57
12:RQ:59:ARG:HA	21:RZ:180:VAL:CG2	2.35	0.57
32:QA:430:A:OP1	35:QD:9:CYS:HB2	2.05	0.57
35:QD:57:ARG:NH2	35:QD:205:GLU:OE1	2.38	0.57
1:YA:2031:A:N3	1:YA:2455:G:O2'	2.35	0.57
3:YD:258:LYS:CE	3:YD:273:ARG:NH1	2.67	0.57
8:YI:92:VAL:HB	8:YI:120:ILE:HG22	1.87	0.57
31:Y9:6:SER:O	31:Y9:6:SER:OG	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:1266:G:N2	32:XA:1269:A:OP2	2.33	0.57
1:RA:140:A:H8	1:RA:1408:C:HO2'	1.52	0.57
6:RG:151:ALA:HB3	6:RG:153:ARG:HH21	1.70	0.57
35:QD:18:LYS:HE2	35:QD:20:TYR:HE1	1.67	0.57
35:QD:120:LEU:HB3	35:QD:126:ILE:HD11	1.86	0.57
5:YF:116:ASP:OD1	5:YF:119:ARG:NH2	2.38	0.57
12:YQ:31:ASP:OD1	12:YQ:134:ARG:NH1	2.38	0.57
15:YT:1:MET:HE2	15:YT:3:ARG:HG2	1.87	0.57
20:YY:17:SER:OG	20:YY:71:LYS:NZ	2.35	0.57
32:XA:272:C:H2'	32:XA:273:A:H8	1.68	0.57
50:XS:41:VAL:HG23	50:XS:43:GLU:H	1.70	0.57
32:QA:1071:C:H2'	32:QA:1072:G:H8	1.70	0.57
44:QM:16:ASP:N	44:QM:16:ASP:OD1	2.37	0.57
1:YA:138:G:N2	19:YX:44:GLU:OE1	2.37	0.57
49:XR:45:SER:HG	49:XR:47:THR:HG1	1.53	0.57
1:RA:18:C:O2'	1:RA:553:U:OP1	2.23	0.56
13:RR:56:LYS:NZ	13:RR:90:ARG:O	2.37	0.56
48:QQ:66:SER:OG	48:QQ:67:LYS:O	2.22	0.56
1:YA:1086:A:O2'	1:YA:1103:A:N6	2.38	0.56
32:XA:1124:G:H1'	41:XJ:38:ILE:HD13	1.87	0.56
1:RA:2547:U:O2	10:RO:23:ARG:NH2	2.37	0.56
3:RD:12:SER:HB3	3:RD:208:LYS:HB3	1.85	0.56
41:QJ:11:PHE:HE2	41:QJ:67:THR:HG22	1.70	0.56
42:QK:52:GLY:H	42:QK:55:LYS:HE2	1.69	0.56
1:YA:2788:C:O2'	1:YA:2809:A:N3	2.35	0.56
1:YA:2867:G:O2'	1:YA:2868:A:O5'	2.23	0.56
9:RN:17:ASP:OD1	9:RN:56:ASN:ND2	2.38	0.56
26:R4:12:ALA:HA	26:R4:29:PRO:HA	1.87	0.56
41:QJ:66:ARG:HB3	41:QJ:68:HIS:CE1	2.39	0.56
1:YA:67:U:H3	1:YA:74:A:H2	1.54	0.56
1:YA:336:C:HO2'	20:YY:35:TYR:HH	1.52	0.56
1:YA:2729:G:H1'	4:YE:187:ALA:HB2	1.87	0.56
1:YA:2743:C:OP1	31:Y9:33:LYS:NZ	2.38	0.56
32:XA:516:U:O2'	32:XA:519:C:N3	2.36	0.56
32:XA:529:G:O6	43:XL:49:ASN:ND2	2.37	0.56
1:RA:1009:A:N3	1:RA:1153:C:O2'	2.37	0.56
32:QA:501:C:H2'	32:QA:502:G:H8	1.70	0.56
48:QQ:81:ARG:HE	48:QQ:84:LEU:HD11	1.71	0.56
1:YA:2306:C:N4	6:YG:42:GLY:O	2.38	0.56
31:Y9:25:VAL:HB	31:Y9:34:GLN:HB2	1.88	0.56
32:XA:768:A:N3	32:XA:1512:U:O2'	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:1238:A:H62	32:XA:1301:U:H3	1.53	0.56
40:XI:53:VAL:HG11	40:XI:85:LEU:HD11	1.86	0.56
46:XO:24:SER:OG	46:XO:25:THR:N	2.39	0.56
1:RA:1812:A:H2'	1:RA:1813:G:H8	1.70	0.56
1:RA:2114:A:N7	1:RA:2168:G:N2	2.52	0.56
32:QA:1314:C:OP2	50:QS:4:SER:OG	2.20	0.56
42:QK:43:SER:OG	42:QK:44:SER:N	2.38	0.56
1:YA:2099:U:O4	1:YA:2190:G:O6	2.22	0.56
1:YA:2335:A:O2'	1:YA:2336:A:H2'	2.06	0.56
2:YB:7:G:H3'	2:YB:8:U:H5''	1.88	0.56
8:YI:99:GLU:OE2	8:YI:103:ARG:NH2	2.38	0.56
1:RA:1542:G:O6	1:RA:1543:A:N6	2.38	0.56
32:QA:1412:C:H2'	32:QA:1413:A:C8	2.41	0.56
35:QD:61:LYS:NZ	35:QD:72:GLU:OE1	2.36	0.56
1:RA:873:G:H4'	12:RQ:63:LYS:NZ	2.20	0.56
1:RA:1041:C:O2	1:RA:1115:G:N2	2.38	0.56
11:RP:118:GLY:O	11:RP:137:LYS:NZ	2.38	0.56
21:RZ:158:PRO:HG2	21:RZ:161:VAL:HG21	1.87	0.56
32:QA:1367:C:H4'	41:QJ:48:THR:HG21	1.87	0.56
7:YH:3:ARG:HH11	7:YH:3:ARG:HG2	1.69	0.56
25:Y3:12:PRO:HA	25:Y3:15:TYR:HD2	1.70	0.56
32:XA:452:A:N7	32:XA:480:U:O4	2.39	0.56
40:XI:9:ARG:HB3	40:XI:104:ARG:HH21	1.70	0.56
43:XL:76:ASN:HD21	43:XL:108:ALA:H	1.54	0.56
1:RA:458:G:N2	1:RA:470:A:OP2	2.31	0.56
32:QA:1096:C:H2'	32:QA:1097:C:H6	1.71	0.56
1:YA:247:G:O6	30:Y8:12:LYS:NZ	2.33	0.56
1:YA:1062:G:H2'	1:YA:1063:G:C8	2.40	0.56
5:YF:117:ARG:NH2	5:YF:189:THR:O	2.39	0.56
32:XA:235:C:H2'	32:XA:236:G:H8	1.71	0.56
32:XA:1224:G:N3	44:XM:102:ARG:NH1	2.45	0.56
36:XE:102:ALA:HB1	36:XE:106:PRO:HG2	1.88	0.56
44:XM:105:THR:OG1	44:XM:106:ASN:N	2.39	0.56
7:RH:70:THR:O	7:RH:74:ASN:N	2.36	0.56
32:QA:56:U:H2'	32:QA:57:G:C8	2.41	0.56
43:QL:71:PRO:O	43:QL:102:ARG:NH1	2.39	0.56
48:QQ:79:SER:OG	48:QQ:80:GLY:N	2.38	0.56
32:XA:1189:C:H5''	34:XC:5:ILE:HG21	1.88	0.56
32:XA:1354:C:H2'	32:XA:1355:G:H8	1.70	0.56
32:XA:1355:G:H2'	32:XA:1356:G:H8	1.71	0.56
32:XA:1450:U:O2'	32:XA:1451:A:N7	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:1533:C:H2'	32:XA:1534:A:H5'	1.86	0.56
48:XQ:6:LEU:HD13	48:XQ:23:VAL:HG11	1.87	0.56
32:QA:501:C:H2'	32:QA:502:G:C8	2.41	0.56
32:QA:953:G:N7	44:QM:104:ARG:NH2	2.54	0.56
39:QH:41:ARG:NH2	39:QH:123:GLU:OE1	2.38	0.56
1:YA:363(B):G:H2'	1:YA:363(C):G:H8	1.70	0.56
1:YA:2134:A:N6	1:YA:2156:G:O2'	2.39	0.56
8:YI:88:ILE:O	8:YI:121:LYS:NZ	2.38	0.56
12:YQ:10:ARG:HD2	21:YZ:196:VAL:HG21	1.87	0.56
34:XC:74:GLY:HA2	34:XC:77:ILE:HD12	1.88	0.56
12:RQ:59:ARG:HG3	21:RZ:180:VAL:CG2	2.36	0.55
32:QA:1067:A:N1	32:QA:1108:G:O2'	2.36	0.55
6:YG:37:VAL:HG22	6:YG:159:VAL:HG12	1.88	0.55
8:YI:110:ASP:OD2	8:YI:113:ARG:NH2	2.39	0.55
27:Y5:16:ARG:NH1	27:Y5:17:ASP:OD1	2.35	0.55
11:RP:52:GLU:OE1	11:RP:55:ARG:NH1	2.40	0.55
12:RQ:58:PHE:CD2	12:RQ:61:GLY:HA3	2.41	0.55
1:YA:29:U:H5''	16:YU:7:GLY:HA2	1.87	0.55
1:RA:2224:G:OP1	3:RD:268:ARG:NH1	2.39	0.55
1:RA:2576:G:O2'	1:RA:2579:C:OP2	2.19	0.55
32:QA:1061:G:OP1	41:QJ:59:SER:OG	2.23	0.55
1:YA:1163:G:OP1	17:YV:24:LYS:NZ	2.39	0.55
1:YA:2784:C:O2'	4:YE:37:ARG:NH1	2.39	0.55
2:YB:40:U:O4	26:Y4:1:MET:N	2.39	0.55
17:YV:62:LEU:HD12	17:YV:93:GLU:HG2	1.87	0.55
32:XA:503:C:OP1	43:XL:119:LYS:NZ	2.34	0.55
32:XA:745:C:OP1	32:XA:851:G:O2'	2.23	0.55
1:RA:907:U:O2'	12:RQ:101:ARG:NH2	2.39	0.55
1:RA:987:G:O2'	1:RA:1000:A:N3	2.37	0.55
1:RA:1788:C:OP1	3:RD:222:ARG:NH2	2.40	0.55
1:RA:2517:C:N3	1:RA:2542:A:N6	2.54	0.55
32:QA:1243:C:H5''	52:QU:8:THR:HG21	1.88	0.55
34:QC:59:ARG:HD3	34:QC:64:VAL:HG12	1.87	0.55
1:YA:1190:G:H5'	11:YP:32:THR:HA	1.88	0.55
21:YZ:183:LEU:O	21:YZ:186:GLU:N	2.39	0.55
32:XA:135:C:H2'	32:XA:136:C:H5'	1.88	0.55
32:XA:1354:C:H2'	32:XA:1355:G:C8	2.41	0.55
32:XA:1446:A:O2'	32:XA:1447:G:O5'	2.23	0.55
1:RA:2814:C:O2'	27:R5:29:THR:OG1	2.17	0.55
4:RE:54:GLN:HB2	4:RE:76:ARG:HG3	1.87	0.55
32:QA:266:G:O2'	32:QA:267:C:OP2	2.23	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:522:C:H41	43:QL:53:ARG:HH22	1.55	0.55
32:QA:689:C:OP2	42:QK:55:LYS:NZ	2.40	0.55
1:YA:620:G:H4'	1:YA:621:A:C5'	2.36	0.55
1:RA:2395:C:O2'	23:R1:30:VAL:O	2.24	0.55
1:RA:2521:C:O2'	1:RA:2564:A:N3	2.37	0.55
22:Y0:27:GLU:HG3	22:Y0:68:GLU:HA	1.87	0.55
32:XA:1342:C:H2'	32:XA:1343:G:H8	1.72	0.55
32:XA:1431:C:H2'	32:XA:1432:G:O4'	2.07	0.55
39:XH:106:GLY:O	39:XH:122:ARG:NH2	2.40	0.55
41:XJ:5:ARG:HE	41:XJ:100:THR:HA	1.71	0.55
48:XQ:18:THR:OG1	48:XQ:69:LYS:NZ	2.39	0.55
1:RA:23:G:OP1	1:RA:504:U:N3	2.36	0.55
21:RZ:31:ARG:NH2	21:RZ:93:ASP:OD2	2.35	0.55
32:QA:1296:C:OP1	44:QM:44:ARG:NH2	2.39	0.55
1:YA:270(N):G:N3	8:YI:50:ARG:NH1	2.54	0.55
1:YA:1509:C:H3'	1:YA:1510:A:H5''	1.88	0.55
1:YA:2068:U:H3	1:YA:2430:A:H2	1.55	0.55
18:YW:12:ILE:O	18:YW:101:SER:OG	2.25	0.55
21:YZ:92:SER:OG	21:YZ:94:GLU:OE1	2.25	0.55
32:XA:80:G:H1	32:XA:89:U:H3	1.54	0.55
32:XA:123:C:OP1	32:XA:311:C:O2'	2.21	0.55
50:XS:32:LYS:HA	50:XS:50:ALA:HB3	1.89	0.55
1:RA:2847:U:OP1	15:RT:98:LYS:NZ	2.33	0.55
32:QA:1347:G:N2	32:QA:1374:A:OP2	2.24	0.55
41:QJ:58:ASP:OD2	41:QJ:58:ASP:N	2.36	0.55
1:YA:2151:G:H2'	1:YA:2152:G:H8	1.72	0.55
32:XA:624:C:H2'	32:XA:625:G:H8	1.70	0.55
34:XC:17:ASP:O	34:XC:54:ARG:NH2	2.39	0.55
35:XD:65:ARG:NH1	35:XD:70:ILE:O	2.39	0.55
38:XG:62:PHE:HA	38:XG:124:LEU:HD11	1.88	0.55
40:XI:13:ALA:HB2	40:XI:68:GLY:HA3	1.89	0.55
1:RA:247:G:H4'	1:RA:386:G:C5	2.41	0.55
1:RA:807:U:O2'	1:RA:2060:A:N1	2.40	0.55
18:RW:88:ARG:NH1	18:RW:94:ASP:OD2	2.40	0.55
33:QB:87:ARG:NH2	33:QB:220:ASP:OD2	2.39	0.55
1:YA:527:C:N4	1:YA:2779:U:OP2	2.40	0.55
1:YA:666:G:N2	30:Y8:2:PRO:O	2.39	0.55
32:XA:170:U:H2'	32:XA:171:A:H8	1.72	0.55
32:XA:657:G:N2	46:XO:22:THR:OG1	2.37	0.55
1:RA:1022:G:N2	1:RA:1023:U:O4	2.38	0.55
30:R8:26:LYS:HD3	30:R8:47:LYS:HB3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:1250:A:OP1	40:QI:67:GLY:N	2.40	0.55
33:QB:178:ARG:NH2	33:QB:196:LEU:O	2.40	0.55
34:QC:20:SER:OG	34:QC:22:TRP:NE1	2.40	0.55
1:YA:617:G:OP1	5:YF:40:GLN:NE2	2.39	0.55
32:XA:264:U:O2'	48:XQ:64:PRO:O	2.23	0.55
40:XI:20:ARG:NH2	40:XI:60:ASP:OD1	2.40	0.55
1:RA:265:A:N6	1:RA:427:U:O2'	2.40	0.54
32:QA:811:C:O2'	32:QA:901:A:N1	2.41	0.54
4:YE:105:THR:HB	4:YE:197:ILE:HG23	1.89	0.54
11:YP:4:SER:O	11:YP:7:ARG:NH2	2.39	0.54
1:RA:1359:A:H62	1:RA:1372:U:H3	1.55	0.54
8:RI:77:LEU:CD2	8:RI:140:LEU:HB3	2.38	0.54
37:QF:30:LEU:HD23	37:QF:75:LEU:HD11	1.89	0.54
3:YD:71:ASP:HB2	3:YD:103:ARG:HH12	1.73	0.54
32:XA:1123:A:H4'	41:XJ:36:GLY:HA3	1.89	0.54
32:XA:1329:A:H5'	44:XM:29:ARG:HE	1.73	0.54
35:XD:4:TYR:OH	35:XD:10:ARG:NH2	2.40	0.54
38:XG:11:GLN:NE2	38:XG:12:LEU:O	2.40	0.54
42:XK:33:THR:HA	42:XK:39:PRO:HA	1.87	0.54
1:RA:1286:A:O2'	1:RA:1288:U:OP2	2.22	0.54
1:RA:1992:G:N2	1:RA:1996:C:O2'	2.40	0.54
1:RA:2680:C:H5'	4:RE:189:PRO:HA	1.88	0.54
50:QS:72:GLY:HA2	50:QS:75:ALA:HB3	1.89	0.54
2:YB:90:C:OP2	12:YQ:16:ARG:NH2	2.40	0.54
33:XB:47:THR:HG23	33:XB:202:PRO:HG2	1.88	0.54
38:XG:94:ARG:NH1	38:XG:98:SER:OG	2.40	0.54
48:XQ:81:ARG:NH2	48:XQ:83:ASP:OD2	2.39	0.54
5:RF:63:LYS:NZ	5:RF:75:HIS:O	2.37	0.54
8:RI:88:ILE:HG13	8:RI:121:LYS:HA	1.89	0.54
16:RU:85:LYS:HG3	16:RU:117:GLN:HG3	1.88	0.54
32:XA:1342:C:H2'	32:XA:1343:G:C8	2.42	0.54
1:RA:675:A:OP1	5:RF:63:LYS:NZ	2.36	0.54
1:RA:2133:G:O2'	1:RA:2158:A:N1	2.41	0.54
1:RA:2183:C:H2'	1:RA:2184:G:C8	2.42	0.54
1:RA:2805:G:H2'	1:RA:2807:G:C8	2.42	0.54
33:QB:23:ARG:NH2	33:QB:191:ASP:OD1	2.40	0.54
1:YA:1427:A:H4'	1:YA:1428:C:O5'	2.07	0.54
1:RA:177:G:H5'	1:RA:178:G:C8	2.42	0.54
1:RA:873:G:H4'	12:RQ:63:LYS:HZ3	1.73	0.54
1:RA:2811:G:C6	1:RA:2891:G:N2	2.75	0.54
4:RE:105:THR:OG1	4:RE:199:ARG:NH2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:RN:30:ILE:HG23	9:RN:52:VAL:HG11	1.89	0.54
21:RZ:163:LEU:HD13	21:RZ:167:PRO:HD3	1.88	0.54
32:QA:673:G:H2'	32:QA:674:G:H8	1.72	0.54
32:QA:1350:A:OP1	40:QI:121:ARG:NH1	2.40	0.54
54:QX:12:A:O2'	54:QX:13:A:N7	2.39	0.54
1:YA:2030:A:H4'	1:YA:2031:A:H8	1.73	0.54
1:YA:2741:A:H5''	31:Y9:22:ARG:HH12	1.73	0.54
32:XA:45:U:H3	32:XA:396:G:H1	1.54	0.54
35:XD:32:ALA:O	35:XD:35:ARG:N	2.38	0.54
1:RA:1731:G:H2'	1:RA:1732:A:H8	1.73	0.54
32:QA:1502:A:H5'	32:QA:1504:G:N7	2.23	0.54
42:QK:16:SER:OG	42:QK:106:LYS:NZ	2.41	0.54
50:QS:32:LYS:HA	50:QS:50:ALA:HB3	1.88	0.54
9:YN:63:THR:OG1	9:YN:64:GLY:N	2.40	0.54
31:Y9:2:LYS:NZ	31:Y9:31:LYS:O	2.39	0.54
32:XA:269:C:H2'	32:XA:270:A:C8	2.43	0.54
32:XA:1290:G:H5'	38:XG:38:LEU:HD11	1.89	0.54
35:XD:20:TYR:O	35:XD:20:TYR:CD1	2.61	0.54
52:XU:6:ARG:HE	52:XU:15:ARG:HH21	1.55	0.54
1:RA:468:G:OP2	29:R7:37:LYS:NZ	2.40	0.54
16:RU:91:ASP:HA	16:RU:95:LEU:HB2	1.88	0.54
43:QL:60:LEU:HD12	43:QL:62:SER:H	1.73	0.54
1:YA:96:G:OP1	24:Y2:46:GLN:NE2	2.40	0.54
1:YA:2335:A:O2'	1:YA:2336:A:O5'	2.26	0.54
1:YA:2684:U:O2'	10:YO:68:GLU:OE1	2.18	0.54
4:YE:92:THR:OG1	4:YE:93:VAL:N	2.40	0.54
6:YG:38:VAL:HG22	6:YG:93:THR:HG22	1.90	0.54
32:XA:753:A:H4'	32:XA:754:C:O5'	2.08	0.54
32:XA:789:U:H4'	54:XX:14:A:C2	2.42	0.54
36:XE:137:GLU:OE1	36:XE:140:ARG:NH1	2.40	0.54
45:XN:23:ARG:HH21	45:XN:30:ALA:HB2	1.73	0.54
1:RA:1800:C:H42	1:RA:1817:G:N2	2.05	0.54
1:RA:2305:A:N6	6:RG:154:GLY:O	2.41	0.54
23:R1:87:PRO:HA	23:R1:90:ILE:HG22	1.89	0.54
32:QA:736:C:H2'	32:QA:737:A:C8	2.43	0.54
34:QC:108:ASN:HD21	34:QC:144:SER:HB3	1.73	0.54
35:QD:2:GLY:N	35:QD:3:ARG:O	2.41	0.54
1:YA:312:G:H5'	1:YA:331:A:O2'	2.08	0.54
1:YA:2712:U:O2'	1:YA:2712(A):A:H8	1.89	0.54
32:XA:129(A):G:N2	32:XA:188:U:O2'	2.41	0.54
33:XB:192:SER:OG	33:XB:193:ASP:N	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:322:A:H5'	1:RA:340:A:H1'	1.89	0.54
1:RA:2364:C:OP1	22:R0:55:ARG:NH1	2.39	0.54
6:RG:124:SER:HB2	6:RG:131:TYR:HE1	1.73	0.54
41:QJ:23:ILE:HG23	41:QJ:85:LEU:HD21	1.90	0.54
1:YA:1019:U:H3	1:YA:1142(A):A:H62	1.56	0.54
1:YA:1097:U:H3'	1:YA:1098:A:H8	1.74	0.54
18:YW:4:LYS:HB2	18:YW:106:ILE:HG12	1.90	0.54
32:XA:1291:G:H4'	40:XI:39:GLY:HA3	1.88	0.54
44:XM:79:LYS:NZ	44:XM:79:LYS:O	2.41	0.54
1:RA:137(A):G:H21	19:RX:41:ASN:HD21	1.55	0.53
3:RD:71:ASP:OD2	3:RD:103:ARG:NH2	2.35	0.53
23:R1:46:LEU:O	23:R1:47:GLN:NE2	2.40	0.53
32:QA:760:G:N2	48:QQ:94:ASN:OD1	2.41	0.53
33:QB:107:THR:HA	33:QB:110:GLN:HG3	1.89	0.53
45:QN:27:CYS:SG	45:QN:28:GLY:N	2.81	0.53
1:YA:336:C:O2'	20:YY:35:TYR:OH	2.23	0.53
10:YO:48:PRO:HB3	32:XA:1422:G:H5''	1.90	0.53
32:XA:958:A:N3	32:XA:985:C:O2'	2.35	0.53
32:XA:1264:C:H2'	32:XA:1265:G:H8	1.73	0.53
33:XB:178:ARG:NH2	33:XB:198:ASP:OD1	2.36	0.53
2:RB:14:U:OP2	2:RB:70:C:O2'	2.22	0.53
6:RG:101:ILE:HD11	26:R4:25:TYR:H	1.74	0.53
10:RO:88:ASN:HD21	10:RO:92:GLU:HB2	1.73	0.53
21:RZ:110:GLY:HA3	21:RZ:174:VAL:HG11	1.90	0.53
32:QA:768:A:N3	32:QA:1512:U:O2'	2.41	0.53
33:QB:8:LYS:H	33:QB:11:LEU:HD12	1.71	0.53
33:QB:98:LEU:HB2	33:QB:101:MET:HE3	1.89	0.53
1:YA:508:G:HO2'	1:YA:509:C:P	2.32	0.53
1:YA:1061:U:H3'	1:YA:1062:G:H5''	1.90	0.53
1:YA:1364:G:OP2	23:Y1:2:SER:N	2.41	0.53
1:YA:1964:G:O2'	1:YA:1967:C:OP2	2.17	0.53
1:YA:2352:A:N6	1:YA:2365:G:O2'	2.42	0.53
32:XA:1277:C:O2'	32:XA:1279:A:H1'	2.09	0.53
1:RA:1286:A:HO2'	1:RA:1288:U:P	2.32	0.53
32:QA:278:G:OP2	48:QQ:92:ARG:NH2	2.41	0.53
5:YF:185:ASP:OD1	5:YF:188:ARG:NH1	2.38	0.53
7:YH:90:LYS:HD3	7:YH:159:GLU:HG2	1.90	0.53
32:XA:1492:A:H1'	32:XA:1493:A:H8	1.72	0.53
34:XC:18:TRP:O	34:XC:54:ARG:NH2	2.40	0.53
36:XE:78:HIS:HB2	39:XH:104:ARG:HG2	1.90	0.53
1:RA:74:A:H4'	1:RA:75:G:O5'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:526:A:O2'	1:RA:2043:C:O2	2.21	0.53
1:RA:2893:G:H5''	1:RA:2894:G:H5'	1.90	0.53
32:QA:56:U:H2'	32:QA:57:G:H8	1.73	0.53
32:QA:359:U:H2'	32:QA:360:A:C8	2.43	0.53
32:QA:552:U:O2'	43:QL:86:ARG:O	2.26	0.53
35:QD:100:ARG:NH2	35:QD:136:PRO:O	2.42	0.53
39:QH:49:GLU:OE2	39:QH:62:TYR:OH	2.26	0.53
1:YA:2429:G:O6	11:YP:61:ARG:NH2	2.34	0.53
41:XJ:51:ARG:HB2	41:XJ:60:ARG:HA	1.91	0.53
1:RA:1138:G:O2'	9:RN:102:ALA:O	2.26	0.53
1:RA:2068:U:H3	1:RA:2430:A:H2	1.55	0.53
1:RA:2115:G:N2	1:RA:2165:G:N7	2.52	0.53
7:RH:71:LEU:HA	7:RH:74:ASN:HB2	1.90	0.53
32:QA:1002:G:H2'	32:QA:1003:G:C8	2.44	0.53
32:QA:1142:G:H3'	32:QA:1143:G:H8	1.73	0.53
1:YA:1869:G:H5'	1:YA:1870:C:OP2	2.08	0.53
5:YF:60:SER:OG	5:YF:61:GLY:N	2.38	0.53
7:YH:101:ARG:HB3	7:YH:117:PRO:HG2	1.91	0.53
32:XA:28:G:O2'	32:XA:296:U:OP1	2.24	0.53
32:XA:1296:C:OP1	44:XM:44:ARG:NH2	2.42	0.53
37:XF:14:LEU:HD22	37:XF:18:GLN:HB2	1.90	0.53
42:XK:34:ASP:OD1	42:XK:38:ASN:N	2.40	0.53
48:XQ:66:SER:OG	48:XQ:67:LYS:N	2.42	0.53
1:RA:2785:C:OP1	4:RE:41:LYS:NZ	2.37	0.53
3:RD:146:GLU:HB2	3:RD:189:CYS:HB3	1.91	0.53
1:YA:1795:C:O2	3:YD:255:LYS:NZ	2.39	0.53
25:Y3:18:ASP:OD1	25:Y3:18:ASP:N	2.36	0.53
32:QA:1386:G:H2'	32:QA:1387:G:H8	1.74	0.53
52:QU:22:ARG:HE	52:QU:23:PRO:HD2	1.74	0.53
4:YE:36:ARG:NH1	4:YE:85:ASN:OD1	2.42	0.53
5:YF:107:LYS:HD2	5:YF:206:ILE:HA	1.91	0.53
12:YQ:56:ARG:HE	21:YZ:180:VAL:HG13	1.74	0.53
32:XA:152:A:N6	32:XA:169:C:N4	2.56	0.53
46:XO:7:GLU:OE2	46:XO:38:ARG:NH2	2.42	0.53
1:RA:848:G:H2'	1:RA:849:A:C8	2.43	0.53
17:RV:60:GLU:OE2	17:RV:97:LYS:NZ	2.40	0.53
52:QU:24:ARG:HH12	52:QU:26:LYS:H	1.57	0.53
1:YA:2576:G:O2'	1:YA:2579:C:OP2	2.23	0.53
3:YD:206:LEU:HA	3:YD:211:ARG:HE	1.73	0.53
32:XA:992:U:O2'	32:XA:993:G:OP2	2.22	0.53
34:XC:20:SER:HG	34:XC:22:TRP:NE1	2.06	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:XD:108:LEU:HD23	35:XD:174:LEU:HD13	1.91	0.53
40:XI:25:LYS:N	40:XI:60:ASP:OD2	2.42	0.53
1:RA:626:U:H5''	1:RA:627:A:H5'	1.91	0.53
1:RA:1056:G:H5''	1:RA:1057:A:H5'	1.90	0.53
25:R3:12:PRO:O	25:R3:20:LYS:NZ	2.42	0.53
32:QA:12:U:O4	32:QA:22:G:O6	2.27	0.53
32:QA:34:C:H2'	32:QA:35:G:H8	1.73	0.53
32:QA:359:U:H2'	32:QA:360:A:H8	1.74	0.53
40:QI:17:VAL:HG22	40:QI:63:ILE:HD12	1.91	0.53
54:QX:7:G:N1	54:QX:8:A:N6	2.56	0.53
1:YA:31:C:O2'	1:YA:1238:G:H5'	2.08	0.53
1:YA:1127:A:N7	1:YA:2488:A:O2'	2.34	0.53
1:YA:2125:G:O2'	1:YA:2173:A:N6	2.41	0.53
7:YH:43:VAL:HG22	7:YH:52:VAL:HG22	1.90	0.53
11:YP:65:ARG:O	11:YP:68:GLN:NE2	2.42	0.53
1:RA:1149:G:H2'	1:RA:1150:C:C6	2.44	0.53
1:RA:2364:C:H2'	1:RA:2365:G:O4'	2.09	0.53
1:RA:2790:A:H2'	1:RA:2791:C:H5''	1.92	0.53
3:RD:69:ARG:NH2	3:RD:128:GLY:O	2.42	0.53
36:QE:122:GLU:O	36:QE:126:ARG:NH2	2.39	0.53
49:QR:31:LEU:HD12	49:QR:66:LEU:HB2	1.91	0.53
1:YA:1340:U:OP2	19:YX:78:LYS:NZ	2.42	0.53
1:YA:2145:C:O2	1:YA:2147:G:N2	2.43	0.53
1:YA:2306:C:H3'	1:YA:2307:G:H5''	1.89	0.53
32:XA:1233:G:O2'	32:XA:1365:G:OP1	2.26	0.53
1:RA:764:A:H5''	3:RD:210:GLY:HA3	1.90	0.52
1:RA:1441:G:H2'	1:RA:1442:G:H8	1.73	0.52
9:RN:58:ASP:OD1	9:RN:58:ASP:N	2.40	0.52
22:R0:18:ALA:O	22:R0:20:ARG:NH1	2.38	0.52
32:QA:209:U:H2'	32:QA:210:U:H4'	1.91	0.52
32:XA:701:C:O2	32:XA:703:G:N1	2.42	0.52
32:XA:890:G:O2'	32:XA:906:G:O6	2.26	0.52
32:XA:953:G:N7	44:XM:104:ARG:NH2	2.57	0.52
35:XD:191:ARG:NH2	35:XD:200:GLU:OE1	2.38	0.52
54:XX:3:C:H2'	54:XX:4:A:H8	1.74	0.52
1:RA:511:U:H4'	1:RA:1235:G:H4'	1.91	0.52
1:RA:995:C:O2	9:RN:3:THR:OG1	2.26	0.52
1:RA:2134:A:N7	1:RA:2157:G:O2'	2.42	0.52
33:QB:76:GLN:NE2	33:QB:206:ASP:OD1	2.41	0.52
37:QF:79:LEU:HB3	37:QF:88:VAL:HG21	1.91	0.52
1:YA:554:U:HO2'	1:YA:556:G:H8	1.56	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1000:A:H2'	1:YA:1001:A:C8	2.44	0.52
1:YA:1363:C:O2'	1:YA:1809:A:N3	2.40	0.52
32:XA:1310:G:O2'	32:XA:1311:G:OP1	2.26	0.52
43:XL:71:PRO:O	43:XL:102:ARG:NH1	2.42	0.52
1:RA:77:C:O3'	24:R2:14:ARG:NH2	2.40	0.52
1:RA:220:G:O2'	1:RA:233:A:N3	2.41	0.52
1:RA:2344:U:OP1	28:R6:37:ARG:NH1	2.38	0.52
17:RV:24:LYS:HA	17:RV:92:THR:HG23	1.90	0.52
32:QA:1151:A:H2'	32:QA:1152:A:C8	2.44	0.52
32:QA:1200:C:O2'	32:QA:1201:A:OP2	2.21	0.52
32:QA:1435:G:H2'	32:QA:1436:U:C6	2.44	0.52
1:YA:30:G:O2'	1:YA:1214:A:N3	2.34	0.52
1:YA:2114:A:H2'	1:YA:2168:G:H1'	1.92	0.52
8:YI:102:SER:OG	8:YI:103:ARG:N	2.38	0.52
9:YN:12:ARG:NH2	9:YN:50:ASP:OD2	2.42	0.52
20:YY:15:VAL:HG21	20:YY:42:VAL:HG11	1.91	0.52
32:XA:1368:G:OP1	40:XI:111:ARG:NH1	2.34	0.52
34:XC:23:TYR:HB2	41:XJ:10:GLY:HA2	1.92	0.52
50:XS:33:THR:HG23	50:XS:35:SER:H	1.73	0.52
1:RA:1482:U:H5'	1:RA:1483:G:OP2	2.09	0.52
18:RW:68:ARG:NE	18:RW:110:LYS:O	2.42	0.52
32:QA:130:A:N6	32:QA:233:C:O2	2.41	0.52
32:QA:1269:A:O2'	32:QA:1325:C:O2'	2.20	0.52
35:QD:3:ARG:HD3	35:QD:118:ARG:HD3	1.91	0.52
38:QG:99:LEU:HD22	38:QG:102:ARG:HH12	1.75	0.52
1:YA:1020:A:N6	1:YA:1141:U:O2'	2.42	0.52
1:YA:2808:U:N3	1:YA:2892:A:C6	2.77	0.52
3:YD:164:GLN:OE1	3:YD:176:ARG:NH2	2.43	0.52
22:Y0:26:TYR:N	22:Y0:29:GLN:OE1	2.41	0.52
27:Y5:41:PRO:O	27:Y5:44:THR:OG1	2.28	0.52
32:XA:335:C:O2'	32:XA:1433:A:N3	2.37	0.52
32:XA:1235:U:H5''	52:XU:3:LYS:HE2	1.91	0.52
46:XO:82:ILE:HB	46:XO:87:ILE:HB	1.91	0.52
1:RA:1786:A:C8	1:RA:1938:A:N6	2.77	0.52
1:RA:2529:G:H5''	1:RA:2530:A:H5''	1.92	0.52
11:RP:62:LEU:HD12	30:R8:30:ARG:HH21	1.74	0.52
16:RU:29:SER:OG	16:RU:30:LYS:NZ	2.40	0.52
33:QB:18:GLY:O	33:QB:204:ASN:ND2	2.43	0.52
40:QI:28:VAL:O	40:QI:31:GLN:N	2.42	0.52
1:YA:263:C:H2'	1:YA:264:C:O4'	2.10	0.52
26:Y4:2:LYS:HB2	26:Y4:5:ILE:HD13	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Y8:11:LYS:NZ	30:Y8:65:GLU:OE1	2.42	0.52
32:XA:17:U:H2'	32:XA:18:C:C6	2.45	0.52
40:XI:26:VAL:HA	40:XI:61:ALA:HB3	1.91	0.52
1:RA:1869:G:H5'	1:RA:1870:C:OP2	2.09	0.52
32:QA:1026:G:H5''	32:QA:1027:C:H5	1.73	0.52
32:QA:1060:C:H2'	32:QA:1061:G:H8	1.75	0.52
1:YA:2845:G:H2'	1:YA:2846:G:C8	2.44	0.52
9:YN:97:ARG:HA	9:YN:100:GLU:HB2	1.90	0.52
1:RA:1681:G:HO2'	1:RA:1762:A:HO2'	1.56	0.52
26:R4:26:SER:OG	26:R4:28:LYS:O	2.27	0.52
32:QA:1112:C:O2	34:QC:179:ARG:NH1	2.43	0.52
40:QI:9:ARG:HG2	40:QI:14:VAL:HG12	1.91	0.52
42:QK:57:THR:HG22	42:QK:59:TYR:H	1.74	0.52
36:XE:81:GLU:HG2	36:XE:90:VAL:HG23	1.92	0.52
1:RA:577:G:O2'	1:RA:1254:A:OP1	2.24	0.52
1:RA:654(A):G:H1	1:RA:654(T):C:H42	1.58	0.52
1:RA:1138:G:H21	9:RN:106:MET:HE3	1.75	0.52
1:RA:2011:U:OP2	18:RW:16:LYS:NZ	2.30	0.52
1:RA:2314:C:H2'	1:RA:2315:G:H8	1.74	0.52
2:RB:13:A:N1	2:RB:69:G:O2'	2.34	0.52
7:RH:40:GLU:OE2	7:RH:60:ARG:NH2	2.43	0.52
33:QB:61:LEU:O	33:QB:65:GLY:N	2.36	0.52
1:YA:996:A:H4'	16:YU:92:ARG:NE	2.24	0.52
1:YA:1695:G:N7	3:YD:14:ARG:NH2	2.57	0.52
1:YA:2154:G:H2'	1:YA:2155:G:H8	1.75	0.52
3:YD:12:SER:HB3	3:YD:208:LYS:HB3	1.91	0.52
32:XA:719:C:H1'	49:XR:49:LYS:HB3	1.91	0.52
32:XA:1412:C:H2'	32:XA:1413:A:C8	2.45	0.52
34:XC:156:ARG:NE	34:XC:160:ALA:O	2.39	0.52
45:XN:27:CYS:SG	45:XN:28:GLY:N	2.82	0.52
1:RA:551:G:H5'	1:RA:1220:A:H1'	1.92	0.52
10:RO:49:ARG:NH1	32:QA:1422:G:O3'	2.42	0.52
33:QB:46:LYS:NZ	33:QB:49:GLU:OE1	2.38	0.52
1:YA:631:A:N3	1:YA:2415:G:O2'	2.35	0.52
1:YA:988:A:C6	25:Y3:13:ILE:HG21	2.45	0.52
9:YN:95:PRO:O	9:YN:97:ARG:N	2.41	0.52
32:XA:946:A:H2'	32:XA:947:G:C8	2.45	0.52
34:XC:88:ARG:HA	34:XC:91:LEU:HD12	1.91	0.52
1:RA:288:C:H2'	1:RA:289:A:H8	1.75	0.52
1:RA:1638:C:O3'	1:RA:2709:G:N2	2.43	0.52
1:RA:1952:A:OP1	10:RO:44:LYS:NZ	2.37	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:RD:259:THR:O	3:RD:259:THR:OG1	2.26	0.52
7:RH:84:SER:OG	7:RH:85:LYS:N	2.43	0.52
14:RS:58:LEU:HD12	14:RS:59:LYS:H	1.75	0.52
32:QA:1352:C:OP1	52:QU:3:LYS:NZ	2.37	0.52
32:QA:1356:G:H2'	32:QA:1357:A:C8	2.45	0.52
35:QD:19:LEU:CD2	35:QD:67:ILE:HG13	2.36	0.52
1:YA:414:C:O2	1:YA:1864:U:O2'	2.27	0.52
1:YA:1021:A:H3'	1:YA:1022:G:H5''	1.92	0.52
4:YE:59:VAL:O	4:YE:64:LYS:NZ	2.36	0.52
12:YQ:122:GLY:HA2	12:YQ:125:LEU:HD12	1.92	0.52
26:Y4:15:ILE:HB	26:Y4:32:TYR:HA	1.92	0.52
32:XA:99:C:H2'	32:XA:101:A:C8	2.45	0.52
32:XA:656:C:O2'	46:XO:28:GLN:OE1	2.20	0.52
32:XA:667:G:H4'	46:XO:51:HIS:CE1	2.44	0.52
32:XA:1287:A:H2	32:XA:1353:G:H1'	1.74	0.52
1:RA:1266:G:O2'	1:RA:2012:G:O6	2.22	0.51
10:RO:19:ILE:HG22	10:RO:43:VAL:HA	1.92	0.51
32:QA:1129:C:H4'	32:QA:1130:A:H8	1.76	0.51
36:QE:12:LEU:HB3	36:QE:31:LEU:HB3	1.90	0.51
44:QM:15:VAL:O	44:QM:19:LEU:HB3	2.10	0.51
1:YA:252:G:OP2	11:YP:50:ARG:NH1	2.43	0.51
1:YA:820:A:H4'	1:YA:836:G:N2	2.25	0.51
1:YA:1266:G:O2'	1:YA:2012:G:O6	2.25	0.51
8:YI:141:LYS:HG3	8:YI:143:SER:HB3	1.91	0.51
23:Y1:49:VAL:HG21	23:Y1:70:VAL:HG21	1.91	0.51
32:XA:581:G:N2	32:XA:582:U:O4	2.44	0.51
32:XA:1240:U:OP1	38:XG:119:ARG:NH2	2.42	0.51
1:RA:2816:C:O2	1:RA:2883:A:O2'	2.24	0.51
32:QA:243:A:H4'	32:QA:244:U:O5'	2.10	0.51
32:QA:244:U:O4	32:QA:893:C:N3	2.42	0.51
35:QD:19:LEU:CD2	35:QD:67:ILE:HG12	2.37	0.51
1:YA:1022:G:N2	1:YA:1023:U:O4	2.42	0.51
25:Y3:15:TYR:CD2	25:Y3:53:LEU:HD21	2.45	0.51
32:XA:606:G:H1	32:XA:631:G:H5''	1.75	0.51
1:RA:1006:C:O2'	9:RN:106:MET:O	2.25	0.51
1:RA:2126:A:H4'	1:RA:2127:G:O5'	2.11	0.51
1:RA:2584:U:H2'	1:RA:2585:U:H2'	1.93	0.51
2:RB:8:U:O4	2:RB:112:G:O6	2.28	0.51
32:QA:946:A:H2'	32:QA:947:G:H8	1.75	0.51
32:QA:1192:C:O2	36:QE:25:ARG:NH2	2.44	0.51
35:QD:62:GLN:O	35:QD:66:ARG:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:QG:50:ILE:HG21	38:QG:61:VAL:HG11	1.92	0.51
1:YA:229:A:OP1	1:YA:229:A:H4'	2.08	0.51
1:YA:247:G:H4'	1:YA:386:G:C5	2.46	0.51
1:YA:758:C:O2'	1:YA:1981:A:N3	2.34	0.51
1:YA:1912:A:O2'	32:XA:1494:G:O2'	2.27	0.51
1:YA:2006:C:O2'	1:YA:2823:A:N3	2.43	0.51
1:YA:2679:A:OP2	4:YE:160:TYR:OH	2.28	0.51
1:YA:2809:A:H2'	1:YA:2810:A:C8	2.45	0.51
32:XA:41:G:H2'	32:XA:42:G:H8	1.75	0.51
32:XA:152:A:N6	32:XA:169:C:C4	2.78	0.51
32:XA:254:G:O2'	48:XQ:16:GLN:O	2.27	0.51
32:XA:375:U:O2	47:XP:28:ARG:NH1	2.44	0.51
32:XA:745:C:H2'	32:XA:746:A:H8	1.73	0.51
32:XA:966:G:C2	53:XV:34:C:H5'	2.45	0.51
1:RA:820:A:H4'	1:RA:836:G:H22	1.76	0.51
1:RA:1786:A:C8	1:RA:1938:A:C6	2.98	0.51
7:RH:89:ILE:HG22	7:RH:162:ILE:HG23	1.92	0.51
14:RS:35:ILE:HD11	14:RS:101:LEU:HD12	1.92	0.51
23:R1:83:GLU:HG2	23:R1:85:LEU:H	1.75	0.51
32:QA:426:G:OP1	35:QD:36:ARG:NH1	2.43	0.51
32:QA:430:A:P	35:QD:22:LYS:NZ	2.82	0.51
32:QA:767:A:O2'	32:QA:1524:C:O2	2.29	0.51
32:QA:778:G:O2'	42:QK:120:ARG:O	2.29	0.51
32:QA:1349:A:H62	32:QA:1373:G:N2	2.08	0.51
1:YA:995:C:O2	9:YN:3:THR:OG1	2.23	0.51
32:XA:180:U:H2'	32:XA:181:G:C8	2.45	0.51
32:XA:545:C:O2'	32:XA:549:C:OP1	2.25	0.51
34:XC:131:ARG:NH1	34:XC:166:GLU:OE1	2.37	0.51
52:XU:4:GLY:HA2	52:XU:15:ARG:HH12	1.76	0.51
1:RA:321:G:O2'	1:RA:340:A:N3	2.44	0.51
1:RA:870:A:OP1	12:RQ:6:ARG:NH1	2.44	0.51
1:RA:1323:U:OP1	18:RW:98:LYS:NZ	2.40	0.51
2:RB:48:A:OP2	14:RS:30:ARG:NH2	2.44	0.51
32:QA:1103:C:H5''	33:QB:98:LEU:HD13	1.92	0.51
32:QA:1287:A:H2'	32:QA:1288:A:C8	2.45	0.51
32:QA:1392:G:H21	32:QA:1502:A:H8	1.57	0.51
35:QD:20:TYR:CE2	37:XF:15:ASP:HB2	2.44	0.51
41:QJ:78:ASN:HB2	41:QJ:81:THR:HG23	1.92	0.51
51:QT:72:LEU:O	51:QT:74:LYS:N	2.44	0.51
1:YA:547:A:H2'	1:YA:548:A:C8	2.45	0.51
1:YA:603:A:N1	1:YA:625:G:O2'	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1056:G:H5''	1:YA:1057:A:H5'	1.92	0.51
1:YA:1063:G:H22	1:YA:1076:C:H1'	1.75	0.51
32:XA:1038:C:H2'	32:XA:1039:C:C6	2.45	0.51
1:RA:1433:U:O4	1:RA:1560:G:O6	2.28	0.51
6:RG:67:LYS:H	26:R4:6:HIS:CE1	2.28	0.51
17:RV:76:LYS:HB2	17:RV:81:TYR:HB3	1.93	0.51
32:QA:376:G:H5''	47:QP:5:ARG:HB2	1.92	0.51
44:QM:102:ARG:HH21	44:QM:105:THR:H	1.57	0.51
50:QS:36:ARG:HH21	50:QS:53:ASN:HA	1.75	0.51
1:YA:249:C:O2	30:Y8:12:LYS:NZ	2.31	0.51
1:YA:606:U:H4'	1:YA:658:C:H4'	1.92	0.51
1:YA:2346:A:H5''	1:YA:2383:G:H1'	1.92	0.51
4:YE:126:PRO:O	4:YE:135:HIS:ND1	2.39	0.51
32:XA:736:C:H2'	32:XA:737:A:H8	1.76	0.51
32:XA:978:A:N6	32:XA:1316:G:O2'	2.44	0.51
32:XA:1172:C:H2'	32:XA:1173:G:H8	1.76	0.51
32:XA:1211:U:H5'	32:XA:1212:U:H5'	1.91	0.51
32:XA:1435:G:H2'	32:XA:1436:U:C6	2.45	0.51
1:RA:270(S):G:H2'	1:RA:270(T):G:H8	1.75	0.51
1:RA:1817:G:OP1	3:RD:88:ARG:NH2	2.42	0.51
1:RA:2712(A):A:H5''	1:RA:2713:A:OP2	2.11	0.51
2:RB:28:C:H2'	2:RB:29:A:C8	2.46	0.51
8:RI:75:LEU:HD13	8:RI:105:HIS:NE2	2.26	0.51
27:R5:41:PRO:O	27:R5:44:THR:OG1	2.28	0.51
36:QE:105:VAL:HG21	36:QE:128:PRO:HB3	1.91	0.51
1:YA:551:G:H5'	1:YA:1220:A:H1'	1.93	0.51
20:YY:83:THR:OG1	20:YY:84:ARG:O	2.27	0.51
44:XM:2:ALA:O	44:XM:9:ILE:CD1	2.49	0.51
1:RA:514:A:N3	1:RA:581:C:O2'	2.37	0.51
1:RA:793:A:OP2	1:RA:2071:A:O2'	2.24	0.51
1:RA:2055:C:OP1	27:R5:8:LYS:NZ	2.38	0.51
21:RZ:183:LEU:HA	21:RZ:186:GLU:HB2	1.92	0.51
32:QA:449:C:H5	47:QP:42:ARG:HH21	1.59	0.51
51:QT:85:MET:HB2	51:QT:104:LEU:HD21	1.93	0.51
1:YA:2577:A:H5'	27:Y5:3:LYS:HD2	1.93	0.51
1:YA:2618:G:H21	4:YE:150:VAL:HG21	1.76	0.51
34:XC:115:LEU:O	34:XC:119:ARG:N	2.42	0.51
40:XI:71:SER:HA	40:XI:74:ILE:HD12	1.92	0.51
1:RA:210:C:OP2	29:R7:29:LYS:NZ	2.43	0.51
1:RA:2291:U:O2'	1:RA:2374:C:O2	2.28	0.51
20:RY:11:ASP:N	20:RY:11:ASP:OD1	2.38	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:QC:123:GLN:O	34:QC:127:ARG:N	2.44	0.51
1:YA:127:A:H5''	1:YA:128:C:C6	2.46	0.51
1:YA:1178:C:H2'	1:YA:1179:C:C6	2.46	0.51
1:YA:1889:A:N3	1:YA:2086:U:O2'	2.42	0.51
46:XO:26:GLU:HG3	46:XO:70:LEU:HD11	1.93	0.51
1:RA:2849:U:OP2	15:RT:95:ARG:NH1	2.44	0.51
10:RO:104:ARG:HH11	10:RO:121:VAL:HG12	1.76	0.51
32:QA:946:A:H2'	32:QA:947:G:C8	2.46	0.51
32:QA:1226:C:OP2	44:QM:103:THR:OG1	2.22	0.51
32:QA:1368:G:H5''	40:QL:112:LYS:HB3	1.93	0.51
32:QA:1499:A:H1'	32:QA:1520:G:H5'	1.92	0.51
35:QD:103:ASN:OD1	35:QD:114:ARG:NE	2.35	0.51
36:QE:7:GLU:OE1	36:QE:37:ARG:NE	2.36	0.51
40:QL:93:ARG:HD3	40:QL:97:LYS:HE2	1.92	0.51
43:QL:114:LYS:O	43:QL:117:ARG:NH1	2.44	0.51
1:YA:321:G:OP2	5:YF:135:LYS:HD3	2.10	0.51
1:YA:1405:U:H2'	1:YA:1406:U:H6	1.76	0.51
13:YR:56:LYS:NZ	13:YR:90:ARG:O	2.43	0.51
28:Y6:23:THR:OG1	28:Y6:24:GLU:N	2.43	0.51
32:XA:736:C:H2'	32:XA:737:A:C8	2.46	0.51
44:XM:34:LEU:HB3	44:XM:41:PRO:HG3	1.92	0.51
16:RU:90:VAL:HG22	17:RV:38:LEU:HB3	1.93	0.50
32:QA:119:A:H4'	32:QA:120:A:O5'	2.10	0.50
35:QD:72:GLU:OE2	35:QD:207:TYR:OH	2.27	0.50
54:QX:2:G:C5	54:QX:3:C:N4	2.79	0.50
1:YA:2186:G:H2'	1:YA:2187:G:C8	2.46	0.50
11:YP:47:ASP:OD2	11:YP:50:ARG:NH2	2.44	0.50
32:XA:452:A:H62	32:XA:480:U:H3	0.74	0.50
32:XA:713:G:H2'	32:XA:714:G:C8	2.45	0.50
1:RA:83:G:H1	1:RA:102:G:HO2'	1.58	0.50
1:RA:630:G:N2	1:RA:633:A:OP2	2.38	0.50
4:RE:24:THR:OG1	4:RE:186:GLY:O	2.27	0.50
8:RI:81:VAL:HG21	8:RI:88:ILE:HD12	1.93	0.50
32:QA:985:C:H2'	32:QA:986:A:H8	1.76	0.50
34:QC:20:SER:HG	34:QC:22:TRP:NE1	2.08	0.50
39:QH:21:LYS:O	39:QH:65:TYR:OH	2.24	0.50
8:YI:81:VAL:HG21	8:YI:88:ILE:HD12	1.92	0.50
32:XA:1127:G:O6	32:XA:1144:G:N1	2.40	0.50
32:XA:1336:C:O2	32:XA:1337:G:N1	2.44	0.50
36:XE:110:LEU:HD13	36:XE:118:ILE:HD13	1.92	0.50
44:XM:81:LEU:HD12	44:XM:88:ARG:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:ZN:44:LEU:HA	45:ZN:47:LEU:HB2	1.94	0.50
1:RA:1048:A:N1	1:RA:1112:G:O2'	2.41	0.50
1:RA:2199:A:OP1	23:R1:50:ARG:NH2	2.45	0.50
6:RG:121:ASN:ND2	6:RG:124:SER:OG	2.44	0.50
12:RQ:52:VAL:HG22	21:RZ:183:LEU:HD22	1.94	0.50
24:R2:45:SER:O	24:R2:46:GLN:NE2	2.44	0.50
32:QA:673:G:O3'	37:QF:87:ARG:NH2	2.44	0.50
40:QI:13:ALA:HB2	40:QI:68:GLY:HA3	1.91	0.50
1:YA:2355:C:H1'	22:Y0:39:ARG:HH21	1.76	0.50
1:YA:2404:C:O3'	11:YP:77:ARG:NH2	2.44	0.50
1:YA:2539:C:H4'	31:Y9:3:VAL:HG21	1.94	0.50
32:XA:619:U:N3	35:XD:134:ASP:OD1	2.40	0.50
32:XA:745:C:H2'	32:XA:746:A:C8	2.47	0.50
38:XG:24:THR:O	38:XG:28:ASN:ND2	2.42	0.50
1:RA:226:G:H2'	1:RA:227:A:C8	2.46	0.50
8:RI:104:GLN:HG2	8:RI:105:HIS:CD2	2.46	0.50
32:QA:45:U:H2'	32:QA:46:G:C8	2.47	0.50
32:QA:516:U:O2'	32:QA:519:C:N3	2.44	0.50
32:QA:1342:C:H2'	32:QA:1343:G:C8	2.47	0.50
34:QC:19:GLU:O	34:QC:40:ARG:NH2	2.45	0.50
44:QM:92:HIS:CE1	44:QM:98:VAL:HG21	2.46	0.50
1:YA:1500:G:N2	3:YD:99:ASP:O	2.38	0.50
32:XA:584:G:H1	32:XA:757:U:H3	1.58	0.50
32:XA:757:U:H2'	32:XA:758:G:O4'	2.12	0.50
32:XA:1055:A:H62	32:XA:1200:C:H42	1.59	0.50
34:XC:153:VAL:O	34:XC:166:GLU:N	2.43	0.50
35:XD:160:GLN:HA	35:XD:163:GLU:HG2	1.93	0.50
48:XQ:83:ASP:N	48:XQ:83:ASP:OD1	2.44	0.50
1:RA:1728:G:H8	1:RA:1732:A:H62	1.59	0.50
1:RA:1800:C:N3	1:RA:1817:G:N1	2.60	0.50
3:RD:254:THR:OG1	3:RD:254:THR:O	2.27	0.50
3:RD:260:ARG:HH22	3:RD:270:ILE:HD12	1.76	0.50
5:RF:149:ASP:OD1	5:RF:149:ASP:N	2.43	0.50
7:RH:149:ARG:NH2	7:RH:167:GLU:OE2	2.38	0.50
15:RT:62:THR:HB	15:RT:75:ILE:HG12	1.93	0.50
44:QM:93:ARG:O	44:QM:94:ARG:NH1	2.44	0.50
51:QT:75:ASN:OD1	51:QT:75:ASN:N	2.42	0.50
1:YA:2469:A:H2	1:YA:2481:G:H21	1.58	0.50
32:XA:1203:C:H2'	32:XA:1204:A:H8	1.76	0.50
32:XA:1264:C:H2'	32:XA:1265:G:C8	2.46	0.50
32:XA:1355:G:H2'	32:XA:1356:G:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:XX:5:A:H2'	54:XX:6:G:H8	1.77	0.50
1:RA:856:C:O2'	1:RA:857:C:OP1	2.20	0.50
1:RA:955:C:OP1	12:RQ:85:LYS:NZ	2.42	0.50
1:RA:1042:G:O6	1:RA:1113:U:O2	2.29	0.50
1:RA:2441:C:OP2	1:RA:2586:C:O2'	2.30	0.50
32:QA:1064:G:H1'	32:QA:1066:C:C6	2.46	0.50
32:QA:1224:G:O2'	32:QA:1322:C:OP2	2.21	0.50
35:QD:187:ARG:NH2	35:QD:193:ASP:OD2	2.33	0.50
37:QF:9:VAL:HB	37:QF:87:ARG:HB2	1.94	0.50
1:YA:2475:C:H42	1:YA:2529:G:H22	1.58	0.50
32:XA:992:U:C2	32:XA:1044:A:N6	2.79	0.50
32:XA:1151:A:H2'	32:XA:1152:A:H8	1.76	0.50
1:RA:2123:G:H2'	1:RA:2124:G:H8	1.77	0.50
3:RD:85:ASP:OD2	3:RD:88:ARG:NH1	2.38	0.50
6:RG:11:TYR:HA	6:RG:15:VAL:HB	1.94	0.50
32:QA:909:A:N3	32:QA:1413:A:O2'	2.33	0.50
1:YA:1265:A:H8	1:YA:1265:A:OP1	1.94	0.50
1:YA:2246:G:H2'	1:YA:2247:A:H8	1.75	0.50
7:YH:3:ARG:CD	7:YH:54:ARG:NH1	2.70	0.50
17:YV:38:LEU:HD13	17:YV:50:PRO:O	2.11	0.50
40:XI:20:ARG:O	40:XI:60:ASP:N	2.44	0.50
41:XJ:38:ILE:HG23	41:XJ:71:LEU:HB3	1.92	0.50
1:RA:232:G:OP2	1:RA:232:G:H8	1.95	0.50
1:RA:2168:G:N2	1:RA:2170:A:N7	2.59	0.50
44:QM:15:VAL:O	44:QM:19:LEU:CB	2.60	0.50
1:YA:1012:U:OP1	16:YU:75:ASN:ND2	2.44	0.50
1:YA:2096:U:O4	1:YA:2193:G:O6	2.29	0.50
1:YA:2547:U:O2	10:YO:23:ARG:NH2	2.45	0.50
32:XA:875:C:H1'	39:XH:15:ASN:HD21	1.75	0.50
32:XA:1296:C:O3'	44:XM:13:LYS:NZ	2.40	0.50
32:XA:1414:U:H2'	32:XA:1415:G:H8	1.76	0.50
41:XJ:24:VAL:HG11	41:XJ:37:PRO:HD3	1.93	0.50
41:XJ:50:ILE:HA	41:XJ:60:ARG:HG2	1.94	0.50
1:RA:1993:U:H4'	4:RE:128:SER:HB3	1.93	0.50
12:RQ:48:GLU:HA	12:RQ:51:ARG:HG2	1.94	0.50
15:RT:1:MET:HE2	15:RT:3:ARG:HG2	1.94	0.50
32:QA:1022:G:H2'	32:QA:1023:G:C8	2.47	0.50
32:QA:1244:C:H2'	32:QA:1245:A:C8	2.46	0.50
32:QA:1274:G:N2	32:QA:1275:A:N7	2.59	0.50
32:QA:1329:A:N7	52:QU:7:ARG:NH2	2.53	0.50
32:QA:1500:A:H5''	32:QA:1508:G:H5''	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:243:U:OP2	1:YA:254:G:N1	2.43	0.50
1:YA:996:A:H4'	16:YU:92:ARG:HE	1.76	0.50
1:YA:2101:G:H2'	1:YA:2102:U:C6	2.47	0.50
1:RA:1509:C:N3	1:RA:1511:A:N6	2.60	0.49
1:RA:2074:U:H2'	1:RA:2075:U:C6	2.47	0.49
21:RZ:140:ASP:OD1	21:RZ:142:SER:OG	2.28	0.49
35:QD:19:LEU:HD23	35:QD:67:ILE:HD11	1.94	0.49
36:QE:8:GLU:HA	36:QE:34:VAL:HG12	1.93	0.49
3:YD:37:LEU:HD13	3:YD:62:TYR:HB2	1.94	0.49
9:YN:16:ILE:HG22	9:YN:18:ALA:HB2	1.94	0.49
1:RA:2296:U:OP2	14:RS:9:ARG:NH1	2.40	0.49
5:RF:185:ASP:HA	5:RF:188:ARG:HD3	1.93	0.49
36:QE:102:ALA:HB1	36:QE:106:PRO:HG2	1.94	0.49
1:YA:1797:C:H4'	3:YD:257:LEU:O	2.12	0.49
1:YA:2074:U:H2'	1:YA:2075:U:C6	2.47	0.49
32:XA:404:U:H2'	32:XA:405:U:H6	1.77	0.49
34:XC:14:ILE:HG12	34:XC:15:THR:HB	1.94	0.49
40:XI:112:LYS:HA	40:XI:119:ALA:HB2	1.95	0.49
7:RH:153:LYS:HB2	7:RH:162:ILE:H	1.77	0.49
25:R3:51:ALA:HA	25:R3:54:VAL:HG12	1.93	0.49
32:QA:152:A:N6	32:QA:169:C:H42	2.08	0.49
34:QC:78:GLY:HA3	34:QC:83:ARG:H	1.78	0.49
37:QF:11:ASN:HB3	37:QF:14:LEU:HD13	1.94	0.49
1:YA:248:G:H5'	1:YA:250:G:N7	2.27	0.49
1:YA:2100:G:H2'	1:YA:2101:G:H8	1.78	0.49
1:YA:2207:C:O2	3:YD:151:LYS:NZ	2.45	0.49
10:YO:80:ASP:OD2	15:YT:64:ARG:NH2	2.45	0.49
19:YX:64:LYS:HZ2	19:YX:73:ARG:HE	1.58	0.49
32:XA:411:A:N3	32:XA:413:G:O2'	2.43	0.49
32:XA:662:G:H2'	32:XA:663:A:C8	2.47	0.49
32:XA:1022:G:H2'	32:XA:1023:G:C8	2.48	0.49
32:XA:1294:G:H2'	32:XA:1295:G:H8	1.76	0.49
33:XB:68:ILE:HG12	33:XB:161:ALA:HB3	1.94	0.49
33:XB:73:THR:OG1	33:XB:170:GLU:OE2	2.30	0.49
1:RA:389:G:H1	11:RP:71:VAL:HG12	1.77	0.49
1:RA:1427:A:H4'	1:RA:1428:C:O5'	2.11	0.49
1:RA:1496:A:H8	1:RA:1577:C:HO2'	1.61	0.49
32:QA:45:U:H2'	32:QA:46:G:H8	1.77	0.49
35:QD:9:CYS:O	35:QD:13:ARG:HB2	2.13	0.49
1:YA:714:U:OP2	46:XO:88:ARG:NH1	2.44	0.49
8:YI:86:THR:H	8:YI:123:LEU:HD12	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:YO:4:PRO:HA	10:YO:21:CYS:HB3	1.95	0.49
30:Y8:6:THR:HG22	30:Y8:63:PRO:HD2	1.92	0.49
32:XA:323:U:H5'	51:XT:23:ARG:HB3	1.93	0.49
34:XC:89:GLU:O	34:XC:93:LYS:N	2.44	0.49
38:XG:66:VAL:HG13	38:XG:67:GLU:HG2	1.93	0.49
1:RA:1464:C:O2'	1:RA:1528:A:H8	1.94	0.49
1:RA:1782:C:C4	1:RA:2587:A:C2	3.00	0.49
5:RF:60:SER:OG	5:RF:61:GLY:N	2.46	0.49
32:QA:1209:C:O2'	32:QA:1214:C:N4	2.40	0.49
47:QP:43:LYS:HG2	47:QP:48:TRP:CD2	2.48	0.49
1:YA:190:A:N3	1:YA:679:C:O2'	2.42	0.49
1:YA:813:U:H2'	1:YA:814:C:C6	2.47	0.49
10:YO:97:ARG:NH2	32:XA:338:A:OP2	2.44	0.49
24:Y2:12:GLU:HA	24:Y2:15:LYS:HE2	1.95	0.49
32:XA:1409:C:H2'	32:XA:1410:G:H8	1.77	0.49
35:XD:19:LEU:O	35:XD:19:LEU:HD12	2.12	0.49
1:RA:11:G:H22	1:RA:2627:G:H5''	1.78	0.49
1:RA:2250:G:C4	12:RQ:82:ARG:HG3	2.48	0.49
1:RA:2327:A:H2'	1:RA:2328:A:C8	2.46	0.49
4:RE:78:LEU:O	4:RE:79:ARG:NH1	2.37	0.49
18:RW:82:LEU:HB2	18:RW:98:LYS:HB2	1.94	0.49
20:RY:39:VAL:HG13	20:RY:42:VAL:HB	1.95	0.49
32:QA:1298:C:OP2	38:QG:114:ARG:NH1	2.45	0.49
39:QH:23:SER:OG	39:QH:24:THR:N	2.46	0.49
42:QK:24:SER:OG	42:QK:27:ASN:N	2.38	0.49
1:YA:1021:A:H8	1:YA:1022:G:H5''	1.78	0.49
6:YG:98:ARG:HA	6:YG:101:ILE:HG22	1.94	0.49
32:XA:708:C:H2'	32:XA:709:G:H8	1.77	0.49
32:XA:711:G:H2'	32:XA:712:A:H8	1.78	0.49
32:XA:983:A:O2'	32:XA:1050:G:OP2	2.29	0.49
32:XA:1129:C:N4	32:XA:1135:U:O4	2.46	0.49
32:XA:1228:C:OP1	44:XM:108:ARG:NH1	2.45	0.49
34:XC:157:ILE:HD12	34:XC:164:ARG:HB2	1.94	0.49
40:XI:96:LEU:O	40:XI:100:GLY:N	2.45	0.49
44:XM:65:LYS:HE2	44:XM:70:LEU:HD23	1.94	0.49
1:RA:1543:A:O2'	1:RA:1544:C:H3'	2.13	0.49
10:RO:13:ASN:ND2	10:RO:96:THR:OG1	2.37	0.49
11:RP:95:VAL:HB	11:RP:125:VAL:HG23	1.94	0.49
16:RU:8:VAL:HG22	16:RU:12:ARG:HD2	1.94	0.49
32:QA:481:G:HO2'	32:QA:482:A:P	2.35	0.49
32:QA:922:G:H4'	36:QE:20:GLN:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:QD:18:LYS:HE2	35:QD:20:TYR:CE1	2.47	0.49
1:YA:1659:U:O2'	1:YA:2712(A):A:N1	2.44	0.49
32:XA:767:A:O2'	32:XA:1524:C:O2	2.28	0.49
33:XB:98:LEU:HB2	33:XB:101:MET:HE3	1.94	0.49
39:XH:91:ARG:NE	48:XQ:32:TYR:O	2.46	0.49
1:RA:1639:U:H2'	1:RA:1640:C:H5''	1.95	0.49
1:RA:2655:G:HO2'	1:RA:2664:G:H1	1.55	0.49
8:RI:86:THR:O	8:RI:87:LYS:CG	2.60	0.49
39:QH:84:ARG:NH2	39:QH:136:GLU:OE2	2.44	0.49
1:YA:183:C:O2'	1:YA:432:A:N3	2.40	0.49
1:YA:1210:A:H5'	1:YA:1210:A:H8	1.78	0.49
32:XA:79:G:H2'	32:XA:80:G:C8	2.47	0.49
32:XA:184:G:H2'	32:XA:185:A:H8	1.76	0.49
32:XA:736:C:O2'	37:XF:90:VAL:O	2.31	0.49
32:XA:1036:G:N7	32:XA:1037:C:N4	2.60	0.49
37:XF:22:GLU:OE2	37:XF:84:ASN:ND2	2.38	0.49
1:RA:30:G:O2'	1:RA:1214:A:N3	2.38	0.49
1:RA:1000:A:H2'	1:RA:1001:A:C8	2.47	0.49
1:RA:1165:U:O4	1:RA:1184:G:O6	2.30	0.49
1:RA:1171:G:H5''	1:RA:1173:G:H5''	1.94	0.49
6:RG:63:ILE:HG13	6:RG:64:THR:HG23	1.95	0.49
8:RI:93:THR:O	8:RI:97:ILE:HG13	2.12	0.49
32:QA:728:A:H2'	32:QA:729:A:H8	1.77	0.49
32:QA:946:A:O2'	32:QA:1333:A:N3	2.42	0.49
32:QA:1065:U:O2'	32:QA:1066:C:OP2	2.26	0.49
32:QA:1347:G:O2'	32:QA:1348:U:OP2	2.27	0.49
1:YA:587:C:O2	11:YP:33:ARG:NH2	2.45	0.49
1:YA:1913:A:O2'	1:YA:1914:C:OP1	2.27	0.49
5:YF:168:ARG:HG3	5:YF:175:THR:HG21	1.95	0.49
7:YH:3:ARG:NH2	7:YH:62:LYS:O	2.46	0.49
32:XA:985:C:H2'	32:XA:986:A:C8	2.47	0.49
32:XA:1287:A:H2'	32:XA:1288:A:C8	2.48	0.49
32:XA:1328:C:OP1	52:XU:21:TYR:OH	2.29	0.49
34:XC:20:SER:HG	34:XC:22:TRP:HE1	1.60	0.49
1:RA:1525:G:H2'	1:RA:1526:G:H8	1.78	0.49
1:RA:1728:G:H3'	1:RA:1729:A:C5'	2.43	0.49
1:RA:2246:G:H2'	1:RA:2247:A:H8	1.78	0.49
1:RA:2692:C:H2'	1:RA:2693:A:C8	2.48	0.49
19:RX:29:TRP:HZ3	19:RX:59:VAL:HG11	1.77	0.49
32:QA:576:G:N2	32:QA:760:G:OP2	2.46	0.49
1:YA:242:G:O2'	1:YA:254:G:O6	2.21	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1031:G:H4'	31:Y9:6:SER:HB2	1.95	0.49
30:Y8:37:SER:OG	30:Y8:38:GLY:N	2.46	0.49
32:XA:60:A:H4'	32:XA:61:G:O5'	2.12	0.49
34:XC:20:SER:HB2	34:XC:40:ARG:HH22	1.78	0.49
40:XI:110:GLU:OE1	40:XI:120:ARG:NH2	2.44	0.49
41:XJ:21:GLN:HA	41:XJ:24:VAL:HG22	1.95	0.49
1:RA:30:G:H2'	1:RA:31:C:C6	2.48	0.48
1:RA:1057:A:O2'	1:RA:1058:G:OP1	2.26	0.48
4:RE:36:ARG:NH1	4:RE:85:ASN:OD1	2.47	0.48
32:QA:677:U:O2	32:QA:777:A:O2'	2.30	0.48
32:QA:1238:A:OP1	32:QA:1335:C:O2'	2.24	0.48
38:QG:39:ALA:HA	38:QG:42:ILE:HD12	1.94	0.48
32:XA:78:G:O2'	32:XA:79:G:OP1	2.25	0.48
32:XA:971:G:H5''	32:XA:972:C:H5''	1.94	0.48
32:XA:1032(A):G:H2'	32:XA:1032(B):G:C8	2.48	0.48
2:RB:15:A:H5'	2:RB:16:G:C8	2.48	0.48
9:RN:96:GLU:HB2	9:RN:122:VAL:HG12	1.95	0.48
32:QA:439:A:OP2	32:QA:493:G:N1	2.34	0.48
34:QC:105:GLU:OE1	34:QC:107:GLN:NE2	2.47	0.48
38:QG:122:HIS:HD2	38:QG:125:MET:HE2	1.79	0.48
1:YA:237:C:O2	1:YA:609:A:O2'	2.27	0.48
1:YA:1055:G:H1	1:YA:1104:C:H42	1.61	0.48
1:YA:1453:A:O2'	1:YA:2702:U:O4	2.31	0.48
9:YN:47:ALA:HB2	9:YN:112:LEU:HD11	1.95	0.48
32:XA:691:G:O6	42:XK:55:LYS:NZ	2.42	0.48
32:XA:1118:C:H1'	32:XA:1179:A:C5	2.48	0.48
32:XA:1175:G:H2'	32:XA:1176:A:C8	2.48	0.48
1:RA:78:A:H2'	1:RA:79:G:H8	1.78	0.48
1:RA:121:G:H4'	1:RA:149:A:H5'	1.95	0.48
1:RA:2867:G:O2'	1:RA:2868:A:H8	1.93	0.48
12:RQ:54:MET:HE1	12:RQ:104:PHE:HB3	1.95	0.48
32:QA:950:U:H2'	32:QA:951:G:C8	2.48	0.48
32:QA:958:A:N3	32:QA:985:C:O2'	2.43	0.48
32:QA:1316:G:N2	32:QA:1319:A:OP2	2.45	0.48
35:QD:79:PHE:HE1	35:QD:204:ILE:HD13	1.78	0.48
40:QI:25:LYS:N	40:QI:60:ASP:OD1	2.46	0.48
1:YA:309:G:N3	1:YA:329:G:O2'	2.44	0.48
1:YA:589:C:H2'	1:YA:590:A:C8	2.48	0.48
1:YA:2185:C:H2'	1:YA:2186:G:H8	1.78	0.48
1:YA:2228:G:OP1	3:YD:261:LYS:NZ	2.40	0.48
1:YA:2774:C:H2'	1:YA:2775:A:O4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:YD:181:GLU:HB2	3:YD:274:ARG:H	1.78	0.48
3:YD:254:THR:OG1	3:YD:254:THR:O	2.31	0.48
26:Y4:53:GLU:HG2	26:Y4:56:VAL:HG13	1.95	0.48
32:XA:41:G:H2'	32:XA:42:G:C8	2.48	0.48
41:XJ:26:ALA:O	41:XJ:30:SER:OG	2.28	0.48
44:XM:53:VAL:HG23	44:XM:57:ARG:HH22	1.78	0.48
1:RA:86:C:H4'	1:RA:104:U:H1'	1.94	0.48
1:RA:1417:C:H2'	1:RA:1418:G:O4'	2.13	0.48
1:RA:2010:G:H5''	18:RW:42:ARG:HB2	1.95	0.48
16:RU:17:ILE:HG13	16:RU:32:PHE:HE1	1.78	0.48
32:QA:235:C:H2'	32:QA:236:G:H8	1.78	0.48
32:QA:438:G:H4'	35:QD:123:HIS:CD2	2.48	0.48
32:QA:1228:C:OP1	44:QM:115:LYS:N	2.40	0.48
35:QD:20:TYR:CE2	37:XF:15:ASP:HA	2.47	0.48
1:YA:288:C:H2'	1:YA:289:A:H8	1.79	0.48
1:YA:443:A:H5''	1:YA:444:C:OP1	2.14	0.48
12:YQ:59:ARG:HA	21:YZ:180:VAL:HG23	1.94	0.48
30:Y8:37:SER:OG	30:Y8:39:LYS:N	2.45	0.48
32:XA:924:C:O2'	32:XA:1502:A:N6	2.46	0.48
34:XC:30:ARG:NH2	45:YN:35:ARG:O	2.42	0.48
35:XD:15:GLU:HB3	35:XD:63:LYS:HE2	1.95	0.48
1:RA:67:U:H3	1:RA:74:A:H2	1.62	0.48
1:RA:270(I):G:H1	1:RA:270(Q):C:H42	1.60	0.48
1:RA:792:G:O2'	1:RA:2440:C:N3	2.47	0.48
1:RA:1638:C:O2	1:RA:2698:U:O2'	2.30	0.48
1:RA:2210:G:H3'	1:RA:2211:G:C8	2.49	0.48
3:RD:131:LEU:HD12	3:RD:136:ILE:HG12	1.95	0.48
11:RP:68:GLN:HG2	30:R8:12:LYS:HG2	1.95	0.48
21:RZ:79:ARG:HB3	21:RZ:80:ARG:HG3	1.95	0.48
25:R3:39:ASP:OD1	25:R3:44:ARG:NH2	2.46	0.48
33:QB:80:ILE:HD13	33:QB:211:ILE:HG22	1.94	0.48
1:YA:956:G:OP2	12:YQ:14:ARG:NH2	2.47	0.48
1:YA:1429:G:H2'	1:YA:1430:C:C6	2.49	0.48
1:YA:1637:A:H4'	1:YA:2711:A:O2'	2.14	0.48
1:YA:2364:C:H2'	1:YA:2365:G:O4'	2.14	0.48
1:YA:2629:A:O2'	1:YA:2630:G:H5''	2.14	0.48
5:YF:77:ASP:OD1	5:YF:77:ASP:N	2.42	0.48
5:YF:132:VAL:HG13	5:YF:162:LEU:HD12	1.95	0.48
35:XD:78:LEU:HD12	35:XD:96:LEU:HB3	1.94	0.48
45:YN:27:CYS:SG	45:YN:29:ARG:N	2.87	0.48
51:XT:55:ILE:O	51:XT:59:ALA:N	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:184:C:O2'	1:RA:217:G:N3	2.42	0.48
1:RA:922:U:H2'	1:RA:923:C:C6	2.48	0.48
1:RA:958:U:OP2	12:RQ:14:ARG:NH1	2.46	0.48
1:RA:2131:G:H4'	1:RA:2132:U:H4'	1.95	0.48
1:RA:2701:C:H3'	1:RA:2702:U:C5'	2.40	0.48
4:RE:36:ARG:HG2	4:RE:47:VAL:HG22	1.95	0.48
24:R2:41:ILE:HD11	24:R2:44:LEU:HG	1.96	0.48
26:R4:12:ALA:HB3	26:R4:24:THR:HG23	1.95	0.48
32:QA:375:U:O2	47:QP:28:ARG:NH1	2.46	0.48
35:QD:201:GLN:NE2	36:QE:116:THR:O	2.45	0.48
50:QS:55:LYS:HG3	50:QS:56:GLN:HB3	1.95	0.48
1:YA:1239:G:H2'	1:YA:1240:U:O4'	2.13	0.48
2:YB:5:C:O2'	2:YB:27:C:O2	2.31	0.48
32:XA:414:A:OP2	32:XA:428:G:N2	2.33	0.48
36:XE:20:GLN:O	36:XE:23:GLY:N	2.43	0.48
41:XJ:53:PRO:HB3	45:XN:42:ILE:HG12	1.94	0.48
1:RA:140:A:H8	1:RA:1408:C:O2'	1.96	0.48
1:RA:855:G:H1	1:RA:922:U:H3	1.61	0.48
1:RA:1031:G:O2'	31:R9:7:VAL:O	2.26	0.48
18:RW:58:ALA:HB1	18:RW:64:MET:HB2	1.96	0.48
32:QA:262:A:H2'	32:QA:263:A:C8	2.47	0.48
32:QA:1326:C:OP1	52:QU:17:THR:OG1	2.30	0.48
1:YA:321:G:O2'	1:YA:340:A:N3	2.40	0.48
1:YA:540:G:H5'	1:YA:541:C:OP2	2.14	0.48
1:YA:1919:A:O2'	32:XA:1517:G:N3	2.46	0.48
1:YA:2740:A:H2'	1:YA:2741:A:C8	2.49	0.48
2:YB:8:U:O2	2:YB:112:G:N2	2.42	0.48
13:YR:28:LEU:HD23	13:YR:48:VAL:HG21	1.96	0.48
29:Y7:10:ARG:HE	29:Y7:14:LYS:HD2	1.79	0.48
32:XA:186(A):C:N3	51:XT:105:SER:OG	2.47	0.48
32:XA:714:G:H2'	32:XA:715:A:C8	2.48	0.48
32:XA:1174:G:H2'	32:XA:1175:G:H8	1.79	0.48
35:XD:98:GLU:HA	35:XD:103:ASN:HD22	1.78	0.48
1:RA:1557:C:OP2	1:RA:1558:A:O2'	2.26	0.48
1:RA:2424:C:O2	1:RA:2429:G:O2'	2.25	0.48
2:RB:50:G:OP1	14:RS:63:THR:HG23	2.12	0.48
21:RZ:108:PRO:HG3	21:RZ:141:VAL:HG23	1.96	0.48
31:R9:6:SER:O	31:R9:6:SER:OG	2.28	0.48
32:QA:272:C:H2'	32:QA:273:A:H8	1.79	0.48
32:QA:452:A:H62	32:QA:480:U:H3	1.62	0.48
34:QC:95:THR:HG23	34:QC:97:LYS:HE2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:QG:76:ARG:NH1	38:QG:89:MET:SD	2.87	0.48
1:YA:2131:G:H4'	1:YA:2132:U:H4'	1.96	0.48
1:YA:2155:G:H3'	1:YA:2156:G:C8	2.48	0.48
3:YD:20:ASP:OD1	3:YD:20:ASP:N	2.47	0.48
7:YH:58:GLU:OE2	7:YH:60:ARG:NH2	2.47	0.48
22:Y0:11:ARG:O	22:Y0:14:ARG:NH2	2.47	0.48
32:XA:22:G:H4'	32:XA:885:G:C8	2.48	0.48
32:XA:911:U:OP2	43:XL:97:ARG:NH2	2.46	0.48
32:XA:1161:C:O2'	32:XA:1162:C:H5'	2.14	0.48
1:RA:784:A:O2'	1:RA:785:G:H5''	2.13	0.48
1:RA:1174:A:O2'	1:RA:1178:C:N4	2.46	0.48
1:RA:1525:G:H2'	1:RA:1526:G:C8	2.48	0.48
1:RA:1593:G:H2'	1:RA:1594:G:C8	2.49	0.48
18:RW:92:ARG:NH1	18:RW:94:ASP:OD1	2.37	0.48
32:QA:1151:A:H2'	32:QA:1152:A:H8	1.79	0.48
32:QA:1172:C:H2'	32:QA:1173:G:H8	1.79	0.48
32:QA:1250:A:H2	32:QA:1370:G:H1'	1.79	0.48
32:QA:1316:G:H4'	45:QN:18:VAL:HG21	1.96	0.48
1:YA:303:U:H2'	1:YA:304:G:H8	1.79	0.48
1:YA:673:C:H5''	5:YF:81:PRO:HD2	1.94	0.48
5:YF:40:GLN:HE22	5:YF:182:ASN:HD22	1.62	0.48
37:XF:30:LEU:HB3	37:XF:35:ALA:HB3	1.94	0.48
1:RA:729:G:O2'	1:RA:763:G:H4'	2.14	0.48
7:RH:27:LYS:HD3	7:RH:32:GLU:HB3	1.95	0.48
11:RP:83:VAL:HB	11:RP:114:ILE:HG22	1.96	0.48
15:RT:24:PRO:HA	15:RT:49:VAL:HG13	1.95	0.48
32:QA:481:G:O2'	32:QA:482:A:O5'	2.29	0.48
32:QA:1150:U:H4'	41:QJ:41:PRO:HB3	1.95	0.48
32:QA:1376:U:OP1	38:QG:94:ARG:NH1	2.44	0.48
1:YA:84:A:N1	1:YA:98:G:O2'	2.37	0.48
1:YA:1799:G:H5'	1:YA:1819:A:N6	2.29	0.48
1:YA:2246:G:H2'	1:YA:2247:A:C8	2.48	0.48
1:YA:2328:A:H2'	1:YA:2329:G:C8	2.49	0.48
1:YA:2853:C:H2'	1:YA:2854:G:H8	1.79	0.48
3:YD:273:ARG:HE	3:YD:274:ARG:HB2	1.79	0.48
16:YU:90:VAL:HG22	17:YV:38:LEU:HD12	1.94	0.48
32:XA:269:C:H2'	32:XA:270:A:H8	1.79	0.48
32:XA:945:G:N2	32:XA:1334:G:O2'	2.46	0.48
32:XA:1406:U:O2	32:XA:1517:G:N2	2.40	0.48
41:XJ:50:ILE:HD13	41:XJ:60:ARG:HD3	1.95	0.48
1:RA:589:C:H2'	1:RA:590:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:RO:66:LYS:NZ	10:RO:80:ASP:O	2.43	0.47
32:QA:539:A:H2'	32:QA:540:G:C8	2.49	0.47
32:QA:581:G:OP1	46:QO:65:ARG:NH1	2.46	0.47
32:QA:713:G:H2'	32:QA:714:G:C8	2.49	0.47
32:QA:1005:A:OP2	32:QA:1006:C:N4	2.47	0.47
35:QD:101:LEU:HB2	35:QD:138:TYR:HB3	1.96	0.47
40:QI:80:GLY:O	40:QI:84:ALA:HB2	2.13	0.47
41:QJ:40:LEU:HB2	41:QJ:69:ASN:HB2	1.96	0.47
44:QM:25:ILE:HG12	44:QM:66:LEU:HD11	1.96	0.47
1:YA:827:U:H5'	1:YA:828:U:O5'	2.14	0.47
1:YA:1968:G:O2'	1:YA:1969:A:O4'	2.26	0.47
1:YA:2361:A:O5'	30:Y8:27:THR:OG1	2.32	0.47
1:YA:2529:G:H5''	1:YA:2530:A:H5''	1.96	0.47
4:YE:1:MET:N	4:YE:83:ASP:O	2.46	0.47
8:YI:40:THR:O	8:YI:44:LEU:N	2.44	0.47
38:XG:21:VAL:O	38:XG:24:THR:OG1	2.29	0.47
48:XQ:4:LYS:H	48:XQ:61:GLU:HB3	1.78	0.47
1:RA:345:A:H2'	1:RA:347:A:H62	1.79	0.47
1:RA:1109:C:H3'	1:RA:1110:G:C8	2.50	0.47
1:RA:2387:U:O2'	22:R0:41:ARG:NH2	2.46	0.47
6:RG:129:GLY:HA2	6:RG:166:ASP:HB3	1.96	0.47
11:RP:100:LEU:O	11:RP:104:GLY:N	2.47	0.47
32:QA:524:G:H2'	32:QA:525:C:C6	2.49	0.47
49:QR:74:ARG:HD3	49:QR:81:PHE:HA	1.96	0.47
1:YA:223:A:O2'	1:YA:420:C:O2	2.29	0.47
1:YA:746:A:HO2'	1:YA:2611:U:HO2'	1.60	0.47
33:XB:87:ARG:NH1	33:XB:220:ASP:OD1	2.47	0.47
34:XC:174:PRO:O	34:XC:177:THR:OG1	2.32	0.47
52:XU:8:THR:OG1	52:XU:9:ARG:N	2.47	0.47
1:RA:1916:A:H61	32:QA:1408:A:HO2'	1.61	0.47
1:RA:2327:A:H5'	21:RZ:201:LYS:HD2	1.96	0.47
7:RH:76:VAL:O	7:RH:80:SER:OG	2.32	0.47
21:RZ:157:LEU:HD23	21:RZ:161:VAL:HG12	1.96	0.47
32:QA:579:G:H5'	32:QA:728:A:H1'	1.96	0.47
32:QA:1228:C:H2'	32:QA:1229:A:H8	1.79	0.47
41:QJ:49:VAL:HG23	45:QN:41:ARG:HB2	1.97	0.47
7:YH:3:ARG:NH2	7:YH:65:HIS:HB3	2.28	0.47
32:XA:986:A:N3	50:XS:52:TYR:OH	2.42	0.47
34:XC:154:SER:HA	34:XC:165:THR:HA	1.97	0.47
43:XL:70:ILE:HG13	43:XL:100:ILE:HD12	1.95	0.47
1:RA:1076:C:H4'	1:RA:1077:A:OP1	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1539:G:H2'	1:RA:1540:G:C8	2.50	0.47
32:QA:122:G:H1	32:QA:239:U:H3	1.62	0.47
32:QA:150:C:H42	32:QA:171:A:N6	2.06	0.47
32:QA:1070:U:O5'	36:QE:25:ARG:NH1	2.47	0.47
33:QB:93:VAL:HG21	33:QB:97:TRP:HD1	1.80	0.47
37:QF:76:ALA:HB1	37:QF:80:ARG:HH12	1.78	0.47
1:YA:670:A:H5''	11:YP:42:SER:O	2.13	0.47
5:YF:155:LEU:HB2	5:YF:189:THR:HG21	1.96	0.47
12:YQ:42:ILE:HD12	12:YQ:97:VAL:HG21	1.95	0.47
32:XA:1178:G:N1	32:XA:1181:G:N7	2.61	0.47
1:RA:51:G:OP2	1:RA:51:G:H8	1.97	0.47
1:RA:443:A:N6	5:RF:41:LEU:O	2.43	0.47
1:RA:1405:U:H2'	1:RA:1406:U:H6	1.79	0.47
1:RA:2019:A:N7	27:R5:9:LYS:NZ	2.46	0.47
1:RA:2137:C:H42	1:RA:2154:G:H22	1.62	0.47
2:RB:28:C:H2'	2:RB:29:A:H8	1.78	0.47
2:RB:42:C:N4	6:RG:91:ARG:HH12	2.12	0.47
10:RO:10:VAL:HG11	10:RO:16:ALA:HB3	1.95	0.47
32:QA:41:G:H2'	32:QA:42:G:H8	1.79	0.47
32:QA:411:A:H62	32:QA:413:G:H21	1.62	0.47
32:QA:426:G:OP1	35:QD:38:TYR:OH	2.24	0.47
32:QA:662:G:H2'	32:QA:663:A:C8	2.49	0.47
35:QD:20:TYR:HE2	37:XF:15:ASP:CB	2.23	0.47
1:YA:330:A:O2'	1:YA:331:A:H8	1.98	0.47
1:YA:964:C:O2'	1:YA:2273:A:N3	2.45	0.47
11:YP:6:LEU:HD23	11:YP:6:LEU:HA	1.81	0.47
13:YR:86:ARG:NH2	13:YR:118:GLU:OXT	2.39	0.47
15:YT:54:ARG:HA	15:YT:59:THR:HG23	1.96	0.47
19:YX:88:LYS:NZ	19:YX:90:GLU:OE2	2.45	0.47
23:Y1:49:VAL:HG23	23:Y1:60:PHE:HB2	1.97	0.47
32:XA:985:C:H2'	32:XA:986:A:H8	1.80	0.47
40:XI:83:ARG:HG2	40:XI:102:LEU:HD11	1.96	0.47
45:XN:7:ILE:HG22	45:XN:23:ARG:HH11	1.79	0.47
54:XX:5:A:H2'	54:XX:6:G:C8	2.50	0.47
1:RA:1419:A:H61	1:RA:1494:A:H61	1.61	0.47
1:RA:1782:C:C4	1:RA:2587:A:N1	2.82	0.47
13:RR:51:LEU:HD22	13:RR:66:VAL:HG13	1.97	0.47
32:QA:731:G:OP1	32:QA:766:A:H1'	2.14	0.47
37:QF:97:PHE:HB3	49:QR:32:ARG:HG3	1.96	0.47
38:QG:70:LYS:HG2	38:QG:100:ALA:HB2	1.95	0.47
1:YA:624:C:H1'	1:YA:657:U:H5'	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1801:G:OP2	3:YD:154:LYS:NZ	2.47	0.47
1:YA:2734:A:H5'	1:YA:2735:G:OP2	2.15	0.47
6:YG:37:VAL:HG23	6:YG:99:MET:HE3	1.97	0.47
32:XA:426:G:OP1	35:XD:38:TYR:OH	2.19	0.47
32:XA:711:G:H2'	32:XA:712:A:C8	2.50	0.47
32:XA:1305:G:H21	32:XA:1332:A:H8	1.63	0.47
42:XK:24:SER:HG	42:XK:27:ASN:H	1.63	0.47
1:RA:1800:C:H42	1:RA:1817:G:H22	1.61	0.47
14:RS:10:ARG:NH1	14:RS:91:PRO:O	2.47	0.47
14:RS:69:VAL:O	14:RS:73:LEU:N	2.46	0.47
16:RU:102:GLU:OE2	17:RV:13:ARG:NH2	2.48	0.47
17:RV:57:VAL:HG22	17:RV:99:ILE:HG23	1.96	0.47
21:RZ:153:SER:OG	21:RZ:154:ASP:OD2	2.29	0.47
32:QA:711:G:P	37:QF:54:LYS:HZ1	2.38	0.47
32:QA:768:A:H5'	32:QA:1524:C:H1'	1.97	0.47
32:QA:801:U:H2'	32:QA:802:A:H8	1.79	0.47
32:QA:806:C:H2'	32:QA:807:A:H8	1.79	0.47
32:QA:985:C:H2'	32:QA:986:A:C8	2.50	0.47
32:QA:1060:C:H2'	32:QA:1061:G:C8	2.50	0.47
32:QA:1187:G:O2'	40:QI:111:ARG:NH1	2.48	0.47
36:QE:66:MET:HE3	36:QE:66:MET:HB3	1.83	0.47
38:QG:70:LYS:HB3	38:QG:96:GLN:HB3	1.97	0.47
1:YA:392:C:H5''	1:YA:409:C:H5''	1.96	0.47
1:YA:1756:G:H4'	1:YA:1758:G:O4'	2.15	0.47
1:YA:2313:C:O4'	6:YG:40:ASN:ND2	2.47	0.47
1:YA:2789:C:O3'	1:YA:2790:A:H4'	2.15	0.47
26:Y4:68:ARG:H	50:XS:16:LEU:HD21	1.78	0.47
32:XA:7:G:O2'	36:XE:120:THR:O	2.32	0.47
32:XA:130:A:N3	32:XA:263:A:O2'	2.42	0.47
32:XA:177:C:H2'	32:XA:178:C:H6	1.80	0.47
32:XA:464:G:N2	32:XA:467:G:N7	2.63	0.47
32:XA:636:U:H2'	32:XA:637:G:H8	1.79	0.47
32:XA:1250:A:H2	32:XA:1370:G:H1'	1.80	0.47
33:XB:69:LEU:HD13	33:XB:91:PRO:HB2	1.97	0.47
37:XF:70:ASP:OD1	37:XF:70:ASP:N	2.40	0.47
38:XG:82:GLY:HA3	54:XX:13:A:H5''	1.96	0.47
39:XH:21:LYS:O	39:XH:65:TYR:OH	2.26	0.47
41:XJ:32:ALA:HB3	41:XJ:76:ASN:HB2	1.97	0.47
41:XJ:51:ARG:HG2	45:XN:45:ARG:HH21	1.80	0.47
45:XN:47:LEU:HB3	45:XN:53:LEU:HD13	1.96	0.47
1:RA:1021:A:H8	1:RA:1022:G:H5''	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1824:G:N3	3:RD:254:THR:OG1	2.48	0.47
1:RA:2302:G:H21	6:RG:126:ASP:HB2	1.79	0.47
2:RB:44:G:H5''	2:RB:45:A:OP1	2.14	0.47
32:QA:429:U:OP2	35:QD:13:ARG:NH2	2.47	0.47
34:QC:47:LEU:HB3	34:QC:50:ALA:HB3	1.95	0.47
1:YA:1062:G:H22	1:YA:1078:U:H1'	1.80	0.47
1:YA:1266:G:O5'	18:YW:15:ARG:NH2	2.48	0.47
1:YA:1759:A:H1'	1:YA:2711:A:C2	2.50	0.47
1:YA:2105:C:H2'	1:YA:2106:G:H8	1.78	0.47
1:YA:2262:U:H5	22:Y0:16:SER:HB3	1.80	0.47
1:YA:2287:A:H62	1:YA:2344:U:H3	1.62	0.47
1:YA:2845:G:H2'	1:YA:2846:G:H8	1.79	0.47
2:YB:31:C:O2'	2:YB:53:A:N1	2.37	0.47
17:YV:8:GLY:O	17:YV:10:LYS:NZ	2.48	0.47
32:XA:434:U:H2'	32:XA:435:C:C6	2.50	0.47
32:XA:719:C:O2'	49:XR:50:ILE:O	2.25	0.47
32:XA:883:C:N4	32:XA:884:U:O4	2.48	0.47
50:XS:53:ASN:HD21	50:XS:56:GLN:HE22	1.63	0.47
1:RA:1478:G:H2'	1:RA:1479:G:H8	1.78	0.47
1:RA:2646:C:OP2	1:RA:2732:G:O2'	2.25	0.47
5:RF:185:ASP:OD1	5:RF:188:ARG:NH1	2.40	0.47
12:RQ:31:ASP:OD1	12:RQ:134:ARG:NH2	2.48	0.47
32:QA:126:G:OP1	32:QA:605:U:O2'	2.25	0.47
32:QA:825:G:O2'	39:QH:12:ARG:NH2	2.47	0.47
32:QA:1321:C:H3'	32:QA:1322:C:H5''	1.96	0.47
35:QD:59:ARG:HD3	35:QD:59:ARG:HA	1.71	0.47
1:YA:249:C:O2'	11:YP:64:LYS:NZ	2.28	0.47
1:YA:340:A:O2'	5:YF:168:ARG:NH2	2.47	0.47
1:YA:862:G:H2'	1:YA:863:A:O4'	2.15	0.47
2:YB:24:G:H5''	2:YB:25:A:OP1	2.14	0.47
32:XA:115:G:H4'	32:XA:116:A:O5'	2.13	0.47
32:XA:484:G:H4'	32:XA:485:G:O5'	2.15	0.47
32:XA:643:C:H2'	32:XA:644:G:C8	2.49	0.47
32:XA:806:C:H2'	32:XA:807:A:H8	1.79	0.47
1:RA:49:A:H61	1:RA:177:G:H2'	1.78	0.47
1:RA:1790:C:H5''	1:RA:1791:A:OP1	2.15	0.47
1:RA:1800:C:O2	1:RA:1817:G:O6	2.32	0.47
6:RG:36:LYS:HE3	6:RG:95:ARG:HH22	1.78	0.47
8:RI:75:LEU:HD13	8:RI:105:HIS:CE1	2.50	0.47
19:RX:34:ALA:O	19:RX:77:LYS:NZ	2.46	0.47
30:R8:29:LYS:HG2	30:R8:44:LYS:HG3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:429:U:C3'	35:QD:22:LYS:HZ1	2.26	0.47
32:QA:1010:G:H2'	32:QA:1011:G:H8	1.78	0.47
43:QL:11:VAL:HG11	48:QQ:36:ILE:HG21	1.96	0.47
50:QS:12:ASP:HB3	50:QS:14:HIS:H	1.80	0.47
1:YA:579:G:H2'	1:YA:580:C:C6	2.50	0.47
1:YA:2211:G:H21	1:YA:2212:A:H2	1.63	0.47
4:YE:57:LYS:HA	4:YE:59:VAL:H	1.80	0.47
22:Y0:68:GLU:HG3	22:Y0:80:HIS:HB2	1.97	0.47
25:Y3:26:LEU:O	25:Y3:35:ARG:NE	2.48	0.47
54:XX:6:G:H2'	54:XX:7:G:C8	2.50	0.47
1:RA:631:A:N3	1:RA:2415:G:O2'	2.41	0.46
1:RA:1550:C:OP1	1:RA:1727:U:O2'	2.27	0.46
24:R2:18:PRO:HA	24:R2:21:LEU:HB2	1.97	0.46
32:QA:59:A:H3'	32:QA:331:G:H22	1.79	0.46
32:QA:493:G:N2	32:QA:494:U:O4	2.48	0.46
32:QA:1175:G:H2'	32:QA:1176:A:H8	1.81	0.46
32:QA:1229:A:O2'	53:QV:30:C:OP1	2.33	0.46
32:QA:1305:G:HO2'	32:QA:1306:A:H8	1.63	0.46
32:QA:1527:C:O2'	32:QA:1528:U:H5'	2.15	0.46
1:YA:528:A:C2	1:YA:2042:A:H2'	2.50	0.46
1:YA:528:A:O2'	1:YA:529:A:H5'	2.15	0.46
1:YA:813:U:H2'	1:YA:814:C:H6	1.79	0.46
5:YF:29:ASN:HB3	5:YF:112:MET:HE1	1.96	0.46
6:YG:179:PRO:HB3	26:Y4:43:TYR:HE2	1.79	0.46
12:YQ:32:TYR:OH	12:YQ:111:GLU:OE1	2.26	0.46
13:YR:67:LEU:HD13	13:YR:76:VAL:HG21	1.97	0.46
32:XA:1219:U:H2'	32:XA:1220:G:C8	2.50	0.46
32:XA:1321:C:H5''	32:XA:1322:C:H2'	1.96	0.46
32:XA:1412:C:H2'	32:XA:1413:A:H8	1.80	0.46
32:XA:1427:U:H2'	32:XA:1428:A:C8	2.50	0.46
40:XI:8:GLY:HA3	40:XI:15:ALA:HB3	1.97	0.46
40:XI:48:GLU:HA	40:XI:51:ARG:HB3	1.96	0.46
1:RA:1800:C:N4	1:RA:1817:G:H22	2.13	0.46
7:RH:88:LEU:HA	7:RH:130:ARG:HA	1.96	0.46
32:QA:625:G:OP1	47:QP:9:PHE:HB3	2.16	0.46
35:QD:173:TRP:CD1	35:QD:174:LEU:HG	2.50	0.46
51:QT:29:LYS:O	51:QT:33:ILE:HG12	2.15	0.46
1:YA:1009:A:N3	1:YA:1153:C:O2'	2.48	0.46
1:YA:1353:A:H2'	1:YA:1354:A:C8	2.49	0.46
16:YU:85:LYS:HA	16:YU:85:LYS:HD3	1.65	0.46
32:XA:359:U:H2'	32:XA:360:A:C8	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:724:U:H2'	1:RA:725:G:O4'	2.15	0.46
1:RA:823:G:H2'	1:RA:824:A:H8	1.81	0.46
1:RA:1590:U:H2'	1:RA:1591:G:H8	1.80	0.46
1:RA:2346:A:H5''	1:RA:2383:G:H1'	1.97	0.46
1:RA:2844:G:H3'	1:RA:2845:G:H8	1.81	0.46
5:RF:149:ASP:CG	5:RF:151:SER:HG	2.24	0.46
7:RH:60:ARG:O	7:RH:63:SER:OG	2.34	0.46
8:RI:86:THR:C	8:RI:87:LYS:HG2	2.40	0.46
8:RI:94:ALA:HA	8:RI:97:ILE:HG13	1.97	0.46
32:QA:1244:C:H2'	32:QA:1245:A:H8	1.79	0.46
33:QB:80:ILE:HG12	33:QB:215:LEU:HD12	1.96	0.46
1:YA:860:U:H1'	1:YA:2268:A:H5'	1.97	0.46
18:YW:35:ILE:O	18:YW:39:THR:OG1	2.27	0.46
21:YZ:140:ASP:OD1	21:YZ:142:SER:OG	2.31	0.46
35:XD:134:ASP:OD1	35:XD:134:ASP:N	2.44	0.46
1:RA:823:G:H2'	1:RA:824:A:C8	2.50	0.46
1:RA:1341:U:OP1	1:RA:1397:U:N3	2.36	0.46
1:RA:1461:G:OP2	1:RA:1461:G:H8	1.98	0.46
1:RA:1991:U:H2'	1:RA:1992:G:H5''	1.98	0.46
8:RI:5:LEU:HD11	8:RI:19:VAL:HG22	1.96	0.46
11:RP:37:GLY:O	11:RP:40:SER:OG	2.27	0.46
32:QA:410:G:H2'	32:QA:429:U:C5	2.49	0.46
32:QA:616:G:OP2	35:QD:141:ARG:NH2	2.46	0.46
32:QA:1129:C:H4'	32:QA:1130:A:C8	2.50	0.46
32:QA:1329:A:H5''	44:QM:26:GLY:H	1.80	0.46
32:QA:1469:G:H2'	32:QA:1470:G:H8	1.80	0.46
32:QA:1539:C:N4	54:QX:5:A:H61	2.06	0.46
33:QB:150:SER:OG	33:QB:151:GLY:N	2.46	0.46
1:YA:270(J):G:H2'	1:YA:270(K):C:O4'	2.16	0.46
1:YA:534:U:H2'	1:YA:535:C:C6	2.50	0.46
1:YA:2115:G:N2	1:YA:2164:C:OP2	2.49	0.46
1:YA:2591:C:H2'	1:YA:2592:G:C8	2.50	0.46
4:YE:12:THR:OG1	4:YE:13:ARG:N	2.48	0.46
13:YR:59:ASP:N	13:YR:59:ASP:OD1	2.35	0.46
23:Y1:17:SER:HB2	23:Y1:40:ARG:HD2	1.96	0.46
33:XB:36:ARG:HG3	33:XB:37:ASN:HB2	1.97	0.46
42:XK:58:PRO:O	42:XK:62:GLN:N	2.45	0.46
1:RA:182:A:H2'	1:RA:183:C:H6	1.80	0.46
1:RA:270(E):G:H1	1:RA:270(U):C:H42	1.64	0.46
1:RA:1668:A:N3	1:RA:1670:C:N4	2.63	0.46
3:RD:260:ARG:NH2	3:RD:266:SER:OG	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:RN:27:ALA:HB1	9:RN:103:VAL:HG22	1.98	0.46
32:QA:356:A:N3	32:QA:368:U:O2'	2.34	0.46
32:QA:736:C:H2'	32:QA:737:A:H8	1.81	0.46
33:QB:132:LYS:HA	33:QB:135:GLN:HB2	1.97	0.46
38:QG:89:MET:HA	38:QG:155:ARG:HH22	1.81	0.46
40:QI:10:ARG:O	40:QI:13:ALA:HB3	2.14	0.46
54:QX:11:U:H2'	54:QX:12:A:C8	2.51	0.46
1:YA:1593:G:H2'	1:YA:1594:G:C8	2.50	0.46
1:YA:2327:A:H2'	1:YA:2328:A:C8	2.51	0.46
3:YD:258:LYS:HZ1	3:YD:273:ARG:NH1	2.13	0.46
32:XA:749:C:H2'	32:XA:750:G:H8	1.81	0.46
32:XA:757:U:O2'	32:XA:879:C:O2	2.30	0.46
32:XA:946:A:H2'	32:XA:947:G:H8	1.80	0.46
1:RA:2428:G:O2'	11:RP:56:SER:OG	2.33	0.46
10:RO:63:VAL:HB	10:RO:102:VAL:HG12	1.96	0.46
12:RQ:32:TYR:CZ	12:RQ:111:GLU:HB3	2.50	0.46
12:RQ:36:ALA:HB2	12:RQ:103:MET:HE2	1.97	0.46
32:QA:114:U:O2'	32:QA:115:G:H5'	2.16	0.46
32:QA:376:G:O3'	47:QP:5:ARG:NH1	2.47	0.46
32:QA:971:G:H22	32:QA:1363:A:P	2.39	0.46
32:QA:1285:A:H1'	32:QA:1286:A:OP2	2.16	0.46
41:QJ:21:GLN:HA	41:QJ:24:VAL:HG12	1.97	0.46
46:QO:84:LYS:HA	46:QO:84:LYS:HD3	1.71	0.46
53:QV:36:G:H1	54:QX:17:C:H42	1.64	0.46
54:QX:13:A:H4'	54:QX:14:A:OP2	2.14	0.46
1:YA:952:G:OP1	12:YQ:16:ARG:NH1	2.49	0.46
1:YA:1006:C:O2'	9:YN:106:MET:O	2.25	0.46
1:YA:1278:A:OP1	13:YR:36:THR:HG22	2.15	0.46
3:YD:146:GLU:HB2	3:YD:189:CYS:HB3	1.97	0.46
22:Y0:18:ALA:O	22:Y0:20:ARG:NH1	2.41	0.46
32:XA:280:C:H3'	32:XA:281:G:H5'	1.98	0.46
32:XA:538:G:H2'	32:XA:539:A:H8	1.81	0.46
32:XA:1250:A:C2	32:XA:1370:G:H1'	2.50	0.46
32:XA:1539:C:H2'	32:XA:1540:U:C6	2.51	0.46
1:RA:2692:C:O2	1:RA:2847:U:O2'	2.33	0.46
13:RR:54:LEU:HB3	13:RR:62:ALA:HB1	1.98	0.46
15:RT:19:LEU:HD22	15:RT:86:ILE:HG22	1.98	0.46
32:QA:1009:G:N2	32:QA:1020:U:O2	2.39	0.46
32:QA:1060:C:OP1	45:QN:45:ARG:NH2	2.43	0.46
33:QB:163:PHE:HE2	33:QB:215:LEU:HD22	1.79	0.46
34:QC:63:ASN:OD1	34:QC:63:ASN:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:QD:175:SER:HB3	35:QD:186:LEU:HD11	1.98	0.46
44:QM:20:THR:HA	44:QM:26:GLY:HA2	1.98	0.46
3:YD:258:LYS:HE2	3:YD:273:ARG:NH1	2.13	0.46
32:XA:737:A:H2'	32:XA:738:C:C6	2.51	0.46
32:XA:1221:G:OP1	50:XS:36:ARG:NH1	2.48	0.46
32:XA:1316:G:H4'	45:XN:18:VAL:HG11	1.96	0.46
32:XA:1323:G:H2'	32:XA:1324:A:C8	2.50	0.46
32:XA:1505:G:H2'	54:XX:15:A:OP2	2.15	0.46
1:RA:94:G:H21	24:R2:47:ASN:HD22	1.64	0.46
1:RA:652:C:H5'	1:RA:653:A:OP2	2.15	0.46
1:RA:863:A:H2'	1:RA:864:G:H8	1.80	0.46
1:RA:1190:G:H5'	11:RP:32:THR:HA	1.98	0.46
3:RD:5:LYS:HG2	3:RD:17:THR:HG22	1.98	0.46
32:QA:254:G:OP1	48:QQ:68:ARG:HB3	2.16	0.46
32:QA:663:A:H61	32:QA:742:G:H1	1.64	0.46
32:QA:674:G:H2'	32:QA:675:A:C8	2.48	0.46
32:QA:757:U:O2'	32:QA:879:C:O2	2.32	0.46
32:QA:1157:A:OP1	32:QA:1158:C:N4	2.49	0.46
33:QB:136:VAL:HA	33:QB:139:LYS:HG2	1.98	0.46
1:YA:2823:A:OP1	4:YE:113:PHE:HB2	2.15	0.46
8:YI:116:LEU:HD13	8:YI:128:LEU:HD11	1.97	0.46
15:YT:9:LEU:O	15:YT:12:SER:OG	2.32	0.46
32:XA:308:C:H2'	32:XA:309:G:H8	1.80	0.46
33:XB:67:THR:HG21	33:XB:155:LEU:HD22	1.96	0.46
33:XB:85:ALA:O	33:XB:89:GLY:N	2.48	0.46
1:RA:38:A:H2'	1:RA:39:C:C6	2.51	0.46
1:RA:574:C:N3	4:RE:145:LYS:NZ	2.45	0.46
1:RA:1864:U:OP1	1:RA:2410:G:O2'	2.34	0.46
6:RG:63:ILE:HG22	6:RG:143:GLU:HB2	1.97	0.46
12:RQ:56:ARG:HA	21:RZ:180:VAL:HG13	1.97	0.46
18:RW:4:LYS:HB2	18:RW:106:ILE:HG12	1.98	0.46
32:QA:945:G:N2	32:QA:1334:G:O2'	2.49	0.46
32:QA:1239:A:H62	32:QA:1299:A:H62	1.62	0.46
32:QA:1522:U:H2'	32:QA:1523:G:H8	1.80	0.46
35:QD:9:CYS:SG	35:QD:32:ALA:HB3	2.55	0.46
1:YA:81:G:HO2'	1:YA:295:G:HO2'	1.63	0.46
1:YA:922:U:H2'	1:YA:923:C:C6	2.51	0.46
1:YA:2306:C:H2'	1:YA:2307:G:H21	1.80	0.46
32:XA:875:C:H1'	39:XH:15:ASN:ND2	2.31	0.46
32:XA:1141:C:H2'	32:XA:1142:G:C8	2.51	0.46
32:XA:1141:C:H2'	32:XA:1142:G:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:XG:79:ARG:HH21	38:XG:82:GLY:HA2	1.81	0.46
1:RA:2744:G:N2	7:RH:143:GLN:OE1	2.41	0.46
4:RE:47:VAL:HG21	4:RE:86:PRO:HD2	1.98	0.46
7:RH:152:ARG:HG2	7:RH:153:LYS:HD2	1.98	0.46
32:QA:652:U:H1'	32:QA:653:A:H2	1.81	0.46
32:QA:974:A:N3	45:QN:31:ARG:NH1	2.64	0.46
1:YA:616:A:C4	5:YF:180:GLY:HA3	2.51	0.46
1:YA:997:G:OP1	16:YU:93:LYS:HE2	2.16	0.46
1:YA:1557:C:OP2	1:YA:1558:A:O2'	2.25	0.46
1:YA:1783:A:H5'	1:YA:2608:G:H4'	1.97	0.46
1:YA:2832:U:H4'	1:YA:2833:G:C5'	2.46	0.46
6:YG:137:GLU:HG3	6:YG:139:LEU:HB2	1.97	0.46
7:YH:11:VAL:HA	7:YH:12:PRO:HD3	1.71	0.46
32:XA:112:G:H4'	32:XA:389:A:H4'	1.97	0.46
32:XA:410:G:H2'	32:XA:429:U:C5	2.50	0.46
32:XA:1022:G:H2'	32:XA:1023:G:H8	1.80	0.46
44:XM:3:ARG:NE	44:XM:3:ARG:N	2.62	0.46
45:XN:40:CYS:SG	45:XN:41:ARG:N	2.88	0.46
1:RA:263:C:H2'	1:RA:264:C:O4'	2.16	0.45
1:RA:671:C:H2'	1:RA:672:C:C6	2.51	0.45
7:RH:107:VAL:O	7:RH:153:LYS:NZ	2.49	0.45
8:RI:113:ARG:HH22	8:RI:115:ALA:HB2	1.81	0.45
29:R7:13:ALA:HB2	29:R7:46:VAL:HG11	1.98	0.45
32:QA:979:C:H42	45:QN:18:VAL:HG12	1.81	0.45
32:QA:1431:C:H2'	32:QA:1432:G:O4'	2.17	0.45
35:QD:31:CYS:HA	57:QD:301:SF4:S4	2.56	0.45
1:YA:1598:C:O3'	19:YX:35:THR:OG1	2.34	0.45
1:YA:2183:C:N4	1:YA:2184:G:O6	2.49	0.45
1:YA:2392:A:H8	11:YP:61:ARG:HG2	1.82	0.45
25:Y3:51:ALA:HA	25:Y3:54:VAL:HG12	1.98	0.45
32:XA:186(D):C:H42	32:XA:191(D):U:H3	1.64	0.45
32:XA:1346:A:H1'	32:XA:1348:U:C2	2.51	0.45
32:XA:1442:G:H1	32:XA:1461:G:H21	1.64	0.45
35:XD:19:LEU:HD13	35:XD:21:LEU:HD21	1.98	0.45
47:XP:11:SER:HB2	47:XP:14:ASN:HB3	1.96	0.45
1:RA:820:A:H4'	1:RA:836:G:N2	2.31	0.45
10:RO:24:VAL:HG13	10:RO:33:ALA:HB2	1.97	0.45
10:RO:104:ARG:NH1	10:RO:121:VAL:O	2.49	0.45
15:RT:20:PRO:HD2	15:RT:86:ILE:HG23	1.97	0.45
23:R1:82:LEU:HD23	23:R1:82:LEU:HA	1.86	0.45
32:QA:115:G:H4'	32:QA:116:A:O5'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:1150:U:H2'	32:QA:1151:A:C8	2.51	0.45
33:QB:6:THR:O	33:QB:217:ARG:NE	2.49	0.45
49:QR:32:ARG:HA	49:QR:69:THR:HG21	1.96	0.45
1:YA:1460:A:H4'	1:YA:1461:G:OP2	2.16	0.45
1:YA:1817:G:OP1	3:YD:88:ARG:NH2	2.47	0.45
1:YA:2756:U:H1'	1:YA:2757:A:H5''	1.97	0.45
32:XA:731:G:OP1	32:XA:766:A:H1'	2.16	0.45
32:XA:737:A:H2'	32:XA:738:C:H6	1.81	0.45
33:XB:132:LYS:HA	33:XB:135:GLN:HB2	1.98	0.45
41:XJ:7:LYS:HB2	41:XJ:97:GLU:HB2	1.98	0.45
47:XP:67:THR:O	47:XP:71:ARG:N	2.49	0.45
1:RA:1203:G:O6	1:RA:1204:A:N6	2.48	0.45
1:RA:1539:G:H2'	1:RA:1540:G:H8	1.80	0.45
2:RB:52:A:HO2'	2:RB:53:A:H8	1.63	0.45
6:RG:32:PRO:HB2	6:RG:172:LEU:HD13	1.97	0.45
7:RH:129:THR:O	7:RH:129:THR:OG1	2.34	0.45
11:RP:76:LYS:HD2	11:RP:79:ARG:HH22	1.81	0.45
15:RT:16:ARG:NH1	15:RT:18:ASP:OD2	2.48	0.45
32:QA:352:C:O2'	32:QA:354:G:OP1	2.29	0.45
32:QA:406:G:N3	35:QD:119:GLN:NE2	2.64	0.45
32:QA:448:A:N7	32:QA:486:U:O4	2.49	0.45
32:QA:657:G:N2	46:QO:22:THR:OG1	2.45	0.45
34:QC:73:PRO:HA	34:QC:76:VAL:HG12	1.98	0.45
39:QH:25:ASP:HB3	39:QH:58:TYR:HD2	1.80	0.45
39:QH:109:ILE:HD11	39:QH:120:THR:HB	1.98	0.45
39:QH:121:ASP:N	39:QH:121:ASP:OD1	2.49	0.45
46:QO:48:LYS:HE2	46:QO:48:LYS:HB2	1.84	0.45
1:YA:189:G:O6	1:YA:205:G:O2'	2.26	0.45
1:YA:1027:A:C2	1:YA:2488:A:H5'	2.52	0.45
1:YA:2023:G:H5'	1:YA:2617:C:H4'	1.97	0.45
1:YA:2836:U:H2'	1:YA:2837:G:C8	2.51	0.45
13:YR:19:ALA:O	13:YR:23:ASN:ND2	2.49	0.45
32:XA:79:G:H2'	32:XA:80:G:H8	1.80	0.45
44:XM:57:ARG:HA	44:XM:60:VAL:HG12	1.98	0.45
1:RA:137(A):G:H2'	1:RA:139:G:N7	2.32	0.45
1:RA:1141:U:H1'	1:RA:1142(A):A:C6	2.51	0.45
1:RA:1485:G:H1	1:RA:1504:C:H42	1.63	0.45
6:RG:37:VAL:HG23	6:RG:99:MET:HE3	1.98	0.45
6:RG:109:VAL:HG11	6:RG:142:PRO:HG3	1.99	0.45
7:RH:20:ALA:HB3	7:RH:23:ARG:HG2	1.98	0.45
10:RO:120:GLU:OE2	15:RT:67:SER:OG	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:940:C:H2'	32:QA:941:G:C8	2.51	0.45
32:QA:1217:C:H2'	32:QA:1218:C:C6	2.51	0.45
41:QJ:3:LYS:HG3	41:QJ:75:ILE:HA	1.99	0.45
42:QK:33:THR:OG1	42:QK:34:ASP:O	2.32	0.45
42:QK:50:TYR:HB3	42:QK:54:ARG:HG3	1.99	0.45
1:YA:363(B):G:H2'	1:YA:363(C):G:C8	2.49	0.45
1:YA:1952:A:OP1	10:YO:44:LYS:NZ	2.43	0.45
6:YG:165:THR:OG1	6:YG:166:ASP:N	2.49	0.45
24:Y2:31:GLU:HB3	24:Y2:53:LEU:HD21	1.99	0.45
32:XA:477:G:H2'	32:XA:478:A:H8	1.80	0.45
32:XA:673:G:O3'	37:XF:87:ARG:NH2	2.50	0.45
32:XA:1151:A:H2'	32:XA:1152:A:C8	2.52	0.45
36:XE:105:VAL:HG21	36:XE:128:PRO:HB3	1.99	0.45
37:XF:67:MET:HE1	37:XF:75:LEU:HD22	1.97	0.45
1:RA:844:C:H2'	1:RA:845:G:O4'	2.17	0.45
1:RA:900:A:H3'	1:RA:901:A:H8	1.81	0.45
1:RA:1283:G:H1'	1:RA:1329:U:H3	1.80	0.45
1:RA:1365:A:O2'	23:R1:11:ARG:NH2	2.46	0.45
1:RA:2313:C:H4'	6:RG:91:ARG:HD3	1.98	0.45
6:RG:166:ASP:OD1	6:RG:166:ASP:N	2.49	0.45
21:RZ:181:GLU:O	21:RZ:181:GLU:HG3	2.15	0.45
32:QA:560:U:H4'	32:QA:561:U:H5''	1.97	0.45
34:QC:40:ARG:HE	34:QC:55:VAL:HB	1.82	0.45
50:QS:32:LYS:HD3	50:QS:57:HIS:CD2	2.52	0.45
1:YA:264:C:C2'	1:YA:265:A:H5''	2.46	0.45
1:YA:529:A:H8	1:YA:530:G:C6	2.35	0.45
1:YA:980:A:N3	1:YA:2037:G:O2'	2.40	0.45
1:YA:1310:G:OP2	29:Y7:9:ARG:NE	2.42	0.45
1:YA:2776:A:H4'	1:YA:2777:G:O5'	2.17	0.45
7:YH:90:LYS:NZ	7:YH:159:GLU:OE1	2.41	0.45
8:YI:67:ARG:HE	8:YI:67:ARG:HB2	1.62	0.45
32:XA:110:C:O2'	47:XP:25:ARG:O	2.34	0.45
32:XA:164:U:H2'	32:XA:165:C:C6	2.52	0.45
32:XA:377:G:OP1	47:XP:3:LYS:HD2	2.16	0.45
32:XA:1492:A:O2'	32:XA:1493:A:H5''	2.16	0.45
42:XK:62:GLN:OE1	42:XK:93:GLN:NE2	2.42	0.45
48:XQ:95:TYR:HA	48:XQ:98:LEU:HD12	1.99	0.45
1:RA:184:C:H2'	1:RA:185:U:H6	1.82	0.45
1:RA:944:G:H5''	1:RA:945:A:O5'	2.17	0.45
1:RA:1073:A:H2'	1:RA:1074:G:H8	1.81	0.45
1:RA:2680:C:OP2	4:RE:111:ARG:NH2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:RF:32:LEU:HD11	5:RF:105:VAL:HG13	1.98	0.45
10:RO:73:ASP:OD1	10:RO:73:ASP:N	2.42	0.45
13:RR:104:ARG:HG3	13:RR:107:ASP:HB3	1.98	0.45
18:RW:18:ARG:HG2	18:RW:76:VAL:HB	1.98	0.45
32:QA:261:U:OP2	51:QT:79:ARG:NH2	2.50	0.45
32:QA:410:G:H21	32:QA:432:A:N6	2.03	0.45
32:QA:1157:A:H62	32:QA:1178:G:N2	2.15	0.45
34:QC:63:ASN:HB3	34:QC:98:ASN:HB2	1.98	0.45
1:YA:746:A:H2'	1:YA:2612:C:H5''	1.98	0.45
1:YA:1833:U:O2'	1:YA:1969:A:N1	2.44	0.45
1:YA:2151:G:H2'	1:YA:2152:G:C8	2.51	0.45
1:YA:2213:U:O2	23:Y1:52:ARG:NH2	2.44	0.45
1:YA:2298:A:H62	1:YA:2318:G:H8	1.65	0.45
10:YO:8:LEU:HB2	10:YO:19:ILE:HG13	1.99	0.45
21:YZ:110:GLY:HA3	21:YZ:174:VAL:HG11	1.97	0.45
32:XA:1540:U:N3	54:XX:2:G:N1	2.64	0.45
46:XO:55:GLY:HA2	46:XO:58:MET:HE3	1.99	0.45
1:RA:249:C:O2	30:R8:12:LYS:NZ	2.38	0.45
1:RA:2236:C:H2'	1:RA:2237:G:O4'	2.17	0.45
19:RX:53:LYS:HB3	19:RX:82:GLN:HB3	1.98	0.45
30:R8:61:LEU:H	30:R8:61:LEU:HG	1.68	0.45
32:QA:922:G:H2'	32:QA:923:A:C8	2.52	0.45
32:QA:987:G:H1'	50:QS:34:TRP:HH2	1.82	0.45
32:QA:1077:G:N2	32:QA:1080:A:OP2	2.47	0.45
50:QS:31:ILE:HG22	50:QS:33:THR:HG23	1.97	0.45
1:YA:81:G:N2	20:YY:1:MET:SD	2.90	0.45
1:YA:443:A:N6	5:YF:41:LEU:O	2.45	0.45
32:XA:603:U:H2'	32:XA:604:G:H8	1.81	0.45
32:XA:627:G:H2'	32:XA:628:G:H8	1.82	0.45
32:XA:1237:C:H5''	32:XA:1238:A:C8	2.51	0.45
32:XA:1513:A:H2'	32:XA:1514:C:C6	2.52	0.45
44:XM:3:ARG:HB3	44:XM:8:GLU:HA	1.99	0.45
1:RA:108:U:H2'	1:RA:109:G:H8	1.81	0.45
1:RA:1210:A:H4'	1:RA:1211:U:O5'	2.17	0.45
1:RA:2086:U:H2'	1:RA:2087:G:C8	2.52	0.45
1:RA:2116:G:H2'	1:RA:2117:A:C4	2.52	0.45
5:RF:116:ASP:OD1	5:RF:119:ARG:NH2	2.36	0.45
18:RW:12:ILE:O	18:RW:101:SER:OG	2.24	0.45
32:QA:8:A:N6	35:QD:205:GLU:O	2.48	0.45
32:QA:17:U:H2'	32:QA:18:C:H6	1.82	0.45
1:YA:18:C:O2'	1:YA:553:U:OP1	2.28	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:278:A:H2'	1:YA:279:C:C6	2.52	0.45
1:YA:475:U:O2'	1:YA:505:A:N3	2.46	0.45
1:YA:2791:C:C5	1:YA:2893:G:H3'	2.51	0.45
6:YG:65:GLY:HA3	26:Y4:9:LEU:HD21	1.97	0.45
10:YO:106:LEU:HB3	10:YO:111:PHE:HB2	1.98	0.45
26:Y4:50:VAL:HG11	44:XM:65:LYS:HG3	1.99	0.45
32:XA:1145:C:H4'	32:XA:1146:A:H5'	1.98	0.45
35:XD:22:LYS:N	35:XD:26:CYS:SG	2.88	0.45
1:RA:807:U:OP2	11:RP:41:ARG:NH1	2.50	0.45
1:RA:848:G:H2'	1:RA:849:A:H8	1.82	0.45
1:RA:2005:A:O2'	1:RA:2049:G:OP1	2.29	0.45
1:RA:2061:G:H5''	1:RA:2503:A:C2	2.52	0.45
2:RB:70:C:H2'	2:RB:71:C:H6	1.82	0.45
32:QA:17:U:H2'	32:QA:18:C:C6	2.52	0.45
32:QA:279:A:OP1	32:QA:280:C:O2'	2.30	0.45
32:QA:1410:G:H2'	32:QA:1411:C:H6	1.82	0.45
32:QA:1497:G:H1'	32:QA:1518:A:H2	1.82	0.45
34:QC:21:ARG:NH2	34:QC:58:GLU:OE2	2.49	0.45
43:QL:45:PRO:HB2	43:QL:92:ASP:HB3	1.98	0.45
1:YA:139:G:N2	1:YA:1596:A:H4'	2.32	0.45
1:YA:888:C:OP1	44:XM:93:ARG:NH2	2.49	0.45
1:YA:2030:A:H4'	1:YA:2031:A:C8	2.52	0.45
5:YF:182:ASN:OD1	5:YF:182:ASN:N	2.48	0.45
32:XA:514:C:H2'	32:XA:515:G:C8	2.47	0.45
33:XB:187:LEU:HA	33:XB:201:ILE:HB	1.98	0.45
42:XK:21:ILE:HB	42:XK:84:VAL:HA	1.99	0.45
44:XM:36:LYS:HE3	44:XM:36:LYS:HB3	1.86	0.45
44:XM:74:VAL:HA	44:XM:77:ASN:HB2	1.99	0.45
45:XN:29:ARG:HG3	45:XN:31:ARG:H	1.82	0.45
1:RA:2532:G:N2	1:RA:2663:G:O2'	2.50	0.45
1:RA:2630:G:H2'	1:RA:2631:G:H8	1.83	0.45
1:RA:2718:G:O2'	1:RA:2847:U:O5'	2.32	0.45
23:R1:58:ILE:HD13	23:R1:87:PRO:HD3	1.99	0.45
32:QA:701:C:H1'	32:QA:703:G:C6	2.52	0.45
32:QA:1095:U:P	32:QA:1108:G:H1	2.39	0.45
48:QQ:92:ARG:HD3	48:QQ:92:ARG:HA	1.82	0.45
1:YA:1639:U:H2'	1:YA:1640:C:H5''	1.98	0.45
1:YA:2154:G:H2'	1:YA:2155:G:C8	2.51	0.45
1:YA:2808:U:N3	1:YA:2892:A:C5	2.85	0.45
17:YV:1:MET:HE2	17:YV:43:GLU:HB2	1.97	0.45
23:Y1:75:GLU:OE2	23:Y1:78:LYS:NZ	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:XD:109:GLY:HA3	35:XD:165:MET:HE2	1.98	0.45
51:XT:75:ASN:N	51:XT:75:ASN:OD1	2.43	0.45
1:RA:414:C:O2	1:RA:1864:U:O2'	2.34	0.44
1:RA:458:G:O2'	1:RA:469:G:O6	2.26	0.44
1:RA:2387:U:O2'	22:R0:19:LYS:NZ	2.50	0.44
1:RA:2627:G:O2'	1:RA:2781:A:N1	2.49	0.44
1:RA:2811:G:C5	1:RA:2891:G:N2	2.85	0.44
22:R0:10:THR:HG22	22:R0:12:ASN:H	1.82	0.44
44:QM:76:ALA:O	44:QM:80:ARG:HG2	2.18	0.44
1:YA:508:G:O2'	1:YA:509:C:P	2.75	0.44
1:YA:1203:G:H5'	11:YP:3:LEU:HD12	2.00	0.44
1:YA:1417:C:H2'	1:YA:1418:G:O4'	2.17	0.44
9:YN:54:VAL:HB	9:YN:122:VAL:HG22	2.00	0.44
32:XA:444:C:H2'	32:XA:445:G:H8	1.82	0.44
32:XA:448:A:OP2	32:XA:485:G:N2	2.39	0.44
35:XD:129:ASN:HA	35:XD:145:GLU:HB2	1.98	0.44
37:XF:50:TYR:OH	49:XR:74:ARG:O	2.33	0.44
1:RA:262:A:N3	1:RA:430:G:O2'	2.45	0.44
1:RA:480:A:N3	1:RA:499:U:O2'	2.44	0.44
2:RB:24:G:H5''	2:RB:25:A:OP1	2.17	0.44
32:QA:714:G:H2'	32:QA:715:A:C8	2.51	0.44
32:QA:728:A:H2'	32:QA:729:A:C8	2.51	0.44
32:QA:1343:G:H4'	40:QI:122:ALA:HB3	1.99	0.44
35:QD:153:ARG:HB3	35:QD:181:MET:HE1	1.98	0.44
40:QI:47:LEU:HG	40:QI:50:LEU:HD12	1.98	0.44
1:YA:262:A:N3	1:YA:430:G:O2'	2.35	0.44
1:YA:455:C:N3	1:YA:473:G:H5'	2.32	0.44
1:YA:581:C:H2'	1:YA:582:G:H8	1.83	0.44
1:YA:589:C:H2'	1:YA:590:A:H8	1.83	0.44
1:YA:639:U:H2'	1:YA:640:C:C6	2.52	0.44
1:YA:1113:U:H2'	1:YA:1114:G:C8	2.52	0.44
1:YA:2577:A:O4'	27:Y5:3:LYS:HB2	2.17	0.44
15:YT:73:GLU:OE2	15:YT:103:ARG:NH2	2.48	0.44
35:XD:176:LEU:HG	35:XD:178:VAL:HG22	1.97	0.44
1:RA:30:G:H2'	1:RA:31:C:H6	1.81	0.44
1:RA:1817:G:H2'	1:RA:1818:U:H5'	2.00	0.44
12:RQ:32:TYR:CE1	12:RQ:133:ARG:HG3	2.53	0.44
32:QA:21:G:H2'	32:QA:22:G:C8	2.52	0.44
32:QA:932:C:OP1	38:QG:4:ARG:NH1	2.49	0.44
32:QA:1228:C:OP2	44:QM:108:ARG:NH2	2.26	0.44
1:YA:657:U:H2'	1:YA:658:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1508:A:O2'	1:YA:1509:C:O4'	2.35	0.44
2:YB:15:A:H5'	2:YB:16:G:C8	2.52	0.44
26:Y4:56:VAL:HG12	26:Y4:57:GLU:H	1.83	0.44
32:XA:855:G:N2	32:XA:1539:C:OP1	2.47	0.44
32:XA:1037:C:H2'	32:XA:1038:C:C6	2.52	0.44
32:XA:1218:C:H2'	32:XA:1219:U:C6	2.52	0.44
32:XA:1244:C:H2'	32:XA:1245:A:C8	2.53	0.44
32:XA:1391:U:H2'	32:XA:1392:G:C8	2.52	0.44
43:XL:67:THR:OG1	43:XL:95:GLY:O	2.34	0.44
1:RA:1338:G:O2'	1:RA:1393:A:N1	2.47	0.44
1:RA:2314:C:H2'	1:RA:2315:G:C8	2.52	0.44
1:RA:2611:U:O4	27:R5:3:LYS:NZ	2.50	0.44
1:RA:2689:U:H4'	1:RA:2690:C:O5'	2.17	0.44
4:RE:144:ARG:HB3	4:RE:145:LYS:H	1.54	0.44
8:RI:118:LYS:O	8:RI:118:LYS:HG2	2.18	0.44
14:RS:28:VAL:HG11	14:RS:98:VAL:HG12	1.99	0.44
32:QA:890:G:O2'	32:QA:906:G:O6	2.26	0.44
32:QA:950:U:H2'	32:QA:951:G:H8	1.82	0.44
32:QA:1145:C:H4'	32:QA:1146:A:H8	1.81	0.44
38:QG:151:TYR:OH	42:QK:54:ARG:NH2	2.51	0.44
46:QO:26:GLU:OE1	46:QO:77:ARG:NH1	2.51	0.44
46:QO:70:LEU:HD21	46:QO:77:ARG:HG3	1.99	0.44
1:YA:38:A:H2'	1:YA:39:C:C6	2.52	0.44
1:YA:855:G:H1	1:YA:922:U:H3	1.65	0.44
1:YA:1394:U:H4'	1:YA:1603:A:H4'	2.00	0.44
3:YD:108:PRO:HG2	3:YD:111:LEU:HG	2.00	0.44
15:YT:24:PRO:HD3	15:YT:52:ILE:HD12	1.98	0.44
32:XA:165:C:H2'	32:XA:166:G:C8	2.53	0.44
32:XA:1314:C:N4	50:XS:2:PRO:O	2.50	0.44
53:XV:39:C:H2'	53:XV:40:G:H8	1.82	0.44
1:RA:99:U:H4'	1:RA:101:G:O5'	2.17	0.44
1:RA:248:G:C2	1:RA:2431:U:H4'	2.53	0.44
1:RA:768:G:O2'	1:RA:1379:A:N6	2.50	0.44
1:RA:796:C:H2'	1:RA:797:C:C6	2.53	0.44
5:RF:107:LYS:HB3	5:RF:107:LYS:HE2	1.83	0.44
11:RP:98:GLU:O	11:RP:102:ARG:NE	2.51	0.44
30:R8:34:TRP:CD1	30:R8:34:TRP:H	2.36	0.44
32:QA:565:U:H3'	32:QA:566:G:H2'	1.99	0.44
32:QA:782:A:O3'	32:QA:1515:C:H4'	2.18	0.44
1:YA:1262:A:OP2	18:YW:97:LYS:NZ	2.50	0.44
1:YA:1930:G:N2	1:YA:1969:A:OP2	2.42	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2291:U:O2'	1:YA:2374:C:O2	2.33	0.44
4:YE:35:GLN:HG2	4:YE:37:ARG:HE	1.81	0.44
32:XA:753:A:OP1	46:XO:69:TYR:OH	2.20	0.44
32:XA:1174:G:H2'	32:XA:1175:G:C8	2.53	0.44
35:XD:159:ARG:O	35:XD:163:GLU:N	2.46	0.44
41:XJ:38:ILE:HD12	41:XJ:39:PRO:HD2	1.98	0.44
49:XR:19:LYS:HB3	49:XR:19:LYS:HE2	1.74	0.44
1:RA:678:C:H2'	1:RA:679:C:C6	2.53	0.44
1:RA:785:G:O2'	1:RA:1779:U:H5''	2.18	0.44
1:RA:1583:A:H4'	1:RA:1586:A:C4	2.52	0.44
2:RB:31:C:O2'	2:RB:53:A:N1	2.48	0.44
10:RO:120:GLU:HG2	10:RO:122:LEU:HG	1.99	0.44
26:R4:37:SER:HA	26:R4:40:HIS:HB2	1.99	0.44
32:QA:514:C:H2'	32:QA:515:G:C8	2.45	0.44
1:YA:65:C:O2	1:YA:456:C:N4	2.51	0.44
1:YA:218:A:N1	1:YA:235:U:H4'	2.33	0.44
1:YA:2140:C:H2'	1:YA:2141:G:C8	2.53	0.44
33:XB:105:PHE:HZ	33:XB:156:LYS:HA	1.82	0.44
35:XD:13:ARG:HB3	35:XD:39:PRO:HA	1.99	0.44
38:XG:58:PRO:HA	38:XG:61:VAL:HG22	1.99	0.44
1:RA:1073:A:HO2'	1:RA:1074:G:C5'	2.30	0.44
32:QA:973:G:H3'	32:QA:974:A:H5''	1.98	0.44
32:QA:1053:G:H5'	32:QA:1054:C:H5'	2.00	0.44
32:QA:1352:C:H2'	32:QA:1353:G:C8	2.53	0.44
33:QB:15:VAL:H	33:QB:16:HIS:CE1	2.35	0.44
35:QD:30:LYS:C	35:QD:32:ALA:H	2.25	0.44
39:QH:103:VAL:HG21	39:QH:110:ALA:HB2	1.99	0.44
44:QM:15:VAL:HG12	44:QM:45:VAL:HG13	1.99	0.44
1:YA:2291:U:H2'	1:YA:2292:C:C6	2.52	0.44
26:Y4:26:SER:OG	26:Y4:27:THR:N	2.51	0.44
32:XA:105:G:H2'	32:XA:106:C:C6	2.53	0.44
32:XA:781:A:O2'	32:XA:1522:U:O2	2.35	0.44
33:XB:131:PRO:HB2	33:XB:133:LYS:HG2	2.00	0.44
33:XB:207:ALA:O	33:XB:210:SER:N	2.44	0.44
34:XC:6:HIS:HD2	34:XC:7:PRO:HD2	1.83	0.44
43:XL:113:ARG:HB3	43:XL:122:THR:HG21	2.00	0.44
49:XR:65:ILE:O	49:XR:69:THR:OG1	2.28	0.44
1:RA:139:G:C2	1:RA:141:A:N6	2.86	0.44
1:RA:956:G:H2'	1:RA:957:A:H2'	2.00	0.44
1:RA:1221:C:H2'	1:RA:1222:C:H6	1.82	0.44
3:RD:20:ASP:OD1	3:RD:20:ASP:N	2.37	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:RQ:7:MET:HB2	12:RQ:7:MET:HE3	1.71	0.44
20:RY:83:THR:OG1	20:RY:84:ARG:N	2.50	0.44
30:R8:25:MET:HE3	30:R8:25:MET:HB3	1.77	0.44
43:QL:77:LEU:HD23	43:QL:77:LEU:HA	1.78	0.44
1:YA:1076:C:H2'	1:YA:1077:A:H5''	1.98	0.44
1:YA:1430:C:H2'	1:YA:1431:U:C6	2.53	0.44
1:YA:2311:A:H8	6:YG:82:LEU:HD11	1.83	0.44
5:YF:7:TYR:HD1	5:YF:21:ALA:HB1	1.81	0.44
8:YI:90:GLY:O	8:YI:121:LYS:NZ	2.49	0.44
9:YN:48:MET:HE2	9:YN:48:MET:HB2	1.85	0.44
20:YY:52:SER:N	20:YY:55:TYR:O	2.51	0.44
32:XA:476:G:H2'	32:XA:477:G:H8	1.82	0.44
32:XA:1427:U:H2'	32:XA:1428:A:H8	1.83	0.44
1:RA:184:C:H2'	1:RA:185:U:C6	2.52	0.44
32:QA:224:C:H2'	32:QA:225:C:H6	1.83	0.44
32:QA:630:G:H2'	32:QA:631:G:H4'	1.99	0.44
32:QA:1391:U:H2'	32:QA:1392:G:C8	2.52	0.44
51:QT:10:LEU:HD23	51:QT:12:ALA:H	1.82	0.44
51:QT:22:ARG:O	51:QT:26:ASN:ND2	2.51	0.44
1:YA:223:A:N1	1:YA:407:G:O2'	2.47	0.44
1:YA:601:C:O2'	1:YA:605:C:OP1	2.35	0.44
1:YA:1779:U:OP2	1:YA:1784:A:N6	2.42	0.44
1:YA:2032:G:H1'	4:YE:145:LYS:HD3	2.00	0.44
1:YA:2591:C:H2'	1:YA:2592:G:H8	1.81	0.44
1:YA:2810:A:H61	1:YA:2891:G:H2'	1.83	0.44
1:YA:2867:G:HO2'	1:YA:2868:A:P	2.40	0.44
3:YD:259:THR:O	3:YD:259:THR:OG1	2.26	0.44
21:YZ:10:ARG:NH2	21:YZ:26:GLY:O	2.51	0.44
32:XA:191(G):G:C5	51:XT:105:SER:HB3	2.53	0.44
32:XA:636:U:H2'	32:XA:637:G:C8	2.52	0.44
32:XA:806:C:H2'	32:XA:807:A:C8	2.53	0.44
32:XA:1015:A:H2'	32:XA:1016:A:C8	2.53	0.44
1:RA:639:U:H2'	1:RA:640:C:C6	2.52	0.43
8:RI:30:LEU:HB3	8:RI:36:ALA:HB3	1.99	0.43
10:RO:73:ASP:OD2	15:RT:32:TYR:OH	2.26	0.43
32:QA:244:U:H4'	32:QA:245:C:O5'	2.16	0.43
32:QA:475:G:H2'	32:QA:476:G:H8	1.83	0.43
32:QA:711:G:H2'	32:QA:712:A:C8	2.53	0.43
32:QA:1152:A:H2'	32:QA:1153:C:C6	2.53	0.43
1:YA:86:C:H4'	1:YA:104:U:H1'	1.99	0.43
1:YA:546:C:H5''	1:YA:547:A:N7	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:607:U:OP1	5:YF:102:PRO:HA	2.18	0.43
1:YA:820:A:H4'	1:YA:836:G:H22	1.83	0.43
1:YA:1729:A:O2'	1:YA:1730:U:H2'	2.18	0.43
1:YA:1790:C:H5''	1:YA:1791:A:OP1	2.18	0.43
1:YA:1792:G:H5'	3:YD:205:VAL:HG13	2.00	0.43
1:YA:2511:U:O2'	4:YE:138:PRO:O	2.34	0.43
32:XA:22:G:O2'	32:XA:913:A:N1	2.38	0.43
32:XA:266:G:H5'	32:XA:268:C:H41	1.83	0.43
32:XA:444:C:H2'	32:XA:445:G:C8	2.53	0.43
32:XA:1098:C:H2'	32:XA:1099:G:H8	1.83	0.43
39:XH:112:LEU:HA	39:XH:134:ILE:HG12	1.99	0.43
50:XS:53:ASN:HD22	50:XS:75:ALA:HB1	1.83	0.43
1:RA:275:G:H3'	1:RA:276:A:H5''	2.00	0.43
1:RA:372:G:HO2'	1:RA:373:U:P	2.41	0.43
1:RA:811:U:H2'	11:RP:21:ARG:HA	1.99	0.43
1:RA:1403:C:C5'	1:RA:1471:A:H1'	2.46	0.43
1:RA:2115:G:N1	1:RA:2164:C:OP2	2.50	0.43
1:RA:2126:A:H1'	1:RA:2127:G:OP2	2.19	0.43
1:RA:2140:C:O2	1:RA:2151:G:N1	2.43	0.43
8:RI:92:VAL:HB	8:RI:120:ILE:CG2	2.48	0.43
10:RO:97:ARG:H	10:RO:117:LEU:HD22	1.82	0.43
26:R4:14:ILE:HB	26:R4:22:ILE:HB	1.99	0.43
32:QA:194:C:H2'	32:QA:195:A:H5''	2.00	0.43
32:QA:963:G:H21	41:QJ:55:LYS:HE3	1.83	0.43
32:QA:1172:C:H2'	32:QA:1173:G:C8	2.52	0.43
32:QA:1287:A:C2	32:QA:1353:G:H1'	2.53	0.43
32:QA:1534:A:C1'	54:QX:10:G:N2	2.68	0.43
39:QH:81:HIS:ND1	39:QH:138:TRP:O	2.38	0.43
1:YA:49:A:H4'	1:YA:50:U:H5''	2.00	0.43
1:YA:184:C:O2'	1:YA:217:G:N3	2.49	0.43
1:YA:492:A:H2'	1:YA:493:G:O4'	2.18	0.43
17:YV:76:LYS:HB2	17:YV:81:TYR:HB3	1.99	0.43
32:XA:34:C:H2'	32:XA:35:G:H8	1.83	0.43
33:XB:48:MET:HA	33:XB:51:LEU:HB2	1.99	0.43
50:XS:50:ALA:HB1	50:XS:57:HIS:HB2	2.00	0.43
1:RA:303:U:H2'	1:RA:304:G:H8	1.83	0.43
1:RA:1823:G:OP1	3:RD:54:ARG:NH1	2.52	0.43
1:RA:2051:A:H5'	1:RA:2578:G:O4'	2.18	0.43
1:RA:2291:U:H2'	1:RA:2292:C:C6	2.53	0.43
1:RA:2572:A:OP1	1:RA:2574:G:H4'	2.18	0.43
6:RG:77:ILE:HG22	6:RG:80:PHE:H	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:RP:65:ARG:HE	11:RP:65:ARG:HB3	1.58	0.43
16:RU:16:LYS:HB2	16:RU:16:LYS:HE2	1.85	0.43
19:RX:46:ALA:HB1	24:R2:33:MET:HE1	1.99	0.43
32:QA:1355:G:H2'	32:QA:1356:G:C8	2.54	0.43
47:QP:21:VAL:HG13	47:QP:34:GLU:H	1.83	0.43
1:YA:396:G:O2'	23:Y1:43:TYR:O	2.36	0.43
1:YA:848:G:H2'	1:YA:849:A:H8	1.83	0.43
1:YA:1359:A:H62	1:YA:1372:U:H3	0.74	0.43
1:YA:1678:G:N2	1:YA:1989:G:H22	2.16	0.43
1:YA:2331:G:O2'	1:YA:2336:A:N1	2.45	0.43
2:YB:39:A:O2'	2:YB:46:A:N1	2.41	0.43
9:YN:6:PRO:HG3	9:YN:41:ASP:HB2	2.00	0.43
32:XA:150:C:N4	32:XA:171:A:H62	2.14	0.43
32:XA:405:U:H3'	32:XA:406:G:H5'	2.00	0.43
32:XA:1030:C:H3'	32:XA:1031:G:C8	2.54	0.43
32:XA:1410:G:H2'	32:XA:1411:C:H6	1.84	0.43
33:XB:14:GLY:H	33:XB:16:HIS:HD1	1.66	0.43
33:XB:115:LEU:HD13	33:XB:145:LEU:HB3	2.00	0.43
35:XD:128:VAL:HG12	35:XD:129:ASN:HB2	1.98	0.43
43:XL:53:ARG:HB3	43:XL:69:TYR:HE1	1.84	0.43
43:XL:76:ASN:OD1	43:XL:76:ASN:N	2.50	0.43
50:XS:19:VAL:HG21	50:XS:44:MET:HG2	2.00	0.43
1:RA:82:G:H5'	1:RA:296:C:H5'	2.01	0.43
1:RA:271(B):G:O2'	1:RA:421:U:OP2	2.32	0.43
1:RA:870:A:H5'	12:RQ:6:ARG:O	2.17	0.43
1:RA:1153:C:H2'	1:RA:1154:G:O4'	2.18	0.43
1:RA:2151:G:H2'	1:RA:2152:G:H8	1.82	0.43
1:RA:2779:U:H5'	1:RA:2780:G:OP1	2.18	0.43
6:RG:165:THR:OG1	6:RG:166:ASP:N	2.51	0.43
12:RQ:60:ARG:HE	12:RQ:60:ARG:HB3	1.67	0.43
13:RR:14:SER:OG	13:RR:15:SER:N	2.51	0.43
32:QA:25:C:H2'	32:QA:26:A:C8	2.52	0.43
32:QA:427:U:OP2	32:QA:428:G:O2'	2.31	0.43
32:QA:619:U:N3	35:QD:134:ASP:OD1	2.34	0.43
32:QA:667:G:H4'	46:QO:51:HIS:CE1	2.53	0.43
32:QA:927:G:H1	32:QA:1390:U:H3	1.66	0.43
43:QL:32:PHE:HE1	43:QL:86:ARG:HG3	1.83	0.43
48:QQ:6:LEU:HD22	48:QQ:23:VAL:HG11	2.00	0.43
50:QS:29:ARG:HG2	50:QS:30:LEU:HD23	1.99	0.43
1:YA:545:G:N2	1:YA:548:A:OP2	2.51	0.43
1:YA:550:G:O2'	1:YA:1220:A:N3	2.42	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:1059:G:OP2	1:YA:1060:U:H5''	2.18	0.43
1:YA:2305:A:N6	6:YG:154:GLY:O	2.52	0.43
1:YA:2502:G:H5''	1:YA:2503:A:H5''	2.00	0.43
4:YE:49:LEU:HD12	4:YE:49:LEU:HA	1.79	0.43
4:YE:144:ARG:HB3	4:YE:145:LYS:H	1.47	0.43
6:YG:166:ASP:O	6:YG:170:ARG:N	2.49	0.43
28:Y6:6:ARG:HA	28:Y6:6:ARG:HD2	1.67	0.43
32:XA:337:C:H2'	32:XA:338:A:C8	2.53	0.43
42:XK:66:LEU:O	42:XK:69:ALA:N	2.50	0.43
1:RA:108:U:H2'	1:RA:109:G:C8	2.54	0.43
1:RA:635:C:O2'	1:RA:639:U:OP1	2.34	0.43
1:RA:1528:A:H2'	1:RA:1529:A:C8	2.53	0.43
1:RA:1917:U:H2'	1:RA:1918:A:C8	2.54	0.43
1:RA:2096:U:O4	1:RA:2193:G:O6	2.36	0.43
28:R6:17:LYS:HB3	28:R6:17:LYS:HE3	1.79	0.43
30:R8:29:LYS:HE2	30:R8:44:LYS:HB2	2.00	0.43
51:QT:56:MET:HE1	51:QT:104:LEU:HG	1.99	0.43
1:YA:286:C:H2'	1:YA:287:C:H6	1.83	0.43
1:YA:2814:C:O2'	27:Y5:29:THR:OG1	2.27	0.43
16:YU:92:ARG:CZ	17:YV:11:GLN:H	2.32	0.43
18:YW:110:LYS:HD2	18:YW:110:LYS:HA	1.86	0.43
32:XA:17:U:H2'	32:XA:18:C:H6	1.81	0.43
1:RA:1033:U:OP1	31:R9:9:ARG:NH1	2.41	0.43
1:RA:1073:A:H2'	1:RA:1074:G:C8	2.53	0.43
1:RA:2808:U:O2	1:RA:2808:U:H2'	2.19	0.43
2:RB:44:G:H1'	2:RB:47:C:N4	2.33	0.43
3:RD:66:ASP:OD2	3:RD:103:ARG:NH1	2.52	0.43
10:RO:107:ARG:HG3	10:RO:112:MET:HE1	2.00	0.43
32:QA:636:U:H2'	32:QA:637:G:H8	1.83	0.43
32:QA:883:C:O2'	32:QA:884:U:H5'	2.19	0.43
32:QA:932:C:OP1	38:QG:4:ARG:HD2	2.19	0.43
32:QA:986:A:H2'	32:QA:987:G:H8	1.83	0.43
32:QA:1228:C:OP1	44:QM:108:ARG:NH1	2.45	0.43
37:QF:70:ASP:OD1	37:QF:70:ASP:N	2.49	0.43
1:YA:205:G:O6	23:Y1:39:LYS:NZ	2.34	0.43
2:YB:66:A:O2'	2:YB:67:G:P	2.76	0.43
3:YD:245:PRO:HA	3:YD:246:PRO:HD3	1.80	0.43
6:YG:139:LEU:HD13	6:YG:144:ILE:HG22	2.00	0.43
32:XA:67:C:H2'	32:XA:68:G:C8	2.54	0.43
32:XA:278:G:OP2	48:XQ:92:ARG:NH2	2.44	0.43
32:XA:792:A:H4'	32:XA:793:U:O5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:1077:G:N2	32:XA:1080:A:OP2	2.41	0.43
35:XD:14:ARG:HD2	35:XD:40:PRO:HD2	1.99	0.43
35:XD:33:MET:HE3	35:XD:33:MET:HB3	1.64	0.43
1:RA:236:C:H2'	1:RA:237:C:H6	1.84	0.43
1:RA:512:G:H4'	1:RA:513:A:O5'	2.18	0.43
1:RA:1859:A:N6	1:RA:1883:G:O2'	2.50	0.43
3:RD:245:PRO:HA	3:RD:246:PRO:HD3	1.90	0.43
9:RN:25:ARG:O	9:RN:29:LYS:NZ	2.52	0.43
11:RP:81:GLN:NE2	11:RP:105:LEU:O	2.52	0.43
32:QA:1218:C:H2'	32:QA:1219:U:C6	2.54	0.43
34:QC:6:HIS:HB3	45:QN:49:HIS:ND1	2.33	0.43
38:QG:68:ASN:HD22	38:QG:128:ALA:HA	1.83	0.43
40:QI:75:ASP:OD2	40:QI:78:LYS:NZ	2.46	0.43
1:YA:1859:A:N6	1:YA:1883:G:O2'	2.51	0.43
2:YB:13:A:N1	2:YB:69:G:O2'	2.45	0.43
10:YO:15:GLY:HA2	10:YO:47:ILE:HG22	2.00	0.43
26:Y4:28:LYS:HA	26:Y4:29:PRO:HD3	1.91	0.43
32:XA:165:C:H2'	32:XA:166:G:H8	1.84	0.43
32:XA:735:C:H5'	49:XR:71:LYS:HD3	2.01	0.43
32:XA:1062:U:H2'	32:XA:1063:C:C6	2.54	0.43
35:XD:94:LEU:O	35:XD:98:GLU:N	2.49	0.43
38:XG:29:LYS:HB3	38:XG:105:VAL:HG21	2.00	0.43
1:RA:1636:C:H2'	1:RA:1637:A:C8	2.54	0.43
32:QA:192:U:H2'	32:QA:193:C:C6	2.54	0.43
32:QA:986:A:H2'	32:QA:987:G:C8	2.53	0.43
35:QD:81:GLU:OE2	35:QD:139:ARG:NH1	2.52	0.43
48:QQ:10:VAL:HA	48:QQ:20:THR:O	2.19	0.43
1:YA:2152:G:H2'	1:YA:2153:G:C8	2.54	0.43
1:YA:2478:A:OP1	31:Y9:31:LYS:HD3	2.19	0.43
1:YA:2661:G:O6	7:YH:175:LYS:NZ	2.39	0.43
10:YO:34:THR:OG1	10:YO:35:VAL:N	2.47	0.43
30:Y8:29:LYS:O	30:Y8:31:HIS:N	2.50	0.43
32:XA:545:C:H5'	35:XD:72:GLU:HG3	2.00	0.43
32:XA:1172:C:H2'	32:XA:1173:G:C8	2.54	0.43
32:XA:1304:G:N2	32:XA:1333:A:H62	2.14	0.43
46:XO:76:GLU:OE1	46:XO:79:ARG:NH1	2.52	0.43
47:XP:72:ARG:HA	47:XP:75:ARG:HB3	2.01	0.43
51:XT:100:ILE:HG23	51:XT:102:GLY:H	1.84	0.43
1:RA:184:C:O3'	1:RA:217:G:N2	2.50	0.43
1:RA:1124:C:O2	31:R9:36:GLN:NE2	2.52	0.43
1:RA:1142(A):A:H4'	9:RN:25:ARG:NH2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1183:G:O3'	25:R3:29:ARG:NH1	2.51	0.43
1:RA:2712:U:H2'	1:RA:2714:G:H5''	2.01	0.43
6:RG:119:GLY:O	6:RG:181:ARG:NE	2.49	0.43
7:RH:87:LEU:HB2	7:RH:131:VAL:HG22	2.01	0.43
12:RQ:59:ARG:HA	21:RZ:180:VAL:HG22	2.00	0.43
19:RX:35:THR:OG1	19:RX:36:LYS:N	2.51	0.43
32:QA:280:C:H3'	32:QA:281:G:H5'	1.99	0.43
32:QA:362:G:N2	32:QA:365:U:OP2	2.52	0.43
32:QA:545:C:O2'	32:QA:549:C:OP1	2.36	0.43
32:QA:868:C:H2'	32:QA:869:G:O4'	2.19	0.43
32:QA:1308:U:H3'	44:QM:99:ARG:HH21	1.84	0.43
35:QD:145:GLU:HG3	35:QD:184:LYS:HE3	2.01	0.43
37:QF:99:ALA:HB1	49:QR:23:LYS:HE3	2.00	0.43
43:QL:56:ALA:HB2	43:QL:70:ILE:HD11	2.01	0.43
48:QQ:52:LYS:N	48:QQ:55:ASP:OD2	2.44	0.43
1:YA:251:A:C5	1:YA:252:G:H1'	2.54	0.43
1:YA:691:C:H2'	1:YA:692:C:H6	1.83	0.43
1:YA:2646:C:OP2	1:YA:2732:G:O2'	2.23	0.43
13:YR:18:LEU:HD12	13:YR:18:LEU:HA	1.90	0.43
21:YZ:183:LEU:HD23	21:YZ:183:LEU:HA	1.74	0.43
30:Y8:28:GLY:HA2	30:Y8:44:LYS:HE2	2.01	0.43
32:XA:21:G:H2'	32:XA:22:G:C8	2.54	0.43
32:XA:148:G:H2'	32:XA:149:A:H8	1.83	0.43
32:XA:315:A:H5''	32:XA:317:G:OP2	2.19	0.43
32:XA:677:U:O2	32:XA:777:A:O2'	2.34	0.43
32:XA:1095:U:P	32:XA:1108:G:H1	2.42	0.43
34:XC:191:THR:OG1	34:XC:194:GLY:O	2.30	0.43
40:XI:37:PHE:HB3	40:XI:40:LEU:HD22	2.01	0.43
52:XU:22:ARG:HD2	52:XU:23:PRO:HD2	1.99	0.43
1:RA:2070:G:H2'	1:RA:2071:A:C8	2.53	0.43
1:RA:2635:C:O2'	4:RE:48:GLN:NE2	2.52	0.43
4:RE:8:LYS:NZ	4:RE:188:VAL:O	2.48	0.43
6:RG:55:LYS:HA	6:RG:58:GLN:HG2	2.00	0.43
8:RI:86:THR:O	8:RI:87:LYS:HD3	2.19	0.43
8:RI:86:THR:HA	8:RI:123:LEU:HD11	2.01	0.43
32:QA:992:U:O2'	32:QA:993:G:OP2	2.34	0.43
32:QA:1143:G:H2'	32:QA:1144:G:C8	2.54	0.43
32:QA:1298:C:H4'	32:QA:1299:A:C4	2.53	0.43
32:QA:1320:C:N4	50:QS:36:ARG:O	2.49	0.43
32:QA:1347:G:N7	40:QI:11:LYS:NZ	2.52	0.43
32:QA:1410:G:H2'	32:QA:1411:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:1532:U:H2'	32:QA:1534:A:H2	1.84	0.43
36:QE:78:HIS:HE1	36:QE:80:ILE:HD13	1.84	0.43
43:QL:57:LYS:NZ	43:QL:65:GLU:OE2	2.49	0.43
1:YA:2064:C:H2'	1:YA:2065:C:C6	2.54	0.43
1:YA:2102:U:H2'	1:YA:2103:C:C6	2.54	0.43
1:YA:2392:A:C8	11:YP:61:ARG:HG2	2.54	0.43
1:YA:2625:G:H2'	1:YA:2626:C:O4'	2.18	0.43
1:YA:2870:C:H2'	1:YA:2871:C:O4'	2.19	0.43
14:YS:32:LEU:O	14:YS:62:LYS:NZ	2.42	0.43
14:YS:62:LYS:HA	14:YS:65:VAL:HG22	2.01	0.43
32:XA:377:G:H2'	32:XA:378:G:C8	2.54	0.43
32:XA:427:U:OP1	35:XD:13:ARG:NH2	2.52	0.43
32:XA:501:C:P	43:XL:117:ARG:HH21	2.41	0.43
32:XA:667:G:H4'	46:XO:51:HIS:ND1	2.34	0.43
32:XA:950:U:H2'	32:XA:951:G:C8	2.53	0.43
35:XD:15:GLU:OE2	35:XD:59:ARG:NH1	2.52	0.43
41:XJ:45:ARG:HH21	45:XN:36:PHE:HB2	1.84	0.43
44:XM:15:VAL:HG22	44:XM:45:VAL:HB	2.00	0.43
1:RA:127:A:H5''	1:RA:128:C:C6	2.54	0.42
1:RA:140:A:C8	1:RA:1408:C:O2'	2.72	0.42
1:RA:2562:U:H1'	10:RO:23:ARG:HE	1.83	0.42
12:RQ:34:LEU:HB2	12:RQ:118:LEU:HD22	2.01	0.42
21:RZ:107:THR:HA	21:RZ:108:PRO:HD3	1.78	0.42
32:QA:1077:G:O6	36:QE:47:LYS:NZ	2.52	0.42
32:QA:1254:C:H2'	32:QA:1255:G:C8	2.53	0.42
33:QB:32:ILE:HD12	33:QB:40:HIS:HB3	2.01	0.42
33:QB:130:ARG:HA	33:QB:131:PRO:HD3	1.90	0.42
54:QX:14:A:H2'	54:QX:15:A:C8	2.54	0.42
1:YA:218:A:C2	1:YA:235:U:H4'	2.54	0.42
1:YA:1243:G:O2'	11:YP:7:ARG:NH2	2.49	0.42
1:YA:2123:G:H2'	1:YA:2124:G:H8	1.83	0.42
9:YN:5:VAL:HA	9:YN:6:PRO:HD3	1.84	0.42
29:Y7:13:ALA:HB2	29:Y7:46:VAL:HG21	2.01	0.42
32:XA:109:A:H5'	32:XA:110:C:H5	1.84	0.42
32:XA:686:U:H2'	32:XA:687:A:C8	2.53	0.42
32:XA:978:A:H2	32:XA:1316:G:H21	1.66	0.42
32:XA:1097:C:O2'	32:XA:1169:A:N3	2.40	0.42
32:XA:1119:C:H2'	32:XA:1120:G:H8	1.84	0.42
35:XD:119:GLN:HE21	35:XD:123:HIS:CE1	2.37	0.42
39:XH:10:LEU:HD22	39:XH:83:ILE:HD11	2.01	0.42
1:RA:639:U:H2'	1:RA:640:C:H6	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:1478:G:H1'	1:RA:1557:C:O2'	2.19	0.42
1:RA:1583:A:H5'	1:RA:1586:A:H1'	2.01	0.42
1:RA:1833:U:O2'	1:RA:1969:A:N1	2.44	0.42
1:RA:2306:C:H3'	1:RA:2307:G:H5''	2.01	0.42
6:RG:34:LEU:HD21	6:RG:172:LEU:HD21	2.01	0.42
32:QA:436:C:H2'	32:QA:437:U:C6	2.54	0.42
32:QA:790:A:OP1	53:QV:38:A:O2'	2.22	0.42
32:QA:1128:C:H1'	32:QA:1146:A:H61	1.84	0.42
32:QA:1391:U:H2'	32:QA:1392:G:H8	1.84	0.42
33:QB:115:LEU:HD13	33:QB:145:LEU:HB3	2.00	0.42
38:QG:115:ARG:HB2	38:QG:118:VAL:HG22	2.02	0.42
1:YA:108:U:H2'	1:YA:109:G:H8	1.85	0.42
1:YA:458:G:O2'	1:YA:469:G:O6	2.32	0.42
1:YA:858:U:O2	1:YA:2268:A:H2'	2.20	0.42
1:YA:1061:U:H3'	1:YA:1062:G:C5'	2.48	0.42
1:YA:1671:U:H2'	1:YA:1673:U:OP2	2.18	0.42
2:YB:79:C:H2'	2:YB:80:U:O4'	2.19	0.42
10:YO:19:ILE:HG22	10:YO:43:VAL:HA	2.00	0.42
17:YV:18:LEU:HA	17:YV:18:LEU:HD12	1.85	0.42
24:Y2:25:VAL:HG13	24:Y2:57:ILE:HG23	2.02	0.42
32:XA:405:U:H5''	32:XA:495:A:H2	1.84	0.42
32:XA:501:C:H2'	32:XA:502:G:H8	1.83	0.42
32:XA:1104:G:H4'	33:XB:111:ARG:NH1	2.34	0.42
32:XA:1159:U:O2'	32:XA:1160:G:N7	2.51	0.42
39:XH:121:ASP:OD1	39:XH:121:ASP:N	2.50	0.42
40:XI:27:THR:OG1	40:XI:61:ALA:O	2.29	0.42
49:XR:26:LEU:HD11	49:XR:39:VAL:HG13	2.00	0.42
1:RA:769:G:H4'	1:RA:1379:A:N1	2.34	0.42
1:RA:1353:A:H2'	1:RA:1354:A:C8	2.54	0.42
1:RA:1448:G:H5'	1:RA:1449:A:OP1	2.19	0.42
1:RA:2611:U:C4	27:R5:3:LYS:HG2	2.54	0.42
6:RG:98:ARG:NH1	26:R4:1:MET:SD	2.92	0.42
10:RO:68:GLU:HG3	10:RO:78:ARG:HD3	2.01	0.42
30:R8:54:GLU:O	30:R8:58:ILE:HG12	2.19	0.42
32:QA:808:C:OP1	46:QO:48:LYS:HD3	2.18	0.42
32:QA:939:G:H4'	38:QG:102:ARG:HH21	1.84	0.42
1:YA:639:U:H2'	1:YA:640:C:H6	1.84	0.42
1:YA:1217:C:OP1	16:YU:15:LYS:NZ	2.49	0.42
1:YA:1539:G:H2'	1:YA:1540:G:C8	2.54	0.42
1:YA:1796:U:H2'	1:YA:1797:C:H6	1.84	0.42
8:YI:100:ALA:O	8:YI:104:GLN:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Y8:2:PRO:HB2	30:Y8:3:LYS:H	1.72	0.42
32:XA:243:A:H5''	32:XA:244:U:H3'	2.02	0.42
32:XA:265:G:H2'	32:XA:266:G:H5''	2.01	0.42
1:RA:448:U:C4	1:RA:583:G:H1'	2.55	0.42
1:RA:1296:G:OP1	1:RA:2709:G:O2'	2.23	0.42
1:RA:1464:C:HO2'	1:RA:1528:A:H8	1.66	0.42
1:RA:1782:C:N4	1:RA:2587:A:C2	2.87	0.42
1:RA:2556:C:H2'	1:RA:2557:G:O4'	2.19	0.42
24:R2:38:GLN:HG2	24:R2:44:LEU:HD12	2.01	0.42
30:R8:54:GLU:HG3	30:R8:57:ARG:HH21	1.85	0.42
32:QA:599:C:O2'	39:QH:129:VAL:O	2.23	0.42
32:QA:924:C:O2'	32:QA:1502:A:N6	2.52	0.42
32:QA:1228:C:P	44:QM:108:ARG:HH12	2.42	0.42
32:QA:1513:A:H2'	32:QA:1514:C:C6	2.55	0.42
36:QE:80:ILE:HD12	36:QE:80:ILE:HA	1.91	0.42
37:QF:3:ARG:NH1	37:QF:66:GLU:OE1	2.52	0.42
49:QR:73:ALA:HB3	49:QR:79:LEU:HD22	2.00	0.42
1:YA:1204:A:O2'	1:YA:1205:U:O5'	2.37	0.42
1:YA:1322:A:OP1	18:YW:11:ARG:HG2	2.19	0.42
1:YA:1454:U:O2'	1:YA:1455:G:N7	2.52	0.42
1:YA:1678:G:H8	1:YA:1678:G:O5'	2.02	0.42
1:YA:1882:C:H5'	1:YA:1883:G:OP2	2.19	0.42
3:YD:177:LEU:HD23	3:YD:177:LEU:HA	1.79	0.42
8:YI:76:THR:OG1	8:YI:139:GLN:NE2	2.53	0.42
9:YN:35:ARG:H	9:YN:35:ARG:HG2	1.71	0.42
15:YT:113:LYS:HA	15:YT:113:LYS:HD3	1.82	0.42
21:YZ:77:ASP:OD2	21:YZ:80:ARG:NH1	2.53	0.42
35:XD:114:ARG:HA	35:XD:117:ALA:HB3	2.01	0.42
41:XJ:15:THR:O	41:XJ:19:SER:N	2.40	0.42
43:XL:46:LYS:HG2	43:XL:47:LYS:H	1.85	0.42
1:RA:524:U:H2'	1:RA:525:U:C6	2.54	0.42
1:RA:2130:U:H2'	1:RA:2131:G:C8	2.55	0.42
1:RA:2183:C:H2'	1:RA:2184:G:H8	1.84	0.42
1:RA:2832:U:O2'	1:RA:2833:G:P	2.77	0.42
2:RB:75:G:H4'	21:RZ:36:LYS:HD3	2.01	0.42
3:RD:108:PRO:HG3	3:RD:143:HIS:CE1	2.55	0.42
8:RI:77:LEU:HD21	8:RI:140:LEU:HB2	1.98	0.42
9:RN:39:ARG:HH11	9:RN:48:MET:HE2	1.83	0.42
17:RV:64:HIS:ND1	17:RV:92:THR:HG22	2.34	0.42
25:R3:4:LEU:N	25:R3:37:LEU:O	2.53	0.42
32:QA:7:G:H5'	32:QA:298:A:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:476:G:H2'	32:QA:477:G:H8	1.85	0.42
33:QB:212:GLN:NE2	33:QB:235:SER:HB3	2.34	0.42
43:QL:117:ARG:HB2	43:QL:122:THR:HB	2.01	0.42
46:QO:26:GLU:HG2	46:QO:81:LEU:HD22	2.02	0.42
1:YA:826:U:H2'	1:YA:828:U:O4'	2.19	0.42
7:YH:121:ILE:HD13	7:YH:121:ILE:HA	1.89	0.42
8:YI:54:GLN:O	8:YI:57:ARG:N	2.51	0.42
15:YT:91:ARG:NE	15:YT:124:ASP:OD2	2.48	0.42
32:XA:673:G:H2'	32:XA:674:G:H8	1.84	0.42
32:XA:1409:C:H2'	32:XA:1410:G:C8	2.53	0.42
51:XT:89:ARG:O	51:XT:93:GLU:N	2.53	0.42
1:RA:29:U:H2'	1:RA:30:G:C8	2.53	0.42
1:RA:142:G:H2'	1:RA:143:C:H6	1.85	0.42
1:RA:332:A:O2'	1:RA:334:C:OP2	2.30	0.42
1:RA:336:C:HO2'	20:RY:35:TYR:HH	1.68	0.42
1:RA:1441:G:H2'	1:RA:1442:G:C8	2.54	0.42
1:RA:2130:U:HO2'	1:RA:2133:G:HO2'	1.66	0.42
1:RA:2853:C:H2'	1:RA:2854:G:C8	2.55	0.42
2:RB:66:A:O2'	2:RB:67:G:OP2	2.30	0.42
6:RG:97:ASP:HA	6:RG:100:TRP:HD1	1.85	0.42
8:RI:56:LYS:O	8:RI:60:GLU:N	2.44	0.42
11:RP:100:LEU:HD23	11:RP:105:LEU:HD22	2.01	0.42
13:RR:75:LEU:HA	13:RR:78:LYS:HB3	2.01	0.42
32:QA:452:A:H2'	32:QA:453:A:C8	2.55	0.42
32:QA:452:A:H2'	32:QA:453:A:H8	1.83	0.42
1:YA:30:G:H2'	1:YA:31:C:H6	1.84	0.42
1:YA:1019:U:O2'	1:YA:1021:A:H2	2.02	0.42
7:YH:40:GLU:OE1	7:YH:60:ARG:NH1	2.52	0.42
12:YQ:24:GLY:H	12:YQ:101:ARG:HD2	1.82	0.42
32:XA:376:G:OP2	47:XP:67:THR:HG21	2.20	0.42
32:XA:452:A:H2'	32:XA:453:A:H8	1.85	0.42
32:XA:1270:C:H2'	32:XA:1271:G:H8	1.85	0.42
1:RA:1273:U:O2	1:RA:2002:G:O2'	2.33	0.42
1:RA:1882:C:H5'	1:RA:1883:G:OP2	2.19	0.42
1:RA:2102:U:H2'	1:RA:2103:C:C6	2.54	0.42
1:RA:2151:G:H2'	1:RA:2152:G:C8	2.54	0.42
2:RB:104:A:OP1	21:RZ:72:ARG:NH1	2.52	0.42
32:QA:404:U:H2'	32:QA:405:U:H6	1.84	0.42
32:QA:1121:U:H2'	32:QA:1122:U:C6	2.54	0.42
32:QA:1273:G:H3'	32:QA:1274:G:H8	1.84	0.42
47:QP:8:ARG:HA	47:QP:17:TYR:HD1	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:530:G:C5	1:YA:2022:U:H5''	2.54	0.42
1:YA:2112:G:O6	1:YA:2169:A:N6	2.53	0.42
5:YF:11:VAL:HB	5:YF:18:ARG:HG3	2.01	0.42
32:XA:1145:C:H4'	32:XA:1146:A:H8	1.85	0.42
32:XA:1295:G:O3'	44:XM:14:ARG:NH1	2.53	0.42
32:XA:1296:C:H5'	44:XM:14:ARG:HD2	2.02	0.42
32:XA:1299:A:N7	32:XA:1301:U:H1'	2.35	0.42
46:XO:4:THR:OG1	46:XO:5:LYS:N	2.52	0.42
1:RA:218:A:N1	1:RA:235:U:H4'	2.35	0.42
1:RA:321:G:C4	5:RF:165:ARG:HD3	2.53	0.42
1:RA:2023:G:H4'	1:RA:2617:C:O3'	2.20	0.42
1:RA:2630:G:H2'	1:RA:2631:G:C8	2.54	0.42
6:RG:67:LYS:HE3	6:RG:67:LYS:HB2	1.88	0.42
12:RQ:60:ARG:NH1	21:RZ:177:PRO:HG2	2.31	0.42
32:QA:408:A:OP1	35:QD:113:SER:OG	2.34	0.42
32:QA:737:A:H2'	32:QA:738:C:H6	1.85	0.42
32:QA:881:G:P	43:QL:12:ARG:HH22	2.42	0.42
32:QA:1298:C:H4'	32:QA:1299:A:C8	2.55	0.42
32:QA:1328:C:OP1	52:QU:21:TYR:OH	2.26	0.42
35:QD:102:ASP:OD1	35:QD:102:ASP:N	2.49	0.42
37:QF:5:GLU:HG3	37:QF:93:SER:HB3	2.01	0.42
37:QF:67:MET:HE3	37:QF:67:MET:HB2	1.76	0.42
38:QG:58:PRO:HA	38:QG:61:VAL:HG12	2.01	0.42
44:QM:74:VAL:O	44:QM:78:ILE:HG12	2.19	0.42
53:QV:34:C:H2'	53:QV:35:G:H8	1.85	0.42
1:YA:363(A):A:H2'	1:YA:363(B):G:H8	1.83	0.42
1:YA:535:C:O3'	16:YU:53:ARG:NH1	2.53	0.42
21:YZ:108:PRO:HG3	21:YZ:141:VAL:HG23	2.02	0.42
32:XA:87:A:O2'	32:XA:88:C:O4'	2.32	0.42
32:XA:244:U:H4'	32:XA:245:C:O5'	2.20	0.42
32:XA:271:C:H2'	32:XA:272:C:H6	1.84	0.42
32:XA:575:G:O2'	32:XA:821:G:H5'	2.20	0.42
32:XA:728:A:H2'	32:XA:729:A:C8	2.54	0.42
32:XA:1219:U:H2'	32:XA:1220:G:H8	1.83	0.42
33:XB:25:ASN:HA	33:XB:26:PRO:HD3	1.88	0.42
38:XG:16:LEU:HD12	38:XG:17:VAL:HG23	2.02	0.42
1:RA:36:G:N3	1:RA:450:G:O2'	2.52	0.42
1:RA:670:A:H5''	11:RP:42:SER:O	2.20	0.42
3:RD:37:LEU:HD12	3:RD:37:LEU:HA	1.90	0.42
7:RH:89:ILE:O	7:RH:129:THR:OG1	2.36	0.42
32:QA:976:G:H5''	32:QA:1358:U:O2'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:1325:C:H4'	52:QU:17:THR:HG21	2.01	0.42
38:QG:13:GLN:HA	38:QG:14:PRO:HD3	1.88	0.42
1:YA:484:C:H2'	1:YA:485:C:H6	1.85	0.42
1:YA:635:C:O2'	1:YA:639:U:OP1	2.37	0.42
1:YA:2533:A:H2'	1:YA:2534:A:O4'	2.20	0.42
26:Y4:10:VAL:N	26:Y4:26:SER:O	2.45	0.42
32:XA:377:G:H2'	32:XA:378:G:H8	1.84	0.42
32:XA:1294:G:H2'	32:XA:1295:G:C8	2.53	0.42
34:XC:108:ASN:HD21	34:XC:144:SER:HB2	1.85	0.42
36:XE:94:ALA:HB1	36:XE:98:THR:HG21	2.02	0.42
41:XJ:11:PHE:O	41:XJ:68:HIS:ND1	2.39	0.42
1:RA:608:A:H2'	1:RA:609:A:C8	2.55	0.42
1:RA:997:G:OP1	16:RU:93:LYS:HB2	2.19	0.42
1:RA:1011:G:H4'	16:RU:75:ASN:ND2	2.35	0.42
1:RA:1084:A:H8	1:RA:1085:A:H4'	1.84	0.42
1:RA:1394:U:H4'	1:RA:1603:A:H4'	2.01	0.42
1:RA:1497:U:H5''	1:RA:1498:C:H5	1.85	0.42
1:RA:2103:C:N4	1:RA:2187:G:O6	2.53	0.42
1:RA:2528:U:H2'	1:RA:2530:A:O5'	2.20	0.42
2:RB:3:C:H2'	2:RB:4:C:H6	1.85	0.42
4:RE:2:LYS:HG2	4:RE:200:GLU:HB2	2.01	0.42
12:RQ:85:LYS:HG2	12:RQ:86:GLY:H	1.85	0.42
14:RS:12:PHE:O	14:RS:16:ASN:ND2	2.53	0.42
20:RY:16:ALA:O	20:RY:21:LYS:HE3	2.18	0.42
21:RZ:69:THR:HG22	21:RZ:90:VAL:HG22	2.02	0.42
32:QA:328:C:H4'	32:QA:329:A:H5'	2.02	0.42
32:QA:410:G:H2'	32:QA:429:U:C4	2.55	0.42
32:QA:429:U:C3'	35:QD:22:LYS:NZ	2.80	0.42
32:QA:639:G:H2'	32:QA:640:A:H8	1.85	0.42
32:QA:974:A:P	45:QN:41:ARG:HH12	2.43	0.42
32:QA:1314:C:H2'	32:QA:1315:U:C6	2.55	0.42
32:QA:1423:G:H2'	32:QA:1424:C:C6	2.54	0.42
44:QM:30:ALA:O	44:QM:34:LEU:HG	2.20	0.42
47:QP:26:ARG:HA	47:QP:26:ARG:HD3	1.87	0.42
1:YA:1286:A:H1'	1:YA:1288:U:OP2	2.20	0.42
1:YA:1394:U:O2	19:YX:16:LYS:NZ	2.50	0.42
1:YA:1411:C:H5'	1:YA:1412:A:OP2	2.19	0.42
1:YA:2086:U:H2'	1:YA:2087:G:C8	2.55	0.42
1:YA:2185:C:H2'	1:YA:2186:G:C8	2.55	0.42
1:YA:2389:G:H5''	1:YA:2390:U:O4'	2.19	0.42
1:YA:2853:C:H2'	1:YA:2854:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:36:C:H2'	32:XA:37:U:O4'	2.20	0.42
32:XA:580:U:H3	32:XA:761:G:H1	1.68	0.42
32:XA:715:A:H2'	32:XA:716:A:C8	2.55	0.42
32:XA:1074:G:H1	32:XA:1083:U:H3	1.67	0.42
32:XA:1368:G:H4'	45:XN:61:TRP:HZ2	1.84	0.42
34:XC:190:ARG:HD2	34:XC:190:ARG:HA	1.84	0.42
41:XJ:78:ASN:O	41:XJ:81:THR:OG1	2.24	0.42
1:RA:746:A:O2'	1:RA:2611:U:O2'	2.31	0.41
1:RA:1204:A:O2'	1:RA:1205:U:O5'	2.37	0.41
1:RA:2208:U:O2'	3:RD:151:LYS:HG2	2.19	0.41
1:RA:2495:G:H5''	12:RQ:81:VAL:HG12	2.01	0.41
1:RA:2740:A:H2'	1:RA:2741:A:C8	2.54	0.41
3:RD:133:LEU:HB3	3:RD:173:VAL:HG21	2.02	0.41
6:RG:36:LYS:HG3	6:RG:95:ARG:NH1	2.35	0.41
12:RQ:17:LEU:HD23	12:RQ:39:PRO:HB2	2.02	0.41
18:RW:110:LYS:HA	18:RW:110:LYS:HD3	1.78	0.41
32:QA:801:U:H2'	32:QA:802:A:C8	2.55	0.41
32:QA:857:C:H2'	32:QA:858:G:O4'	2.20	0.41
32:QA:948:C:H2'	32:QA:949:A:H8	1.83	0.41
32:QA:1355:G:H2'	32:QA:1356:G:H8	1.85	0.41
41:QJ:100:THR:O	41:QJ:100:THR:OG1	2.33	0.41
49:QR:53:ARG:NE	49:QR:58:LEU:O	2.48	0.41
1:YA:1149:G:H2'	1:YA:1150:C:C6	2.55	0.41
1:YA:1178:C:H2'	1:YA:1179:C:H6	1.84	0.41
1:YA:2111:C:C2	1:YA:2118:U:H4'	2.55	0.41
1:YA:2140:C:N4	1:YA:2141:G:O6	2.53	0.41
3:YD:60:ARG:NH1	3:YD:86:PRO:O	2.53	0.41
16:YU:17:ILE:HG13	16:YU:32:PHE:HE1	1.85	0.41
16:YU:29:SER:OG	16:YU:30:LYS:NZ	2.52	0.41
23:Y1:82:LEU:HD23	23:Y1:82:LEU:HA	1.93	0.41
24:Y2:57:ILE:HG22	24:Y2:61:LEU:HD12	2.02	0.41
29:Y7:6:GLN:HA	29:Y7:7:PRO:HD3	1.90	0.41
38:XG:63:LYS:HB3	38:XG:63:LYS:HE3	1.89	0.41
48:XQ:89:LEU:O	48:XQ:93:GLN:N	2.52	0.41
1:RA:250:G:H2'	1:RA:251:A:C8	2.55	0.41
1:RA:442:G:H1'	5:RF:48:THR:HG21	2.02	0.41
1:RA:769:G:H5'	1:RA:1379:A:N6	2.35	0.41
1:RA:1695:G:N7	3:RD:14:ARG:NH2	2.67	0.41
1:RA:2197:U:H1'	1:RA:2198:A:C8	2.54	0.41
1:RA:2287:A:N6	1:RA:2344:U:H3	2.18	0.41
1:RA:2315:G:OP1	6:RG:36:LYS:NZ	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:RE:5:LEU:HD11	4:RE:79:ARG:HB2	2.02	0.41
5:RF:182:ASN:OD1	5:RF:182:ASN:N	2.52	0.41
6:RG:102:PHE:HD1	6:RG:103:LEU:HD23	1.85	0.41
8:RI:86:THR:O	8:RI:87:LYS:CD	2.69	0.41
15:RT:9:LEU:O	15:RT:12:SER:OG	2.37	0.41
32:QA:139:G:H2'	32:QA:140:A:H8	1.85	0.41
32:QA:537:G:H5''	43:QL:113:ARG:HH12	1.85	0.41
32:QA:628:G:H2'	32:QA:629:G:C8	2.55	0.41
32:QA:806:C:H2'	32:QA:807:A:C8	2.54	0.41
32:QA:1372:U:OP1	40:QI:72:GLY:N	2.54	0.41
1:YA:307:G:H21	1:YA:330:A:N6	2.17	0.41
1:YA:1796:U:H2'	1:YA:1797:C:C6	2.56	0.41
1:YA:1871:A:H2'	1:YA:1872:A:C8	2.55	0.41
6:YG:59:GLU:OE2	6:YG:153:ARG:NH2	2.38	0.41
30:Y8:29:LYS:H	30:Y8:29:LYS:HG2	1.66	0.41
32:XA:434:U:H2'	32:XA:435:C:H6	1.84	0.41
32:XA:481:G:O2'	32:XA:482:A:O5'	2.37	0.41
32:XA:1288:A:N1	32:XA:1371:G:H1'	2.35	0.41
44:XM:106:ASN:N	44:XM:106:ASN:OD1	2.53	0.41
1:RA:1608:A:H1'	1:RA:1610:A:OP2	2.20	0.41
1:RA:2537:U:H2'	1:RA:2538:C:C6	2.54	0.41
1:RA:2636:U:H5'	4:RE:80:GLU:HB2	2.02	0.41
1:RA:2832:U:HO2'	1:RA:2833:G:P	2.42	0.41
4:RE:97:LYS:HB2	4:RE:97:LYS:HE3	1.83	0.41
6:RG:135:LEU:HD23	6:RG:155:MET:HG2	2.02	0.41
12:RQ:41:TRP:HB3	12:RQ:94:VAL:HG21	2.03	0.41
12:RQ:58:PHE:HD2	12:RQ:61:GLY:HA3	1.83	0.41
20:RY:65:ALA:HA	20:RY:66:PRO:HD3	1.95	0.41
24:R2:38:GLN:HB3	24:R2:45:SER:HB2	2.01	0.41
32:QA:41:G:H2'	32:QA:42:G:C8	2.54	0.41
32:QA:110:C:H2'	32:QA:111:G:O4'	2.20	0.41
32:QA:224:C:H2'	32:QA:225:C:C6	2.55	0.41
32:QA:466:C:H4'	32:QA:467:G:OP2	2.20	0.41
32:QA:1043:C:H2'	32:QA:1044:A:C8	2.55	0.41
32:QA:1308:U:H2'	32:QA:1309:G:C8	2.55	0.41
40:QI:93:ARG:HB2	40:QI:97:LYS:HE2	2.03	0.41
1:YA:37:C:H4'	1:YA:451:C:OP1	2.21	0.41
1:YA:1021:A:H2'	1:YA:1023:U:H5'	2.02	0.41
1:YA:1657:C:H2'	1:YA:1658:C:C6	2.56	0.41
1:YA:2487:G:H2'	1:YA:2488:A:C8	2.55	0.41
8:YI:74:ASN:OD1	8:YI:74:ASN:N	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:XA:861:G:HO2'	32:XA:874:G:HO2'	1.64	0.41
32:XA:1222:G:H5''	50:XS:78:ARG:HD2	2.02	0.41
32:XA:1532:U:H1'	32:XA:1533:C:H5	1.86	0.41
38:XG:103:TRP:HA	38:XG:106:GLN:HB2	2.02	0.41
43:XL:77:LEU:HD23	43:XL:77:LEU:HA	1.83	0.41
51:XT:68:LYS:O	51:XT:73:HIS:NE2	2.54	0.41
1:RA:29:U:H2'	1:RA:30:G:H8	1.85	0.41
1:RA:242:G:O2'	1:RA:254:G:O6	2.33	0.41
1:RA:863:A:H2'	1:RA:864:G:C8	2.55	0.41
1:RA:1064:C:H3'	1:RA:1065:U:H5'	2.02	0.41
1:RA:2305:A:H5''	6:RG:134:GLY:HA3	2.02	0.41
1:RA:2820:A:C5	13:RR:4:LEU:HD11	2.56	0.41
2:RB:15:A:H5'	2:RB:16:G:H8	1.85	0.41
14:RS:101:LEU:O	14:RS:105:ALA:N	2.53	0.41
25:R3:8:LEU:HD21	25:R3:23:LEU:HD21	2.02	0.41
32:QA:708:C:H2'	32:QA:709:G:H8	1.85	0.41
32:QA:753:A:H4'	32:QA:754:C:O5'	2.20	0.41
32:QA:1446:A:HO2'	32:QA:1447:G:P	2.43	0.41
33:QB:7:VAL:HB	33:QB:217:ARG:HD2	2.03	0.41
33:QB:82:ARG:HB2	33:QB:94:ASN:HD21	1.86	0.41
35:QD:9:CYS:SG	35:QD:32:ALA:CB	3.08	0.41
1:YA:184:C:H2'	1:YA:185:U:H6	1.84	0.41
1:YA:314:A:N6	1:YA:315:G:O6	2.52	0.41
1:YA:1225:C:O2'	17:YV:85:LYS:HA	2.20	0.41
1:YA:2105:C:H2'	1:YA:2106:G:C8	2.55	0.41
1:YA:2543:G:H2'	1:YA:2544:G:C8	2.56	0.41
8:YI:78:THR:HG22	8:YI:141:LYS:HB3	2.02	0.41
32:XA:164:U:H2'	32:XA:165:C:H6	1.85	0.41
32:XA:397:A:H5'	32:XA:398:C:OP1	2.20	0.41
32:XA:452:A:H2'	32:XA:453:A:C8	2.56	0.41
32:XA:1299:A:C8	32:XA:1301:U:H1'	2.55	0.41
32:XA:1326:C:H5''	52:XU:12:LYS:HZ3	1.85	0.41
32:XA:1346:A:O3'	32:XA:1347:G:H4'	2.20	0.41
33:XB:115:LEU:HA	33:XB:118:LEU:HB2	2.01	0.41
45:XN:26:ARG:HD3	45:XN:43:CYS:SG	2.61	0.41
1:RA:969:U:H2'	1:RA:970:C:C6	2.55	0.41
1:RA:1756:G:H4'	1:RA:1758:G:O4'	2.20	0.41
1:RA:2136:C:H2'	1:RA:2137:C:H6	1.85	0.41
5:RF:186:ILE:HD12	5:RF:192:LEU:HD11	2.02	0.41
9:RN:112:LEU:HD12	9:RN:112:LEU:HA	1.85	0.41
23:R1:65:SER:OG	23:R1:66:HIS:ND1	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:323:U:H5'	51:QT:23:ARG:HB3	2.03	0.41
32:QA:563:A:H2'	32:QA:567:G:C8	2.55	0.41
32:QA:963:G:H21	41:QJ:55:LYS:HG2	1.85	0.41
32:QA:1133:G:H2'	32:QA:1134:G:C8	2.55	0.41
34:QC:57:ILE:HA	34:QC:65:ALA:O	2.20	0.41
34:QC:72:LYS:HD2	34:QC:72:LYS:HA	1.86	0.41
36:QE:92:LYS:HB3	36:QE:119:LEU:HB2	2.03	0.41
41:QJ:61:GLU:OE2	45:QN:45:ARG:NE	2.53	0.41
42:QK:51:LYS:HE2	42:QK:51:LYS:HB2	1.82	0.41
1:YA:36:G:N3	1:YA:450:G:O2'	2.52	0.41
1:YA:579:G:H2'	1:YA:580:C:H6	1.84	0.41
1:YA:807:U:OP2	11:YP:41:ARG:NH1	2.54	0.41
1:YA:867:C:N3	1:YA:912:C:O2'	2.36	0.41
1:YA:1018:C:O3'	1:YA:1120:G:N2	2.53	0.41
1:YA:1657:C:H2'	1:YA:1658:C:H6	1.86	0.41
1:YA:1923:U:H2'	1:YA:1924:C:C6	2.55	0.41
1:YA:2137:C:H2'	1:YA:2138:C:C6	2.55	0.41
3:YD:5:LYS:HE3	3:YD:5:LYS:HB3	1.80	0.41
10:YO:73:ASP:OD1	10:YO:73:ASP:N	2.41	0.41
32:XA:227:G:N2	47:XP:62:VAL:O	2.52	0.41
32:XA:356:A:O2'	32:XA:367:U:O2'	2.30	0.41
32:XA:627:G:H2'	32:XA:628:G:C8	2.55	0.41
35:XD:101:LEU:HB2	35:XD:138:TYR:HB3	2.03	0.41
1:RA:78:A:H2'	1:RA:79:G:C8	2.54	0.41
1:RA:125:G:OP1	29:R7:14:LYS:NZ	2.54	0.41
1:RA:302:C:P	20:RY:73:ARG:HH12	2.44	0.41
1:RA:919:G:N2	1:RA:2269:A:OP2	2.53	0.41
1:RA:960:A:H61	12:RQ:82:ARG:HH12	1.67	0.41
1:RA:1005:C:H2'	1:RA:1006:C:C6	2.55	0.41
1:RA:1063:G:OP1	1:RA:1065:U:O2'	2.39	0.41
1:RA:1536:A:H5''	1:RA:1537:C:C6	2.56	0.41
1:RA:1541:U:H2'	1:RA:1542:G:C8	2.56	0.41
12:RQ:18:LYS:HE2	12:RQ:18:LYS:HB3	1.78	0.41
32:QA:35:G:N3	43:QL:118:SER:OG	2.49	0.41
32:QA:1130:A:N6	32:QA:1131:G:O6	2.53	0.41
34:QC:95:THR:HG22	34:QC:97:LYS:H	1.84	0.41
1:YA:2314:C:H2'	1:YA:2315:G:H8	1.86	0.41
1:YA:2611:U:H3'	1:YA:2611:U:OP2	2.20	0.41
1:YA:2626:C:H2'	1:YA:2627:G:C8	2.56	0.41
1:YA:2712:U:OP1	1:YA:2714:G:H4'	2.21	0.41
21:YZ:19:ARG:NH1	21:YZ:84:GLU:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Y1:86:SER:OG	23:Y1:89:GLU:OE2	2.31	0.41
32:XA:148:G:H2'	32:XA:149:A:C8	2.55	0.41
32:XA:477:G:H2'	32:XA:478:A:C8	2.56	0.41
32:XA:678:U:H2'	32:XA:679:C:C6	2.56	0.41
32:XA:868:C:H2'	32:XA:869:G:O4'	2.21	0.41
32:XA:1531:A:H5'	32:XA:1532:U:OP1	2.20	0.41
35:XD:129:ASN:OD1	35:XD:145:GLU:N	2.53	0.41
38:XG:93:PRO:HA	38:XG:96:GLN:HB3	2.02	0.41
1:RA:372:G:O2'	1:RA:373:U:O5'	2.36	0.41
1:RA:625:G:P	30:R8:64:TYR:HB3	2.59	0.41
1:RA:2326:C:O3'	21:RZ:201:LYS:NZ	2.54	0.41
6:RG:101:ILE:HD12	6:RG:101:ILE:HA	1.96	0.41
32:QA:977:A:N6	32:QA:1224:G:OP1	2.53	0.41
33:QB:223:ILE:HD12	33:QB:230:VAL:HG23	2.02	0.41
33:QB:233:SER:O	33:QB:233:SER:OG	2.29	0.41
36:QE:71:LEU:HD23	36:QE:71:LEU:HA	1.88	0.41
43:QL:51:ALA:HB3	43:QL:53:ARG:HE	1.86	0.41
44:QM:81:LEU:HD13	44:QM:88:ARG:HB3	2.03	0.41
1:YA:27:G:N2	1:YA:512:G:O2'	2.54	0.41
1:YA:83:G:H1	1:YA:102:G:HO2'	1.64	0.41
1:YA:141:A:H5''	1:YA:141(A):C:OP2	2.20	0.41
1:YA:581:C:H2'	1:YA:582:G:C8	2.56	0.41
1:YA:932:G:H4'	1:YA:933:A:O5'	2.21	0.41
1:YA:2781:A:H5''	1:YA:2782:G:H5'	2.02	0.41
14:YS:5:THR:OG1	14:YS:8:GLU:OE2	2.36	0.41
14:YS:15:ARG:NE	14:YS:88:ASP:OD2	2.53	0.41
23:Y1:50:ARG:HG2	23:Y1:59:THR:HG22	2.03	0.41
32:XA:80:G:H22	32:XA:89:U:H3	1.68	0.41
32:XA:324:G:OP1	51:XT:70:SER:HB2	2.20	0.41
32:XA:378:G:N1	32:XA:386:C:N3	2.69	0.41
32:XA:1043:C:H2'	32:XA:1044:A:C8	2.56	0.41
32:XA:1491:G:H5'	43:XL:47:LYS:HE2	2.01	0.41
36:XE:69:VAL:HG21	36:XE:113:ALA:HB1	2.03	0.41
50:XS:7:LYS:HB3	50:XS:7:LYS:HE3	1.77	0.41
51:XT:57:ARG:O	51:XT:61:SER:OG	2.35	0.41
1:RA:29:U:H5''	16:RU:7:GLY:HA2	2.03	0.41
1:RA:673:C:H5''	5:RF:81:PRO:HD2	2.03	0.41
1:RA:1657:C:H2'	1:RA:1658:C:H6	1.85	0.41
1:RA:2574:G:N2	4:RE:142:GLY:O	2.37	0.41
1:RA:2685:G:P	15:RT:51:ARG:HH22	2.44	0.41
12:RQ:21:THR:HB	12:RQ:22:LYS:H	1.70	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:RQ:24:GLY:H	12:RQ:101:ARG:HD2	1.86	0.41
27:R5:56:LYS:NZ	27:R5:59:GLU:OE2	2.44	0.41
32:QA:1238:A:H62	32:QA:1301:U:H3	1.69	0.41
44:QM:19:LEU:HD12	44:QM:22:ILE:HD13	2.02	0.41
1:YA:307:G:H21	1:YA:330:A:H62	1.67	0.41
1:YA:805:G:N2	1:YA:829:A:OP1	2.52	0.41
1:YA:1186:G:H2'	1:YA:1187:G:O4'	2.21	0.41
1:YA:2183:C:H2'	1:YA:2184:G:C8	2.56	0.41
1:YA:2845:G:OP1	15:YT:54:ARG:HB3	2.19	0.41
2:YB:48:A:P	14:YS:30:ARG:HH12	2.44	0.41
5:YF:9:ILE:O	5:YF:20:LEU:N	2.51	0.41
5:YF:192:LEU:HD21	5:YF:194:MET:HE3	2.01	0.41
8:YI:83:ALA:HB1	8:YI:123:LEU:HD11	2.03	0.41
32:XA:8:A:N6	35:XD:205:GLU:O	2.53	0.41
32:XA:19:C:H2'	32:XA:20:U:C6	2.56	0.41
32:XA:407:G:H2'	32:XA:408:A:H8	1.84	0.41
32:XA:464:G:C6	32:XA:466:C:H5'	2.56	0.41
32:XA:636:U:H5'	48:XQ:2:PRO:HG3	2.02	0.41
32:XA:707:C:H2'	32:XA:708:C:H6	1.84	0.41
42:XK:31:THR:HA	42:XK:42:TRP:HA	2.03	0.41
44:XM:16:ASP:OD1	44:XM:16:ASP:N	2.53	0.41
46:XO:36:ILE:O	46:XO:40:SER:N	2.42	0.41
51:XT:10:LEU:HD23	51:XT:12:ALA:H	1.85	0.41
51:XT:50:GLU:HG2	51:XT:99:LEU:HD12	2.02	0.41
1:RA:237:C:O2	1:RA:609:A:O2'	2.37	0.41
1:RA:239:U:O2'	1:RA:622:G:O2'	2.37	0.41
1:RA:241:A:OP1	1:RA:243:U:H1'	2.21	0.41
1:RA:451:C:H41	1:RA:454:A:H5'	1.86	0.41
1:RA:923:C:H2'	1:RA:924:C:C6	2.56	0.41
1:RA:1181:C:H2'	1:RA:1182:A:C8	2.56	0.41
1:RA:1300:U:H4'	1:RA:1301:A:H5''	2.01	0.41
1:RA:2053:G:OP1	4:RE:144:ARG:HG2	2.21	0.41
1:RA:2389:G:H5''	1:RA:2390:U:O4'	2.21	0.41
1:RA:2687:U:H2'	1:RA:2688:U:O4'	2.21	0.41
1:RA:2699:C:H2'	1:RA:2700:C:O4'	2.21	0.41
1:RA:2820:A:OP1	13:RR:2:ARG:NH2	2.54	0.41
6:RG:59:GLU:OE2	6:RG:153:ARG:NH1	2.53	0.41
7:RH:102:ALA:HA	7:RH:117:PRO:HD3	2.01	0.41
21:RZ:53:ILE:HG22	21:RZ:71:VAL:HG13	2.02	0.41
32:QA:25:C:H2'	32:QA:26:A:H8	1.86	0.41
32:QA:153:C:N3	32:QA:169:C:N4	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:865:A:N3	32:QA:918:A:O2'	2.50	0.41
32:QA:1071:C:H2'	32:QA:1072:G:C8	2.54	0.41
32:QA:1277:C:O2'	32:QA:1279:A:H8	2.04	0.41
32:QA:1411:C:H2'	32:QA:1412:C:C6	2.56	0.41
35:QD:20:TYR:HE2	37:XF:15:ASP:HB2	1.85	0.41
37:QF:3:ARG:HA	37:QF:65:VAL:O	2.20	0.41
39:QH:73:ASP:OD2	39:QH:75:ARG:NH1	2.54	0.41
1:YA:776:G:N7	1:YA:793:A:O2'	2.53	0.41
1:YA:2544:G:H1'	1:YA:2646:C:H4'	2.03	0.41
1:YA:2698:U:H2'	1:YA:2699:C:C6	2.55	0.41
1:YA:2699:C:H2'	1:YA:2700:C:O4'	2.21	0.41
2:YB:13:A:O2'	2:YB:15:A:O5'	2.39	0.41
4:YE:51:PHE:CD2	4:YE:52:LEU:HG	2.56	0.41
6:YG:114:ILE:HG13	6:YG:115:ARG:H	1.85	0.41
8:YI:88:ILE:HG12	8:YI:122:GLU:H	1.86	0.41
9:YN:128:HIS:O	9:YN:131:GLN:NE2	2.53	0.41
11:YP:71:VAL:HG22	11:YP:72:PRO:HA	2.01	0.41
32:XA:243:A:H4'	32:XA:244:U:H3'	2.03	0.41
32:XA:272:C:H2'	32:XA:273:A:C8	2.52	0.41
32:XA:279:A:OP1	32:XA:280:C:O2'	2.24	0.41
32:XA:406:G:H5''	35:XD:5:ILE:HG12	2.02	0.41
32:XA:1446:A:HO2'	32:XA:1447:G:P	2.44	0.41
32:XA:1510:U:H2'	32:XA:1511:G:C8	2.56	0.41
35:XD:71:SER:O	35:XD:75:PHE:N	2.50	0.41
40:XI:21:PRO:HA	40:XI:59:PHE:HD1	1.86	0.41
41:XJ:69:ASN:HD22	41:XJ:69:ASN:HA	1.68	0.41
43:XL:53:ARG:HH12	43:XL:92:ASP:HB2	1.86	0.41
43:XL:77:LEU:HD21	43:XL:107:ALA:HB2	2.03	0.41
44:XM:87:TYR:OH	44:XM:91:ARG:NH2	2.48	0.41
51:XT:89:ARG:HH21	51:XT:104:LEU:HD21	1.85	0.41
1:RA:177:G:H3'	1:RA:178:G:H8	1.86	0.41
1:RA:2731:G:OP1	4:RE:169:ASN:ND2	2.45	0.41
1:RA:2803:C:H2'	1:RA:2804:C:C6	2.56	0.41
32:QA:358:U:H2'	32:QA:359:U:H6	1.86	0.41
32:QA:384:G:H2'	32:QA:385:C:C6	2.56	0.41
32:QA:709:G:H2'	32:QA:710:G:H8	1.86	0.41
32:QA:1326:C:OP2	52:QU:6:ARG:NH1	2.54	0.41
34:QC:189:ALA:HB3	34:QC:196:LEU:HB2	2.03	0.41
35:QD:20:TYR:CE2	37:XF:15:ASP:CA	3.04	0.41
1:YA:1062:G:N2	1:YA:1077:A:N1	2.69	0.41
1:YA:1639:U:C2'	1:YA:1640:C:H5''	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:YA:2867:G:O2'	1:YA:2868:A:P	2.79	0.41
32:XA:842:C:H5'	32:XA:843:U:OP1	2.21	0.41
32:XA:1367:C:OP1	40:XI:115:GLY:N	2.40	0.41
32:XA:1511:G:H2'	32:XA:1512:U:O4'	2.20	0.41
33:XB:216:SER:OG	33:XB:217:ARG:N	2.54	0.41
1:RA:582:G:OP1	16:RU:14:HIS:ND1	2.49	0.40
1:RA:764:A:H5''	3:RD:210:GLY:CA	2.51	0.40
1:RA:1188:U:H5'	17:RV:79:VAL:HG13	2.02	0.40
1:RA:1224:G:N2	1:RA:1227:A:OP2	2.52	0.40
1:RA:1638:C:H2'	1:RA:1639:U:O4'	2.21	0.40
1:RA:1786:A:H2'	1:RA:1786:A:N3	2.35	0.40
3:RD:177:LEU:HA	3:RD:177:LEU:HD23	1.83	0.40
9:RN:1:MET:HE1	16:RU:95:LEU:HD21	2.03	0.40
9:RN:48:MET:HE2	9:RN:48:MET:HB2	1.94	0.40
14:RS:27:SER:HA	14:RS:88:ASP:HB3	2.02	0.40
32:QA:57:G:H2'	32:QA:58:C:C6	2.56	0.40
32:QA:636:U:H2'	32:QA:637:G:C8	2.55	0.40
32:QA:1154:G:H2'	32:QA:1155:G:H8	1.86	0.40
32:QA:1220:G:H1'	50:QS:52:TYR:HD2	1.86	0.40
32:QA:1342:C:H2'	32:QA:1343:G:H8	1.87	0.40
36:QE:127:ASN:HA	36:QE:128:PRO:HD3	1.93	0.40
1:YA:924:C:H2'	1:YA:925:C:H6	1.86	0.40
1:YA:1348:G:H2'	1:YA:1349:A:H5''	2.03	0.40
1:YA:1818:U:H2'	3:YD:157:ARG:HB2	2.02	0.40
1:YA:2287:A:O2'	1:YA:2288:A:O5'	2.38	0.40
4:YE:36:ARG:HH12	4:YE:86:PRO:HD2	1.86	0.40
6:YG:99:MET:HE3	6:YG:99:MET:HB2	1.87	0.40
8:YI:130:TYR:HB3	8:YI:136:VAL:HG22	2.03	0.40
11:YP:33:ARG:HD3	11:YP:40:SER:HA	2.03	0.40
32:XA:538:G:H2'	32:XA:539:A:C8	2.56	0.40
32:XA:781:A:H4'	32:XA:1522:U:O2'	2.20	0.40
32:XA:939:G:H4'	38:XG:102:ARG:NH2	2.36	0.40
32:XA:998:G:H2'	32:XA:998(A):C:C6	2.57	0.40
32:XA:1191:A:OP1	34:XC:3:ASN:HB3	2.21	0.40
32:XA:1348:U:N3	32:XA:1374:A:H2	2.20	0.40
1:RA:58:G:O2'	1:RA:73:A:N1	2.49	0.40
1:RA:1266:G:O5'	18:RW:15:ARG:NH2	2.54	0.40
1:RA:1542:G:H5''	1:RA:1543:A:OP2	2.21	0.40
1:RA:1593:G:H2'	1:RA:1594:G:H8	1.85	0.40
3:RD:95:LEU:HD11	3:RD:105:ILE:HG12	2.04	0.40
4:RE:52:LEU:HD23	4:RE:52:LEU:HA	1.92	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:RO:70:LYS:HE3	10:RO:70:LYS:HB3	1.76	0.40
12:RQ:42:ILE:HD12	12:RQ:97:VAL:HG21	2.04	0.40
17:RV:97:LYS:HD3	17:RV:97:LYS:HA	1.81	0.40
32:QA:553:A:H2'	32:QA:554:C:C6	2.56	0.40
32:QA:616:G:OP1	35:QD:141:ARG:NH1	2.54	0.40
32:QA:1217:C:H2'	32:QA:1218:C:H6	1.86	0.40
47:QP:14:ASN:OD1	47:QP:16:HIS:NE2	2.55	0.40
1:YA:129:C:OP1	1:YA:1599:C:O2'	2.39	0.40
1:YA:184:C:H2'	1:YA:185:U:C6	2.56	0.40
1:YA:221:A:H4'	1:YA:222:A:O5'	2.20	0.40
1:YA:270(U):C:H2'	1:YA:270(V):G:H8	1.86	0.40
1:YA:1429:G:H2'	1:YA:1430:C:H6	1.85	0.40
1:YA:2832:U:O2'	1:YA:2833:G:P	2.79	0.40
6:YG:11:TYR:HA	6:YG:15:VAL:HB	2.03	0.40
6:YG:102:PHE:HE1	6:YG:141:PHE:HE2	1.69	0.40
25:Y3:8:LEU:HD21	25:Y3:23:LEU:HD21	2.04	0.40
28:Y6:35:GLU:OE2	28:Y6:50:ARG:NH2	2.55	0.40
32:XA:407:G:H2'	32:XA:408:A:C8	2.55	0.40
32:XA:743:U:H2'	32:XA:744:C:C6	2.56	0.40
36:XE:145:LYS:HA	36:XE:148:VAL:HG22	2.03	0.40
38:XG:36:LYS:O	38:XG:40:ALA:N	2.44	0.40
38:XG:94:ARG:O	38:XG:98:SER:OG	2.31	0.40
46:XO:85:LEU:HD23	46:XO:85:LEU:HA	1.89	0.40
48:XQ:45:HIS:NE2	48:XQ:47:PRO:HG3	2.37	0.40
51:XT:61:SER:O	51:XT:65:LYS:HG3	2.22	0.40
1:RA:297:C:H2'	1:RA:298:G:O4'	2.22	0.40
1:RA:411:G:OP2	1:RA:2406:U:O2'	2.33	0.40
1:RA:587:C:O2'	11:RP:19:VAL:HG22	2.21	0.40
1:RA:1252:G:N2	16:RU:37:GLU:OE2	2.39	0.40
1:RA:2334:G:O6	22:R0:74:ARG:NH2	2.51	0.40
1:RA:2361:A:O5'	30:R8:27:THR:OG1	2.39	0.40
1:RA:2760:C:H2'	1:RA:2761:G:H5''	2.03	0.40
1:RA:2847:U:O2	1:RA:2847:U:H2'	2.22	0.40
13:RR:67:LEU:HD13	13:RR:76:VAL:HG21	2.03	0.40
19:RX:8:ILE:HD11	19:RX:42:ALA:HB1	2.03	0.40
32:QA:128:G:O2'	48:QQ:3:LYS:NZ	2.54	0.40
32:QA:288:A:H2'	32:QA:289:G:H4'	2.02	0.40
32:QA:384:G:H2'	32:QA:385:C:H6	1.86	0.40
32:QA:478:A:H2'	32:QA:479:C:H6	1.86	0.40
32:QA:940:C:H2'	32:QA:941:G:H8	1.86	0.40
32:QA:1305:G:O2'	32:QA:1306:A:O4'	2.40	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:QA:1505:G:H2'	54:QX:16:C:OP2	2.21	0.40
43:QL:24:VAL:HG13	43:QL:98:TYR:HE1	1.86	0.40
44:QM:91:ARG:HH21	44:QM:97:PRO:HD2	1.85	0.40
47:QP:1:MET:HG3	47:QP:65:GLN:HB2	2.03	0.40
51:QT:85:MET:HE2	51:QT:85:MET:HB3	1.90	0.40
1:YA:676:A:H2	1:YA:802:A:H61	1.68	0.40
1:YA:724:U:H2'	1:YA:725:G:O4'	2.22	0.40
5:YF:51:THR:HG23	5:YF:92:PRO:HD2	2.04	0.40
12:YQ:64:ILE:HG13	21:YZ:178:GLU:HG3	2.01	0.40
25:Y3:12:PRO:HB2	25:Y3:20:LYS:HG2	2.04	0.40
31:Y9:1:MET:HE2	31:Y9:1:MET:HB2	1.91	0.40
32:XA:151:A:H62	32:XA:170:U:H3	1.68	0.40
32:XA:976:G:P	45:XN:32:SER:H	2.44	0.40
32:XA:1133:G:H2'	32:XA:1134:G:C8	2.56	0.40
32:XA:1134:G:H2'	32:XA:1135:U:O4'	2.20	0.40
32:XA:1532:U:H1'	32:XA:1533:C:C5	2.56	0.40
33:XB:223:ILE:HA	33:XB:226:ARG:HB2	2.03	0.40
49:XR:86:VAL:HG12	49:XR:87:ARG:HG2	2.04	0.40
1:RA:345:A:H5''	1:RA:346:A:OP1	2.22	0.40
1:RA:690:G:H2'	1:RA:691:C:C6	2.56	0.40
1:RA:893:C:H2'	1:RA:894:C:H6	1.87	0.40
1:RA:2798:C:H2'	1:RA:2799:A:N7	2.37	0.40
4:RE:11:MET:HE2	4:RE:11:MET:HB3	1.93	0.40
4:RE:14:ILE:HG13	4:RE:21:VAL:HG13	2.03	0.40
6:RG:173:LEU:O	6:RG:177:GLY:N	2.53	0.40
15:RT:110:ILE:HD13	15:RT:110:ILE:HG21	1.92	0.40
21:RZ:4:ARG:HA	21:RZ:59:LEU:H	1.86	0.40
32:QA:323:U:H2'	32:QA:324:G:O4'	2.21	0.40
38:QG:60:LYS:HA	38:QG:63:LYS:HG2	2.04	0.40
41:QJ:12:ASP:HB3	41:QJ:15:THR:HG22	2.02	0.40
43:QL:93:LEU:HA	43:QL:94:PRO:HD3	1.94	0.40
45:QN:2:ALA:HB1	45:QN:6:LEU:HD21	2.04	0.40
47:QP:1:MET:SD	47:QP:1:MET:N	2.83	0.40
1:YA:180:G:N2	1:YA:215:G:O6	2.53	0.40
1:YA:581:C:OP1	16:YU:31:SER:OG	2.35	0.40
1:YA:1657:C:H4'	4:YE:133:LYS:HB3	2.04	0.40
1:YA:2438:U:O2'	1:YA:2440:C:OP1	2.36	0.40
1:YA:2712:U:O2'	1:YA:2712(A):A:C8	2.64	0.40
1:YA:2788:C:P	4:YE:61:ARG:HH21	2.45	0.40
4:YE:181:LEU:HD21	15:YT:6:LEU:HG	2.04	0.40
5:YF:78:ILE:H	5:YF:78:ILE:HG13	1.71	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:YH:3:ARG:HD3	7:YH:6:ARG:HG2	2.02	0.40
15:YT:16:ARG:NH1	15:YT:18:ASP:OD2	2.54	0.40
19:YX:31:HIS:HA	19:YX:32:PRO:HD3	1.93	0.40
25:Y3:30:ARG:HH21	25:Y3:33:GLN:NE2	2.20	0.40
32:XA:337:C:H2'	32:XA:338:A:H8	1.86	0.40
32:XA:489:C:H2'	32:XA:490:G:H8	1.86	0.40
32:XA:950:U:H2'	32:XA:951:G:H8	1.84	0.40
32:XA:1220:G:H2'	32:XA:1221:G:H8	1.86	0.40
32:XA:1222:G:H5''	50:XS:78:ARG:HH11	1.87	0.40
33:XB:217:ARG:HA	33:XB:220:ASP:HB2	2.02	0.40
47:XP:8:ARG:HA	47:XP:17:TYR:HD1	1.86	0.40
50:XS:10:PHE:HE2	50:XS:16:LEU:HD13	1.86	0.40
1:RA:172:C:H2'	1:RA:173:G:C8	2.56	0.40
1:RA:307:G:H21	1:RA:330:A:H62	1.70	0.40
1:RA:530:G:C5	1:RA:2022:U:H5''	2.57	0.40
1:RA:1368:G:OP1	29:R7:28:ARG:NH2	2.55	0.40
1:RA:1796:U:H2'	1:RA:1797:C:H6	1.87	0.40
1:RA:2059:A:H5'	1:RA:2060:A:OP2	2.21	0.40
1:RA:2712:U:H1'	1:RA:2712(A):A:C8	2.57	0.40
1:RA:2836:U:H2'	1:RA:2837:G:C8	2.57	0.40
4:RE:2:LYS:HD3	4:RE:95:ILE:HB	2.03	0.40
5:RF:154:VAL:HG22	5:RF:191:ARG:HB3	2.03	0.40
7:RH:87:LEU:HD22	7:RH:162:ILE:HG22	2.04	0.40
8:RI:72:LEU:HD13	8:RI:107:VAL:HG11	2.03	0.40
11:RP:121:LYS:HB3	11:RP:123:LEU:HD22	2.03	0.40
21:RZ:54:HIS:ND1	21:RZ:101:PRO:HG3	2.37	0.40
32:QA:510:A:N3	32:QA:543:C:H1'	2.36	0.40
32:QA:707:C:H1'	42:QK:39:PRO:HG3	2.03	0.40
32:QA:1007:C:H2'	32:QA:1008:C:C6	2.57	0.40
32:QA:1293:G:H2'	32:QA:1294:G:H8	1.85	0.40
32:QA:1524:C:H2'	32:QA:1525:G:C8	2.56	0.40
33:QB:189:ASP:OD1	33:QB:189:ASP:N	2.54	0.40
37:QF:82:ARG:HB2	37:QF:85:VAL:HG23	2.04	0.40
52:QU:6:ARG:HH21	52:QU:15:ARG:HE	1.69	0.40
1:YA:1113:U:H2'	1:YA:1114:G:H8	1.86	0.40
1:YA:1590:U:H2'	1:YA:1591:G:H8	1.86	0.40
1:YA:2484:G:O2'	12:YQ:124:LYS:O	2.33	0.40
1:YA:2632:A:O2'	1:YA:2811:G:O2'	2.31	0.40
11:YP:46:LYS:HA	11:YP:46:LYS:HD2	1.91	0.40
11:YP:101:VAL:HB	11:YP:106:LEU:HB3	2.04	0.40
18:YW:10:VAL:HG12	18:YW:12:ILE:HG22	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:YX:43:VAL:HG13	19:YX:47:PHE:HD2	1.86	0.40
22:Y0:64:ASP:OD1	22:Y0:64:ASP:N	2.53	0.40
32:XA:191(B):G:H2'	32:XA:191(C):G:C8	2.57	0.40
32:XA:524:G:H2'	32:XA:525:C:C6	2.56	0.40
32:XA:704:A:H8	32:XA:704:A:OP2	2.04	0.40
32:XA:1410:G:H2'	32:XA:1411:C:C6	2.56	0.40
34:XC:44:GLU:HB3	34:XC:52:LEU:HD11	2.03	0.40
38:XG:67:GLU:HA	38:XG:70:LYS:HB2	2.03	0.40
39:XH:109:ILE:HD11	39:XH:120:THR:HB	2.03	0.40

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:RA:307:G:O6	24:Y2:71:ASN:O[3_555]	1.47	0.73
7:YH:46:GLU:CB	20:YY:22:GLY:O[4_445]	1.82	0.38
8:RI:82:ARG:NH1	32:XA:56:U:O2'[4_555]	2.05	0.15
8:RI:91:SER:OG	32:XA:368:U:OP1[4_555]	2.07	0.13
18:RW:63:ASP:OD1	20:YY:92:ASN:ND2[3_555]	2.08	0.12

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	RD	270/276 (98%)	257 (95%)	13 (5%)	0	100	100
3	YD	271/276 (98%)	261 (96%)	10 (4%)	0	100	100
4	RE	202/206 (98%)	190 (94%)	12 (6%)	0	100	100
4	YE	203/206 (98%)	170 (84%)	32 (16%)	1 (0%)	24	54
5	RF	200/210 (95%)	191 (96%)	9 (4%)	0	100	100
5	YF	200/210 (95%)	182 (91%)	18 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	RG	179/182 (98%)	153 (86%)	25 (14%)	1 (1%)	21	50
6	YG	179/182 (98%)	151 (84%)	27 (15%)	1 (1%)	21	50
7	RH	172/180 (96%)	149 (87%)	21 (12%)	2 (1%)	10	35
7	YH	172/180 (96%)	164 (95%)	8 (5%)	0	100	100
8	RI	144/148 (97%)	119 (83%)	24 (17%)	1 (1%)	18	47
8	YI	144/148 (97%)	122 (85%)	22 (15%)	0	100	100
9	RN	136/140 (97%)	121 (89%)	15 (11%)	0	100	100
9	YN	138/140 (99%)	125 (91%)	12 (9%)	1 (1%)	18	47
10	RO	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
10	YO	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
11	RP	146/150 (97%)	122 (84%)	24 (16%)	0	100	100
11	YP	145/150 (97%)	129 (89%)	15 (10%)	1 (1%)	18	47
12	RQ	139/141 (99%)	120 (86%)	18 (13%)	1 (1%)	18	47
12	YQ	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
13	RR	116/118 (98%)	106 (91%)	10 (9%)	0	100	100
13	YR	115/118 (98%)	106 (92%)	9 (8%)	0	100	100
14	RS	109/112 (97%)	91 (84%)	18 (16%)	0	100	100
14	YS	108/112 (96%)	106 (98%)	2 (2%)	0	100	100
15	RT	135/146 (92%)	121 (90%)	14 (10%)	0	100	100
15	YT	135/146 (92%)	127 (94%)	8 (6%)	0	100	100
16	RU	115/118 (98%)	107 (93%)	7 (6%)	1 (1%)	14	42
16	YU	115/118 (98%)	107 (93%)	7 (6%)	1 (1%)	14	42
17	RV	99/101 (98%)	95 (96%)	4 (4%)	0	100	100
17	YV	99/101 (98%)	92 (93%)	6 (6%)	1 (1%)	12	40
18	RW	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
18	YW	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
19	RX	90/96 (94%)	85 (94%)	5 (6%)	0	100	100
19	YX	92/96 (96%)	84 (91%)	8 (9%)	0	100	100
20	RY	105/110 (96%)	99 (94%)	6 (6%)	0	100	100
20	YY	105/110 (96%)	102 (97%)	3 (3%)	0	100	100
21	RZ	201/206 (98%)	180 (90%)	20 (10%)	1 (0%)	24	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	YZ	199/206 (97%)	188 (94%)	9 (4%)	2 (1%)	12	40
22	R0	74/85 (87%)	71 (96%)	3 (4%)	0	100	100
22	Y0	73/85 (86%)	69 (94%)	4 (6%)	0	100	100
23	R1	95/98 (97%)	83 (87%)	12 (13%)	0	100	100
23	Y1	91/98 (93%)	91 (100%)	0	0	100	100
24	R2	67/72 (93%)	64 (96%)	3 (4%)	0	100	100
24	Y2	70/72 (97%)	69 (99%)	1 (1%)	0	100	100
25	R3	57/60 (95%)	53 (93%)	4 (7%)	0	100	100
25	Y3	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
26	R4	67/71 (94%)	56 (84%)	11 (16%)	0	100	100
26	Y4	67/71 (94%)	58 (87%)	9 (13%)	0	100	100
27	R5	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
27	Y5	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
28	R6	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
28	Y6	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
29	R7	45/49 (92%)	45 (100%)	0	0	100	100
29	Y7	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
30	R8	62/65 (95%)	54 (87%)	8 (13%)	0	100	100
30	Y8	62/65 (95%)	56 (90%)	6 (10%)	0	100	100
31	R9	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
31	Y9	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
33	QB	233/256 (91%)	201 (86%)	32 (14%)	0	100	100
33	XB	234/256 (91%)	205 (88%)	29 (12%)	0	100	100
34	QC	203/239 (85%)	187 (92%)	16 (8%)	0	100	100
34	XC	203/239 (85%)	186 (92%)	17 (8%)	0	100	100
35	QD	206/209 (99%)	191 (93%)	13 (6%)	2 (1%)	12	40
35	XD	206/209 (99%)	191 (93%)	13 (6%)	2 (1%)	12	40
36	QE	149/162 (92%)	139 (93%)	10 (7%)	0	100	100
36	XE	149/162 (92%)	135 (91%)	14 (9%)	0	100	100
37	QF	99/101 (98%)	95 (96%)	4 (4%)	0	100	100
37	XF	99/101 (98%)	98 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	QG	153/156 (98%)	146 (95%)	7 (5%)	0	100	100
38	XG	153/156 (98%)	146 (95%)	7 (5%)	0	100	100
39	QH	135/138 (98%)	123 (91%)	12 (9%)	0	100	100
39	XH	135/138 (98%)	129 (96%)	6 (4%)	0	100	100
40	QI	125/128 (98%)	115 (92%)	10 (8%)	0	100	100
40	XI	124/128 (97%)	110 (89%)	14 (11%)	0	100	100
41	QJ	97/105 (92%)	86 (89%)	11 (11%)	0	100	100
41	XJ	94/105 (90%)	84 (89%)	10 (11%)	0	100	100
42	QK	114/129 (88%)	104 (91%)	10 (9%)	0	100	100
42	XK	114/129 (88%)	108 (95%)	6 (5%)	0	100	100
43	QL	123/132 (93%)	108 (88%)	15 (12%)	0	100	100
43	XL	120/132 (91%)	106 (88%)	14 (12%)	0	100	100
44	QM	118/126 (94%)	104 (88%)	13 (11%)	1 (1%)	16	44
44	XM	117/126 (93%)	105 (90%)	10 (8%)	2 (2%)	7	28
45	QN	58/61 (95%)	51 (88%)	7 (12%)	0	100	100
45	XN	58/61 (95%)	51 (88%)	7 (12%)	0	100	100
46	QO	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
46	XO	85/89 (96%)	82 (96%)	3 (4%)	0	100	100
47	QP	82/88 (93%)	76 (93%)	6 (7%)	0	100	100
47	XP	82/88 (93%)	75 (92%)	7 (8%)	0	100	100
48	QQ	98/105 (93%)	92 (94%)	6 (6%)	0	100	100
48	XQ	98/105 (93%)	92 (94%)	6 (6%)	0	100	100
49	QR	68/88 (77%)	62 (91%)	6 (9%)	0	100	100
49	XR	68/88 (77%)	64 (94%)	4 (6%)	0	100	100
50	QS	81/93 (87%)	73 (90%)	8 (10%)	0	100	100
50	XS	82/93 (88%)	68 (83%)	13 (16%)	1 (1%)	10	35
51	QT	97/106 (92%)	89 (92%)	8 (8%)	0	100	100
51	XT	97/106 (92%)	86 (89%)	11 (11%)	0	100	100
52	QU	23/27 (85%)	22 (96%)	1 (4%)	0	100	100
52	XU	23/27 (85%)	22 (96%)	1 (4%)	0	100	100
All	All	11486/12128 (95%)	10518 (92%)	945 (8%)	23 (0%)	43	71

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	YV	49	THR
35	XD	32	ALA
21	YZ	52	SER
16	RU	93	LYS
35	QD	32	ALA
35	XD	20	TYR
44	XM	5	ALA
6	RG	81	LYS
21	RZ	53	ILE
44	QM	106	ASN
6	YG	81	LYS
16	YU	93	LYS
7	RH	86	GLU
8	RI	118	LYS
12	RQ	78	PRO
35	QD	33	MET
9	YN	22	THR
21	YZ	183	LEU
50	XS	30	LEU
7	RH	55	PRO
11	YP	7	ARG
4	YE	116	VAL
44	XM	9	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	RD	214/218 (98%)	212 (99%)	2 (1%)	70	76
3	YD	215/218 (99%)	212 (99%)	3 (1%)	59	70
4	RE	165/166 (99%)	162 (98%)	3 (2%)	51	67
4	YE	165/166 (99%)	162 (98%)	3 (2%)	51	67
5	RF	161/166 (97%)	158 (98%)	3 (2%)	50	66
5	YF	161/166 (97%)	160 (99%)	1 (1%)	78	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	RG	155/156 (99%)	154 (99%)	1 (1%)	78	80
6	YG	155/156 (99%)	155 (100%)	0	100	100
7	RH	145/148 (98%)	143 (99%)	2 (1%)	59	70
7	YH	145/148 (98%)	138 (95%)	7 (5%)	23	50
8	RI	122/124 (98%)	107 (88%)	15 (12%)	4	18
8	YI	122/124 (98%)	119 (98%)	3 (2%)	42	62
9	RN	117/119 (98%)	115 (98%)	2 (2%)	53	67
9	YN	119/119 (100%)	116 (98%)	3 (2%)	42	62
10	RO	100/100 (100%)	99 (99%)	1 (1%)	68	75
10	YO	100/100 (100%)	99 (99%)	1 (1%)	68	75
11	RP	115/116 (99%)	114 (99%)	1 (1%)	70	76
11	YP	114/116 (98%)	112 (98%)	2 (2%)	51	67
12	RQ	111/111 (100%)	108 (97%)	3 (3%)	39	60
12	YQ	111/111 (100%)	109 (98%)	2 (2%)	51	67
13	RR	101/101 (100%)	101 (100%)	0	100	100
13	YR	100/101 (99%)	99 (99%)	1 (1%)	68	75
14	RS	87/88 (99%)	86 (99%)	1 (1%)	65	74
14	YS	87/88 (99%)	86 (99%)	1 (1%)	65	74
15	RT	120/127 (94%)	118 (98%)	2 (2%)	53	67
15	YT	120/127 (94%)	120 (100%)	0	100	100
16	RU	93/94 (99%)	93 (100%)	0	100	100
16	YU	93/94 (99%)	92 (99%)	1 (1%)	65	74
17	RV	82/82 (100%)	78 (95%)	4 (5%)	22	49
17	YV	82/82 (100%)	80 (98%)	2 (2%)	43	62
18	RW	92/92 (100%)	91 (99%)	1 (1%)	65	74
18	YW	92/92 (100%)	92 (100%)	0	100	100
19	RX	74/78 (95%)	70 (95%)	4 (5%)	20	47
19	YX	76/78 (97%)	72 (95%)	4 (5%)	20	47
20	RY	88/91 (97%)	88 (100%)	0	100	100
20	YY	88/91 (97%)	88 (100%)	0	100	100
21	RZ	174/179 (97%)	170 (98%)	4 (2%)	44	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	YZ	173/179 (97%)	170 (98%)	3 (2%)	53	67
22	R0	61/67 (91%)	61 (100%)	0	100	100
22	Y0	61/67 (91%)	61 (100%)	0	100	100
23	R1	82/83 (99%)	82 (100%)	0	100	100
23	Y1	78/83 (94%)	78 (100%)	0	100	100
24	R2	64/67 (96%)	64 (100%)	0	100	100
24	Y2	67/67 (100%)	67 (100%)	0	100	100
25	R3	51/52 (98%)	50 (98%)	1 (2%)	48	65
25	Y3	51/52 (98%)	50 (98%)	1 (2%)	48	65
26	R4	62/63 (98%)	60 (97%)	2 (3%)	34	58
26	Y4	62/63 (98%)	62 (100%)	0	100	100
27	R5	51/52 (98%)	50 (98%)	1 (2%)	48	65
27	Y5	51/52 (98%)	50 (98%)	1 (2%)	48	65
28	R6	51/52 (98%)	51 (100%)	0	100	100
28	Y6	51/52 (98%)	50 (98%)	1 (2%)	48	65
29	R7	40/42 (95%)	40 (100%)	0	100	100
29	Y7	41/42 (98%)	41 (100%)	0	100	100
30	R8	54/55 (98%)	53 (98%)	1 (2%)	50	66
30	Y8	54/55 (98%)	54 (100%)	0	100	100
31	R9	34/34 (100%)	34 (100%)	0	100	100
31	Y9	34/34 (100%)	34 (100%)	0	100	100
33	QB	203/220 (92%)	201 (99%)	2 (1%)	68	75
33	XB	204/220 (93%)	203 (100%)	1 (0%)	81	81
34	QC	159/188 (85%)	158 (99%)	1 (1%)	78	80
34	XC	159/188 (85%)	158 (99%)	1 (1%)	78	80
35	QD	180/181 (99%)	178 (99%)	2 (1%)	65	74
35	XD	180/181 (99%)	174 (97%)	6 (3%)	33	57
36	QE	116/123 (94%)	114 (98%)	2 (2%)	53	67
36	XE	116/123 (94%)	113 (97%)	3 (3%)	40	61
37	QF	90/90 (100%)	90 (100%)	0	100	100
37	XF	90/90 (100%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	QG	126/127 (99%)	126 (100%)	0	100	100
38	XG	126/127 (99%)	124 (98%)	2 (2%)	55	68
39	QH	118/119 (99%)	118 (100%)	0	100	100
39	XH	118/119 (99%)	118 (100%)	0	100	100
40	QI	98/99 (99%)	96 (98%)	2 (2%)	48	65
40	XI	97/99 (98%)	97 (100%)	0	100	100
41	QJ	89/92 (97%)	88 (99%)	1 (1%)	65	74
41	XJ	86/92 (94%)	86 (100%)	0	100	100
42	QK	88/99 (89%)	87 (99%)	1 (1%)	65	74
42	XK	88/99 (89%)	87 (99%)	1 (1%)	65	74
43	QL	104/109 (95%)	104 (100%)	0	100	100
43	XL	103/109 (94%)	103 (100%)	0	100	100
44	QM	96/101 (95%)	94 (98%)	2 (2%)	47	64
44	XM	95/101 (94%)	93 (98%)	2 (2%)	47	64
45	QN	49/50 (98%)	49 (100%)	0	100	100
45	XN	49/50 (98%)	48 (98%)	1 (2%)	48	65
46	QO	79/80 (99%)	78 (99%)	1 (1%)	61	71
46	XO	79/80 (99%)	79 (100%)	0	100	100
47	QP	72/74 (97%)	71 (99%)	1 (1%)	59	70
47	XP	72/74 (97%)	71 (99%)	1 (1%)	59	70
48	QQ	95/97 (98%)	95 (100%)	0	100	100
48	XQ	95/97 (98%)	94 (99%)	1 (1%)	65	74
49	QR	61/77 (79%)	61 (100%)	0	100	100
49	XR	61/77 (79%)	61 (100%)	0	100	100
50	QS	72/80 (90%)	71 (99%)	1 (1%)	59	70
50	XS	73/80 (91%)	72 (99%)	1 (1%)	59	70
51	QT	76/82 (93%)	76 (100%)	0	100	100
51	XT	76/82 (93%)	76 (100%)	0	100	100
52	QU	20/22 (91%)	19 (95%)	1 (5%)	22	49
52	XU	20/22 (91%)	20 (100%)	0	100	100
All	All	9712/10066 (96%)	9581 (99%)	131 (1%)	61	71

All (131) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	RD	61	LEU
3	RD	138	VAL
4	RE	9	VAL
4	RE	21	VAL
4	RE	75	VAL
5	RF	183	VAL
5	RF	201	VAL
5	RF	204	ASN
6	RG	172	LEU
7	RH	7	LEU
7	RH	105	LEU
8	RI	9	LEU
8	RI	77	LEU
8	RI	85	GLU
8	RI	86	THR
8	RI	91	SER
8	RI	97	ILE
8	RI	103	ARG
8	RI	117	GLU
8	RI	118	LYS
8	RI	120	ILE
8	RI	121	LYS
8	RI	123	LEU
8	RI	133	HIS
8	RI	136	VAL
8	RI	138	ILE
9	RN	5	VAL
9	RN	32	THR
10	RO	47	ILE
11	RP	70	GLN
12	RQ	21	THR
12	RQ	60	ARG
12	RQ	63	LYS
14	RS	85	VAL
15	RT	62	THR
15	RT	99	LEU
17	RV	7	THR
17	RV	47	VAL
17	RV	72	VAL
17	RV	79	VAL
18	RW	17	VAL
19	RX	54	VAL

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Mol	Chain	Res	Type
19	RX	59	VAL
19	RX	66	LEU
19	RX	81	VAL
21	RZ	9	TYR
21	RZ	180	VAL
21	RZ	182	LYS
21	RZ	185	GLU
25	R3	36	VAL
26	R4	40	HIS
26	R4	46	GLN
27	R5	6	VAL
30	R8	61	LEU
33	QB	215	LEU
33	QB	230	VAL
34	QC	63	ASN
35	QD	31	CYS
35	QD	33	MET
36	QE	51	VAL
36	QE	90	VAL
40	QI	28	VAL
40	QI	53	VAL
41	QJ	42	THR
42	QK	33	THR
44	QM	7	VAL
44	QM	45	VAL
46	QO	87	ILE
47	QP	67	THR
50	QS	33	THR
52	QU	8	THR
3	YD	138	VAL
3	YD	273	ARG
3	YD	274	ARG
4	YE	33	VAL
4	YE	197	ILE
4	YE	201	THR
5	YF	183	VAL
7	YH	2	SER
7	YH	3	ARG
7	YH	4	ILE
7	YH	15	VAL
7	YH	45	VAL
7	YH	49	VAL

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Mol	Chain	Res	Type
7	YH	136	ILE
8	YI	15	VAL
8	YI	38	LEU
8	YI	136	VAL
9	YN	120	LEU
9	YN	138	LEU
9	YN	140	VAL
10	YO	38	VAL
11	YP	71	VAL
11	YP	125	VAL
12	YQ	21	THR
12	YQ	55	VAL
13	YR	114	VAL
14	YS	85	VAL
16	YU	91	ASP
17	YV	46	VAL
17	YV	72	VAL
19	YX	27	THR
19	YX	49	VAL
19	YX	59	VAL
19	YX	80	ILE
21	YZ	86	VAL
21	YZ	126	VAL
21	YZ	183	LEU
25	Y3	13	ILE
27	Y5	58	LEU
28	Y6	52	VAL
33	XB	172	ILE
34	XC	198	VAL
35	XD	8	VAL
35	XD	18	LYS
35	XD	19	LEU
35	XD	21	LEU
35	XD	22	LYS
35	XD	33	MET
36	XE	11	ILE
36	XE	33	VAL
36	XE	116	THR
38	XG	23	VAL
38	XG	37	ASN
42	XK	30	VAL
44	XM	3	ARG

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Mol	Chain	Res	Type
44	XM	7	VAL
45	XN	53	LEU
47	XP	67	THR
48	XQ	31	LEU
50	XS	11	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (71) such sidechains are listed below:

Mol	Chain	Res	Type
3	RD	227	ASN
4	RE	48	GLN
4	RE	180	ASN
5	RF	40	GLN
6	RG	26	GLN
14	RS	68	GLN
17	RV	11	GLN
19	RX	41	ASN
21	RZ	34	ASN
21	RZ	73	GLN
22	R0	17	GLN
24	R2	46	GLN
24	R2	47	ASN
24	R2	71	ASN
26	R4	6	HIS
26	R4	47	GLN
30	R8	31	HIS
31	R9	34	GLN
33	QB	19	HIS
33	QB	25	ASN
33	QB	94	ASN
33	QB	204	ASN
34	QC	108	ASN
34	QC	118	GLN
38	QG	51	GLN
38	QG	64	GLN
40	QI	29	ASN
41	QJ	69	ASN
41	QJ	84	GLN
42	QK	38	ASN
42	QK	78	GLN
46	QO	62	GLN
5	YF	203	GLN

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Mol	Chain	Res	Type
6	YG	40	ASN
6	YG	132	ASN
8	YI	28	ASN
10	YO	89	ASN
11	YP	68	GLN
11	YP	81	GLN
12	YQ	57	HIS
14	YS	68	GLN
15	YT	79	HIS
16	YU	44	ASN
16	YU	72	HIS
16	YU	75	ASN
21	YZ	32	HIS
21	YZ	34	ASN
22	Y0	17	GLN
30	Y8	7	HIS
30	Y8	31	HIS
33	XB	37	ASN
33	XB	40	HIS
34	XC	37	GLN
34	XC	98	ASN
34	XC	104	GLN
34	XC	181	ASN
35	XD	161	ASN
36	XE	141	GLN
37	XF	7	ASN
37	XF	73	ASN
38	XG	28	ASN
39	XH	82	HIS
40	XI	3	GLN
40	XI	31	GLN
40	XI	34	ASN
40	XI	73	GLN
41	XJ	76	ASN
42	XK	117	ASN
48	XQ	94	ASN
50	XS	53	ASN
50	XS	83	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	RA	2877/2915 (98%)	581 (20%)	41 (1%)
1	YA	2880/2915 (98%)	558 (19%)	40 (1%)
2	RB	119/122 (97%)	19 (15%)	1 (0%)
2	YB	119/122 (97%)	23 (19%)	2 (1%)
32	QA	1510/1521 (99%)	292 (19%)	37 (2%)
32	XA	1509/1521 (99%)	277 (18%)	29 (1%)
53	QV	16/17 (94%)	1 (6%)	0
53	XV	14/17 (82%)	0	0
54	QX	17/19 (89%)	5 (29%)	1 (5%)
54	XX	18/19 (94%)	9 (50%)	1 (5%)
All	All	9079/9188 (98%)	1765 (19%)	152 (1%)

All (1765) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	RA	9	U
1	RA	15	G
1	RA	34	C
1	RA	35	G
1	RA	46	C
1	RA	51	G
1	RA	55	G
1	RA	63	U
1	RA	72	U
1	RA	73	A
1	RA	74	A
1	RA	75	G
1	RA	82	G
1	RA	83	G
1	RA	90	U
1	RA	95	G
1	RA	101	G
1	RA	103	A
1	RA	118	A
1	RA	120	U
1	RA	131	G
1	RA	140	A
1	RA	177	G
1	RA	181	A
1	RA	196	A
1	RA	199	A
1	RA	214	G
1	RA	215	G

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Mol	Chain	Res	Type
1	RA	216	A
1	RA	221	A
1	RA	222	A
1	RA	223	A
1	RA	229	A
1	RA	230	U
1	RA	248	G
1	RA	249	C
1	RA	252	G
1	RA	265	A
1	RA	266	G
1	RA	269	U
1	RA	270(L)	U
1	RA	270(M)	U
1	RA	270(N)	G
1	RA	270(P)	C
1	RA	271(C)	U
1	RA	273(F)	C
1	RA	275	G
1	RA	276	A
1	RA	277	C
1	RA	299	A
1	RA	311	A
1	RA	316	C
1	RA	323	G
1	RA	324	A
1	RA	329	G
1	RA	330	A
1	RA	342	G
1	RA	346	A
1	RA	352	G
1	RA	363(F)	A
1	RA	364	C
1	RA	371	A
1	RA	372	G
1	RA	373	U
1	RA	386	G
1	RA	395	U
1	RA	405	U
1	RA	411	G
1	RA	412	A
1	RA	428	A

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Mol	Chain	Res	Type
1	RA	435	C
1	RA	444	C
1	RA	448	U
1	RA	454	A
1	RA	455	C
1	RA	456	C
1	RA	457	A
1	RA	458	G
1	RA	470	A
1	RA	481	G
1	RA	501	A
1	RA	503	A
1	RA	504	U
1	RA	505	A
1	RA	509	C
1	RA	513	A
1	RA	528	A
1	RA	529	A
1	RA	530	G
1	RA	531	C
1	RA	532	A
1	RA	533	G
1	RA	537	C
1	RA	539	G
1	RA	540	G
1	RA	546	C
1	RA	547	A
1	RA	556	G
1	RA	563	G
1	RA	573	G
1	RA	574	C
1	RA	575	A
1	RA	583	G
1	RA	588	U
1	RA	603	A
1	RA	607	U
1	RA	614	U
1	RA	615	G
1	RA	616	A
1	RA	617	G
1	RA	626	U
1	RA	627	A

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Mol	Chain	Res	Type
1	RA	631	A
1	RA	637	A
1	RA	638	G
1	RA	645	C
1	RA	646	A
1	RA	647	G
1	RA	650	C
1	RA	651	G
1	RA	652	C
1	RA	654	A
1	RA	654(A)	G
1	RA	669	G
1	RA	670	A
1	RA	686	G
1	RA	702	G
1	RA	717	G
1	RA	722	A
1	RA	726	G
1	RA	730	C
1	RA	752	A
1	RA	753	C
1	RA	765	G
1	RA	776	G
1	RA	782	A
1	RA	783	A
1	RA	784	A
1	RA	785	G
1	RA	790	C
1	RA	791	C
1	RA	792	G
1	RA	805	G
1	RA	812	C
1	RA	819	A
1	RA	827	U
1	RA	828	U
1	RA	830	G
1	RA	831	G
1	RA	846	C
1	RA	847	U
1	RA	856	C
1	RA	857	C
1	RA	859	G

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Mol	Chain	Res	Type
1	RA	866	A
1	RA	869	G
1	RA	882	G
1	RA	884	C
1	RA	885	C
1	RA	886	C
1	RA	888	C
1	RA	889	C
1	RA	896	A
1	RA	897	C
1	RA	900	A
1	RA	901	A
1	RA	907	U
1	RA	910	A
1	RA	914	C
1	RA	915	C
1	RA	917	A
1	RA	932	G
1	RA	941	A
1	RA	945	A
1	RA	946	G
1	RA	953	A
1	RA	957	A
1	RA	959	A
1	RA	961	C
1	RA	973	A
1	RA	974	G
1	RA	974(A)	C
1	RA	980	A
1	RA	983	A
1	RA	996	A
1	RA	1003	G
1	RA	1005	C
1	RA	1008	C
1	RA	1012	U
1	RA	1013	C
1	RA	1020	A
1	RA	1022	G
1	RA	1023	U
1	RA	1025	G
1	RA	1026	U
1	RA	1027	A

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Mol	Chain	Res	Type
1	RA	1033	U
1	RA	1042	G
1	RA	1045	A
1	RA	1046	A
1	RA	1047	G
1	RA	1048	A
1	RA	1052	C
1	RA	1054	A
1	RA	1058	G
1	RA	1060	U
1	RA	1063	G
1	RA	1064	C
1	RA	1065	U
1	RA	1066	U
1	RA	1067	A
1	RA	1068	G
1	RA	1069	A
1	RA	1070	A
1	RA	1071	G
1	RA	1073	A
1	RA	1074	G
1	RA	1076	C
1	RA	1078	U
1	RA	1079	C
1	RA	1082	U
1	RA	1083	U
1	RA	1084	A
1	RA	1085	A
1	RA	1086	A
1	RA	1088	A
1	RA	1090	U
1	RA	1091	G
1	RA	1092	C
1	RA	1093	G
1	RA	1094	U
1	RA	1109	C
1	RA	1110	G
1	RA	1111	A
1	RA	1112	G
1	RA	1122	G
1	RA	1129	A
1	RA	1130	U

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Mol	Chain	Res	Type
1	RA	1135	C
1	RA	1136	G
1	RA	1139	G
1	RA	1140	C
1	RA	1142	U
1	RA	1142(A)	A
1	RA	1173	G
1	RA	1174	A
1	RA	1175	U
1	RA	1176	G
1	RA	1178	C
1	RA	1181	C
1	RA	1195	G
1	RA	1204	A
1	RA	1205	U
1	RA	1210	A
1	RA	1211	U
1	RA	1220	A
1	RA	1236	G
1	RA	1238	G
1	RA	1248	G
1	RA	1250	G
1	RA	1253	A
1	RA	1256	G
1	RA	1265	A
1	RA	1272	A
1	RA	1281	G
1	RA	1300	U
1	RA	1301	A
1	RA	1312	U
1	RA	1313	U
1	RA	1314	C
1	RA	1321	A
1	RA	1329	U
1	RA	1349	A
1	RA	1352	U
1	RA	1365	A
1	RA	1370	C
1	RA	1379	A
1	RA	1384	A
1	RA	1385	G
1	RA	1386	C

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Mol	Chain	Res	Type
1	RA	1390	U
1	RA	1391	U
1	RA	1395	A
1	RA	1407	C
1	RA	1408	C
1	RA	1411	C
1	RA	1416	G
1	RA	1419	A
1	RA	1420	U
1	RA	1421	G
1	RA	1428	C
1	RA	1444(A)	A
1	RA	1445	C
1	RA	1449	A
1	RA	1449(A)	G
1	RA	1455	G
1	RA	1460	A
1	RA	1461	G
1	RA	1471	A
1	RA	1480	G
1	RA	1482	U
1	RA	1483	G
1	RA	1487	G
1	RA	1493	C
1	RA	1494	A
1	RA	1495	A
1	RA	1497	U
1	RA	1504	C
1	RA	1505	C
1	RA	1506	C
1	RA	1507	A
1	RA	1508	A
1	RA	1509	C
1	RA	1510	A
1	RA	1511	A
1	RA	1513	C
1	RA	1514	U
1	RA	1515	C
1	RA	1519	G
1	RA	1522	G
1	RA	1533	C
1	RA	1535	U

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Mol	Chain	Res	Type
1	RA	1536	A
1	RA	1537	C
1	RA	1538	G
1	RA	1543	A
1	RA	1544	C
1	RA	1545	A
1	RA	1547	C
1	RA	1558	A
1	RA	1559	G
1	RA	1566	A
1	RA	1569	A
1	RA	1578	U
1	RA	1580	A
1	RA	1586	A
1	RA	1587	A
1	RA	1598	C
1	RA	1599	C
1	RA	1608	A
1	RA	1609	A
1	RA	1616	A
1	RA	1617	C
1	RA	1634	A
1	RA	1640	C
1	RA	1648	C
1	RA	1654	A
1	RA	1667	G
1	RA	1674	G
1	RA	1678	G
1	RA	1725	G
1	RA	1728	G
1	RA	1729	A
1	RA	1730	U
1	RA	1731	G
1	RA	1733	G
1	RA	1742	C
1	RA	1743	G
1	RA	1750	G
1	RA	1756	G
1	RA	1762	A
1	RA	1763	G
1	RA	1764	G
1	RA	1773	A

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Mol	Chain	Res	Type
1	RA	1776	G
1	RA	1780	A
1	RA	1782	C
1	RA	1787	A
1	RA	1791	A
1	RA	1799	G
1	RA	1800	C
1	RA	1801	G
1	RA	1816	G
1	RA	1820	U
1	RA	1829	A
1	RA	1835	G
1	RA	1847	A
1	RA	1848	A
1	RA	1858	G
1	RA	1869	G
1	RA	1870	C
1	RA	1872	A
1	RA	1878	G
1	RA	1882	C
1	RA	1888	G
1	RA	1889	A
1	RA	1900	A
1	RA	1903	G
1	RA	1906	G
1	RA	1909	C
1	RA	1913	A
1	RA	1914	C
1	RA	1929	G
1	RA	1930	G
1	RA	1936	A
1	RA	1939	U
1	RA	1955	U
1	RA	1963	U
1	RA	1967	C
1	RA	1969	A
1	RA	1970	A
1	RA	1971	A
1	RA	1972	A
1	RA	1982	C
1	RA	1991	U
1	RA	1992	G

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Mol	Chain	Res	Type
1	RA	1993	U
1	RA	2020	A
1	RA	2023	G
1	RA	2030	A
1	RA	2031	A
1	RA	2032	G
1	RA	2033	A
1	RA	2043	C
1	RA	2055	C
1	RA	2056	G
1	RA	2059	A
1	RA	2060	A
1	RA	2061	G
1	RA	2062	A
1	RA	2069	G
1	RA	2089	U
1	RA	2093	G
1	RA	2099	U
1	RA	2101	G
1	RA	2107	C
1	RA	2111	C
1	RA	2113	U
1	RA	2114	A
1	RA	2115	G
1	RA	2116	G
1	RA	2117	A
1	RA	2118	U
1	RA	2126	A
1	RA	2127	G
1	RA	2128	C
1	RA	2131	G
1	RA	2132	U
1	RA	2133	G
1	RA	2135	A
1	RA	2141	G
1	RA	2145	C
1	RA	2146	C
1	RA	2147	G
1	RA	2148	G
1	RA	2158	A
1	RA	2160	G
1	RA	2166	G

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Mol	Chain	Res	Type
1	RA	2168	G
1	RA	2169	A
1	RA	2170	A
1	RA	2173	A
1	RA	2181	G
1	RA	2189	U
1	RA	2190	G
1	RA	2191	G
1	RA	2192	G
1	RA	2198	A
1	RA	2210	G
1	RA	2211	G
1	RA	2212	A
1	RA	2215	G
1	RA	2225	A
1	RA	2238	G
1	RA	2239	G
1	RA	2243	U
1	RA	2266	A
1	RA	2275	C
1	RA	2278	A
1	RA	2280	G
1	RA	2283	C
1	RA	2287	A
1	RA	2288	A
1	RA	2305	A
1	RA	2307	G
1	RA	2308	G
1	RA	2309	A
1	RA	2311	A
1	RA	2312	U
1	RA	2320	A
1	RA	2325	G
1	RA	2334	G
1	RA	2336	A
1	RA	2345	G
1	RA	2346	A
1	RA	2347	C
1	RA	2350	C
1	RA	2383	G
1	RA	2385	C
1	RA	2403	C

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Mol	Chain	Res	Type
1	RA	2406	U
1	RA	2424	C
1	RA	2425	A
1	RA	2427	C
1	RA	2429	G
1	RA	2430	A
1	RA	2435	A
1	RA	2439	A
1	RA	2440	C
1	RA	2441	C
1	RA	2448	A
1	RA	2465	C
1	RA	2469	A
1	RA	2473	U
1	RA	2475	C
1	RA	2480	C
1	RA	2482	G
1	RA	2494	G
1	RA	2502	G
1	RA	2505	G
1	RA	2518	A
1	RA	2519	U
1	RA	2529	G
1	RA	2542	A
1	RA	2543	G
1	RA	2554	U
1	RA	2564	A
1	RA	2566	A
1	RA	2567	G
1	RA	2569	G
1	RA	2572	A
1	RA	2573	C
1	RA	2602	A
1	RA	2609	U
1	RA	2611	U
1	RA	2612	C
1	RA	2615	U
1	RA	2623	G
1	RA	2629	A
1	RA	2636	U
1	RA	2641	G
1	RA	2654	A

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Mol	Chain	Res	Type
1	RA	2655	G
1	RA	2665	A
1	RA	2673	G
1	RA	2689	U
1	RA	2690	C
1	RA	2702	U
1	RA	2703	C
1	RA	2707	G
1	RA	2712(A)	A
1	RA	2713	A
1	RA	2714	G
1	RA	2726	U
1	RA	2732	G
1	RA	2733	A
1	RA	2744	G
1	RA	2748	A
1	RA	2751	G
1	RA	2757	A
1	RA	2758	A
1	RA	2761	G
1	RA	2762	G
1	RA	2764	A
1	RA	2765	A
1	RA	2766	G
1	RA	2778	A
1	RA	2779	U
1	RA	2780	G
1	RA	2789	C
1	RA	2790	A
1	RA	2791	C
1	RA	2797	U
1	RA	2798	C
1	RA	2799	A
1	RA	2807	G
1	RA	2813	A
1	RA	2818	G
1	RA	2820	A
1	RA	2821	A
1	RA	2833	G
1	RA	2834	G
1	RA	2847	U
1	RA	2867	G

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Mol	Chain	Res	Type
1	RA	2868	A
1	RA	2872	G
1	RA	2880	C
1	RA	2892	A
1	RA	2894	G
1	RA	2895	U
1	RA	2897	U
2	RB	2	C
2	RB	8	U
2	RB	13	A
2	RB	15	A
2	RB	16	G
2	RB	19	G
2	RB	21	G
2	RB	25	A
2	RB	31	C
2	RB	41	U
2	RB	42	C
2	RB	44	G
2	RB	45	A
2	RB	52	A
2	RB	56	G
2	RB	67	G
2	RB	73	A
2	RB	108	C
2	RB	109	G
32	QA	6	G
32	QA	7	G
32	QA	9	G
32	QA	32	A
32	QA	39	G
32	QA	47	C
32	QA	48	C
32	QA	51	A
32	QA	59	A
32	QA	64	G
32	QA	65	U
32	QA	66	G
32	QA	76	G
32	QA	82	U
32	QA	90	C
32	QA	91	C

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Mol	Chain	Res	Type
32	QA	95	G
32	QA	101	A
32	QA	116	A
32	QA	120	A
32	QA	121	C
32	QA	129(A)	G
32	QA	144	G
32	QA	146	G
32	QA	158	G
32	QA	159	G
32	QA	162	A
32	QA	163	C
32	QA	169	C
32	QA	173	U
32	QA	174	C
32	QA	182	U
32	QA	187	C
32	QA	188	U
32	QA	190	G
32	QA	191(A)	G
32	QA	195	A
32	QA	197	A
32	QA	208	U
32	QA	209	U
32	QA	210	U
32	QA	216	G
32	QA	220	G
32	QA	244	U
32	QA	245	C
32	QA	247	G
32	QA	250	A
32	QA	251	G
32	QA	267	C
32	QA	270	A
32	QA	281	G
32	QA	289	G
32	QA	298	A
32	QA	306	G
32	QA	321	A
32	QA	328	C
32	QA	329	A
32	QA	332	G

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Mol	Chain	Res	Type
32	QA	344	A
32	QA	346	G
32	QA	347	G
32	QA	352	C
32	QA	353	A
32	QA	354	G
32	QA	356	A
32	QA	367	U
32	QA	372	C
32	QA	373	A
32	QA	389	A
32	QA	390	C
32	QA	397	A
32	QA	398	C
32	QA	406	G
32	QA	411	A
32	QA	412	A
32	QA	413	G
32	QA	414	A
32	QA	421	U
32	QA	422	C
32	QA	423	G
32	QA	424	G
32	QA	429	U
32	QA	430	A
32	QA	435	C
32	QA	439	A
32	QA	442	C
32	QA	466	C
32	QA	482	A
32	QA	485	G
32	QA	486	U
32	QA	495	A
32	QA	496	A
32	QA	497	U
32	QA	505	G
32	QA	508	C
32	QA	509	A
32	QA	510	A
32	QA	511	C
32	QA	518	C
32	QA	521	G

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Mol	Chain	Res	Type
32	QA	527	G
32	QA	532	A
32	QA	533	A
32	QA	545	C
32	QA	547	A
32	QA	559	A
32	QA	564	C
32	QA	568	G
32	QA	572	A
32	QA	573	A
32	QA	576	G
32	QA	577	G
32	QA	596	C
32	QA	618	C
32	QA	630	G
32	QA	631	G
32	QA	632	A
32	QA	633	G
32	QA	653	A
32	QA	657	G
32	QA	665	A
32	QA	666	G
32	QA	686	U
32	QA	688	G
32	QA	701	C
32	QA	702	A
32	QA	703	G
32	QA	704	A
32	QA	722	A
32	QA	724	G
32	QA	731	G
32	QA	748	C
32	QA	749	C
32	QA	754	C
32	QA	755	G
32	QA	760	G
32	QA	777	A
32	QA	786	G
32	QA	792	A
32	QA	793	U
32	QA	794	A
32	QA	812	C

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Mol	Chain	Res	Type
32	QA	813	U
32	QA	817	C
32	QA	819	A
32	QA	821	G
32	QA	828	A
32	QA	841	U
32	QA	842	C
32	QA	843	U
32	QA	848	C
32	QA	859	A
32	QA	870	U
32	QA	871	U
32	QA	872	A
32	QA	885	G
32	QA	889	A
32	QA	902	G
32	QA	914	A
32	QA	927	G
32	QA	934	C
32	QA	935	A
32	QA	960	U
32	QA	961	U
32	QA	968	A
32	QA	969	A
32	QA	971	G
32	QA	974	A
32	QA	976	G
32	QA	977	A
32	QA	982	U
32	QA	991	U
32	QA	992	U
32	QA	993	G
32	QA	994	A
32	QA	1004	A
32	QA	1005	A
32	QA	1006	C
32	QA	1008	C
32	QA	1009	G
32	QA	1020	U
32	QA	1024	G
32	QA	1025	U
32	QA	1027	C

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Mol	Chain	Res	Type
32	QA	1029	G
32	QA	1030	C
32	QA	1031	G
32	QA	1032(A)	G
32	QA	1033	G
32	QA	1034	G
32	QA	1042	G
32	QA	1054	C
32	QA	1064	G
32	QA	1065	U
32	QA	1066	C
32	QA	1080	A
32	QA	1081	G
32	QA	1094	G
32	QA	1095	U
32	QA	1101	A
32	QA	1108	G
32	QA	1124	G
32	QA	1125	U
32	QA	1126	U
32	QA	1130	A
32	QA	1131	G
32	QA	1136	U
32	QA	1137	C
32	QA	1138	G
32	QA	1139	G
32	QA	1140	C
32	QA	1146	A
32	QA	1157	A
32	QA	1158	C
32	QA	1159	U
32	QA	1160	G
32	QA	1181	G
32	QA	1183	A
32	QA	1184	G
32	QA	1187	G
32	QA	1190	G
32	QA	1196	U
32	QA	1201	A
32	QA	1202	G
32	QA	1212	U
32	QA	1213	A

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Mol	Chain	Res	Type
32	QA	1215	G
32	QA	1224	G
32	QA	1240	U
32	QA	1241	G
32	QA	1256	A
32	QA	1257	U
32	QA	1258	G
32	QA	1260	C
32	QA	1270	C
32	QA	1279	A
32	QA	1280	A
32	QA	1281	U
32	QA	1286	A
32	QA	1287	A
32	QA	1297	C
32	QA	1298	C
32	QA	1299	A
32	QA	1301	U
32	QA	1302	U
32	QA	1303	C
32	QA	1305	G
32	QA	1317	C
32	QA	1321	C
32	QA	1322	C
32	QA	1323	G
32	QA	1331	G
32	QA	1334	G
32	QA	1335	C
32	QA	1336	C
32	QA	1337	G
32	QA	1347	G
32	QA	1348	U
32	QA	1362(A)	C
32	QA	1370	G
32	QA	1379	G
32	QA	1397	C
32	QA	1398	A
32	QA	1419	G
32	QA	1439	C
32	QA	1442	G
32	QA	1446	A
32	QA	1447	G

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Mol	Chain	Res	Type
32	QA	1452	C
32	QA	1453	G
32	QA	1487	G
32	QA	1492	A
32	QA	1494	G
32	QA	1497	G
32	QA	1499	A
32	QA	1503	A
32	QA	1504	G
32	QA	1506	U
32	QA	1517	G
32	QA	1519	A
32	QA	1520	G
32	QA	1529	G
32	QA	1530	G
32	QA	1531	A
32	QA	1532	U
32	QA	1533	C
32	QA	1534	A
32	QA	1535	C
32	QA	1537	U
32	QA	1538	C
32	QA	1539	C
32	QA	1541	U
53	QV	43	G
54	QX	8	A
54	QX	12	A
54	QX	13	A
54	QX	14	A
54	QX	15	A
1	YA	9	U
1	YA	14	A
1	YA	15	G
1	YA	23	G
1	YA	26	G
1	YA	34	C
1	YA	35	G
1	YA	46	C
1	YA	55	G
1	YA	63	U
1	YA	64	A
1	YA	72	U

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Mol	Chain	Res	Type
1	YA	74	A
1	YA	75	G
1	YA	90	U
1	YA	95	G
1	YA	99	U
1	YA	101	G
1	YA	102	G
1	YA	118	A
1	YA	120	U
1	YA	125	G
1	YA	131	G
1	YA	140	A
1	YA	161	U
1	YA	162	U
1	YA	181	A
1	YA	196	A
1	YA	199	A
1	YA	204	A
1	YA	216	A
1	YA	221	A
1	YA	222	A
1	YA	223	A
1	YA	226	G
1	YA	228	A
1	YA	229	A
1	YA	230	U
1	YA	232	G
1	YA	233	A
1	YA	242	G
1	YA	243	U
1	YA	248	G
1	YA	252	G
1	YA	265	A
1	YA	266	G
1	YA	269	U
1	YA	270(L)	U
1	YA	270(M)	U
1	YA	270(N)	G
1	YA	270(P)	C
1	YA	271(C)	U
1	YA	271(D)	G
1	YA	274	G

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Mol	Chain	Res	Type
1	YA	275	G
1	YA	276	A
1	YA	278	A
1	YA	279	C
1	YA	299	A
1	YA	311	A
1	YA	323	G
1	YA	324	A
1	YA	327	G
1	YA	329	G
1	YA	330	A
1	YA	331	A
1	YA	332	A
1	YA	333	G
1	YA	352	G
1	YA	363(E)	U
1	YA	364	C
1	YA	371	A
1	YA	372	G
1	YA	386	G
1	YA	387	U
1	YA	396	G
1	YA	405	U
1	YA	411	G
1	YA	412	A
1	YA	428	A
1	YA	443	A
1	YA	444	C
1	YA	448	U
1	YA	457	A
1	YA	470	A
1	YA	481	G
1	YA	504	U
1	YA	505	A
1	YA	508	G
1	YA	509	C
1	YA	512	G
1	YA	530	G
1	YA	531	C
1	YA	532	A
1	YA	533	G
1	YA	537	C

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Mol	Chain	Res	Type
1	YA	539	G
1	YA	540	G
1	YA	546	C
1	YA	547	A
1	YA	563	G
1	YA	573	G
1	YA	574	C
1	YA	575	A
1	YA	586	A
1	YA	603	A
1	YA	607	U
1	YA	609(A)	G
1	YA	614	U
1	YA	617	G
1	YA	618	G
1	YA	622	G
1	YA	627	A
1	YA	634	C
1	YA	637	A
1	YA	638	G
1	YA	645	C
1	YA	646	A
1	YA	651	G
1	YA	654	A
1	YA	654(A)	G
1	YA	657	U
1	YA	669	G
1	YA	686	G
1	YA	701	G
1	YA	722	A
1	YA	730	C
1	YA	752	A
1	YA	753	C
1	YA	764	A
1	YA	782	A
1	YA	784	A
1	YA	785	G
1	YA	790	C
1	YA	791	C
1	YA	792	G
1	YA	805	G
1	YA	812	C

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Mol	Chain	Res	Type
1	YA	819	A
1	YA	827	U
1	YA	828	U
1	YA	831	G
1	YA	847	U
1	YA	856	C
1	YA	857	C
1	YA	860	U
1	YA	866	A
1	YA	878	A
1	YA	881	G
1	YA	882	G
1	YA	884	C
1	YA	886	C
1	YA	888	C
1	YA	889	C
1	YA	896	A
1	YA	897	C
1	YA	898	C
1	YA	900	A
1	YA	901	A
1	YA	904	C
1	YA	905	U
1	YA	907	U
1	YA	910	A
1	YA	915	C
1	YA	917	A
1	YA	918	A
1	YA	932	G
1	YA	938	G
1	YA	941	A
1	YA	945	A
1	YA	946	G
1	YA	953	A
1	YA	957	A
1	YA	959	A
1	YA	961	C
1	YA	974	G
1	YA	974(A)	C
1	YA	980	A
1	YA	983	A
1	YA	989	G

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Mol	Chain	Res	Type
1	YA	996	A
1	YA	1011	G
1	YA	1012	U
1	YA	1013	C
1	YA	1015	G
1	YA	1021	A
1	YA	1022	G
1	YA	1023	U
1	YA	1025	G
1	YA	1026	U
1	YA	1027	A
1	YA	1033	U
1	YA	1045	A
1	YA	1046	A
1	YA	1047	G
1	YA	1050	A
1	YA	1051	G
1	YA	1057	A
1	YA	1059	G
1	YA	1060	U
1	YA	1061	U
1	YA	1065	U
1	YA	1066	U
1	YA	1067	A
1	YA	1068	G
1	YA	1070	A
1	YA	1071	G
1	YA	1073	A
1	YA	1076	C
1	YA	1077	A
1	YA	1078	U
1	YA	1082	U
1	YA	1083	U
1	YA	1084	A
1	YA	1085	A
1	YA	1086	A
1	YA	1088	A
1	YA	1093	G
1	YA	1095	A
1	YA	1096	A
1	YA	1097	U
1	YA	1103	A

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Mol	Chain	Res	Type
1	YA	1104	C
1	YA	1105	U
1	YA	1110	G
1	YA	1111	A
1	YA	1122	G
1	YA	1126	A
1	YA	1130	U
1	YA	1131	G
1	YA	1135	C
1	YA	1136	G
1	YA	1142	U
1	YA	1142(A)	A
1	YA	1143	A
1	YA	1168	G
1	YA	1173	G
1	YA	1174	A
1	YA	1175	U
1	YA	1176	G
1	YA	1177	A
1	YA	1179	C
1	YA	1204	A
1	YA	1205	U
1	YA	1211	U
1	YA	1220	A
1	YA	1221	C
1	YA	1238	G
1	YA	1244	G
1	YA	1253	A
1	YA	1256	G
1	YA	1265	A
1	YA	1271	G
1	YA	1272	A
1	YA	1273	U
1	YA	1300	U
1	YA	1301	A
1	YA	1329	U
1	YA	1341	U
1	YA	1345	C
1	YA	1349	A
1	YA	1352	U
1	YA	1365	A
1	YA	1368	G

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Mol	Chain	Res	Type
1	YA	1370	C
1	YA	1379	A
1	YA	1384	A
1	YA	1385	G
1	YA	1395	A
1	YA	1407	C
1	YA	1411	C
1	YA	1416	G
1	YA	1419	A
1	YA	1420	U
1	YA	1421	G
1	YA	1428	C
1	YA	1444(A)	A
1	YA	1445	C
1	YA	1449	A
1	YA	1449(A)	G
1	YA	1455	G
1	YA	1459	G
1	YA	1460	A
1	YA	1461	G
1	YA	1467	C
1	YA	1471	A
1	YA	1478	G
1	YA	1482	U
1	YA	1483	G
1	YA	1485	G
1	YA	1493	C
1	YA	1494	A
1	YA	1497	U
1	YA	1504	C
1	YA	1506	C
1	YA	1507	A
1	YA	1510	A
1	YA	1511	A
1	YA	1515	C
1	YA	1520	U
1	YA	1522	G
1	YA	1533	C
1	YA	1534	G
1	YA	1535	U
1	YA	1536	A
1	YA	1537	C

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Mol	Chain	Res	Type
1	YA	1538	G
1	YA	1540	G
1	YA	1543	A
1	YA	1544	C
1	YA	1545	A
1	YA	1558	A
1	YA	1559	G
1	YA	1566	A
1	YA	1569	A
1	YA	1578	U
1	YA	1585	C
1	YA	1586	A
1	YA	1598	C
1	YA	1607	C
1	YA	1608	A
1	YA	1609	A
1	YA	1610	A
1	YA	1617	C
1	YA	1618	A
1	YA	1640	C
1	YA	1648	C
1	YA	1654	A
1	YA	1674	G
1	YA	1675	C
1	YA	1687	G
1	YA	1693	U
1	YA	1695	G
1	YA	1725	G
1	YA	1728	G
1	YA	1729	A
1	YA	1730	U
1	YA	1731	G
1	YA	1743	G
1	YA	1754	C
1	YA	1756	G
1	YA	1762	A
1	YA	1763	G
1	YA	1764	G
1	YA	1773	A
1	YA	1780	A
1	YA	1787	A
1	YA	1791	A

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Mol	Chain	Res	Type
1	YA	1799	G
1	YA	1800	C
1	YA	1801	G
1	YA	1816	G
1	YA	1835	G
1	YA	1847	A
1	YA	1858	G
1	YA	1869	G
1	YA	1870	C
1	YA	1872	A
1	YA	1878	G
1	YA	1882	C
1	YA	1884	A
1	YA	1885	A
1	YA	1889	A
1	YA	1899	G
1	YA	1903	G
1	YA	1906	G
1	YA	1913	A
1	YA	1914	C
1	YA	1919	A
1	YA	1929	G
1	YA	1930	G
1	YA	1936	A
1	YA	1938	A
1	YA	1939	U
1	YA	1940	U
1	YA	1955	U
1	YA	1960	A
1	YA	1963	U
1	YA	1965	C
1	YA	1967	C
1	YA	1969	A
1	YA	1970	A
1	YA	1971	A
1	YA	1972	A
1	YA	1982	C
1	YA	1992	G
1	YA	1993	U
1	YA	2020	A
1	YA	2021	C
1	YA	2023	G

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Mol	Chain	Res	Type
1	YA	2031	A
1	YA	2033	A
1	YA	2039	C
1	YA	2043	C
1	YA	2051	A
1	YA	2052	G
1	YA	2055	C
1	YA	2056	G
1	YA	2059	A
1	YA	2060	A
1	YA	2061	G
1	YA	2062	A
1	YA	2069	G
1	YA	2093	G
1	YA	2099	U
1	YA	2105	C
1	YA	2111	C
1	YA	2112	G
1	YA	2113	U
1	YA	2114	A
1	YA	2115	G
1	YA	2116	G
1	YA	2118	U
1	YA	2119	A
1	YA	2120	G
1	YA	2122	U
1	YA	2126	A
1	YA	2127	G
1	YA	2128	C
1	YA	2131	G
1	YA	2132	U
1	YA	2136	C
1	YA	2146	C
1	YA	2156	G
1	YA	2158	A
1	YA	2159	G
1	YA	2160	G
1	YA	2166	G
1	YA	2168	G
1	YA	2169	A
1	YA	2173	A
1	YA	2176	A

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Mol	Chain	Res	Type
1	YA	2180	U
1	YA	2187	G
1	YA	2189	U
1	YA	2190	G
1	YA	2192	G
1	YA	2193	G
1	YA	2198	A
1	YA	2210	G
1	YA	2211	G
1	YA	2212	A
1	YA	2213	U
1	YA	2215	G
1	YA	2225	A
1	YA	2238	G
1	YA	2239	G
1	YA	2243	U
1	YA	2246	G
1	YA	2266	A
1	YA	2273	A
1	YA	2275	C
1	YA	2280	G
1	YA	2283	C
1	YA	2287	A
1	YA	2288	A
1	YA	2307	G
1	YA	2308	G
1	YA	2310	A
1	YA	2311	A
1	YA	2320	A
1	YA	2325	G
1	YA	2334	G
1	YA	2342	C
1	YA	2346	A
1	YA	2347	C
1	YA	2350	C
1	YA	2354	G
1	YA	2383	G
1	YA	2385	C
1	YA	2392	A
1	YA	2401	U
1	YA	2402	C
1	YA	2406	U

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Mol	Chain	Res	Type
1	YA	2410	G
1	YA	2423	U
1	YA	2424	C
1	YA	2425	A
1	YA	2429	G
1	YA	2430	A
1	YA	2435	A
1	YA	2439	A
1	YA	2441	C
1	YA	2448	A
1	YA	2450	A
1	YA	2465	C
1	YA	2469	A
1	YA	2470	G
1	YA	2473	U
1	YA	2474	C
1	YA	2475	C
1	YA	2480	C
1	YA	2494	G
1	YA	2502	G
1	YA	2504	U
1	YA	2505	G
1	YA	2518	A
1	YA	2525	G
1	YA	2529	G
1	YA	2542	A
1	YA	2554	U
1	YA	2567	G
1	YA	2573	C
1	YA	2578	G
1	YA	2585	U
1	YA	2586	C
1	YA	2602	A
1	YA	2609	U
1	YA	2611	U
1	YA	2612	C
1	YA	2615	U
1	YA	2629	A
1	YA	2654	A
1	YA	2655	G
1	YA	2665	A
1	YA	2666	C

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Mol	Chain	Res	Type
1	YA	2673	G
1	YA	2675	A
1	YA	2682	U
1	YA	2689	U
1	YA	2702	U
1	YA	2707	G
1	YA	2712	U
1	YA	2712(A)	A
1	YA	2713	A
1	YA	2714	G
1	YA	2726	U
1	YA	2733	A
1	YA	2739	U
1	YA	2744	G
1	YA	2751	G
1	YA	2757	A
1	YA	2758	A
1	YA	2762	G
1	YA	2764	A
1	YA	2765	A
1	YA	2766	G
1	YA	2777	G
1	YA	2778	A
1	YA	2779	U
1	YA	2789	C
1	YA	2790	A
1	YA	2791	C
1	YA	2797	U
1	YA	2798	C
1	YA	2808	U
1	YA	2820	A
1	YA	2821	A
1	YA	2833	G
1	YA	2834	G
1	YA	2867	G
1	YA	2868	A
1	YA	2872	G
1	YA	2880	C
1	YA	2891	G
1	YA	2892	A
1	YA	2893	G
1	YA	2894	G

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Mol	Chain	Res	Type
2	YB	7	G
2	YB	8	U
2	YB	9	G
2	YB	12	C
2	YB	13	A
2	YB	15	A
2	YB	16	G
2	YB	19	G
2	YB	21	G
2	YB	25	A
2	YB	31	C
2	YB	41	U
2	YB	42	C
2	YB	44	G
2	YB	45	A
2	YB	52	A
2	YB	56	G
2	YB	67	G
2	YB	73	A
2	YB	81	G
2	YB	82	G
2	YB	108	C
2	YB	109	G
32	XA	6	G
32	XA	32	A
32	XA	39	G
32	XA	48	C
32	XA	51	A
32	XA	59	A
32	XA	61	G
32	XA	64	G
32	XA	65	U
32	XA	66	G
32	XA	79	G
32	XA	89	U
32	XA	92	G
32	XA	95	G
32	XA	101	A
32	XA	108	G
32	XA	116	A
32	XA	120	A
32	XA	121	C

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Mol	Chain	Res	Type
32	XA	130	A
32	XA	144	G
32	XA	163	C
32	XA	169	C
32	XA	172	A
32	XA	174	C
32	XA	188	U
32	XA	190	G
32	XA	195	A
32	XA	197	A
32	XA	209	U
32	XA	210	U
32	XA	231	G
32	XA	244	U
32	XA	245	C
32	XA	247	G
32	XA	251	G
32	XA	267	C
32	XA	281	G
32	XA	289	G
32	XA	298	A
32	XA	306	G
32	XA	321	A
32	XA	328	C
32	XA	329	A
32	XA	332	G
32	XA	344	A
32	XA	345	C
32	XA	347	G
32	XA	348	G
32	XA	351	G
32	XA	352	C
32	XA	353	A
32	XA	354	G
32	XA	356	A
32	XA	367	U
32	XA	372	C
32	XA	389	A
32	XA	397	A
32	XA	398	C
32	XA	411	A
32	XA	412	A

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Mol	Chain	Res	Type
32	XA	413	G
32	XA	414	A
32	XA	421	U
32	XA	422	C
32	XA	423	G
32	XA	424	G
32	XA	429	U
32	XA	430	A
32	XA	435	C
32	XA	438	G
32	XA	439	A
32	XA	465	A
32	XA	466	C
32	XA	467	G
32	XA	482	A
32	XA	484	G
32	XA	485	G
32	XA	486	U
32	XA	496	A
32	XA	497	U
32	XA	509	A
32	XA	510	A
32	XA	511	C
32	XA	518	C
32	XA	519	C
32	XA	527	G
32	XA	531	U
32	XA	532	A
32	XA	533	A
32	XA	547	A
32	XA	548	G
32	XA	559	A
32	XA	561	U
32	XA	564	C
32	XA	568	G
32	XA	572	A
32	XA	573	A
32	XA	576	G
32	XA	577	G
32	XA	579	G
32	XA	618	C
32	XA	630	G

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Mol	Chain	Res	Type
32	XA	631	G
32	XA	632	A
32	XA	633	G
32	XA	653	A
32	XA	657	G
32	XA	665	A
32	XA	686	U
32	XA	688	G
32	XA	703	G
32	XA	704	A
32	XA	721	G
32	XA	723	U
32	XA	731	G
32	XA	734	G
32	XA	749	C
32	XA	753	A
32	XA	754	C
32	XA	755	G
32	XA	777	A
32	XA	792	A
32	XA	793	U
32	XA	794	A
32	XA	799	G
32	XA	816	A
32	XA	817	C
32	XA	821	G
32	XA	828	A
32	XA	841	U
32	XA	842	C
32	XA	843	U
32	XA	848	C
32	XA	855	G
32	XA	859	A
32	XA	870	U
32	XA	871	U
32	XA	872	A
32	XA	902	G
32	XA	914	A
32	XA	926	G
32	XA	927	G
32	XA	934	C
32	XA	935	A

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Mol	Chain	Res	Type
32	XA	960	U
32	XA	966	G
32	XA	968	A
32	XA	969	A
32	XA	972	C
32	XA	974	A
32	XA	975	A
32	XA	976	G
32	XA	977	A
32	XA	981	U
32	XA	982	U
32	XA	991	U
32	XA	992	U
32	XA	993	G
32	XA	1004	A
32	XA	1006	C
32	XA	1009	G
32	XA	1024	G
32	XA	1025	U
32	XA	1028	C
32	XA	1028(A)	C
32	XA	1029	G
32	XA	1030	C
32	XA	1031	G
32	XA	1032	A
32	XA	1032(A)	G
32	XA	1038	C
32	XA	1039	C
32	XA	1040	U
32	XA	1042	G
32	XA	1053	G
32	XA	1054	C
32	XA	1064	G
32	XA	1066	C
32	XA	1081	G
32	XA	1094	G
32	XA	1101	A
32	XA	1108	G
32	XA	1124	G
32	XA	1125	U
32	XA	1126	U
32	XA	1127	G

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Mol	Chain	Res	Type
32	XA	1129	C
32	XA	1130	A
32	XA	1136	U
32	XA	1137	C
32	XA	1138	G
32	XA	1139	G
32	XA	1145	C
32	XA	1146	A
32	XA	1157	A
32	XA	1158	C
32	XA	1159	U
32	XA	1160	G
32	XA	1162	C
32	XA	1176	A
32	XA	1177	G
32	XA	1181	G
32	XA	1183	A
32	XA	1196	U
32	XA	1212	U
32	XA	1224	G
32	XA	1225	A
32	XA	1226	C
32	XA	1236	A
32	XA	1238	A
32	XA	1240	U
32	XA	1241	G
32	XA	1256	A
32	XA	1257	U
32	XA	1258	G
32	XA	1260	C
32	XA	1263	C
32	XA	1270	C
32	XA	1273	G
32	XA	1278	U
32	XA	1280	A
32	XA	1281	U
32	XA	1286	A
32	XA	1287	A
32	XA	1290	G
32	XA	1298	C
32	XA	1300	G
32	XA	1301	U

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Mol	Chain	Res	Type
32	XA	1302	U
32	XA	1303	C
32	XA	1305	G
32	XA	1310	G
32	XA	1311	G
32	XA	1320	C
32	XA	1322	C
32	XA	1323	G
32	XA	1331	G
32	XA	1332	A
32	XA	1335	C
32	XA	1336	C
32	XA	1347	G
32	XA	1348	U
32	XA	1357	A
32	XA	1362(A)	C
32	XA	1364	U
32	XA	1378	C
32	XA	1399	C
32	XA	1419	G
32	XA	1442	G
32	XA	1446	A
32	XA	1447	G
32	XA	1452	C
32	XA	1453	G
32	XA	1454	G
32	XA	1487	G
32	XA	1492	A
32	XA	1493	A
32	XA	1497	G
32	XA	1499	A
32	XA	1502	A
32	XA	1503	A
32	XA	1504	G
32	XA	1506	U
32	XA	1517	G
32	XA	1520	G
32	XA	1529	G
32	XA	1530	G
32	XA	1532	U
32	XA	1533	C
32	XA	1534	A

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Mol	Chain	Res	Type
32	XA	1536	C
32	XA	1537	U
32	XA	1538	C
32	XA	1539	C
32	XA	1541	U
32	XA	1542	U
54	XX	2	G
54	XX	7	G
54	XX	10	G
54	XX	11	U
54	XX	12	A
54	XX	13	A
54	XX	14	A
54	XX	15	A
54	XX	19	U

All (152) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	RA	74	A
1	RA	99	U
1	RA	221	A
1	RA	222	A
1	RA	229	A
1	RA	271(B)	G
1	RA	345	A
1	RA	372	G
1	RA	404	C
1	RA	503	A
1	RA	508	G
1	RA	512	G
1	RA	587	C
1	RA	637	A
1	RA	752	A
1	RA	846	C
1	RA	856	C
1	RA	1022	G
1	RA	1053	C
1	RA	1057	A
1	RA	1065	U
1	RA	1067	A
1	RA	1073	A

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Mol	Chain	Res	Type
1	RA	1204	A
1	RA	1210	A
1	RA	1312	U
1	RA	1427	A
1	RA	1508	A
1	RA	1558	A
1	RA	1653	G
1	RA	1819	A
1	RA	1992	G
1	RA	2060	A
1	RA	2126	A
1	RA	2439	A
1	RA	2566	A
1	RA	2610	C
1	RA	2689	U
1	RA	2756	U
1	RA	2832	U
1	RA	2867	G
2	RB	66	A
32	QA	5	U
32	QA	64	G
32	QA	115	G
32	QA	119	A
32	QA	181	G
32	QA	243	A
32	QA	244	U
32	QA	250	A
32	QA	266	G
32	QA	328	C
32	QA	410	G
32	QA	412	A
32	QA	428	G
32	QA	429	U
32	QA	481	G
32	QA	484	G
32	QA	485	G
32	QA	509	A
32	QA	687	A
32	QA	703	G
32	QA	753	A
32	QA	792	A
32	QA	812	C

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Mol	Chain	Res	Type
32	QA	913	A
32	QA	960	U
32	QA	992	U
32	QA	1065	U
32	QA	1200	C
32	QA	1201	A
32	QA	1285	A
32	QA	1297	C
32	QA	1336	C
32	QA	1346	A
32	QA	1347	G
32	QA	1446	A
32	QA	1498	U
32	QA	1528	U
54	QX	13	A
1	YA	99	U
1	YA	196	A
1	YA	221	A
1	YA	229	A
1	YA	242	G
1	YA	271(B)	G
1	YA	278	A
1	YA	404	C
1	YA	503	A
1	YA	508	G
1	YA	637	A
1	YA	752	A
1	YA	846	C
1	YA	856	C
1	YA	859	G
1	YA	1012	U
1	YA	1022	G
1	YA	1026	U
1	YA	1085	A
1	YA	1109	C
1	YA	1130	U
1	YA	1178	C
1	YA	1204	A
1	YA	1210	A
1	YA	1427	A
1	YA	1460	A
1	YA	1558	A

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Mol	Chain	Res	Type
1	YA	1653	G
1	YA	1694	C
1	YA	1799	G
1	YA	1913	A
1	YA	1992	G
1	YA	2406	U
1	YA	2566	A
1	YA	2681	C
1	YA	2712	U
1	YA	2756	U
1	YA	2776	A
1	YA	2832	U
1	YA	2867	G
2	YB	24	G
2	YB	66	A
32	XA	60	A
32	XA	78	G
32	XA	115	G
32	XA	243	A
32	XA	244	U
32	XA	250	A
32	XA	266	G
32	XA	328	C
32	XA	388	G
32	XA	410	G
32	XA	412	A
32	XA	429	U
32	XA	481	G
32	XA	484	G
32	XA	485	G
32	XA	509	A
32	XA	560	U
32	XA	687	A
32	XA	703	G
32	XA	753	A
32	XA	913	A
32	XA	992	U
32	XA	1027	C
32	XA	1285	A
32	XA	1297	C
32	XA	1310	G
32	XA	1446	A

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Mol	Chain	Res	Type
32	XA	1498	U
32	XA	1537	U
54	XX	12	A

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
53	1MG	QV	37	53	23,26,27	1.15	3 (13%)	33,39,42	1.73	5 (15%)
53	1MG	XV	37	53	23,26,27	1.15	2 (8%)	33,39,42	1.79	5 (15%)

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
53	1MG	QV	37	53	-	0/7/25/26	0/3/3/3
53	1MG	XV	37	53	-	0/7/25/26	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	QV	37	1MG	C5-C4	3.06	1.47	1.38
53	XV	37	1MG	C5-C4	3.00	1.47	1.38
53	XV	37	1MG	C5-N7	-2.48	1.34	1.39
53	QV	37	1MG	C5-N7	-2.31	1.34	1.39
53	QV	37	1MG	C2-N1	2.07	1.41	1.37

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	XV	37	1MG	C5-C4-N3	-6.01	118.83	128.39
53	QV	37	1MG	C5-C4-N3	-5.46	119.71	128.39
53	XV	37	1MG	N9-C4-N3	4.53	135.00	125.95
53	XV	37	1MG	C2-N3-C4	4.52	122.14	111.98
53	QV	37	1MG	N9-C4-N3	4.12	134.19	125.95
53	QV	37	1MG	C2-N3-C4	4.12	121.23	111.98
53	QV	37	1MG	C4-C5-N7	-2.73	106.35	110.67
53	XV	37	1MG	C4-C5-N7	-2.54	106.64	110.67
53	QV	37	1MG	C6-C5-N7	2.48	134.88	129.36
53	XV	37	1MG	C6-C5-N7	2.28	134.42	129.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1213 ligands modelled in this entry, 1211 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	$\# Z > 2$
57	SF4	XD	301	35	0,12,12	-	-	-		
57	SF4	QD	301	35	0,12,12	-	-	-		

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
57	SF4	XD	301	35	-	-	0/6/5/5
57	SF4	QD	301	35	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	XD	301	SF4	3	0
57	QD	301	SF4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	RA	2881/2915 (98%)	0.00	99 (3%) 48 35	42, 74, 214, 568	0
1	YA	2883/2915 (98%)	-0.14	78 (2%) 56 42	29, 52, 212, 440	0
2	RB	120/122 (98%)	0.26	2 (1%) 69 54	79, 127, 167, 200	0
2	YB	120/122 (98%)	-0.15	1 (0%) 82 71	51, 77, 104, 135	0
3	RD	272/276 (98%)	0.29	5 (1%) 67 53	41, 65, 98, 124	0
3	YD	273/276 (98%)	0.12	1 (0%) 88 81	32, 52, 78, 104	0
4	RE	204/206 (99%)	0.14	2 (0%) 79 66	40, 70, 108, 132	0
4	YE	205/206 (99%)	0.38	13 (6%) 26 20	31, 56, 103, 184	0
5	RF	202/210 (96%)	0.41	5 (2%) 58 43	43, 81, 139, 181	0
5	YF	202/210 (96%)	0.49	12 (5%) 28 22	26, 57, 122, 164	0
6	RG	181/182 (99%)	1.37	42 (23%) 2 3	108, 165, 236, 297	0
6	YG	181/182 (99%)	0.93	16 (8%) 15 14	77, 119, 184, 221	0
7	RH	174/180 (96%)	1.31	34 (19%) 3 4	91, 130, 171, 232	0
7	YH	174/180 (96%)	0.20	8 (4%) 37 27	38, 69, 100, 122	0
8	RI	146/148 (98%)	1.17	30 (20%) 2 4	63, 121, 154, 186	0
8	YI	146/148 (98%)	0.75	18 (12%) 8 9	59, 103, 141, 161	0
9	RN	138/140 (98%)	0.63	5 (3%) 46 33	50, 81, 123, 160	0
9	YN	140/140 (100%)	0.33	4 (2%) 53 39	37, 55, 95, 146	0
10	RO	122/122 (100%)	0.23	3 (2%) 58 43	46, 72, 105, 123	0
10	YO	122/122 (100%)	0.16	0 100 100	36, 58, 92, 109	0
11	RP	148/150 (98%)	0.80	13 (8%) 15 14	49, 91, 132, 176	0
11	YP	147/150 (98%)	0.39	4 (2%) 56 42	29, 60, 96, 129	0
12	RQ	141/141 (100%)	0.78	21 (14%) 5 7	59, 90, 135, 232	0
12	YQ	141/141 (100%)	0.35	10 (7%) 22 18	40, 60, 90, 128	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	RR	118/118 (100%)	0.47	4 (3%) 48 35	44, 71, 102, 124	0
13	YR	117/118 (99%)	0.36	4 (3%) 48 35	33, 54, 78, 122	0
14	RS	111/112 (99%)	0.98	15 (13%) 7 8	97, 120, 175, 207	0
14	YS	110/112 (98%)	0.41	9 (8%) 17 16	51, 77, 105, 118	0
15	RT	137/146 (93%)	0.42	9 (6%) 24 19	52, 79, 139, 185	0
15	YT	137/146 (93%)	0.32	5 (3%) 46 33	36, 63, 122, 178	0
16	RU	117/118 (99%)	0.74	12 (10%) 12 12	45, 79, 129, 241	0
16	YU	117/118 (99%)	0.43	5 (4%) 40 29	29, 47, 91, 196	0
17	RV	101/101 (100%)	0.33	1 (0%) 79 66	58, 96, 129, 140	0
17	YV	101/101 (100%)	0.15	6 (5%) 28 22	31, 57, 91, 175	0
18	RW	113/113 (100%)	0.32	5 (4%) 39 28	42, 63, 103, 213	0
18	YW	113/113 (100%)	0.14	4 (3%) 47 34	33, 47, 83, 195	0
19	RX	92/96 (95%)	0.44	3 (3%) 49 36	54, 80, 111, 135	0
19	YX	94/96 (97%)	0.24	3 (3%) 50 37	35, 54, 92, 123	0
20	RY	107/110 (97%)	0.73	8 (7%) 20 17	67, 94, 130, 157	0
20	YY	107/110 (97%)	0.40	5 (4%) 36 27	42, 67, 103, 137	0
21	RZ	203/206 (98%)	0.80	16 (7%) 18 16	88, 123, 159, 219	0
21	YZ	201/206 (97%)	0.16	4 (1%) 65 49	51, 84, 126, 143	0
22	R0	76/85 (89%)	0.80	8 (10%) 11 12	66, 86, 108, 129	0
22	Y0	75/85 (88%)	0.28	2 (2%) 56 42	35, 60, 84, 93	0
23	R1	97/98 (98%)	0.84	10 (10%) 12 12	51, 77, 134, 245	0
23	Y1	93/98 (94%)	0.32	2 (2%) 62 47	35, 60, 93, 117	0
24	R2	69/72 (95%)	0.91	7 (10%) 12 12	59, 96, 143, 158	0
24	Y2	72/72 (100%)	0.54	6 (8%) 17 15	35, 61, 112, 216	0
25	R3	59/60 (98%)	0.22	2 (3%) 48 35	53, 83, 134, 175	0
25	Y3	59/60 (98%)	0.21	0 100 100	32, 57, 102, 150	0
26	R4	69/71 (97%)	0.92	5 (7%) 21 18	131, 200, 263, 278	0
26	Y4	69/71 (97%)	0.88	7 (10%) 12 12	110, 173, 242, 272	0
27	R5	59/60 (98%)	0.43	2 (3%) 48 35	42, 61, 104, 135	0
27	Y5	59/60 (98%)	0.14	1 (1%) 69 54	34, 51, 91, 147	0
28	R6	53/54 (98%)	0.15	3 (5%) 29 22	66, 87, 115, 184	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	Y6	53/54 (98%)	0.19	0 100 100	52, 65, 88, 102	0
29	R7	47/49 (95%)	0.41	2 (4%) 40 29	40, 59, 89, 106	0
29	Y7	48/49 (97%)	0.29	1 (2%) 63 48	32, 45, 78, 125	0
30	R8	64/65 (98%)	1.39	16 (25%) 2 3	59, 81, 119, 190	0
30	Y8	64/65 (98%)	0.47	3 (4%) 36 27	40, 54, 85, 115	0
31	R9	36/37 (97%)	0.98	4 (11%) 10 11	77, 99, 123, 160	0
31	Y9	37/37 (100%)	0.52	3 (8%) 18 16	50, 68, 100, 155	0
32	QA	1511/1521 (99%)	0.41	111 (7%) 21 18	62, 108, 271, 392	0
32	XA	1511/1521 (99%)	0.45	99 (6%) 24 19	51, 119, 271, 367	0
33	QB	235/256 (91%)	0.96	24 (10%) 12 12	100, 141, 197, 229	0
33	XB	236/256 (92%)	1.15	39 (16%) 4 6	99, 142, 187, 221	0
34	QC	205/239 (85%)	1.15	38 (18%) 3 4	115, 160, 216, 243	0
34	XC	205/239 (85%)	1.17	37 (18%) 3 5	116, 167, 212, 242	0
35	QD	208/209 (99%)	0.73	18 (8%) 16 14	77, 106, 139, 163	0
35	XD	208/209 (99%)	0.95	31 (14%) 5 7	81, 118, 164, 191	0
36	QE	151/162 (93%)	0.54	10 (6%) 24 19	75, 104, 142, 174	0
36	XE	151/162 (93%)	0.53	11 (7%) 21 18	65, 105, 142, 200	0
37	QF	101/101 (100%)	0.41	3 (2%) 52 39	74, 109, 145, 189	0
37	XF	101/101 (100%)	0.62	9 (8%) 15 14	76, 106, 142, 180	0
38	QG	155/156 (99%)	1.14	27 (17%) 4 5	127, 176, 231, 274	0
38	XG	155/156 (99%)	1.14	24 (15%) 5 7	120, 164, 209, 253	0
39	QH	137/138 (99%)	0.57	14 (10%) 12 12	71, 107, 137, 154	0
39	XH	137/138 (99%)	0.63	9 (6%) 24 19	76, 110, 142, 179	0
40	QI	127/128 (99%)	1.63	44 (34%) 1 1	124, 195, 235, 268	0
40	XI	126/128 (98%)	1.50	34 (26%) 1 2	123, 184, 231, 253	0
41	QJ	99/105 (94%)	1.81	29 (29%) 1 2	161, 191, 229, 260	0
41	XJ	96/105 (91%)	1.60	27 (28%) 1 2	162, 186, 228, 245	0
42	QK	116/129 (89%)	0.60	10 (8%) 16 15	67, 117, 152, 189	0
42	XK	116/129 (89%)	0.54	1 (0%) 81 68	69, 106, 141, 194	0
43	QL	125/132 (94%)	0.51	8 (6%) 25 20	63, 89, 130, 209	0
43	XL	122/132 (92%)	1.00	17 (13%) 6 8	69, 94, 123, 166	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	QM	120/126 (95%)	1.38	28 (23%) 2 3	134, 196, 241, 277	0
44	XM	119/126 (94%)	1.53	31 (26%) 1 3	136, 193, 260, 292	0
45	QN	60/61 (98%)	2.03	28 (46%) 0 1	137, 169, 213, 260	0
45	XN	60/61 (98%)	1.62	19 (31%) 1 1	133, 173, 216, 242	0
46	QO	88/89 (98%)	0.65	7 (7%) 18 16	59, 103, 138, 165	0
46	XO	87/89 (97%)	0.51	1 (1%) 78 65	65, 95, 136, 162	0
47	QP	84/88 (95%)	0.99	11 (13%) 7 8	75, 101, 140, 169	0
47	XP	84/88 (95%)	1.15	12 (14%) 6 8	78, 121, 165, 184	0
48	QQ	100/105 (95%)	0.46	3 (3%) 52 39	69, 94, 119, 171	0
48	XQ	100/105 (95%)	0.49	4 (4%) 42 30	65, 99, 138, 144	0
49	QR	70/88 (79%)	0.80	9 (12%) 7 9	68, 106, 143, 157	0
49	XR	70/88 (79%)	0.35	1 (1%) 73 59	68, 102, 140, 159	0
50	QS	83/93 (89%)	1.39	19 (22%) 2 4	165, 199, 249, 272	0
50	XS	84/93 (90%)	1.62	27 (32%) 1 1	152, 199, 239, 260	0
51	QT	99/106 (93%)	0.65	4 (4%) 42 30	68, 93, 150, 184	0
51	XT	99/106 (93%)	0.98	16 (16%) 4 6	82, 113, 165, 174	0
52	QU	25/27 (92%)	2.27	13 (52%) 0 0	135, 157, 199, 211	0
52	XU	25/27 (92%)	2.22	12 (48%) 0 1	128, 175, 233, 253	0
53	QV	16/17 (94%)	0.79	2 (12%) 8 9	177, 204, 219, 223	0
53	XV	14/17 (82%)	0.83	0 100 100	176, 181, 204, 205	0
54	QX	18/19 (94%)	2.15	8 (44%) 0 1	136, 267, 324, 335	0
54	XX	19/19 (100%)	2.21	11 (57%) 0 0	125, 256, 314, 321	0
All	All	20775/21316 (97%)	0.45	1568 (7%) 20 17	26, 89, 218, 568	0

All (1568) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	YA	2602	A	9.4
41	QJ	48	THR	8.5
41	QJ	62	HIS	8.1
12	YQ	112	GLU	8.0
6	RG	137	GLU	7.8
44	QM	121	LYS	7.6
6	RG	135	LEU	7.5

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Mol	Chain	Res	Type	RSRZ
7	RH	155	SER	7.4
43	XL	89	ARG	7.3
41	QJ	47	PHE	7.3
36	XE	24	ARG	7.3
44	QM	7	VAL	7.2
7	RH	166	GLY	7.2
6	YG	137	GLU	7.1
1	RA	2134	A	7.1
51	XT	18	GLN	7.0
7	RH	169	VAL	6.9
40	QI	115	GLY	6.9
8	RI	20	ASP	6.7
41	QJ	46	ARG	6.6
34	XC	158	GLY	6.5
44	QM	120	LYS	6.4
44	QM	119	GLY	6.3
1	RA	2175	C	6.3
52	QU	2	GLY	6.3
33	XB	195	ASP	6.2
50	XS	71	LEU	6.2
15	RT	106	SER	6.2
52	XU	14	TRP	6.1
34	QC	158	GLY	6.1
41	XJ	98	ILE	6.0
7	RH	152	ARG	6.0
9	YN	68	GLU	5.9
44	XM	102	ARG	5.9
32	XA	1286	A	5.9
24	R2	8	LYS	5.9
40	QI	128	ARG	5.8
6	RG	62	LEU	5.8
32	QA	1353	G	5.8
36	XE	21	ALA	5.7
35	QD	50	ARG	5.6
7	RH	170	ARG	5.6
1	RA	2159	G	5.6
32	XA	1212	U	5.5
6	YG	26	GLN	5.5
8	YI	1	MET	5.4
11	RP	65	ARG	5.4
1	RA	229	A	5.4
1	RA	2130	U	5.4

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Mol	Chain	Res	Type	RSRZ
32	XA	1451	A	5.4
8	YI	117	GLU	5.3
30	R8	65	GLU	5.3
1	YA	2112	G	5.3
8	RI	117	GLU	5.3
1	YA	2113	U	5.2
1	RA	2104	G	5.2
12	RQ	141	GLN	5.2
24	Y2	11	GLU	5.2
41	XJ	100	THR	5.2
45	XN	2	ALA	5.2
33	XB	27	LYS	5.2
16	RU	97	ASP	5.2
32	QA	1092	A	5.1
38	XG	42	ILE	5.1
1	RA	2602	A	5.1
1	YA	2141	G	5.1
44	XM	7	VAL	5.0
50	XS	56	GLN	5.0
38	QG	38	LEU	5.0
14	RS	2	ALA	5.0
35	QD	163	GLU	5.0
40	QI	64	THR	5.0
42	QK	126	ARG	5.0
45	QN	2	ALA	5.0
16	YU	118	GLY	5.0
35	XD	77	ASN	4.9
40	XI	102	LEU	4.9
32	QA	1116	C	4.9
8	RI	12	LEU	4.9
38	XG	16	LEU	4.9
15	RT	104	ASN	4.9
41	XJ	48	THR	4.9
41	XJ	47	PHE	4.9
17	YV	48	GLY	4.9
24	Y2	12	GLU	4.9
40	QI	123	PRO	4.9
40	XI	81	ILE	4.9
7	RH	168	PRO	4.9
44	XM	107	ALA	4.9
1	YA	2142	C	4.9
40	QI	125	TYR	4.9

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Mol	Chain	Res	Type	RSRZ
45	QN	56	VAL	4.8
40	XI	12	GLU	4.8
32	QA	1235	U	4.8
1	RA	2160	G	4.8
6	RG	133	LEU	4.8
47	XP	29	ASP	4.8
38	QG	27	ILE	4.8
1	RA	2129	C	4.8
35	XD	130	GLY	4.8
32	QA	1224	G	4.8
32	QA	1234	C	4.7
1	RA	1046	A	4.7
38	QG	79	ARG	4.7
15	RT	112	ARG	4.7
6	RG	136	ARG	4.6
45	QN	35	ARG	4.6
1	RA	614	U	4.6
1	RA	1070	A	4.6
6	RG	145	THR	4.6
40	QI	77	ILE	4.6
50	QS	15	LEU	4.6
1	RA	2165	G	4.6
52	QU	14	TRP	4.6
6	RG	90	LEU	4.6
44	XM	2	ALA	4.6
1	RA	1764	G	4.6
11	RP	61	ARG	4.6
21	RZ	165	VAL	4.5
30	R8	64	TYR	4.5
44	XM	4	ILE	4.5
8	RI	10	GLU	4.5
43	XL	27	LEU	4.5
8	RI	84	GLY	4.5
23	R1	98	LEU	4.5
32	QA	1364	U	4.5
50	QS	69	HIS	4.5
6	RG	139	LEU	4.5
35	QD	56	VAL	4.5
34	QC	91	LEU	4.5
16	YU	117	GLN	4.5
6	YG	139	LEU	4.4
36	XE	23	GLY	4.4

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Mol	Chain	Res	Type	RSRZ
7	RH	4	ILE	4.4
33	XB	31	TYR	4.4
8	YI	118	LYS	4.4
41	QJ	58	ASP	4.4
12	YQ	21	THR	4.4
40	XI	105	ASP	4.4
4	YE	204	ALA	4.3
39	QH	2	LEU	4.3
6	RG	138	GLN	4.3
1	YA	1536	A	4.3
38	QG	84	ASN	4.3
5	YF	198	ALA	4.3
44	QM	96	LEU	4.3
32	QA	1533	C	4.3
40	XI	14	VAL	4.3
37	XF	54	LYS	4.3
38	QG	82	GLY	4.3
52	QU	4	GLY	4.3
1	RA	2106	G	4.3
1	YA	2116	G	4.2
38	XG	38	LEU	4.2
6	RG	28	VAL	4.2
33	XB	227	GLY	4.2
44	XM	106	ASN	4.2
34	XC	164	ARG	4.2
40	XI	15	ALA	4.2
42	QK	127	LYS	4.2
44	XM	31	LYS	4.2
47	XP	34	GLU	4.2
44	QM	17	VAL	4.2
1	RA	1763	G	4.2
50	XS	74	PHE	4.2
31	Y9	37	GLY	4.2
45	XN	17	LYS	4.2
41	QJ	34	VAL	4.2
8	RI	11	ASN	4.2
32	QA	89	U	4.2
47	XP	68	ASP	4.2
54	QX	5	A	4.2
1	RA	2174	C	4.2
32	QA	1149	C	4.2
50	QS	79	THR	4.2

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Mol	Chain	Res	Type	RSRZ
41	QJ	66	ARG	4.2
30	R8	62	LEU	4.1
6	RG	155	MET	4.1
8	RI	14	ASP	4.1
50	XS	57	HIS	4.1
51	QT	73	HIS	4.1
32	QA	1352	C	4.1
8	YI	122	GLU	4.1
54	XX	1	G	4.1
52	QU	5	ASP	4.1
44	XM	6	GLY	4.1
1	RA	2109	U	4.1
32	QA	975	A	4.1
40	QI	62	TYR	4.1
32	QA	82	U	4.1
26	R4	27	THR	4.1
49	QR	47	THR	4.1
1	RA	2133	G	4.1
52	QU	11	GLY	4.1
7	RH	7	LEU	4.0
20	RY	1	MET	4.0
29	R7	47	ARG	4.0
41	QJ	65	LEU	4.0
51	XT	73	HIS	4.0
7	YH	175	LYS	4.0
41	XJ	55	LYS	4.0
6	RG	146	TYR	4.0
7	YH	170	ARG	4.0
44	QM	97	PRO	4.0
38	QG	81	GLY	4.0
7	RH	8	PRO	4.0
32	QA	312	C	4.0
33	XB	12	GLU	4.0
8	RI	16	GLY	4.0
20	RY	41	GLY	4.0
33	XB	30	ARG	3.9
35	XD	73	ARG	3.9
32	XA	1453	G	3.9
43	XL	16	GLU	3.9
32	QA	974	A	3.9
32	QA	1115	C	3.9
24	R2	7	ARG	3.9

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Mol	Chain	Res	Type	RSRZ
47	XP	1	MET	3.9
1	RA	2135	A	3.9
38	QG	32	ARG	3.9
39	XH	58	TYR	3.9
39	XH	93	VAL	3.9
36	XE	18	ARG	3.9
1	RA	34	C	3.9
5	YF	131	GLY	3.9
45	QN	55	GLY	3.9
45	XN	15	LYS	3.9
20	YY	91	GLU	3.8
44	QM	62	ASN	3.8
1	YA	11	G	3.8
1	YA	614	U	3.8
14	RS	52	SER	3.8
50	XS	10	PHE	3.8
8	RI	2	LYS	3.8
51	XT	12	ALA	3.8
1	RA	2108	C	3.8
1	YA	1092	C	3.8
20	YY	63	LYS	3.8
36	QE	11	ILE	3.8
8	RI	17	GLN	3.8
42	QK	89	ALA	3.8
44	XM	16	ASP	3.8
43	XL	91	LYS	3.8
32	QA	1367	C	3.8
34	QC	159	GLY	3.8
40	QI	74	ILE	3.8
7	RH	125	VAL	3.8
41	XJ	59	SER	3.8
38	QG	33	ASP	3.8
41	QJ	63	PHE	3.8
2	YB	1	U	3.8
1	RA	1091	G	3.7
6	RG	157	ILE	3.7
24	R2	11	GLU	3.7
4	YE	205	ALA	3.7
34	XC	169	ALA	3.7
45	QN	25	VAL	3.7
13	YR	7	GLY	3.7
1	RA	2110	G	3.7

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Mol	Chain	Res	Type	RSRZ
26	Y4	52	THR	3.7
1	RA	161	U	3.7
16	RU	118	GLY	3.7
44	XM	32	GLU	3.7
7	RH	150	ALA	3.7
50	XS	9	VAL	3.7
7	RH	111	HIS	3.7
32	XA	524	G	3.7
34	XC	167	TRP	3.7
31	R9	21	GLY	3.7
12	RQ	140	ALA	3.7
1	YA	277	C	3.7
1	YA	2143	C	3.7
18	YW	113	LYS	3.7
1	RA	2120	G	3.6
18	RW	93	ALA	3.6
32	XA	108	G	3.6
34	QC	188	LEU	3.6
40	XI	47	LEU	3.6
9	RN	84	LYS	3.6
45	QN	15	LYS	3.6
33	QB	137	ARG	3.6
1	YA	2107	C	3.6
44	XM	15	VAL	3.6
16	RU	91	ASP	3.6
34	XC	159	GLY	3.6
44	QM	6	GLY	3.6
45	QN	23	ARG	3.6
32	QA	1349	A	3.6
33	XB	154	LEU	3.6
50	XS	4	SER	3.6
36	QE	20	GLN	3.6
12	RQ	104	PHE	3.6
26	Y4	4	GLY	3.6
34	QC	172	ARG	3.6
8	RI	122	GLU	3.6
34	XC	35	GLU	3.6
33	XB	70	PHE	3.5
6	RG	65	GLY	3.5
6	RG	134	GLY	3.5
20	RY	22	GLY	3.5
41	QJ	57	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
6	RG	152	LEU	3.5
52	XU	18	TYR	3.5
1	YA	1420	U	3.5
44	QM	102	ARG	3.5
14	YS	12	PHE	3.5
42	QK	125	PHE	3.5
51	XT	11	SER	3.5
35	XD	74	GLN	3.5
38	QG	35	LYS	3.5
44	QM	5	ALA	3.5
32	QA	1286	A	3.5
1	RA	615	G	3.5
53	QV	35	G	3.5
32	QA	824	C	3.5
35	XD	80	GLU	3.5
34	XC	184	TYR	3.5
9	YN	61	ARG	3.5
44	XM	103	THR	3.5
11	RP	109	GLY	3.5
14	YS	76	LYS	3.5
33	XB	188	ALA	3.5
40	QI	81	ILE	3.5
1	RA	2119	A	3.5
32	QA	1288	A	3.5
38	QG	37	ASN	3.5
1	RA	2105	C	3.5
19	RX	33	LYS	3.5
37	XF	83	ASP	3.5
51	XT	80	ARG	3.5
52	XU	3	LYS	3.5
12	YQ	33	GLY	3.5
32	XA	1288	A	3.5
54	XX	4	A	3.5
51	XT	16	HIS	3.5
10	RO	81	ASP	3.5
1	RA	2156	G	3.5
1	YA	615	G	3.5
32	XA	111	G	3.5
41	XJ	60	ARG	3.5
48	XQ	24	GLU	3.4
18	YW	91	GLY	3.4
45	QN	6	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
7	RH	10	PRO	3.4
52	XU	15	ARG	3.4
32	QA	1368	G	3.4
33	XB	232	PRO	3.4
41	QJ	35	SER	3.4
41	XJ	7	LYS	3.4
24	R2	52	ASP	3.4
41	XJ	54	PHE	3.4
32	XA	532	A	3.4
8	YI	35	LEU	3.4
38	QG	28	ASN	3.4
5	YF	96	ASP	3.4
6	YG	35	GLU	3.4
8	YI	9	LEU	3.4
35	QD	49	ARG	3.4
1	RA	6	A	3.4
45	QN	13	THR	3.4
32	QA	1354	C	3.4
54	QX	3	C	3.4
26	Y4	53	GLU	3.4
34	XC	55	VAL	3.4
32	QA	1371	G	3.4
23	R1	79	GLY	3.4
34	QC	2	GLY	3.4
52	XU	16	GLY	3.4
34	QC	15	THR	3.4
1	YA	1096	A	3.3
28	R6	50	ARG	3.3
35	XD	81	GLU	3.3
49	QR	83	GLU	3.3
22	R0	71	ASP	3.3
7	RH	129	THR	3.3
17	YV	49	THR	3.3
54	QX	6	G	3.3
35	XD	179	GLU	3.3
32	QA	994	A	3.3
32	XA	1350	A	3.3
6	YG	63	ILE	3.3
16	YU	91	ASP	3.3
37	QF	83	ASP	3.3
46	QO	86	GLY	3.3
32	XA	1194	U	3.3

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Mol	Chain	Res	Type	RSRZ
30	Y8	35	GLN	3.3
38	QG	36	LYS	3.3
1	YA	2173	A	3.3
34	QC	87	LEU	3.3
24	Y2	15	LYS	3.3
34	QC	152	ILE	3.3
30	R8	38	GLY	3.3
50	QS	80	TYR	3.3
6	RG	147	ASP	3.3
18	RW	22	ASP	3.3
32	QA	570	G	3.3
44	QM	105	THR	3.3
33	QB	133	LYS	3.3
33	XB	229	VAL	3.3
40	XI	108	VAL	3.3
50	XS	70	LYS	3.3
32	QA	1287	A	3.3
32	XA	134	A	3.3
32	XA	262	A	3.3
7	YH	58	GLU	3.3
33	XB	29	ALA	3.3
54	QX	16	C	3.3
36	XE	25	ARG	3.2
41	QJ	60	ARG	3.2
45	QN	21	TYR	3.2
38	XG	20	ASP	3.2
45	QN	30	ALA	3.2
41	QJ	61	GLU	3.2
32	QA	311	C	3.2
34	XC	52	LEU	3.2
30	R8	48	PHE	3.2
36	XE	20	GLN	3.2
43	XL	19	ARG	3.2
51	XT	17	ARG	3.2
11	RP	64	LYS	3.2
34	XC	4	LYS	3.2
51	XT	20	LEU	3.2
54	XX	19	U	3.2
50	QS	2	PRO	3.2
14	YS	27	SER	3.2
1	RA	2188	C	3.2
34	XC	39	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
41	QJ	6	ILE	3.2
6	YG	136	ARG	3.2
21	RZ	97	GLU	3.2
38	QG	101	LEU	3.2
40	QI	5	TYR	3.2
44	XM	97	PRO	3.2
16	RU	77	SER	3.2
40	QI	117	HIS	3.2
1	RA	1089	G	3.2
32	XA	1002	G	3.2
32	XA	1160	G	3.2
32	XA	1182	G	3.2
1	RA	2107	C	3.2
6	RG	142	PRO	3.2
17	YV	50	PRO	3.2
38	XG	61	VAL	3.2
24	Y2	70	GLN	3.2
40	QI	66	ARG	3.2
23	R1	77	ALA	3.2
40	XI	103	THR	3.2
6	RG	116	ASP	3.1
18	YW	67	ASP	3.1
32	QA	1532	U	3.1
32	XA	1020	U	3.1
43	XL	114	LYS	3.1
43	QL	27	LEU	3.1
7	RH	167	GLU	3.1
1	YA	276	A	3.1
40	QI	89	ASN	3.1
51	QT	9	ASN	3.1
1	YA	2896	C	3.1
20	RY	5	MET	3.1
40	QI	63	ILE	3.1
46	QO	87	ILE	3.1
7	RH	90	LYS	3.1
40	QI	127	LYS	3.1
33	XB	228	GLY	3.1
44	XM	56	LEU	3.1
44	XM	96	LEU	3.1
7	RH	159	GLU	3.1
54	QX	11	U	3.1
39	XH	94	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
44	XM	41	PRO	3.1
48	QQ	101	ARG	3.1
32	QA	1534	A	3.1
54	QX	4	A	3.1
45	QN	11	LYS	3.1
41	QJ	20	ALA	3.1
1	RA	2896	C	3.1
32	XA	1223	C	3.1
40	QI	85	LEU	3.1
8	YI	7	GLU	3.1
11	RP	117	GLU	3.1
45	XN	16	PHE	3.1
46	QO	88	ARG	3.1
44	QM	113	PRO	3.1
50	XS	2	PRO	3.1
35	QD	54	TYR	3.1
44	XM	22	ILE	3.1
51	XT	14	LYS	3.1
34	XC	71	ALA	3.1
30	Y8	38	GLY	3.1
43	QL	29	GLY	3.1
44	XM	105	THR	3.1
1	YA	2146	C	3.1
12	RQ	80	GLU	3.1
31	Y9	12	ASP	3.1
35	QD	209	ARG	3.1
6	RG	87	PRO	3.1
13	RR	9	LYS	3.1
1	YA	2697	G	3.1
32	QA	1139	G	3.1
32	XA	1353	G	3.1
33	QB	13	ALA	3.1
38	QG	25	ALA	3.1
33	QB	110	GLN	3.1
54	QX	19	U	3.1
40	QI	67	GLY	3.1
46	QO	64	ARG	3.1
5	RF	132	VAL	3.1
14	RS	27	SER	3.1
33	QB	136	VAL	3.1
10	RO	9	GLU	3.1
12	RQ	139	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
33	XB	134	GLU	3.1
47	QP	29	ASP	3.1
50	XS	76	PRO	3.1
14	RS	34	HIS	3.0
1	RA	1980	G	3.0
1	RA	2319	G	3.0
17	RV	67	GLY	3.0
32	QA	631	G	3.0
32	QA	1365	G	3.0
32	QA	1302	U	3.0
40	QI	108	VAL	3.0
49	QR	46	GLU	3.0
45	QN	54	PRO	3.0
52	XU	13	ILE	3.0
15	RT	114	LEU	3.0
34	QC	187	ALA	3.0
34	QC	3	ASN	3.0
47	QP	65	GLN	3.0
41	QJ	67	THR	3.0
50	XS	39	THR	3.0
1	YA	2130	U	3.0
35	XD	207	TYR	3.0
14	RS	20	ARG	3.0
40	QI	11	LYS	3.0
1	RA	1536	A	3.0
1	YA	229	A	3.0
40	XI	101	PHE	3.0
1	RA	1765	C	3.0
1	RA	2111	C	3.0
22	R0	53	MET	3.0
32	QA	466	C	3.0
50	XS	5	LEU	3.0
14	RS	36	TYR	3.0
14	YS	3	ARG	3.0
50	XS	80	TYR	3.0
8	YI	20	ASP	3.0
43	XL	115	LYS	3.0
44	QM	100	GLY	3.0
1	YA	2131	G	3.0
46	QO	62	GLN	3.0
20	RY	40	GLU	3.0
36	XE	81	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	YA	6	A	3.0
5	YF	95	ARG	3.0
52	QU	6	ARG	3.0
1	RA	2161	C	3.0
49	QR	49	LYS	3.0
13	YR	106	GLY	3.0
50	XS	8	GLY	3.0
32	QA	1065	U	3.0
6	RG	71	THR	3.0
6	RG	59	GLU	2.9
18	RW	92	ARG	2.9
1	RA	2121	G	2.9
32	QA	1117	G	2.9
23	R1	78	LYS	2.9
32	QA	1360	A	2.9
50	QS	9	VAL	2.9
26	Y4	14	ILE	2.9
40	XI	85	LEU	2.9
30	R8	52	LYS	2.9
33	XB	194	PRO	2.9
34	QC	18	TRP	2.9
12	YQ	27	VAL	2.9
38	XG	81	GLY	2.9
32	XA	951	G	2.9
33	XB	193	ASP	2.9
35	XD	154	ASN	2.9
1	YA	2188	C	2.9
8	RI	119	PRO	2.9
18	RW	78	GLU	2.9
32	QA	1007	C	2.9
32	XA	308	C	2.9
32	XA	1226	C	2.9
32	XA	1538	C	2.9
44	QM	2	ALA	2.9
32	XA	950	U	2.9
6	RG	38	VAL	2.9
16	YU	90	VAL	2.9
6	RG	141	PHE	2.9
34	XC	87	LEU	2.9
37	XF	18	GLN	2.9
45	XN	22	THR	2.9
32	QA	1248	A	2.9

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Mol	Chain	Res	Type	RSRZ
40	XI	109	VAL	2.9
1	YA	967	C	2.9
5	RF	131	GLY	2.9
50	XS	40	ILE	2.9
12	RQ	28	ALA	2.9
30	R8	53	PRO	2.9
40	QI	27	THR	2.9
42	QK	57	THR	2.9
44	QM	18	ALA	2.9
35	QD	24	GLU	2.9
34	QC	64	VAL	2.9
34	XC	70	VAL	2.9
34	XC	153	VAL	2.9
7	RH	157	TYR	2.9
22	R0	44	ARG	2.9
40	QI	18	PHE	2.9
1	RA	2131	G	2.9
1	YA	1176	G	2.9
9	YN	70	LYS	2.9
32	XA	1222	G	2.9
32	XA	1287	A	2.9
43	XL	47	LYS	2.9
50	QS	40	ILE	2.9
32	QA	1128	C	2.8
32	XA	1196	U	2.8
54	XX	3	C	2.8
8	YI	132	PRO	2.8
26	R4	7	PRO	2.8
41	QJ	37	PRO	2.8
44	QM	10	PRO	2.8
45	QN	22	THR	2.8
11	RP	16	ARG	2.8
22	Y0	57	PHE	2.8
34	QC	150	LYS	2.8
28	R6	54	ILE	2.8
37	XF	50	TYR	2.8
32	QA	1324	A	2.8
32	XA	101	A	2.8
40	QI	119	ALA	2.8
1	RA	2166	G	2.8
1	RA	2182	G	2.8
32	QA	1323	G	2.8

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Mol	Chain	Res	Type	RSRZ
32	XA	1343	G	2.8
20	RY	12	THR	2.8
27	R5	26	THR	2.8
34	QC	177	THR	2.8
19	RX	68	ARG	2.8
24	Y2	51	ARG	2.8
51	XT	83	ARG	2.8
45	QN	61	TRP	2.8
52	QU	3	LYS	2.8
12	RQ	92	GLY	2.8
36	XE	22	GLY	2.8
51	XT	55	ILE	2.8
45	XN	14	PRO	2.8
16	RU	89	GLU	2.8
30	R8	56	GLU	2.8
1	RA	529	A	2.8
8	YI	96	ASP	2.8
31	R9	12	ASP	2.8
33	QB	22	LYS	2.8
36	QE	92	LYS	2.8
7	RH	109	PHE	2.8
32	QA	1450	U	2.8
32	XA	261	U	2.8
32	XA	1450	U	2.8
33	QB	57	PHE	2.8
1	RA	944	G	2.8
1	YA	2161	C	2.8
32	QA	1369	C	2.8
32	XA	525	C	2.8
35	XD	14	ARG	2.8
22	R0	75	LEU	2.8
33	QB	141	GLU	2.8
34	QC	143	GLU	2.8
43	QL	73	GLU	2.8
14	RS	29	PHE	2.8
34	XC	186	PHE	2.8
47	QP	59	TRP	2.8
20	YY	1	MET	2.8
38	XG	37	ASN	2.8
42	QK	117	ASN	2.8
1	YA	2144	U	2.8
32	QA	965	A	2.8

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Mol	Chain	Res	Type	RSRZ
32	QA	1090	U	2.8
1	RA	2179	C	2.8
43	XL	30	ALA	2.8
1	RA	2154	G	2.8
32	XA	1003	G	2.8
11	RP	59	LEU	2.8
33	XB	155	LEU	2.8
33	XB	196	LEU	2.8
8	RI	4	ILE	2.8
38	XG	19	GLY	2.7
35	XD	4	TYR	2.7
34	XC	163	ALA	2.7
5	YF	132	VAL	2.7
7	RH	99	VAL	2.7
32	QA	1250	A	2.7
8	RI	137	PRO	2.7
34	QC	32	LEU	2.7
45	QN	39	LEU	2.7
1	YA	2108	C	2.7
5	YF	56	GLU	2.7
8	RI	1	MET	2.7
32	XA	110	C	2.7
32	XA	1320	C	2.7
23	Y1	26	ARG	2.7
30	R8	42	ARG	2.7
45	QN	31	ARG	2.7
52	QU	10	ARG	2.7
42	QK	50	TYR	2.7
34	XC	137	ALA	2.7
8	RI	9	LEU	2.7
34	XC	34	LEU	2.7
41	QJ	71	LEU	2.7
41	XJ	39	PRO	2.7
32	QA	1358	U	2.7
46	QO	3	ILE	2.7
33	QB	20	GLU	2.7
1	YA	2117	A	2.7
26	R4	66	SER	2.7
32	XA	949	A	2.7
50	QS	68	GLY	2.7
13	RR	68	ARG	2.7
35	QD	73	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
35	XD	76	ARG	2.7
20	RY	21	LYS	2.7
29	Y7	48	LYS	2.7
32	QA	1509	C	2.7
32	XA	1354	C	2.7
24	Y2	71	ASN	2.7
30	R8	51	ALA	2.7
8	RI	18	VAL	2.7
40	XI	17	VAL	2.7
43	XL	101	VAL	2.7
4	YE	195	LEU	2.7
37	XF	48	LEU	2.7
1	YA	2121	G	2.7
32	QA	81	G	2.7
32	QA	1511	G	2.7
32	XA	1216	G	2.7
6	YG	13	GLU	2.7
33	XB	231	GLU	2.7
45	XN	46	GLU	2.7
7	YH	60	ARG	2.7
45	XN	29	ARG	2.7
52	QU	8	THR	2.7
32	XA	1341	U	2.7
32	XA	1364	U	2.7
1	RA	1084	A	2.7
32	QA	452	A	2.7
32	QA	1493	A	2.7
35	QD	53	ASP	2.7
52	QU	18	TYR	2.7
38	QG	118	VAL	2.7
39	XH	2	LEU	2.7
41	XJ	62	HIS	2.7
32	XA	63	C	2.7
34	QC	134	ILE	2.7
12	RQ	7	MET	2.7
34	XC	10	PHE	2.7
41	QJ	31	GLY	2.7
50	XS	68	GLY	2.7
12	RQ	21	THR	2.7
1	RA	1087	G	2.7
1	RA	2802	G	2.7
32	QA	823	G	2.7

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Mol	Chain	Res	Type	RSRZ
32	XA	112	G	2.7
32	XA	190	G	2.7
17	YV	73	SER	2.7
44	QM	118	ALA	2.7
1	RA	2172	U	2.7
1	YA	2109	U	2.7
11	RP	110	TYR	2.7
23	R1	85	LEU	2.7
34	QC	55	VAL	2.7
39	QH	15	ASN	2.7
1	RA	2320	A	2.6
1	YA	1762	A	2.6
32	XA	1531	A	2.6
33	XB	214	ILE	2.6
33	XB	222	ILE	2.6
33	XB	48	MET	2.6
54	XX	13	A	2.6
54	XX	14	A	2.6
38	XG	32	ARG	2.6
41	XJ	46	ARG	2.6
3	RD	38	LYS	2.6
40	XI	127	LYS	2.6
1	YA	591	C	2.6
2	RB	12	C	2.6
20	YY	62	GLU	2.6
32	QA	88	C	2.6
32	QA	1223	C	2.6
32	QA	1249	C	2.6
32	QA	1389	C	2.6
51	XT	71	THR	2.6
8	RI	38	LEU	2.6
35	XD	56	VAL	2.6
38	XG	99	LEU	2.6
21	RZ	121	HIS	2.6
50	XS	69	HIS	2.6
1	RA	2115	G	2.6
32	XA	631	G	2.6
1	RA	1097	U	2.6
24	R2	9	GLN	2.6
27	R5	9	LYS	2.6
34	QC	142	MET	2.6
32	XA	1148	U	2.6

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Mol	Chain	Res	Type	RSRZ
35	QD	161	ASN	2.6
40	QI	113	LYS	2.6
41	XJ	63	PHE	2.6
20	YY	64	GLU	2.6
32	QA	1191	A	2.6
32	QA	1357	A	2.6
41	QJ	64	GLU	2.6
34	XC	165	THR	2.6
34	XC	192	THR	2.6
50	XS	41	VAL	2.6
1	RA	2178	C	2.6
38	QG	77	SER	2.6
43	XL	81	SER	2.6
4	YE	149	ARG	2.6
43	XL	23	LYS	2.6
8	RI	132	PRO	2.6
12	RQ	65	PHE	2.6
6	RG	41	GLN	2.6
1	RA	1090	U	2.6
1	RA	2150	U	2.6
7	YH	46	GLU	2.6
15	RT	109	GLU	2.6
32	QA	955	U	2.6
32	QA	1125	U	2.6
32	QA	1148	U	2.6
35	QD	150	GLU	2.6
1	RA	2116	G	2.6
1	RA	2155	G	2.6
32	QA	929	G	2.6
54	XX	9	G	2.6
4	YE	52	LEU	2.6
44	XM	45	VAL	2.6
45	XN	13	THR	2.6
32	QA	1289	A	2.6
32	XA	965	A	2.6
52	XU	10	ARG	2.6
34	XC	134	ILE	2.6
33	XB	28	PHE	2.6
33	XB	91	PRO	2.6
40	XI	123	PRO	2.6
32	XA	442	C	2.6
7	RH	120	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
12	RQ	27	VAL	2.6
16	RU	96	ALA	2.6
33	XB	197	VAL	2.6
40	QI	43	ALA	2.6
41	QJ	15	THR	2.6
45	XN	5	ALA	2.6
1	RA	2585	U	2.6
30	R8	5	LYS	2.6
32	QA	956	U	2.6
38	XG	103	TRP	2.6
1	YA	2894	G	2.6
32	XA	1033	G	2.6
54	XX	10	G	2.6
38	XG	58	PRO	2.6
35	XD	201	GLN	2.6
44	QM	16	ASP	2.6
34	XC	33	LEU	2.6
1	RA	1767	C	2.6
16	RU	37	GLU	2.6
34	XC	116	VAL	2.6
35	XD	10	ARG	2.6
35	XD	66	ARG	2.6
38	XG	118	VAL	2.6
39	QH	30	ARG	2.6
40	QI	17	VAL	2.6
45	XN	25	VAL	2.6
45	QN	50	LYS	2.6
47	QP	8	ARG	2.6
47	QP	26	ARG	2.6
33	QB	24	TRP	2.5
41	XJ	96	ILE	2.5
32	QA	1240	U	2.5
32	QA	1510	U	2.5
44	QM	87	TYR	2.5
21	RZ	166	SER	2.5
33	XB	233	SER	2.5
40	XI	126	SER	2.5
34	QC	9	GLY	2.5
35	XD	78	LEU	2.5
1	RA	2157	G	2.5
1	YA	2793	G	2.5
4	YE	55	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
8	RI	118	LYS	2.5
9	RN	74	ARG	2.5
43	XL	18	VAL	2.5
48	XQ	101	ARG	2.5
1	RA	265	A	2.5
32	QA	1251	A	2.5
48	QQ	24	GLU	2.5
41	XJ	50	ILE	2.5
1	RA	1092	C	2.5
1	RA	2798	C	2.5
53	QV	34	C	2.5
1	RA	2506	U	2.5
8	RI	13	GLY	2.5
11	RP	28	GLY	2.5
15	YT	47	GLY	2.5
35	XD	71	SER	2.5
41	XJ	90	LEU	2.5
50	XS	38	SER	2.5
33	XB	22	LYS	2.5
39	XH	91	ARG	2.5
52	XU	9	ARG	2.5
9	RN	92	ALA	2.5
15	YT	104	ASN	2.5
15	YT	107	ASP	2.5
47	QP	68	ASP	2.5
33	XB	200	ILE	2.5
33	QB	101	MET	2.5
1	YA	2476	A	2.5
54	XX	12	A	2.5
1	YA	2166	G	2.5
1	YA	2181	G	2.5
37	XF	56	PRO	2.5
40	XI	117	HIS	2.5
12	RQ	18	LYS	2.5
12	YQ	18	LYS	2.5
14	RS	110	LEU	2.5
30	R8	29	LYS	2.5
30	R8	50	LEU	2.5
31	Y9	13	LYS	2.5
34	QC	94	LEU	2.5
36	QE	31	LEU	2.5
32	XA	1244	C	2.5

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Mol	Chain	Res	Type	RSRZ
35	XD	2	GLY	2.5
40	QI	30	GLY	2.5
43	QL	114	LYS	2.5
47	QP	27	LYS	2.5
52	QU	15	ARG	2.5
22	R0	17	GLN	2.5
38	QG	86	GLN	2.5
43	QL	116	SER	2.5
21	RZ	113	ALA	2.5
34	QC	137	ALA	2.5
38	QG	150	ALA	2.5
39	QH	28	ALA	2.5
47	XP	84	ALA	2.5
11	YP	136	GLU	2.5
32	XA	5	U	2.5
39	QH	136	GLU	2.5
50	QS	27	GLU	2.5
37	XF	55	ASP	2.5
38	XG	15	ASP	2.5
41	QJ	50	ILE	2.5
33	QB	190	THR	2.5
40	QI	7	THR	2.5
50	QS	33	THR	2.5
52	XU	17	THR	2.5
6	YG	72	ARG	2.5
14	YS	7	TYR	2.5
25	R3	41	PRO	2.5
16	RU	98	LEU	2.5
40	XI	9	ARG	2.5
32	QA	814	A	2.5
32	QA	815	A	2.5
1	YA	1093	G	2.5
1	YA	2792	G	2.5
32	XA	1312	G	2.5
38	QG	83	ALA	2.5
38	XG	117	ALA	2.5
40	QI	106	ALA	2.5
50	QS	35	SER	2.5
7	RH	81	GLU	2.5
35	XD	156	GLU	2.5
19	YX	1	MET	2.5
32	XA	1159	U	2.5

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Mol	Chain	Res	Type	RSRZ
12	RQ	130	LYS	2.5
6	RG	82	LEU	2.5
6	YG	43	LEU	2.5
8	RI	27	ARG	2.5
18	RW	37	ARG	2.5
47	XP	25	ARG	2.5
34	XC	2	GLY	2.5
40	XI	68	GLY	2.5
16	RU	90	VAL	2.5
33	XB	136	VAL	2.5
34	QC	66	VAL	2.5
41	QJ	33	GLN	2.5
21	YZ	197	ILE	2.4
47	XP	19	ILE	2.4
32	QA	1350	A	2.4
33	XB	117	GLU	2.4
23	R1	91	LYS	2.4
44	QM	27	LYS	2.4
50	QS	53	ASN	2.4
32	QA	630	G	2.4
32	QA	947	G	2.4
32	XA	1032(A)	G	2.4
32	XA	1317	C	2.4
38	QG	16	LEU	2.4
44	QM	19	LEU	2.4
44	XM	43	THR	2.4
32	QA	1226	C	2.4
7	RH	108	GLY	2.4
33	XB	230	VAL	2.4
45	XN	56	VAL	2.4
44	QM	72	ALA	2.4
45	QN	5	ALA	2.4
34	XC	8	ILE	2.4
12	RQ	1	MET	2.4
22	R0	16	SER	2.4
16	RU	16	LYS	2.4
41	QJ	54	PHE	2.4
16	YU	92	ARG	2.4
21	RZ	79	ARG	2.4
21	RZ	81	ARG	2.4
45	QN	41	ARG	2.4
33	QB	221	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
34	QC	52	LEU	2.4
37	QF	21	LEU	2.4
41	XJ	71	LEU	2.4
44	XM	19	LEU	2.4
32	QA	313	A	2.4
32	XA	1245	A	2.4
32	XA	1349	A	2.4
33	QB	6	THR	2.4
40	XI	7	THR	2.4
54	XX	5	A	2.4
22	R0	78	TYR	2.4
40	XI	125	TYR	2.4
23	R1	54	ALA	2.4
32	QA	308	C	2.4
32	QA	930	C	2.4
32	QA	995	C	2.4
32	QA	1141	C	2.4
32	XA	1342	C	2.4
1	RA	2181	G	2.4
1	RA	2807	G	2.4
1	YA	275	G	2.4
32	XA	1240	U	2.4
33	XB	42	ILE	2.4
51	QT	55	ILE	2.4
12	YQ	7	MET	2.4
29	R7	1	MET	2.4
38	QG	31	MET	2.4
7	RH	97	ARG	2.4
8	RI	113	ARG	2.4
21	RZ	6	LYS	2.4
27	Y5	59	GLU	2.4
33	QB	86	GLU	2.4
40	XI	83	ARG	2.4
47	QP	34	GLU	2.4
52	QU	23	PRO	2.4
8	RI	145	VAL	2.4
13	RR	73	VAL	2.4
20	RY	107	ASP	2.4
4	YE	151	TYR	2.4
19	YX	94	GLY	2.4
34	XC	6	HIS	2.4
41	XJ	10	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
33	QB	41	ILE	2.4
38	QG	147	ALA	2.4
40	XI	119	ALA	2.4
1	YA	1095	A	2.4
41	QJ	45	ARG	2.4
45	QN	16	PHE	2.4
45	QN	36	PHE	2.4
1	RA	2145	C	2.4
32	QA	1129	C	2.4
32	XA	307	C	2.4
32	XA	395	C	2.4
32	XA	1344	C	2.4
1	RA	11	G	2.4
1	RA	1989	G	2.4
32	QA	1233	G	2.4
6	RG	29	TRP	2.4
7	RH	112	PRO	2.4
34	QC	174	PRO	2.4
6	YG	97	ASP	2.4
12	YQ	19	GLY	2.4
33	XB	18	GLY	2.4
38	XG	68	ASN	2.4
40	XI	115	GLY	2.4
40	QI	114	TYR	2.4
12	RQ	103	MET	2.4
37	XF	94	GLN	2.4
7	RH	71	LEU	2.4
35	XD	96	LEU	2.4
6	YG	30	GLU	2.4
21	RZ	168	GLU	2.4
32	QA	262	A	2.4
32	QA	687	A	2.4
36	XE	7	GLU	2.4
39	QH	33	GLU	2.4
40	XI	48	GLU	2.4
54	XX	8	A	2.4
1	RA	1083	U	2.4
1	YA	2189	U	2.4
8	YI	119	PRO	2.4
50	QS	41	VAL	2.4
32	XA	989	C	2.3
5	YF	133	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
21	RZ	133	ILE	2.3
43	QL	26	ALA	2.3
50	QS	6	LYS	2.3
35	QD	115	ARG	2.3
38	XG	18	TYR	2.3
45	XN	3	ARG	2.3
52	QU	13	ILE	2.3
12	RQ	29	PHE	2.3
14	RS	32	LEU	2.3
21	RZ	5	LEU	2.3
40	QI	37	PHE	2.3
40	QI	99	LEU	2.3
30	R8	54	GLU	2.3
32	QA	1451	A	2.3
40	QI	71	SER	2.3
40	QI	116	LYS	2.3
5	YF	106	ARG	2.3
35	XD	209	ARG	2.3
36	QE	24	ARG	2.3
44	QM	103	THR	2.3
45	XN	23	ARG	2.3
45	XN	26	ARG	2.3
36	QE	21	ALA	2.3
32	XA	1211	U	2.3
39	QH	58	TYR	2.3
39	QH	54	ASP	2.3
46	QO	49	ASP	2.3
23	R1	97	LEU	2.3
40	XI	19	LEU	2.3
41	XJ	65	LEU	2.3
13	YR	118	GLU	2.3
43	QL	127	GLU	2.3
1	RA	101	G	2.3
1	RA	171	G	2.3
32	XA	630	G	2.3
21	RZ	199	LYS	2.3
43	XL	28	LYS	2.3
35	XD	65	ARG	2.3
39	XH	18	ARG	2.3
3	RD	216	GLY	2.3
21	RZ	200	GLY	2.3
38	QG	42	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
39	QH	55	GLY	2.3
21	RZ	107	THR	2.3
34	QC	165	THR	2.3
40	XI	106	ALA	2.3
45	QN	59	ALA	2.3
5	RF	133	ASN	2.3
49	QR	85	LEU	2.3
51	XT	10	LEU	2.3
32	QA	977	A	2.3
32	XA	523	A	2.3
41	XJ	73	ASP	2.3
50	XS	12	ASP	2.3
32	XA	1540	U	2.3
1	YA	2174	C	2.3
32	QA	1362(A)	C	2.3
32	XA	1195	C	2.3
33	XB	15	VAL	2.3
44	XM	27	LYS	2.3
22	Y0	44	ARG	2.3
45	QN	26	ARG	2.3
7	RH	100	GLY	2.3
41	QJ	74	ILE	2.3
43	XL	103	GLY	2.3
8	YI	146	ALA	2.3
35	QD	164	ALA	2.3
51	XT	106	ALA	2.3
12	RQ	75	THR	2.3
34	QC	20	SER	2.3
34	XC	177	THR	2.3
5	RF	33	LEU	2.3
9	RN	72	TYR	2.3
32	QA	1370	G	2.3
32	XA	105	G	2.3
32	XA	1021	G	2.3
47	XP	32	TYR	2.3
54	QX	10	G	2.3
37	XF	57	GLN	2.3
46	XO	62	GLN	2.3
1	RA	2117	A	2.3
1	YA	1073	A	2.3
1	YA	2169	A	2.3
4	YE	7	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
4	YE	79	ARG	2.3
6	RG	14	GLU	2.3
26	R4	56	VAL	2.3
32	XA	1041	A	2.3
34	QC	68	VAL	2.3
48	QQ	58	GLU	2.3
1	YA	2132	U	2.3
32	XA	118	U	2.3
32	XA	1532	U	2.3
33	QB	14	GLY	2.3
36	XE	17	ALA	2.3
38	QG	144	MET	2.3
51	QT	77	ALA	2.3
6	RG	3	LEU	2.3
9	YN	93	THR	2.3
43	XL	44	THR	2.3
44	QM	90	LEU	2.3
45	XN	6	LEU	2.3
33	QB	113	HIS	2.3
8	RI	25	TYR	2.3
4	YE	76	ARG	2.3
14	RS	97	ARG	2.3
17	YV	80	GLN	2.3
12	RQ	102	VAL	2.3
12	RQ	105	GLU	2.2
35	XD	60	GLU	2.2
40	QI	110	GLU	2.2
1	RA	508	G	2.2
1	YA	1087	G	2.2
1	YA	1933	G	2.2
1	YA	2168	G	2.2
32	XA	104	G	2.2
32	XA	971	G	2.2
32	XA	1224	G	2.2
44	QM	9	ILE	2.2
34	XC	51	GLY	2.2
44	XM	113	PRO	2.2
6	RG	158	ALA	2.2
1	RA	896	A	2.2
1	RA	1026	U	2.2
1	YA	1759	A	2.2
6	YG	29	TRP	2.2

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Mol	Chain	Res	Type	RSRZ
32	QA	1363	A	2.2
6	RG	178	PHE	2.2
21	RZ	78	LYS	2.2
34	XC	193	TYR	2.2
48	XQ	37	LYS	2.2
1	RA	2164	C	2.2
32	QA	1066	C	2.2
34	XC	68	VAL	2.2
51	XT	9	ASN	2.2
36	QE	81	GLU	2.2
7	RH	89	ILE	2.2
36	XE	80	ILE	2.2
7	RH	154	PRO	2.2
12	RQ	83	MET	2.2
34	XC	73	PRO	2.2
34	XC	115	LEU	2.2
44	XM	30	ALA	2.2
50	QS	16	LEU	2.2
5	YF	39	TRP	2.2
26	Y4	49	PHE	2.2
33	QB	152	PHE	2.2
1	YA	2110	G	2.2
32	QA	928	G	2.2
32	QA	953	G	2.2
32	QA	1087	G	2.2
32	XA	933	G	2.2
32	XA	1516	G	2.2
39	QH	3	THR	2.2
47	XP	27	LYS	2.2
52	XU	25	LYS	2.2
5	YF	97	TYR	2.2
32	QA	723	U	2.2
32	QA	1372	U	2.2
39	XH	84	ARG	2.2
1	YA	1379	A	2.2
7	RH	63	SER	2.2
11	YP	133	SER	2.2
14	YS	52	SER	2.2
50	QS	11	VAL	2.2
13	RR	71	GLN	2.2
39	XH	78	GLN	2.2
14	YS	16	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
6	RG	144	ILE	2.2
15	RT	102	ILE	2.2
34	XC	166	GLU	2.2
35	XD	15	GLU	2.2
4	YE	1	MET	2.2
6	YG	94	LEU	2.2
14	RS	88	ASP	2.2
15	YT	124	ASP	2.2
32	QA	1538	C	2.2
32	XA	366	C	2.2
32	XA	1018	C	2.2
8	YI	36	ALA	2.2
11	RP	62	LEU	2.2
49	QR	33	ASP	2.2
26	Y4	54	GLY	2.2
40	QI	46	ALA	2.2
40	XI	69	GLY	2.2
45	QN	10	ALA	2.2
49	QR	60	ALA	2.2
50	XS	50	ALA	2.2
50	XS	75	ALA	2.2
8	RI	95	LYS	2.2
19	RX	60	ARG	2.2
40	XI	66	ARG	2.2
3	RD	220	HIS	2.2
3	RD	259	THR	2.2
9	RN	75	TYR	2.2
6	RG	159	VAL	2.2
1	RA	1060	U	2.2
2	RB	1	U	2.2
6	RG	39	ILE	2.2
1	RA	2173	A	2.2
1	YA	1091	G	2.2
1	YA	1460	A	2.2
1	YA	1510	A	2.2
1	YA	2120	G	2.2
32	QA	1024	G	2.2
32	QA	1094	G	2.2
32	XA	1094	G	2.2
39	QH	99	GLU	2.2
50	QS	71	LEU	2.2
40	QI	6	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
40	XI	13	ALA	2.2
44	XM	5	ALA	2.2
14	YS	9	ARG	2.2
24	R2	69	ARG	2.2
41	XJ	43	ARG	2.2
1	RA	2103	C	2.2
1	RA	2177	C	2.2
32	QA	1321	C	2.2
32	XA	418	C	2.2
15	RT	40	THR	2.2
43	QL	99	HIS	2.2
19	YX	52	VAL	2.2
34	QC	99	VAL	2.2
7	YH	2	SER	2.2
24	R2	46	GLN	2.2
40	QI	126	SER	2.2
6	RG	7	LEU	2.2
11	YP	107	LYS	2.2
28	R6	32	ASN	2.2
34	QC	189	ALA	2.2
35	QD	199	ASN	2.2
38	XG	39	ALA	2.2
30	R8	63	PRO	2.2
32	QA	1351	U	2.2
40	QI	49	PRO	2.2
44	XM	85	GLY	2.2
14	RS	3	ARG	2.2
23	Y1	11	ARG	2.2
33	QB	144	ARG	2.2
36	QE	15	ARG	2.2
39	XH	121	ASP	2.2
1	YA	2114	A	2.2
32	XA	452	A	2.2
32	QA	1312	G	2.2
32	XA	929	G	2.2
43	XL	99	HIS	2.2
5	YF	70	THR	2.1
40	QI	14	VAL	2.1
41	XJ	44	VAL	2.1
49	XR	82	THR	2.1
50	XS	58	VAL	2.1
47	XP	17	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	YA	2129	C	2.1
32	XA	1322	C	2.1
32	XA	1397	C	2.1
42	QK	48	ILE	2.1
50	QS	31	ILE	2.1
35	QD	201	GLN	2.1
41	QJ	16	LEU	2.1
6	RG	148	MET	2.1
41	XJ	99	LYS	2.1
48	XQ	100	LYS	2.1
4	YE	53	PRO	2.1
21	YZ	80	ARG	2.1
6	RG	40	ASN	2.1
25	R3	2	PRO	2.1
30	Y8	46	ARG	2.1
1	YA	1535	U	2.1
1	YA	2167	U	2.1
1	YA	2180	U	2.1
47	QP	23	ASP	2.1
44	XM	64	TRP	2.1
26	R4	6	HIS	2.1
50	XS	60	VAL	2.1
47	XP	44	THR	2.1
1	RA	1177	A	2.1
23	R1	18	ILE	2.1
32	XA	958	A	2.1
32	XA	975	A	2.1
45	QN	34	TYR	2.1
8	YI	12	LEU	2.1
12	RQ	37	LEU	2.1
36	QE	88	LYS	2.1
1	RA	530	G	2.1
1	RA	1573	G	2.1
1	YA	352	G	2.1
1	YA	1056	G	2.1
15	YT	1	MET	2.1
32	QA	1186	G	2.1
35	QD	168	ARG	2.1
41	XJ	66	ARG	2.1
44	QM	99	ARG	2.1
15	RT	69	GLY	2.1
21	YZ	162	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
21	YZ	200	GLY	2.1
35	QD	83	SER	2.1
1	YA	1537	C	2.1
1	YA	2794	C	2.1
35	XD	121	VAL	2.1
44	QM	60	VAL	2.1
50	XS	51	VAL	2.1
11	RP	35	HIS	2.1
34	QC	69	HIS	2.1
34	QC	176	HIS	2.1
15	RT	42	ILE	2.1
34	QC	95	THR	2.1
38	XG	59	LEU	2.1
45	XN	47	LEU	2.1
47	QP	33	ILE	2.1
6	RG	131	TYR	2.1
49	QR	84	LYS	2.1
11	RP	111	ARG	2.1
12	YQ	1	MET	2.1
4	RE	20	ALA	2.1
38	XG	116	ALA	2.1
1	RA	2176	A	2.1
1	YA	2801	A	2.1
22	R0	76	GLY	2.1
41	XJ	97	GLU	2.1
50	XS	59	PRO	2.1
33	QB	109	SER	2.1
37	QF	97	PHE	2.1
50	XS	35	SER	2.1
34	XC	3	ASN	2.1
40	QI	29	ASN	2.1
1	YA	2148	G	2.1
8	RI	107	VAL	2.1
38	QG	66	VAL	2.1
32	XA	135	C	2.1
10	RO	18	LYS	2.1
31	R9	15	LYS	2.1
34	QC	167	TRP	2.1
45	QN	9	LYS	2.1
7	RH	88	LEU	2.1
7	YH	171	LEU	2.1
41	QJ	4	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
8	RI	86	THR	2.1
8	RI	93	THR	2.1
21	RZ	112	ARG	2.1
33	XB	186	ALA	2.1
36	QE	94	ALA	2.1
1	RA	1766	U	2.1
32	QA	1159	U	2.1
35	XD	42	GLN	2.1
4	YE	193	GLY	2.1
6	RG	154	GLY	2.1
8	RI	85	GLU	2.1
8	YI	134	PRO	2.1
12	YQ	80	GLU	2.1
14	YS	8	GLU	2.1
23	R1	83	GLU	2.1
44	XM	10	PRO	2.1
50	QS	38	SER	2.1
7	RH	17	VAL	2.1
42	QK	47	VAL	2.1
1	RA	2801	A	2.1
1	YA	2311	A	2.1
47	QP	31	LYS	2.1
49	QR	68	LYS	2.1
8	YI	6	LEU	2.1
11	YP	6	LEU	2.1
40	QI	102	LEU	2.1
42	QK	120	ARG	2.1
44	XM	78	ILE	2.1
33	QB	40	HIS	2.1
52	XU	6	ARG	2.1
3	RD	71	ASP	2.1
40	QI	105	ASP	2.1
6	YG	64	THR	2.1
1	RA	2128	C	2.1
32	QA	381	C	2.1
32	QA	1359	C	2.1
32	XA	1262	C	2.1
1	YA	669	G	2.1
32	QA	1187	G	2.1
32	QA	1190	G	2.1
32	XA	147	G	2.1
32	XA	1233	G	2.1

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Mol	Chain	Res	Type	RSRZ
47	XP	7	ALA	2.1
4	RE	130	GLY	2.1
6	RG	26	GLN	2.1
8	YI	90	GLY	2.1
38	XG	43	PHE	2.1
1	RA	362	U	2.0
1	YA	2449	U	2.0
16	RU	84	LYS	2.0
32	XA	323	U	2.0
34	XC	66	VAL	2.0
38	QG	29	LYS	2.0
38	XG	80	VAL	2.0
40	XI	11	LYS	2.0
40	XI	41	VAL	2.0
44	XM	117	VAL	2.0
6	RG	53	LEU	2.0
7	YH	3	ARG	2.0
12	YQ	79	LEU	2.0
13	YR	2	ARG	2.0
35	XD	97	LEU	2.0
41	QJ	38	ILE	2.0
41	XJ	38	ILE	2.0
45	XN	35	ARG	2.0
33	XB	40	HIS	2.0
1	RA	1103	A	2.0
3	YD	230	ASP	2.0
7	RH	164	TYR	2.0
18	YW	94	ASP	2.0
32	QA	1111	A	2.0
32	QA	1225	A	2.0
33	XB	160	ASP	2.0
33	XB	220	ASP	2.0
44	XM	87	TYR	2.0
5	YF	40	GLN	2.0
7	RH	91	GLY	2.0
1	RA	1537	C	2.0
1	RA	2791	C	2.0
1	YA	2699	C	2.0
1	YA	2803	C	2.0
11	RP	36	LYS	2.0
30	R8	49	VAL	2.0
32	XA	466	C	2.0

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Mol	Chain	Res	Type	RSRZ
32	XA	1243	C	2.0
34	QC	199	LYS	2.0
52	XU	12	LYS	2.0
33	XB	7	VAL	2.0
38	QG	80	VAL	2.0
41	XJ	49	VAL	2.0
1	RA	2162	G	2.0
1	RA	2805	G	2.0
14	RS	54	LEU	2.0
32	XA	44	G	2.0
32	XA	1184	G	2.0
32	XA	1386	G	2.0
32	XA	1387	G	2.0
33	QB	102	LEU	2.0
35	XD	11	LEU	2.0
45	QN	47	LEU	2.0
14	RS	53	SER	2.0
35	QD	52	SER	2.0
35	XD	83	SER	2.0
1	RA	2312	U	2.0
34	QC	181	ASN	2.0
5	RF	128	ALA	2.0
6	YG	25	TYR	2.0
17	YV	81	TYR	2.0
26	Y4	24	THR	2.0
40	QI	84	ALA	2.0
39	QH	4	ASP	2.0
39	QH	25	ASP	2.0
6	RG	102	PHE	2.0
6	YG	2	PRO	2.0
8	YI	121	LYS	2.0
14	RS	57	LYS	2.0
16	RU	34	LYS	2.0
31	R9	36	GLN	2.0
38	XG	106	GLN	2.0
42	XK	115	PRO	2.0
1	YA	2119	A	2.0
1	YA	2790	A	2.0
32	QA	1531	A	2.0
35	XD	50	ARG	2.0
38	XG	69	VAL	2.0
45	XN	19	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
39	QH	112	LEU	2.0
40	QI	79	LEU	2.0
40	XI	79	LEU	2.0
51	XT	72	LEU	2.0
33	QB	162	ILE	2.0
34	QC	157	ILE	2.0
40	XI	77	ILE	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	RSCC	RSR	B-factors(Å ²)	Q<0.9
53	1MG	QV	37	24/25	0.78	0.10	84,144,150,160	0
53	1MG	XV	37	24/25	0.80	0.13	171,173,175,184	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	RSCC	RSR	B-factors(Å ²)	Q<0.9
55	MG	YA	3390	1/1	0.36	0.40	86,86,86,86	0
55	MG	RA	3205	1/1	0.39	0.33	95,95,95,95	0
55	MG	RF	301	1/1	0.40	0.54	83,83,83,83	0
55	MG	RA	3246	1/1	0.44	0.46	91,91,91,91	0
55	MG	RA	3193	1/1	0.47	0.23	77,77,77,77	0
55	MG	RA	3312	1/1	0.49	0.34	80,80,80,80	0
55	MG	YA	3333	1/1	0.50	0.07	19,19,19,19	0
55	MG	RA	3147	1/1	0.55	0.21	60,60,60,60	0
55	MG	RA	3137	1/1	0.55	0.29	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	RB	208	1/1	0.56	0.19	63,63,63,63	0
55	MG	YA	3330	1/1	0.56	0.23	58,58,58,58	0
55	MG	RA	3316	1/1	0.57	0.37	74,74,74,74	0
55	MG	YA	3449	1/1	0.58	0.24	54,54,54,54	0
55	MG	RA	3176	1/1	0.59	0.18	75,75,75,75	0
55	MG	YA	3212	1/1	0.59	0.32	62,62,62,62	0
55	MG	QA	1642	1/1	0.60	0.16	79,79,79,79	0
55	MG	RA	3440	1/1	0.60	0.31	61,61,61,61	0
55	MG	RA	3411	1/1	0.61	0.32	87,87,87,87	0
55	MG	RA	3301	1/1	0.62	0.19	72,72,72,72	0
55	MG	QA	1648	1/1	0.63	0.18	77,77,77,77	0
55	MG	RA	3389	1/1	0.63	0.33	62,62,62,62	0
55	MG	RA	3315	1/1	0.63	0.31	81,81,81,81	0
55	MG	YA	3293	1/1	0.65	0.13	62,62,62,62	0
55	MG	RA	3068	1/1	0.65	0.13	66,66,66,66	0
55	MG	YA	3081	1/1	0.65	0.19	55,55,55,55	0
55	MG	RA	3111	1/1	0.65	0.22	92,92,92,92	0
55	MG	YA	3288	1/1	0.65	0.20	60,60,60,60	0
55	MG	RA	3249	1/1	0.66	0.14	60,60,60,60	0
55	MG	RA	3156	1/1	0.66	0.18	78,78,78,78	0
55	MG	YA	3402	1/1	0.67	0.21	74,74,74,74	0
55	MG	YA	3358	1/1	0.67	0.18	32,32,32,32	0
55	MG	XA	1668	1/1	0.67	0.09	77,77,77,77	0
55	MG	XA	1674	1/1	0.67	0.22	64,64,64,64	0
55	MG	YA	3464	1/1	0.68	0.21	63,63,63,63	0
55	MG	YA	3494	1/1	0.68	0.31	56,56,56,56	0
55	MG	YA	3206	1/1	0.68	0.30	64,64,64,64	0
55	MG	YA	3393	1/1	0.68	0.42	69,69,69,69	0
55	MG	RA	3432	1/1	0.69	0.26	81,81,81,81	0
55	MG	RA	3186	1/1	0.69	0.24	76,76,76,76	0
55	MG	YA	3429	1/1	0.70	0.26	82,82,82,82	0
55	MG	RA	3129	1/1	0.70	0.21	58,58,58,58	0
55	MG	YA	3380	1/1	0.70	0.29	70,70,70,70	0
55	MG	RA	3243	1/1	0.70	0.21	57,57,57,57	0
55	MG	YA	3210	1/1	0.70	0.13	59,59,59,59	0
55	MG	RA	3419	1/1	0.70	0.21	61,61,61,61	0
55	MG	XA	1681	1/1	0.70	0.20	82,82,82,82	0
55	MG	YA	3324	1/1	0.71	0.23	55,55,55,55	0
55	MG	YA	3472	1/1	0.71	0.18	68,68,68,68	0
55	MG	RA	3372	1/1	0.71	0.17	66,66,66,66	0
55	MG	YA	3321	1/1	0.72	0.17	63,63,63,63	0
55	MG	YA	3184	1/1	0.72	0.18	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	QA	1634	1/1	0.72	0.32	65,65,65,65	0
55	MG	YA	3208	1/1	0.72	0.18	51,51,51,51	0
55	MG	RA	3308	1/1	0.72	0.24	66,66,66,66	0
55	MG	RA	3183	1/1	0.72	0.30	90,90,90,90	0
55	MG	YA	3500	1/1	0.72	0.30	79,79,79,79	0
55	MG	XA	1645	1/1	0.72	0.21	78,78,78,78	0
55	MG	YA	3382	1/1	0.72	0.32	53,53,53,53	0
55	MG	QA	1622	1/1	0.72	0.18	96,96,96,96	0
55	MG	YA	3136	1/1	0.72	0.17	43,43,43,43	0
55	MG	QA	1618	1/1	0.73	0.26	108,108,108,108	0
55	MG	YA	3342	1/1	0.73	0.36	61,61,61,61	0
55	MG	XA	1640	1/1	0.73	0.20	65,65,65,65	0
55	MG	RA	3008	1/1	0.73	0.23	65,65,65,65	0
55	MG	RA	3447	1/1	0.73	0.17	55,55,55,55	0
55	MG	YA	3215	1/1	0.73	0.26	56,56,56,56	0
55	MG	YA	3229	1/1	0.73	0.25	47,47,47,47	0
55	MG	RA	3204	1/1	0.74	0.22	62,62,62,62	0
55	MG	YE	303	1/1	0.74	0.21	44,44,44,44	0
55	MG	RA	3306	1/1	0.74	0.14	51,51,51,51	0
55	MG	QA	1662	1/1	0.74	0.24	57,57,57,57	0
55	MG	RA	3361	1/1	0.74	0.12	68,68,68,68	0
55	MG	RA	3084	1/1	0.74	0.14	33,33,33,33	0
55	MG	RA	3207	1/1	0.74	0.22	81,81,81,81	0
55	MG	YA	3193	1/1	0.75	0.40	70,70,70,70	0
55	MG	RA	3053	1/1	0.75	0.19	36,36,36,36	0
55	MG	RA	3148	1/1	0.75	0.18	56,56,56,56	0
55	MG	RA	3357	1/1	0.75	0.26	73,73,73,73	0
55	MG	RA	3212	1/1	0.75	0.21	67,67,67,67	0
55	MG	YA	3366	1/1	0.75	0.12	32,32,32,32	0
55	MG	RA	3056	1/1	0.75	0.12	61,61,61,61	0
55	MG	XA	1630	1/1	0.75	0.14	39,39,39,39	0
55	MG	RA	3386	1/1	0.75	0.19	61,61,61,61	0
55	MG	RA	3387	1/1	0.75	0.14	56,56,56,56	0
55	MG	YA	3180	1/1	0.75	0.18	67,67,67,67	0
55	MG	RA	3093	1/1	0.75	0.18	57,57,57,57	0
55	MG	YA	3419	1/1	0.75	0.13	60,60,60,60	0
55	MG	R0	101	1/1	0.76	0.19	40,40,40,40	0
55	MG	RA	3211	1/1	0.76	0.17	73,73,73,73	0
55	MG	YA	3261	1/1	0.76	0.25	53,53,53,53	0
55	MG	YA	3497	1/1	0.76	0.12	51,51,51,51	0
55	MG	XA	1670	1/1	0.76	0.13	59,59,59,59	0
55	MG	RA	3167	1/1	0.76	0.17	80,80,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	RA	3144	1/1	0.76	0.22	47,47,47,47	0
55	MG	RA	3474	1/1	0.77	0.34	58,58,58,58	0
55	MG	YA	3123	1/1	0.77	0.17	29,29,29,29	0
55	MG	RA	3300	1/1	0.77	0.26	60,60,60,60	0
55	MG	QA	1639	1/1	0.77	0.13	73,73,73,73	0
55	MG	RA	3121	1/1	0.77	0.14	59,59,59,59	0
55	MG	RA	3285	1/1	0.77	0.23	67,67,67,67	0
55	MG	RA	3457	1/1	0.77	0.25	51,51,51,51	0
55	MG	YA	3317	1/1	0.77	0.30	47,47,47,47	0
55	MG	YA	3011	1/1	0.77	0.22	40,40,40,40	0
55	MG	RA	3108	1/1	0.78	0.14	83,83,83,83	0
55	MG	YA	3119	1/1	0.78	0.18	43,43,43,43	0
55	MG	RA	3145	1/1	0.78	0.10	36,36,36,36	0
55	MG	RA	3269	1/1	0.78	0.27	70,70,70,70	0
55	MG	YA	3149	1/1	0.78	0.18	36,36,36,36	0
55	MG	QA	1635	1/1	0.78	0.21	59,59,59,59	0
55	MG	RA	3466	1/1	0.78	0.34	74,74,74,74	0
55	MG	RA	3399	1/1	0.78	0.24	69,69,69,69	0
55	MG	YA	3410	1/1	0.78	0.16	40,40,40,40	0
55	MG	RA	3358	1/1	0.78	0.21	68,68,68,68	0
55	MG	RA	3200	1/1	0.78	0.25	45,45,45,45	0
55	MG	RA	3287	1/1	0.78	0.32	58,58,58,58	0
55	MG	YA	3458	1/1	0.78	0.12	47,47,47,47	0
55	MG	XA	1683	1/1	0.78	0.23	155,155,155,155	0
56	ZN	Y4	101	1/1	0.78	0.16	196,196,196,196	0
55	MG	RT	201	1/1	0.79	0.35	82,82,82,82	0
55	MG	YA	3144	1/1	0.79	0.23	41,41,41,41	0
55	MG	XA	1620	1/1	0.79	0.14	62,62,62,62	0
55	MG	RA	3413	1/1	0.79	0.19	68,68,68,68	0
55	MG	XA	1639	1/1	0.79	0.12	42,42,42,42	0
55	MG	RA	3314	1/1	0.79	0.21	51,51,51,51	0
55	MG	RA	3237	1/1	0.79	0.20	57,57,57,57	0
55	MG	RB	204	1/1	0.79	0.33	57,57,57,57	0
55	MG	YA	3462	1/1	0.79	0.14	39,39,39,39	0
55	MG	YA	3202	1/1	0.79	0.11	47,47,47,47	0
55	MG	YA	3296	1/1	0.79	0.17	48,48,48,48	0
55	MG	RA	3271	1/1	0.79	0.23	79,79,79,79	0
55	MG	RA	3181	1/1	0.79	0.18	57,57,57,57	0
55	MG	RA	3394	1/1	0.80	0.23	52,52,52,52	0
55	MG	YA	3370	1/1	0.80	0.17	44,44,44,44	0
55	MG	RA	3371	1/1	0.80	0.18	70,70,70,70	0
55	MG	RA	3340	1/1	0.80	0.18	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	YA	3016	1/1	0.80	0.39	74,74,74,74	0
55	MG	YA	3197	1/1	0.80	0.30	58,58,58,58	0
55	MG	YA	3305	1/1	0.80	0.11	33,33,33,33	0
55	MG	RA	3379	1/1	0.80	0.22	79,79,79,79	0
55	MG	RA	3475	1/1	0.80	0.18	68,68,68,68	0
55	MG	RA	3248	1/1	0.80	0.22	45,45,45,45	0
55	MG	YA	3328	1/1	0.80	0.10	43,43,43,43	0
55	MG	YA	3132	1/1	0.80	0.19	35,35,35,35	0
55	MG	RA	3171	1/1	0.80	0.15	65,65,65,65	0
55	MG	RA	3262	1/1	0.80	0.20	63,63,63,63	0
55	MG	YA	3216	1/1	0.80	0.10	36,36,36,36	0
55	MG	RA	3260	1/1	0.81	0.30	66,66,66,66	0
55	MG	YA	3178	1/1	0.81	0.24	47,47,47,47	0
55	MG	YA	3420	1/1	0.81	0.17	52,52,52,52	0
55	MG	RA	3299	1/1	0.81	0.10	35,35,35,35	0
55	MG	YA	3310	1/1	0.81	0.33	69,69,69,69	0
55	MG	QA	1641	1/1	0.81	0.18	70,70,70,70	0
55	MG	YA	3318	1/1	0.81	0.12	41,41,41,41	0
55	MG	RA	3236	1/1	0.81	0.29	48,48,48,48	0
55	MG	RA	3396	1/1	0.81	0.17	64,64,64,64	0
55	MG	QA	1654	1/1	0.81	0.14	65,65,65,65	0
55	MG	RA	3268	1/1	0.81	0.35	67,67,67,67	0
55	MG	RA	3410	1/1	0.81	0.12	39,39,39,39	0
55	MG	YA	3507	1/1	0.81	0.34	21,21,21,21	0
55	MG	RA	3201	1/1	0.81	0.25	44,44,44,44	0
55	MG	YA	3353	1/1	0.81	0.16	42,42,42,42	0
55	MG	RA	3136	1/1	0.81	0.12	57,57,57,57	0
55	MG	RA	3309	1/1	0.81	0.11	59,59,59,59	0
55	MG	RA	3310	1/1	0.81	0.27	76,76,76,76	0
55	MG	YA	3371	1/1	0.81	0.09	27,27,27,27	0
55	MG	YA	3224	1/1	0.81	0.22	30,30,30,30	0
55	MG	XA	1669	1/1	0.81	0.31	51,51,51,51	0
55	MG	RA	3276	1/1	0.81	0.24	67,67,67,67	0
55	MG	QA	1630	1/1	0.81	0.09	70,70,70,70	0
55	MG	YA	3282	1/1	0.81	0.18	44,44,44,44	0
55	MG	YA	3394	1/1	0.81	0.32	70,70,70,70	0
55	MG	XL	201	1/1	0.81	0.09	69,69,69,69	0
55	MG	XS	101	1/1	0.81	0.11	89,89,89,89	0
55	MG	RA	3250	1/1	0.81	0.18	70,70,70,70	0
55	MG	YA	3002	1/1	0.82	0.13	37,37,37,37	0
55	MG	YA	3008	1/1	0.82	0.11	32,32,32,32	0
55	MG	QA	1617	1/1	0.82	0.08	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	RA	3338	1/1	0.82	0.17	51,51,51,51	0
55	MG	YA	3351	1/1	0.82	0.20	36,36,36,36	0
55	MG	YA	3496	1/1	0.82	0.23	72,72,72,72	0
55	MG	RA	3242	1/1	0.82	0.30	43,43,43,43	0
55	MG	YA	3110	1/1	0.82	0.15	31,31,31,31	0
55	MG	RA	3345	1/1	0.82	0.11	43,43,43,43	0
55	MG	YA	3121	1/1	0.82	0.14	16,16,16,16	0
55	MG	XA	1610	1/1	0.82	0.19	70,70,70,70	0
55	MG	RA	3352	1/1	0.82	0.24	79,79,79,79	0
55	MG	RA	3292	1/1	0.82	0.11	39,39,39,39	0
55	MG	XA	1631	1/1	0.82	0.11	51,51,51,51	0
55	MG	XA	1637	1/1	0.82	0.11	106,106,106,106	0
55	MG	RA	3294	1/1	0.82	0.28	65,65,65,65	0
55	MG	RA	3175	1/1	0.82	0.23	63,63,63,63	0
55	MG	YA	3147	1/1	0.82	0.22	70,70,70,70	0
55	MG	XA	1657	1/1	0.82	0.17	59,59,59,59	0
55	MG	RA	3254	1/1	0.82	0.20	54,54,54,54	0
55	MG	YA	3170	1/1	0.82	0.20	60,60,60,60	0
55	MG	QA	1643	1/1	0.82	0.12	58,58,58,58	0
55	MG	QA	1645	1/1	0.82	0.10	81,81,81,81	0
55	MG	RA	3122	1/1	0.82	0.18	42,42,42,42	0
55	MG	RA	3376	1/1	0.82	0.16	58,58,58,58	0
55	MG	YA	3434	1/1	0.82	0.10	27,27,27,27	0
55	MG	RA	3166	1/1	0.82	0.22	61,61,61,61	0
55	MG	YA	3453	1/1	0.82	0.22	89,89,89,89	0
55	MG	YA	3498	1/1	0.83	0.22	61,61,61,61	0
55	MG	RA	3151	1/1	0.83	0.10	42,42,42,42	0
55	MG	RA	3405	1/1	0.83	0.26	64,64,64,64	0
55	MG	YE	302	1/1	0.83	0.13	51,51,51,51	0
55	MG	RA	3154	1/1	0.83	0.10	33,33,33,33	0
55	MG	YA	3403	1/1	0.83	0.28	63,63,63,63	0
55	MG	RA	3045	1/1	0.83	0.12	30,30,30,30	0
55	MG	YA	3214	1/1	0.83	0.20	34,34,34,34	0
55	MG	RA	3141	1/1	0.83	0.20	75,75,75,75	0
55	MG	YA	3161	1/1	0.83	0.16	48,48,48,48	0
55	MG	RA	3349	1/1	0.83	0.12	54,54,54,54	0
55	MG	YA	3442	1/1	0.83	0.15	52,52,52,52	0
55	MG	YA	3042	1/1	0.83	0.40	194,194,194,194	0
55	MG	RA	3103	1/1	0.83	0.27	48,48,48,48	0
55	MG	YA	3454	1/1	0.83	0.19	88,88,88,88	0
55	MG	YA	3280	1/1	0.83	0.22	54,54,54,54	0
55	MG	RA	3125	1/1	0.83	0.28	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	YA	3186	1/1	0.83	0.21	40,40,40,40	0
55	MG	YA	3468	1/1	0.83	0.16	43,43,43,43	0
55	MG	RA	3114	1/1	0.83	0.18	43,43,43,43	0
55	MG	XE	201	1/1	0.83	0.17	72,72,72,72	0
55	MG	YA	3194	1/1	0.83	0.15	60,60,60,60	0
55	MG	RA	3119	1/1	0.83	0.15	56,56,56,56	0
55	MG	QA	1650	1/1	0.83	0.19	44,44,44,44	0
55	MG	YA	3487	1/1	0.84	0.26	53,53,53,53	0
55	MG	YA	3223	1/1	0.84	0.08	54,54,54,54	0
55	MG	YA	3166	1/1	0.84	0.21	44,44,44,44	0
55	MG	YA	3014	1/1	0.84	0.12	39,39,39,39	0
55	MG	YA	3175	1/1	0.84	0.17	34,34,34,34	0
55	MG	RA	3120	1/1	0.84	0.23	32,32,32,32	0
55	MG	YA	3039	1/1	0.84	0.43	28,28,28,28	0
55	MG	RA	3206	1/1	0.84	0.27	66,66,66,66	0
55	MG	RB	203	1/1	0.84	0.08	64,64,64,64	0
55	MG	YA	3190	1/1	0.84	0.15	23,23,23,23	0
55	MG	XA	1617	1/1	0.84	0.24	43,43,43,43	0
55	MG	RA	3153	1/1	0.84	0.23	65,65,65,65	0
55	MG	RA	3127	1/1	0.84	0.22	40,40,40,40	0
55	MG	RA	3431	1/1	0.84	0.37	84,84,84,84	0
55	MG	RA	3393	1/1	0.84	0.08	63,63,63,63	0
55	MG	YA	3425	1/1	0.84	0.16	52,52,52,52	0
55	MG	RA	3187	1/1	0.84	0.14	62,62,62,62	0
55	MG	YA	3433	1/1	0.84	0.22	60,60,60,60	0
55	MG	XA	1647	1/1	0.84	0.08	133,133,133,133	0
55	MG	RA	3265	1/1	0.84	0.19	39,39,39,39	0
55	MG	YA	3440	1/1	0.84	0.21	58,58,58,58	0
55	MG	RA	3232	1/1	0.84	0.11	34,34,34,34	0
55	MG	RA	3458	1/1	0.84	0.25	63,63,63,63	0
55	MG	YA	3213	1/1	0.84	0.13	28,28,28,28	0
55	MG	YA	3339	1/1	0.84	0.31	83,83,83,83	0
55	MG	RA	3464	1/1	0.84	0.10	42,42,42,42	0
55	MG	YA	3150	1/1	0.84	0.21	35,35,35,35	0
55	MG	RA	3347	1/1	0.84	0.17	61,61,61,61	0
55	MG	YA	3218	1/1	0.84	0.26	66,66,66,66	0
55	MG	YA	3359	1/1	0.84	0.20	56,56,56,56	0
55	MG	RA	3444	1/1	0.85	0.22	82,82,82,82	0
55	MG	RA	3403	1/1	0.85	0.15	20,20,20,20	0
55	MG	RA	3178	1/1	0.85	0.16	59,59,59,59	0
55	MG	YA	3153	1/1	0.85	0.19	34,34,34,34	0
55	MG	YE	304	1/1	0.85	0.14	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	XA	1607	1/1	0.85	0.18	44,44,44,44	0
55	MG	YA	3156	1/1	0.85	0.28	34,34,34,34	0
55	MG	RA	3077	1/1	0.85	0.14	26,26,26,26	0
55	MG	RA	3326	1/1	0.85	0.16	46,46,46,46	0
55	MG	RA	3412	1/1	0.85	0.16	73,73,73,73	0
55	MG	RA	3327	1/1	0.85	0.09	69,69,69,69	0
55	MG	YA	3075	1/1	0.85	0.20	65,65,65,65	0
55	MG	YA	3450	1/1	0.85	0.17	53,53,53,53	0
55	MG	YA	3451	1/1	0.85	0.16	35,35,35,35	0
55	MG	YA	3251	1/1	0.85	0.25	56,56,56,56	0
55	MG	YA	3360	1/1	0.85	0.14	43,43,43,43	0
55	MG	XA	1653	1/1	0.85	0.10	89,89,89,89	0
55	MG	RA	3007	1/1	0.85	0.19	56,56,56,56	0
55	MG	XA	1658	1/1	0.85	0.21	55,55,55,55	0
55	MG	YA	3459	1/1	0.85	0.16	41,41,41,41	0
55	MG	YA	3101	1/1	0.85	0.22	41,41,41,41	0
55	MG	YA	3105	1/1	0.85	0.26	34,34,34,34	0
55	MG	RA	3420	1/1	0.85	0.17	54,54,54,54	0
55	MG	XA	1679	1/1	0.85	0.08	90,90,90,90	0
55	MG	RA	3423	1/1	0.85	0.12	62,62,62,62	0
55	MG	RA	3280	1/1	0.85	0.36	73,73,73,73	0
55	MG	RA	3281	1/1	0.85	0.18	54,54,54,54	0
55	MG	RQ	201	1/1	0.85	0.10	59,59,59,59	0
55	MG	RA	3435	1/1	0.85	0.11	70,70,70,70	0
55	MG	RA	3006	1/1	0.85	0.11	53,53,53,53	0
55	MG	RA	3282	1/1	0.86	0.26	57,57,57,57	0
55	MG	QA	1647	1/1	0.86	0.20	67,67,67,67	0
55	MG	RA	3049	1/1	0.86	0.13	39,39,39,39	0
55	MG	YA	3426	1/1	0.86	0.35	54,54,54,54	0
55	MG	XA	1601	1/1	0.86	0.19	45,45,45,45	0
55	MG	RA	3321	1/1	0.86	0.19	33,33,33,33	0
55	MG	XA	1608	1/1	0.86	0.15	57,57,57,57	0
55	MG	YA	3228	1/1	0.86	0.26	46,46,46,46	0
55	MG	RA	3192	1/1	0.86	0.10	60,60,60,60	0
55	MG	RA	3470	1/1	0.86	0.27	47,47,47,47	0
55	MG	YA	3259	1/1	0.86	0.20	47,47,47,47	0
55	MG	YA	3446	1/1	0.86	0.30	78,78,78,78	0
55	MG	RA	3150	1/1	0.86	0.21	33,33,33,33	0
55	MG	YA	3263	1/1	0.86	0.13	23,23,23,23	0
55	MG	YA	3004	1/1	0.86	0.11	36,36,36,36	0
55	MG	RA	3012	1/1	0.86	0.18	23,23,23,23	0
55	MG	RA	3482	1/1	0.86	0.19	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	YA	3374	1/1	0.86	0.18	53,53,53,53	0
55	MG	YA	3375	1/1	0.86	0.15	57,57,57,57	0
55	MG	RB	202	1/1	0.86	0.08	51,51,51,51	0
55	MG	YA	3207	1/1	0.86	0.16	42,42,42,42	0
55	MG	YA	3465	1/1	0.86	0.14	31,31,31,31	0
55	MG	YA	3385	1/1	0.86	0.31	57,57,57,57	0
55	MG	YA	3471	1/1	0.86	0.13	43,43,43,43	0
55	MG	RA	3442	1/1	0.86	0.24	61,61,61,61	0
55	MG	RA	3443	1/1	0.86	0.09	76,76,76,76	0
55	MG	RA	3172	1/1	0.86	0.13	40,40,40,40	0
55	MG	YA	3399	1/1	0.86	0.29	44,44,44,44	0
55	MG	RA	3165	1/1	0.86	0.12	39,39,39,39	0
55	MG	XQ	201	1/1	0.86	0.09	86,86,86,86	0
55	MG	QA	1644	1/1	0.86	0.27	62,62,62,62	0
55	MG	YA	3092	1/1	0.86	0.24	22,22,22,22	0
55	MG	YA	3376	1/1	0.87	0.17	29,29,29,29	0
55	MG	RA	3373	1/1	0.87	0.23	57,57,57,57	0
55	MG	RA	3215	1/1	0.87	0.09	71,71,71,71	0
55	MG	RA	3263	1/1	0.87	0.12	30,30,30,30	0
55	MG	YA	3192	1/1	0.87	0.21	26,26,26,26	0
55	MG	QA	1666	1/1	0.87	0.18	58,58,58,58	0
55	MG	YA	3502	1/1	0.87	0.14	30,30,30,30	0
55	MG	RA	3478	1/1	0.87	0.10	50,50,50,50	0
55	MG	QA	1631	1/1	0.87	0.11	35,35,35,35	0
55	MG	YA	3200	1/1	0.87	0.13	24,24,24,24	0
55	MG	RA	3198	1/1	0.87	0.13	42,42,42,42	0
55	MG	Y0	102	1/1	0.87	0.14	32,32,32,32	0
55	MG	YA	3405	1/1	0.87	0.14	43,43,43,43	0
55	MG	XA	1604	1/1	0.87	0.09	114,114,114,114	0
55	MG	YA	3203	1/1	0.87	0.10	49,49,49,49	0
55	MG	YA	3415	1/1	0.87	0.09	40,40,40,40	0
55	MG	YA	3312	1/1	0.87	0.22	51,51,51,51	0
55	MG	YA	3204	1/1	0.87	0.10	42,42,42,42	0
55	MG	YA	3009	1/1	0.87	0.14	40,40,40,40	0
55	MG	RA	3162	1/1	0.87	0.09	49,49,49,49	0
55	MG	YA	3427	1/1	0.87	0.10	56,56,56,56	0
55	MG	XA	1635	1/1	0.87	0.11	63,63,63,63	0
55	MG	YA	3323	1/1	0.87	0.17	48,48,48,48	0
55	MG	YA	3431	1/1	0.87	0.30	58,58,58,58	0
55	MG	RA	3018	1/1	0.87	0.11	7,7,7,7	0
55	MG	YA	3325	1/1	0.87	0.19	43,43,43,43	0
55	MG	RA	3445	1/1	0.87	0.19	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	XA	1652	1/1	0.87	0.11	104,104,104,104	0
55	MG	YA	3017	1/1	0.87	0.17	42,42,42,42	0
55	MG	RA	3202	1/1	0.87	0.27	58,58,58,58	0
55	MG	YA	3337	1/1	0.87	0.19	80,80,80,80	0
55	MG	XA	1667	1/1	0.87	0.14	42,42,42,42	0
55	MG	RA	3337	1/1	0.87	0.07	57,57,57,57	0
55	MG	YA	3162	1/1	0.87	0.26	36,36,36,36	0
55	MG	YA	3056	1/1	0.87	0.27	41,41,41,41	0
55	MG	XA	1673	1/1	0.87	0.14	50,50,50,50	0
55	MG	YA	3167	1/1	0.87	0.26	30,30,30,30	0
55	MG	XA	1675	1/1	0.87	0.18	49,49,49,49	0
55	MG	YA	3221	1/1	0.87	0.17	42,42,42,42	0
55	MG	RA	3293	1/1	0.87	0.17	75,75,75,75	0
55	MG	YA	3173	1/1	0.87	0.16	60,60,60,60	0
55	MG	YA	3225	1/1	0.87	0.27	55,55,55,55	0
55	MG	RA	3426	1/1	0.87	0.20	44,44,44,44	0
55	MG	RA	3107	1/1	0.87	0.13	35,35,35,35	0
55	MG	YA	3241	1/1	0.87	0.29	49,49,49,49	0
55	MG	QA	1613	1/1	0.87	0.13	50,50,50,50	0
55	MG	YR	201	1/1	0.88	0.34	33,33,33,33	0
55	MG	QA	1628	1/1	0.88	0.08	63,63,63,63	0
55	MG	YA	3163	1/1	0.88	0.12	47,47,47,47	0
55	MG	RA	3105	1/1	0.88	0.12	27,27,27,27	0
55	MG	RA	3115	1/1	0.88	0.26	35,35,35,35	0
55	MG	YA	3267	1/1	0.88	0.17	65,65,65,65	0
55	MG	RA	3449	1/1	0.88	0.14	55,55,55,55	0
55	MG	XA	1614	1/1	0.88	0.11	59,59,59,59	0
55	MG	RA	3046	1/1	0.88	0.12	34,34,34,34	0
55	MG	QA	1638	1/1	0.88	0.21	40,40,40,40	0
55	MG	YA	3291	1/1	0.88	0.37	74,74,74,74	0
55	MG	YA	3292	1/1	0.88	0.29	56,56,56,56	0
55	MG	YA	3372	1/1	0.88	0.25	38,38,38,38	0
55	MG	YA	3176	1/1	0.88	0.20	30,30,30,30	0
55	MG	YA	3295	1/1	0.88	0.09	29,29,29,29	0
55	MG	RA	3311	1/1	0.88	0.17	51,51,51,51	0
55	MG	YA	3299	1/1	0.88	0.43	74,74,74,74	0
55	MG	RA	3074	1/1	0.88	0.24	37,37,37,37	0
55	MG	XA	1648	1/1	0.88	0.07	61,61,61,61	0
55	MG	XA	1649	1/1	0.88	0.12	63,63,63,63	0
55	MG	YA	3383	1/1	0.88	0.27	51,51,51,51	0
55	MG	RA	3247	1/1	0.88	0.15	29,29,29,29	0
55	MG	XA	1656	1/1	0.88	0.08	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	YA	3387	1/1	0.88	0.26	65,65,65,65	0
55	MG	RA	3406	1/1	0.88	0.22	44,44,44,44	0
55	MG	XA	1662	1/1	0.88	0.15	54,54,54,54	0
55	MG	XA	1665	1/1	0.88	0.10	53,53,53,53	0
55	MG	YA	3316	1/1	0.88	0.24	67,67,67,67	0
55	MG	YA	3486	1/1	0.88	0.25	28,28,28,28	0
55	MG	RA	3050	1/1	0.88	0.17	31,31,31,31	0
55	MG	YA	3488	1/1	0.88	0.17	19,19,19,19	0
55	MG	YA	3222	1/1	0.88	0.22	27,27,27,27	0
55	MG	RA	3283	1/1	0.88	0.21	54,54,54,54	0
55	MG	RA	3168	1/1	0.88	0.18	46,46,46,46	0
55	MG	YA	3053	1/1	0.88	0.15	18,18,18,18	0
55	MG	RA	3323	1/1	0.88	0.17	60,60,60,60	0
55	MG	YA	3069	1/1	0.88	0.20	28,28,28,28	0
55	MG	QA	1624	1/1	0.88	0.09	54,54,54,54	0
55	MG	YB	205	1/1	0.88	0.10	63,63,63,63	0
55	MG	YA	3243	1/1	0.88	0.24	51,51,51,51	0
55	MG	YA	3336	1/1	0.88	0.13	23,23,23,23	0
55	MG	YA	3248	1/1	0.88	0.20	54,54,54,54	0
55	MG	QA	1649	1/1	0.89	0.10	79,79,79,79	0
55	MG	YA	3127	1/1	0.89	0.20	22,22,22,22	0
55	MG	YA	3300	1/1	0.89	0.13	55,55,55,55	0
55	MG	YA	3303	1/1	0.89	0.12	41,41,41,41	0
55	MG	YA	3304	1/1	0.89	0.32	67,67,67,67	0
55	MG	RA	3185	1/1	0.89	0.13	27,27,27,27	0
55	MG	Y1	101	1/1	0.89	0.17	41,41,41,41	0
55	MG	YA	3414	1/1	0.89	0.09	37,37,37,37	0
55	MG	RA	3094	1/1	0.89	0.08	34,34,34,34	0
55	MG	YA	3137	1/1	0.89	0.16	30,30,30,30	0
55	MG	RA	3274	1/1	0.89	0.18	43,43,43,43	0
55	MG	YA	3424	1/1	0.89	0.22	71,71,71,71	0
55	MG	RQ	202	1/1	0.89	0.09	55,55,55,55	0
55	MG	YA	3148	1/1	0.89	0.10	23,23,23,23	0
55	MG	YA	3001	1/1	0.89	0.23	39,39,39,39	0
55	MG	RA	3441	1/1	0.89	0.18	48,48,48,48	0
55	MG	YA	3151	1/1	0.89	0.17	42,42,42,42	0
55	MG	RA	3161	1/1	0.89	0.15	41,41,41,41	0
55	MG	YA	3326	1/1	0.89	0.09	64,64,64,64	0
55	MG	RA	3397	1/1	0.89	0.28	48,48,48,48	0
55	MG	YA	3220	1/1	0.89	0.12	44,44,44,44	0
55	MG	RA	3036	1/1	0.89	0.19	36,36,36,36	0
55	MG	RA	3402	1/1	0.89	0.07	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	RA	3446	1/1	0.89	0.13	39,39,39,39	0
55	MG	RA	3140	1/1	0.89	0.23	45,45,45,45	0
55	MG	RA	3177	1/1	0.89	0.07	67,67,67,67	0
55	MG	RA	3128	1/1	0.89	0.15	49,49,49,49	0
55	MG	YA	3171	1/1	0.89	0.15	33,33,33,33	0
55	MG	RA	3407	1/1	0.89	0.08	57,57,57,57	0
55	MG	RA	3463	1/1	0.89	0.12	49,49,49,49	0
55	MG	RA	3225	1/1	0.89	0.19	36,36,36,36	0
55	MG	RA	3370	1/1	0.89	0.12	42,42,42,42	0
55	MG	YA	3466	1/1	0.89	0.13	46,46,46,46	0
55	MG	YA	3257	1/1	0.89	0.27	37,37,37,37	0
55	MG	RA	3286	1/1	0.89	0.25	57,57,57,57	0
55	MG	YA	3182	1/1	0.89	0.13	55,55,55,55	0
55	MG	RA	3082	1/1	0.89	0.22	36,36,36,36	0
55	MG	YA	3185	1/1	0.89	0.10	42,42,42,42	0
55	MG	RA	3291	1/1	0.89	0.08	34,34,34,34	0
55	MG	YA	3492	1/1	0.89	0.17	25,25,25,25	0
55	MG	YA	3281	1/1	0.89	0.12	40,40,40,40	0
55	MG	XA	1682	1/1	0.89	0.12	132,132,132,132	0
55	MG	RA	3233	1/1	0.89	0.19	39,39,39,39	0
55	MG	RA	3234	1/1	0.89	0.15	33,33,33,33	0
55	MG	RA	3135	1/1	0.89	0.13	57,57,57,57	0
55	MG	RA	3428	1/1	0.89	0.17	41,41,41,41	0
55	MG	YA	3120	1/1	0.89	0.21	57,57,57,57	0
55	MG	RA	3203	1/1	0.89	0.09	59,59,59,59	0
55	MG	YA	3391	1/1	0.90	0.20	41,41,41,41	0
55	MG	RA	3229	1/1	0.90	0.24	50,50,50,50	0
55	MG	YA	3508	1/1	0.90	0.26	31,31,31,31	0
55	MG	YB	202	1/1	0.90	0.17	35,35,35,35	0
55	MG	RX	101	1/1	0.90	0.21	57,57,57,57	0
55	MG	YA	3395	1/1	0.90	0.18	43,43,43,43	0
55	MG	YA	3397	1/1	0.90	0.14	50,50,50,50	0
55	MG	RA	3332	1/1	0.90	0.21	65,65,65,65	0
55	MG	RA	3062	1/1	0.90	0.07	29,29,29,29	0
55	MG	RA	3409	1/1	0.90	0.20	56,56,56,56	0
55	MG	YA	3306	1/1	0.90	0.18	35,35,35,35	0
55	MG	Y8	101	1/1	0.90	0.14	30,30,30,30	0
55	MG	RA	3088	1/1	0.90	0.23	23,23,23,23	0
55	MG	RA	3450	1/1	0.90	0.17	37,37,37,37	0
55	MG	RA	3149	1/1	0.90	0.09	34,34,34,34	0
55	MG	RA	3344	1/1	0.90	0.20	27,27,27,27	0
55	MG	XA	1609	1/1	0.90	0.22	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	YA	3157	1/1	0.90	0.18	33,33,33,33	0
55	MG	RA	3461	1/1	0.90	0.16	25,25,25,25	0
55	MG	RA	3252	1/1	0.90	0.18	31,31,31,31	0
55	MG	XA	1619	1/1	0.90	0.28	56,56,56,56	0
55	MG	RA	3031	1/1	0.90	0.24	21,21,21,21	0
55	MG	RA	3298	1/1	0.90	0.12	61,61,61,61	0
55	MG	YA	3065	1/1	0.90	0.10	28,28,28,28	0
55	MG	RA	3392	1/1	0.90	0.19	56,56,56,56	0
55	MG	YA	3071	1/1	0.90	0.17	28,28,28,28	0
55	MG	YA	3226	1/1	0.90	0.22	59,59,59,59	0
55	MG	YA	3438	1/1	0.90	0.15	52,52,52,52	0
55	MG	XA	1642	1/1	0.90	0.13	37,37,37,37	0
55	MG	YA	3172	1/1	0.90	0.16	27,27,27,27	0
55	MG	XA	1646	1/1	0.90	0.22	47,47,47,47	0
55	MG	RA	3424	1/1	0.90	0.06	70,70,70,70	0
55	MG	YA	3444	1/1	0.90	0.25	63,63,63,63	0
55	MG	YA	3239	1/1	0.90	0.19	7,7,7,7	0
55	MG	RA	3351	1/1	0.90	0.10	55,55,55,55	0
55	MG	YA	3343	1/1	0.90	0.20	49,49,49,49	0
55	MG	XA	1654	1/1	0.90	0.14	44,44,44,44	0
55	MG	YA	3090	1/1	0.90	0.17	28,28,28,28	0
55	MG	RA	3112	1/1	0.90	0.15	36,36,36,36	0
55	MG	YA	3357	1/1	0.90	0.26	50,50,50,50	0
55	MG	YA	3096	1/1	0.90	0.14	30,30,30,30	0
55	MG	RA	3051	1/1	0.90	0.22	18,18,18,18	0
55	MG	RB	201	1/1	0.90	0.22	70,70,70,70	0
55	MG	YA	3365	1/1	0.90	0.23	47,47,47,47	0
55	MG	YA	3108	1/1	0.90	0.08	36,36,36,36	0
55	MG	RA	3029	1/1	0.90	0.12	8,8,8,8	0
55	MG	RA	3398	1/1	0.90	0.23	43,43,43,43	0
55	MG	YA	3279	1/1	0.90	0.12	51,51,51,51	0
55	MG	RA	3437	1/1	0.90	0.17	39,39,39,39	0
55	MG	XA	1676	1/1	0.90	0.16	43,43,43,43	0
55	MG	RA	3360	1/1	0.90	0.20	63,63,63,63	0
55	MG	RA	3400	1/1	0.90	0.19	55,55,55,55	0
55	MG	YA	3379	1/1	0.90	0.27	29,29,29,29	0
55	MG	YA	3195	1/1	0.90	0.13	35,35,35,35	0
55	MG	XA	1687	1/1	0.90	0.14	79,79,79,79	0
55	MG	RN	201	1/1	0.90	0.22	60,60,60,60	0
55	MG	YA	3199	1/1	0.90	0.18	56,56,56,56	0
55	MG	RA	3039	1/1	0.90	0.15	22,22,22,22	0
55	MG	YA	3135	1/1	0.90	0.28	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	RA	3363	1/1	0.90	0.07	25,25,25,25	0
55	MG	YA	3275	1/1	0.91	0.18	31,31,31,31	0
55	MG	YA	3277	1/1	0.91	0.18	56,56,56,56	0
55	MG	YA	3504	1/1	0.91	0.11	33,33,33,33	0
55	MG	RA	3258	1/1	0.91	0.21	29,29,29,29	0
55	MG	RA	3047	1/1	0.91	0.21	24,24,24,24	0
55	MG	RA	3427	1/1	0.91	0.15	39,39,39,39	0
55	MG	RA	3472	1/1	0.91	0.18	37,37,37,37	0
55	MG	RA	3473	1/1	0.91	0.16	56,56,56,56	0
55	MG	YA	3290	1/1	0.91	0.20	22,22,22,22	0
55	MG	RA	3261	1/1	0.91	0.22	55,55,55,55	0
55	MG	YO	201	1/1	0.91	0.07	63,63,63,63	0
55	MG	RA	3353	1/1	0.91	0.13	60,60,60,60	0
55	MG	Y0	101	1/1	0.91	0.23	41,41,41,41	0
55	MG	RA	3354	1/1	0.91	0.10	51,51,51,51	0
55	MG	YA	3294	1/1	0.91	0.07	25,25,25,25	0
55	MG	RA	3480	1/1	0.91	0.21	55,55,55,55	0
55	MG	RA	3481	1/1	0.91	0.11	58,58,58,58	0
55	MG	YA	3111	1/1	0.91	0.22	28,28,28,28	0
55	MG	RA	3180	1/1	0.91	0.16	50,50,50,50	0
55	MG	YA	3302	1/1	0.91	0.29	36,36,36,36	0
55	MG	RA	3210	1/1	0.91	0.11	44,44,44,44	0
55	MG	RA	3401	1/1	0.91	0.12	43,43,43,43	0
55	MG	XA	1611	1/1	0.91	0.14	46,46,46,46	0
55	MG	YA	3416	1/1	0.91	0.13	47,47,47,47	0
55	MG	RA	3317	1/1	0.91	0.11	49,49,49,49	0
55	MG	RA	3319	1/1	0.91	0.08	26,26,26,26	0
55	MG	YA	3129	1/1	0.91	0.15	5,5,5,5	0
55	MG	YA	3130	1/1	0.91	0.20	24,24,24,24	0
55	MG	RB	206	1/1	0.91	0.21	36,36,36,36	0
55	MG	YA	3133	1/1	0.91	0.17	38,38,38,38	0
55	MG	RA	3146	1/1	0.91	0.17	35,35,35,35	0
55	MG	RA	3182	1/1	0.91	0.09	52,52,52,52	0
55	MG	QA	1658	1/1	0.91	0.10	49,49,49,49	0
55	MG	XA	1641	1/1	0.91	0.09	68,68,68,68	0
55	MG	QA	1660	1/1	0.91	0.23	41,41,41,41	0
55	MG	YA	3437	1/1	0.91	0.09	29,29,29,29	0
55	MG	RA	3214	1/1	0.91	0.23	27,27,27,27	0
55	MG	QA	1663	1/1	0.91	0.17	67,67,67,67	0
55	MG	RP	202	1/1	0.91	0.10	47,47,47,47	0
55	MG	RA	3164	1/1	0.91	0.20	38,38,38,38	0
55	MG	YA	3332	1/1	0.91	0.27	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	RA	3038	1/1	0.91	0.14	13,13,13,13	0
55	MG	YA	3334	1/1	0.91	0.16	33,33,33,33	0
55	MG	RA	3228	1/1	0.91	0.09	48,48,48,48	0
55	MG	RA	3303	1/1	0.91	0.15	26,26,26,26	0
55	MG	RA	3453	1/1	0.91	0.24	52,52,52,52	0
55	MG	QA	1601	1/1	0.91	0.20	47,47,47,47	0
55	MG	XA	1663	1/1	0.91	0.17	51,51,51,51	0
55	MG	QA	1604	1/1	0.91	0.13	34,34,34,34	0
55	MG	QA	1611	1/1	0.91	0.19	26,26,26,26	0
55	MG	YA	3233	1/1	0.91	0.08	34,34,34,34	0
55	MG	YA	3356	1/1	0.91	0.11	42,42,42,42	0
55	MG	QA	1612	1/1	0.91	0.10	35,35,35,35	0
55	MG	YA	3467	1/1	0.91	0.07	24,24,24,24	0
55	MG	RA	3028	1/1	0.91	0.27	38,38,38,38	0
55	MG	QA	1614	1/1	0.91	0.12	68,68,68,68	0
55	MG	YA	3045	1/1	0.91	0.16	3,3,3,3	0
55	MG	YA	3476	1/1	0.91	0.12	26,26,26,26	0
55	MG	YA	3477	1/1	0.91	0.15	24,24,24,24	0
55	MG	QA	1616	1/1	0.91	0.10	60,60,60,60	0
55	MG	YA	3255	1/1	0.91	0.21	35,35,35,35	0
55	MG	XA	1685	1/1	0.91	0.08	82,82,82,82	0
55	MG	RA	3076	1/1	0.91	0.25	34,34,34,34	0
55	MG	YA	3057	1/1	0.91	0.15	17,17,17,17	0
55	MG	RA	3253	1/1	0.91	0.28	52,52,52,52	0
55	MG	YA	3177	1/1	0.91	0.19	46,46,46,46	0
55	MG	RA	3189	1/1	0.91	0.22	31,31,31,31	0
55	MG	YA	3270	1/1	0.91	0.10	41,41,41,41	0
55	MG	YA	3091	1/1	0.92	0.10	26,26,26,26	0
55	MG	YA	3268	1/1	0.92	0.23	31,31,31,31	0
55	MG	YA	3269	1/1	0.92	0.18	39,39,39,39	0
55	MG	YA	3179	1/1	0.92	0.16	40,40,40,40	0
55	MG	RA	3418	1/1	0.92	0.09	53,53,53,53	0
55	MG	RA	3208	1/1	0.92	0.11	68,68,68,68	0
55	MG	YA	3278	1/1	0.92	0.22	49,49,49,49	0
55	MG	RA	3118	1/1	0.92	0.11	35,35,35,35	0
55	MG	YA	3506	1/1	0.92	0.15	42,42,42,42	0
55	MG	RA	3023	1/1	0.92	0.19	14,14,14,14	0
55	MG	YA	3106	1/1	0.92	0.24	21,21,21,21	0
55	MG	YA	3509	1/1	0.92	0.20	6,6,6,6	0
55	MG	YA	3510	1/1	0.92	0.13	40,40,40,40	0
55	MG	YB	201	1/1	0.92	0.11	12,12,12,12	0
55	MG	RA	3092	1/1	0.92	0.13	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	YA	3386	1/1	0.92	0.18	47,47,47,47	0
55	MG	RA	3375	1/1	0.92	0.08	45,45,45,45	0
55	MG	YA	3388	1/1	0.92	0.19	38,38,38,38	0
55	MG	YA	3289	1/1	0.92	0.11	12,12,12,12	0
55	MG	RA	3289	1/1	0.92	0.24	46,46,46,46	0
55	MG	RA	3066	1/1	0.92	0.11	28,28,28,28	0
55	MG	RA	3381	1/1	0.92	0.13	69,69,69,69	0
55	MG	RA	3385	1/1	0.92	0.20	42,42,42,42	0
55	MG	RA	3188	1/1	0.92	0.27	62,62,62,62	0
55	MG	RA	3224	1/1	0.92	0.19	11,11,11,11	0
55	MG	YA	3401	1/1	0.92	0.14	35,35,35,35	0
55	MG	RA	3439	1/1	0.92	0.10	39,39,39,39	0
55	MG	YA	3297	1/1	0.92	0.26	80,80,80,80	0
55	MG	YA	3298	1/1	0.92	0.15	59,59,59,59	0
55	MG	YA	3407	1/1	0.92	0.14	28,28,28,28	0
55	MG	RA	3333	1/1	0.92	0.13	34,34,34,34	0
55	MG	YA	3412	1/1	0.92	0.09	39,39,39,39	0
55	MG	XA	1613	1/1	0.92	0.14	63,63,63,63	0
55	MG	RA	3334	1/1	0.92	0.15	66,66,66,66	0
55	MG	XA	1616	1/1	0.92	0.14	18,18,18,18	0
55	MG	RA	3033	1/1	0.92	0.15	28,28,28,28	0
55	MG	YA	3134	1/1	0.92	0.14	23,23,23,23	0
55	MG	YA	3417	1/1	0.92	0.14	45,45,45,45	0
55	MG	RA	3169	1/1	0.92	0.07	46,46,46,46	0
55	MG	RA	3395	1/1	0.92	0.24	68,68,68,68	0
55	MG	XA	1633	1/1	0.92	0.08	49,49,49,49	0
55	MG	RA	3170	1/1	0.92	0.24	45,45,45,45	0
55	MG	YA	3142	1/1	0.92	0.12	26,26,26,26	0
55	MG	YA	3311	1/1	0.92	0.38	46,46,46,46	0
55	MG	RA	3342	1/1	0.92	0.13	45,45,45,45	0
55	MG	YA	3145	1/1	0.92	0.16	43,43,43,43	0
55	MG	YA	3430	1/1	0.92	0.20	58,58,58,58	0
55	MG	XA	1643	1/1	0.92	0.16	39,39,39,39	0
55	MG	RA	3035	1/1	0.92	0.13	44,44,44,44	0
55	MG	RA	3075	1/1	0.92	0.12	37,37,37,37	0
55	MG	RA	3024	1/1	0.92	0.19	32,32,32,32	0
55	MG	YA	3435	1/1	0.92	0.07	40,40,40,40	0
55	MG	YA	3322	1/1	0.92	0.50	96,96,96,96	0
55	MG	RA	3235	1/1	0.92	0.16	60,60,60,60	0
55	MG	YA	3030	1/1	0.92	0.23	26,26,26,26	0
55	MG	RA	3307	1/1	0.92	0.22	31,31,31,31	0
55	MG	RA	3017	1/1	0.92	0.13	3,3,3,3	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	RA	3130	1/1	0.92	0.19	19,19,19,19	0
55	MG	YA	3158	1/1	0.92	0.13	26,26,26,26	0
55	MG	XA	1661	1/1	0.92	0.24	32,32,32,32	0
55	MG	RA	3081	1/1	0.92	0.25	24,24,24,24	0
55	MG	RA	3355	1/1	0.92	0.17	49,49,49,49	0
55	MG	YA	3452	1/1	0.92	0.20	40,40,40,40	0
55	MG	RA	3278	1/1	0.92	0.23	41,41,41,41	0
55	MG	YA	3058	1/1	0.92	0.11	13,13,13,13	0
55	MG	YA	3456	1/1	0.92	0.23	35,35,35,35	0
55	MG	RA	3467	1/1	0.92	0.20	54,54,54,54	0
55	MG	XA	1671	1/1	0.92	0.09	57,57,57,57	0
55	MG	YA	3338	1/1	0.92	0.15	50,50,50,50	0
55	MG	YA	3461	1/1	0.92	0.10	45,45,45,45	0
55	MG	RA	3015	1/1	0.92	0.14	29,29,29,29	0
55	MG	YA	3070	1/1	0.92	0.24	34,34,34,34	0
55	MG	XA	1678	1/1	0.92	0.19	50,50,50,50	0
55	MG	RA	3313	1/1	0.92	0.14	60,60,60,60	0
55	MG	YA	3350	1/1	0.92	0.14	44,44,44,44	0
55	MG	YA	3252	1/1	0.92	0.17	24,24,24,24	0
55	MG	YA	3253	1/1	0.92	0.29	49,49,49,49	0
55	MG	YA	3074	1/1	0.92	0.12	28,28,28,28	0
55	MG	YA	3256	1/1	0.92	0.17	39,39,39,39	0
55	MG	YA	3174	1/1	0.92	0.19	36,36,36,36	0
55	MG	YA	3258	1/1	0.92	0.28	22,22,22,22	0
55	MG	RA	3030	1/1	0.92	0.22	29,29,29,29	0
55	MG	RA	3086	1/1	0.92	0.21	30,30,30,30	0
56	ZN	R4	101	1/1	0.92	0.08	319,319,319,319	0
55	MG	RA	3415	1/1	0.92	0.08	34,34,34,34	0
55	MG	RA	3220	1/1	0.93	0.17	41,41,41,41	0
55	MG	RA	3040	1/1	0.93	0.13	42,42,42,42	0
55	MG	RA	3422	1/1	0.93	0.14	40,40,40,40	0
55	MG	RA	3335	1/1	0.93	0.12	38,38,38,38	0
55	MG	YA	3076	1/1	0.93	0.26	23,23,23,23	0
55	MG	YA	3080	1/1	0.93	0.09	28,28,28,28	0
55	MG	YA	3183	1/1	0.93	0.16	39,39,39,39	0
55	MG	QA	1636	1/1	0.93	0.11	40,40,40,40	0
55	MG	YB	207	1/1	0.93	0.28	70,70,70,70	0
55	MG	YA	3082	1/1	0.93	0.20	21,21,21,21	0
55	MG	RA	3382	1/1	0.93	0.17	48,48,48,48	0
55	MG	RA	3336	1/1	0.93	0.21	51,51,51,51	0
55	MG	RA	3131	1/1	0.93	0.14	31,31,31,31	0
55	MG	YQ	201	1/1	0.93	0.11	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	RA	3226	1/1	0.93	0.37	71,71,71,71	0
55	MG	YA	3100	1/1	0.93	0.22	15,15,15,15	0
55	MG	YA	3404	1/1	0.93	0.09	47,47,47,47	0
55	MG	RA	3429	1/1	0.93	0.14	64,64,64,64	0
55	MG	RA	3484	1/1	0.93	0.07	47,47,47,47	0
55	MG	YA	3408	1/1	0.93	0.11	3,3,3,3	0
55	MG	RA	3430	1/1	0.93	0.12	50,50,50,50	0
55	MG	QA	1646	1/1	0.93	0.08	56,56,56,56	0
55	MG	RA	3305	1/1	0.93	0.31	61,61,61,61	0
55	MG	RA	3010	1/1	0.93	0.14	31,31,31,31	0
55	MG	RA	3116	1/1	0.93	0.15	42,42,42,42	0
55	MG	RA	3231	1/1	0.93	0.18	52,52,52,52	0
55	MG	XA	1612	1/1	0.93	0.20	36,36,36,36	0
55	MG	QA	1652	1/1	0.93	0.10	41,41,41,41	0
55	MG	RA	3191	1/1	0.93	0.13	125,125,125,125	0
55	MG	YA	3209	1/1	0.93	0.13	14,14,14,14	0
55	MG	YA	3125	1/1	0.93	0.11	27,27,27,27	0
55	MG	YA	3314	1/1	0.93	0.09	43,43,43,43	0
55	MG	YA	3315	1/1	0.93	0.13	22,22,22,22	0
55	MG	XA	1623	1/1	0.93	0.12	34,34,34,34	0
55	MG	QA	1656	1/1	0.93	0.21	25,25,25,25	0
55	MG	QA	1657	1/1	0.93	0.12	60,60,60,60	0
55	MG	RA	3157	1/1	0.93	0.21	38,38,38,38	0
55	MG	XA	1634	1/1	0.93	0.05	114,114,114,114	0
55	MG	RA	3255	1/1	0.93	0.24	50,50,50,50	0
55	MG	RA	3009	1/1	0.93	0.22	25,25,25,25	0
55	MG	XA	1638	1/1	0.93	0.15	39,39,39,39	0
55	MG	YA	3217	1/1	0.93	0.21	30,30,30,30	0
55	MG	YA	3436	1/1	0.93	0.24	58,58,58,58	0
55	MG	RA	3259	1/1	0.93	0.26	77,77,77,77	0
55	MG	RA	3101	1/1	0.93	0.14	29,29,29,29	0
55	MG	RA	3089	1/1	0.93	0.12	25,25,25,25	0
55	MG	RA	3184	1/1	0.93	0.22	43,43,43,43	0
55	MG	YA	3443	1/1	0.93	0.20	65,65,65,65	0
55	MG	YA	3139	1/1	0.93	0.16	27,27,27,27	0
55	MG	RA	3239	1/1	0.93	0.16	48,48,48,48	0
55	MG	YA	3143	1/1	0.93	0.18	68,68,68,68	0
55	MG	R1	300	1/1	0.93	0.25	46,46,46,46	0
55	MG	RA	3359	1/1	0.93	0.08	9,9,9,9	0
55	MG	YA	3010	1/1	0.93	0.10	44,44,44,44	0
55	MG	RA	3173	1/1	0.93	0.09	51,51,51,51	0
55	MG	YA	3235	1/1	0.93	0.27	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	YA	3340	1/1	0.93	0.28	57,57,57,57	0
55	MG	XA	1659	1/1	0.93	0.07	53,53,53,53	0
55	MG	QA	1610	1/1	0.93	0.13	20,20,20,20	0
55	MG	RA	3451	1/1	0.93	0.17	37,37,37,37	0
55	MG	YA	3346	1/1	0.93	0.15	34,34,34,34	0
55	MG	XA	1664	1/1	0.93	0.14	56,56,56,56	0
55	MG	RA	3266	1/1	0.93	0.10	43,43,43,43	0
55	MG	YA	3026	1/1	0.93	0.24	13,13,13,13	0
55	MG	YA	3154	1/1	0.93	0.25	36,36,36,36	0
55	MG	YA	3354	1/1	0.93	0.15	54,54,54,54	0
55	MG	RA	3322	1/1	0.93	0.13	48,48,48,48	0
55	MG	YA	3031	1/1	0.93	0.09	14,14,14,14	0
55	MG	RA	3366	1/1	0.93	0.19	49,49,49,49	0
55	MG	YA	3160	1/1	0.93	0.16	34,34,34,34	0
55	MG	YA	3473	1/1	0.93	0.33	56,56,56,56	0
55	MG	RA	3459	1/1	0.93	0.14	25,25,25,25	0
55	MG	RA	3295	1/1	0.93	0.18	29,29,29,29	0
55	MG	YA	3050	1/1	0.93	0.19	20,20,20,20	0
55	MG	XA	1680	1/1	0.93	0.09	23,23,23,23	0
55	MG	RA	3296	1/1	0.93	0.06	45,45,45,45	0
55	MG	YA	3262	1/1	0.93	0.17	40,40,40,40	0
55	MG	YA	3054	1/1	0.93	0.09	25,25,25,25	0
55	MG	QA	1619	1/1	0.93	0.07	67,67,67,67	0
55	MG	RA	3297	1/1	0.93	0.10	43,43,43,43	0
55	MG	RA	3330	1/1	0.93	0.10	27,27,27,27	0
55	MG	QA	1626	1/1	0.93	0.10	36,36,36,36	0
55	MG	YA	3499	1/1	0.93	0.07	37,37,37,37	0
55	MG	YA	3273	1/1	0.93	0.18	38,38,38,38	0
55	MG	YA	3068	1/1	0.93	0.20	32,32,32,32	0
55	MG	RA	3267	1/1	0.93	0.17	33,33,33,33	0
55	MG	QA	1603	1/1	0.94	0.23	25,25,25,25	0
55	MG	RA	3142	1/1	0.94	0.21	40,40,40,40	0
55	MG	YP	202	1/1	0.94	0.09	22,22,22,22	0
55	MG	YA	3319	1/1	0.94	0.08	33,33,33,33	0
55	MG	YA	3320	1/1	0.94	0.25	18,18,18,18	0
55	MG	YA	3159	1/1	0.94	0.08	31,31,31,31	0
55	MG	RA	3190	1/1	0.94	0.18	25,25,25,25	0
55	MG	YA	3421	1/1	0.94	0.16	68,68,68,68	0
55	MG	RA	3159	1/1	0.94	0.09	29,29,29,29	0
55	MG	RA	3364	1/1	0.94	0.04	36,36,36,36	0
55	MG	XA	1603	1/1	0.94	0.18	30,30,30,30	0
55	MG	YA	3079	1/1	0.94	0.11	10,10,10,10	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	YA	3164	1/1	0.94	0.05	64,64,64,64	0
55	MG	YA	3247	1/1	0.94	0.27	30,30,30,30	0
55	MG	YA	3165	1/1	0.94	0.11	26,26,26,26	0
55	MG	YA	3250	1/1	0.94	0.18	40,40,40,40	0
55	MG	YA	3432	1/1	0.94	0.11	37,37,37,37	0
55	MG	RA	3160	1/1	0.94	0.13	47,47,47,47	0
55	MG	RA	3436	1/1	0.94	0.08	57,57,57,57	0
55	MG	YA	3335	1/1	0.94	0.18	44,44,44,44	0
55	MG	RA	3113	1/1	0.94	0.10	38,38,38,38	0
55	MG	RA	3476	1/1	0.94	0.17	21,21,21,21	0
55	MG	RA	3196	1/1	0.94	0.15	50,50,50,50	0
55	MG	QF	201	1/1	0.94	0.08	50,50,50,50	0
55	MG	RA	3277	1/1	0.94	0.08	36,36,36,36	0
55	MG	YA	3097	1/1	0.94	0.17	27,27,27,27	0
55	MG	QA	1620	1/1	0.94	0.16	45,45,45,45	0
55	MG	YA	3345	1/1	0.94	0.06	30,30,30,30	0
55	MG	RA	3087	1/1	0.94	0.14	26,26,26,26	0
55	MG	YA	3102	1/1	0.94	0.15	16,16,16,16	0
55	MG	YA	3266	1/1	0.94	0.26	22,22,22,22	0
55	MG	YA	3104	1/1	0.94	0.19	12,12,12,12	0
55	MG	RA	3374	1/1	0.94	0.10	47,47,47,47	0
55	MG	QA	1625	1/1	0.94	0.23	55,55,55,55	0
55	MG	YA	3455	1/1	0.94	0.11	56,56,56,56	0
55	MG	RA	3199	1/1	0.94	0.23	48,48,48,48	0
55	MG	RA	3320	1/1	0.94	0.12	32,32,32,32	0
55	MG	YA	3012	1/1	0.94	0.19	42,42,42,42	0
55	MG	YA	3117	1/1	0.94	0.06	34,34,34,34	0
55	MG	RA	3377	1/1	0.94	0.12	80,80,80,80	0
55	MG	RA	3348	1/1	0.94	0.05	60,60,60,60	0
55	MG	YA	3369	1/1	0.94	0.07	61,61,61,61	0
55	MG	XA	1651	1/1	0.94	0.13	40,40,40,40	0
55	MG	QA	1633	1/1	0.94	0.11	41,41,41,41	0
55	MG	RA	3152	1/1	0.94	0.10	31,31,31,31	0
55	MG	RB	205	1/1	0.94	0.18	38,38,38,38	0
55	MG	XA	1655	1/1	0.94	0.18	40,40,40,40	0
55	MG	YA	3373	1/1	0.94	0.12	43,43,43,43	0
55	MG	YA	3284	1/1	0.94	0.09	3,3,3,3	0
55	MG	YA	3286	1/1	0.94	0.18	48,48,48,48	0
55	MG	YA	3474	1/1	0.94	0.22	65,65,65,65	0
55	MG	XA	1660	1/1	0.94	0.07	51,51,51,51	0
55	MG	RA	3448	1/1	0.94	0.20	47,47,47,47	0
55	MG	YA	3034	1/1	0.94	0.17	8,8,8,8	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	YA	3485	1/1	0.94	0.10	3,3,3,3	0
55	MG	YA	3035	1/1	0.94	0.23	12,12,12,12	0
55	MG	YA	3131	1/1	0.94	0.08	25,25,25,25	0
55	MG	RA	3350	1/1	0.94	0.14	39,39,39,39	0
55	MG	RA	3218	1/1	0.94	0.20	33,33,33,33	0
55	MG	YA	3043	1/1	0.94	0.12	13,13,13,13	0
55	MG	YA	3495	1/1	0.94	0.17	51,51,51,51	0
55	MG	YA	3044	1/1	0.94	0.15	18,18,18,18	0
55	MG	QA	1640	1/1	0.94	0.11	46,46,46,46	0
55	MG	YA	3046	1/1	0.94	0.27	24,24,24,24	0
55	MG	RA	3240	1/1	0.94	0.23	24,24,24,24	0
55	MG	RA	3174	1/1	0.94	0.18	31,31,31,31	0
55	MG	RA	3455	1/1	0.94	0.15	10,10,10,10	0
55	MG	YA	3055	1/1	0.94	0.23	33,33,33,33	0
55	MG	RA	3042	1/1	0.94	0.23	20,20,20,20	0
55	MG	YA	3146	1/1	0.94	0.17	26,26,26,26	0
55	MG	RA	3079	1/1	0.94	0.09	26,26,26,26	0
55	MG	RA	3356	1/1	0.94	0.22	49,49,49,49	0
55	MG	XA	1684	1/1	0.94	0.20	41,41,41,41	0
55	MG	YA	3062	1/1	0.94	0.22	25,25,25,25	0
55	MG	YA	3064	1/1	0.94	0.20	3,3,3,3	0
55	MG	RA	3331	1/1	0.94	0.08	42,42,42,42	0
55	MG	YB	203	1/1	0.94	0.07	36,36,36,36	0
55	MG	YA	3313	1/1	0.94	0.16	48,48,48,48	0
55	MG	YA	3066	1/1	0.94	0.24	17,17,17,17	0
55	MG	RA	3288	1/1	0.94	0.45	67,67,67,67	0
55	MG	RA	3106	1/1	0.94	0.11	16,16,16,16	0
55	MG	RA	3217	1/1	0.95	0.16	28,28,28,28	0
55	MG	YA	3489	1/1	0.95	0.21	37,37,37,37	0
55	MG	YA	3361	1/1	0.95	0.23	45,45,45,45	0
55	MG	RB	207	1/1	0.95	0.17	26,26,26,26	0
55	MG	YA	3260	1/1	0.95	0.34	64,64,64,64	0
55	MG	YA	3367	1/1	0.95	0.19	39,39,39,39	0
55	MG	RA	3195	1/1	0.95	0.06	46,46,46,46	0
55	MG	RE	302	1/1	0.95	0.14	33,33,33,33	0
55	MG	RA	3102	1/1	0.95	0.14	34,34,34,34	0
55	MG	YA	3265	1/1	0.95	0.20	25,25,25,25	0
55	MG	RA	3284	1/1	0.95	0.18	43,43,43,43	0
55	MG	YA	3503	1/1	0.95	0.14	2,2,2,2	0
55	MG	RO	201	1/1	0.95	0.05	79,79,79,79	0
55	MG	QA	1651	1/1	0.95	0.07	36,36,36,36	0
55	MG	RA	3044	1/1	0.95	0.18	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	RA	3085	1/1	0.95	0.12	16,16,16,16	0
55	MG	YA	3272	1/1	0.95	0.13	38,38,38,38	0
55	MG	YA	3381	1/1	0.95	0.10	20,20,20,20	0
55	MG	RA	3143	1/1	0.95	0.17	40,40,40,40	0
55	MG	YA	3274	1/1	0.95	0.26	40,40,40,40	0
55	MG	YA	3384	1/1	0.95	0.10	35,35,35,35	0
55	MG	RA	3027	1/1	0.95	0.11	22,22,22,22	0
55	MG	YB	206	1/1	0.95	0.10	10,10,10,10	0
55	MG	YA	3276	1/1	0.95	0.17	16,16,16,16	0
55	MG	RA	3256	1/1	0.95	0.11	38,38,38,38	0
55	MG	YA	3089	1/1	0.95	0.06	22,22,22,22	0
55	MG	RA	3124	1/1	0.95	0.23	27,27,27,27	0
55	MG	QA	1661	1/1	0.95	0.17	75,75,75,75	0
55	MG	RA	3404	1/1	0.95	0.15	56,56,56,56	0
55	MG	RA	3004	1/1	0.95	0.23	27,27,27,27	0
55	MG	RA	3324	1/1	0.95	0.18	40,40,40,40	0
55	MG	YA	3285	1/1	0.95	0.23	45,45,45,45	0
55	MG	YA	3398	1/1	0.95	0.12	36,36,36,36	0
55	MG	RA	3078	1/1	0.95	0.14	20,20,20,20	0
55	MG	YA	3400	1/1	0.95	0.23	44,44,44,44	0
55	MG	QA	1605	1/1	0.95	0.25	27,27,27,27	0
55	MG	QA	1607	1/1	0.95	0.05	37,37,37,37	0
55	MG	YA	3103	1/1	0.95	0.09	11,11,11,11	0
55	MG	XA	1606	1/1	0.95	0.13	35,35,35,35	0
55	MG	YA	3003	1/1	0.95	0.13	49,49,49,49	0
55	MG	YA	3188	1/1	0.95	0.04	28,28,28,28	0
55	MG	RA	3069	1/1	0.95	0.16	23,23,23,23	0
55	MG	RA	3080	1/1	0.95	0.13	39,39,39,39	0
55	MG	RA	3367	1/1	0.95	0.17	28,28,28,28	0
55	MG	YA	3411	1/1	0.95	0.09	61,61,61,61	0
55	MG	YA	3109	1/1	0.95	0.08	3,3,3,3	0
55	MG	RA	3072	1/1	0.95	0.15	24,24,24,24	0
55	MG	XA	1615	1/1	0.95	0.10	22,22,22,22	0
55	MG	RA	3264	1/1	0.95	0.14	34,34,34,34	0
55	MG	YA	3112	1/1	0.95	0.21	19,19,19,19	0
55	MG	XA	1618	1/1	0.95	0.31	54,54,54,54	0
55	MG	YA	3113	1/1	0.95	0.12	16,16,16,16	0
55	MG	YA	3115	1/1	0.95	0.10	18,18,18,18	0
55	MG	QA	1615	1/1	0.95	0.07	46,46,46,46	0
55	MG	XA	1627	1/1	0.95	0.20	22,22,22,22	0
55	MG	YA	3013	1/1	0.95	0.13	14,14,14,14	0
55	MG	YA	3422	1/1	0.95	0.15	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	YA	3423	1/1	0.95	0.09	41,41,41,41	0
55	MG	RA	3060	1/1	0.95	0.12	27,27,27,27	0
55	MG	YA	3015	1/1	0.95	0.12	3,3,3,3	0
55	MG	YA	3308	1/1	0.95	0.04	39,39,39,39	0
55	MG	RA	3416	1/1	0.95	0.15	49,49,49,49	0
55	MG	YA	3428	1/1	0.95	0.25	41,41,41,41	0
55	MG	YA	3124	1/1	0.95	0.10	17,17,17,17	0
55	MG	RA	3209	1/1	0.95	0.10	25,25,25,25	0
55	MG	YA	3211	1/1	0.95	0.06	29,29,29,29	0
55	MG	YA	3126	1/1	0.95	0.17	3,3,3,3	0
55	MG	YA	3018	1/1	0.95	0.19	15,15,15,15	0
55	MG	YA	3128	1/1	0.95	0.17	49,49,49,49	0
55	MG	RA	3134	1/1	0.95	0.14	33,33,33,33	0
55	MG	YA	3027	1/1	0.95	0.22	19,19,19,19	0
55	MG	RA	3095	1/1	0.95	0.14	21,21,21,21	0
55	MG	RA	3302	1/1	0.95	0.18	43,43,43,43	0
55	MG	YA	3219	1/1	0.95	0.09	49,49,49,49	0
55	MG	RA	3241	1/1	0.95	0.27	38,38,38,38	0
55	MG	RA	3339	1/1	0.95	0.13	66,66,66,66	0
55	MG	RA	3425	1/1	0.95	0.21	62,62,62,62	0
55	MG	YA	3040	1/1	0.95	0.12	3,3,3,3	0
55	MG	YA	3447	1/1	0.95	0.16	34,34,34,34	0
55	MG	YA	3041	1/1	0.95	0.15	3,3,3,3	0
55	MG	YA	3327	1/1	0.95	0.11	14,14,14,14	0
55	MG	QA	1627	1/1	0.95	0.05	51,51,51,51	0
55	MG	RA	3380	1/1	0.95	0.06	44,44,44,44	0
55	MG	RA	3477	1/1	0.95	0.14	42,42,42,42	0
55	MG	RA	3270	1/1	0.95	0.17	33,33,33,33	0
55	MG	YA	3231	1/1	0.95	0.08	23,23,23,23	0
55	MG	RA	3099	1/1	0.95	0.13	28,28,28,28	0
55	MG	YA	3457	1/1	0.95	0.13	74,74,74,74	0
55	MG	YA	3234	1/1	0.95	0.11	35,35,35,35	0
55	MG	YA	3049	1/1	0.95	0.21	3,3,3,3	0
55	MG	YA	3460	1/1	0.95	0.18	85,85,85,85	0
55	MG	YA	3237	1/1	0.95	0.14	3,3,3,3	0
55	MG	RA	3384	1/1	0.95	0.25	60,60,60,60	0
55	MG	RA	3213	1/1	0.95	0.06	36,36,36,36	0
55	MG	RA	3483	1/1	0.95	0.14	30,30,30,30	0
55	MG	YA	3246	1/1	0.95	0.15	17,17,17,17	0
55	MG	YA	3344	1/1	0.95	0.07	40,40,40,40	0
55	MG	RA	3244	1/1	0.95	0.20	39,39,39,39	0
55	MG	YA	3469	1/1	0.95	0.20	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	RA	3346	1/1	0.95	0.11	41,41,41,41	0
55	MG	YA	3249	1/1	0.95	0.24	32,32,32,32	0
55	MG	YA	3152	1/1	0.95	0.09	30,30,30,30	0
55	MG	RA	3433	1/1	0.95	0.12	42,42,42,42	0
55	MG	RA	3245	1/1	0.95	0.17	40,40,40,40	0
55	MG	YA	3061	1/1	0.95	0.24	27,27,27,27	0
55	MG	YA	3479	1/1	0.95	0.22	3,3,3,3	0
55	MG	YA	3480	1/1	0.95	0.19	3,3,3,3	0
55	MG	YA	3481	1/1	0.95	0.18	3,3,3,3	0
55	MG	RA	3155	1/1	0.95	0.12	41,41,41,41	0
55	MG	YA	3063	1/1	0.95	0.08	8,8,8,8	0
55	MG	RA	3083	1/1	0.95	0.15	5,5,5,5	0
55	MG	YA	3088	1/1	0.96	0.07	9,9,9,9	0
55	MG	Y5	102	1/1	0.96	0.07	25,25,25,25	0
55	MG	YA	3441	1/1	0.96	0.08	38,38,38,38	0
55	MG	YA	3362	1/1	0.96	0.12	27,27,27,27	0
55	MG	YA	3364	1/1	0.96	0.30	72,72,72,72	0
55	MG	YA	3020	1/1	0.96	0.09	3,3,3,3	0
55	MG	YA	3445	1/1	0.96	0.06	32,32,32,32	0
55	MG	YA	3023	1/1	0.96	0.15	3,3,3,3	0
55	MG	YA	3025	1/1	0.96	0.12	19,19,19,19	0
55	MG	RA	3064	1/1	0.96	0.14	26,26,26,26	0
55	MG	YA	3094	1/1	0.96	0.17	18,18,18,18	0
55	MG	RA	3465	1/1	0.96	0.15	61,61,61,61	0
55	MG	RA	3343	1/1	0.96	0.14	34,34,34,34	0
55	MG	RA	3090	1/1	0.96	0.11	27,27,27,27	0
55	MG	R5	101	1/1	0.96	0.10	43,43,43,43	0
55	MG	RA	3132	1/1	0.96	0.12	40,40,40,40	0
55	MG	YA	3037	1/1	0.96	0.07	3,3,3,3	0
55	MG	YA	3377	1/1	0.96	0.16	26,26,26,26	0
55	MG	YA	3378	1/1	0.96	0.16	23,23,23,23	0
55	MG	YA	3038	1/1	0.96	0.16	14,14,14,14	0
55	MG	RA	3471	1/1	0.96	0.13	20,20,20,20	0
55	MG	YA	3232	1/1	0.96	0.21	22,22,22,22	0
55	MG	XA	1625	1/1	0.96	0.05	59,59,59,59	0
55	MG	RA	3133	1/1	0.96	0.06	31,31,31,31	0
55	MG	RA	3251	1/1	0.96	0.10	30,30,30,30	0
55	MG	YA	3168	1/1	0.96	0.17	41,41,41,41	0
55	MG	XA	1632	1/1	0.96	0.17	25,25,25,25	0
55	MG	RA	3273	1/1	0.96	0.07	31,31,31,31	0
55	MG	RA	3179	1/1	0.96	0.12	54,54,54,54	0
55	MG	RA	3438	1/1	0.96	0.12	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	XA	1636	1/1	0.96	0.05	77,77,77,77	0
55	MG	YA	3242	1/1	0.96	0.19	3,3,3,3	0
55	MG	YA	3389	1/1	0.96	0.10	39,39,39,39	0
55	MG	RA	3091	1/1	0.96	0.14	15,15,15,15	0
55	MG	YA	3245	1/1	0.96	0.25	11,11,11,11	0
55	MG	RA	3378	1/1	0.96	0.15	41,41,41,41	0
55	MG	YA	3048	1/1	0.96	0.20	3,3,3,3	0
55	MG	QA	1655	1/1	0.96	0.32	34,34,34,34	0
55	MG	RA	3479	1/1	0.96	0.09	44,44,44,44	0
55	MG	RA	3065	1/1	0.96	0.17	32,32,32,32	0
55	MG	RA	3011	1/1	0.96	0.09	16,16,16,16	0
55	MG	YA	3122	1/1	0.96	0.16	1,1,1,1	0
55	MG	RA	3279	1/1	0.96	0.08	43,43,43,43	0
55	MG	RA	3019	1/1	0.96	0.16	3,3,3,3	0
55	MG	RA	3383	1/1	0.96	0.10	37,37,37,37	0
55	MG	RA	3414	1/1	0.96	0.20	45,45,45,45	0
55	MG	YA	3491	1/1	0.96	0.26	29,29,29,29	0
55	MG	YA	3060	1/1	0.96	0.13	5,5,5,5	0
55	MG	YA	3493	1/1	0.96	0.06	22,22,22,22	0
55	MG	YA	3187	1/1	0.96	0.12	10,10,10,10	0
55	MG	RA	3257	1/1	0.96	0.17	44,44,44,44	0
55	MG	RA	3238	1/1	0.96	0.08	20,20,20,20	0
55	MG	RA	3139	1/1	0.96	0.12	37,37,37,37	0
55	MG	RA	3058	1/1	0.96	0.25	12,12,12,12	0
55	MG	YA	3413	1/1	0.96	0.07	42,42,42,42	0
55	MG	YA	3264	1/1	0.96	0.23	14,14,14,14	0
55	MG	RA	3096	1/1	0.96	0.16	38,38,38,38	0
55	MG	RA	3391	1/1	0.96	0.18	65,65,65,65	0
55	MG	XA	1666	1/1	0.96	0.08	61,61,61,61	0
55	MG	QA	1629	1/1	0.96	0.14	25,25,25,25	0
55	MG	YA	3505	1/1	0.96	0.23	39,39,39,39	0
55	MG	YA	3198	1/1	0.96	0.23	28,28,28,28	0
55	MG	RA	3222	1/1	0.96	0.15	34,34,34,34	0
55	MG	RA	3223	1/1	0.96	0.21	37,37,37,37	0
55	MG	QA	1632	1/1	0.96	0.07	39,39,39,39	0
55	MG	YA	3138	1/1	0.96	0.11	14,14,14,14	0
55	MG	RA	3003	1/1	0.96	0.20	16,16,16,16	0
55	MG	YA	3205	1/1	0.96	0.14	41,41,41,41	0
55	MG	YA	3140	1/1	0.96	0.17	17,17,17,17	0
55	MG	YB	204	1/1	0.96	0.17	23,23,23,23	0
55	MG	YA	3347	1/1	0.96	0.13	40,40,40,40	0
55	MG	YA	3349	1/1	0.96	0.17	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	RA	3100	1/1	0.96	0.18	58,58,58,58	0
55	MG	YD	301	1/1	0.96	0.10	32,32,32,32	0
55	MG	RA	3460	1/1	0.96	0.08	33,33,33,33	0
55	MG	YA	3352	1/1	0.96	0.24	42,42,42,42	0
55	MG	XA	1686	1/1	0.96	0.18	34,34,34,34	0
55	MG	YA	3078	1/1	0.96	0.18	19,19,19,19	0
55	MG	RA	3365	1/1	0.96	0.18	40,40,40,40	0
55	MG	QA	1637	1/1	0.96	0.16	31,31,31,31	0
55	MG	RA	3462	1/1	0.96	0.08	59,59,59,59	0
55	MG	RA	3041	1/1	0.96	0.12	30,30,30,30	0
55	MG	YA	3084	1/1	0.96	0.10	11,11,11,11	0
55	MG	YA	3085	1/1	0.96	0.11	13,13,13,13	0
56	ZN	XN	101	1/1	0.96	0.08	184,184,184,184	0
55	MG	YA	3007	1/1	0.97	0.06	32,32,32,32	0
55	MG	QA	1623	1/1	0.97	0.06	43,43,43,43	0
55	MG	Y7	101	1/1	0.97	0.08	28,28,28,28	0
55	MG	YA	3073	1/1	0.97	0.11	3,3,3,3	0
55	MG	YA	3283	1/1	0.97	0.09	8,8,8,8	0
55	MG	RA	3043	1/1	0.97	0.10	10,10,10,10	0
55	MG	YA	3363	1/1	0.97	0.07	29,29,29,29	0
55	MG	RA	3325	1/1	0.97	0.10	30,30,30,30	0
55	MG	RA	3362	1/1	0.97	0.09	24,24,24,24	0
55	MG	YA	3287	1/1	0.97	0.14	64,64,64,64	0
55	MG	YA	3077	1/1	0.97	0.14	22,22,22,22	0
55	MG	RA	3052	1/1	0.97	0.09	27,27,27,27	0
55	MG	RA	3020	1/1	0.97	0.04	21,21,21,21	0
55	MG	RA	3329	1/1	0.97	0.24	59,59,59,59	0
55	MG	RA	3158	1/1	0.97	0.05	31,31,31,31	0
55	MG	RA	3098	1/1	0.97	0.10	28,28,28,28	0
55	MG	RA	3138	1/1	0.97	0.07	27,27,27,27	0
55	MG	RA	3408	1/1	0.97	0.09	56,56,56,56	0
55	MG	YA	3155	1/1	0.97	0.15	28,28,28,28	0
55	MG	YA	3086	1/1	0.97	0.16	3,3,3,3	0
55	MG	YA	3087	1/1	0.97	0.13	0,0,0,0	0
55	MG	YA	3019	1/1	0.97	0.12	7,7,7,7	0
55	MG	XA	1621	1/1	0.97	0.11	34,34,34,34	0
55	MG	XA	1622	1/1	0.97	0.06	40,40,40,40	0
55	MG	RA	3117	1/1	0.97	0.10	30,30,30,30	0
55	MG	YA	3463	1/1	0.97	0.25	38,38,38,38	0
55	MG	XA	1626	1/1	0.97	0.08	10,10,10,10	0
55	MG	YA	3301	1/1	0.97	0.06	31,31,31,31	0
55	MG	XA	1628	1/1	0.97	0.09	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	YA	3021	1/1	0.97	0.10	13,13,13,13	0
55	MG	RA	3054	1/1	0.97	0.16	22,22,22,22	0
55	MG	YA	3230	1/1	0.97	0.17	16,16,16,16	0
55	MG	RA	3163	1/1	0.97	0.18	39,39,39,39	0
55	MG	RA	3070	1/1	0.97	0.13	11,11,11,11	0
55	MG	RA	3452	1/1	0.97	0.19	8,8,8,8	0
55	MG	YA	3028	1/1	0.97	0.14	6,6,6,6	0
55	MG	YA	3029	1/1	0.97	0.14	3,3,3,3	0
55	MG	RA	3071	1/1	0.97	0.15	12,12,12,12	0
55	MG	RA	3055	1/1	0.97	0.09	3,3,3,3	0
55	MG	YA	3392	1/1	0.97	0.14	46,46,46,46	0
55	MG	YA	3240	1/1	0.97	0.17	3,3,3,3	0
55	MG	YA	3033	1/1	0.97	0.18	12,12,12,12	0
55	MG	RA	3456	1/1	0.97	0.07	8,8,8,8	0
55	MG	XA	1644	1/1	0.97	0.12	54,54,54,54	0
55	MG	YA	3483	1/1	0.97	0.08	3,3,3,3	0
55	MG	YA	3484	1/1	0.97	0.12	3,3,3,3	0
55	MG	YA	3396	1/1	0.97	0.08	43,43,43,43	0
55	MG	RA	3272	1/1	0.97	0.25	45,45,45,45	0
55	MG	RA	3073	1/1	0.97	0.24	25,25,25,25	0
55	MG	XA	1650	1/1	0.97	0.20	32,32,32,32	0
55	MG	RA	3417	1/1	0.97	0.18	47,47,47,47	0
55	MG	RA	3216	1/1	0.97	0.14	37,37,37,37	0
55	MG	YA	3490	1/1	0.97	0.29	23,23,23,23	0
55	MG	RA	3275	1/1	0.97	0.10	32,32,32,32	0
55	MG	RA	3123	1/1	0.97	0.15	16,16,16,16	0
55	MG	RA	3421	1/1	0.97	0.12	34,34,34,34	0
55	MG	QA	1602	1/1	0.97	0.24	39,39,39,39	0
55	MG	RA	3104	1/1	0.97	0.07	45,45,45,45	0
55	MG	YA	3406	1/1	0.97	0.13	8,8,8,8	0
55	MG	RA	3219	1/1	0.97	0.18	13,13,13,13	0
55	MG	YA	3254	1/1	0.97	0.17	4,4,4,4	0
55	MG	RA	3021	1/1	0.97	0.15	12,12,12,12	0
55	MG	YA	3329	1/1	0.97	0.09	12,12,12,12	0
55	MG	YA	3501	1/1	0.97	0.18	70,70,70,70	0
55	MG	YA	3047	1/1	0.97	0.16	16,16,16,16	0
55	MG	QA	1653	1/1	0.97	0.10	45,45,45,45	0
55	MG	RA	3194	1/1	0.97	0.14	38,38,38,38	0
55	MG	QA	1608	1/1	0.97	0.06	42,42,42,42	0
55	MG	RA	3469	1/1	0.97	0.19	22,22,22,22	0
55	MG	YA	3189	1/1	0.97	0.26	44,44,44,44	0
55	MG	RA	3022	1/1	0.97	0.05	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	XA	1672	1/1	0.97	0.09	34,34,34,34	0
55	MG	YA	3191	1/1	0.97	0.11	27,27,27,27	0
55	MG	RA	3013	1/1	0.97	0.11	15,15,15,15	0
55	MG	QA	1659	1/1	0.97	0.06	73,73,73,73	0
55	MG	RA	3001	1/1	0.97	0.06	15,15,15,15	0
55	MG	RA	3109	1/1	0.97	0.05	33,33,33,33	0
55	MG	YA	3059	1/1	0.97	0.08	7,7,7,7	0
55	MG	RA	3227	1/1	0.97	0.22	38,38,38,38	0
55	MG	RA	3318	1/1	0.97	0.19	27,27,27,27	0
55	MG	YA	3271	1/1	0.97	0.08	25,25,25,25	0
55	MG	YA	3348	1/1	0.97	0.04	25,25,25,25	0
55	MG	YE	301	1/1	0.97	0.21	24,24,24,24	0
55	MG	RA	3110	1/1	0.97	0.08	39,39,39,39	0
55	MG	YA	3201	1/1	0.97	0.07	28,28,28,28	0
55	MG	RA	3063	1/1	0.97	0.10	12,12,12,12	0
55	MG	RA	3230	1/1	0.97	0.15	40,40,40,40	0
55	MG	YP	201	1/1	0.97	0.10	22,22,22,22	0
55	MG	RA	3016	1/1	0.97	0.16	23,23,23,23	0
55	MG	QA	1621	1/1	0.97	0.07	35,35,35,35	0
55	MG	YA	3355	1/1	0.97	0.10	33,33,33,33	0
55	MG	RA	3290	1/1	0.97	0.18	32,32,32,32	0
55	MG	YA	3006	1/1	0.97	0.17	40,40,40,40	0
55	MG	YA	3181	1/1	0.98	0.04	18,18,18,18	0
55	MG	QA	1664	1/1	0.98	0.20	35,35,35,35	0
55	MG	QA	1665	1/1	0.98	0.06	27,27,27,27	0
55	MG	YA	3051	1/1	0.98	0.08	3,3,3,3	0
55	MG	YA	3341	1/1	0.98	0.19	24,24,24,24	0
55	MG	YA	3478	1/1	0.98	0.15	3,3,3,3	0
55	MG	YA	3052	1/1	0.98	0.15	17,17,17,17	0
55	MG	YA	3116	1/1	0.98	0.05	19,19,19,19	0
55	MG	RA	3048	1/1	0.98	0.17	24,24,24,24	0
55	MG	YA	3482	1/1	0.98	0.19	3,3,3,3	0
55	MG	YA	3118	1/1	0.98	0.13	14,14,14,14	0
55	MG	RA	3026	1/1	0.98	0.11	5,5,5,5	0
55	MG	RA	3221	1/1	0.98	0.25	44,44,44,44	0
55	MG	YA	3227	1/1	0.98	0.09	18,18,18,18	0
55	MG	RA	3034	1/1	0.98	0.07	9,9,9,9	0
55	MG	XA	1605	1/1	0.98	0.05	33,33,33,33	0
55	MG	YA	3307	1/1	0.98	0.04	48,48,48,48	0
55	MG	YA	3439	1/1	0.98	0.07	27,27,27,27	0
55	MG	RA	3005	1/1	0.98	0.22	31,31,31,31	0
55	MG	YA	3309	1/1	0.98	0.15	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	QA	1606	1/1	0.98	0.09	51,51,51,51	0
55	MG	YA	3005	1/1	0.98	0.18	28,28,28,28	0
55	MG	RA	3388	1/1	0.98	0.11	40,40,40,40	0
55	MG	RA	3304	1/1	0.98	0.18	29,29,29,29	0
55	MG	QA	1609	1/1	0.98	0.06	9,9,9,9	0
55	MG	RA	3390	1/1	0.98	0.14	42,42,42,42	0
55	MG	YA	3448	1/1	0.98	0.06	36,36,36,36	0
55	MG	YA	3236	1/1	0.98	0.10	9,9,9,9	0
55	MG	YA	3093	1/1	0.98	0.10	3,3,3,3	0
55	MG	YA	3238	1/1	0.98	0.14	3,3,3,3	0
55	MG	RA	3067	1/1	0.98	0.06	3,3,3,3	0
55	MG	YA	3095	1/1	0.98	0.13	3,3,3,3	0
55	MG	RP	201	1/1	0.98	0.16	49,49,49,49	0
55	MG	RA	3434	1/1	0.98	0.15	40,40,40,40	0
55	MG	XA	1624	1/1	0.98	0.04	34,34,34,34	0
55	MG	YA	3067	1/1	0.98	0.24	29,29,29,29	0
55	MG	YA	3244	1/1	0.98	0.17	28,28,28,28	0
55	MG	YA	3368	1/1	0.98	0.04	33,33,33,33	0
55	MG	RA	3197	1/1	0.98	0.13	42,42,42,42	0
55	MG	XA	1629	1/1	0.98	0.10	6,6,6,6	0
55	MG	RA	3341	1/1	0.98	0.05	28,28,28,28	0
55	MG	RA	3468	1/1	0.98	0.04	33,33,33,33	0
55	MG	RA	3485	1/1	0.98	0.05	64,64,64,64	0
55	MG	YA	3072	1/1	0.98	0.06	1,1,1,1	0
55	MG	YA	3418	1/1	0.98	0.13	19,19,19,19	0
55	MG	RA	3025	1/1	0.98	0.07	3,3,3,3	0
55	MG	YA	3141	1/1	0.98	0.07	3,3,3,3	0
55	MG	YA	3107	1/1	0.98	0.18	17,17,17,17	0
55	MG	RA	3126	1/1	0.98	0.12	12,12,12,12	0
55	MG	RA	3037	1/1	0.98	0.15	1,1,1,1	0
56	ZN	QN	101	1/1	0.98	0.08	174,174,174,174	0
55	MG	YA	3470	1/1	0.98	0.21	40,40,40,40	0
55	MG	R8	101	1/1	0.98	0.32	37,37,37,37	0
57	SF4	QD	301	8/8	0.98	0.05	82,98,127,192	0
57	SF4	XD	301	8/8	0.98	0.06	82,105,120,139	0
55	MG	RA	3032	1/1	0.99	0.04	19,19,19,19	0
55	MG	XA	1602	1/1	0.99	0.06	40,40,40,40	0
55	MG	YA	3331	1/1	0.99	0.08	22,22,22,22	0
55	MG	YA	3196	1/1	0.99	0.06	53,53,53,53	0
55	MG	YA	3032	1/1	0.99	0.12	15,15,15,15	0
55	MG	YA	3169	1/1	0.99	0.06	16,16,16,16	0
55	MG	RA	3097	1/1	0.99	0.05	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	MG	RA	3328	1/1	0.99	0.06	16,16,16,16	0
55	MG	RA	3061	1/1	0.99	0.05	18,18,18,18	0
55	MG	YA	3036	1/1	0.99	0.12	3,3,3,3	0
55	MG	RA	3057	1/1	0.99	0.25	8,8,8,8	0
55	MG	RA	3002	1/1	0.99	0.14	36,36,36,36	0
55	MG	YA	3083	1/1	0.99	0.04	13,13,13,13	0
55	MG	RA	3369	1/1	0.99	0.05	18,18,18,18	0
55	MG	YA	3475	1/1	0.99	0.06	3,3,3,3	0
56	ZN	R5	102	1/1	0.99	0.06	117,117,117,117	0
56	ZN	R6	101	1/1	0.99	0.04	93,93,93,93	0
56	ZN	R9	101	1/1	0.99	0.06	100,100,100,100	0
55	MG	RE	301	1/1	0.99	0.04	12,12,12,12	0
56	ZN	YY	201	1/1	0.99	0.03	74,74,74,74	0
55	MG	YA	3098	1/1	0.99	0.05	6,6,6,6	0
56	ZN	Y5	101	1/1	0.99	0.03	74,74,74,74	0
56	ZN	Y6	101	1/1	0.99	0.02	46,46,46,46	0
56	ZN	Y9	101	1/1	0.99	0.05	63,63,63,63	0
55	MG	YA	3409	1/1	0.99	0.12	36,36,36,36	0
55	MG	RA	3454	1/1	0.99	0.07	2,2,2,2	0
55	MG	XA	1677	1/1	0.99	0.11	39,39,39,39	0
55	MG	YA	3024	1/1	1.00	0.04	3,3,3,3	0
55	MG	RA	3059	1/1	1.00	0.04	21,21,21,21	0
56	ZN	RY	201	1/1	1.00	0.04	116,116,116,116	0
55	MG	YA	3114	1/1	1.00	0.05	0,0,0,0	0
55	MG	RA	3368	1/1	1.00	0.02	13,13,13,13	0
55	MG	YA	3022	1/1	1.00	0.06	7,7,7,7	0
55	MG	RA	3014	1/1	1.00	0.06	8,8,8,8	0
55	MG	YA	3099	1/1	1.00	0.04	4,4,4,4	0

6.5 Other polymers [i](#)

There are no such residues in this entry.