



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 17, 2023 – 09:37 PM EDT

PDB ID : 4YZV  
Title : Precleavage 70S structure of the *P. vulgaris* HigB deltaH92 toxin bound to the ACA codon  
Authors : Schureck, M.A.; Dunkle, J.A.; Maehigashi, T.; Dunham, C.M.  
Deposited on : 2015-03-25  
Resolution : 3.10 Å (reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<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>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35.1

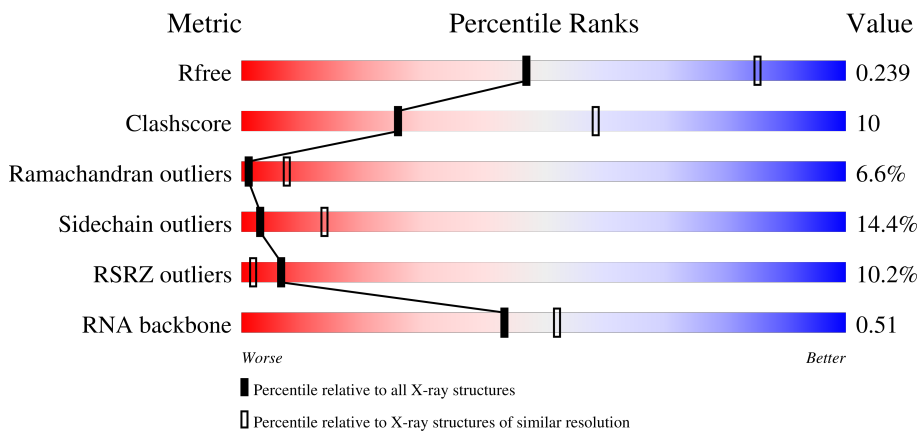
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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))
$R_{free}$	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)
RNA backbone	3102	1116 (3.40-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	QA	1522	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">12%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">57%</div> <div style="text-align: center;">31%</div> <div style="text-align: center;">11%</div> <div style="font-size: 0.8em;">..</div> </div>
1	XA	1522	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">7%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">58%</div> <div style="text-align: center;">32%</div> <div style="text-align: center;">8%</div> <div style="font-size: 0.8em;">..</div> </div>
2	QB	256	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">34%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">52%</div> <div style="text-align: center;">32%</div> <div style="text-align: center;">8%</div> <div style="font-size: 0.8em;">• 8%</div> </div>
2	XB	256	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">19%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: center;">50%</div> <div style="text-align: center;">34%</div> <div style="text-align: center;">8%</div> <div style="font-size: 0.8em;">8%</div> </div>

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Mol	Chain	Length	Quality of chain
3	QC	239	
3	XC	239	
4	QD	209	
4	XD	209	
5	QE	162	
5	XE	162	
6	QF	101	
6	XF	101	
7	QG	156	
7	XG	156	
8	QH	138	
8	XH	138	
9	QI	128	
9	XI	128	
10	QJ	105	
10	XJ	105	
11	QK	129	
11	XK	129	
12	QL	132	
12	XL	132	
13	QM	126	
13	XM	126	
14	QN	61	
14	XN	61	
15	QO	89	

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Mol	Chain	Length	Quality of chain
15	XO	89	6% 72% 24% . .
16	QP	88	3% 67% 25% . 5%
16	XP	88	5% 73% 22% . 5%
17	QQ	105	3% 70% 22% . 5%
17	XQ	105	% 70% 23% . . 5%
18	QR	88	11% 64% 15% . 19%
18	XR	88	3% 47% 30% 5% 19%
19	QS	93	27% 32% 37% 19% 12%
19	XS	93	37% 39% 35% 14% 12%
20	QT	106	22% 61% 25% 7% . 7%
20	XT	106	4% 55% 32% 6% . 7%
21	QU	25	64% 48% 44% 8%
21	XU	25	84% 44% 44% 12%
22	QV	77	10% 68% 29% .
22	XV	77	5% 70% 22% 8%
23	QX	24	54% 17% 33% 21% 12% 17%
23	XX	24	50% 33% 21% 17% 12% 17%
24	QY	117	3% 55% 22% . 22%
24	XY	117	5% 62% 14% . 22%
25	RA	2916	10% 60% 30% 9% .
25	YA	2916	10% 59% 31% 7% .
26	RB	124	7% 60% 30% 9% .
26	YB	124	7% 59% 33% 6% .
27	RD	276	2% 62% 30% 7% .
27	YD	276	% 62% 28% 8% .

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Mol	Chain	Length	Quality of chain
28	RE	206	5% 49% 36% 12% .
28	YE	206	5% 49% 39% 10% .
29	RF	210	5% 60% 30% 8% .
29	YF	210	11% 55% 34% 10% .
30	RG	182	4% 61% 34% . .
30	YG	182	17% 55% 38% 7% .
31	RH	180	28% 43% 38% 12% . 6%
31	YH	180	15% 38% 40% 14% . 6%
32	RI	148	18% 59% 28% 11% . .
32	YI	148	8% 59% 29% 10% . .
33	RN	140	2% 74% 21% . .
33	YN	140	% 69% 25% . . .
34	RO	122	65% 31% .
34	YO	122	69% 26% . .
35	RP	150	7% 41% 39% 15% 6%
35	YP	150	8% 41% 38% 13% 7%
36	RQ	141	2% 65% 27% 6% . .
36	YQ	141	3% 58% 30% 9% . .
37	RR	118	3% 70% 23% 6% .
37	YR	118	3% 67% 27% 5% .
38	RS	112	31% 60% 33% 5% . .
38	YS	112	15% 53% 38% 8% . .
39	RT	146	3% 52% 38% . . 6%
39	YT	146	5% 53% 32% 8% . 6%
40	RU	118	5% 66% 30% . . .

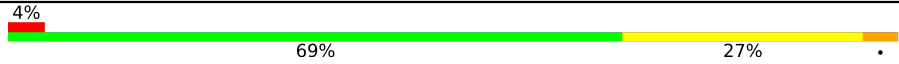

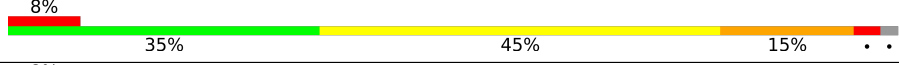
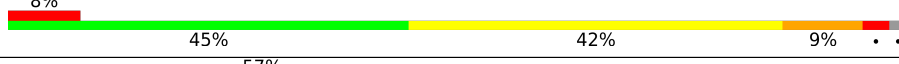

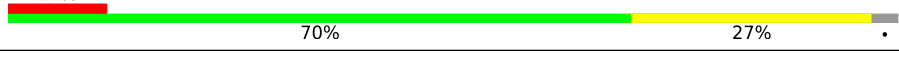
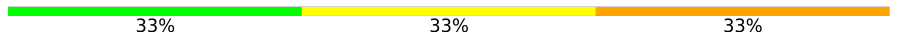
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Mol	Chain	Length	Quality of chain
40	YU	118	4% 68% 27% ...
41	RV	101	6% 40% 45% 12% .
41	YV	101	11% 42% 45% 11% .
42	RW	113	% 66% 29% .
42	YW	113	65% 27% 8%
43	RX	96	3% 73% 20% ..
43	YX	96	67% 27% ..
44	RY	110	18% 34% 39% 14% 6% 7%
44	YY	110	19% 33% 40% 18% . 7%
45	RZ	206	19% 41% 31% 14% 15%
45	YZ	206	9% 48% 30% 10% . 11%
46	R0	85	% 64% 31% ..
46	Y0	85	6% 56% 36% 5% .
47	R1	98	6% 50% 38% 9% ..
47	Y1	98	5% 59% 35% . ...
48	R2	72	6% 53% 31% 10% . .
48	Y2	72	7% 61% 25% 7% . .
49	R3	60	70% 22% 7% .
49	Y3	60	67% 28% ..
50	R4	71	37% 45% 35% 18% .
50	Y4	71	28% 32% 45% 20% ..
51	R5	60	12% 70% 23% . ...
51	Y5	60	8% 55% 33% 5% . 5%
52	R6	54	59% 24% 37% 28% 11%
52	Y6	54	56% 22% 31% 31% . 11%

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Mol	Chain	Length	Quality of chain
53	R7	49	
53	Y7	49	
54	R8	65	
54	Y8	65	
55	R9	37	
55	Y9	37	
56	Z6	3	
56	Z7	3	

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
57	MG	QA	1697	-	-	-	X
57	MG	QA	1751	-	-	-	X
57	MG	R0	102	-	-	-	X
57	MG	RA	3075	-	-	-	X
57	MG	RA	3092	-	-	-	X
57	MG	RA	3102	-	-	-	X
57	MG	RA	3146	-	-	-	X
57	MG	RA	3176	-	-	-	X
57	MG	RA	3182	-	-	-	X
57	MG	RA	3188	-	-	-	X
57	MG	RA	3210	-	-	-	X
57	MG	RA	3292	-	-	-	X
57	MG	RA	3298	-	-	-	X
57	MG	RA	3300	-	-	-	X
57	MG	RA	3302	-	-	-	X
57	MG	RA	3322	-	-	-	X
57	MG	RA	3323	-	-	-	X
57	MG	RA	3329	-	-	-	X
57	MG	RA	3338	-	-	-	X
57	MG	RA	3341	-	-	-	X
57	MG	RA	3351	-	-	-	X
57	MG	RA	3353	-	-	-	X
57	MG	RA	3361	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	RA	3370	-	-	-	X
57	MG	RA	3376	-	-	-	X
57	MG	RA	3387	-	-	-	X
57	MG	RA	3392	-	-	-	X
57	MG	RA	3438	-	-	-	X
57	MG	RY	202	-	-	-	X
57	MG	XA	1639	-	-	-	X
57	MG	XA	1646	-	-	-	X
57	MG	XA	1669	-	-	-	X
57	MG	XA	1685	-	-	-	X
57	MG	XA	1702	-	-	-	X
57	MG	XA	1704	-	-	-	X
57	MG	XA	1725	-	-	-	X
57	MG	XA	1756	-	-	-	X
57	MG	YA	3001	-	-	-	X
57	MG	YA	3100	-	-	-	X
57	MG	YA	3104	-	-	-	X
57	MG	YA	3111	-	-	-	X
57	MG	YA	3134	-	-	-	X
57	MG	YA	3147	-	-	-	X
57	MG	YA	3186	-	-	-	X
57	MG	YA	3197	-	-	-	X
57	MG	YA	3215	-	-	-	X
57	MG	YA	3255	-	-	-	X
57	MG	YA	3268	-	-	-	X
57	MG	YA	3283	-	-	-	X
57	MG	YA	3287	-	-	-	X
57	MG	YA	3297	-	-	-	X
57	MG	YA	3300	-	-	-	X
57	MG	YA	3327	-	-	-	X
57	MG	YA	3340	-	-	-	X
57	MG	YA	3348	-	-	-	X
57	MG	YA	3353	-	-	-	X
57	MG	YA	3362	-	-	-	X
57	MG	YA	3365	-	-	-	X
57	MG	YA	3371	-	-	-	X
57	MG	YA	3374	-	-	-	X
57	MG	YA	3391	-	-	-	X
57	MG	YA	3444	-	-	-	X
57	MG	YA	3448	-	-	-	X
57	MG	YA	3490	-	-	-	X
57	MG	YA	3499	-	-	-	X

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<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
57	MG	YA	3502	-	-	-	X
57	MG	YU	201	-	-	-	X

## 2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 294445 atoms, of which 18 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 16S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	QA	1511	Total 32472	C 14453	N 6011	O 10497	P 1511	0	0	0
1	XA	1508	Total 32409	C 14425	N 6001	O 10475	P 1508	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	QB	236	Total 1915	C 1223	N 343	O 344	S 5	0	0	0
2	XB	236	Total 1915	C 1223	N 343	O 344	S 5	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	QC	206	Total 1612	C 1016	N 314	O 281	S 1	0	0	0
3	XC	206	Total 1612	C 1016	N 314	O 281	S 1	0	0	0

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	QE	154	Total	C	N	O	S	0	0	0
			1178	743	221	210	4			
5	XE	154	Total	C	N	O	S	0	0	0
			1178	743	221	210	4			

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	QI	128	Total	C	N	O	S	0	0	0
			1018	644	198	175	1			
9	XI	128	Total	C	N	O	S	0	0	0
			1018	644	198	175	1			

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
11	QK	121	901	560	171	167	3	0	0	0
11	XK	121	901	560	171	167	3	0	0	0

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
13	QM	118	937	579	193	163	2	0	0	0
13	XM	118	937	579	193	163	2	0	0	0

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
18	QR	71	Total 585	C 373	N 116	O 96	0	0	0
18	XR	71	Total 585	C 373	N 116	O 96	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
19	QS	82	Total 656	C 419	N 121	O 114	S 2	0	0	0
19	XS	82	Total 656	C 419	N 121	O 114	S 2	0	0	0

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

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

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

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

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

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

- Molecule 23 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	QX	20	Total	C	H	N	O	P	0	0	0
			444	198	9	87	131	19			
23	XX	20	Total	C	H	N	O	P	0	0	0
			444	198	9	87	131	19			

- Molecule 24 is a protein called Killer protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
24	QY	91	Total	C	N	O	0	0	0
			746	478	131	137			
24	XY	91	Total	C	N	O	0	0	0
			746	478	131	137			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
QY	0	MET	-	initiating methionine	UNP Q7A225
QY	1	GLY	-	expression tag	UNP Q7A225
QY	92	LYS	-	expression tag	UNP Q7A225
QY	93	LEU	-	expression tag	UNP Q7A225
QY	94	GLY	-	expression tag	UNP Q7A225
QY	95	PRO	-	expression tag	UNP Q7A225
QY	96	GLU	-	expression tag	UNP Q7A225
QY	97	GLN	-	expression tag	UNP Q7A225
QY	98	LYS	-	expression tag	UNP Q7A225
QY	99	LEU	-	expression tag	UNP Q7A225
QY	100	ILE	-	expression tag	UNP Q7A225

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Chain	Residue	Modelled	Actual	Comment	Reference
QY	101	SER	-	expression tag	UNP Q7A225
QY	102	GLU	-	expression tag	UNP Q7A225
QY	103	GLU	-	expression tag	UNP Q7A225
QY	104	ASP	-	expression tag	UNP Q7A225
QY	105	LEU	-	expression tag	UNP Q7A225
QY	106	ASN	-	expression tag	UNP Q7A225
QY	107	SER	-	expression tag	UNP Q7A225
QY	108	ALA	-	expression tag	UNP Q7A225
QY	109	VAL	-	expression tag	UNP Q7A225
QY	110	ASP	-	expression tag	UNP Q7A225
QY	111	HIS	-	expression tag	UNP Q7A225
QY	112	HIS	-	expression tag	UNP Q7A225
QY	113	HIS	-	expression tag	UNP Q7A225
QY	114	HIS	-	expression tag	UNP Q7A225
QY	115	HIS	-	expression tag	UNP Q7A225
QY	116	HIS	-	expression tag	UNP Q7A225
XY	0	MET	-	initiating methionine	UNP Q7A225
XY	1	GLY	-	expression tag	UNP Q7A225
XY	92	LYS	-	expression tag	UNP Q7A225
XY	93	LEU	-	expression tag	UNP Q7A225
XY	94	GLY	-	expression tag	UNP Q7A225
XY	95	PRO	-	expression tag	UNP Q7A225
XY	96	GLU	-	expression tag	UNP Q7A225
XY	97	GLN	-	expression tag	UNP Q7A225
XY	98	LYS	-	expression tag	UNP Q7A225
XY	99	LEU	-	expression tag	UNP Q7A225
XY	100	ILE	-	expression tag	UNP Q7A225
XY	101	SER	-	expression tag	UNP Q7A225
XY	102	GLU	-	expression tag	UNP Q7A225
XY	103	GLU	-	expression tag	UNP Q7A225
XY	104	ASP	-	expression tag	UNP Q7A225
XY	105	LEU	-	expression tag	UNP Q7A225
XY	106	ASN	-	expression tag	UNP Q7A225
XY	107	SER	-	expression tag	UNP Q7A225
XY	108	ALA	-	expression tag	UNP Q7A225
XY	109	VAL	-	expression tag	UNP Q7A225
XY	110	ASP	-	expression tag	UNP Q7A225
XY	111	HIS	-	expression tag	UNP Q7A225
XY	112	HIS	-	expression tag	UNP Q7A225
XY	113	HIS	-	expression tag	UNP Q7A225
XY	114	HIS	-	expression tag	UNP Q7A225
XY	115	HIS	-	expression tag	UNP Q7A225

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Chain	Residue	Modelled	Actual	Comment	Reference
XY	116	HIS	-	expression tag	UNP Q7A225

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	RA	2891	Total	C	N	O	P	0	0	0
			62269	27713	11649	20016	2891			
25	YA	2875	Total	C	N	O	P	0	0	0
			61924	27560	11583	19906	2875			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	RB	122	Total	C	N	O	P	0	0	0
			2617	1166	486	844	121			
26	YB	122	Total	C	N	O	P	0	0	0
			2617	1166	486	844	121			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	RF	208	Total	C	N	O	S	0	0	0
			1627	1037	304	283	3			
29	YF	208	Total	C	N	O	S	0	0	0
			1627	1037	304	283	3			



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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	RQ	140	Total	C	N	O	S	0	0	0
			1112	710	210	185	7			
36	YQ	139	Total	C	N	O	S	0	0	0
			1107	707	209	184	7			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
37	RR	117	Total	C	N	O	0	0	0
			960	599	202	159			
37	YR	117	Total	C	N	O	0	0	0
			960	599	202	159			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
45	RZ	176	1404	897	252	252	3	0	0	0
45	YZ	183	1461	933	260	265	3	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
46	R0	83	Total 657	C 407	N 139	O 110	S 1	0	0	0
46	Y0	83	Total 657	C 407	N 139	O 110	S 1	0	0	0

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
50	R4	70	Total 573	C 359	N 107	O 103	S 4	0	0	0
50	Y4	70	Total 573	C 359	N 107	O 103	S 4	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	R5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			
51	Y5	57	Total	C	N	O	S	0	0	0
			442	278	88	71	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	R6	48	Total	C	N	O	S	0	0	0
			417	259	86	68	4			
52	Y6	48	Total	C	N	O	S	0	0	0
			417	259	86	68	4			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	R9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
55	Y9	36	Total	C	N	O	S	0	0	0
			299	183	67	46	3			

- Molecule 56 is a RNA chain called CC-puromycin.

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

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
56	Z7	3	74	40	13	19	2	0	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	QA	151	Total 151	Mg 151	0	0
57	QD	2	Total 2	Mg 2	0	0
57	QE	1	Total 1	Mg 1	0	0
57	QL	1	Total 1	Mg 1	0	0
57	QN	1	Total 1	Mg 1	0	0
57	QV	5	Total 5	Mg 5	0	0
57	RA	451	Total 451	Mg 451	0	0
57	RB	5	Total 5	Mg 5	0	0
57	RD	2	Total 2	Mg 2	0	0
57	RE	3	Total 3	Mg 3	0	0
57	RF	1	Total 1	Mg 1	0	0
57	RP	2	Total 2	Mg 2	0	0
57	RQ	2	Total 2	Mg 2	0	0
57	RR	1	Total 1	Mg 1	0	0
57	RV	1	Total 1	Mg 1	0	0
57	RY	2	Total 2	Mg 2	0	0
57	R0	2	Total 2	Mg 2	0	0
57	R2	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	R5	3	Total Mg 3 3	0	0
57	XA	164	Total Mg 164 164	0	0
57	XD	1	Total Mg 1 1	0	0
57	XE	1	Total Mg 1 1	0	0
57	XF	1	Total Mg 1 1	0	0
57	XK	1	Total Mg 1 1	0	0
57	XL	1	Total Mg 1 1	0	0
57	XN	1	Total Mg 1 1	0	0
57	XS	1	Total Mg 1 1	0	0
57	XV	4	Total Mg 4 4	0	0
57	YA	504	Total Mg 504 504	0	0
57	YB	6	Total Mg 6 6	0	0
57	YD	1	Total Mg 1 1	0	0
57	YE	2	Total Mg 2 2	0	0
57	YF	2	Total Mg 2 2	0	0
57	YG	1	Total Mg 1 1	0	0
57	YH	2	Total Mg 2 2	0	0
57	YN	1	Total Mg 1 1	0	0
57	YO	1	Total Mg 1 1	0	0
57	YP	2	Total Mg 2 2	0	0
57	YQ	2	Total Mg 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	YR	1	Total Mg 1 1	0	0
57	YU	1	Total Mg 1 1	0	0
57	YV	1	Total Mg 1 1	0	0
57	YW	1	Total Mg 1 1	0	0
57	Y0	1	Total Mg 1 1	0	0
57	Y5	3	Total Mg 3 3	0	0
57	Y7	1	Total Mg 1 1	0	0
57	Z7	1	Total Mg 1 1	0	0

- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

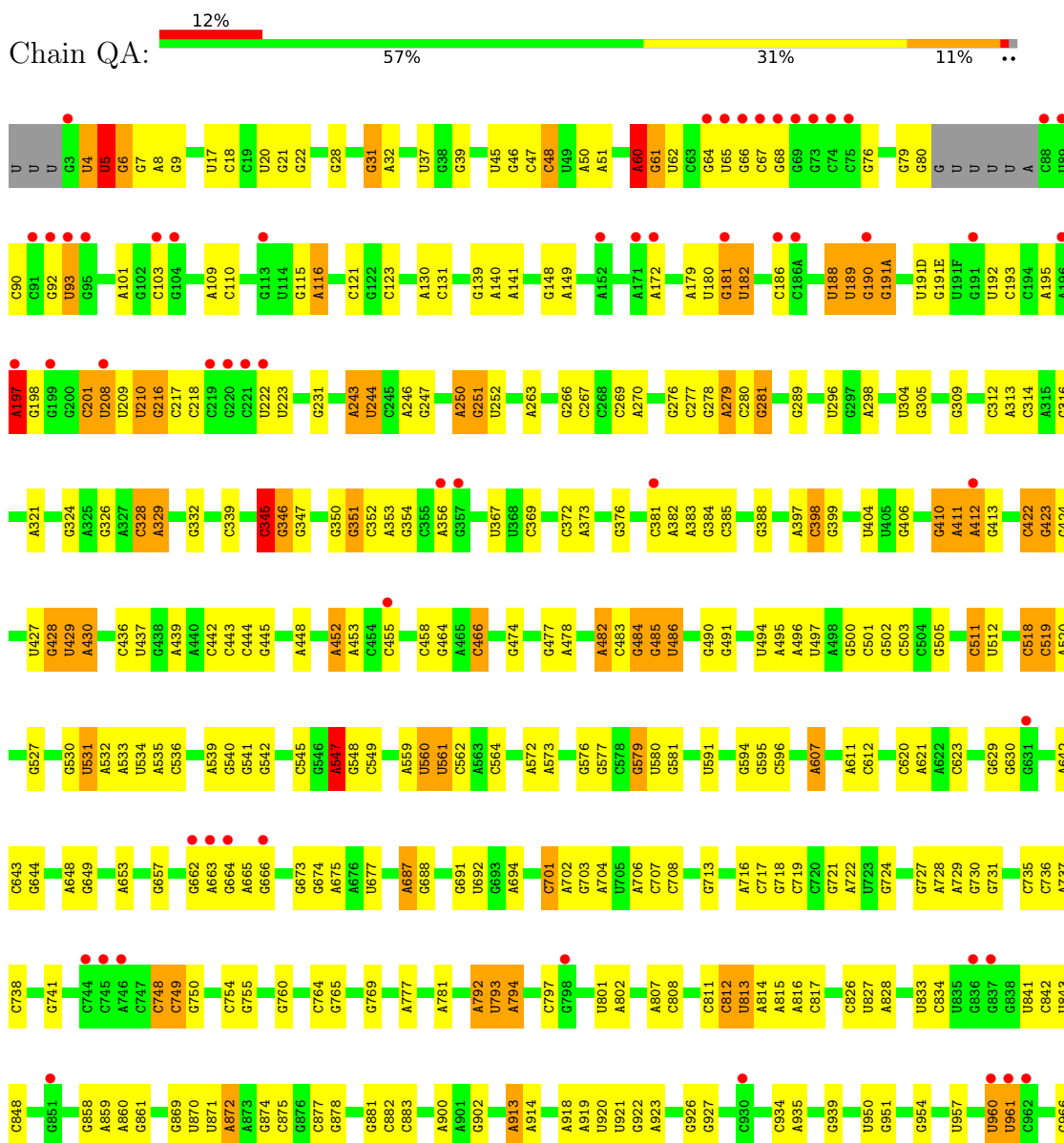
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	QD	1	Total Zn 1 1	0	0
58	QN	1	Total Zn 1 1	0	0
58	XD	1	Total Zn 1 1	0	0
58	XN	1	Total Zn 1 1	0	0

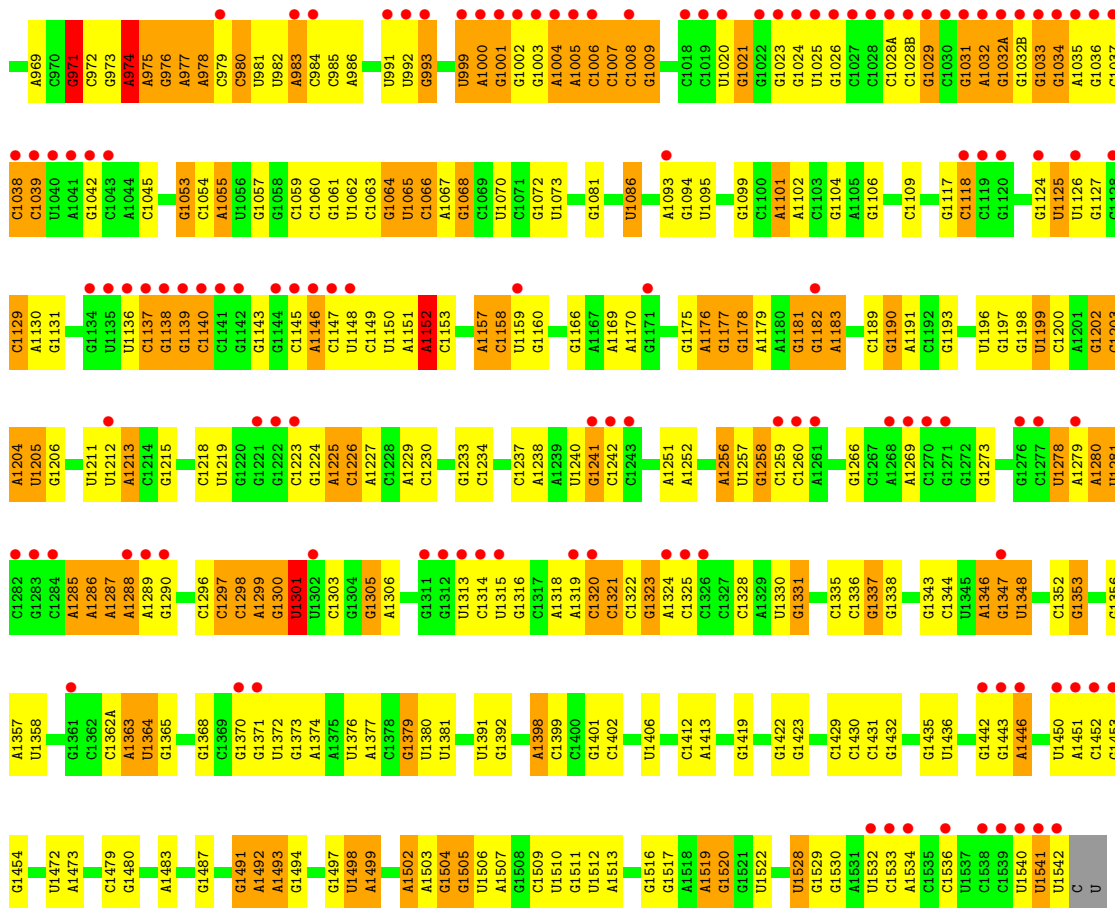


### 3 Residue-property plots [i](#)

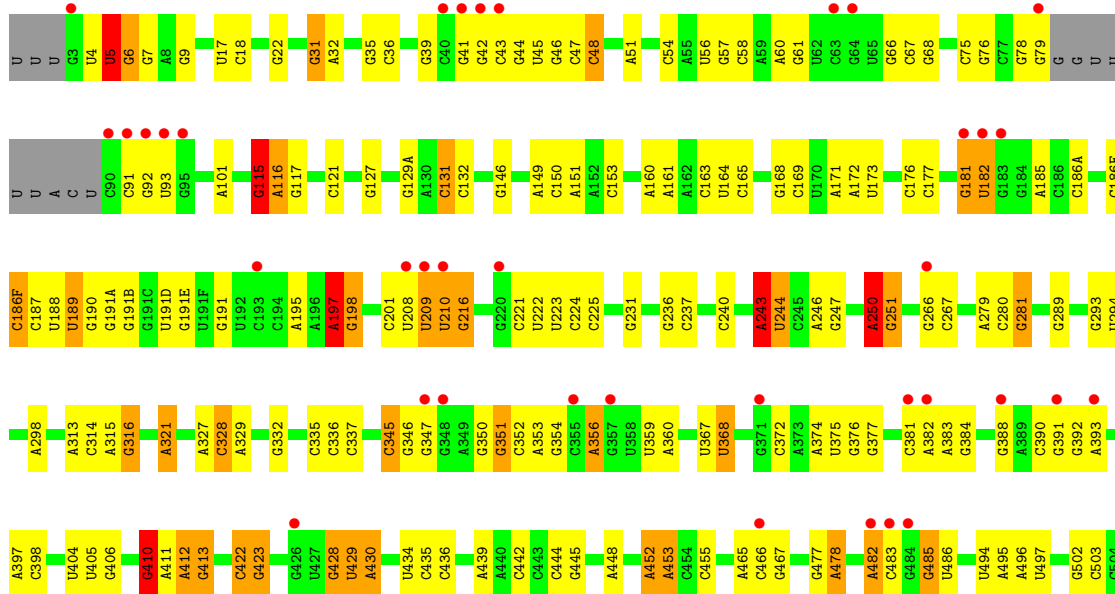
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: 16S rRNA

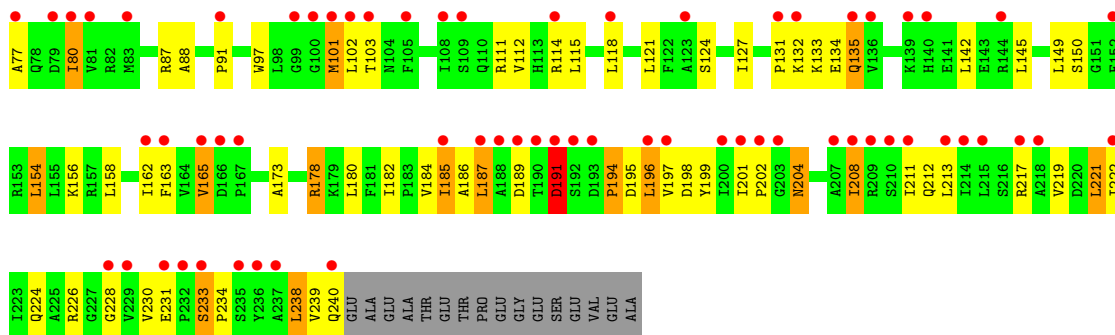




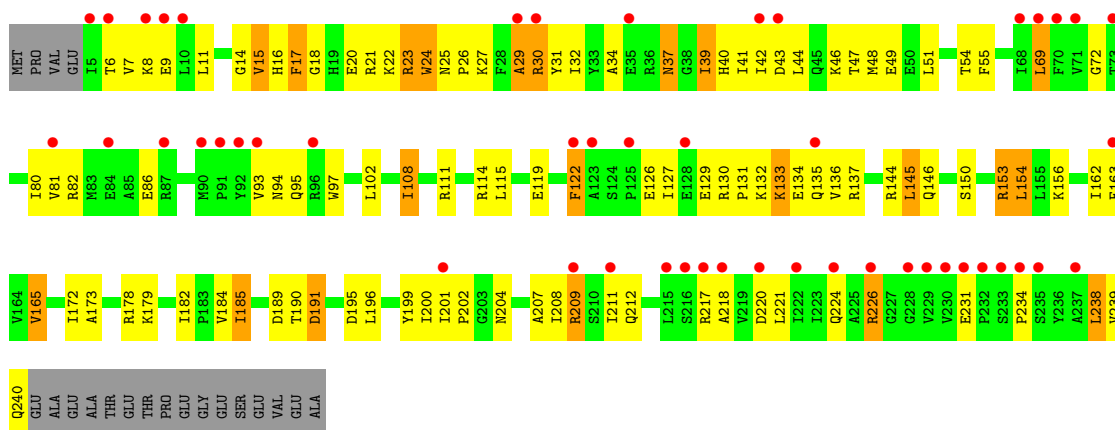
• Molecule 1: 16S rRNA



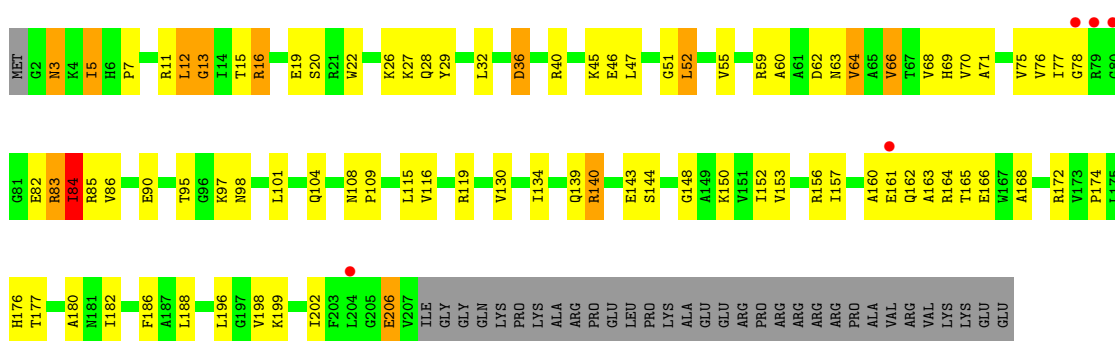




• Molecule 2: 30S ribosomal protein S2

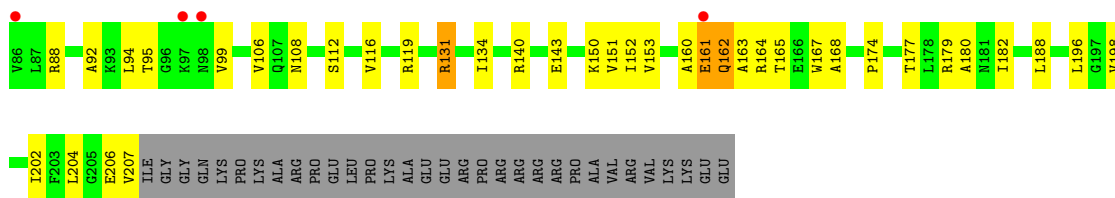


• Molecule 3: 30S ribosomal protein S3

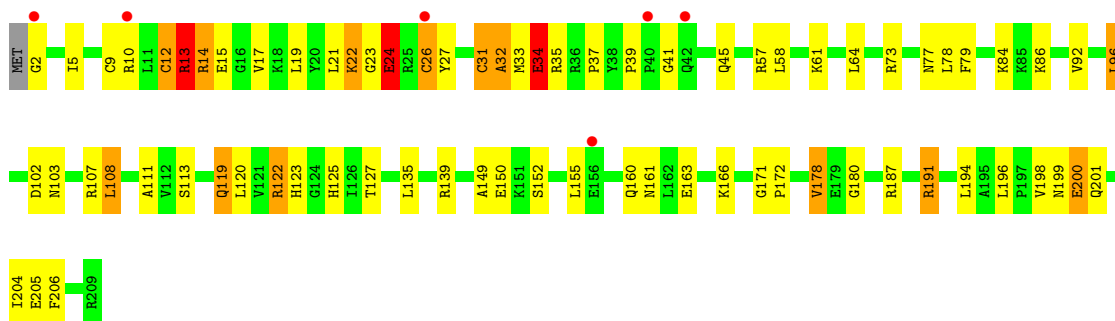


• Molecule 3: 30S ribosomal protein S3

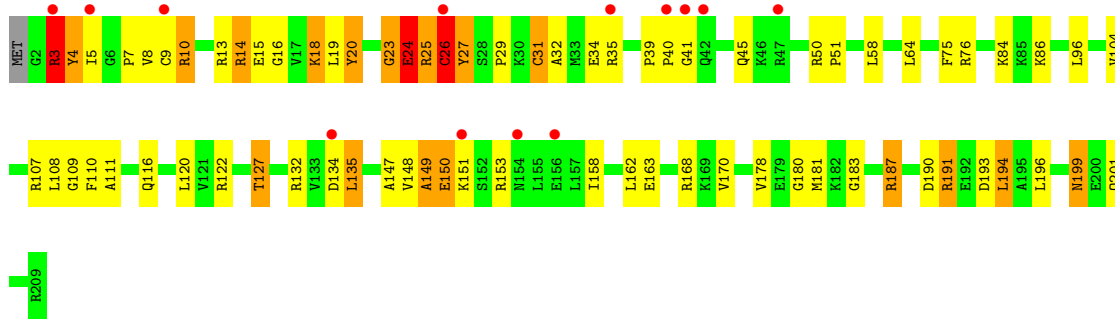




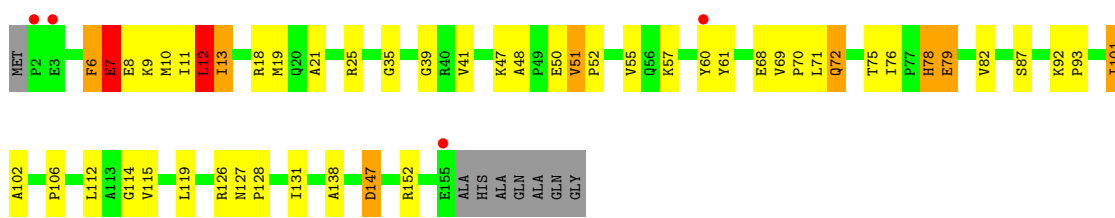
• Molecule 4: 30S ribosomal protein S4



• Molecule 4: 30S ribosomal protein S4

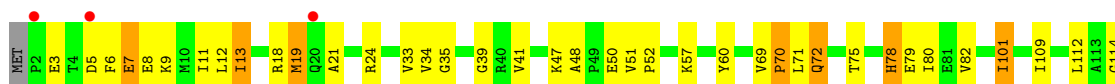


• Molecule 5: 30S ribosomal protein S5

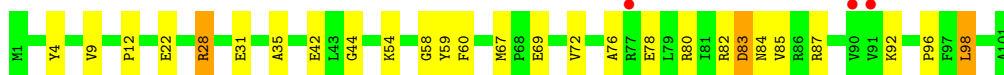
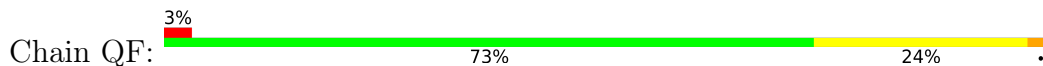


• Molecule 5: 30S ribosomal protein S5

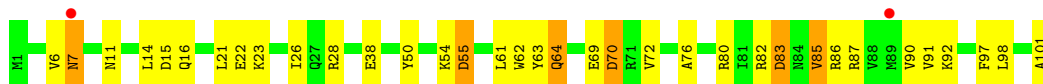




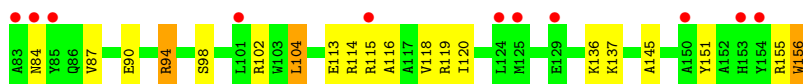
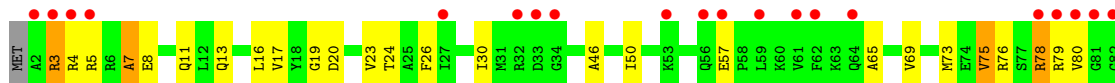
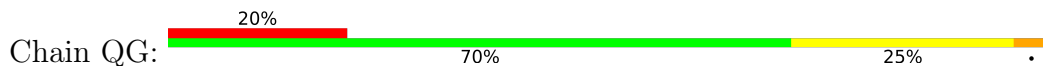
- Molecule 6: 30S ribosomal protein S6



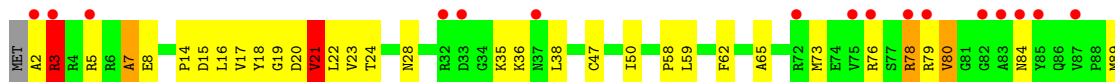
- Molecule 6: 30S ribosomal protein S6



- Molecule 7: 30S ribosomal protein S7

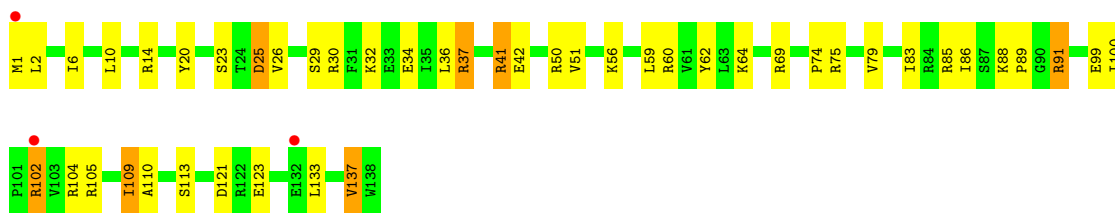


- Molecule 7: 30S ribosomal protein S7



- Molecule 8: 30S ribosomal protein S8

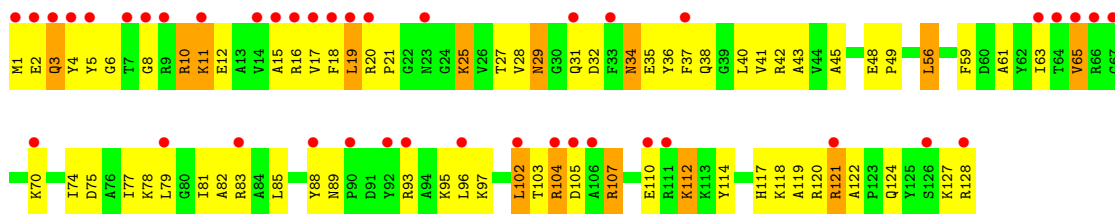




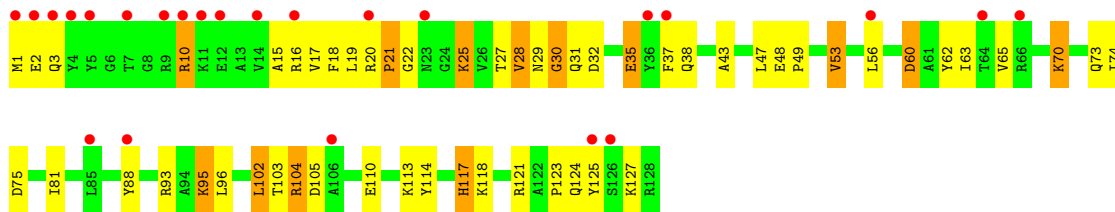
• Molecule 8: 30S ribosomal protein S8



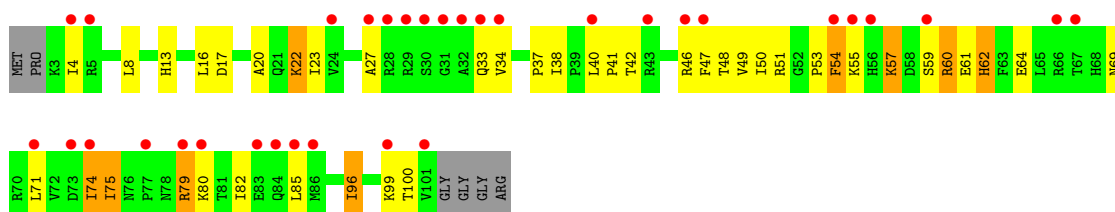
• Molecule 9: 30S ribosomal protein S9



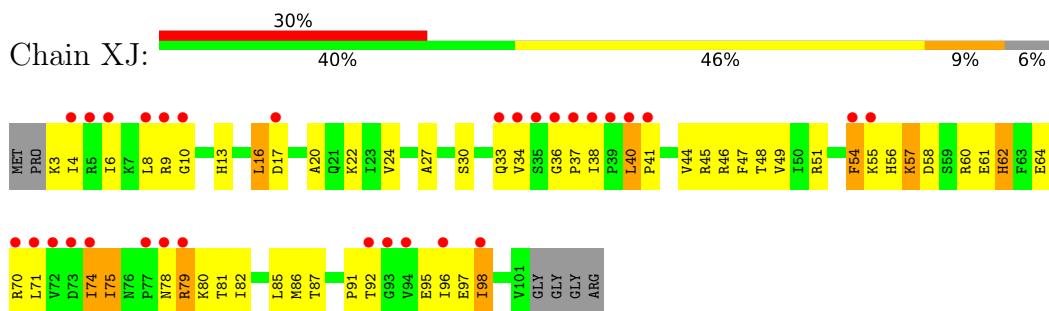
• Molecule 9: 30S ribosomal protein S9



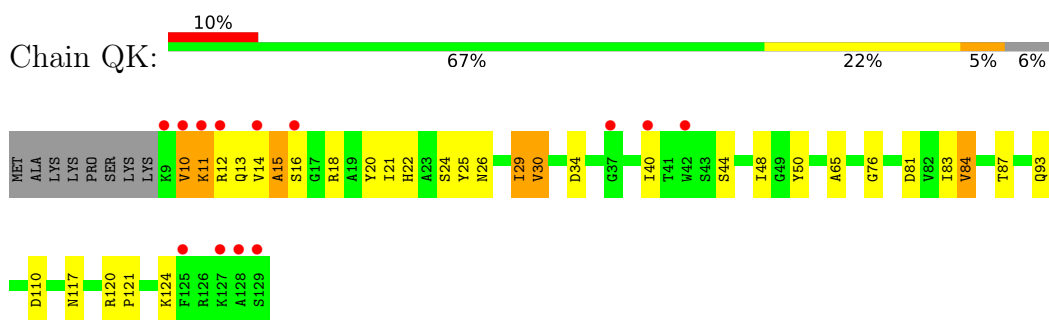
• Molecule 10: 30S ribosomal protein S10



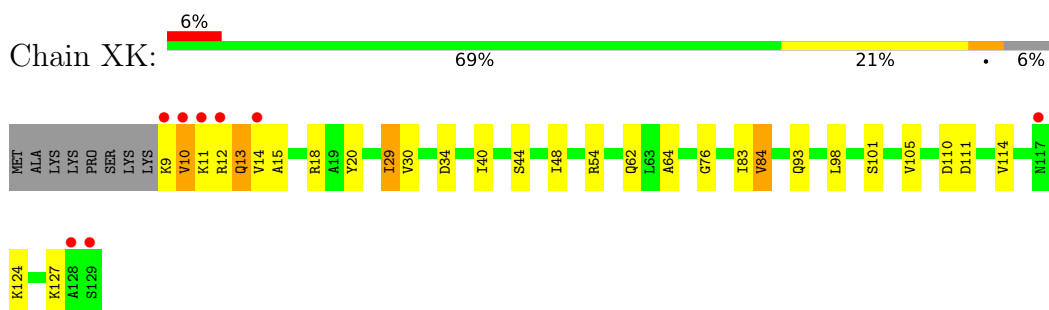
- Molecule 10: 30S ribosomal protein S10



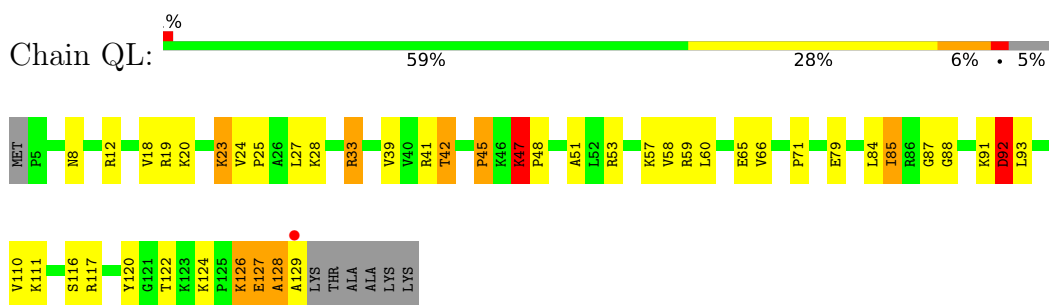
- Molecule 11: 30S ribosomal protein S11



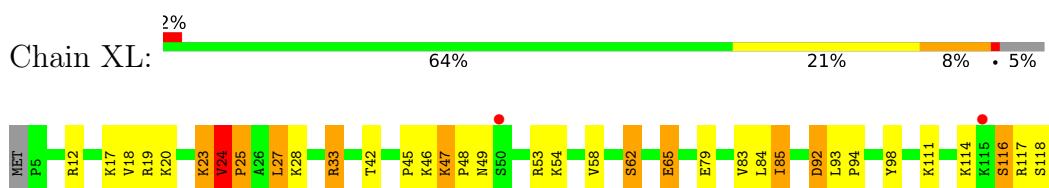
- Molecule 11: 30S ribosomal protein S11



- Molecule 12: 30S ribosomal protein S12



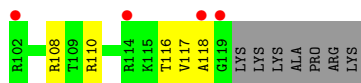
- Molecule 12: 30S ribosomal protein S12



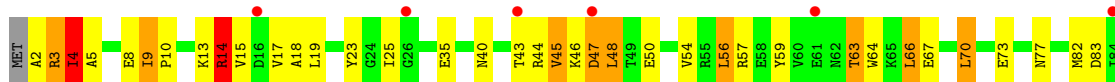




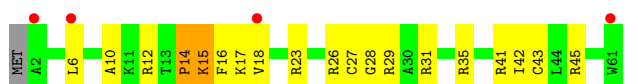
- Molecule 13: 30S ribosomal protein S13



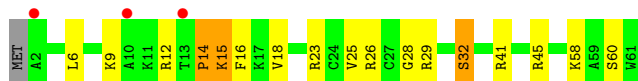
- Molecule 13: 30S ribosomal protein S13



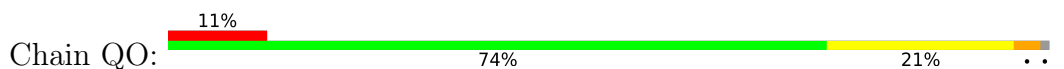
- Molecule 14: 30S ribosomal protein S14 type Z



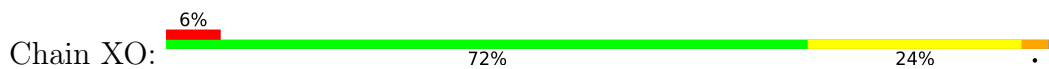
- Molecule 14: 30S ribosomal protein S14 type Z



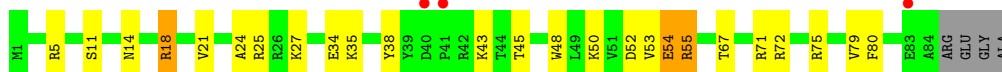
- Molecule 15: 30S ribosomal protein S15



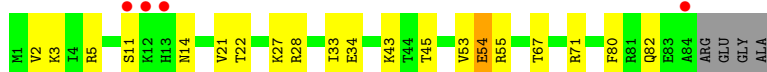
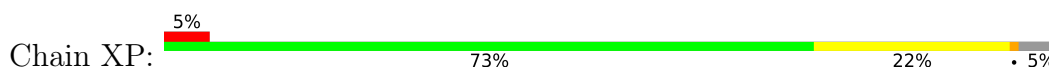
- Molecule 15: 30S ribosomal protein S15



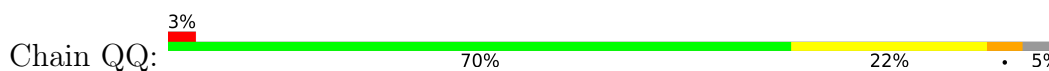
- Molecule 16: 30S ribosomal protein S16



- Molecule 16: 30S ribosomal protein S16



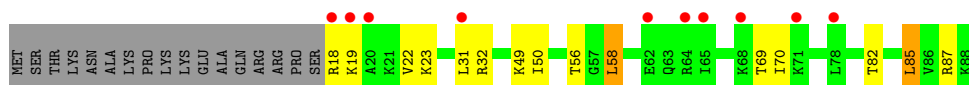
- Molecule 17: 30S ribosomal protein S17



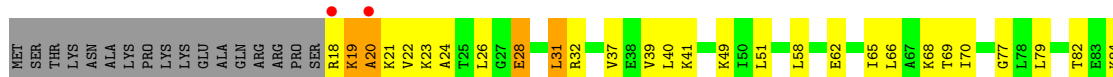
- Molecule 17: 30S ribosomal protein S17



- Molecule 18: 30S ribosomal protein S18

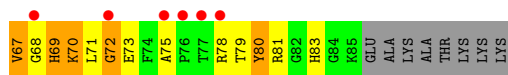
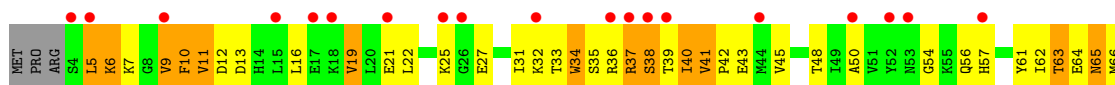


- Molecule 18: 30S ribosomal protein S18

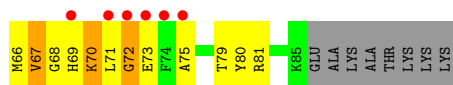
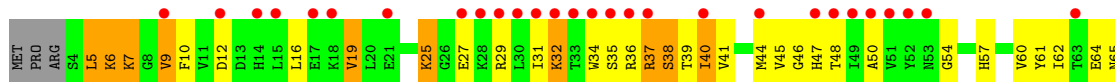




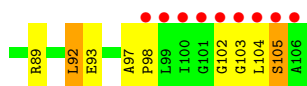
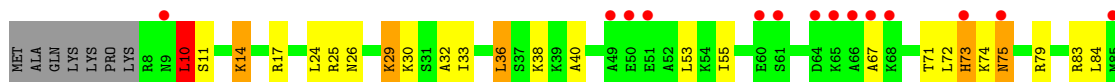
• Molecule 19: 30S ribosomal protein S19



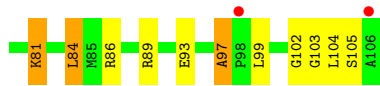
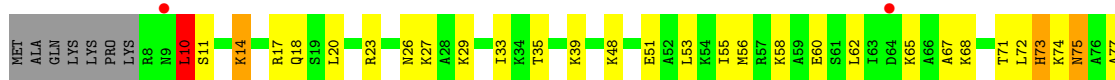
• Molecule 19: 30S ribosomal protein S19



• Molecule 20: 30S ribosomal protein S20

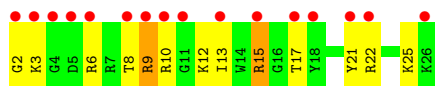


• Molecule 20: 30S ribosomal protein S20

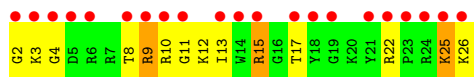
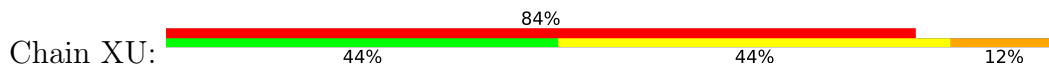


• Molecule 21: 30S ribosomal protein Thx





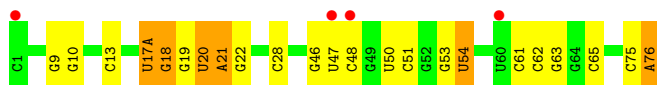
• Molecule 21: 30S ribosomal protein Thx



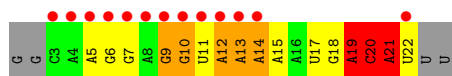
• Molecule 22: P-site tRNA-fMet



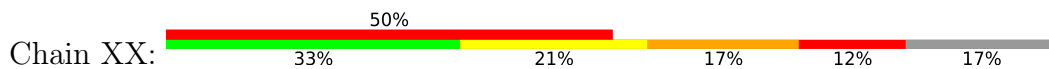
• Molecule 22: P-site tRNA-fMet



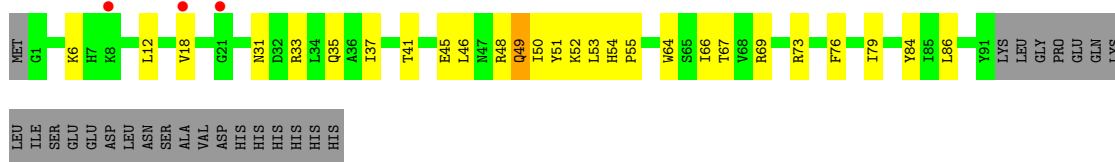
• Molecule 23: messenger RNA



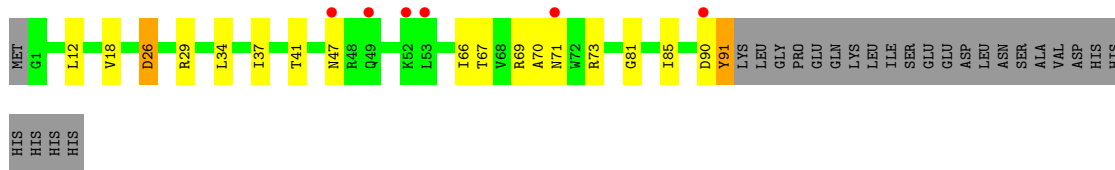
• Molecule 23: messenger RNA



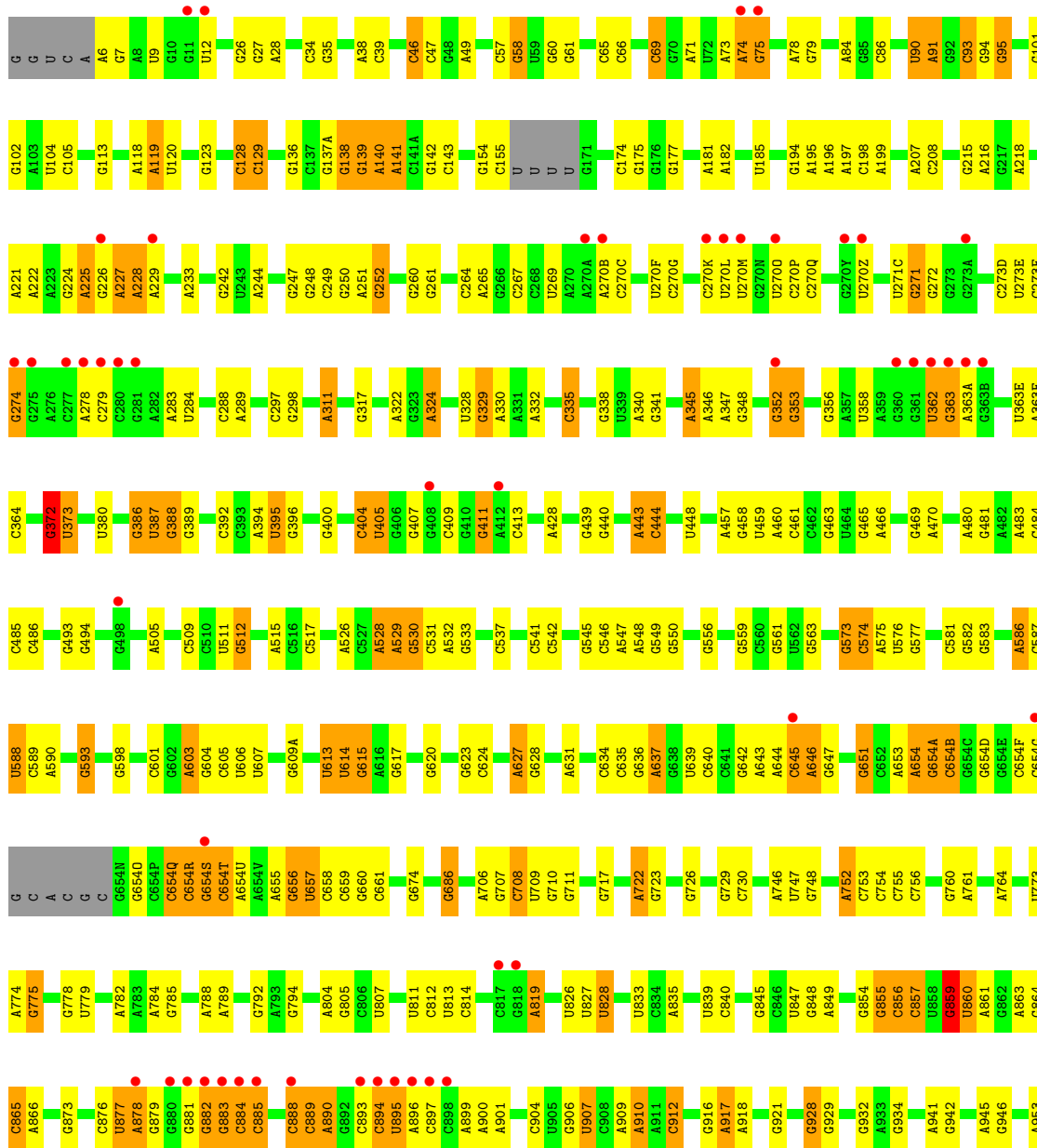
• Molecule 24: Killer protein

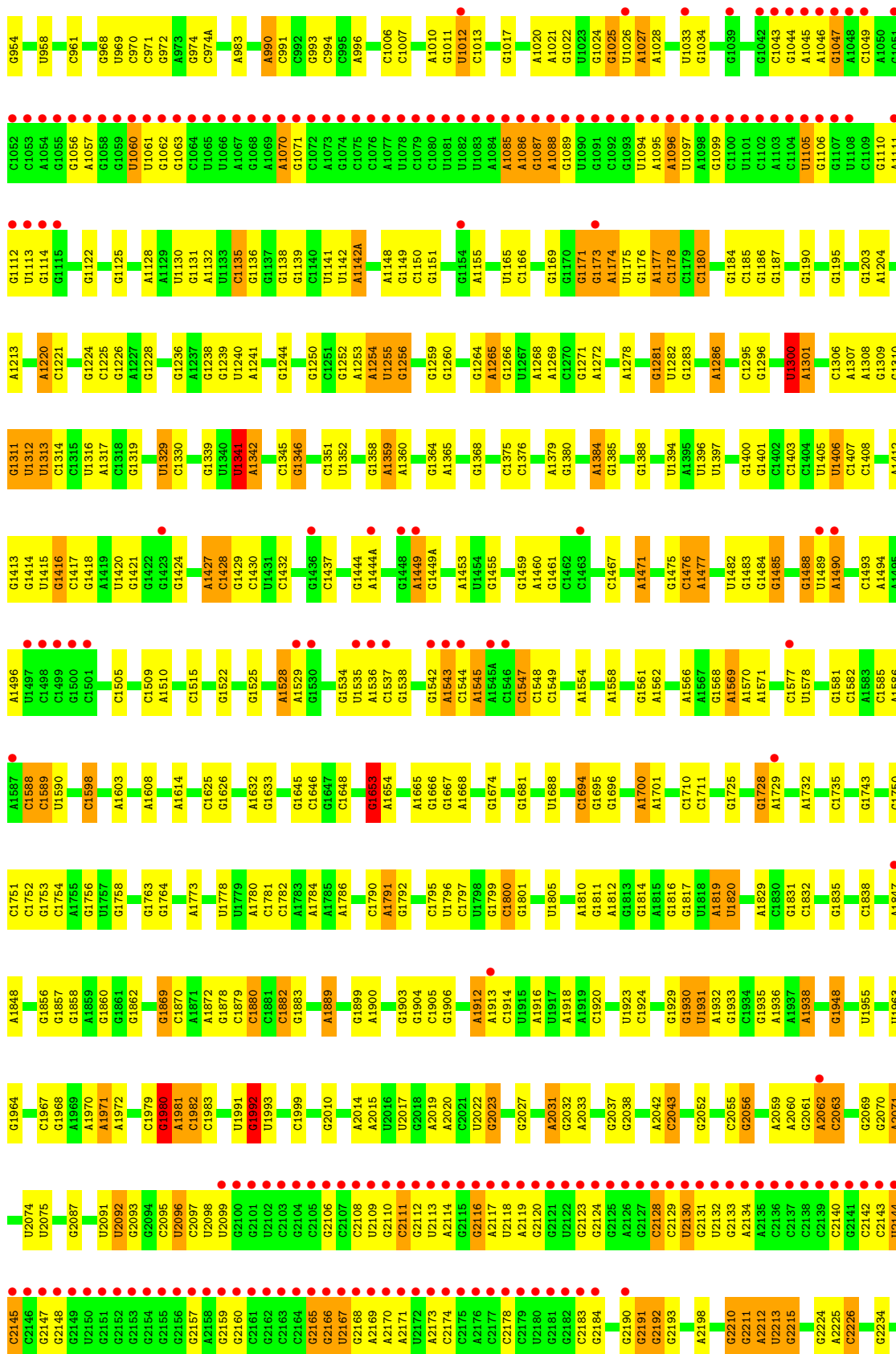


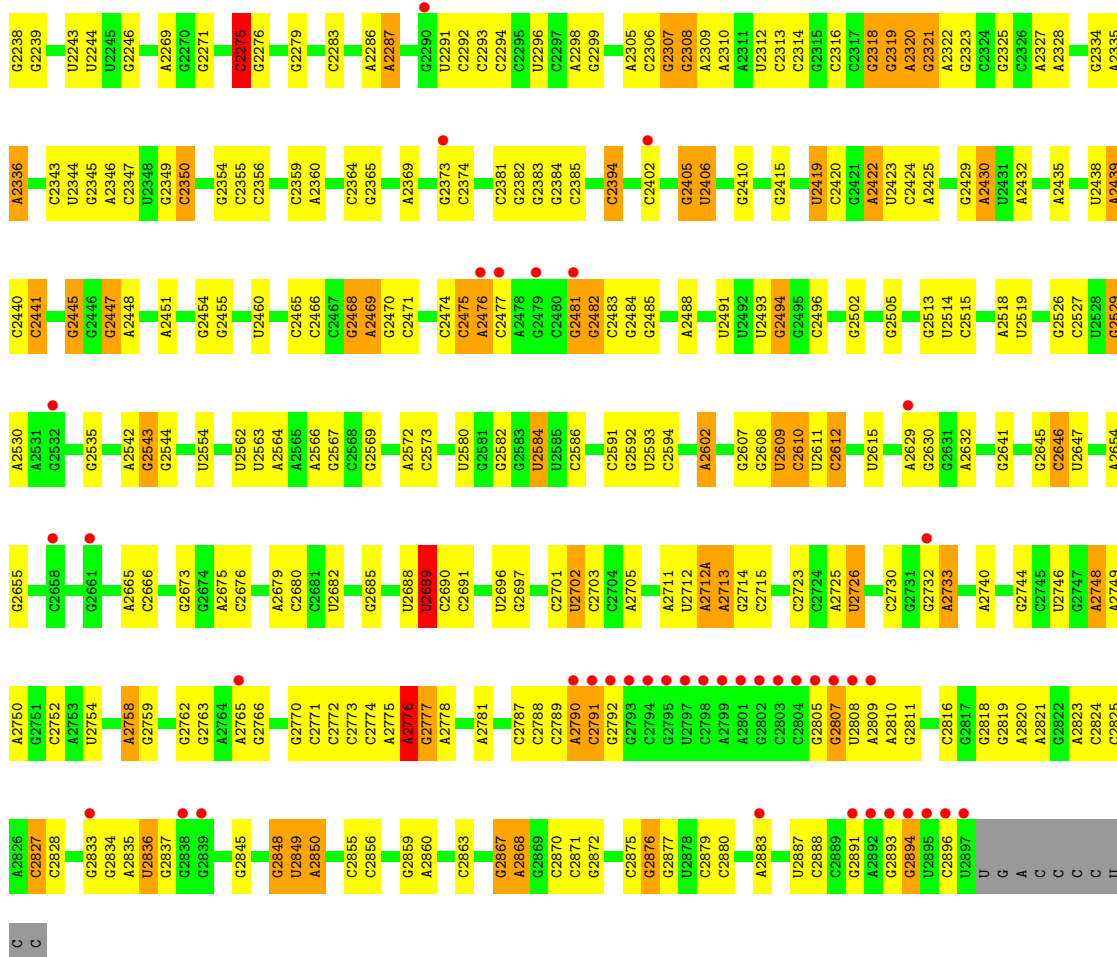
• Molecule 24: Killer protein



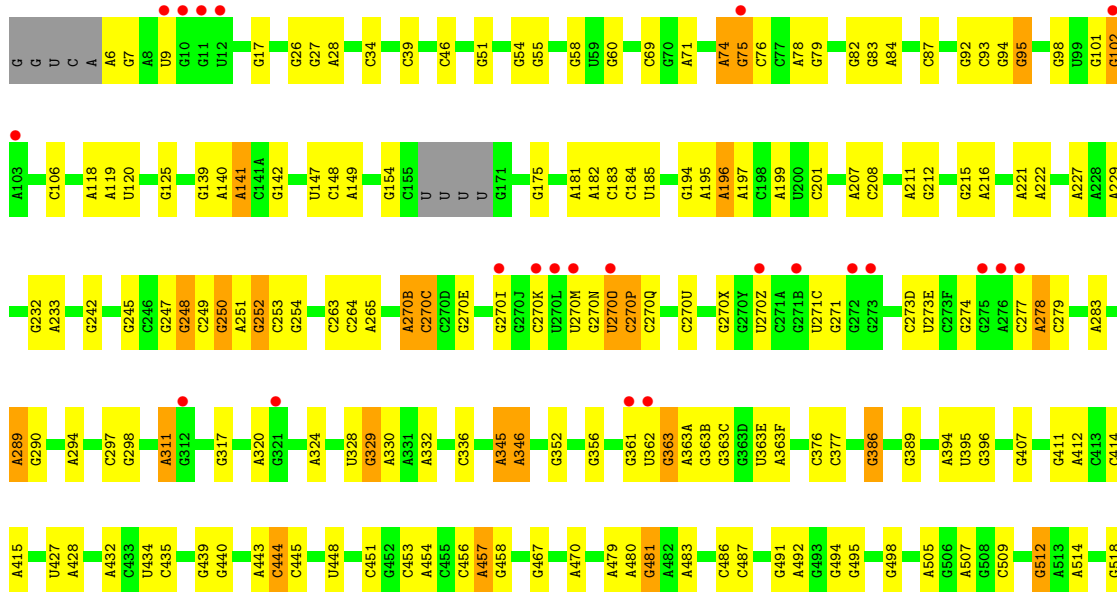
• Molecule 25: 23S rRNA





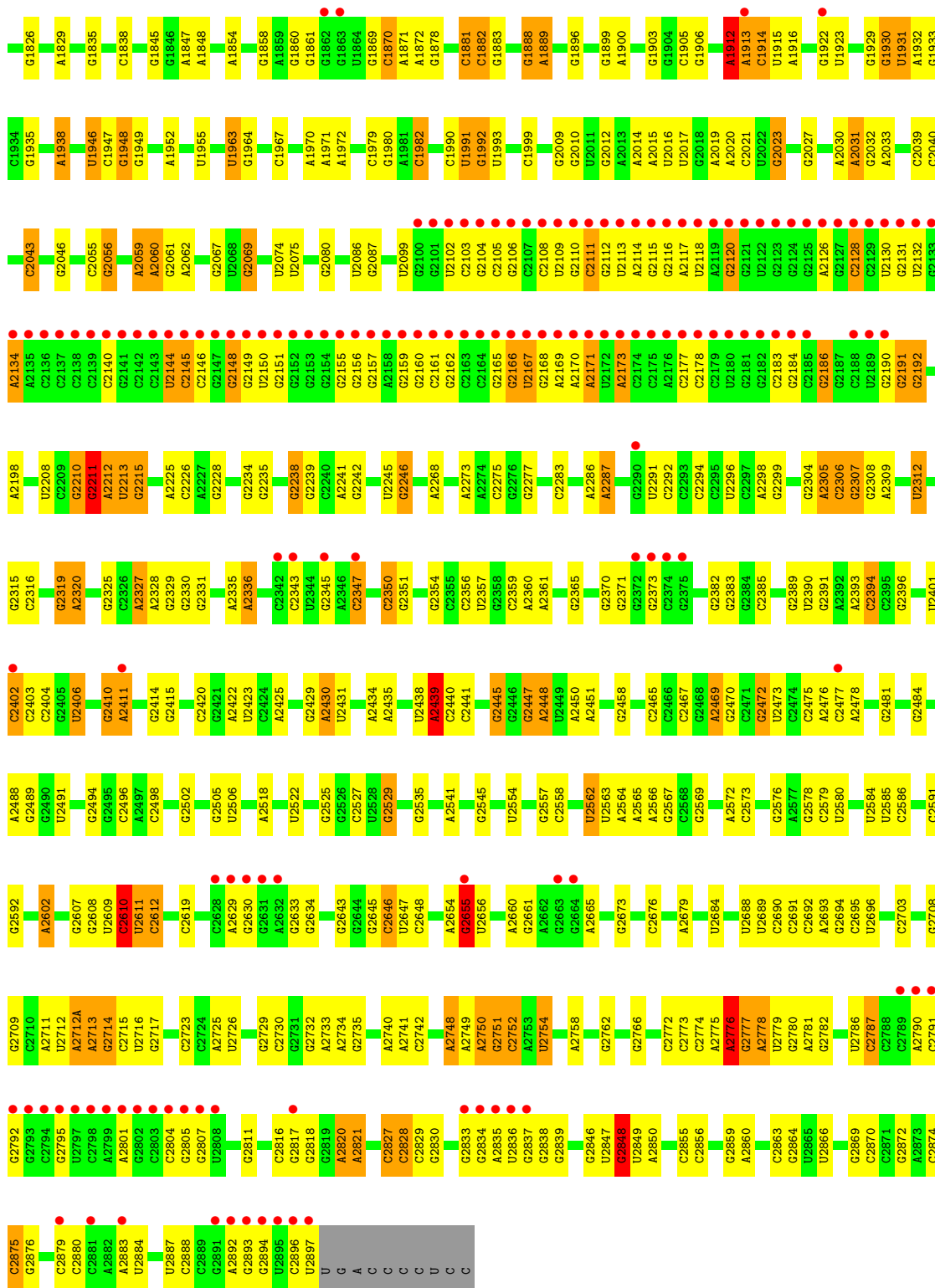


• Molecule 25: 23S rRNA



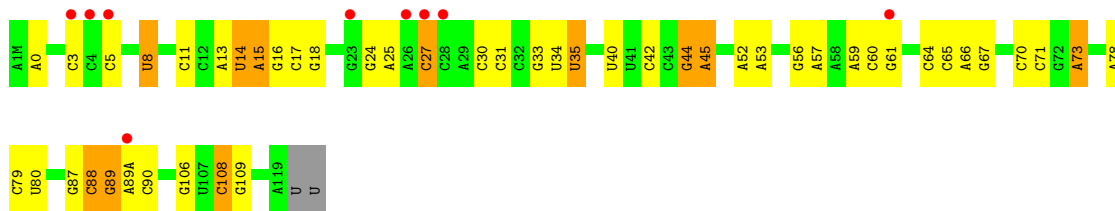
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G579	G580	G581	G582	G583	G586	G587	G588	G589	G590	G593	G598	G599	A603	U607	G612	U613	U614	U615	U616	U617	G618	G619	G620	G621	G622	G623	G624	G625	G626	G627	G631	G632	G633	G635	G636	G637	G638	G639	G640	G641	G642	G643	G644	G645	G646	G647	G648	G649	G650	G651	G652	G653	G654	G655	G656	G657	G658	G659	G660	G661	G662	G663	G664	G665	G666	G667	G668																																			
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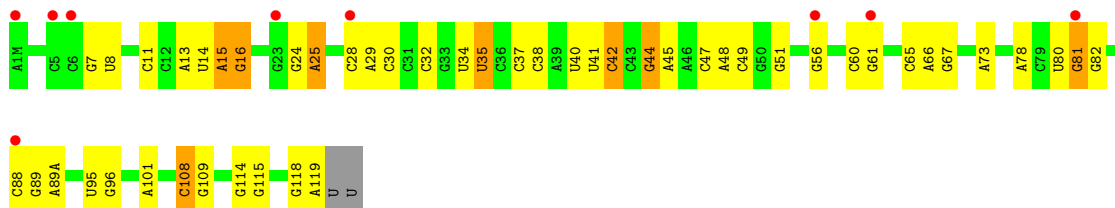


• Molecule 26: 5S rRNA

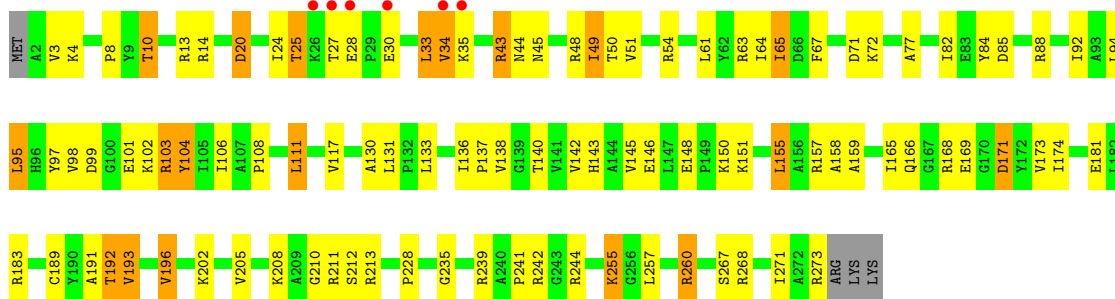




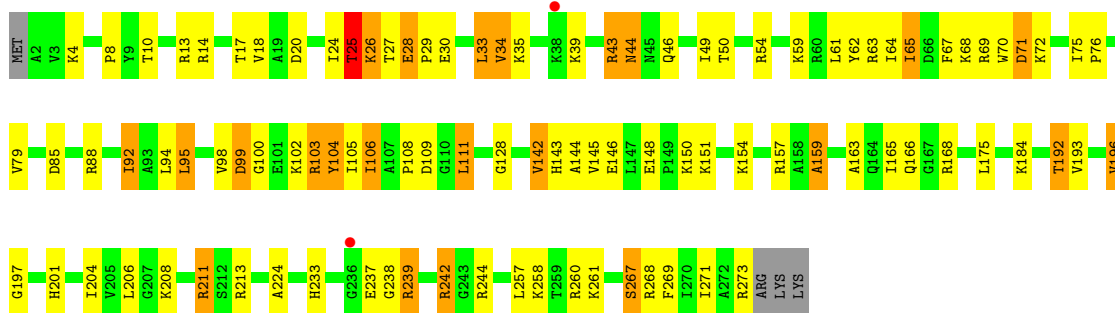
- Molecule 26: 5S rRNA



- Molecule 27: 50S ribosomal protein L2

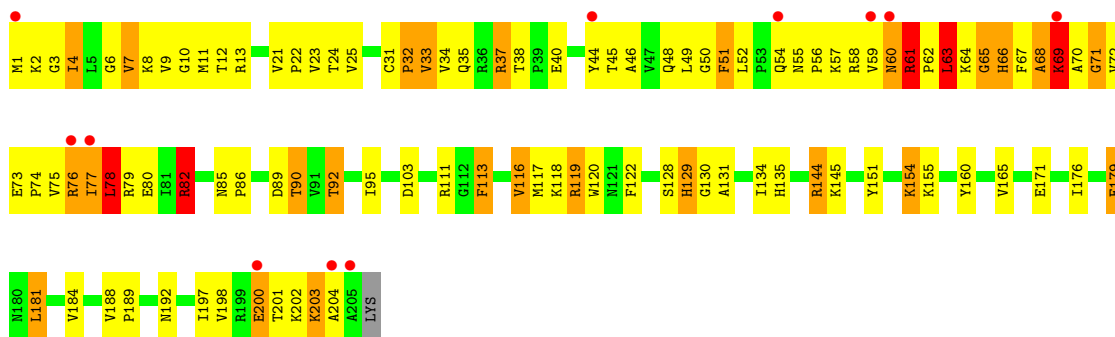


- Molecule 27: 50S ribosomal protein L2

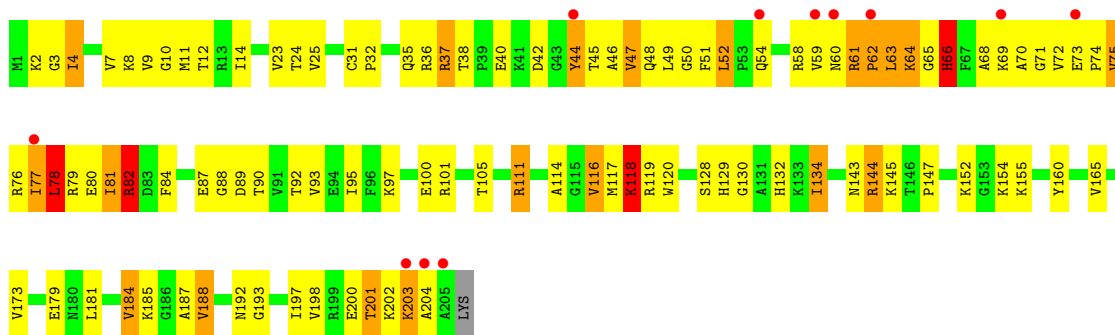


- Molecule 28: 50S ribosomal protein L3

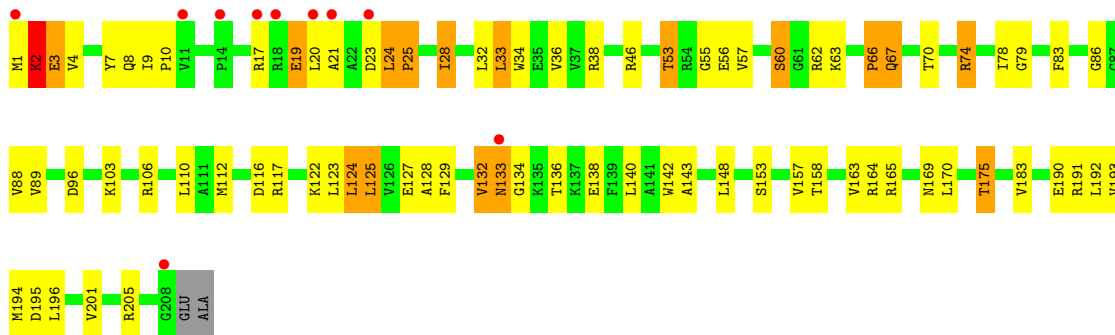




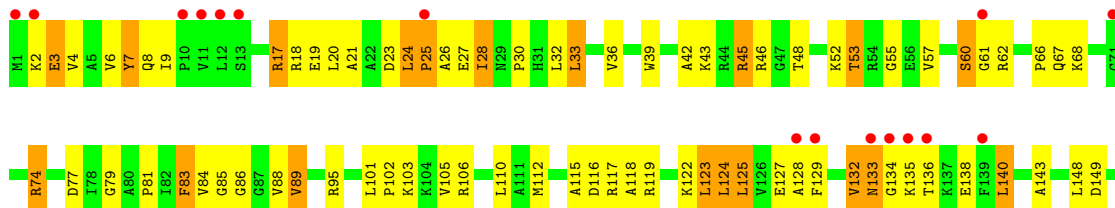
• Molecule 28: 50S ribosomal protein L3



• Molecule 29: 50S ribosomal protein L4



• Molecule 29: 50S ribosomal protein L4

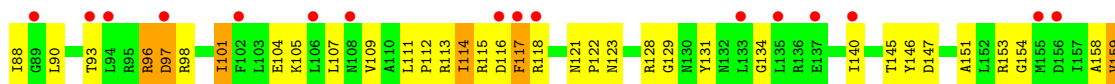
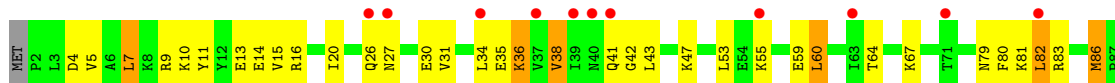




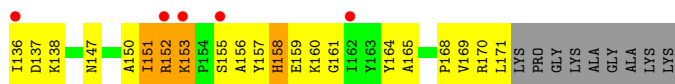
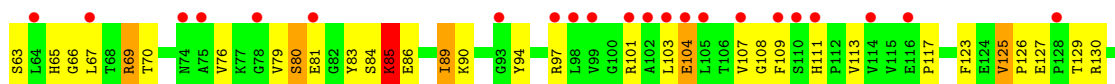
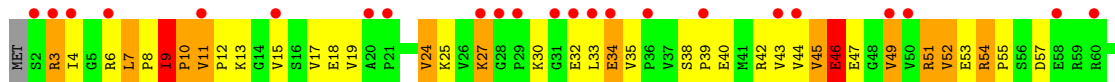
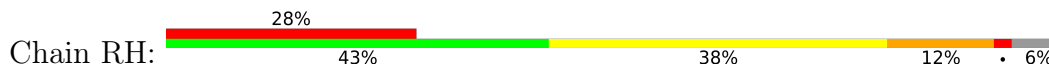
- Molecule 30: 50S ribosomal protein L5



- Molecule 30: 50S ribosomal protein L5

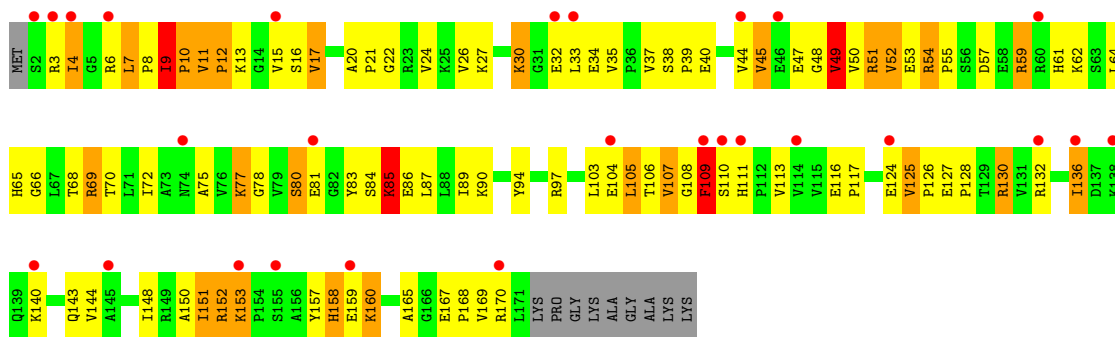


- Molecule 31: 50S ribosomal protein L6

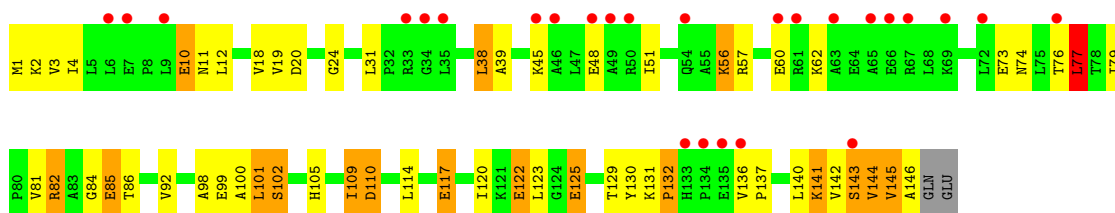


- Molecule 31: 50S ribosomal protein L6

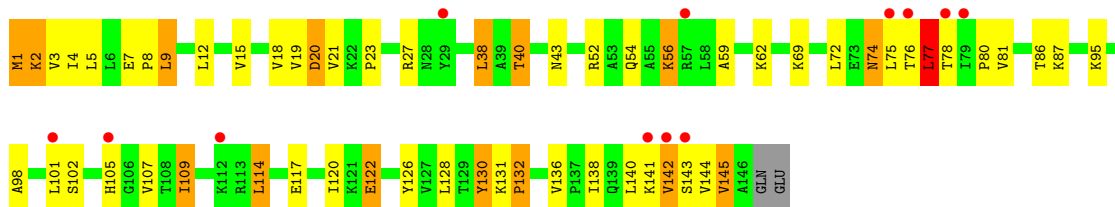




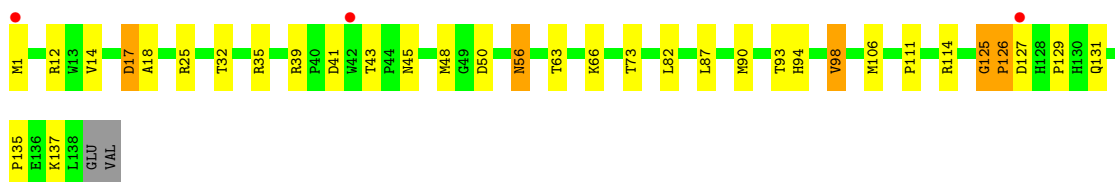
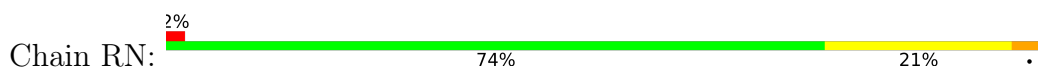
• Molecule 32: 50S ribosomal protein L9



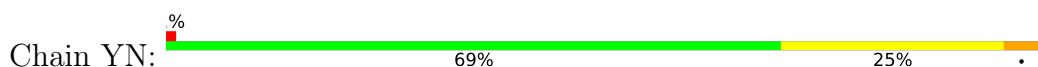
• Molecule 32: 50S ribosomal protein L9



• Molecule 33: 50S ribosomal protein L13



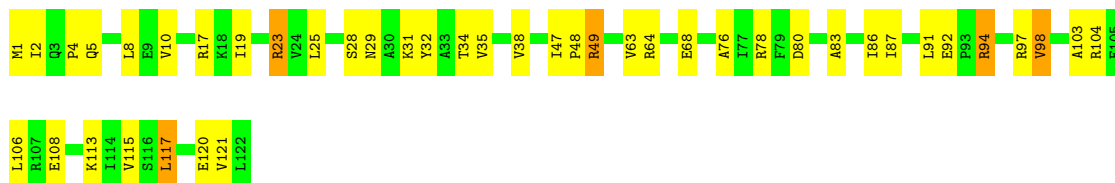
• Molecule 33: 50S ribosomal protein L13





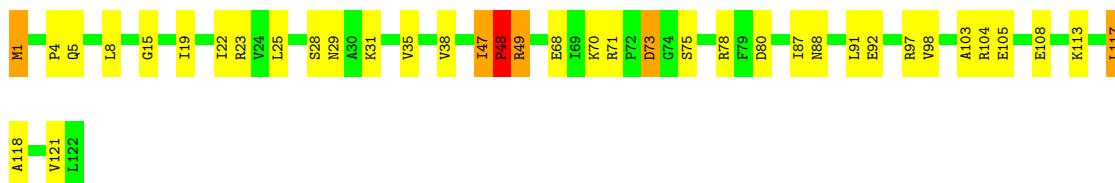
- Molecule 34: 50S ribosomal protein L14

Chain RO: 65% 31%



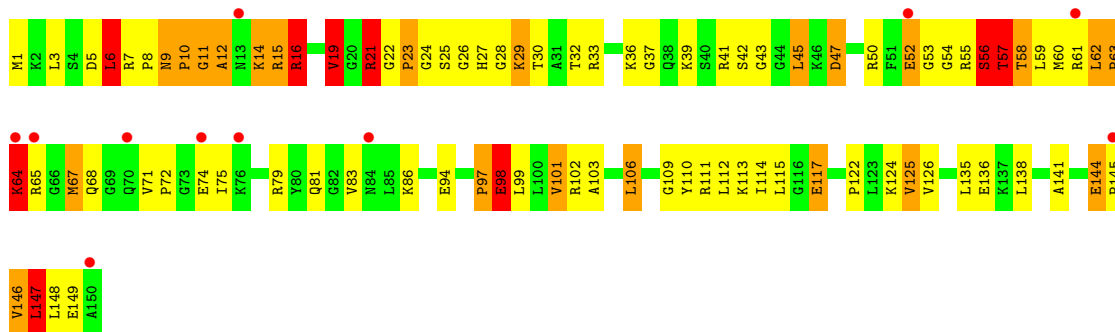
- Molecule 34: 50S ribosomal protein L14

Chain YO: 69% 26%



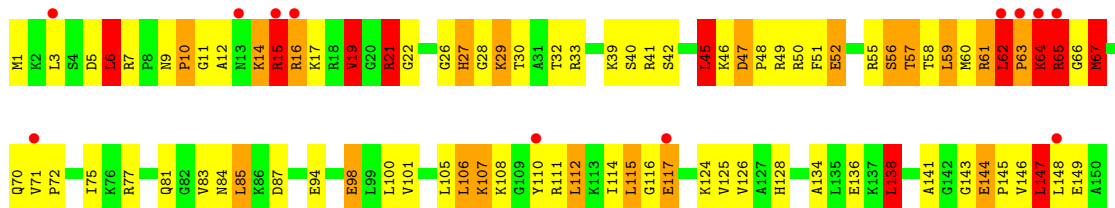
- Molecule 35: 50S ribosomal protein L15

Chain RP: 7% 41% 39% 15% 6%

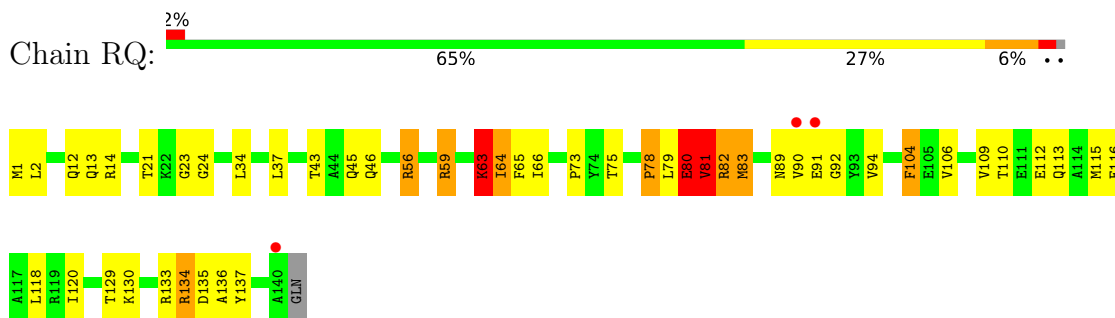


- Molecule 35: 50S ribosomal protein L15

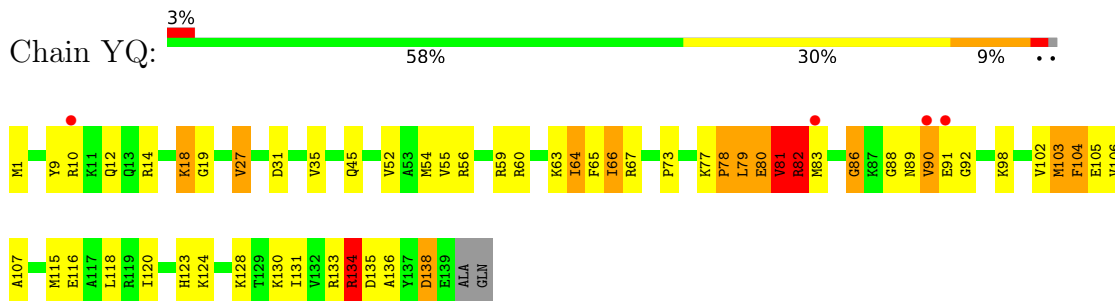
Chain YP: 8% 41% 38% 13% 7%



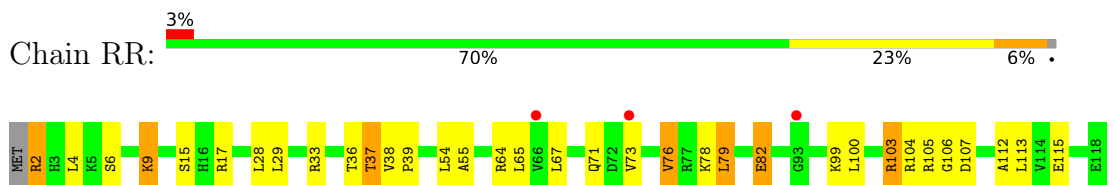
- Molecule 36: 50S ribosomal protein L16



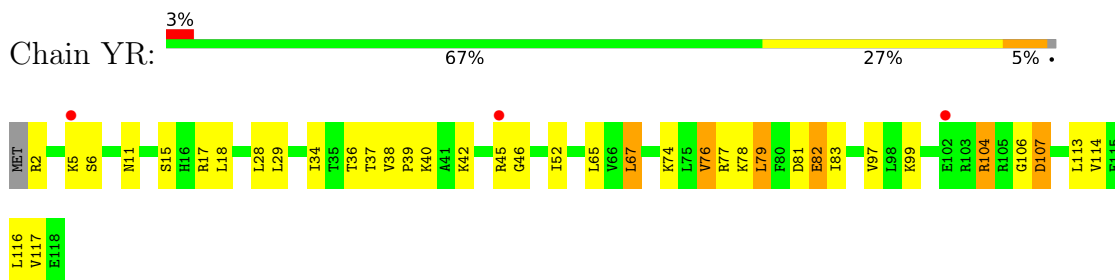
• Molecule 36: 50S ribosomal protein L16



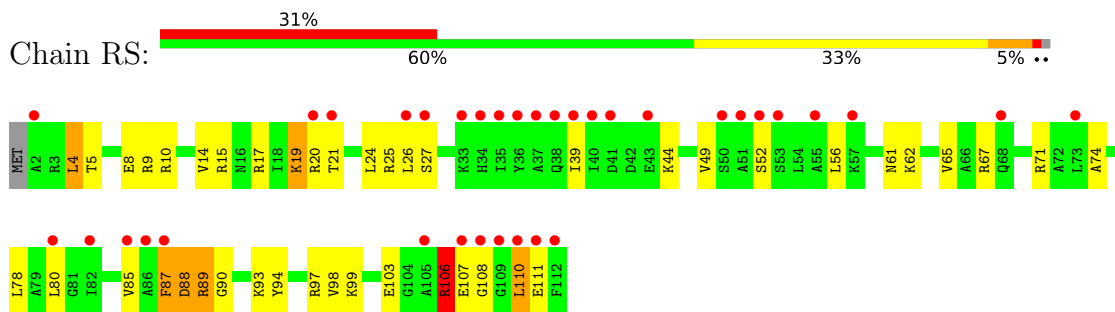
• Molecule 37: 50S ribosomal protein L17



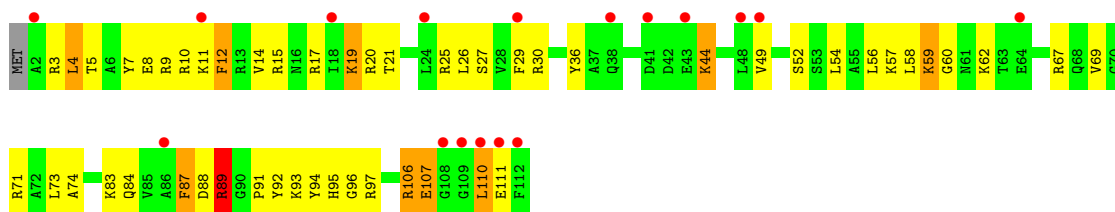
• Molecule 37: 50S ribosomal protein L17



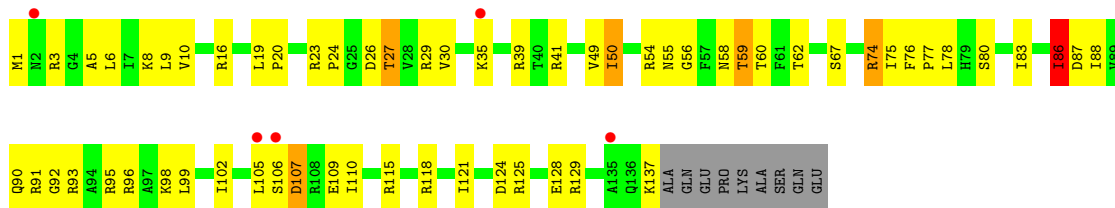
• Molecule 38: 50S ribosomal protein L18



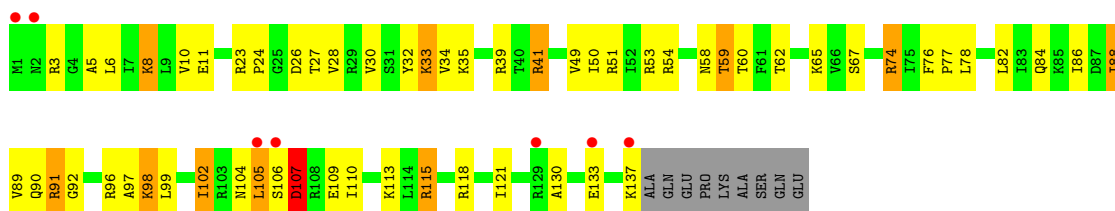
• Molecule 38: 50S ribosomal protein L18



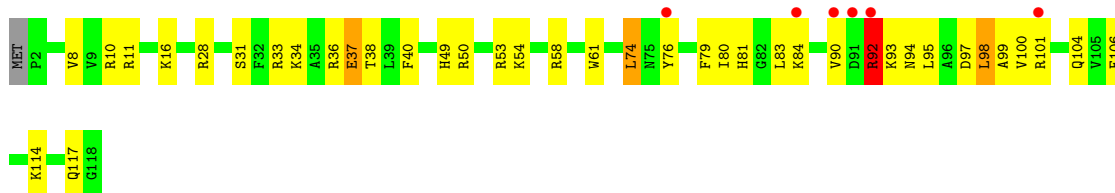
- Molecule 39: 50S ribosomal protein L19



- Molecule 39: 50S ribosomal protein L19



- Molecule 40: 50S ribosomal protein L20



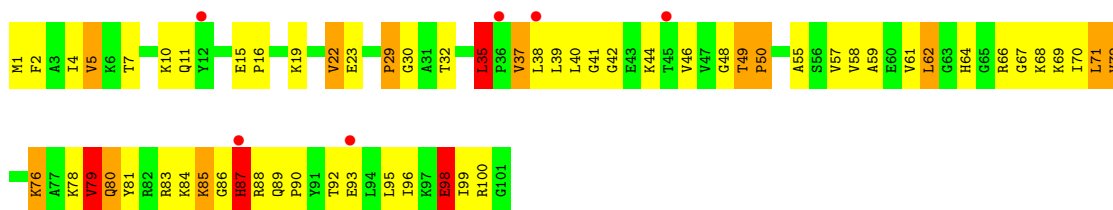
- Molecule 40: 50S ribosomal protein L20



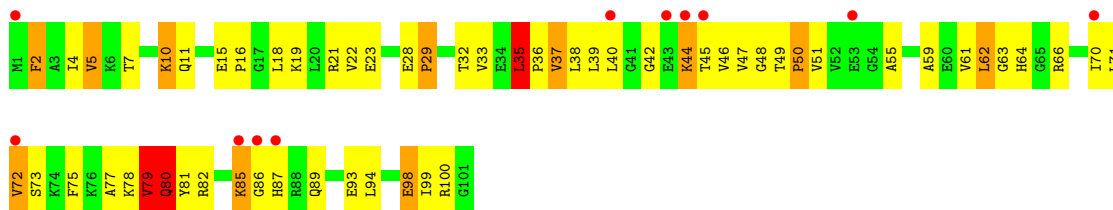
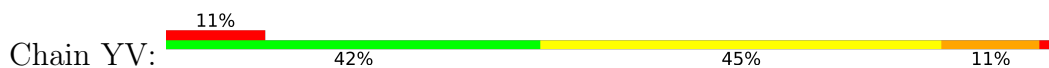




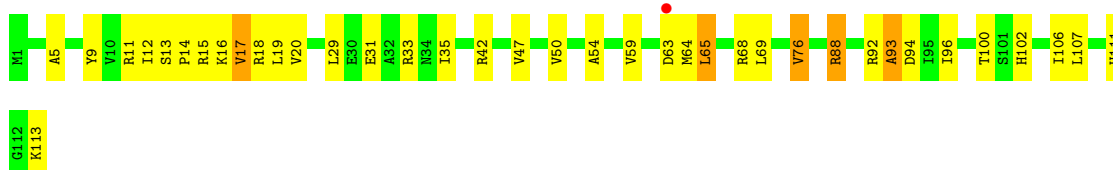
- Molecule 41: 50S ribosomal protein L21



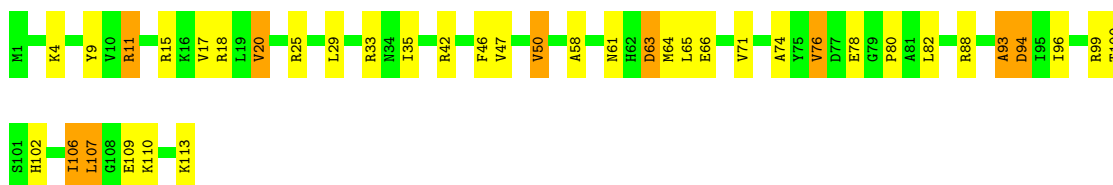
- Molecule 41: 50S ribosomal protein L21



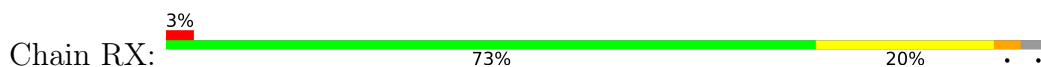
- Molecule 42: 50S ribosomal protein L22

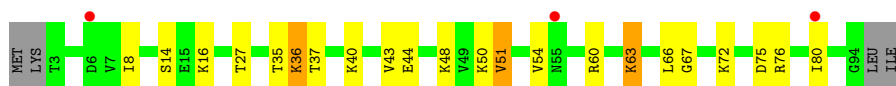


- Molecule 42: 50S ribosomal protein L22

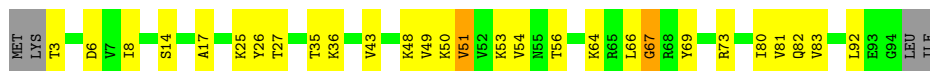


- Molecule 43: 50S ribosomal protein L23





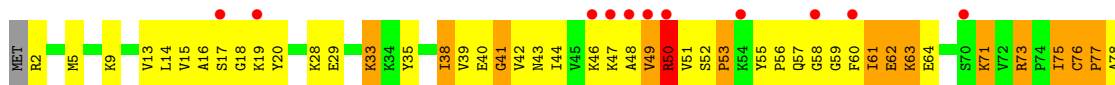
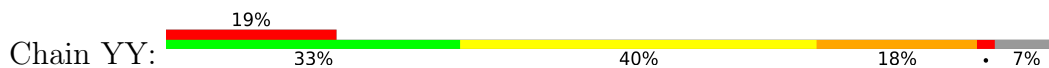
• Molecule 43: 50S ribosomal protein L23



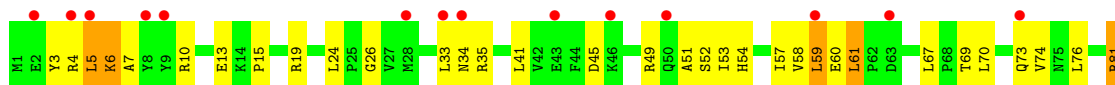
• Molecule 44: 50S ribosomal protein L24



• Molecule 44: 50S ribosomal protein L24

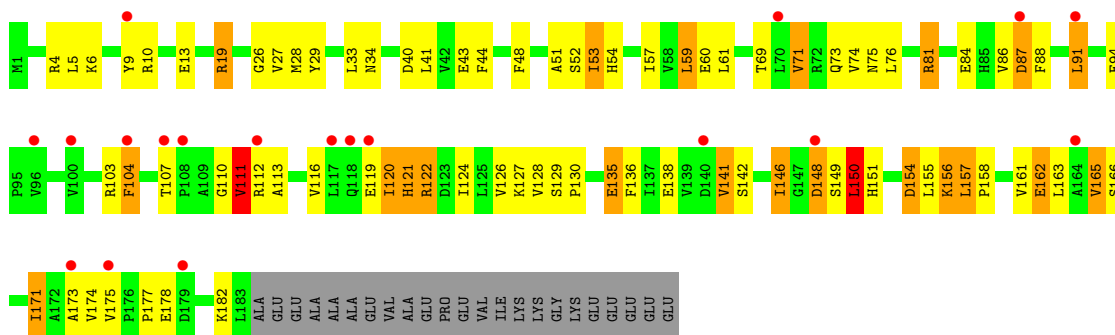


• Molecule 45: 50S ribosomal protein L25



• Molecule 45: 50S ribosomal protein L25





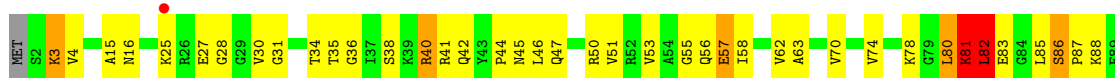
- Molecule 46: 50S ribosomal protein L27



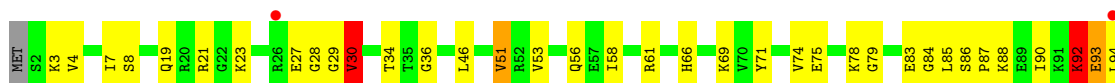
- Molecule 46: 50S ribosomal protein L27



- Molecule 47: 50S ribosomal protein L28

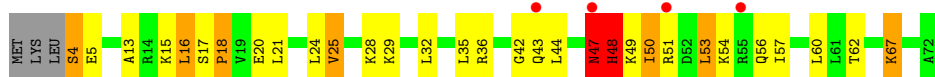


- Molecule 47: 50S ribosomal protein L28

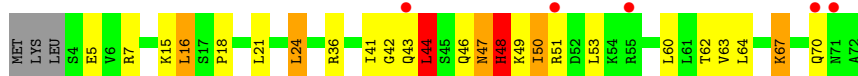


- Molecule 48: 50S ribosomal protein L29

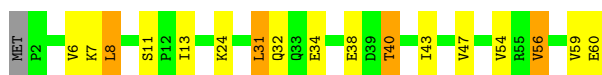




- Molecule 48: 50S ribosomal protein L29



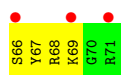
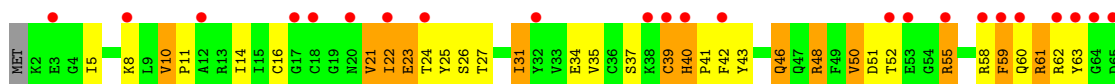
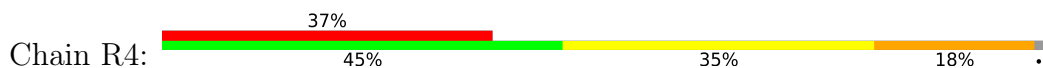
- Molecule 49: 50S ribosomal protein L30



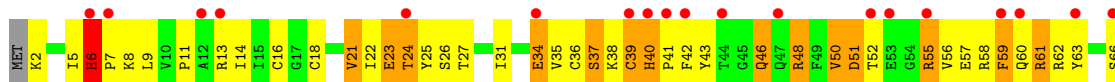
- Molecule 49: 50S ribosomal protein L30



- Molecule 50: 50S ribosomal protein L31



- Molecule 50: 50S ribosomal protein L31



- Molecule 51: 50S ribosomal protein L32

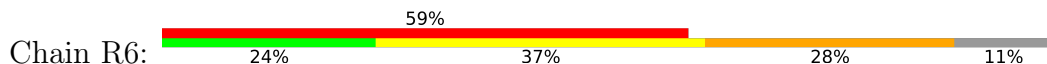




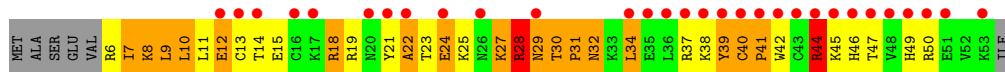
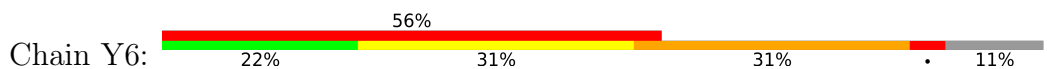
- Molecule 51: 50S ribosomal protein L32



- Molecule 52: 50S ribosomal protein L33



- Molecule 52: 50S ribosomal protein L33



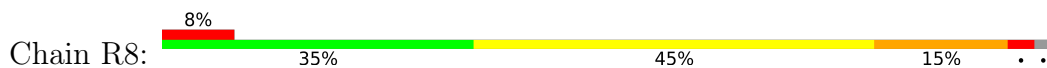
- Molecule 53: 50S ribosomal protein L34



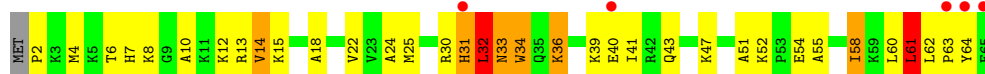
- Molecule 53: 50S ribosomal protein L34



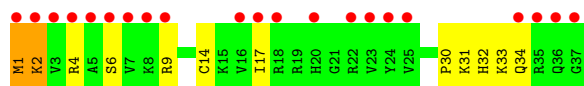
- Molecule 54: 50S ribosomal protein L35



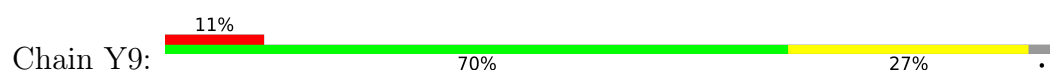
- Molecule 54: 50S ribosomal protein L35



- Molecule 55: 50S ribosomal protein L36



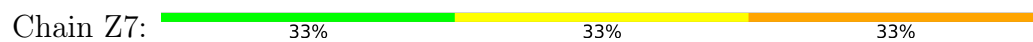
- Molecule 55: 50S ribosomal protein L36



- Molecule 56: CC-puromycin



- Molecule 56: CC-puromycin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	214.20Å 453.27Å 609.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.93 – 3.10 96.01 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.3 (34.93-3.10) 99.3 (96.01-3.10)	Depositor EDS
$R_{merge}$	0.20	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 3.13Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.203 , 0.237 0.206 , 0.239	Depositor DCC
$R_{free}$ test set	49438 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	62.6	Xtrriage
Anisotropy	0.145	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 70.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	294445	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	75.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.46% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: A2M, ZN, OMC, MG, PPU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	QA	0.31	0/36346	0.80	17/56724 (0.0%)
1	XA	0.34	2/36276 (0.0%)	0.81	23/56615 (0.0%)
2	QB	0.25	0/1950	0.49	0/2630
2	XB	0.25	0/1950	0.49	1/2630 (0.0%)
3	QC	0.24	0/1636	0.47	0/2205
3	XC	0.27	0/1636	0.48	0/2205
4	QD	0.28	0/1733	0.50	0/2318
4	XD	0.28	0/1733	0.50	0/2318
5	QE	0.28	0/1195	0.48	0/1609
5	XE	0.29	0/1195	0.48	0/1609
6	QF	0.25	0/856	0.44	0/1154
6	XF	0.28	0/856	0.45	0/1154
7	QG	0.23	0/1276	0.45	0/1709
7	XG	0.26	0/1276	0.46	0/1709
8	QH	0.24	0/1136	0.47	0/1527
8	XH	0.27	0/1136	0.45	0/1527
9	QI	0.24	0/1037	0.48	0/1389
9	XI	0.26	0/1037	0.48	0/1389
10	QJ	0.24	0/814	0.45	0/1095
10	XJ	0.24	0/814	0.46	0/1095
11	QK	0.24	0/916	0.44	0/1234
11	XK	0.28	0/916	0.48	0/1234
12	QL	0.31	0/991	0.52	1/1327 (0.1%)
12	XL	0.36	1/991 (0.1%)	0.56	1/1327 (0.1%)
13	QM	0.26	0/947	0.53	1/1270 (0.1%)
13	XM	0.25	0/947	0.53	0/1270
14	QN	0.25	0/501	0.47	0/664
14	XN	0.29	0/501	0.49	0/664
15	QO	0.24	0/745	0.39	0/992
15	XO	0.26	0/745	0.43	0/992
16	QP	0.26	0/721	0.46	0/970
16	XP	0.25	0/721	0.45	0/970



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
17	QQ	0.26	0/847	0.46	0/1131
17	XQ	0.30	0/847	0.47	0/1131
18	QR	0.25	0/590	0.48	0/782
18	XR	0.26	0/590	0.51	0/782
19	QS	0.27	0/670	0.53	0/901
19	XS	0.29	0/670	0.52	0/901
20	QT	0.24	0/765	0.49	1/1007 (0.1%)
20	XT	0.25	0/765	0.48	0/1007
21	QU	0.23	0/221	0.47	0/288
21	XU	0.24	0/221	0.45	0/288
22	QV	0.31	0/1832	0.79	0/2855
22	XV	0.32	0/1832	0.76	0/2855
23	QX	0.36	0/414	0.77	0/645
23	XX	0.35	0/414	0.86	0/645
24	QY	0.31	0/762	0.45	0/1028
24	XY	0.25	0/762	0.42	0/1028
25	RA	0.40	1/69742 (0.0%)	0.86	33/108874 (0.0%)
25	YA	0.42	1/69356 (0.0%)	0.87	27/108271 (0.0%)
26	RB	0.30	0/2928	0.81	0/4568
26	YB	0.31	0/2928	0.81	0/4568
27	RD	0.34	0/2165	0.56	0/2919
27	YD	0.37	0/2165	0.60	0/2919
28	RE	0.30	0/1601	0.55	0/2160
28	YE	0.34	0/1601	0.58	0/2160
29	RF	0.35	0/1662	0.58	0/2249
29	YF	0.31	0/1662	0.57	0/2249
30	RG	0.24	0/1499	0.46	0/2016
30	YG	0.25	0/1499	0.46	0/2016
31	RH	0.25	0/1332	0.60	1/1802 (0.1%)
31	YH	0.27	0/1332	0.61	1/1802 (0.1%)
32	RI	0.24	0/1151	0.54	0/1558
32	YI	0.28	0/1151	0.58	0/1558
33	RN	0.28	0/1131	0.50	0/1525
33	YN	0.29	0/1131	0.50	0/1525
34	RO	0.32	0/943	0.51	0/1269
34	YO	0.33	0/943	0.53	0/1269
35	RP	0.34	0/1162	0.66	0/1544
35	YP	0.35	0/1162	0.69	2/1544 (0.1%)
36	RQ	0.34	0/1133	0.57	0/1515
36	YQ	0.35	0/1128	0.58	1/1508 (0.1%)
37	RR	0.27	0/974	0.51	0/1302
37	YR	0.30	0/974	0.53	0/1302
38	RS	0.25	0/892	0.48	0/1187

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
38	YS	0.29	0/892	0.54	0/1187
39	RT	0.27	0/1155	0.46	0/1542
39	YT	0.30	0/1155	0.47	0/1542
40	RU	0.32	0/982	0.53	0/1306
40	YU	0.33	0/982	0.52	0/1306
41	RV	0.38	0/790	0.69	1/1057 (0.1%)
41	YV	0.35	0/790	0.67	1/1057 (0.1%)
42	RW	0.30	0/911	0.51	0/1220
42	YW	0.30	0/911	0.52	0/1220
43	RX	0.32	0/739	0.51	0/993
43	YX	0.35	0/739	0.52	0/993
44	RY	0.33	0/798	0.59	0/1064
44	YY	0.32	0/798	0.59	0/1064
45	RZ	0.28	0/1435	0.56	0/1947
45	YZ	0.30	0/1493	0.60	0/2026
46	R0	0.32	0/666	0.52	0/885
46	Y0	0.32	0/666	0.58	0/885
47	R1	0.31	0/770	0.57	0/1022
47	Y1	0.36	0/770	0.59	0/1022
48	R2	0.28	0/583	0.58	0/771
48	Y2	0.33	0/583	0.59	1/771 (0.1%)
49	R3	0.29	0/474	0.44	0/635
49	Y3	0.28	0/474	0.47	0/635
50	R4	0.24	0/586	0.46	0/785
50	Y4	0.30	0/586	0.51	0/785
51	R5	0.30	0/473	0.58	1/639 (0.2%)
51	Y5	0.50	1/456 (0.2%)	0.71	2/617 (0.3%)
52	R6	0.29	0/424	0.67	0/565
52	Y6	0.44	0/424	0.82	0/565
53	R7	0.33	0/438	0.49	0/575
53	Y7	0.34	0/438	0.53	0/575
54	R8	0.42	0/525	0.75	0/691
54	Y8	0.38	0/525	0.66	0/691
55	R9	0.26	0/310	0.42	0/407
55	Y9	0.24	0/302	0.41	0/397
56	Z6	0.53	0/40	0.56	0/60
56	Z7	0.38	0/40	0.62	0/60
All	All	0.36	6/318202 (0.0%)	0.77	116/475540 (0.0%)

All (6) bond length outliers are listed below:

*Continued on next page...*

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	RA	1983	C	O3'-P	-5.65	1.54	1.61
25	YA	2643	G	O3'-P	-5.59	1.54	1.61
1	XA	1296	C	O3'-P	-5.42	1.54	1.61
1	XA	1156	G	O3'-P	-5.28	1.54	1.61
51	Y5	7	PRO	N-CD	5.26	1.55	1.47
12	XL	25	PRO	N-CD	5.01	1.54	1.47

All (116) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	XA	1157	A	P-O3'-C3'	8.78	130.23	119.70
1	XA	115	G	P-O3'-C3'	8.69	130.12	119.70
25	YA	1912	A	P-O3'-C3'	6.44	127.43	119.70
1	XA	1156	G	P-O3'-C3'	-6.17	112.29	119.70
1	QA	345	C	P-O3'-C3'	6.01	126.91	119.70
25	YA	1558	A	P-O3'-C3'	6.00	126.90	119.70
51	Y5	4	HIS	C-N-CD	5.99	140.98	128.40
12	XL	24	VAL	C-N-CD	5.99	140.98	128.40
25	RA	2447	G	P-O3'-C3'	5.96	126.85	119.70
25	YA	613	U	N3-C2-O2	-5.95	118.03	122.20
25	YA	2477	C	C2-N1-C1'	5.94	125.33	118.80
1	QA	1301	U	C2-N1-C1'	5.93	124.82	117.70
1	XA	1065	U	P-O3'-C3'	5.91	126.79	119.70
1	XA	687	A	P-O3'-C3'	5.87	126.74	119.70
1	XA	960	U	P-O3'-C3'	5.87	126.74	119.70
35	YP	138	LEU	CA-CB-CG	5.85	128.75	115.30
1	XA	818	G	P-O3'-C3'	5.77	126.62	119.70
20	QT	10	LEU	CA-CB-CG	5.75	128.52	115.30
25	RA	2275	C	C6-N1-C2	-5.74	118.00	120.30
1	XA	197	A	P-O3'-C3'	5.71	126.56	119.70
25	RA	1992	G	P-O3'-C3'	5.67	126.50	119.70
1	QA	687	A	P-O3'-C3'	5.65	126.48	119.70
41	RV	35	LEU	CA-CB-CG	5.65	128.29	115.30
1	QA	1528	U	C4'-C3'-O3'	5.64	124.28	113.00
1	XA	960	U	C2-N1-C1'	5.61	124.43	117.70
25	YA	2619	C	C6-N1-C2	5.60	122.54	120.30
25	YA	298	G	N1-C6-O6	5.58	123.25	119.90
25	YA	1781	C	C2-N1-C1'	5.58	124.94	118.80
1	XA	547	A	P-O3'-C3'	5.57	126.38	119.70
25	YA	2655	G	O4'-C1'-N9	5.57	112.65	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	QA	547	A	P-O3'-C3'	5.55	126.36	119.70
25	YA	528	A	P-O3'-C3'	5.54	126.35	119.70
25	YA	856	C	C6-N1-C2	-5.54	118.08	120.30
1	QA	197	A	P-O3'-C3'	5.54	126.34	119.70
51	Y5	6	VAL	C-N-CD	5.53	140.02	128.40
25	RA	227	A	P-O3'-C3'	5.53	126.33	119.70
25	RA	856	C	C2-N1-C1'	5.52	124.88	118.80
25	YA	774	A	C8-N9-C4	-5.52	103.59	105.80
1	XA	1094	G	P-O3'-C3'	5.51	126.31	119.70
25	YA	1313	U	C2-N1-C1'	5.51	124.31	117.70
25	RA	387	U	P-O3'-C3'	5.51	126.31	119.70
1	QA	754	C	C2-N1-C1'	5.50	124.85	118.80
25	RA	1300	U	P-O3'-C3'	5.49	126.28	119.70
25	YA	2447	G	P-O3'-C3'	5.49	126.28	119.70
25	YA	933	A	O4'-C1'-N9	5.47	112.58	108.20
25	RA	912	C	N1-C2-O2	5.46	122.17	118.90
25	RA	1980	G	P-O3'-C3'	5.46	126.25	119.70
25	YA	2211	G	P-O3'-C3'	5.46	126.25	119.70
1	QA	1065	U	P-O3'-C3'	5.42	126.21	119.70
1	XA	1502	A	N7-C8-N9	5.42	116.51	113.80
25	YA	746	A	O4'-C1'-N9	5.42	112.54	108.20
25	YA	748	G	O4'-C1'-N9	5.41	112.53	108.20
25	RA	2776	A	P-O3'-C3'	5.39	126.17	119.70
25	RA	2689	U	N3-C2-O2	-5.38	118.43	122.20
25	RA	1341	U	C2'-C3'-O3'	5.38	122.30	113.70
1	XA	792	A	P-O3'-C3'	5.36	126.14	119.70
25	YA	2335	A	O4'-C1'-N9	5.36	112.49	108.20
25	RA	603	A	P-O3'-C3'	5.34	126.11	119.70
1	QA	754	C	N1-C2-O2	5.33	122.10	118.90
1	QA	913	A	P-O3'-C3'	5.32	126.08	119.70
25	YA	1963	U	C2-N1-C1'	5.31	124.07	117.70
41	YV	35	LEU	CA-CB-CG	5.31	127.51	115.30
25	RA	119	A	P-O3'-C3'	5.30	126.06	119.70
25	RA	372	G	OP2-P-O3'	5.29	116.84	105.20
25	RA	1653	G	P-O3'-C3'	5.28	126.04	119.70
35	YP	85	LEU	CA-CB-CG	5.28	127.44	115.30
25	RA	2405	G	P-O3'-C3'	5.28	126.03	119.70
25	RA	1914	C	N1-C2-O2	5.28	122.06	118.90
1	XA	1155	G	O3'-P-O5'	-5.27	93.98	104.00
25	RA	1528	A	C5-C6-N1	5.27	120.34	117.70
13	QM	70	LEU	CA-CB-CG	5.27	127.41	115.30
25	RA	613	U	O4'-C1'-N1	5.25	112.40	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	YA	2776	A	P-O3'-C3'	5.23	125.98	119.70
25	YA	298	G	O5'-P-OP1	-5.23	101.00	105.70
25	RA	974(A)	C	N3-C2-O2	-5.22	118.25	121.90
1	XA	5	U	P-O3'-C3'	5.22	125.96	119.70
2	XB	154	LEU	CA-CB-CG	5.21	127.28	115.30
1	QA	792	A	P-O3'-C3'	5.20	125.94	119.70
25	RA	847	U	C5-C6-N1	-5.20	120.10	122.70
1	XA	410	G	P-O3'-C3'	5.20	125.94	119.70
1	XA	1086	U	C2-N1-C1'	5.18	123.92	117.70
1	XA	1067	A	P-O3'-C3'	5.17	125.91	119.70
1	XA	243	A	P-O3'-C3'	5.17	125.90	119.70
25	RA	1781	C	N1-C2-O2	5.17	122.00	118.90
25	YA	2211	G	OP2-P-O3'	5.17	116.56	105.20
48	Y2	16	LEU	CA-CB-CG	5.17	127.18	115.30
12	QL	47	LYS	C-N-CD	5.14	139.19	128.40
25	RA	2610	C	P-O3'-C3'	5.14	125.87	119.70
31	RH	9	ILE	C-N-CD	-5.14	109.29	120.60
36	YQ	82	ARG	N-CA-C	5.13	124.86	111.00
25	RA	752	A	P-O3'-C3'	5.13	125.85	119.70
25	RA	859	G	P-O3'-C3'	5.12	125.85	119.70
1	XA	913	A	P-O3'-C3'	5.12	125.85	119.70
25	RA	748	G	C4-N9-C1'	-5.12	119.84	126.50
25	YA	1300	U	P-O3'-C3'	5.12	125.84	119.70
25	YA	2439	A	P-O3'-C3'	5.12	125.84	119.70
25	YA	2610	C	P-O3'-C3'	5.11	125.84	119.70
31	YH	9	ILE	C-N-CD	-5.10	109.38	120.60
1	XA	1065	U	C5-C4-O4	5.10	128.96	125.90
1	QA	1498	U	P-O3'-C3'	5.08	125.80	119.70
25	RA	2275	C	P-O3'-C3'	5.08	125.79	119.70
25	RA	2688	U	N3-C2-O2	-5.07	118.65	122.20
51	R5	4	HIS	C-N-CD	5.07	139.05	128.40
1	QA	5	U	P-O3'-C3'	5.07	125.78	119.70
1	XA	1157	A	C3'-C2'-O2'	-5.07	98.60	113.30
25	RA	372	G	P-O3'-C3'	5.07	125.78	119.70
1	QA	971	G	C4-N9-C1'	5.06	133.08	126.50
25	RA	2422	A	C3'-C2'-C1'	5.06	105.55	101.50
25	RA	2689	U	P-O3'-C3'	5.04	125.75	119.70
1	XA	250	A	P-O3'-C3'	5.04	125.75	119.70
1	QA	974	A	O4'-C1'-N9	5.02	112.22	108.20
25	YA	2848	G	P-O3'-C3'	5.02	125.73	119.70
1	QA	60	A	P-O3'-C3'	5.01	125.71	119.70
25	RA	2584	U	N3-C2-O2	-5.01	118.69	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	QA	1152	A	O4'-C1'-N9	5.00	112.20	108.20
25	YA	1992	G	C2'-C3'-O3'	5.00	121.71	113.70

There are no chirality outliers.

There are no planarity outliers.

## 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	QA	32472	0	16393	410	0
1	XA	32409	0	16361	373	0
2	QB	1915	0	1969	57	0
2	XB	1915	0	1969	60	0
3	QC	1612	0	1677	51	0
3	XC	1612	0	1677	34	0
4	QD	1703	0	1765	41	0
4	XD	1703	0	1766	39	0
5	QE	1178	0	1233	30	0
5	XE	1178	0	1234	24	0
6	QF	843	0	857	16	0
6	XF	843	0	857	19	0
7	QG	1257	0	1296	23	0
7	XG	1257	0	1296	31	0
8	QH	1116	0	1177	34	0
8	XH	1116	0	1177	27	0
9	QI	1018	0	1049	55	0
9	XI	1018	0	1049	40	0
10	QJ	801	0	849	34	0
10	XJ	801	0	849	46	0
11	QK	901	0	926	19	0
11	XK	901	0	926	19	0
12	QL	975	0	1062	26	0
12	XL	975	0	1062	22	0
13	QM	937	0	994	29	0
13	XM	937	0	994	59	0
14	QN	492	0	529	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	XN	492	0	529	11	0
15	QO	734	0	771	14	0
15	XO	734	0	771	16	0
16	QP	705	0	725	13	0
16	XP	705	0	725	10	0
17	QQ	834	0	904	15	0
17	XQ	834	0	904	15	0
18	QR	585	0	657	9	0
18	XR	585	0	657	19	0
19	QS	656	0	678	46	0
19	XS	656	0	678	40	0
20	QT	763	0	861	21	0
20	XT	763	0	861	27	0
21	QU	217	0	234	9	0
21	XU	217	0	234	13	0
22	QV	1640	0	837	11	0
22	XV	1640	0	837	12	0
23	QX	435	9	225	18	0
23	XX	435	9	225	16	0
24	QY	746	0	742	15	0
24	XY	746	0	742	12	0
25	RA	62269	0	31392	690	0
25	YA	61924	0	31214	645	0
26	RB	2617	0	1328	27	0
26	YB	2617	0	1328	25	0
27	RD	2115	0	2195	66	0
27	YD	2115	0	2195	71	0
28	RE	1568	0	1634	104	0
28	YE	1568	0	1634	75	0
29	RF	1627	0	1680	52	0
29	YF	1627	0	1680	55	0
30	RG	1474	0	1535	43	0
30	YG	1474	0	1535	46	0
31	RH	1307	0	1382	95	0
31	YH	1307	0	1381	82	0
32	RI	1136	0	1223	53	0
32	YI	1136	0	1223	69	0
33	RN	1104	0	1180	15	0
33	YN	1104	0	1180	21	0
34	RO	933	0	996	28	0
34	YO	933	0	996	28	0
35	RP	1145	0	1228	113	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	YP	1145	0	1228	141	0
36	RQ	1112	0	1170	32	0
36	YQ	1107	0	1165	36	0
37	RR	960	0	1021	15	0
37	YR	960	0	1021	25	0
38	RS	882	0	943	29	0
38	YS	882	0	943	34	0
39	RT	1141	0	1202	44	0
39	YT	1141	0	1202	38	0
40	RU	964	0	1022	36	0
40	YU	964	0	1022	34	0
41	RV	779	0	852	58	0
41	YV	779	0	852	57	0
42	RW	900	0	964	23	0
42	YW	900	0	964	21	0
43	RX	725	0	778	17	0
43	YX	725	0	778	17	0
44	RY	785	0	877	68	0
44	YY	785	0	878	47	0
45	RZ	1404	0	1437	90	0
45	YZ	1461	0	1493	47	0
46	R0	657	0	683	21	0
46	Y0	657	0	683	24	0
47	R1	763	0	848	28	0
47	Y1	763	0	848	22	0
48	R2	581	0	629	17	0
48	Y2	581	0	629	16	0
49	R3	469	0	518	9	0
49	Y3	469	0	518	9	0
50	R4	573	0	565	22	0
50	Y4	573	0	565	37	0
51	R5	459	0	480	10	0
51	Y5	442	0	465	22	0
52	R6	417	0	441	24	0
52	Y6	417	0	441	51	0
53	R7	430	0	480	8	0
53	Y7	430	0	480	12	0
54	R8	517	0	582	49	0
54	Y8	517	0	582	69	0
55	R9	307	0	338	8	0
55	Y9	299	0	326	6	0
56	Z6	74	0	51	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	Z7	74	0	51	10	0
57	QA	151	0	0	0	0
57	QD	2	0	0	0	0
57	QE	1	0	0	0	0
57	QL	1	0	0	0	0
57	QN	1	0	0	0	0
57	QV	5	0	0	0	0
57	R0	2	0	0	0	0
57	R2	1	0	0	0	0
57	R5	3	0	0	0	0
57	RA	451	0	0	0	0
57	RB	5	0	0	0	0
57	RD	2	0	0	0	0
57	RE	3	0	0	0	0
57	RF	1	0	0	0	0
57	RP	2	0	0	0	0
57	RQ	2	0	0	0	0
57	RR	1	0	0	0	0
57	RV	1	0	0	0	0
57	RY	2	0	0	0	0
57	XA	164	0	0	0	0
57	XD	1	0	0	0	0
57	XE	1	0	0	0	0
57	XF	1	0	0	0	0
57	XK	1	0	0	0	0
57	XL	1	0	0	0	0
57	XN	1	0	0	0	0
57	XS	1	0	0	0	0
57	XV	4	0	0	0	0
57	Y0	1	0	0	0	0
57	Y5	3	0	0	0	0
57	Y7	1	0	0	0	0
57	YA	504	0	0	0	0
57	YB	6	0	0	0	0
57	YD	1	0	0	0	0
57	YE	2	0	0	0	0
57	YF	2	0	0	0	0
57	YG	1	0	0	0	0
57	YH	2	0	0	0	0
57	YN	1	0	0	0	0
57	YO	1	0	0	0	0
57	YP	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	YQ	2	0	0	0	0
57	YR	1	0	0	0	0
57	YU	1	0	0	0	0
57	YV	1	0	0	0	0
57	YW	1	0	0	0	0
57	Z7	1	0	0	0	0
58	QD	1	0	0	0	0
58	QN	1	0	0	0	0
58	XD	1	0	0	0	0
58	XN	1	0	0	0	0
All	All	294427	18	199944	4997	0

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 10.

All (4997) 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)
41:YV:49:THR:CG2	41:YV:50:PRO:HD3	1.35	1.52
31:RH:9:ILE:CG2	31:RH:10:PRO:HA	1.36	1.51
50:Y4:6:HIS:HB2	50:Y4:7:PRO:CD	1.43	1.47
31:YH:9:ILE:CG2	31:YH:10:PRO:HA	1.39	1.47
41:RV:49:THR:CG2	41:RV:50:PRO:HD3	1.48	1.42
32:RI:143:SER:O	32:RI:144:VAL:HG22	1.19	1.37
28:RE:51:PHE:O	28:RE:74:PRO:HB3	1.29	1.31
31:RH:9:ILE:HB	31:RH:10:PRO:CB	1.61	1.31
31:YH:9:ILE:HB	31:YH:10:PRO:CB	1.57	1.30
45:RZ:156:LYS:O	45:RZ:157:LEU:HG	1.29	1.30
5:QE:10:MET:SD	5:QE:13:ILE:HD12	1.72	1.28
13:XM:8:GLU:O	13:XM:9:ILE:HG22	1.09	1.26
35:YP:64:LYS:HG2	54:Y8:25:MET:CG	1.67	1.22
52:Y6:30:THR:HA	52:Y6:31:PRO:O	1.34	1.22
44:RY:76:CYS:SG	44:RY:77:PRO:HD3	1.80	1.21
41:YV:49:THR:HG22	41:YV:50:PRO:CD	1.70	1.20
35:RP:58:THR:HG22	35:RP:61:ARG:NH2	1.56	1.20
32:YI:78:THR:H	32:YI:142:VAL:CG2	1.54	1.19
45:RZ:163:LEU:HD11	45:RZ:165:VAL:CG1	1.72	1.19
25:RA:1547:C:O2'	25:RA:1548:C:H5'	1.42	1.18
41:YV:49:THR:CB	41:YV:50:PRO:HD3	1.71	1.18
45:YZ:155:LEU:HD12	45:YZ:155:LEU:O	1.42	1.16
35:RP:64:LYS:NZ	54:R8:30:ARG:HA	1.60	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:RA:1981:A:H5''	25:RA:1982:C:OP2	1.43	1.16
35:RP:56:SER:O	35:RP:57:THR:HG22	1.44	1.15
44:RY:75:ILE:HG13	44:RY:80:GLY:H	1.02	1.15
45:RZ:163:LEU:CD1	45:RZ:165:VAL:HG12	1.75	1.15
31:YH:9:ILE:HG22	31:YH:10:PRO:CA	1.77	1.15
32:YI:78:THR:H	32:YI:142:VAL:HG23	1.04	1.13
31:RH:9:ILE:HG22	31:RH:10:PRO:CA	1.78	1.13
5:QE:10:MET:SD	5:QE:13:ILE:CD1	2.35	1.13
41:RV:49:THR:HB	41:RV:50:PRO:CD	1.79	1.12
32:YI:77:LEU:HD12	32:YI:142:VAL:CG2	1.79	1.12
5:QE:11:ILE:O	5:QE:12:LEU:HB2	1.48	1.11
28:RE:61:ARG:HB3	28:RE:62:PRO:CD	1.79	1.10
13:XM:9:ILE:HG13	13:XM:10:PRO:HD2	1.33	1.10
28:RE:61:ARG:CB	28:RE:62:PRO:HD3	1.80	1.10
31:RH:9:ILE:HB	31:RH:10:PRO:CA	1.81	1.10
41:RV:49:THR:CB	41:RV:50:PRO:CD	2.30	1.10
13:XM:8:GLU:O	13:XM:9:ILE:CG2	1.97	1.10
32:YI:141:LYS:HB3	32:YI:142:VAL:HA	1.18	1.09
41:RV:49:THR:CG2	41:RV:50:PRO:CD	2.30	1.09
31:RH:9:ILE:CG2	31:RH:10:PRO:CA	2.30	1.09
45:RZ:158:PRO:CB	45:RZ:159:PRO:CD	2.30	1.09
50:Y4:6:HIS:CB	50:Y4:7:PRO:CD	2.30	1.09
41:RV:49:THR:HG22	41:RV:50:PRO:CD	1.82	1.09
32:YI:77:LEU:HD12	32:YI:142:VAL:HG21	1.16	1.09
31:RH:9:ILE:CB	31:RH:10:PRO:HA	1.80	1.09
41:RV:49:THR:HB	41:RV:50:PRO:HD2	1.24	1.09
32:RI:143:SER:O	32:RI:144:VAL:CG2	2.01	1.08
45:RZ:156:LYS:O	45:RZ:157:LEU:CG	2.00	1.08
31:YH:9:ILE:HB	31:YH:10:PRO:CA	1.83	1.08
35:YP:64:LYS:HG2	54:Y8:25:MET:HG2	1.21	1.08
32:RI:125:GLU:HA	32:RI:141:LYS:HB3	1.34	1.08
31:YH:9:ILE:CB	31:YH:10:PRO:CA	2.30	1.08
45:RZ:155:LEU:O	45:RZ:156:LYS:HG2	1.53	1.08
31:YH:9:ILE:CG2	31:YH:10:PRO:CA	2.30	1.08
25:YA:2645:G:H3'	25:YA:2646:C:C5'	1.82	1.08
35:YP:63:PRO:HA	54:Y8:13:ARG:HA	1.17	1.08
35:RP:62:LEU:H	35:RP:62:LEU:HD12	1.11	1.07
31:RH:9:ILE:CB	31:RH:10:PRO:CA	2.30	1.07
1:XA:1156:G:H5''	1:XA:1157:A:OP2	1.54	1.07
25:YA:631:A:H5'	35:YP:65:ARG:HG3	1.34	1.07
50:Y4:6:HIS:HB2	50:Y4:7:PRO:HD2	1.09	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:YI:78:THR:N	32:YI:142:VAL:HG23	1.69	1.07
1:XA:1183:A:OP2	1:XA:1183:A:H4'	1.36	1.06
51:Y5:4:HIS:HB3	51:Y5:5:PRO:HD3	1.36	1.06
28:RE:60:ASN:O	28:RE:62:PRO:HD2	1.53	1.06
45:RZ:158:PRO:HB2	45:RZ:159:PRO:HD2	1.33	1.06
13:QM:99:ARG:HH11	13:QM:101:GLN:HG2	1.10	1.05
35:RP:62:LEU:HD13	35:RP:62:LEU:O	1.54	1.05
52:Y6:31:PRO:O	52:Y6:32:ASN:HB2	1.49	1.05
25:RA:1543:A:H8	25:RA:1543:A:H5''	1.10	1.05
28:YE:60:ASN:C	28:YE:62:PRO:HD2	1.76	1.05
35:YP:63:PRO:HA	54:Y8:13:ARG:CA	1.87	1.05
13:QM:99:ARG:NH1	13:QM:101:GLN:HG2	1.70	1.05
25:RA:2584:U:H5'	56:Z7:76:PPU:H103	1.36	1.05
45:RZ:157:LEU:HD22	45:RZ:161:VAL:HG11	1.36	1.05
41:YV:49:THR:CG2	41:YV:50:PRO:CD	2.30	1.04
32:RI:82:ARG:HD2	32:RI:146:ALA:HB3	1.32	1.03
25:RA:1543:A:H5''	25:RA:1543:A:C8	1.93	1.03
31:RH:9:ILE:HB	31:RH:10:PRO:HB3	1.08	1.03
32:YI:141:LYS:HB3	32:YI:142:VAL:CA	1.87	1.03
25:YA:631:A:C5'	35:YP:65:ARG:CG	2.36	1.02
25:YA:2645:G:H3'	25:YA:2646:C:H5'	1.05	1.02
25:RA:2701:C:H3'	25:RA:2702:U:H5''	1.40	1.02
41:RV:49:THR:HG22	41:RV:50:PRO:HD3	1.03	1.02
31:YH:9:ILE:HB	31:YH:10:PRO:HB3	1.04	1.02
32:YI:77:LEU:HB2	32:YI:142:VAL:HG22	1.03	1.02
45:RZ:158:PRO:CB	45:RZ:159:PRO:HD2	1.88	1.01
25:YA:631:A:C5'	35:YP:65:ARG:HG3	1.89	1.01
31:YH:9:ILE:CB	31:YH:10:PRO:HA	1.84	1.01
28:YE:63:LEU:O	28:YE:64:LYS:HB2	1.57	1.00
44:RY:76:CYS:CB	44:RY:77:PRO:CD	2.38	1.00
1:XA:1157:A:N6	1:XA:1178:G:H21	1.57	1.00
28:RE:35:GLN:HG3	28:RE:64:LYS:NZ	1.76	1.00
44:RY:76:CYS:HB3	44:RY:77:PRO:HD2	1.41	1.00
41:YV:49:THR:CB	41:YV:50:PRO:CD	2.38	1.00
45:RZ:163:LEU:HD12	45:RZ:165:VAL:HG12	1.42	0.99
32:YI:144:VAL:O	32:YI:145:VAL:HG12	1.62	0.99
31:RH:7:LEU:HD11	31:RH:66:GLY:HA2	1.42	0.99
35:YP:63:PRO:CA	54:Y8:13:ARG:HA	1.90	0.99
35:RP:62:LEU:HD12	35:RP:62:LEU:N	1.77	0.98
25:RA:2787:C:H1'	28:RE:62:PRO:HG3	1.46	0.98
35:YP:64:LYS:CG	54:Y8:25:MET:HG2	1.92	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:YH:9:ILE:CB	31:YH:10:PRO:HB3	1.94	0.97
32:YI:77:LEU:HB2	32:YI:141:LYS:HB2	1.46	0.97
31:YH:7:LEU:HD22	31:YH:69:ARG:HG2	1.47	0.97
44:RY:75:ILE:HG13	44:RY:80:GLY:N	1.79	0.97
25:YA:1386:C:OP2	25:YA:1396:U:H5	1.46	0.97
32:YI:77:LEU:CB	32:YI:142:VAL:HG22	1.93	0.97
52:Y6:30:THR:HA	52:Y6:31:PRO:C	1.82	0.97
28:RE:61:ARG:HB3	28:RE:62:PRO:HD3	0.98	0.96
35:RP:58:THR:CG2	35:RP:61:ARG:NH2	2.27	0.96
45:RZ:163:LEU:HD11	45:RZ:165:VAL:HG13	1.47	0.96
44:RY:76:CYS:SG	44:RY:77:PRO:CD	2.51	0.96
45:YZ:121:HIS:H	45:YZ:171:ILE:HG13	1.28	0.96
32:RI:123:LEU:CD1	32:RI:144:VAL:HG11	1.96	0.96
25:YA:1396:U:H2'	25:YA:1396:U:O2	1.63	0.96
52:Y6:28:ARG:HB3	52:Y6:30:THR:H	1.30	0.95
47:Y1:87:PRO:HA	47:Y1:90:ILE:HG22	1.45	0.95
50:Y4:6:HIS:HB2	50:Y4:7:PRO:HD3	1.48	0.95
41:YV:49:THR:HG22	41:YV:50:PRO:HD3	0.97	0.95
25:RA:598:G:O4'	35:RP:11:GLY:HA3	1.66	0.95
45:RZ:155:LEU:C	45:RZ:156:LYS:HG2	1.84	0.95
35:RP:64:LYS:HZ1	54:R8:30:ARG:HA	1.14	0.95
31:YH:8:PRO:C	31:YH:9:ILE:HG12	1.84	0.95
52:Y6:28:ARG:HA	52:Y6:29:ASN:HB3	1.49	0.94
25:YA:2645:G:C3'	25:YA:2646:C:H5'	1.96	0.94
25:RA:2810:A:O3'	28:RE:61:ARG:HG3	1.67	0.94
41:YV:49:THR:HB	41:YV:50:PRO:CD	1.98	0.94
13:XM:9:ILE:CG1	13:XM:10:PRO:HD2	1.98	0.94
25:RA:1225:C:H4'	41:RV:85:LYS:HB2	1.48	0.94
35:RP:56:SER:C	35:RP:57:THR:HG22	1.88	0.93
35:RP:62:LEU:N	35:RP:62:LEU:CD1	2.30	0.93
28:YE:134:ILE:HD13	28:YE:134:ILE:C	1.88	0.93
1:XA:1182:G:H4'	1:XA:1183:A:OP2	1.66	0.93
32:RI:79:ILE:O	32:RI:142:VAL:HG21	1.69	0.93
1:XA:1241:G:H1	1:XA:1296:C:H42	0.99	0.93
44:RY:78:ALA:HB2	44:RY:98:VAL:HG11	1.51	0.93
25:YA:631:A:H5'	35:YP:65:ARG:CG	1.99	0.93
31:RH:8:PRO:C	31:RH:9:ILE:HG12	1.90	0.92
31:YH:9:ILE:CB	31:YH:10:PRO:CB	2.48	0.92
32:YI:77:LEU:HB2	32:YI:142:VAL:CG2	1.97	0.91
45:RZ:157:LEU:HB3	45:RZ:161:VAL:HB	1.50	0.91
1:XA:1502:A:H2	1:XA:1505:G:H1	1.16	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:YI:77:LEU:CB	32:YI:141:LYS:HB2	1.98	0.91
1:QA:1502:A:H2	1:QA:1505:G:H1	1.16	0.91
32:RI:79:ILE:C	32:RI:142:VAL:HG21	1.91	0.91
52:Y6:28:ARG:HG3	52:Y6:30:THR:O	1.71	0.91
52:Y6:28:ARG:HD2	52:Y6:29:ASN:HB3	1.51	0.91
28:RE:35:GLN:HG3	28:RE:64:LYS:HZ1	1.35	0.90
25:YA:631:A:C5'	35:YP:65:ARG:HG2	2.01	0.90
32:YI:141:LYS:CB	32:YI:142:VAL:HA	1.99	0.90
35:YP:63:PRO:CA	54:Y8:13:ARG:HG2	2.02	0.90
51:Y5:4:HIS:HB3	51:Y5:5:PRO:CD	2.01	0.90
1:XA:1241:G:H1	1:XA:1296:C:N4	1.69	0.89
44:RY:76:CYS:HB3	44:RY:77:PRO:CD	1.95	0.89
25:YA:1586:A:H2'	25:YA:1587:A:H5''	1.55	0.89
45:RZ:158:PRO:HB2	45:RZ:159:PRO:CD	1.95	0.89
35:YP:63:PRO:CB	54:Y8:13:ARG:HG2	2.03	0.89
45:RZ:163:LEU:CD1	45:RZ:165:VAL:CG1	2.41	0.89
25:YA:631:A:H5''	35:YP:65:ARG:CG	2.00	0.89
5:QE:50:GLU:HG3	5:QE:52:PRO:HD2	1.55	0.88
32:RI:82:ARG:HD2	32:RI:146:ALA:CB	2.02	0.88
1:XA:1157:A:N3	1:XA:1158:C:N4	2.20	0.88
35:YP:63:PRO:HB3	54:Y8:13:ARG:HG2	1.53	0.88
9:QI:11:LYS:HD2	9:QI:107:ARG:O	1.73	0.88
32:RI:123:LEU:HD22	32:RI:144:VAL:CG1	2.03	0.88
13:QM:99:ARG:HH11	13:QM:101:GLN:CG	1.87	0.88
23:QX:12:A:H3'	23:QX:13:A:H5''	1.54	0.88
35:RP:9:ASN:HB2	35:RP:10:PRO:HD2	1.53	0.88
1:XA:1302:U:C5	13:XM:17:VAL:HG21	2.09	0.88
5:QE:9:LYS:HG2	5:QE:112:LEU:HD11	1.54	0.88
28:RE:63:LEU:HD23	28:RE:64:LYS:N	1.89	0.87
45:YZ:148:ASP:HB3	45:YZ:149:SER:HA	1.56	0.87
25:RA:655:A:H4'	25:RA:656:G:H5'	1.55	0.87
1:XA:1157:A:H1'	1:XA:1158:C:N3	1.90	0.87
35:RP:62:LEU:HD23	35:RP:64:LYS:HD2	1.57	0.87
25:RA:1542:G:H3'	25:RA:1543:A:C5'	2.04	0.87
44:RY:17:SER:HB2	44:RY:71:LYS:HE2	1.56	0.87
22:XV:53:G:O2'	22:XV:54:U:H5'	1.74	0.87
25:YA:1913:A:OP2	25:YA:1913:A:H4'	1.74	0.87
31:RH:9:ILE:CB	31:RH:10:PRO:HB3	2.01	0.87
1:QA:1203:C:H2'	1:QA:1204:A:H5'	1.57	0.86
32:YI:78:THR:N	32:YI:142:VAL:CG2	2.32	0.86
54:R8:30:ARG:O	54:R8:31:HIS:ND1	2.09	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:YA:1586:A:H3'	25:YA:1587:A:H5'	1.57	0.86
45:YZ:155:LEU:O	45:YZ:155:LEU:CD1	2.22	0.86
25:RA:2394:C:OP1	35:RP:63:PRO:HD2	1.74	0.85
25:YA:1225:C:H4'	41:YV:85:LYS:HB2	1.57	0.85
25:YA:1587:A:H5'	25:YA:1587:A:H8	1.38	0.85
28:YE:134:ILE:HD13	28:YE:134:ILE:O	1.76	0.85
9:QI:10:ARG:HH21	9:QI:11:LYS:HD3	1.41	0.85
39:YT:54:ARG:HA	39:YT:59:THR:HB	1.57	0.85
35:RP:58:THR:HG22	35:RP:61:ARG:HH22	1.36	0.85
25:YA:2711:A:H5''	25:YA:2712:U:H5''	1.59	0.85
35:YP:64:LYS:HG2	54:Y8:25:MET:CE	2.06	0.85
19:QS:36:ARG:HD2	19:QS:71:LEU:H	1.42	0.85
25:YA:273(E):U:H3	25:YA:363(A):A:H61	1.23	0.85
25:RA:2584:U:C5'	56:Z7:76:PPU:H103	2.07	0.85
28:YE:60:ASN:C	28:YE:62:PRO:CD	2.45	0.85
52:Y6:28:ARG:HA	52:Y6:29:ASN:CB	2.07	0.84
28:YE:134:ILE:C	28:YE:134:ILE:CD1	2.44	0.84
2:XB:185:ILE:HG22	2:XB:199:TYR:HB2	1.58	0.84
31:RH:9:ILE:HG22	31:RH:10:PRO:HA	0.86	0.84
1:XA:953:G:H5'	1:XA:965:A:H61	1.42	0.84
35:YP:64:LYS:CG	54:Y8:25:MET:HE3	2.07	0.84
35:RP:58:THR:CG2	35:RP:61:ARG:HH22	1.87	0.84
1:XA:1157:A:O2'	1:XA:1158:C:P	2.35	0.84
41:RV:49:THR:CB	41:RV:50:PRO:HD3	2.03	0.83
29:RF:1:MET:HB3	29:RF:2:LYS:HE3	1.58	0.83
25:RA:2701:C:H3'	25:RA:2702:U:C5'	2.07	0.83
28:YE:63:LEU:O	28:YE:64:LYS:CB	2.24	0.83
25:YA:2393:A:H5'	35:YP:62:LEU:HD23	1.60	0.83
54:R8:40:GLU:H	54:R8:43:GLN:HG3	1.44	0.83
35:YP:52:GLU:HG2	35:YP:55:ARG:HE	1.42	0.83
44:RY:75:ILE:CG1	44:RY:80:GLY:H	1.90	0.83
51:R5:4:HIS:HB3	51:R5:5:PRO:HD3	1.58	0.83
32:YI:78:THR:CA	32:YI:142:VAL:HG23	2.09	0.83
28:RE:61:ARG:CB	28:RE:62:PRO:CD	2.43	0.83
13:XM:10:PRO:CG	13:XM:18:ALA:HA	2.08	0.82
32:YI:144:VAL:O	32:YI:145:VAL:CG1	2.26	0.82
31:YH:7:LEU:HD11	31:YH:66:GLY:HA2	1.62	0.82
35:YP:63:PRO:HB3	54:Y8:13:ARG:CG	2.10	0.82
41:YV:85:LYS:HG3	41:YV:87:HIS:H	1.44	0.82
31:YH:9:ILE:HG22	31:YH:10:PRO:HA	0.82	0.82
32:RI:123:LEU:CD2	32:RI:144:VAL:CG1	2.58	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:RP:62:LEU:CD2	35:RP:64:LYS:HB2	2.10	0.82
4:XD:31:CYS:SG	4:XD:32:ALA:N	2.52	0.82
31:RH:69:ARG:HG3	31:RH:69:ARG:HH11	1.44	0.81
25:YA:1204:A:H62	25:YA:1241:A:H2	1.28	0.81
45:RZ:156:LYS:C	45:RZ:157:LEU:HG	2.00	0.81
25:RA:2419:U:O4	54:R8:31:HIS:CD2	2.34	0.81
44:YY:17:SER:HB2	44:YY:71:LYS:HE2	1.60	0.81
35:RP:19:VAL:HG13	35:RP:21:ARG:H	1.44	0.81
25:RA:2420:C:OP1	54:R8:34:TRP:HB3	1.81	0.81
35:YP:64:LYS:HG2	54:Y8:25:MET:CB	2.10	0.81
19:XS:36:ARG:HD2	19:XS:71:LEU:H	1.44	0.81
41:YV:5:VAL:HG23	41:YV:37:VAL:HG11	1.63	0.81
32:YI:140:LEU:O	32:YI:141:LYS:HG3	1.81	0.81
35:YP:9:ASN:HB2	35:YP:10:PRO:HD2	1.63	0.80
45:RZ:7:ALA:HB2	45:RZ:59:LEU:HD11	1.62	0.80
25:RA:2419:U:O4	54:R8:31:HIS:CG	2.33	0.80
35:RP:63:PRO:HB3	54:R8:13:ARG:HG2	1.63	0.80
25:RA:883:G:H1	25:RA:893:C:H42	1.30	0.80
1:XA:1156:G:C5'	1:XA:1157:A:OP2	2.30	0.80
23:XX:14:A:O2'	23:XX:15:A:H5'	1.80	0.80
28:RE:60:ASN:O	28:RE:62:PRO:CD	2.30	0.80
44:RY:97:ARG:HH21	44:RY:98:VAL:HB	1.45	0.80
5:QE:10:MET:SD	5:QE:13:ILE:HD11	2.22	0.79
35:YP:64:LYS:CG	54:Y8:25:MET:CE	2.59	0.79
28:RE:61:ARG:O	28:RE:63:LEU:HD22	1.83	0.79
25:YA:910:A:H62	36:YQ:12:GLN:HA	1.46	0.79
35:RP:56:SER:O	35:RP:57:THR:CG2	2.30	0.79
25:YA:571:A:H5'	25:YA:2030:A:H62	1.48	0.79
4:QD:31:CYS:SG	4:QD:32:ALA:N	2.56	0.79
29:RF:3:GLU:HA	29:RF:24:LEU:HG	1.65	0.79
25:RA:1542:G:H3'	25:RA:1543:A:H5'	1.65	0.79
10:QJ:79:ARG:HA	10:QJ:82:ILE:HB	1.63	0.78
25:RA:2419:U:O4	54:R8:31:HIS:CE1	2.36	0.78
9:XI:10:ARG:HD3	9:XI:75:ASP:HB3	1.65	0.78
35:YP:61:ARG:O	35:YP:62:LEU:HB2	1.82	0.78
25:RA:598:G:C4'	35:RP:11:GLY:HA3	2.12	0.78
25:YA:832:G:H5'	35:YP:45:LEU:HD21	1.66	0.78
32:YI:77:LEU:CD1	32:YI:142:VAL:CG2	2.61	0.78
25:YA:2777:G:H5''	25:YA:2778:A:H5'	1.65	0.78
25:RA:1414:G:H1	25:RA:1588:C:H42	1.28	0.78
35:RP:63:PRO:C	35:RP:65:ARG:H	1.87	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:YA:242:G:H5''	54:Y8:62:LEU:HD13	1.64	0.78
25:YA:686:G:H5''	53:Y7:11:LYS:HE2	1.65	0.78
25:YA:1543:A:H1'	25:YA:1545:A:O4'	1.83	0.78
44:RY:17:SER:OG	44:RY:18:GLY:N	2.14	0.78
25:RA:774:A:H2'	25:RA:774:A:N3	1.96	0.78
45:RZ:156:LYS:O	45:RZ:157:LEU:CB	2.30	0.78
1:QA:664:G:H22	1:QA:741:G:H1	1.29	0.78
25:RA:910:A:H62	36:RQ:12:GLN:HA	1.47	0.77
44:YY:97:ARG:HH21	44:YY:98:VAL:HB	1.48	0.77
25:YA:74:A:H4'	25:YA:75:G:O5'	1.83	0.77
15:QO:39:LEU:HD12	15:QO:56:LEU:HB2	1.67	0.77
1:XA:1157:A:H62	1:XA:1178:G:H21	1.31	0.77
44:YY:19:LYS:HE3	44:YY:71:LYS:HZ1	1.49	0.77
1:XA:1493:A:N6	25:YA:1913:A:N3	2.32	0.77
25:YA:6:A:O2'	25:YA:7:G:H5'	1.85	0.77
25:RA:1204:A:H62	25:RA:1241:A:H2	1.29	0.77
25:RA:2451:A:N1	56:Z7:76:PPU:HE2	2.00	0.77
25:RA:2527:C:H5'	55:R9:30:PRO:HB2	1.67	0.77
1:XA:677:U:H3	1:XA:713:G:H22	1.29	0.77
40:RU:92:ARG:HD2	40:RU:94:ASN:HB3	1.67	0.76
12:XL:53:ARG:HG3	12:XL:93:LEU:HD21	1.67	0.76
25:YA:1386:C:OP2	25:YA:1396:U:C5	2.36	0.76
32:RI:144:VAL:HG23	32:RI:145:VAL:HG23	1.68	0.76
36:RQ:75:THR:HA	36:RQ:89:ASN:H	1.49	0.76
54:R8:56:GLU:HA	54:R8:59:LYS:HE2	1.67	0.76
29:RF:4:VAL:HA	29:RF:19:GLU:HB3	1.67	0.76
45:RZ:157:LEU:HB3	45:RZ:161:VAL:CB	2.14	0.76
2:QB:77:ALA:HB2	2:QB:211:ILE:HD13	1.67	0.76
50:Y4:6:HIS:CB	50:Y4:7:PRO:HD3	2.09	0.76
5:XE:50:GLU:HG3	5:XE:52:PRO:HD2	1.66	0.76
44:YY:102:CYS:SG	44:YY:103:GLY:N	2.59	0.76
13:QM:87:TYR:HB3	19:QS:73:GLU:HG2	1.67	0.76
25:RA:273(E):U:H3	25:RA:363(A):A:H61	1.32	0.76
44:RY:76:CYS:HB3	44:RY:96:ILE:HD11	1.68	0.76
25:RA:1138:G:H21	33:RN:106:MET:HE3	1.50	0.76
29:YF:4:VAL:HA	29:YF:19:GLU:HB3	1.66	0.76
1:QA:1202:G:H2'	1:QA:1203:C:O5'	1.86	0.75
25:RA:1981:A:C5'	25:RA:1982:C:OP2	2.30	0.75
44:RY:76:CYS:CB	44:RY:77:PRO:HD2	2.09	0.75
25:YA:1728:G:N7	25:YA:1731:G:N2	2.34	0.75
27:YD:206:LEU:HD22	27:YD:211:ARG:HG2	1.66	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:RP:125:VAL:HG13	35:RP:144:GLU:HB3	1.68	0.75
45:RZ:118:GLN:HG3	45:RZ:173:ALA:H	1.49	0.75
35:YP:64:LYS:HG3	54:Y8:25:MET:HE3	1.67	0.75
28:RE:52:LEU:O	28:RE:74:PRO:HA	1.85	0.75
44:RY:95:LYS:NZ	44:RY:96:ILE:O	2.20	0.75
40:YU:95:LEU:HD13	41:YV:4:ILE:HG13	1.69	0.75
25:RA:709:U:O4	25:RA:722:A:N6	2.20	0.75
35:RP:63:PRO:O	35:RP:65:ARG:N	2.20	0.75
35:RP:56:SER:C	35:RP:57:THR:CG2	2.54	0.75
43:RX:35:THR:HG22	43:RX:37:THR:H	1.52	0.74
28:RE:38:THR:HG22	28:RE:40:GLU:H	1.51	0.74
31:RH:69:ARG:HH11	31:RH:69:ARG:CG	2.00	0.74
5:XE:71:LEU:HD11	5:XE:114:GLY:HA3	1.69	0.74
40:YU:90:VAL:HG22	41:YV:39:LEU:HB3	1.69	0.74
25:RA:1414:G:C6	25:RA:1415:U:C4	2.74	0.74
1:QA:339:C:OP2	34:RO:97:ARG:NH1	2.20	0.74
2:QB:8:LYS:HB3	2:QB:217:ARG:HD3	1.69	0.74
25:RA:1598:C:H5'	43:RX:36:LYS:HB3	1.68	0.74
37:RR:33:ARG:HG2	37:RR:115:GLU:HG2	1.69	0.74
1:QA:1086:U:H3	1:QA:1099:G:H22	1.31	0.74
25:YA:631:A:H5''	35:YP:65:ARG:HG2	1.64	0.74
32:YI:78:THR:H	32:YI:142:VAL:HG22	1.51	0.74
2:QB:54:THR:HG21	2:QB:201:ILE:HD11	1.70	0.74
44:YY:95:LYS:NZ	44:YY:99:CYS:O	2.21	0.74
1:XA:1305:G:H22	1:XA:1331:G:H2'	1.52	0.74
38:YS:106:ARG:NH1	38:YS:106:ARG:O	2.21	0.74
35:RP:14:LYS:O	35:RP:16:ARG:N	2.21	0.73
45:RZ:158:PRO:HB3	45:RZ:159:PRO:CD	2.14	0.73
12:XL:25:PRO:HD2	12:XL:98:TYR:OH	1.87	0.73
27:YD:44:ASN:HB3	27:YD:49:ILE:HA	1.68	0.73
39:RT:55:ASN:H	39:RT:59:THR:HB	1.52	0.73
40:YU:92:ARG:HD2	40:YU:94:ASN:HB3	1.71	0.73
38:RS:62:LYS:HB3	38:RS:97:ARG:HD3	1.71	0.73
1:XA:1118:C:OP1	9:XI:104:ARG:NH1	2.21	0.73
27:YD:85:ASP:HB2	27:YD:92:ILE:HD13	1.71	0.73
25:RA:857:C:H4'	46:R0:23:VAL:HG21	1.70	0.73
35:RP:62:LEU:CD2	35:RP:64:LYS:HD2	2.17	0.73
52:Y6:28:ARG:CD	52:Y6:29:ASN:HB3	2.18	0.73
25:YA:1728:G:N1	25:YA:1730:U:OP2	2.21	0.73
2:QB:48:MET:HA	2:QB:51:LEU:HD12	1.71	0.73
25:RA:1547:C:O2'	25:RA:1548:C:C5'	2.30	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:RI:123:LEU:HD13	32:RI:144:VAL:HG11	1.69	0.73
22:XV:53:G:C2'	22:XV:54:U:H5'	2.18	0.73
25:YA:1587:A:H5'	25:YA:1587:A:C8	2.22	0.73
1:XA:1070:U:OP1	5:XE:18:ARG:NH1	2.22	0.73
52:Y6:6:ARG:HG2	52:Y6:8:LYS:H	1.52	0.73
25:RA:142:G:H4'	43:RX:35:THR:HG21	1.71	0.73
25:RA:2031:A:O2'	25:RA:2454:G:N2	2.21	0.73
47:R1:83:GLU:HG2	47:R1:85:LEU:H	1.52	0.73
25:RA:6:A:O2'	25:RA:7:G:H5'	1.88	0.73
25:RA:1414:G:N1	25:RA:1588:C:N4	2.35	0.73
25:RA:2438:U:O3'	25:RA:2439:A:H3'	1.88	0.73
41:RV:49:THR:HG21	41:RV:50:PRO:HD3	1.69	0.73
9:QI:27:THR:OG1	9:QI:28:VAL:N	2.22	0.72
25:YA:1586:A:H3'	25:YA:1587:A:C5'	2.19	0.72
32:YI:78:THR:HA	32:YI:142:VAL:HG23	1.71	0.72
35:YP:14:LYS:O	35:YP:16:ARG:N	2.22	0.72
25:RA:2134:A:N6	25:RA:2157:G:O2'	2.22	0.72
28:RE:1:MET:N	28:RE:200:GLU:OE2	2.22	0.72
45:RZ:157:LEU:HD13	45:RZ:161:VAL:HG12	1.71	0.72
1:XA:933:G:OP2	7:XG:2:ALA:N	2.23	0.72
2:XB:69:LEU:HB3	2:XB:162:ILE:HG22	1.70	0.72
24:XY:12:LEU:HB3	24:XY:18:VAL:HB	1.72	0.72
25:YA:2292:C:OP1	38:YS:17:ARG:NH2	2.22	0.72
41:YV:49:THR:HB	41:YV:50:PRO:HD3	1.60	0.72
47:Y1:83:GLU:HG2	47:Y1:85:LEU:H	1.54	0.72
50:Y4:5:ILE:HG13	50:Y4:6:HIS:HB3	1.72	0.72
25:RA:345:A:O2'	25:RA:346:A:N7	2.22	0.72
37:RR:100:LEU:HD21	37:RR:113:LEU:HD13	1.71	0.72
2:QB:185:ILE:HG22	2:QB:199:TYR:HB2	1.70	0.72
29:RF:153:SER:HB2	29:RF:190:GLU:H	1.55	0.72
1:XA:1322:C:H5''	13:XM:100:GLY:HA3	1.69	0.72
25:RA:69:C:O2	25:RA:69:C:H5''	1.89	0.72
34:RO:92:GLU:OE1	34:RO:113:LYS:NZ	2.22	0.72
25:YA:1138:G:H21	33:YN:106:MET:HE3	1.54	0.72
45:YZ:146:ILE:HA	45:YZ:174:VAL:HG23	1.72	0.72
28:RE:63:LEU:HD23	28:RE:64:LYS:H	1.54	0.72
35:YP:63:PRO:HA	54:Y8:13:ARG:CB	2.19	0.72
52:Y6:28:ARG:CA	52:Y6:29:ASN:HB3	2.20	0.72
1:XA:542:G:OP1	4:XD:10:ARG:NH2	2.22	0.72
39:YT:60:THR:HG22	39:YT:77:PRO:HA	1.72	0.72
1:QA:218:C:H5'	1:QA:466:C:H42	1.53	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:RA:1414:G:H1	25:RA:1588:C:N4	1.88	0.71
1:XA:974:A:OP1	14:XN:29:ARG:NH2	2.23	0.71
10:XJ:49:VAL:HG13	14:XN:41:ARG:HD2	1.70	0.71
29:YF:3:GLU:HA	29:YF:24:LEU:HG	1.70	0.71
1:QA:1203:C:C2'	1:QA:1204:A:H5'	2.19	0.71
1:XA:1178:G:H5'	9:XI:93:ARG:HH21	1.55	0.71
25:RA:2712(A):A:H5''	25:RA:2713:A:OP2	1.91	0.71
45:YZ:150:LEU:HB2	45:YZ:171:ILE:HG22	1.72	0.71
41:RV:71:LEU:HD11	41:RV:83:ARG:HE	1.54	0.71
25:RA:2580:U:H4'	28:RE:130:GLY:HA3	1.71	0.71
32:RI:123:LEU:HD11	32:RI:144:VAL:HG11	1.70	0.71
1:QA:1323:G:H2'	1:QA:1324:A:C8	2.25	0.71
35:YP:62:LEU:HD12	54:Y8:25:MET:O	1.90	0.71
34:RO:25:LEU:HB2	34:RO:38:VAL:HG23	1.72	0.71
1:XA:664:G:H22	1:XA:741:G:H1	1.37	0.71
25:YA:1728:G:H8	25:YA:1732:A:H62	1.39	0.71
23:QX:12:A:H3'	23:QX:13:A:C5'	2.21	0.71
41:YV:15:GLU:HG3	41:YV:16:PRO:HD2	1.72	0.71
25:RA:1021:A:H3'	25:RA:1021:A:N3	2.06	0.71
1:XA:1061:G:OP2	3:XC:3:ASN:ND2	2.23	0.71
31:YH:44:VAL:O	31:YH:51:ARG:NH1	2.24	0.71
52:Y6:28:ARG:CB	52:Y6:30:THR:H	2.02	0.71
54:Y8:14:VAL:HG13	54:Y8:24:ALA:HB2	1.72	0.71
25:YA:2103:C:H42	25:YA:2186:G:H1	1.38	0.70
1:QA:957:U:O2	1:QA:960:U:C2	2.44	0.70
29:RF:24:LEU:HD13	29:RF:25:PRO:HD2	1.71	0.70
36:RQ:89:ASN:O	36:RQ:91:GLU:N	2.24	0.70
13:XM:10:PRO:HG3	13:XM:18:ALA:HA	1.70	0.70
25:RA:1148:A:H5''	25:RA:1148:A:H8	1.55	0.70
25:RA:2867:G:HO2'	25:RA:2868:A:H8	1.36	0.70
25:YA:320:A:N3	29:YF:169:ASN:ND2	2.39	0.70
27:YD:35:LYS:HG2	27:YD:64:ILE:N	2.05	0.70
31:RH:9:ILE:CB	31:RH:10:PRO:CB	2.53	0.70
3:XC:84:ILE:HD12	3:XC:88:ARG:HH21	1.57	0.70
31:YH:8:PRO:O	31:YH:9:ILE:CG1	2.39	0.70
25:RA:2420:C:H41	54:R8:31:HIS:HB3	1.55	0.70
36:RQ:89:ASN:O	36:RQ:92:GLY:N	2.25	0.70
44:RY:75:ILE:HG12	44:RY:76:CYS:N	2.05	0.70
19:XS:50:ALA:HB1	19:XS:57:HIS:HB3	1.71	0.70
25:YA:1587:A:H2'	25:YA:1588:C:C6	2.26	0.70
35:YP:9:ASN:CB	35:YP:10:PRO:HD2	2.19	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:RZ:157:LEU:CD2	45:RZ:161:VAL:HG11	2.18	0.70
20:XT:67:ALA:HA	20:XT:73:HIS:H	1.57	0.70
28:YE:134:ILE:H	28:YE:134:ILE:HD12	1.57	0.70
25:RA:1254:A:H5'	25:RA:1255:U:H5'	1.74	0.70
52:R6:14:THR:OG1	52:R6:15:GLU:N	2.25	0.70
28:YE:60:ASN:O	28:YE:61:ARG:HB2	1.91	0.70
28:YE:61:ARG:N	28:YE:62:PRO:HD2	2.06	0.70
31:YH:17:VAL:HG21	31:YH:49:VAL:HG23	1.73	0.70
34:YO:98:VAL:HG13	34:YO:117:LEU:HB3	1.73	0.70
19:QS:36:ARG:NH1	19:QS:73:GLU:HB2	2.07	0.70
35:RP:62:LEU:HD22	35:RP:64:LYS:H	1.56	0.70
25:YA:2016:U:H1'	51:Y5:6:VAL:CG1	2.21	0.70
25:YA:2712(A):A:H5''	25:YA:2713:A:OP2	1.92	0.70
48:Y2:42:GLY:O	48:Y2:44:LEU:N	2.25	0.70
9:QI:10:ARG:HD3	9:QI:75:ASP:HB3	1.74	0.70
12:QL:60:LEU:HD21	12:QL:66:VAL:HG22	1.72	0.70
35:RP:64:LYS:NZ	54:R8:30:ARG:CA	2.50	0.70
35:YP:64:LYS:CD	54:Y8:25:MET:HG2	2.22	0.70
44:YY:50:ARG:HB3	44:YY:53:PRO:HG3	1.73	0.70
11:QK:10:VAL:HG12	11:QK:11:LYS:HG2	1.71	0.70
25:RA:1589:C:O2'	25:RA:1590:U:H5'	1.91	0.70
54:R8:54:GLU:HG3	54:R8:57:ARG:HH21	1.55	0.70
17:XQ:26:GLN:HG2	17:XQ:37:LYS:HG2	1.74	0.70
25:YA:2527:C:H5'	55:Y9:30:PRO:HB2	1.73	0.70
29:YF:53:THR:HG23	29:YF:55:GLY:H	1.57	0.70
25:RA:2096:U:H3	25:RA:2193:G:H1	1.39	0.69
1:XA:1157:A:N6	1:XA:1178:G:N2	2.37	0.69
23:XX:13:A:O2'	23:XX:14:A:H5''	1.91	0.69
31:YH:7:LEU:HD13	31:YH:69:ARG:HB3	1.74	0.69
35:YP:29:LYS:HD2	35:YP:30:THR:HG23	1.74	0.69
52:Y6:6:ARG:CD	52:Y6:8:LYS:HB3	2.22	0.69
25:YA:2401:U:H5'	52:Y6:18:ARG:HH12	1.55	0.69
3:QC:19:GLU:O	3:QC:40:ARG:NH2	2.25	0.69
29:RF:2:LYS:HB2	29:RF:24:LEU:HD12	1.73	0.69
41:RV:49:THR:O	41:RV:50:PRO:C	2.30	0.69
27:YD:34:VAL:HG22	27:YD:35:LYS:HG3	1.73	0.69
31:YH:8:PRO:O	31:YH:9:ILE:HG12	1.91	0.69
12:QL:53:ARG:HG3	12:QL:93:LEU:HD21	1.74	0.69
35:YP:94:GLU:HG3	35:YP:124:LYS:HB3	1.73	0.69
1:XA:531:U:OP2	24:XY:69:ARG:NH1	2.25	0.69
1:XA:1001:G:N1	1:XA:1039:C:N3	2.38	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:YA:574:C:O2	28:YE:145:LYS:NZ	2.26	0.69
35:YP:64:LYS:CG	54:Y8:25:MET:CG	2.57	0.69
19:QS:5:LEU:HD13	19:QS:9:VAL:HA	1.75	0.69
25:RA:1266:G:O5'	42:RW:15:ARG:NH2	2.26	0.69
25:RA:1413:G:C2	25:RA:1414:G:C8	2.80	0.69
25:YA:2294:C:OP1	38:YS:89:ARG:NH2	2.26	0.69
29:YF:60:SER:O	29:YF:60:SER:OG	2.06	0.69
25:RA:660:G:H21	35:RP:12:ALA:HB2	1.58	0.69
25:RA:1024:G:H3'	25:RA:1025:G:H5''	1.75	0.69
25:RA:2134:A:OP2	25:RA:2157:G:N2	2.25	0.69
29:RF:53:THR:HG23	29:RF:55:GLY:H	1.57	0.69
35:RP:55:ARG:O	35:RP:56:SER:O	2.09	0.69
27:YD:25:THR:O	27:YD:27:THR:N	2.25	0.69
28:YE:60:ASN:CA	28:YE:62:PRO:HD2	2.23	0.69
30:YG:83:ARG:H	30:YG:86:MET:HG3	1.58	0.69
52:Y6:6:ARG:HD3	52:Y6:8:LYS:HB3	1.73	0.69
1:QA:1028(B):C:H3'	1:QA:1029:G:H4'	1.75	0.69
42:RW:18:ARG:HD3	42:RW:76:VAL:HG13	1.75	0.69
52:R6:9:LEU:H	52:R6:27:LYS:HA	1.58	0.69
25:YA:2438:U:O3'	25:YA:2439:A:H3'	1.93	0.69
29:YF:103:LYS:HA	29:YF:106:ARG:HG3	1.75	0.69
38:YS:106:ARG:NH1	38:YS:107:GLU:OE2	2.23	0.69
31:YH:158:HIS:HA	31:YH:170:ARG:HG2	1.75	0.69
32:YI:80:PRO:CB	32:YI:143:SER:O	2.40	0.69
43:YX:43:VAL:HG23	43:YX:51:VAL:HG21	1.74	0.69
4:QD:13:ARG:O	4:QD:15:GLU:N	2.26	0.68
25:RA:593:G:H4'	54:R8:61:LEU:HD22	1.75	0.68
30:RG:16:ARG:HE	30:RG:31:VAL:HG11	1.57	0.68
54:R8:56:GLU:OE1	54:R8:56:GLU:N	2.24	0.68
25:YA:1309:G:H4'	53:Y7:7:PRO:HB2	1.74	0.68
17:QQ:45:HIS:HB2	17:QQ:65:ILE:HD13	1.75	0.68
35:RP:62:LEU:HD21	54:R8:25:MET:HB3	1.75	0.68
12:XL:117:ARG:HB3	12:XL:122:THR:HB	1.73	0.68
25:YA:2645:G:C3'	25:YA:2646:C:C5'	2.64	0.68
32:YI:77:LEU:HB3	32:YI:141:LYS:HB2	1.76	0.68
1:QA:1202:G:C2'	1:QA:1203:C:O5'	2.41	0.68
25:YA:974:G:O2'	25:YA:975:G:N7	2.24	0.68
12:QL:47:LYS:HB3	12:QL:48:PRO:HD3	1.76	0.68
35:RP:57:THR:C	35:RP:59:LEU:H	1.96	0.68
1:XA:1302:U:H5	13:XM:17:VAL:HG21	1.57	0.68
25:YA:2684:U:OP1	39:YT:53:ARG:HD3	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:QA:345:C:O2'	1:QA:346:G:P	2.52	0.68
1:QA:1325:C:H4'	21:QU:17:THR:HG21	1.76	0.68
25:RA:242:G:H5''	54:R8:62:LEU:HD13	1.76	0.68
25:RA:1414:G:C6	25:RA:1588:C:N4	2.56	0.68
25:RA:2010:G:H5''	42:RW:42:ARG:HB2	1.75	0.68
30:RG:66:GLN:NE2	30:RG:93:THR:O	2.26	0.68
34:RO:68:GLU:OE2	34:RO:78:ARG:NH1	2.26	0.68
45:RZ:157:LEU:HB3	45:RZ:161:VAL:CG1	2.23	0.68
1:XA:673:G:H2'	1:XA:674:G:C8	2.29	0.68
1:QA:1347:G:N7	9:QI:11:LYS:HE3	2.09	0.68
32:RI:110:ASP:OD1	32:RI:110:ASP:N	2.26	0.68
13:XM:8:GLU:C	13:XM:9:ILE:HG22	2.10	0.68
28:RE:63:LEU:O	28:RE:64:LYS:HB3	1.92	0.68
35:RP:9:ASN:CB	35:RP:10:PRO:HD2	2.15	0.68
25:YA:278:A:H61	25:YA:362:U:H3	1.39	0.68
52:Y6:40:CYS:HB3	52:Y6:46:HIS:CE1	2.27	0.68
4:QD:191:ARG:NH1	4:QD:200:GLU:OE1	2.27	0.68
25:RA:1169:G:H1	25:RA:1180:C:H42	1.40	0.68
25:RA:1310:G:H2'	25:RA:1311:G:H5''	1.75	0.68
31:RH:125:VAL:HG22	31:RH:126:PRO:HA	1.76	0.68
1:QA:1289:A:OP1	21:QU:9:ARG:NH2	2.27	0.67
2:QB:115:LEU:HD13	2:QB:145:LEU:HB3	1.76	0.67
25:YA:1396:U:O2	25:YA:1396:U:C2'	2.37	0.67
25:RA:2119:A:N6	25:RA:2170:A:N7	2.41	0.67
10:XJ:51:ARG:HB2	10:XJ:60:ARG:HA	1.73	0.67
3:QC:164:ARG:NH2	3:QC:166:GLU:OE2	2.27	0.67
17:XQ:66:SER:O	17:XQ:70:ARG:NH1	2.26	0.67
25:YA:1300:U:H4'	25:YA:1301:A:H5''	1.74	0.67
33:YN:125:GLY:HA3	33:YN:126:PRO:O	1.93	0.67
49:Y3:8:LEU:HD13	49:Y3:31:LEU:HD12	1.76	0.67
1:QA:973:G:OP1	10:QJ:57:LYS:NZ	2.27	0.67
25:RA:1403:C:H5''	25:RA:1471:A:H1'	1.74	0.67
32:RI:123:LEU:HD22	32:RI:144:VAL:HG12	1.75	0.67
9:XI:27:THR:OG1	9:XI:28:VAL:N	2.27	0.67
13:XM:9:ILE:CG1	13:XM:10:PRO:CD	2.71	0.67
25:YA:833:U:O2	35:YP:55:ARG:NH1	2.27	0.67
30:YG:161:THR:HG22	30:YG:163:ALA:H	1.57	0.67
25:RA:270(Q):C:H5'	32:RI:45:LYS:HE3	1.77	0.67
28:RE:179:GLU:HB3	28:RE:181:LEU:HD22	1.77	0.67
28:YE:37:ARG:HG3	28:YE:46:ALA:HB3	1.77	0.67
2:QB:204:ASN:OD1	2:QB:204:ASN:N	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:RZ:158:PRO:CB	45:RZ:159:PRO:HD3	2.24	0.67
1:XA:422:C:O2'	1:XA:423:G:N2	2.27	0.67
25:YA:1586:A:C3'	25:YA:1587:A:C5'	2.73	0.67
31:YH:8:PRO:C	31:YH:9:ILE:CG1	2.62	0.67
52:Y6:12:GLU:HB2	52:Y6:22:ALA:HB3	1.77	0.67
31:RH:19:VAL:HG13	31:RH:43:VAL:HG22	1.77	0.67
54:Y8:6:THR:HG21	54:Y8:63:PRO:HD3	1.77	0.67
23:QX:14:A:O2'	23:QX:15:A:H5'	1.95	0.67
25:YA:1421:G:N2	25:YA:1495:A:N1	2.43	0.67
31:YH:10:PRO:O	31:YH:11:VAL:CG1	2.42	0.67
52:Y6:28:ARG:HG3	52:Y6:30:THR:C	2.14	0.67
25:RA:1171:G:H1	25:RA:1178:C:H42	1.41	0.67
54:R8:8:LYS:HB3	54:R8:12:LYS:HE3	1.77	0.67
12:XL:27:LEU:HD12	12:XL:33:ARG:HB2	1.77	0.67
29:YF:122:LYS:O	29:YF:124:LEU:N	2.27	0.67
36:YQ:89:ASN:O	36:YQ:91:GLU:N	2.27	0.67
56:Z6:75:C:H2'	56:Z6:76:PPU:C8	2.25	0.67
30:RG:161:THR:HG22	30:RG:163:ALA:H	1.60	0.66
32:RI:120:ILE:HG22	32:RI:122:GLU:H	1.60	0.66
10:XJ:79:ARG:HA	10:XJ:82:ILE:HB	1.77	0.66
20:XT:60:GLU:HG3	20:XT:81:LYS:HD2	1.76	0.66
25:RA:1414:G:C5	25:RA:1415:U:C5	2.82	0.66
25:YA:480:A:H1'	44:YY:44:ILE:HD13	1.78	0.66
25:YA:857:C:H4'	46:Y0:23:VAL:HG21	1.78	0.66
25:YA:2580:U:H4'	28:YE:130:GLY:HA3	1.77	0.66
35:YP:65:ARG:HH11	35:YP:65:ARG:HB2	1.59	0.66
10:QJ:8:LEU:HG	10:QJ:96:ILE:HG22	1.77	0.66
45:RZ:10:ARG:NH1	45:RZ:26:GLY:O	2.28	0.66
52:R6:15:GLU:OE1	52:R6:44:ARG:NH2	2.28	0.66
25:YA:1586:A:C2'	25:YA:1587:A:H5''	2.25	0.66
25:YA:2415:G:O3'	35:YP:66:GLY:HA3	1.94	0.66
31:YH:80:SER:OG	31:YH:81:GLU:N	2.29	0.66
44:YY:76:CYS:SG	44:YY:77:PRO:HD2	2.35	0.66
1:QA:1305:G:H22	1:QA:1331:G:H2'	1.60	0.66
20:QT:75:ASN:OD1	20:QT:75:ASN:N	2.29	0.66
30:RG:96:ARG:O	30:RG:98:ARG:N	2.28	0.66
35:RP:146:VAL:HG22	35:RP:147:LEU:HD13	1.77	0.66
3:XC:71:ALA:HA	3:XC:106:VAL:HB	1.76	0.66
31:YH:45:VAL:HG23	31:YH:49:VAL:HA	1.78	0.66
32:YI:144:VAL:C	32:YI:145:VAL:HG12	2.15	0.66
1:QA:673:G:H2'	1:QA:674:G:C8	2.31	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:RA:2445:G:OP1	29:RF:74:ARG:NH2	2.27	0.66
35:RP:23:PRO:O	35:RP:25:SER:N	2.28	0.66
36:RQ:64:ILE:HG22	36:RQ:106:VAL:HG12	1.76	0.66
44:RY:33:LYS:H	44:RY:33:LYS:HD3	1.61	0.66
44:RY:50:ARG:HB3	44:RY:53:PRO:HG3	1.78	0.66
31:YH:86:GLU:HG3	31:YH:165:ALA:HB2	1.78	0.66
52:Y6:28:ARG:HB3	52:Y6:30:THR:N	2.07	0.66
47:R1:51:VAL:HG11	47:R1:74:VAL:HG21	1.76	0.66
54:R8:14:VAL:HG13	54:R8:24:ALA:HB2	1.77	0.66
1:XA:674:G:H2'	1:XA:675:A:H8	1.61	0.66
1:XA:1157:A:C6	1:XA:1181:G:O6	2.49	0.66
2:XB:178:ARG:HH12	8:XH:68:ARG:HH22	1.41	0.66
19:XS:67:VAL:HG21	50:Y4:59:PHE:HB3	1.78	0.66
25:YA:252:G:OP2	35:YP:50:ARG:NH2	2.27	0.66
36:YQ:18:LYS:HB2	36:YQ:98:LYS:HZ1	1.60	0.66
32:RI:123:LEU:HD13	32:RI:144:VAL:CG1	2.25	0.66
4:XD:13:ARG:O	4:XD:15:GLU:N	2.29	0.66
25:YA:660:G:H21	35:YP:12:ALA:HB2	1.59	0.66
35:YP:63:PRO:HD3	54:Y8:13:ARG:HH11	1.61	0.66
25:RA:2746:U:H5''	31:RH:138:LYS:HE3	1.77	0.66
46:R0:48:GLY:O	46:R0:80:HIS:ND1	2.29	0.66
25:YA:2610:C:H4'	25:YA:2611:U:OP2	1.95	0.66
35:RP:11:GLY:O	35:RP:12:ALA:HB3	1.96	0.65
29:YF:66:PRO:O	29:YF:68:LYS:N	2.29	0.65
53:Y7:34:ARG:NH1	53:Y7:41:ARG:O	2.29	0.65
12:QL:117:ARG:HB3	12:QL:122:THR:HB	1.78	0.65
25:RA:993:G:OP1	40:RU:50:ARG:NH2	2.29	0.65
35:RP:97:PRO:O	35:RP:99:LEU:N	2.27	0.65
38:RS:26:LEU:HB3	38:RS:87:PHE:HA	1.79	0.65
44:RY:61:ILE:HG22	44:RY:62:GLU:HG3	1.77	0.65
44:RY:88:LYS:O	44:RY:90:LEU:N	2.28	0.65
25:YA:987:G:O2'	25:YA:1000:A:N3	2.27	0.65
49:Y3:39:ASP:OD2	49:Y3:44:ARG:NH2	2.29	0.65
2:QB:194:PRO:O	2:QB:196:LEU:N	2.29	0.65
44:RY:89:PHE:HB2	44:RY:90:LEU:HD22	1.79	0.65
1:XA:974:A:OP2	14:XN:41:ARG:NH1	2.29	0.65
2:XB:195:ASP:O	8:XH:68:ARG:NH2	2.29	0.65
13:XM:97:PRO:HA	13:XM:110:ARG:HD3	1.79	0.65
25:YA:1598:C:H5'	43:YX:36:LYS:HB3	1.79	0.65
25:YA:2134:A:N6	25:YA:2157:G:O2'	2.30	0.65
29:YF:132:VAL:HG22	29:YF:133:ASN:H	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:Y6:30:THR:CA	52:Y6:31:PRO:C	2.64	0.65
31:RH:10:PRO:O	31:RH:11:VAL:CG1	2.44	0.65
1:XA:971:G:N2	1:XA:1363:A:OP2	2.29	0.65
13:XM:10:PRO:HG2	13:XM:18:ALA:HA	1.79	0.65
28:YE:61:ARG:N	28:YE:62:PRO:CD	2.58	0.65
32:YI:80:PRO:HB3	32:YI:143:SER:O	1.96	0.65
32:YI:141:LYS:CB	32:YI:142:VAL:CA	2.67	0.65
19:QS:62:ILE:HA	19:QS:66:MET:HE1	1.77	0.65
25:RA:1542:G:H5''	25:RA:1543:A:OP2	1.96	0.65
28:RE:8:LYS:HB3	28:RE:192:ASN:HA	1.77	0.65
44:RY:13:VAL:HG21	44:RY:72:VAL:HB	1.77	0.65
2:XB:43:ASP:HB3	2:XB:46:LYS:HB2	1.78	0.65
1:QA:974:A:OP2	14:QN:29:ARG:NH2	2.29	0.65
1:QA:1348:U:H3	1:QA:1374:A:H2	1.42	0.65
7:QG:73:MET:HG2	7:QG:90:GLU:HA	1.79	0.65
20:QT:67:ALA:HA	20:QT:73:HIS:H	1.62	0.65
9:XI:28:VAL:HG21	9:XI:63:ILE:N	2.09	0.65
25:YA:620:G:H5'	25:YA:620:G:N3	2.12	0.65
25:YA:1247:A:OP1	29:YF:95:ARG:NH2	2.30	0.65
32:YI:120:ILE:HG22	32:YI:122:GLU:H	1.61	0.65
40:YU:92:ARG:HH22	41:YV:10:LYS:HA	1.61	0.65
45:RZ:87:ASP:OD2	45:RZ:87:ASP:N	2.30	0.65
48:R2:17:SER:HB2	48:R2:18:PRO:HA	1.78	0.65
35:YP:64:LYS:O	35:YP:65:ARG:C	2.35	0.65
38:YS:26:LEU:HB3	38:YS:87:PHE:HA	1.77	0.65
29:RF:79:GLY:HA2	29:RF:86:GLY:HA2	1.78	0.65
35:RP:62:LEU:HD13	35:RP:62:LEU:C	2.12	0.65
25:YA:27:G:N1	25:YA:512:G:O2'	2.27	0.65
25:YA:27:G:N2	25:YA:512:G:O2'	2.30	0.65
25:YA:1614:A:H62	42:YW:93:ALA:HB2	1.60	0.65
1:QA:1346:A:H4'	1:QA:1347:G:O5'	1.97	0.65
25:RA:1547:C:HO2'	25:RA:1548:C:H5'	1.58	0.65
31:RH:7:LEU:HD13	31:RH:69:ARG:HB3	1.79	0.65
3:XC:11:ARG:HE	3:XC:180:ALA:HB3	1.62	0.65
7:XG:15:ASP:HB3	7:XG:24:THR:HG22	1.79	0.65
31:YH:24:VAL:HG22	31:YH:35:VAL:HB	1.79	0.65
47:Y1:34:THR:HG22	47:Y1:36:GLY:H	1.61	0.65
1:QA:662:G:H2'	1:QA:663:A:C8	2.31	0.64
7:QG:16:LEU:HD23	9:QI:41:VAL:HG12	1.80	0.64
27:RD:171:ASP:OD2	27:RD:171:ASP:N	2.29	0.64
27:YD:35:LYS:HD2	27:YD:104:TYR:CE1	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:QA:1346:A:H4'	1:QA:1347:G:C5'	2.26	0.64
31:RH:8:PRO:O	31:RH:9:ILE:CG1	2.45	0.64
25:YA:530:G:N1	25:YA:2023:G:OP1	2.27	0.64
25:YA:1024:G:H3'	25:YA:1025:G:H5''	1.79	0.64
25:YA:2016:U:H1'	51:Y5:6:VAL:HG12	1.79	0.64
28:YE:80:GLU:O	28:YE:82:ARG:N	2.30	0.64
36:YQ:64:ILE:HG22	36:YQ:106:VAL:HG12	1.79	0.64
9:QI:34:ASN:O	9:QI:36:TYR:N	2.30	0.64
25:RA:2420:C:N4	54:R8:31:HIS:HB3	2.12	0.64
1:XA:666:G:H5'	1:XA:726:C:H1'	1.79	0.64
13:XM:99:ARG:O	13:XM:101:GLN:NE2	2.30	0.64
25:RA:69:C:O2	25:RA:69:C:O4'	2.13	0.64
1:XA:1006:C:N3	1:XA:1023:G:N2	2.43	0.64
4:XD:148:VAL:HG11	4:XD:158:ILE:HG21	1.79	0.64
27:YD:39:LYS:HB2	27:YD:62:TYR:HB2	1.78	0.64
27:YD:44:ASN:OD1	27:YD:44:ASN:N	2.29	0.64
1:QA:1152:A:H5''	10:QJ:13:HIS:CD2	2.32	0.64
25:RA:833:U:O2	35:RP:55:ARG:NH1	2.29	0.64
1:XA:1392:G:N2	1:XA:1502:A:H8	1.94	0.64
33:YN:49:GLY:O	33:YN:119:ARG:NH1	2.29	0.64
45:YZ:121:HIS:N	45:YZ:171:ILE:HG13	2.08	0.64
35:RP:52:GLU:OE1	35:RP:54:GLY:N	2.20	0.64
42:RW:65:LEU:HD13	42:RW:68:ARG:HD2	1.79	0.64
1:XA:1348:U:H3	1:XA:1374:A:H2	1.44	0.64
4:XD:23:GLY:O	4:XD:24:GLU:HB2	1.97	0.64
25:YA:1300:U:H4'	25:YA:1301:A:C5'	2.27	0.64
25:YA:2415:G:H4'	35:YP:67:MET:N	2.13	0.64
44:YY:17:SER:OG	44:YY:18:GLY:N	2.28	0.64
14:QN:12:ARG:HG2	14:QN:14:PRO:HD3	1.79	0.64
35:RP:62:LEU:HB2	54:R8:30:ARG:HH11	1.63	0.64
2:XB:111:ARG:HA	2:XB:111:ARG:HH11	1.63	0.64
7:XG:35:LYS:HB3	7:XG:38:LEU:HD13	1.79	0.64
7:XG:151:TYR:OH	11:XK:54:ARG:NH2	2.30	0.64
25:YA:2134:A:OP2	25:YA:2157:G:N2	2.31	0.64
29:YF:135:LYS:HB3	29:YF:138:GLU:HG3	1.79	0.64
31:YH:69:ARG:HG3	31:YH:70:THR:N	2.12	0.64
35:YP:146:VAL:HG22	35:YP:147:LEU:H	1.62	0.64
52:Y6:28:ARG:CG	52:Y6:31:PRO:HD2	2.26	0.64
25:RA:764:A:N3	27:RD:213:ARG:NH1	2.46	0.64
25:RA:2419:U:O4	54:R8:31:HIS:ND1	2.31	0.64
31:RH:158:HIS:HA	31:RH:170:ARG:HG2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:RO:86:ILE:HG22	34:RO:94:ARG:HG3	1.79	0.64
4:XD:109:GLY:O	4:XD:111:ALA:N	2.30	0.64
9:XI:25:LYS:HD3	9:XI:25:LYS:H	1.61	0.64
20:XT:56:MET:HG3	20:XT:84:LEU:HD12	1.79	0.64
25:YA:857:C:OP2	46:Y0:77:ARG:NH2	2.30	0.64
1:QA:971:G:N2	1:QA:1233:G:H1'	2.12	0.64
25:RA:394:A:H2'	25:RA:395:U:H5''	1.79	0.64
25:RA:614:U:H5''	25:RA:615:G:OP1	1.98	0.64
25:RA:642:G:H21	25:RA:646:A:H2	1.44	0.64
28:YE:92:THR:OG1	28:YE:93:VAL:N	2.31	0.64
1:QA:974:A:OP2	14:QN:41:ARG:NH1	2.31	0.64
25:RA:857:C:H1'	46:R0:26:TYR:HE2	1.62	0.64
39:RT:19:LEU:HD22	39:RT:86:ILE:HG22	1.79	0.64
25:YA:39:C:O2	29:YF:46:ARG:NH2	2.31	0.64
44:YY:73:ARG:HH21	44:YY:82:PRO:HD3	1.63	0.64
25:RA:686:G:H5''	53:R7:11:LYS:HE2	1.79	0.63
28:RE:62:PRO:O	28:RE:64:LYS:N	2.30	0.63
31:RH:51:ARG:HH21	31:RH:53:GLU:H	1.44	0.63
1:XA:1157:A:N1	1:XA:1181:G:O6	2.31	0.63
1:XA:1454:G:OP1	20:XT:39:LYS:NZ	2.25	0.63
13:XM:9:ILE:HG13	13:XM:10:PRO:CD	2.21	0.63
25:YA:999:U:H2'	25:YA:1000:A:H5''	1.80	0.63
30:YG:114:ILE:HG22	30:YG:117:PHE:HB2	1.78	0.63
4:XD:25:ARG:O	4:XD:27:TYR:N	2.31	0.63
30:YG:47:LYS:HD3	30:YG:81:LYS:HB2	1.80	0.63
31:YH:3:ARG:HH11	31:YH:6:ARG:HE	1.44	0.63
38:YS:62:LYS:HB3	38:YS:97:ARG:HD3	1.79	0.63
1:QA:954:G:H21	1:QA:1227:A:H62	1.45	0.63
1:QA:1346:A:C4'	1:QA:1347:G:O5'	2.46	0.63
25:RA:2849:U:OP1	39:RT:95:ARG:NH1	2.31	0.63
50:R4:22:ILE:HG12	50:R4:23:GLU:H	1.63	0.63
1:XA:448:A:OP2	1:XA:485:G:N2	2.31	0.63
23:XX:12:A:H3'	23:XX:13:A:H5''	1.80	0.63
25:YA:2469:A:H2	25:YA:2481:G:H21	1.44	0.63
28:YE:31:CYS:HB3	28:YE:49:LEU:HB3	1.80	0.63
35:YP:146:VAL:HG22	35:YP:147:LEU:HD13	1.80	0.63
25:RA:247:G:H4'	25:RA:386:G:C5	2.33	0.63
25:RA:583:G:OP2	40:RU:10:ARG:NH1	2.30	0.63
25:RA:1112:G:OP1	31:RH:3:ARG:NH2	2.31	0.63
31:RH:44:VAL:H	31:RH:51:ARG:HH12	1.45	0.63
35:YP:64:LYS:O	35:YP:66:GLY:N	2.30	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:YQ:67:ARG:NH1	36:YQ:105:GLU:OE2	2.32	0.63
51:Y5:4:HIS:CB	51:Y5:5:PRO:HD3	2.22	0.63
8:QH:42:GLU:HG3	8:QH:109:ILE:HD12	1.79	0.63
32:RI:143:SER:O	32:RI:144:VAL:CB	2.46	0.63
41:RV:35:LEU:O	41:RV:37:VAL:HG22	1.99	0.63
1:XA:1179:A:H5'	9:XI:102:LEU:HD22	1.80	0.63
16:XP:22:THR:HA	16:XP:33:ILE:HG12	1.80	0.63
25:YA:1403:C:H5''	25:YA:1471:A:H1'	1.81	0.63
34:YO:68:GLU:OE2	34:YO:78:ARG:NH1	2.31	0.63
50:Y4:37:SER:OG	50:Y4:38:LYS:N	2.28	0.63
3:QC:156:ARG:H	3:QC:163:ALA:HA	1.64	0.63
23:QX:12:A:H2'	23:QX:13:A:C8	2.33	0.63
31:RH:97:ARG:HB2	31:RH:104:GLU:HB2	1.79	0.63
39:RT:125:ARG:O	39:RT:129:ARG:NH1	2.32	0.63
10:XJ:46:ARG:HG2	10:XJ:64:GLU:HB3	1.81	0.63
20:XT:75:ASN:N	20:XT:75:ASN:OD1	2.31	0.63
25:YA:586:A:H5'	29:YF:89:VAL:HG21	1.81	0.63
25:YA:1056:G:H4'	25:YA:1086:A:H1'	1.81	0.63
25:YA:1171:G:H1	25:YA:1178:C:H42	1.45	0.63
50:Y4:61:ARG:HB3	50:Y4:62:ARG:HH21	1.62	0.63
1:QA:1178:G:H5'	9:QI:93:ARG:HH21	1.63	0.63
2:XB:51:LEU:HD23	2:XB:201:ILE:HD12	1.81	0.63
5:XE:78:HIS:HA	8:XH:105:ARG:HG3	1.81	0.63
26:YB:80:U:H2'	26:YB:81:G:H21	1.61	0.63
29:RF:116:ASP:OD2	35:RP:1:MET:N	2.32	0.63
36:RQ:37:LEU:HD21	36:RQ:130:LYS:HD3	1.81	0.63
42:RW:68:ARG:NH1	42:RW:111:HIS:O	2.32	0.63
45:RZ:119:GLU:OE1	45:RZ:122:ARG:NH2	2.31	0.63
49:R3:11:SER:OG	49:R3:13:ILE:HG12	1.99	0.63
1:XA:1435:G:H2'	1:XA:1436:U:C6	2.34	0.63
2:XB:32:ILE:HD11	2:XB:40:HIS:HB3	1.80	0.63
25:YA:2855:C:H2'	25:YA:2856:C:H6	1.64	0.63
35:YP:62:LEU:CD1	54:Y8:25:MET:HB3	2.28	0.63
1:QA:1131:G:H1	1:QA:1143:G:H21	1.45	0.63
35:RP:57:THR:O	35:RP:59:LEU:N	2.31	0.63
45:RZ:156:LYS:N	45:RZ:156:LYS:HE3	2.14	0.63
45:RZ:158:PRO:HB3	45:RZ:159:PRO:HD3	1.81	0.63
52:R6:39:TYR:HB3	52:R6:41:PRO:HD3	1.80	0.63
31:YH:125:VAL:HG22	31:YH:126:PRO:HA	1.81	0.63
35:YP:64:LYS:CG	54:Y8:25:MET:CB	2.76	0.63
52:Y6:28:ARG:CA	52:Y6:29:ASN:CB	2.77	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:QP:71:ARG:HG3	16:QP:80:PHE:HE1	1.63	0.62
25:RA:1329:U:H5''	25:RA:1330:C:H5	1.64	0.62
1:XA:1412:C:H2'	1:XA:1413:A:C8	2.34	0.62
35:YP:47:ASP:OD2	35:YP:50:ARG:NH1	2.32	0.62
35:YP:62:LEU:HD13	54:Y8:25:MET:HB3	1.80	0.62
35:YP:64:LYS:HG2	54:Y8:25:MET:SD	2.39	0.62
1:QA:345:C:OP2	39:RT:39:ARG:NH2	2.32	0.62
9:QI:63:ILE:HG21	9:QI:77:ILE:HG12	1.81	0.62
25:RA:2867:G:O2'	25:RA:2868:A:H8	1.81	0.62
31:RH:84:SER:OG	31:RH:85:LYS:N	2.32	0.62
32:RI:123:LEU:CD2	32:RI:144:VAL:HG11	2.28	0.62
40:RU:90:VAL:HG22	41:RV:39:LEU:HB3	1.81	0.62
1:XA:530:G:C4	23:XX:21:A2M:H2	2.34	0.62
38:YS:83:LYS:HE2	38:YS:84:GLN:HG3	1.80	0.62
9:QI:103:THR:HG22	9:QI:105:ASP:H	1.63	0.62
25:RA:873:G:O3'	36:RQ:63:LYS:NZ	2.26	0.62
45:YZ:87:ASP:OD2	45:YZ:87:ASP:N	2.32	0.62
9:QI:25:LYS:H	9:QI:25:LYS:HD3	1.63	0.62
23:QX:13:A:C3'	23:QX:14:A:H5''	2.29	0.62
23:QX:13:A:O2'	23:QX:14:A:H3'	2.00	0.62
25:RA:2451:A:C6	56:Z7:76:PPU:HE2	2.34	0.62
31:RH:8:PRO:O	31:RH:9:ILE:HG12	1.97	0.62
46:R0:27:GLU:HG3	46:R0:68:GLU:HA	1.81	0.62
19:XS:16:LEU:HA	19:XS:19:VAL:HG12	1.81	0.62
31:YH:10:PRO:C	31:YH:11:VAL:HG12	2.20	0.62
35:YP:63:PRO:HA	54:Y8:13:ARG:HG2	1.80	0.62
35:YP:64:LYS:HB2	54:Y8:25:MET:HB2	1.81	0.62
46:Y0:6:GLY:HA3	46:Y0:7:LEU:HD22	1.82	0.62
10:QJ:79:ARG:H	10:QJ:79:ARG:HD3	1.64	0.62
15:QO:56:LEU:HA	15:QO:59:MET:HE2	1.79	0.62
28:RE:51:PHE:O	28:RE:74:PRO:CB	2.25	0.62
28:YE:70:ALA:O	28:YE:72:VAL:N	2.32	0.62
45:YZ:138:GLU:OE1	45:YZ:138:GLU:N	2.30	0.62
50:Y4:40:HIS:H	50:Y4:41:PRO:HD2	1.64	0.62
2:QB:184:VAL:N	2:QB:198:ASP:OD1	2.33	0.62
4:QD:64:LEU:HD13	4:QD:198:VAL:HG21	1.81	0.62
9:QI:8:GLY:HA2	9:QI:79:LEU:HD12	1.81	0.62
25:RA:654(D):G:H1	25:RA:654(Q):C:H42	1.45	0.62
25:RA:1569:A:H5'	27:RD:61:LEU:HD21	1.81	0.62
32:RI:123:LEU:CD1	32:RI:144:VAL:CG1	2.76	0.62
40:RU:76:TYR:OH	40:RU:93:LYS:HE2	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:QF:28:ARG:NH2	6:QF:31:GLU:OE1	2.33	0.62
41:YV:85:LYS:HG3	41:YV:87:HIS:N	2.13	0.62
45:YZ:19:ARG:NH1	45:YZ:84:GLU:O	2.33	0.62
45:YZ:150:LEU:HD21	45:YZ:155:LEU:HD23	1.80	0.62
4:QD:23:GLY:O	4:QD:24:GLU:HB2	1.99	0.62
9:QI:17:VAL:HG11	9:QI:81:ILE:HA	1.81	0.62
9:QI:17:VAL:HG22	9:QI:63:ILE:HG12	1.81	0.62
19:QS:67:VAL:HG21	50:R4:59:PHE:HB3	1.82	0.62
31:RH:7:LEU:HB3	31:RH:69:ARG:HD3	1.82	0.62
19:XS:36:ARG:NH1	19:XS:73:GLU:HB2	2.14	0.62
27:YD:35:LYS:NZ	27:YD:64:ILE:O	2.27	0.62
39:YT:105:LEU:HD22	39:YT:109:GLU:HG3	1.80	0.62
1:QA:1158:C:O2	1:QA:1158:C:H2'	1.99	0.62
5:QE:102:ALA:HB1	5:QE:106:PRO:HG2	1.81	0.62
9:QI:4:TYR:HB2	9:QI:18:PHE:O	2.00	0.62
10:QJ:34:VAL:HG22	10:QJ:74:ILE:HG22	1.80	0.62
31:RH:42:ARG:O	31:RH:51:ARG:NH2	2.32	0.62
15:XO:82:ILE:HD11	15:XO:88:ARG:HB2	1.81	0.62
35:YP:64:LYS:CB	54:Y8:25:MET:HB2	2.30	0.62
25:RA:128:C:H2'	25:RA:129:C:C6	2.35	0.62
25:RA:573:G:N1	25:RA:2031:A:OP2	2.23	0.62
25:RA:1265:A:H8	25:RA:1265:A:OP1	1.82	0.62
29:RF:157:VAL:HB	29:RF:194:MET:HB3	1.82	0.62
35:RP:11:GLY:O	35:RP:12:ALA:CB	2.47	0.62
52:R6:9:LEU:HB3	52:R6:27:LYS:HA	1.82	0.62
25:YA:833:U:H5''	35:YP:48:PRO:HB2	1.82	0.62
32:YI:141:LYS:HB2	32:YI:142:VAL:HG22	1.81	0.62
9:QI:96:LEU:HD23	9:QI:102:LEU:HD12	1.81	0.61
2:XB:24:TRP:HD1	2:XB:24:TRP:H	1.46	0.61
25:YA:2056:G:N2	51:Y5:4:HIS:O	2.33	0.61
25:YA:2584:U:C5'	56:Z6:76:PPU:H92	2.29	0.61
31:YH:51:ARG:HH21	31:YH:53:GLU:H	1.48	0.61
25:RA:1056:G:H4'	25:RA:1086:A:H1'	1.81	0.61
45:RZ:118:GLN:HG3	45:RZ:173:ALA:N	2.14	0.61
25:YA:483:A:H5'	44:YY:49:VAL:HA	1.82	0.61
1:QA:1177:G:OP2	9:QI:97:LYS:NZ	2.30	0.61
25:RA:1444:G:C2	25:RA:1548:C:N3	2.68	0.61
3:QC:153:VAL:HG22	3:QC:198:VAL:HG22	1.82	0.61
27:RD:35:LYS:HG2	27:RD:64:ILE:N	2.15	0.61
29:RF:132:VAL:O	29:RF:134:GLY:N	2.30	0.61
32:RI:82:ARG:CD	32:RI:146:ALA:HB3	2.20	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:XB:47:THR:HA	2:XB:202:PRO:HG2	1.81	0.61
13:XM:2:ALA:O	13:XM:4:ILE:N	2.32	0.61
23:XX:5:A:H2'	23:XX:6:G:H8	1.64	0.61
25:YA:2016:U:O4'	51:Y5:6:VAL:HG11	2.00	0.61
32:YI:141:LYS:HD3	32:YI:142:VAL:HG13	1.82	0.61
50:Y4:66:SER:HA	50:Y4:68:ARG:HH11	1.65	0.61
1:QA:422:C:O2'	1:QA:423:G:N2	2.33	0.61
2:QB:29:ALA:HB1	2:QB:30:ARG:HH21	1.65	0.61
19:QS:50:ALA:HB1	19:QS:57:HIS:HB3	1.82	0.61
1:XA:422:C:HO2'	1:XA:423:G:N2	1.98	0.61
1:XA:1325:C:H4'	21:XU:17:THR:HG21	1.82	0.61
25:YA:1566:A:OP1	27:YD:211:ARG:NH1	2.34	0.61
31:YH:26:VAL:HG11	31:YH:75:ALA:HB1	1.83	0.61
1:QA:1510:U:H2'	1:QA:1511:G:C8	2.36	0.61
31:RH:10:PRO:C	31:RH:11:VAL:HG12	2.21	0.61
32:RI:31:LEU:HD21	32:RI:38:LEU:HG	1.82	0.61
32:RI:143:SER:O	32:RI:144:VAL:HG13	2.00	0.61
48:R2:15:LYS:HA	48:R2:67:LYS:HZ1	1.65	0.61
8:XH:33:GLU:OE1	8:XH:50:ARG:NH1	2.34	0.61
26:YB:8:U:O3'	38:YS:25:ARG:NH2	2.33	0.61
29:YF:79:GLY:HA2	29:YF:86:GLY:HA2	1.82	0.61
50:Y4:6:HIS:CB	50:Y4:7:PRO:HD2	2.05	0.61
54:Y8:8:LYS:HB3	54:Y8:12:LYS:HE3	1.83	0.61
28:RE:34:VAL:HG12	28:RE:64:LYS:NZ	2.16	0.61
35:YP:65:ARG:HB2	35:YP:65:ARG:NH1	2.15	0.61
1:QA:1346:A:H4'	1:QA:1347:G:H5'	1.83	0.61
8:QH:110:ALA:HB3	8:QH:121:ASP:HB3	1.81	0.61
49:R3:6:VAL:HG22	49:R3:56:VAL:HG23	1.83	0.61
1:XA:1157:A:C5	1:XA:1181:G:C6	2.89	0.61
21:XU:25:LYS:HG2	21:XU:26:LYS:HG2	1.82	0.61
25:YA:956:G:OP2	36:YQ:14:ARG:NH2	2.34	0.61
52:Y6:34:LEU:HD23	52:Y6:34:LEU:H	1.65	0.61
1:QA:1061:G:OP2	3:QC:3:ASN:ND2	2.33	0.61
1:QA:1379:G:C8	7:QG:3:ARG:HD3	2.36	0.61
25:RA:1413:G:H21	25:RA:1414:G:H1'	1.64	0.61
27:RD:44:ASN:HB3	27:RD:49:ILE:HA	1.82	0.61
45:RZ:5:LEU:CB	45:RZ:59:LEU:HA	2.31	0.61
8:XH:25:ASP:N	8:XH:25:ASP:OD1	2.33	0.61
34:YO:92:GLU:OE1	34:YO:113:LYS:NZ	2.33	0.61
52:Y6:15:GLU:OE1	52:Y6:44:ARG:NH2	2.28	0.61
1:QA:1227:A:C4	13:QM:117:VAL:HG21	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:QB:24:TRP:H	2:QB:24:TRP:HD1	1.48	0.61
50:R4:40:HIS:H	50:R4:41:PRO:HD2	1.66	0.61
7:XG:113:GLU:HB2	7:XG:119:ARG:HG2	1.83	0.61
1:QA:376:G:H5''	16:QP:5:ARG:HB2	1.83	0.60
2:QB:55:PHE:HD1	2:QB:221:LEU:HD21	1.66	0.60
4:QD:107:ARG:HH21	4:QD:194:LEU:HD12	1.66	0.60
35:RP:62:LEU:HD11	54:R8:25:MET:O	2.01	0.60
13:XM:10:PRO:HG2	13:XM:18:ALA:CB	2.31	0.60
25:YA:637:A:H5''	35:YP:117:GLU:HG3	1.83	0.60
41:YV:49:THR:HG22	41:YV:50:PRO:CG	2.30	0.60
1:QA:1379:G:N2	1:QA:1381:U:O4	2.31	0.60
31:RH:18:GLU:HB2	31:RH:25:LYS:HB2	1.84	0.60
45:RZ:58:VAL:O	45:RZ:60:GLU:N	2.34	0.60
25:YA:631:A:H4'	35:YP:65:ARG:HG2	1.83	0.60
25:YA:2208:U:H4'	27:YD:151:LYS:HG2	1.83	0.60
31:YH:10:PRO:O	31:YH:11:VAL:HG13	2.01	0.60
44:YY:76:CYS:HB3	44:YY:96:ILE:HD11	1.82	0.60
1:QA:975:A:H5''	1:QA:976:G:H5'	1.84	0.60
1:QA:1152:A:H5''	10:QJ:13:HIS:HD2	1.66	0.60
1:QA:1443:G:H3'	1:QA:1446:A:H5''	1.84	0.60
2:QB:32:ILE:HD11	2:QB:40:HIS:HB3	1.82	0.60
12:QL:88:GLY:H	12:QL:98:TYR:HA	1.65	0.60
25:RA:2732:G:H3'	25:RA:2733:A:H5'	1.82	0.60
44:RY:76:CYS:SG	44:RY:77:PRO:HD2	2.41	0.60
1:XA:1182:G:C4'	1:XA:1183:A:OP2	2.47	0.60
2:QB:47:THR:HA	2:QB:202:PRO:HG2	1.83	0.60
25:RA:686:G:H21	25:RA:788:A:H61	1.49	0.60
31:RH:155:SER:O	31:RH:155:SER:OG	2.19	0.60
35:RP:63:PRO:C	35:RP:65:ARG:N	2.55	0.60
49:R3:8:LEU:HD13	49:R3:31:LEU:HD12	1.82	0.60
4:XD:127:THR:HA	4:XD:132:ARG:HA	1.83	0.60
3:QC:60:ALA:O	3:QC:63:ASN:ND2	2.34	0.60
32:RI:4:ILE:HG12	32:RI:18:VAL:HG22	1.82	0.60
41:RV:71:LEU:N	41:RV:86:GLY:HA3	2.16	0.60
52:R6:33:LYS:HD2	52:R6:34:LEU:H	1.66	0.60
21:XU:12:LYS:HB3	21:XU:22:ARG:HD2	1.83	0.60
32:YI:141:LYS:HB3	32:YI:142:VAL:CB	2.32	0.60
1:QA:345:C:H5''	1:QA:345:C:C6	2.36	0.60
44:RY:13:VAL:HG23	44:RY:73:ARG:O	2.00	0.60
1:XA:1143:G:H2'	1:XA:1144:G:H8	1.66	0.60
1:XA:1376:U:H2'	1:XA:1377:A:C8	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:1392:G:H21	1:XA:1502:A:H8	1.49	0.60
35:YP:64:LYS:HB3	54:Y8:25:MET:HE2	1.83	0.60
1:QA:1237:C:O2'	1:QA:1300:G:N2	2.33	0.60
23:QX:14:A:C2'	23:QX:15:A:H5'	2.32	0.60
27:RD:35:LYS:HG2	27:RD:64:ILE:H	1.67	0.60
27:RD:35:LYS:HD2	27:RD:104:TYR:CE1	2.37	0.60
29:RF:1:MET:O	29:RF:2:LYS:O	2.20	0.60
41:RV:69:LYS:HD2	41:RV:85:LYS:HD2	1.82	0.60
32:YI:131:LYS:HB3	32:YI:132:PRO:HA	1.84	0.60
18:QR:22:VAL:HG12	18:QR:56:THR:HA	1.82	0.60
9:XI:110:GLU:OE2	9:XI:113:LYS:NZ	2.33	0.60
27:YD:17:THR:O	27:YD:211:ARG:NH2	2.35	0.60
27:YD:95:LEU:HD11	27:YD:105:ILE:HG23	1.83	0.60
12:QL:23:LYS:H	12:QL:23:LYS:HD3	1.67	0.60
25:RA:1869:G:H5'	25:RA:1870:C:OP2	2.02	0.60
54:R8:29:LYS:O	54:R8:31:HIS:N	2.34	0.60
25:YA:102:G:OP1	48:Y2:7:ARG:NH2	2.35	0.60
1:QA:8:A:N6	4:QD:205:GLU:O	2.33	0.60
2:QB:87:ARG:HH21	2:QB:233:SER:HB2	1.67	0.60
25:RA:637:A:H5''	35:RP:117:GLU:HG3	1.83	0.60
27:RD:108:PRO:HG2	27:RD:111:LEU:HB2	1.83	0.60
32:RI:143:SER:C	32:RI:144:VAL:HG13	2.23	0.60
35:RP:62:LEU:HD22	35:RP:64:LYS:HB2	1.81	0.60
44:RY:14:LEU:HA	44:RY:24:VAL:HA	1.83	0.60
52:R6:11:LEU:HD12	52:R6:53:LYS:HB3	1.82	0.60
2:XB:25:ASN:O	2:XB:27:LYS:N	2.34	0.60
13:XM:99:ARG:HD3	13:XM:101:GLN:HG3	1.84	0.60
44:YY:75:ILE:HG13	44:YY:79:CYS:HA	1.82	0.60
1:QA:448:A:OP2	1:QA:485:G:N2	2.31	0.59
25:RA:6:A:H8	25:RA:6:A:O5'	1.84	0.59
25:RA:755:C:H2'	25:RA:756:C:C6	2.37	0.59
25:RA:2836:U:H2'	25:RA:2837:G:C8	2.37	0.59
44:RY:42:VAL:HG13	44:RY:65:ALA:HB3	1.83	0.59
1:XA:1145:C:H4'	1:XA:1146:A:H5'	1.82	0.59
5:XE:137:GLU:OE1	5:XE:141:GLN:NE2	2.35	0.59
25:YA:1639:U:H2'	25:YA:1640:C:H5''	1.83	0.59
27:YD:237:GLU:O	27:YD:239:ARG:N	2.35	0.59
42:RW:19:LEU:HB3	51:R5:25:LEU:HD12	1.85	0.59
45:RZ:157:LEU:O	45:RZ:158:PRO:C	2.40	0.59
31:YH:152:ARG:HG3	31:YH:153:LYS:HG2	1.83	0.59
39:YT:118:ARG:HA	39:YT:121:ILE:HB	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:QA:1060:C:H2'	1:QA:1061:G:H8	1.67	0.59
2:QB:132:LYS:O	2:QB:134:GLU:N	2.35	0.59
25:RA:2680:C:H5'	28:RE:189:PRO:HA	1.85	0.59
39:RT:27:THR:HG23	39:RT:90:GLN:HB3	1.84	0.59
43:RX:63:LYS:HZ2	43:RX:63:LYS:H	1.50	0.59
2:XB:115:LEU:HD13	2:XB:145:LEU:HB3	1.85	0.59
7:XG:73:MET:HG2	7:XG:90:GLU:HA	1.84	0.59
10:XJ:61:GLU:OE2	14:YN:45:ARG:NH1	2.35	0.59
19:XS:48:THR:HG22	19:XS:61:TYR:HD1	1.67	0.59
25:YA:994:C:OP1	40:YU:53:ARG:NH2	2.35	0.59
25:YA:2105:C:H2'	25:YA:2106:G:H8	1.68	0.59
1:QA:1158:C:O2	1:QA:1158:C:C2'	2.49	0.59
4:QD:111:ALA:HB2	4:QD:120:LEU:HD12	1.84	0.59
25:RA:1979:C:H2'	25:RA:1980:G:H5'	1.83	0.59
1:XA:1227:A:C4	13:XM:117:VAL:HG21	2.38	0.59
25:YA:2286:A:H4'	25:YA:2287:A:O5'	2.00	0.59
28:YE:63:LEU:HG	28:YE:64:LYS:N	2.16	0.59
28:YE:111:ARG:HA	37:YR:2:ARG:NH1	2.16	0.59
29:YF:116:ASP:OD2	35:YP:1:MET:N	2.36	0.59
34:YO:35:VAL:HG11	34:YO:103:ALA:HB3	1.82	0.59
52:Y6:14:THR:OG1	52:Y6:15:GLU:N	2.34	0.59
1:QA:827:U:H3	1:QA:872:A:H62	1.50	0.59
25:YA:1482:U:H5'	25:YA:1483:G:OP2	2.02	0.59
32:YI:141:LYS:HB3	32:YI:142:VAL:HG13	1.84	0.59
35:YP:83:VAL:HG12	35:YP:112:LEU:HD21	1.84	0.59
3:QC:108:ASN:HD21	3:QC:144:SER:HB2	1.68	0.59
7:QG:5:ARG:HH21	7:QG:7:ALA:HA	1.67	0.59
46:R0:37:LEU:N	46:R0:59:LEU:O	2.26	0.59
25:YA:783:A:N3	25:YA:783:A:H2'	2.18	0.59
25:YA:2692:C:H2'	25:YA:2693:A:H8	1.66	0.59
32:YI:77:LEU:CD1	32:YI:142:VAL:HG22	2.31	0.59
39:YT:106:SER:HA	39:YT:110:ILE:HG13	1.84	0.59
46:Y0:27:GLU:HG3	46:Y0:68:GLU:HA	1.84	0.59
25:RA:2748:A:H2	25:RA:2754:U:H3	1.50	0.59
16:XP:11:SER:HB2	16:XP:14:ASN:HB3	1.84	0.59
25:RA:140:A:H8	25:RA:1408:C:HO2'	1.49	0.59
25:RA:1225:C:H5''	41:RV:85:LYS:HE2	1.84	0.59
25:RA:1311:G:H5'	25:RA:1311:G:H8	1.67	0.59
25:RA:2790:A:H2'	25:RA:2791:C:H5'	1.85	0.59
45:RZ:59:LEU:C	45:RZ:60:GLU:HG3	2.23	0.59
3:XC:150:LYS:HE2	3:XC:152:ILE:HD11	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:YF:132:VAL:O	29:YF:134:GLY:N	2.34	0.59
29:YF:143:ALA:HB1	29:YF:148:LEU:HB2	1.84	0.59
52:Y6:13:CYS:H	52:Y6:22:ALA:HB3	1.67	0.59
55:Y9:8:LYS:O	55:Y9:34:GLN:NE2	2.35	0.59
23:QX:17:U:O2'	23:QX:18:G:H5'	2.03	0.59
31:RH:44:VAL:H	31:RH:51:ARG:NH1	2.01	0.59
35:RP:9:ASN:O	35:RP:11:GLY:N	2.36	0.59
19:XS:5:LEU:HD13	19:XS:9:VAL:HA	1.83	0.59
25:YA:883:G:H1	25:YA:893:C:H42	1.51	0.59
27:YD:35:LYS:HB3	27:YD:63:ARG:HA	1.83	0.59
30:YG:129:GLY:HA2	30:YG:166:ASP:HA	1.85	0.59
51:Y5:2:ALA:O	51:Y5:3:LYS:HD2	2.03	0.59
1:QA:1223:C:H5''	1:QA:1224:G:H5''	1.85	0.59
25:RA:58:G:H1	25:RA:69:C:H5	1.49	0.59
25:RA:2310:A:N6	30:RG:79:ASN:OD1	2.36	0.59
25:RA:2789:C:O2	25:RA:2894:G:N2	2.34	0.59
25:RA:2848:G:O2'	25:RA:2849:U:O5'	2.20	0.59
31:RH:44:VAL:HG22	31:RH:51:ARG:HH11	1.68	0.59
39:RT:24:PRO:HA	39:RT:49:VAL:HG13	1.84	0.59
25:YA:631:A:H5''	35:YP:65:ARG:HG3	1.72	0.59
25:YA:1174:A:H62	25:YA:1177:A:H4'	1.68	0.59
25:YA:2331:G:O2'	46:Y0:43:THR:HG22	2.03	0.59
28:YE:37:ARG:HD3	28:YE:44:TYR:OH	2.03	0.59
48:Y2:41:ILE:HD11	48:Y2:44:LEU:HD12	1.85	0.59
1:QA:1031:G:H21	1:QA:1032:A:H1'	1.67	0.58
1:QA:1368:G:H5''	9:QI:112:LYS:HB3	1.84	0.58
25:RA:2308:G:HO2'	25:RA:2310:A:H2	1.51	0.58
35:RP:26:GLY:O	35:RP:28:GLY:N	2.35	0.58
35:RP:55:ARG:HG2	35:RP:56:SER:N	2.18	0.58
45:RZ:158:PRO:HB3	45:RZ:159:PRO:HD2	1.76	0.58
15:XO:87:ILE:HG22	15:XO:88:ARG:H	1.67	0.58
19:XS:45:VAL:HG13	19:XS:62:ILE:HG22	1.85	0.58
35:YP:128:HIS:O	35:YP:147:LEU:HB3	2.03	0.58
44:YY:33:LYS:H	44:YY:33:LYS:HD3	1.68	0.58
45:YZ:27:VAL:HG13	45:YZ:87:ASP:HB3	1.84	0.58
50:Y4:8:LYS:C	50:Y4:9:LEU:HD12	2.22	0.58
20:QT:53:LEU:HB3	20:QT:102:GLY:HA3	1.85	0.58
25:RA:1341:U:O2'	25:RA:1342:A:OP1	2.21	0.58
25:RA:1414:G:C6	25:RA:1415:U:C5	2.92	0.58
25:RA:1416:G:N2	25:RA:1582:C:O2	2.35	0.58
26:RB:15:A:H5'	26:RB:16:G:C8	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:RW:59:VAL:HG23	42:RW:65:LEU:H	1.68	0.58
45:RZ:125:LEU:HG	45:RZ:164:ALA:HB3	1.84	0.58
13:XM:86:CYS:HB2	19:XS:73:GLU:HB3	1.85	0.58
28:YE:60:ASN:HB3	28:YE:62:PRO:HD2	1.84	0.58
25:RA:1254:A:H5'	25:RA:1255:U:C5'	2.32	0.58
25:RA:2451:A:C2	56:Z7:76:PPU:HE2	2.38	0.58
25:RA:2788:C:O2'	25:RA:2809:A:N3	2.36	0.58
44:RY:78:ALA:O	44:RY:79:CYS:HB2	2.01	0.58
25:YA:1266:G:O5'	42:YW:15:ARG:NH2	2.37	0.58
9:QI:10:ARG:NH2	9:QI:11:LYS:HD3	2.14	0.58
32:RI:125:GLU:CA	32:RI:141:LYS:HB3	2.23	0.58
35:RP:9:ASN:O	35:RP:10:PRO:C	2.42	0.58
51:R5:4:HIS:HB3	51:R5:5:PRO:CD	2.31	0.58
1:XA:560:U:H5'	1:XA:566:G:N2	2.19	0.58
27:YD:148:GLU:HB2	27:YD:151:LYS:HD2	1.86	0.58
41:YV:2:PHE:CD2	41:YV:42:GLY:HA2	2.38	0.58
1:QA:1320:C:H2'	1:QA:1321:C:O5'	2.04	0.58
9:QI:28:VAL:HG11	9:QI:63:ILE:H	1.67	0.58
25:RA:674:G:O2'	29:RF:74:ARG:HG3	2.03	0.58
27:RD:169:GLU:HG2	27:RD:174:ILE:HD11	1.85	0.58
36:RQ:80:GLU:HG3	46:R0:5:LYS:HB3	1.84	0.58
44:RY:47:LYS:HA	44:RY:60:PHE:HB3	1.84	0.58
50:R4:66:SER:HA	50:R4:68:ARG:HH11	1.68	0.58
7:XG:20:ASP:OD2	7:XG:23:VAL:N	2.35	0.58
9:XI:2:GLU:O	9:XI:20:ARG:NH1	2.37	0.58
13:XM:23:TYR:HB3	13:XM:67:GLU:HA	1.85	0.58
25:YA:2439:A:C8	25:YA:2439:A:H5'	2.38	0.58
45:YZ:5:LEU:HB3	45:YZ:59:LEU:HA	1.85	0.58
6:QF:83:ASP:N	6:QF:83:ASP:OD2	2.36	0.58
25:RA:586:A:H5'	29:RF:89:VAL:HG21	1.86	0.58
25:RA:2128:C:N4	25:RA:2159:G:O6	2.37	0.58
25:RA:2320:A:N3	25:RA:2320:A:H2'	2.18	0.58
6:XF:70:ASP:OD1	6:XF:70:ASP:N	2.37	0.58
25:YA:642:G:H21	25:YA:646:A:H2	1.52	0.58
25:YA:1112:G:OP1	31:YH:3:ARG:NH2	2.36	0.58
25:YA:1454:U:OP1	37:YR:77:ARG:NH1	2.35	0.58
50:Y4:55:ARG:HE	50:Y4:56:VAL:H	1.51	0.58
2:QB:32:ILE:HG12	2:QB:33:TYR:H	1.67	0.58
25:RA:958:U:H5'	36:RQ:14:ARG:HD3	1.85	0.58
25:RA:1148:A:H5''	25:RA:1148:A:C8	2.37	0.58
25:RA:1831:G:H2'	25:RA:1832:C:C6	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:674:G:H2'	1:XA:675:A:C8	2.38	0.58
1:XA:1152:A:H5''	10:XJ:13:HIS:CD2	2.38	0.58
2:XB:14:GLY:O	2:XB:209:ARG:NH1	2.35	0.58
28:YE:95:ILE:H	28:YE:95:ILE:HD12	1.68	0.58
1:QA:960:U:O2'	1:QA:961:U:P	2.62	0.58
25:RA:1753:G:OP2	39:RT:115:ARG:NH2	2.36	0.58
25:RA:1754:C:OP1	39:RT:96:ARG:NH1	2.37	0.58
28:RE:11:MET:HA	28:RE:24:THR:HA	1.86	0.58
1:XA:186(A):C:H5''	20:XT:86:ARG:HG3	1.86	0.58
19:XS:72:GLY:HA2	19:XS:75:ALA:HB3	1.86	0.58
25:YA:270(B):A:H5'	25:YA:270(C):C:OP2	2.03	0.58
25:YA:2751:G:H1'	31:YH:4:ILE:HG13	1.84	0.58
1:QA:503:C:OP2	12:QL:116:SER:HB3	2.04	0.58
13:QM:97:PRO:HA	13:QM:110:ARG:HD3	1.86	0.58
13:QM:118:ALA:HB2	22:QV:29:G:H5'	1.86	0.58
21:QU:6:ARG:CZ	21:QU:15:ARG:HH21	2.17	0.58
28:RE:63:LEU:N	28:RE:63:LEU:CD2	2.67	0.58
52:R6:42:TRP:HD1	52:R6:44:ARG:HG2	1.68	0.58
2:XB:55:PHE:HD1	2:XB:221:LEU:HD21	1.68	0.58
25:YA:2750:A:H2'	25:YA:2752:C:N4	2.18	0.58
28:YE:52:LEU:O	28:YE:74:PRO:HA	2.04	0.58
30:YG:67:LYS:HD2	50:Y4:5:ILE:HG12	1.86	0.58
52:Y6:10:LEU:HA	52:Y6:24:GLU:OE1	2.04	0.58
1:QA:411:A:C4	1:QA:413:G:H1'	2.39	0.58
1:QA:1125:U:H2'	1:QA:1126:U:H2'	1.85	0.58
1:QA:1347:G:C5	9:QI:11:LYS:HE3	2.39	0.58
29:RF:122:LYS:O	29:RF:124:LEU:N	2.37	0.58
29:RF:132:VAL:HG22	29:RF:133:ASN:H	1.69	0.58
1:XA:1299:A:H8	1:XA:1299:A:H3'	1.69	0.58
8:XH:41:ARG:NH2	8:XH:123:GLU:OE2	2.37	0.58
35:YP:63:PRO:HA	54:Y8:13:ARG:CG	2.34	0.58
1:QA:1006:C:N3	1:QA:1023:G:N2	2.51	0.57
19:QS:36:ARG:O	19:QS:38:SER:N	2.36	0.57
27:RD:8:PRO:HB3	27:RD:14:ARG:HB2	1.85	0.57
42:RW:88:ARG:HB3	42:RW:92:ARG:HB3	1.86	0.57
1:XA:652:U:H1'	1:XA:653:A:H2	1.68	0.57
1:XA:1183:A:H2'	1:XA:1183:A:N3	2.18	0.57
13:XM:19:LEU:HB3	13:XM:25:ILE:HG21	1.86	0.57
25:YA:2714:G:O2'	25:YA:2715:C:H5'	2.04	0.57
45:YZ:165:VAL:HG22	45:YZ:166:SER:H	1.68	0.57
1:QA:1126:U:O2	1:QA:1280:A:H5''	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:QH:10:LEU:HD22	8:QH:83:ILE:HD11	1.86	0.57
25:RA:581:C:H2'	25:RA:582:G:H8	1.69	0.57
25:RA:1728:G:H8	25:RA:1732:A:H62	1.51	0.57
25:RA:2015:A:H1'	51:R5:2:ALA:HA	1.85	0.57
25:RA:2701:C:C3'	25:RA:2702:U:H5''	2.25	0.57
28:RE:50:GLY:C	28:RE:74:PRO:HG2	2.24	0.57
41:RV:29:PRO:HA	41:RV:61:VAL:HG13	1.86	0.57
44:RY:76:CYS:CB	44:RY:96:ILE:HD11	2.33	0.57
1:XA:7:G:H2'	5:XE:119:LEU:HD22	1.85	0.57
24:XY:37:ILE:HD11	24:XY:66:ILE:HD11	1.85	0.57
25:YA:141:A:C8	25:YA:1408:C:H1'	2.38	0.57
25:YA:2347:C:OP1	25:YA:2347:C:H4'	2.03	0.57
35:RP:94:GLU:HG3	35:RP:124:LYS:HB3	1.86	0.57
35:RP:106:LEU:HD11	35:RP:112:LEU:HG	1.85	0.57
3:XC:26:LYS:HD3	10:XJ:45:ARG:HH22	1.69	0.57
25:YA:141:A:H8	25:YA:1595:G:H21	1.51	0.57
25:YA:582:G:H2'	25:YA:583:G:C8	2.38	0.57
25:YA:582:G:H2'	25:YA:583:G:H8	1.68	0.57
25:YA:1252:G:N3	40:YU:33:ARG:HD2	2.19	0.57
24:QY:12:LEU:HB3	24:QY:18:VAL:HB	1.85	0.57
25:RA:873:G:H1	25:RA:904:C:H42	1.52	0.57
27:RD:85:ASP:HB2	27:RD:92:ILE:HD13	1.87	0.57
30:RG:6:ALA:N	50:R4:23:GLU:OE2	2.31	0.57
45:RZ:19:ARG:NH1	45:RZ:84:GLU:O	2.37	0.57
45:RZ:91:LEU:H	45:RZ:91:LEU:HD23	1.69	0.57
47:R1:50:ARG:NH1	47:R1:57:GLU:OE1	2.38	0.57
1:XA:1320:C:C2	19:XS:36:ARG:HG2	2.39	0.57
22:XV:76:A:H2'	25:YA:2602:A:N6	2.19	0.57
27:YD:79:VAL:HG21	27:YD:111:LEU:HD11	1.87	0.57
29:YF:178:PRO:HB2	29:YF:201:VAL:HG11	1.86	0.57
1:QA:579:G:H5'	1:QA:728:A:H1'	1.86	0.57
1:QA:1179:A:OP2	9:QI:93:ARG:NH2	2.38	0.57
25:RA:1413:G:N2	25:RA:1414:G:C4	2.73	0.57
28:RE:128:SER:OG	28:RE:129:HIS:N	2.37	0.57
29:RF:143:ALA:HB1	29:RF:148:LEU:HB2	1.86	0.57
17:XQ:60:ILE:HB	17:XQ:74:LEU:HD23	1.86	0.57
27:YD:72:LYS:NZ	27:YD:99:ASP:OD1	2.28	0.57
1:QA:1068:G:OP2	1:QA:1068:G:H8	1.88	0.57
25:RA:2356:C:H4'	46:R0:20:ARG:HG3	1.85	0.57
1:XA:1422:G:O3'	34:YO:49:ARG:NH1	2.36	0.57
25:YA:1930:G:H1'	25:YA:1931:U:OP2	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:QA:31:G:O2'	1:QA:48:C:N4	2.38	0.57
1:QA:534:U:H5'	1:QA:535:A:OP2	2.05	0.57
1:QA:1318:A:H4'	19:QS:10:PHE:CE2	2.40	0.57
25:RA:2319:G:C6	25:RA:2320:A:N6	2.73	0.57
25:RA:2875:C:H4'	39:RT:5:ALA:HB2	1.87	0.57
26:RB:8:U:O3'	38:RS:25:ARG:NH2	2.38	0.57
1:XA:1129:C:H5''	9:XI:16:ARG:HH22	1.69	0.57
9:XI:15:ALA:HB2	9:XI:65:VAL:HG23	1.85	0.57
29:YF:153:SER:HB2	29:YF:190:GLU:H	1.70	0.57
25:RA:270(B):A:H5'	25:RA:270(C):C:OP2	2.05	0.57
35:RP:52:GLU:HB2	35:RP:55:ARG:HB3	1.86	0.57
1:XA:186(A):C:O2'	20:XT:89:ARG:NE	2.36	0.57
1:XA:189:U:O2	17:XQ:63:ARG:NH1	2.37	0.57
1:XA:963:G:H21	10:XJ:55:LYS:HD3	1.69	0.57
1:XA:1056:U:H5'	3:XC:163:ALA:HB2	1.85	0.57
19:XS:5:LEU:HA	19:XS:6:LYS:HE3	1.85	0.57
25:YA:458:G:C8	53:Y7:37:LYS:HG2	2.39	0.57
26:YB:65:C:N4	26:YB:108:C:H2'	2.19	0.57
35:YP:105:LEU:O	35:YP:107:LYS:N	2.36	0.57
39:YT:115:ARG:H	39:YT:115:ARG:HD3	1.70	0.57
31:RH:117:PRO:HB3	31:RH:123:PHE:CE1	2.40	0.57
1:XA:345:C:OP2	39:YT:39:ARG:NH2	2.38	0.57
1:XA:518:C:H2'	1:XA:530:G:C8	2.40	0.57
8:XH:10:LEU:HD22	8:XH:83:ILE:HD11	1.86	0.57
19:XS:36:ARG:O	19:XS:38:SER:N	2.37	0.57
25:YA:27:G:O2'	25:YA:28:A:OP2	2.21	0.57
39:YT:26:ASP:HB3	39:YT:92:GLY:H	1.69	0.57
42:YW:35:ILE:HG23	51:Y5:28:PRO:HD2	1.87	0.57
4:QD:125:HIS:ND1	4:QD:152:SER:OG	2.29	0.57
25:RA:2439:A:H5'	25:RA:2439:A:C8	2.39	0.57
1:XA:1157:A:C2	1:XA:1158:C:N4	2.73	0.57
8:XH:103:VAL:HG21	8:XH:110:ALA:HB2	1.87	0.57
30:YG:96:ARG:O	30:YG:98:ARG:N	2.37	0.57
31:YH:126:PRO:HB2	31:YH:127:GLU:HA	1.86	0.57
36:YQ:89:ASN:O	36:YQ:92:GLY:N	2.36	0.57
1:QA:345:C:O2'	1:QA:346:G:H5''	2.04	0.56
1:QA:1060:C:H5''	10:QJ:51:ARG:HG2	1.87	0.56
5:QE:9:LYS:CG	5:QE:112:LEU:HD11	2.31	0.56
19:QS:64:GLU:O	19:QS:66:MET:N	2.37	0.56
25:RA:2811:G:N2	25:RA:2891:G:H1'	2.20	0.56
35:RP:64:LYS:HZ3	54:R8:30:ARG:HA	1.62	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:RT:74:ARG:HD3	39:RT:76:PHE:CZ	2.40	0.56
47:R1:87:PRO:HA	47:R1:90:ILE:HG22	1.87	0.56
1:XA:1002:G:N2	1:XA:1039:C:O2	2.37	0.56
3:XC:131:ARG:NH2	3:XC:167:TRP:O	2.38	0.56
4:XD:108:LEU:HD21	4:XD:183:GLY:HA3	1.86	0.56
6:XF:101:ALA:HA	18:XR:28:GLU:HB3	1.85	0.56
14:YN:12:ARG:HG2	14:YN:14:PRO:HD3	1.86	0.56
25:YA:2522:U:O2'	25:YA:2647:U:OP1	2.21	0.56
28:YE:74:PRO:HG2	28:YE:78:LEU:HD23	1.87	0.56
1:QA:815:A:N7	1:QA:1509:C:O2'	2.34	0.56
13:QM:53:VAL:HG12	13:QM:57:ARG:HD3	1.87	0.56
25:RA:1882:C:H5'	25:RA:1883:G:OP2	2.05	0.56
28:RE:37:ARG:HG3	28:RE:46:ALA:HB3	1.85	0.56
38:RS:49:VAL:HG22	38:RS:80:LEU:HD12	1.87	0.56
39:RT:125:ARG:NH1	39:RT:128:GLU:OE1	2.38	0.56
9:XI:32:ASP:HB2	9:XI:35:GLU:HB2	1.87	0.56
25:YA:2467:C:O2	36:YQ:124:LYS:NZ	2.38	0.56
41:YV:4:ILE:HG22	41:YV:39:LEU:HD13	1.86	0.56
1:QA:1380:U:H5	7:QG:3:ARG:HG2	1.69	0.56
10:QJ:38:ILE:HB	10:QJ:71:LEU:HB3	1.86	0.56
25:RA:928:G:H5'	25:RA:929:G:OP2	2.05	0.56
29:RF:34:TRP:NE1	35:RP:8:PRO:HD3	2.21	0.56
43:RX:8:ILE:O	48:R2:36:ARG:NH2	2.38	0.56
1:XA:1060:C:H5''	10:XJ:51:ARG:HG2	1.87	0.56
2:XB:119:GLU:OE2	2:XB:153:ARG:NH2	2.38	0.56
10:XJ:48:THR:HA	10:XJ:62:HIS:HB3	1.87	0.56
25:YA:2010:G:H5''	42:YW:42:ARG:HB2	1.87	0.56
25:YA:2115:G:O2'	25:YA:2171:A:N6	2.37	0.56
35:YP:63:PRO:HD3	54:Y8:13:ARG:NH1	2.20	0.56
36:YQ:54:MET:HE1	36:YQ:118:LEU:HD23	1.85	0.56
41:YV:49:THR:HB	41:YV:50:PRO:HD2	1.81	0.56
52:Y6:31:PRO:O	52:Y6:32:ASN:CB	2.36	0.56
1:QA:750:G:N3	15:QO:23:GLY:HA3	2.21	0.56
12:QL:126:LYS:HD3	12:QL:126:LYS:H	1.70	0.56
17:QQ:90:ILE:O	17:QQ:94:ASN:ND2	2.39	0.56
31:RH:69:ARG:CG	31:RH:69:ARG:NH1	2.62	0.56
1:XA:1068:G:H8	1:XA:1068:G:OP2	1.87	0.56
2:XB:189:ASP:O	2:XB:191:ASP:N	2.39	0.56
5:XE:19:MET:HA	5:XE:24:ARG:HA	1.86	0.56
10:XJ:34:VAL:HG22	10:XJ:74:ILE:HG22	1.87	0.56
25:YA:142:G:H4'	43:YX:35:THR:HG21	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:YA:631:A:C4'	35:YP:65:ARG:HG2	2.35	0.56
25:YA:1400:G:H2'	25:YA:1401:G:C8	2.41	0.56
25:YA:2445:G:OP1	29:YF:74:ARG:NH2	2.33	0.56
32:YI:98:ALA:HA	32:YI:109:ILE:HD11	1.87	0.56
40:YU:93:LYS:HD3	40:YU:93:LYS:N	2.21	0.56
46:Y0:4:LYS:H	46:Y0:5:LYS:HB3	1.70	0.56
1:QA:736:C:H2'	1:QA:737:A:C8	2.40	0.56
23:QX:6:G:H2'	23:QX:7:G:H8	1.71	0.56
25:RA:582:G:H2'	25:RA:583:G:H8	1.71	0.56
25:RA:839:U:H2'	25:RA:840:C:C6	2.40	0.56
1:XA:455:C:H42	1:XA:477:G:H1	1.54	0.56
1:XA:656:C:O2'	15:XO:28:GLN:OE1	2.22	0.56
1:XA:1299:A:C6	1:XA:1301:U:C2	2.93	0.56
3:XC:82:GLU:HG3	3:XC:83:ARG:H	1.70	0.56
4:XD:199:ASN:O	4:XD:201:GLN:N	2.35	0.56
5:XE:8:GLU:HG2	5:XE:34:VAL:HG22	1.87	0.56
6:XF:55:ASP:HB2	6:XF:86:ARG:HH12	1.69	0.56
1:QA:1300:G:O2'	1:QA:1301:U:O5'	2.24	0.56
1:QA:1348:U:N3	1:QA:1374:A:H2	2.03	0.56
11:QK:84:VAL:HG23	11:QK:110:ASP:HA	1.87	0.56
25:RA:58:G:H22	25:RA:69:C:H5	1.54	0.56
25:RA:574:C:O2	28:RE:145:LYS:NZ	2.36	0.56
31:RH:24:VAL:HG22	31:RH:35:VAL:HB	1.88	0.56
45:RZ:124:ILE:HD11	45:RZ:165:VAL:HG11	1.87	0.56
46:R0:36:ILE:HA	46:R0:60:PHE:HA	1.88	0.56
1:XA:1513:A:H2'	1:XA:1514:C:C6	2.41	0.56
25:YA:587:C:N3	35:YP:33:ARG:NH1	2.53	0.56
35:YP:52:GLU:HG2	35:YP:55:ARG:NE	2.16	0.56
25:RA:480:A:H1'	44:RY:44:ILE:HD13	1.87	0.56
25:RA:848:G:H2'	25:RA:849:A:C8	2.40	0.56
27:RD:146:GLU:HB2	27:RD:189:CYS:HB3	1.87	0.56
28:RE:37:ARG:HD3	28:RE:44:TYR:OH	2.06	0.56
29:RF:125:LEU:HD23	29:RF:125:LEU:H	1.70	0.56
25:YA:2584:U:O2	25:YA:2585:U:C4	2.59	0.56
27:YD:159:ALA:H	27:YD:196:VAL:HG11	1.71	0.56
31:YH:127:GLU:HG3	31:YH:128:PRO:HD2	1.87	0.56
1:QA:1320:C:C4	19:QS:36:ARG:HG2	2.40	0.56
25:RA:2343:C:HO2'	25:RA:2373:G:HO2'	1.40	0.56
28:RE:63:LEU:O	28:RE:64:LYS:CB	2.54	0.56
45:RZ:116:VAL:O	45:RZ:118:GLN:NE2	2.39	0.56
52:R6:34:LEU:HD11	52:R6:50:ARG:HH21	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:1157:A:C2	1:XA:1181:G:O6	2.59	0.56
1:XA:1423:G:OP1	34:YO:49:ARG:NH2	2.39	0.56
2:XB:80:ILE:HD11	2:XB:211:ILE:HG22	1.88	0.56
27:YD:35:LYS:HG2	27:YD:64:ILE:H	1.69	0.56
31:YH:11:VAL:HG23	31:YH:13:LYS:HG2	1.88	0.56
42:YW:29:LEU:HD21	42:YW:33:ARG:HH21	1.70	0.56
44:YY:39:VAL:HG23	44:YY:41:GLY:H	1.70	0.56
1:QA:1347:G:H1'	1:QA:1348:U:OP2	2.06	0.56
13:QM:23:TYR:CD1	13:QM:71:ARG:HD2	2.40	0.56
25:RA:1414:G:N1	25:RA:1415:U:C4	2.74	0.56
25:RA:2346:A:H2	52:R6:25:LYS:HB3	1.71	0.56
30:RG:68:PRO:HA	30:RG:92:VAL:HB	1.88	0.56
28:YE:8:LYS:HB3	28:YE:193:GLY:H	1.71	0.56
1:QA:1321:C:C5	1:QA:1322:C:C4	2.94	0.56
10:QJ:50:ILE:HD13	10:QJ:60:ARG:HD3	1.88	0.56
25:RA:372:G:O2'	25:RA:373:U:OP2	2.24	0.56
25:RA:2384:G:OP2	46:R0:55:ARG:NH2	2.30	0.56
1:XA:1175:G:H2'	1:XA:1176:A:C8	2.41	0.56
17:XQ:12:SER:HB3	17:XQ:20:THR:HB	1.88	0.56
31:YH:6:ARG:HB3	31:YH:54:ARG:HH12	1.71	0.56
31:YH:12:PRO:HG3	31:YH:48:GLY:HA2	1.88	0.56
1:QA:189:U:O2	17:QQ:63:ARG:NH1	2.40	0.55
1:QA:345:C:H1'	1:QA:346:G:C2	2.40	0.55
1:QA:1320:C:C2'	1:QA:1321:C:O5'	2.54	0.55
4:QD:73:ARG:O	4:QD:77:ASN:ND2	2.40	0.55
18:QR:22:VAL:HG22	18:QR:23:LYS:H	1.70	0.55
28:RE:67:PHE:O	28:RE:68:ALA:C	2.43	0.55
36:RQ:80:GLU:HG2	36:RQ:81:VAL:H	1.72	0.55
1:XA:878:G:H5'	8:XH:89:PRO:HG2	1.88	0.55
10:XJ:10:GLY:HA3	10:XJ:16:LEU:HD21	1.88	0.55
25:YA:2693:A:H2'	25:YA:2694:G:H8	1.71	0.55
35:YP:63:PRO:HB2	54:Y8:12:LYS:O	2.06	0.55
45:YZ:151:HIS:O	45:YZ:154:ASP:HB3	2.05	0.55
52:Y6:30:THR:O	52:Y6:30:THR:HG23	2.06	0.55
9:QI:2:GLU:H	9:QI:20:ARG:HH11	1.51	0.55
10:QJ:4:ILE:HA	10:QJ:100:THR:HG22	1.87	0.55
25:RA:2287:A:H2	25:RA:2346:A:H62	1.53	0.55
25:RA:2476:A:H62	25:RA:2477:C:N4	2.05	0.55
27:RD:44:ASN:N	27:RD:44:ASN:OD1	2.39	0.55
27:RD:101:GLU:OE1	27:RD:103:ARG:NH1	2.39	0.55
31:RH:30:LYS:HB3	31:RH:136:ILE:HG21	1.86	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:XE:13:ILE:HD13	5:XE:13:ILE:H	1.70	0.55
18:XR:31:LEU:HD13	18:XR:65:ILE:HD13	1.89	0.55
31:RH:86:GLU:HG3	31:RH:165:ALA:HB2	1.88	0.55
32:RI:123:LEU:CD2	32:RI:144:VAL:HG12	2.31	0.55
32:RI:144:VAL:O	32:RI:145:VAL:HB	2.04	0.55
1:XA:530:G:N3	23:XX:21:A2M:H2	2.21	0.55
2:XB:9:GLU:HG2	2:XB:48:MET:HG3	1.88	0.55
25:YA:655:A:H4'	25:YA:656:G:H5'	1.89	0.55
25:YA:2315:G:OP1	30:YG:36:LYS:NZ	2.38	0.55
30:YG:131:TYR:HB3	30:YG:159:VAL:HG13	1.87	0.55
36:YQ:31:ASP:H	36:YQ:107:ALA:HB2	1.71	0.55
38:YS:19:LYS:O	38:YS:21:THR:N	2.35	0.55
1:QA:1145:C:H4'	1:QA:1146:A:C8	2.42	0.55
1:QA:1494:G:O2'	25:RA:1912:A:O2'	2.23	0.55
25:RA:1252:G:N7	40:RU:36:ARG:NH1	2.54	0.55
31:RH:45:VAL:HG13	31:RH:46:GLU:H	1.71	0.55
44:RY:96:ILE:HG12	44:RY:101:LYS:HG3	1.88	0.55
45:RZ:121:HIS:H	45:RZ:171:ILE:HG12	1.72	0.55
1:XA:413:G:H21	1:XA:428:G:H1'	1.72	0.55
1:XA:972:C:O3'	10:XJ:57:LYS:HG2	2.07	0.55
15:XO:26:GLU:OE2	15:XO:77:ARG:NH1	2.39	0.55
26:YB:65:C:H41	26:YB:108:C:H2'	1.72	0.55
29:YF:102:PRO:HB2	29:YF:105:VAL:HG23	1.89	0.55
30:YG:27:ASN:HB3	30:YG:30:GLU:HG3	1.88	0.55
38:YS:93:LYS:HG2	38:YS:95:HIS:HB2	1.88	0.55
51:Y5:41:PRO:O	51:Y5:44:THR:OG1	2.23	0.55
1:QA:4:U:O2	8:QH:102:ARG:NH1	2.39	0.55
1:QA:1435:G:H2'	1:QA:1436:U:C6	2.41	0.55
3:QC:52:LEU:HD23	3:QC:52:LEU:H	1.72	0.55
9:QI:27:THR:HG21	9:QI:32:ASP:HA	1.88	0.55
9:QI:28:VAL:HG21	9:QI:63:ILE:N	2.22	0.55
25:RA:58:G:H1	25:RA:69:C:H41	1.54	0.55
42:RW:59:VAL:HA	42:RW:64:MET:H	1.72	0.55
45:RZ:69:THR:HG22	45:RZ:90:VAL:HA	1.89	0.55
1:XA:35:G:H2'	1:XA:36:C:C6	2.41	0.55
1:XA:966:G:O2'	9:XI:127:LYS:O	2.25	0.55
25:YA:1247:A:OP2	35:YP:15:ARG:NH1	2.38	0.55
25:YA:2393:A:H4'	35:YP:62:LEU:H	1.72	0.55
25:YA:2820:A:O2'	25:YA:2821:A:OP1	2.24	0.55
27:YD:26:LYS:H	27:YD:26:LYS:HD2	1.71	0.55
1:QA:304:U:H2'	1:QA:305:G:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:QI:15:ALA:HB2	9:QI:65:VAL:HG23	1.88	0.55
15:QO:3:ILE:H	15:QO:3:ILE:HD13	1.72	0.55
15:QO:87:ILE:HG22	15:QO:88:ARG:H	1.72	0.55
25:RA:6:A:H2'	25:RA:7:G:H8	1.70	0.55
25:RA:710:G:H2'	25:RA:711:G:C8	2.42	0.55
25:RA:774:A:O2'	25:RA:775:G:OP2	2.21	0.55
25:RA:1931:U:O2	25:RA:1931:U:H2'	2.05	0.55
1:XA:327:A:C3'	1:XA:328:C:H5''	2.37	0.55
3:XC:134:ILE:HG23	3:XC:151:VAL:HB	1.89	0.55
12:XL:126:LYS:H	12:XL:126:LYS:HD3	1.72	0.55
25:YA:1416:G:O2'	25:YA:1417:C:OP2	2.25	0.55
25:YA:1786:A:H1'	25:YA:1938:A:N6	2.21	0.55
31:YH:64:LEU:O	31:YH:68:THR:OG1	2.23	0.55
32:YI:3:VAL:HG12	32:YI:38:LEU:HA	1.88	0.55
48:Y2:18:PRO:HA	48:Y2:21:LEU:HB2	1.88	0.55
1:QA:1363:A:H4'	1:QA:1364:U:H5''	1.89	0.55
2:QB:187:LEU:HA	2:QB:201:ILE:HB	1.87	0.55
2:QB:219:VAL:HA	2:QB:222:ILE:HD12	1.89	0.55
25:RA:990:A:H5'	25:RA:990:A:H8	1.71	0.55
25:RA:1935:G:H1'	25:RA:1964:G:N2	2.20	0.55
39:RT:3:ARG:HG2	39:RT:6:LEU:HB2	1.88	0.55
45:RZ:5:LEU:HB3	45:RZ:59:LEU:HA	1.89	0.55
47:R1:80:LEU:H	47:R1:80:LEU:HD13	1.72	0.55
25:YA:813:U:H2'	25:YA:814:C:C6	2.42	0.55
25:YA:2306:C:N4	30:YG:42:GLY:O	2.37	0.55
28:YE:60:ASN:CB	28:YE:62:PRO:HD2	2.37	0.55
40:YU:92:ARG:HH12	41:YV:11:GLN:H	1.53	0.55
1:QA:139:G:H2'	1:QA:140:A:H8	1.71	0.55
1:QA:1399:C:C2	1:QA:1502:A:N6	2.75	0.55
2:QB:76:GLN:HG3	2:QB:208:ILE:HG12	1.89	0.55
25:RA:1413:G:N3	25:RA:1414:G:C8	2.75	0.55
25:RA:2496:C:OP1	36:RQ:82:ARG:HD3	2.06	0.55
31:RH:3:ARG:HH11	31:RH:6:ARG:HE	1.54	0.55
47:R1:53:VAL:HG22	47:R1:74:VAL:HG13	1.88	0.55
1:XA:750:G:N3	15:XO:23:GLY:HA3	2.22	0.55
1:XA:1137:C:H4'	1:XA:1138:G:O5'	2.06	0.55
1:XA:1391:U:H2'	1:XA:1392:G:C8	2.42	0.55
1:XA:1502:A:H2	1:XA:1505:G:N1	1.96	0.55
20:XT:29:LYS:O	20:XT:33:ILE:HG12	2.06	0.55
32:YI:76:THR:OG1	32:YI:77:LEU:N	2.39	0.55
8:QH:69:ARG:NH1	8:QH:75:ARG:O	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:RE:80:GLU:O	28:RE:82:ARG:N	2.39	0.55
2:XB:7:VAL:HG13	2:XB:8:LYS:H	1.72	0.55
3:XC:92:ALA:HA	3:XC:95:THR:HB	1.88	0.55
6:XF:11:ASN:HB3	6:XF:14:LEU:HG	1.89	0.55
12:XL:23:LYS:HD3	12:XL:23:LYS:H	1.72	0.55
20:XT:26:ASN:HB2	20:XT:71:THR:HG23	1.87	0.55
25:YA:1653:G:O6	37:YR:11:ASN:OD1	2.23	0.55
32:YI:86:THR:HG22	32:YI:122:GLU:HG3	1.89	0.55
35:YP:62:LEU:HD12	54:Y8:25:MET:C	2.26	0.55
1:QA:501:C:H2'	1:QA:502:G:C8	2.42	0.55
1:QA:1541:U:O2'	18:QR:18:ARG:NH2	2.39	0.55
25:RA:2776:A:OP1	25:RA:2776:A:H3'	2.07	0.55
26:RB:60:C:H2'	26:RB:61:G:H8	1.72	0.55
30:RG:125:PHE:HB3	30:RG:166:ASP:HB2	1.89	0.55
31:RH:11:VAL:HG23	31:RH:13:LYS:HG2	1.89	0.55
42:RW:18:ARG:NH1	42:RW:76:VAL:O	2.40	0.55
1:XA:209:U:O2	1:XA:209:U:H2'	2.07	0.55
1:XA:316:G:OP1	1:XA:351:G:O2'	2.24	0.55
1:XA:742:G:OP2	15:XO:35:ARG:NH2	2.40	0.55
1:XA:1126:U:H3	10:XJ:40:LEU:HD21	1.72	0.55
30:YG:16:ARG:HE	30:YG:31:VAL:HG11	1.72	0.55
35:YP:59:LEU:HD21	54:Y8:10:ALA:HA	1.89	0.55
47:Y1:8:SER:HB3	47:Y1:66:HIS:CD2	2.42	0.55
52:Y6:28:ARG:NH2	52:Y6:30:THR:HG23	2.22	0.55
54:Y8:61:LEU:HD12	54:Y8:62:LEU:H	1.72	0.55
1:QA:993:G:O6	1:QA:1045:C:N4	2.33	0.54
1:QA:1266:G:N2	1:QA:1269:A:OP2	2.39	0.54
2:QB:102:LEU:HD23	2:QB:182:ILE:HD12	1.88	0.54
9:QI:121:ARG:NH1	9:QI:122:ALA:O	2.40	0.54
44:RY:43:ASN:HB3	44:RY:64:GLU:HA	1.89	0.54
1:XA:1157:A:C6	1:XA:1181:G:C6	2.95	0.54
6:XF:7:ASN:HD22	6:XF:7:ASN:N	2.06	0.54
21:XU:8:THR:HG22	21:XU:10:ARG:H	1.71	0.54
25:YA:807:U:OP2	35:YP:41:ARG:NH1	2.40	0.54
27:YD:35:LYS:HZ1	27:YD:65:ILE:HA	1.71	0.54
31:YH:10:PRO:C	31:YH:11:VAL:CG1	2.75	0.54
32:YI:140:LEU:O	32:YI:141:LYS:CG	2.52	0.54
1:QA:1316:G:H5''	14:QN:17:LYS:HE3	1.90	0.54
25:RA:1094:U:O2'	25:RA:1096:A:OP1	2.25	0.54
25:RA:2212:A:H1'	25:RA:2215:G:C4	2.42	0.54
31:RH:89:ILE:HD12	31:RH:129:THR:HA	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:RH:150:ALA:O	31:RH:152:ARG:N	2.39	0.54
41:RV:59:ALA:HB2	41:RV:96:ILE:HD13	1.89	0.54
1:XA:1217:C:OP1	14:XN:9:LYS:HD2	2.07	0.54
16:XP:71:ARG:HG3	16:XP:80:PHE:HE1	1.72	0.54
25:YA:1731:G:N1	25:YA:1732:A:N7	2.55	0.54
27:YD:106:ILE:HD11	27:YD:196:VAL:HG13	1.89	0.54
32:YI:2:LYS:HA	32:YI:20:ASP:HA	1.89	0.54
1:QA:1129:C:O2'	1:QA:1130:A:OP2	2.24	0.54
19:QS:72:GLY:HA2	19:QS:75:ALA:HB3	1.88	0.54
20:QT:10:LEU:HD22	20:QT:11:SER:N	2.22	0.54
25:RA:61:G:H1	25:RA:93:C:H42	1.56	0.54
25:RA:581:C:H2'	25:RA:582:G:C8	2.42	0.54
26:RB:14:U:O4'	26:RB:106:G:N2	2.40	0.54
27:RD:130:ALA:HA	27:RD:192:THR:HA	1.89	0.54
32:RI:131:LYS:HB3	32:RI:132:PRO:HA	1.88	0.54
45:RZ:157:LEU:HD13	45:RZ:161:VAL:CG1	2.37	0.54
50:R4:39:CYS:O	50:R4:40:HIS:ND1	2.40	0.54
1:XA:1493:A:C6	25:YA:1913:A:H1'	2.42	0.54
6:XF:22:GLU:O	6:XF:26:ILE:HG13	2.07	0.54
11:XK:98:LEU:O	11:XK:101:SER:OG	2.21	0.54
13:XM:44:ARG:HB3	13:XM:46:LYS:HB3	1.88	0.54
25:YA:2144:U:O2'	25:YA:2145:C:O5'	2.22	0.54
25:YA:2830:G:H5'	28:YE:58:ARG:HH11	1.73	0.54
2:QB:80:ILE:HD13	2:QB:212:GLN:HA	1.89	0.54
25:RA:819:A:OP2	25:RA:1187:G:N2	2.33	0.54
30:RG:41:GLN:NE2	30:RG:154:GLY:O	2.34	0.54
35:RP:58:THR:HG21	35:RP:61:ARG:HH22	1.70	0.54
42:RW:12:ILE:HD13	42:RW:17:VAL:HG13	1.89	0.54
52:R6:8:LYS:HB2	52:R6:27:LYS:HB2	1.88	0.54
1:XA:186(E):C:H42	1:XA:191(B):G:H1	1.55	0.54
1:XA:706:A:O4'	11:XK:29:ILE:HD11	2.08	0.54
10:XJ:4:ILE:HB	10:XJ:74:ILE:HD11	1.88	0.54
25:YA:2734:A:H5'	25:YA:2735:G:OP2	2.07	0.54
29:YF:42:ALA:O	29:YF:45:ARG:HB2	2.07	0.54
49:Y3:59:VAL:HG12	49:Y3:60:GLU:H	1.72	0.54
9:QI:2:GLU:HG3	9:QI:3:GLN:H	1.72	0.54
25:RA:411:G:OP2	25:RA:2406:U:O2'	2.22	0.54
25:RA:1412:A:H2'	25:RA:1413:G:H8	1.72	0.54
33:RN:39:ARG:HH21	33:RN:41:ASP:HB2	1.73	0.54
5:XE:33:VAL:HG12	5:XE:112:LEU:HD12	1.90	0.54
28:YE:8:LYS:HG2	28:YE:192:ASN:HA	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:YP:64:LYS:HD3	54:Y8:25:MET:HG2	1.89	0.54
43:YX:36:LYS:HD3	43:YX:56:THR:HG23	1.90	0.54
44:YY:88:LYS:O	44:YY:90:LEU:N	2.39	0.54
45:YZ:27:VAL:HG22	45:YZ:29:TYR:HD2	1.73	0.54
48:Y2:47:ASN:O	48:Y2:49:LYS:N	2.32	0.54
1:QA:542:G:OP1	4:QD:10:ARG:NH2	2.41	0.54
1:QA:1305:G:N2	1:QA:1331:G:H2'	2.22	0.54
3:QC:11:ARG:O	3:QC:13:GLY:N	2.39	0.54
20:QT:67:ALA:O	20:QT:73:HIS:ND1	2.40	0.54
25:RA:606:U:H4'	25:RA:658:C:H4'	1.90	0.54
25:RA:1782:C:H1'	25:RA:2609:U:H5''	1.89	0.54
25:RA:2091:U:H1'	47:R1:47:GLN:NE2	2.22	0.54
27:RD:65:ILE:HD11	27:RD:67:PHE:CE2	2.43	0.54
28:RE:64:LYS:O	28:RE:65:GLY:C	2.45	0.54
45:RZ:118:GLN:O	45:RZ:120:ILE:HG22	2.07	0.54
1:XA:1183:A:OP2	1:XA:1183:A:C4'	2.30	0.54
5:XE:101:ILE:HG13	5:XE:119:LEU:HD23	1.88	0.54
25:YA:969:U:H2'	25:YA:970:C:C6	2.43	0.54
29:YF:101:LEU:O	29:YF:106:ARG:NH1	2.40	0.54
52:Y6:28:ARG:NH2	52:Y6:30:THR:O	2.41	0.54
5:QE:75:THR:OG1	5:QE:76:ILE:N	2.40	0.54
25:RA:582:G:H2'	25:RA:583:G:C8	2.43	0.54
25:RA:888:C:H4'	25:RA:889:C:H5	1.73	0.54
25:RA:2419:U:O4	54:R8:31:HIS:NE2	2.40	0.54
36:RQ:12:GLN:HG2	36:RQ:73:PRO:HD2	1.90	0.54
18:XR:62:GLU:HA	18:XR:65:ILE:HD11	1.90	0.54
25:YA:637:A:O5'	35:YP:116:GLY:HA2	2.07	0.54
25:YA:911:A:H2'	36:YQ:9:TYR:OH	2.07	0.54
35:YP:100:LEU:HB3	35:YP:106:LEU:HD13	1.88	0.54
45:YZ:120:ILE:HG23	45:YZ:171:ILE:HA	1.88	0.54
1:QA:1323:G:H2'	1:QA:1324:A:H8	1.70	0.54
25:RA:136:G:H1	25:RA:143:C:H42	1.55	0.54
25:RA:639:U:H2'	25:RA:640:C:C6	2.42	0.54
25:RA:1007:C:OP1	33:RN:35:ARG:NH1	2.41	0.54
1:XA:579:G:H5'	1:XA:728:A:H1'	1.88	0.54
1:XA:1151:A:H2'	1:XA:1152:A:C8	2.42	0.54
25:YA:862:G:O2'	26:YB:78:A:N3	2.39	0.54
25:YA:1570:A:H2'	25:YA:1571:A:C8	2.43	0.54
36:YQ:12:GLN:HG2	36:YQ:73:PRO:HD2	1.88	0.54
28:RE:34:VAL:HG12	28:RE:64:LYS:CE	2.38	0.54
44:RY:76:CYS:HB3	44:RY:96:ILE:CD1	2.36	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:1440:C:O2'	1:XA:1442:G:N2	2.41	0.54
3:XC:60:ALA:O	3:XC:63:ASN:ND2	2.40	0.54
13:XM:46:LYS:O	13:XM:48:LEU:N	2.40	0.54
25:YA:1914:C:OP1	25:YA:1915:U:OP2	2.24	0.54
25:YA:2211:G:H4'	25:YA:2212:A:OP2	2.08	0.54
25:YA:2795:G:H21	25:YA:2801:A:H62	1.56	0.54
31:YH:97:ARG:HB2	31:YH:104:GLU:HB2	1.90	0.54
36:YQ:66:ILE:HD13	36:YQ:66:ILE:H	1.72	0.54
39:YT:24:PRO:HA	39:YT:49:VAL:HG13	1.90	0.54
41:YV:7:THR:HG23	41:YV:22:VAL:HG21	1.90	0.54
45:YZ:10:ARG:NH1	45:YZ:26:GLY:O	2.41	0.54
47:Y1:23:LYS:HE3	47:Y1:28:GLY:HA3	1.88	0.54
1:QA:1423:G:OP1	34:RO:49:ARG:NH2	2.40	0.54
4:QD:78:LEU:HD22	4:QD:96:LEU:HB3	1.90	0.54
25:RA:722:A:H5'	25:RA:723:G:OP2	2.08	0.54
25:RA:2345:G:N3	25:RA:2381:C:H2'	2.23	0.54
34:RO:115:VAL:HG13	34:RO:121:VAL:HG21	1.90	0.54
35:RP:146:VAL:HG22	35:RP:147:LEU:H	1.72	0.54
37:RR:33:ARG:HD2	51:R5:55:ARG:HD2	1.88	0.54
44:RY:97:ARG:H	44:RY:97:ARG:HD3	1.72	0.54
1:XA:1123:A:H4'	10:XJ:36:GLY:HA3	1.90	0.54
4:XD:150:GLU:HG2	4:XD:151:LYS:H	1.72	0.54
20:XT:89:ARG:HB2	20:XT:104:LEU:HD21	1.90	0.54
25:YA:1007:C:OP1	33:YN:35:ARG:NH1	2.41	0.54
25:YA:1171:G:O2'	25:YA:1173:G:O5'	2.26	0.54
29:YF:39:TRP:O	29:YF:43:LYS:HG2	2.07	0.54
41:YV:35:LEU:O	41:YV:37:VAL:HG22	2.08	0.54
45:YZ:69:THR:HB	45:YZ:88:PHE:HB3	1.90	0.54
47:Y1:3:LYS:H	47:Y1:61:ARG:HH12	1.55	0.54
13:QM:118:ALA:CB	22:QV:29:G:H5'	2.38	0.53
25:RA:859:G:O2'	25:RA:860:U:P	2.66	0.53
25:RA:2748:A:H2'	25:RA:2749:A:O4'	2.08	0.53
26:RB:65:C:H41	26:RB:108:C:H2'	1.72	0.53
38:RS:99:LYS:O	38:RS:103:GLU:HG2	2.08	0.53
40:RU:97:ASP:OD2	40:RU:101:ARG:NH2	2.41	0.53
1:XA:1033:G:O2'	1:XA:1034:G:OP1	2.25	0.53
1:XA:1483:A:H1'	25:YA:1948:G:H1'	1.90	0.53
4:QD:33:MET:O	4:QD:34:GLU:HG2	2.08	0.53
25:RA:2111:C:C2	25:RA:2118:U:H1'	2.43	0.53
28:RE:58:ARG:O	28:RE:60:ASN:N	2.41	0.53
6:XF:82:ARG:O	6:XF:85:VAL:HG23	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:Y2:46:GLN:HB2	48:Y2:49:LYS:HZ1	1.73	0.53
3:QC:22:TRP:CG	3:QC:59:ARG:HD2	2.44	0.53
13:QM:118:ALA:HB1	22:QV:28:C:O3'	2.09	0.53
25:RA:1311:G:H5'	25:RA:1311:G:C8	2.44	0.53
25:RA:1862:G:H1	25:RA:1880:C:H42	1.54	0.53
28:RE:3:GLY:HA2	28:RE:198:VAL:O	2.08	0.53
31:RH:107:VAL:HB	31:RH:153:LYS:HG3	1.90	0.53
1:XA:580:U:H2'	1:XA:581:G:O4'	2.08	0.53
18:XR:18:ARG:HG2	18:XR:20:ALA:H	1.72	0.53
23:XX:12:A:H2'	23:XX:13:A:C8	2.42	0.53
24:XY:67:THR:HA	24:XY:73:ARG:HD3	1.89	0.53
24:XY:71:ASN:ND2	24:XY:90:ASP:OD1	2.41	0.53
42:YW:80:PRO:O	42:YW:100:THR:HG22	2.08	0.53
47:Y1:56:GLN:N	47:Y1:56:GLN:OE1	2.41	0.53
1:QA:250:A:H4'	1:QA:251:G:O5'	2.09	0.53
1:QA:482:A:H5'	1:QA:483:C:OP2	2.07	0.53
1:QA:1347:G:H4'	1:QA:1348:U:C6	2.44	0.53
3:QC:82:GLU:HG3	3:QC:83:ARG:H	1.74	0.53
25:RA:547:A:H2'	25:RA:548:A:C8	2.44	0.53
25:RA:1085:A:H2'	25:RA:1086:A:C8	2.44	0.53
25:RA:1416:G:H2'	25:RA:1417:C:C6	2.44	0.53
25:RA:2564:A:C2	25:RA:2647:U:H4'	2.43	0.53
25:RA:2746:U:H4'	31:RH:138:LYS:HG3	1.90	0.53
32:RI:143:SER:O	32:RI:144:VAL:CG1	2.57	0.53
45:RZ:155:LEU:O	45:RZ:156:LYS:CG	2.42	0.53
47:R1:82:LEU:HD11	47:R1:86:SER:HB3	1.91	0.53
1:XA:652:U:H1'	1:XA:653:A:C2	2.43	0.53
25:YA:1379:A:H4'	25:YA:1380:G:OP2	2.07	0.53
35:YP:125:VAL:HG13	35:YP:144:GLU:HB3	1.89	0.53
1:QA:982:U:H5''	14:QN:6:LEU:HD11	1.89	0.53
1:QA:1104:G:O3'	2:QB:111:ARG:NH2	2.42	0.53
1:QA:1166:G:N2	1:QA:1170:A:OP2	2.40	0.53
1:QA:1204:A:H2'	1:QA:1205:U:O5'	2.08	0.53
5:QE:6:PHE:O	5:QE:7:GLU:O	2.26	0.53
8:QH:86:ILE:HG13	8:QH:133:LEU:HD22	1.91	0.53
25:RA:74:A:H5''	25:RA:75:G:O4'	2.08	0.53
25:RA:1085:A:H2'	25:RA:1086:A:H8	1.73	0.53
25:RA:1490:A:O2'	27:RD:99:ASP:OD1	2.26	0.53
25:RA:2451:A:C2	56:Z7:76:PPU:CE2	2.91	0.53
25:RA:2740:A:H62	25:RA:2763:G:H2'	1.74	0.53
28:RE:62:PRO:C	28:RE:64:LYS:N	2.62	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:RG:60:LEU:O	30:RG:64:THR:HG22	2.08	0.53
40:RU:98:LEU:C	40:RU:100:VAL:H	2.11	0.53
1:XA:115:G:N2	1:XA:116:A:N6	2.57	0.53
1:XA:173:U:O2	1:XA:197:A:N6	2.42	0.53
18:XR:19:LYS:O	18:XR:21:LYS:N	2.40	0.53
25:YA:184:C:H2'	25:YA:185:U:C6	2.44	0.53
25:YA:1165:U:H2'	25:YA:1166:C:C6	2.43	0.53
28:YE:117:MET:O	28:YE:118:LYS:HB2	2.08	0.53
32:YI:141:LYS:HB3	32:YI:142:VAL:CG1	2.38	0.53
13:QM:11:ARG:O	13:QM:13:LYS:N	2.41	0.53
13:QM:46:LYS:O	13:QM:48:LEU:N	2.42	0.53
25:RA:517:C:OP1	51:R5:16:ARG:NH2	2.42	0.53
25:RA:1070:A:H5'	25:RA:1071:G:H5''	1.89	0.53
25:RA:1224:G:H5'	25:RA:1225:C:OP2	2.09	0.53
25:RA:1856:G:H2'	25:RA:1857:G:H5'	1.91	0.53
25:RA:2327:A:H2'	25:RA:2328:A:C8	2.43	0.53
1:XA:1299:A:C6	1:XA:1301:U:O2	2.62	0.53
6:XF:6:VAL:HG13	6:XF:90:VAL:HG22	1.89	0.53
9:XI:2:GLU:H	9:XI:20:ARG:HD3	1.73	0.53
10:XJ:49:VAL:O	10:XJ:60:ARG:HB2	2.08	0.53
25:YA:2529:G:O6	55:Y9:31:LYS:NZ	2.42	0.53
37:YR:37:THR:HG22	37:YR:39:PRO:HD2	1.89	0.53
40:YU:92:ARG:HG3	40:YU:95:LEU:H	1.73	0.53
2:QB:162:ILE:HD11	2:QB:184:VAL:HG22	1.90	0.53
6:QF:22:GLU:OE1	6:QF:84:ASN:ND2	2.37	0.53
25:RA:252:G:OP2	35:RP:50:ARG:NH2	2.42	0.53
25:RA:775:G:C4	25:RA:794:G:C8	2.97	0.53
25:RA:1427:A:H4'	25:RA:1428:C:O5'	2.08	0.53
1:XA:972:C:OP2	10:XJ:57:LYS:HE3	2.09	0.53
25:YA:1860:G:H1	25:YA:1882:C:H42	1.57	0.53
25:YA:2572:A:H62	28:YE:145:LYS:HG3	1.73	0.53
36:YQ:78:PRO:O	36:YQ:79:LEU:HG	2.08	0.53
46:Y0:17:GLN:O	46:Y0:19:LYS:NZ	2.42	0.53
54:Y8:14:VAL:HG11	54:Y8:22:VAL:HG12	1.91	0.53
1:QA:316:G:OP2	1:QA:351:G:O2'	2.26	0.53
1:QA:826:C:H2'	1:QA:827:U:C6	2.44	0.53
1:QA:1313:U:P	19:QS:6:LYS:HD3	2.49	0.53
3:QC:164:ARG:NH1	3:QC:166:GLU:OE1	2.39	0.53
8:QH:51:VAL:HG11	8:QH:60:ARG:HH11	1.74	0.53
10:QJ:40:LEU:HG	10:QJ:41:PRO:HD2	1.90	0.53
25:RA:137(A):G:H2'	25:RA:139:G:N7	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:RA:1300:U:H4'	25:RA:1301:A:C5'	2.38	0.53
25:RA:2287:A:H62	25:RA:2344:U:H3	1.56	0.53
27:RD:34:VAL:HG22	27:RD:35:LYS:HG3	1.89	0.53
28:RE:31:CYS:HB3	28:RE:49:LEU:HB3	1.90	0.53
50:R4:10:VAL:O	50:R4:25:TYR:HA	2.09	0.53
1:XA:939:G:H5''	7:XG:102:ARG:NH2	2.24	0.53
1:XA:1151:A:H2'	1:XA:1152:A:H8	1.74	0.53
25:YA:1336:A:P	43:YX:64:LYS:HZ2	2.32	0.53
25:YA:2016:U:C1'	51:Y5:6:VAL:HG11	2.39	0.53
25:YA:2402:C:HO2'	25:YA:2403:C:H5	1.57	0.53
32:YI:145:VAL:HG13	32:YI:145:VAL:O	2.09	0.53
35:YP:26:GLY:O	35:YP:28:GLY:N	2.42	0.53
4:QD:57:ARG:HB3	4:QD:206:PHE:HB2	1.90	0.53
11:QK:24:SER:OG	11:QK:25:TYR:N	2.42	0.53
25:RA:1025:G:H8	25:RA:1025:G:OP1	1.92	0.53
25:RA:1028:A:N6	25:RA:1125:G:H2'	2.24	0.53
25:RA:2294:C:P	38:RS:89:ARG:HH22	2.32	0.53
25:RA:2415:G:H4'	35:RP:67:MET:N	2.24	0.53
28:RE:131:ALA:HB1	28:RE:135:HIS:HE1	1.74	0.53
30:RG:53:LEU:HG	30:RG:90:LEU:HD21	1.90	0.53
31:RH:113:VAL:HG11	31:RH:151:ILE:HG21	1.91	0.53
35:RP:57:THR:C	35:RP:59:LEU:N	2.62	0.53
36:RQ:80:GLU:HG2	46:R0:7:LEU:HD21	1.91	0.53
45:RZ:118:GLN:HG3	45:RZ:174:VAL:H	1.73	0.53
1:XA:115:G:N2	1:XA:116:A:H62	2.07	0.53
1:XA:833:U:H2'	1:XA:834:C:C6	2.44	0.53
1:XA:1075:C:OP1	2:XB:179:LYS:HE2	2.09	0.53
10:XJ:56:HIS:O	10:XJ:58:ASP:N	2.41	0.53
25:YA:2031:A:C6	25:YA:2498:C:H1'	2.43	0.53
1:QA:520:A:N1	1:QA:536:C:H1'	2.24	0.53
1:QA:960:U:O2'	1:QA:1223:C:H4'	2.09	0.53
25:RA:653:A:H5''	25:RA:654:A:OP1	2.09	0.53
25:RA:1113:U:H2'	25:RA:1114:G:C8	2.44	0.53
28:RE:35:GLN:HG3	28:RE:64:LYS:CE	2.38	0.53
28:RE:37:ARG:N	28:RE:46:ALA:O	2.37	0.53
30:RG:55:LYS:HD2	30:RG:58:GLN:HE21	1.74	0.53
34:RO:113:LYS:O	34:RO:117:LEU:HB2	2.08	0.53
1:XA:7:G:H5'	1:XA:298:A:O4'	2.09	0.53
1:XA:17:U:H2'	1:XA:18:C:C6	2.43	0.53
1:XA:1299:A:H3'	1:XA:1299:A:C8	2.44	0.53
1:XA:1306:A:N6	1:XA:1331:G:H1'	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:XC:180:ALA:HB1	3:XC:182:ILE:HG13	1.90	0.53
6:XF:62:TRP:CH2	6:XF:64:GLN:HB2	2.44	0.53
25:YA:2086:U:H2'	25:YA:2087:G:C8	2.44	0.53
25:YA:2327:A:H2'	25:YA:2328:A:C8	2.44	0.53
25:YA:2343:C:HO2'	25:YA:2373:G:HO2'	1.56	0.53
1:QA:1147:C:H2'	9:QI:16:ARG:HD3	1.90	0.52
1:QA:1328:C:OP1	21:QU:21:TYR:OH	2.25	0.52
3:QC:52:LEU:HD12	3:QC:55:VAL:HG22	1.90	0.52
4:QD:119:GLN:HG2	4:QD:123:HIS:CE1	2.44	0.52
13:QM:4:ILE:HA	13:QM:57:ARG:HG2	1.90	0.52
25:RA:2772:C:H2'	25:RA:2773:C:C6	2.44	0.52
27:RD:148:GLU:HB2	27:RD:151:LYS:HD2	1.90	0.52
28:RE:50:GLY:CA	28:RE:74:PRO:HG2	2.39	0.52
28:RE:61:ARG:C	28:RE:63:LEU:H	2.13	0.52
45:RZ:58:VAL:HG12	45:RZ:60:GLU:HG2	1.90	0.52
1:XA:1126:U:O2	1:XA:1280:A:H5''	2.09	0.52
1:XA:1298:C:H2'	7:XG:114:ARG:HH12	1.74	0.52
1:XA:1380:U:H5	7:XG:3:ARG:HG2	1.74	0.52
13:XM:4:ILE:HG23	13:XM:5:ALA:H	1.74	0.52
13:XM:88:ARG:HG3	13:XM:98:VAL:HG13	1.90	0.52
40:YU:88:ILE:HA	41:YV:49:THR:O	2.09	0.52
1:QA:345:C:O2'	1:QA:346:G:C5'	2.57	0.52
19:QS:67:VAL:HG13	19:QS:68:GLY:H	1.73	0.52
21:QU:12:LYS:HB3	21:QU:22:ARG:HD2	1.91	0.52
25:RA:546:C:H2'	25:RA:547:A:O4'	2.09	0.52
27:RD:228:PRO:HD3	27:RD:235:GLY:CA	2.40	0.52
1:XA:452:A:OP1	16:XP:43:LYS:NZ	2.43	0.52
1:XA:1187:G:H21	14:XN:60:SER:HB3	1.74	0.52
25:YA:1754:C:H5''	39:YT:113:LYS:HE3	1.90	0.52
1:QA:518:C:H4'	1:QA:519:C:O5'	2.08	0.52
25:RA:1799:G:O2'	27:RD:181:GLU:OE2	2.25	0.52
35:RP:12:ALA:C	35:RP:14:LYS:H	2.12	0.52
35:RP:62:LEU:HD13	35:RP:62:LEU:N	2.24	0.52
48:R2:47:ASN:O	48:R2:49:LYS:N	2.36	0.52
1:XA:1000:A:H3'	1:XA:1001:G:H5''	1.91	0.52
25:YA:389:G:H1	35:YP:71:VAL:HG12	1.74	0.52
25:YA:2306:C:N4	25:YA:2307:G:O6	2.42	0.52
26:YB:60:C:H2'	26:YB:61:G:H8	1.73	0.52
1:QA:642:A:N3	8:QH:113:SER:OG	2.42	0.52
8:QH:41:ARG:NH2	8:QH:123:GLU:OE2	2.41	0.52
29:RF:66:PRO:O	29:RF:67:GLN:HB3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:RH:10:PRO:O	31:RH:11:VAL:HG12	2.08	0.52
45:RZ:91:LEU:HD12	45:RZ:130:PRO:HB3	1.90	0.52
1:XA:78:G:O6	1:XA:91:C:N4	2.43	0.52
25:YA:768:G:O2'	25:YA:1379:A:N6	2.42	0.52
25:YA:1416:G:HO2'	25:YA:1417:C:H5	1.53	0.52
25:YA:2875:C:O2'	39:YT:3:ARG:HG3	2.09	0.52
26:YB:60:C:H2'	26:YB:61:G:C8	2.44	0.52
31:YH:97:ARG:N	31:YH:104:GLU:O	2.40	0.52
41:YV:2:PHE:HE1	41:YV:4:ILE:HD13	1.74	0.52
52:Y6:28:ARG:HD2	52:Y6:29:ASN:CB	2.34	0.52
1:QA:76:G:H1	1:QA:93:U:H3	1.56	0.52
1:QA:1137:C:H4'	1:QA:1138:G:O5'	2.08	0.52
1:QA:1259:C:N4	1:QA:1260:C:O2	2.43	0.52
1:QA:1297:C:O2'	7:QG:114:ARG:NH2	2.42	0.52
2:QB:73:THR:HG21	2:QB:97:TRP:HB2	1.91	0.52
25:RA:128:C:H2'	25:RA:129:C:H6	1.73	0.52
30:RG:118:ARG:HB3	30:RG:181:ARG:HG3	1.91	0.52
45:RZ:7:ALA:HB2	45:RZ:59:LEU:CD1	2.34	0.52
1:XA:327:A:H3'	1:XA:328:C:H5''	1.91	0.52
25:YA:2296:U:OP2	38:YS:9:ARG:NH1	2.43	0.52
25:YA:2748:A:H2	25:YA:2754:U:H3	1.57	0.52
26:YB:51:G:N7	38:YS:62:LYS:NZ	2.49	0.52
27:YD:4:LYS:HE3	27:YD:20:ASP:HA	1.91	0.52
35:YP:63:PRO:HB3	54:Y8:13:ARG:HG3	1.90	0.52
45:YZ:94:GLU:HG3	45:YZ:129:SER:HB3	1.89	0.52
47:Y1:85:LEU:HD22	47:Y1:88:LYS:HG3	1.90	0.52
1:QA:1504:G:OP1	1:QA:1507:A:H4'	2.10	0.52
8:QH:34:GLU:OE1	8:QH:37:ARG:NH1	2.43	0.52
25:RA:252:G:P	35:RP:50:ARG:NH2	2.82	0.52
25:RA:686:G:N2	25:RA:788:A:H61	2.07	0.52
32:RI:129:THR:HA	32:RI:137:PRO:HA	1.92	0.52
1:XA:56:U:H2'	1:XA:57:G:C8	2.44	0.52
1:XA:382:A:H2'	1:XA:383:A:C8	2.45	0.52
25:YA:825:C:H1'	35:YP:55:ARG:HH21	1.74	0.52
25:YA:1405:U:H2'	25:YA:1406:U:C6	2.45	0.52
30:YG:67:LYS:H	50:Y4:6:HIS:CE1	2.27	0.52
32:YI:77:LEU:HA	32:YI:141:LYS:H	1.74	0.52
38:YS:67:ARG:O	38:YS:71:ARG:HG3	2.09	0.52
15:QO:64:ARG:HH11	15:QO:68:ARG:HH21	1.58	0.52
19:QS:16:LEU:HD11	19:QS:41:VAL:HG11	1.90	0.52
25:RA:708:C:H5'	25:RA:709:U:OP2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:RN:14:VAL:HA	33:RN:135:PRO:HD2	1.92	0.52
1:XA:41:G:H2'	1:XA:42:G:C8	2.45	0.52
1:XA:1296:C:H5''	1:XA:1297:C:OP2	2.10	0.52
25:YA:1096:A:C5	25:YA:1097:U:H1'	2.45	0.52
25:YA:2564:A:OP1	25:YA:2648:C:H4'	2.09	0.52
25:YA:2576:G:O2'	25:YA:2579:C:OP2	2.23	0.52
35:YP:11:GLY:O	35:YP:12:ALA:HB3	2.10	0.52
35:YP:61:ARG:O	35:YP:62:LEU:CB	2.53	0.52
40:YU:28:ARG:NH1	40:YU:38:THR:OG1	2.36	0.52
44:YY:95:LYS:HA	44:YY:101:LYS:HB2	1.91	0.52
54:Y8:40:GLU:H	54:Y8:43:GLN:HG3	1.75	0.52
1:QA:216:G:H2'	1:QA:217:C:C6	2.45	0.52
1:QA:1298:C:H4'	1:QA:1299:A:C8	2.44	0.52
2:QB:97:TRP:HZ2	2:QB:102:LEU:HD13	1.74	0.52
3:QC:95:THR:HG22	3:QC:97:LYS:H	1.75	0.52
4:QD:26:CYS:HA	4:QD:31:CYS:HB2	1.91	0.52
9:QI:45:ALA:O	9:QI:78:LYS:NZ	2.42	0.52
25:RA:529:A:H8	25:RA:530:G:C6	2.27	0.52
25:RA:2313:C:H2'	25:RA:2314:C:H6	1.75	0.52
25:RA:2712:U:H5	25:RA:2715:C:OP1	1.93	0.52
25:RA:2849:U:O2'	25:RA:2868:A:N3	2.42	0.52
44:RY:99:CYS:SG	44:RY:100:ALA:N	2.83	0.52
47:R1:56:GLN:OE1	47:R1:56:GLN:N	2.43	0.52
49:R3:7:LYS:HB2	49:R3:34:GLU:HG2	1.91	0.52
8:XH:29:SER:HB3	8:XH:32:LYS:HG3	1.91	0.52
10:XJ:44:VAL:HG22	10:XJ:66:ARG:HG2	1.92	0.52
13:XM:19:LEU:HD21	13:XM:56:LEU:HD11	1.91	0.52
19:XS:65:ASN:HA	50:Y4:55:ARG:HD2	1.91	0.52
25:YA:1222:C:H2'	25:YA:1223:C:H6	1.75	0.52
25:YA:1400:G:H2'	25:YA:1401:G:H8	1.75	0.52
1:QA:501:C:H1'	1:QA:549:C:H1'	1.92	0.52
1:QA:1002:G:N2	1:QA:1039:C:O2	2.43	0.52
1:QA:1288:A:H2'	1:QA:1289:A:H8	1.75	0.52
1:QA:1314:C:OP2	19:QS:6:LYS:HD2	2.10	0.52
1:QA:1499:A:H1'	1:QA:1520:G:H5'	1.92	0.52
16:QP:18:ARG:HD3	16:QP:35:LYS:HD2	1.92	0.52
17:QQ:66:SER:O	17:QQ:70:ARG:NH1	2.43	0.52
40:RU:81:HIS:HD2	40:RU:84:LYS:HD3	1.75	0.52
41:RV:4:ILE:HG22	41:RV:39:LEU:HD13	1.92	0.52
45:RZ:151:HIS:ND1	45:RZ:151:HIS:O	2.43	0.52
55:R9:9:ARG:NH1	55:R9:14:CYS:O	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:881:G:P	12:XL:12:ARG:HH22	2.32	0.52
1:XA:1287:A:H2'	1:XA:1288:A:C8	2.45	0.52
1:XA:1504:G:OP1	1:XA:1507:A:H4'	2.10	0.52
3:XC:20:SER:OG	3:XC:40:ARG:NH2	2.40	0.52
9:XI:17:VAL:HG11	9:XI:81:ILE:HA	1.92	0.52
25:YA:1112:G:H5'	31:YH:3:ARG:HE	1.74	0.52
32:YI:27:ARG:HD2	47:Y1:71:TYR:CE1	2.44	0.52
33:YN:34:LEU:O	33:YN:49:GLY:HA3	2.10	0.52
41:YV:87:HIS:NE2	41:YV:89:GLN:OE1	2.33	0.52
43:YX:3:THR:HA	43:YX:6:ASP:OD2	2.10	0.52
2:QB:118:LEU:HB3	2:QB:142:LEU:HD12	1.92	0.52
25:RA:177:G:OP2	25:RA:177:G:N2	2.35	0.52
25:RA:1384:A:N3	25:RA:1405:U:H1'	2.25	0.52
25:RA:1568:G:OP1	27:RD:63:ARG:NH1	2.38	0.52
28:RE:7:VAL:HG11	39:RT:1:MET:HE1	1.92	0.52
28:RE:70:ALA:O	28:RE:72:VAL:N	2.43	0.52
30:RG:47:LYS:HD3	30:RG:81:LYS:HB2	1.91	0.52
31:RH:10:PRO:O	31:RH:11:VAL:HG13	2.10	0.52
36:RQ:64:ILE:HD13	36:RQ:64:ILE:H	1.74	0.52
1:XA:1007:C:H3'	1:XA:1008:C:H5''	1.92	0.52
25:YA:1500:G:H21	27:YD:100:GLY:HA3	1.75	0.52
25:YA:2633:G:H1'	28:YE:62:PRO:CB	2.39	0.52
27:YD:8:PRO:HB3	27:YD:14:ARG:HB2	1.92	0.52
27:YD:76:PRO:HG2	27:YD:98:VAL:HG21	1.92	0.52
48:Y2:24:LEU:HD13	48:Y2:60:LEU:HD21	1.92	0.52
1:QA:1223:C:P	19:QS:78:ARG:HH21	2.33	0.51
23:QX:6:G:H2'	23:QX:7:G:C8	2.45	0.51
25:RA:857:C:H1'	46:R0:26:TYR:CE2	2.42	0.51
25:RA:1444:G:N2	25:RA:1548:C:C2	2.78	0.51
25:RA:2469:A:O2'	36:RQ:56:ARG:HG2	2.09	0.51
25:RA:2513:G:O2'	28:RE:154:LYS:NZ	2.34	0.51
9:XI:2:GLU:H	9:XI:20:ARG:HH11	1.57	0.51
25:YA:2105:C:H2'	25:YA:2106:G:C8	2.45	0.51
35:YP:64:LYS:HG2	54:Y8:25:MET:HB2	1.90	0.51
45:YZ:5:LEU:HD21	45:YZ:44:PHE:HA	1.92	0.51
1:QA:735:C:H2'	1:QA:736:C:H6	1.75	0.51
2:QB:69:LEU:HD23	2:QB:91:PRO:HB2	1.92	0.51
13:QM:88:ARG:HG3	13:QM:98:VAL:HG13	1.92	0.51
1:XA:534:U:H5'	1:XA:535:A:OP2	2.10	0.51
1:XA:538:G:H5''	12:XL:114:LYS:HB2	1.92	0.51
1:XA:1157:A:H62	1:XA:1178:G:N2	2.03	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:1251:A:H2'	1:XA:1252:A:C8	2.45	0.51
5:XE:33:VAL:HG21	5:XE:109:ILE:HG12	1.93	0.51
25:YA:2712:U:O2'	25:YA:2712(A):A:P	2.68	0.51
28:YE:24:THR:HG21	28:YE:188:VAL:HG12	1.92	0.51
37:YR:78:LYS:O	37:YR:82:GLU:HB3	2.10	0.51
1:QA:382:A:H2'	1:QA:383:A:C8	2.46	0.51
1:QA:1053:G:HO2'	1:QA:1199:U:H5	1.57	0.51
25:RA:1414:G:C4	25:RA:1415:U:C5	2.98	0.51
25:RA:1561:G:H2'	25:RA:1562:A:C8	2.45	0.51
33:RN:125:GLY:HA3	33:RN:126:PRO:O	2.10	0.51
45:RZ:149:SER:OG	45:RZ:150:LEU:N	2.43	0.51
1:XA:246:A:N6	1:XA:281:G:H1'	2.25	0.51
1:XA:620:C:C2	4:XD:135:LEU:HG	2.46	0.51
1:XA:1178:G:H5'	9:XI:93:ARG:NH2	2.24	0.51
1:XA:1299:A:C5	1:XA:1301:U:C2	2.98	0.51
1:XA:1427:U:H2'	1:XA:1428:A:C8	2.46	0.51
5:XE:48:ALA:HB2	5:XE:57:LYS:HD3	1.91	0.51
22:XV:61:C:H2'	22:XV:62:C:H6	1.75	0.51
25:YA:6:A:H8	25:YA:6:A:O5'	1.94	0.51
25:YA:1544:C:O2'	25:YA:1545:A:OP1	2.25	0.51
25:YA:1587:A:H2'	25:YA:1588:C:H6	1.72	0.51
25:YA:2016:U:C1'	51:Y5:6:VAL:CG1	2.89	0.51
25:RA:2296:U:OP2	38:RS:9:ARG:NH1	2.43	0.51
25:RA:2777:G:OP2	25:RA:2781:A:O2'	2.20	0.51
30:RG:15:VAL:HG21	30:RG:176:LEU:HD23	1.93	0.51
49:R3:59:VAL:HG12	49:R3:60:GLU:H	1.75	0.51
25:YA:1225:C:O3'	41:YV:85:LYS:HD3	2.11	0.51
25:YA:1861:G:H1	25:YA:1881:C:H42	1.58	0.51
25:YA:2749:A:N1	25:YA:2750:A:N6	2.55	0.51
30:YG:60:LEU:O	30:YG:64:THR:HG22	2.09	0.51
30:YG:151:ALA:HB3	30:YG:153:ARG:NH1	2.25	0.51
54:Y8:60:LEU:O	54:Y8:62:LEU:N	2.44	0.51
1:QA:20:U:H2'	1:QA:21:G:O4'	2.11	0.51
1:QA:738:C:H5''	6:QF:69:GLU:HB2	1.91	0.51
2:QB:51:LEU:HD23	2:QB:201:ILE:HD12	1.93	0.51
25:RA:643:A:N1	25:RA:2369:A:O2'	2.38	0.51
25:RA:2124:G:H1	25:RA:2174:C:H42	1.58	0.51
25:RA:2811:G:OP1	28:RE:61:ARG:HG2	2.10	0.51
28:RE:119:ARG:HG2	28:RE:160:TYR:HB2	1.93	0.51
37:RR:38:VAL:HG22	37:RR:112:ALA:HB2	1.92	0.51
41:RV:71:LEU:HD11	41:RV:83:ARG:NE	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:RX:63:LYS:HA	43:RX:72:LYS:HA	1.92	0.51
44:RY:95:LYS:NZ	44:RY:99:CYS:O	2.42	0.51
1:XA:1127:G:H1'	1:XA:1280:A:C6	2.45	0.51
25:YA:1313:U:H2'	25:YA:1610:A:C2	2.45	0.51
25:YA:1688:U:H1'	25:YA:1701:A:C6	2.46	0.51
25:YA:2420:C:OP1	54:Y8:34:TRP:HB3	2.11	0.51
28:YE:66:HIS:C	28:YE:68:ALA:H	2.14	0.51
29:YF:132:VAL:C	29:YF:134:GLY:H	2.13	0.51
1:QA:1198:G:H2'	1:QA:1199:U:O4'	2.11	0.51
3:QC:150:LYS:HE2	3:QC:152:ILE:HD11	1.92	0.51
20:QT:40:ALA:HB2	20:QT:55:ILE:HG22	1.93	0.51
23:QX:19:A2M:H4'	23:QX:20:OMC:O4'	2.11	0.51
25:RA:859:G:H2'	25:RA:916:G:O6	2.10	0.51
25:RA:1341:U:H1'	25:RA:1342:A:OP1	2.11	0.51
25:RA:1963:U:H3'	25:RA:1963:U:O2	2.10	0.51
25:RA:2144:U:O2'	25:RA:2145:C:O5'	2.24	0.51
31:RH:137:ASP:OD1	31:RH:138:LYS:N	2.39	0.51
1:XA:1412:C:H2'	1:XA:1413:A:H8	1.76	0.51
25:YA:1930:G:O2'	25:YA:1931:U:OP2	2.28	0.51
28:YE:101:ARG:O	28:YE:201:THR:OG1	2.29	0.51
2:QB:9:GLU:O	2:QB:12:GLU:HG3	2.10	0.51
4:QD:33:MET:HE3	4:QD:37:PRO:HA	1.93	0.51
25:RA:2211:G:H2'	25:RA:2211:G:N3	2.25	0.51
25:RA:2572:A:N7	28:RE:145:LYS:HG3	2.25	0.51
25:RA:2824:C:H2'	25:RA:2825:C:O4'	2.10	0.51
26:RB:14:U:H4'	26:RB:70:C:O2	2.11	0.51
32:RI:77:LEU:HA	32:RI:140:LEU:HD12	1.92	0.51
39:RT:54:ARG:HA	39:RT:59:THR:HB	1.92	0.51
45:RZ:155:LEU:C	45:RZ:156:LYS:CG	2.68	0.51
1:XA:1157:A:C4	1:XA:1181:G:N1	2.78	0.51
9:XI:17:VAL:HG22	9:XI:63:ILE:HG12	1.92	0.51
12:XL:27:LEU:HD11	12:XL:85:ILE:HG22	1.93	0.51
25:YA:363(B):G:H2'	25:YA:363(C):G:H8	1.75	0.51
25:YA:1688:U:O2	25:YA:1700:A:H5'	2.11	0.51
30:YG:11:TYR:HA	30:YG:15:VAL:HB	1.92	0.51
31:YH:33:LEU:HD21	31:YH:140:LYS:HE2	1.92	0.51
35:YP:19:VAL:HG13	35:YP:21:ARG:H	1.76	0.51
37:YR:97:VAL:HG22	37:YR:114:VAL:HG22	1.93	0.51
12:QL:59:ARG:HA	12:QL:65:GLU:HA	1.91	0.51
25:RA:1542:G:P	25:RA:1543:A:H3'	2.50	0.51
39:RT:26:ASP:O	39:RT:49:VAL:HG12	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:R1:44:PRO:O	47:R1:46:LEU:N	2.43	0.51
52:R6:12:GLU:HB2	52:R6:22:ALA:HB3	1.92	0.51
1:XA:530:G:C2	23:XX:21:A2M:H2	2.45	0.51
2:XB:72:GLY:HA3	2:XB:81:VAL:HG21	1.93	0.51
19:XS:65:ASN:OD1	50:Y4:55:ARG:NH1	2.44	0.51
20:XT:48:LYS:HB3	20:XT:51:GLU:HG3	1.93	0.51
25:YA:876:C:H2'	25:YA:877:U:O4'	2.10	0.51
25:YA:1225:C:H4'	41:YV:85:LYS:CB	2.36	0.51
25:YA:1445:C:H2'	25:YA:1446:C:H6	1.75	0.51
25:YA:1870:C:H2'	25:YA:1871:A:O4'	2.11	0.51
42:YW:25:ARG:NH2	42:YW:74:ALA:O	2.44	0.51
49:Y3:6:VAL:HG13	49:Y3:54:VAL:HG11	1.93	0.51
1:QA:1008:C:H42	1:QA:1021:G:H1	1.57	0.51
20:QT:10:LEU:HD22	20:QT:11:SER:H	1.74	0.51
25:RA:388:G:H5'	47:R1:25:LYS:HB2	1.93	0.51
25:RA:877:U:H2'	25:RA:878:A:H5''	1.92	0.51
32:RI:143:SER:C	32:RI:144:VAL:HG22	2.16	0.51
39:RT:62:THR:HG22	39:RT:75:ILE:HG23	1.92	0.51
40:RU:95:LEU:C	40:RU:97:ASP:H	2.14	0.51
21:XU:12:LYS:HG2	21:XU:22:ARG:HB3	1.92	0.51
25:YA:993:G:OP1	40:YU:50:ARG:NH2	2.35	0.51
25:YA:2245:U:H5'	25:YA:2246:G:H5'	1.93	0.51
25:YA:2584:U:H5''	56:Z6:76:PPU:H92	1.91	0.51
54:Y8:33:ASN:HB2	54:Y8:36:LYS:HD3	1.92	0.51
1:QA:313:A:H2'	1:QA:314:C:C6	2.46	0.51
4:QD:9:CYS:HA	4:QD:12:CYS:HB2	1.93	0.51
8:QH:20:TYR:CE2	8:QH:75:ARG:HB3	2.46	0.51
16:QP:53:VAL:HG12	16:QP:79:VAL:HG22	1.92	0.51
25:RA:990:A:C6	25:RA:1186:G:H1'	2.46	0.51
25:RA:1415:U:O2	25:RA:1415:U:H2'	2.11	0.51
28:RE:33:VAL:HG12	28:RE:90:THR:H	1.74	0.51
30:RG:131:TYR:HB3	30:RG:159:VAL:HG13	1.92	0.51
32:RI:101:LEU:HD23	32:RI:101:LEU:H	1.76	0.51
44:RY:69:ALA:O	44:RY:72:VAL:HG22	2.11	0.51
44:RY:76:CYS:C	44:RY:78:ALA:H	2.14	0.51
9:XI:37:PHE:HE2	9:XI:70:LYS:HG3	1.76	0.51
25:YA:1681:G:HO2'	25:YA:1762:A:HO2'	1.58	0.51
26:YB:15:A:H5'	26:YB:16:G:C8	2.46	0.51
26:YB:42:C:O2	30:YG:93:THR:N	2.40	0.51
27:YD:43:ARG:HH11	27:YD:44:ASN:ND2	2.08	0.51
36:YQ:115:MET:HG3	36:YQ:131:ILE:HG21	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:YW:78:GLU:OE1	42:YW:99:ARG:NH1	2.41	0.51
47:Y1:94:LEU:HD23	47:Y1:94:LEU:H	1.76	0.51
54:Y8:31:HIS:CG	54:Y8:32:LEU:H	2.27	0.51
1:QA:591:U:OP2	8:QH:30:ARG:NH1	2.43	0.50
1:QA:1358:U:OP1	14:QN:35:ARG:HG2	2.10	0.50
7:QG:20:ASP:OD2	7:QG:23:VAL:N	2.45	0.50
25:RA:1283:G:N2	25:RA:1286:A:OP2	2.41	0.50
25:RA:1476:C:H2'	25:RA:1477:A:C8	2.46	0.50
25:RA:2116:G:N2	25:RA:2165:G:O6	2.44	0.50
31:RH:126:PRO:HB2	31:RH:127:GLU:HA	1.94	0.50
6:XF:76:ALA:O	6:XF:80:ARG:HG3	2.11	0.50
25:YA:2128:C:N4	25:YA:2159:G:O6	2.44	0.50
36:YQ:19:GLY:H	36:YQ:98:LYS:NZ	2.08	0.50
43:YX:36:LYS:HG3	43:YX:54:VAL:HB	1.92	0.50
1:QA:1001:G:H4'	1:QA:1001:G:OP1	2.11	0.50
9:QI:82:ALA:HB1	9:QI:96:LEU:HD21	1.93	0.50
10:QJ:49:VAL:O	10:QJ:60:ARG:HB2	2.12	0.50
25:RA:754:C:H2'	25:RA:755:C:C6	2.46	0.50
25:RA:774:A:N3	25:RA:774:A:C2'	2.73	0.50
25:RA:1259:G:H2'	25:RA:1260:G:C8	2.46	0.50
25:RA:1414:G:H3'	25:RA:1415:U:H6	1.76	0.50
25:RA:2827:C:H5'	25:RA:2828:C:OP2	2.12	0.50
28:RE:68:ALA:O	28:RE:70:ALA:N	2.44	0.50
39:RT:107:ASP:N	39:RT:107:ASP:OD1	2.43	0.50
41:RV:49:THR:HG22	41:RV:50:PRO:N	2.27	0.50
44:RY:48:ALA:O	44:RY:50:ARG:N	2.43	0.50
1:XA:503:C:OP2	12:XL:116:SER:HB3	2.11	0.50
9:XI:28:VAL:HG22	9:XI:29:ASN:N	2.26	0.50
10:XJ:79:ARG:HD3	10:XJ:79:ARG:H	1.76	0.50
23:XX:12:A:H2'	23:XX:13:A:N7	2.27	0.50
25:YA:859:G:O2'	25:YA:860:U:P	2.69	0.50
31:YH:7:LEU:HD13	31:YH:69:ARG:CB	2.41	0.50
1:QA:1150:U:O4	1:QA:1151:A:N6	2.44	0.50
1:QA:1493:A:H1'	24:QY:54:HIS:HA	1.92	0.50
2:QB:18:GLY:HA2	2:QB:40:HIS:O	2.11	0.50
11:QK:20:TYR:CE2	11:QK:83:ILE:HD12	2.46	0.50
23:QX:9:G:H4'	23:QX:10:G:OP2	2.12	0.50
31:RH:10:PRO:C	31:RH:11:VAL:CG1	2.79	0.50
36:RQ:34:LEU:HB2	36:RQ:118:LEU:HD22	1.92	0.50
40:RU:74:LEU:HD13	40:RU:79:PHE:HB2	1.92	0.50
45:RZ:5:LEU:HB3	45:RZ:59:LEU:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:1305:G:N2	1:XA:1331:G:H2'	2.24	0.50
2:XB:132:LYS:O	2:XB:134:GLU:N	2.44	0.50
3:XC:23:TYR:HD2	10:XJ:10:GLY:HA2	1.76	0.50
9:XI:27:THR:HG21	9:XI:32:ASP:HA	1.94	0.50
13:XM:8:GLU:O	13:XM:8:GLU:HG3	2.10	0.50
13:XM:10:PRO:HG2	13:XM:18:ALA:CA	2.40	0.50
41:YV:62:LEU:HB3	41:YV:93:GLU:O	2.12	0.50
1:QA:404:U:H5'	4:QD:122:ARG:HD2	1.93	0.50
1:QA:1000:A:H3'	1:QA:1001:G:H5''	1.93	0.50
1:QA:1033:G:HO2'	1:QA:1034:G:P	2.32	0.50
5:QE:147:ASP:OD2	5:QE:147:ASP:N	2.24	0.50
10:QJ:53:PRO:HA	14:QN:42:ILE:HD12	1.93	0.50
19:QS:45:VAL:HG13	19:QS:62:ILE:HG22	1.94	0.50
25:RA:729:G:C5	27:RD:208:LYS:HB2	2.46	0.50
25:RA:1980:G:O2'	25:RA:1982:C:OP2	2.29	0.50
25:RA:2876:G:O2'	39:RT:3:ARG:NH1	2.45	0.50
30:RG:107:LEU:HA	30:RG:111:LEU:HD12	1.93	0.50
41:RV:5:VAL:HB	41:RV:37:VAL:HG21	1.93	0.50
1:XA:327:A:O2'	1:XA:328:C:O4'	2.27	0.50
1:XA:776:G:HO2'	1:XA:777:A:H8	1.58	0.50
1:XA:1183:A:O2'	1:XA:1184:G:OP1	2.30	0.50
11:XK:20:TYR:CE2	11:XK:83:ILE:HD12	2.47	0.50
13:XM:9:ILE:HG12	13:XM:10:PRO:N	2.26	0.50
21:XU:9:ARG:HH21	21:XU:10:ARG:HE	1.59	0.50
30:YG:36:LYS:HD2	30:YG:160:VAL:HG21	1.93	0.50
45:YZ:74:VAL:HG13	45:YZ:86:VAL:HG22	1.94	0.50
52:Y6:8:LYS:HA	52:Y6:27:LYS:HA	1.93	0.50
1:QA:1412:C:H2'	1:QA:1413:A:C8	2.47	0.50
19:QS:21:GLU:HG3	19:QS:22:LEU:HD22	1.93	0.50
24:QY:55:PRO:HD3	24:QY:64:TRP:CZ3	2.47	0.50
25:RA:1062:G:H2'	25:RA:1063:G:H8	1.76	0.50
25:RA:1364:G:H5'	47:R1:3:LYS:HE3	1.94	0.50
25:RA:1548:C:H2'	25:RA:1549:C:C6	2.46	0.50
26:RB:56:G:H5'	30:RG:27:ASN:HD21	1.77	0.50
33:RN:73:THR:HB	33:RN:82:LEU:HD11	1.94	0.50
2:XB:48:MET:HA	2:XB:51:LEU:HD12	1.94	0.50
4:XD:127:THR:HG23	4:XD:147:ALA:HB3	1.92	0.50
5:XE:82:VAL:HG21	5:XE:138:ALA:HA	1.93	0.50
10:XJ:9:ARG:HB2	10:XJ:95:GLU:HB3	1.92	0.50
13:XM:10:PRO:CG	13:XM:18:ALA:CA	2.86	0.50
1:QA:648:A:H2'	1:QA:649:G:H8	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:QA:765:G:N2	1:QA:813:U:OP2	2.41	0.50
1:QA:1227:A:N3	13:QM:117:VAL:HG21	2.26	0.50
20:QT:89:ARG:HB2	20:QT:104:LEU:HD21	1.94	0.50
25:RA:2070:G:H2'	25:RA:2071:A:C8	2.46	0.50
25:RA:2106:G:N2	25:RA:2183:C:O2	2.45	0.50
25:RA:2676:C:OP1	34:RO:31:LYS:NZ	2.41	0.50
28:RE:151:TYR:HD2	28:RE:154:LYS:HZ2	1.58	0.50
31:RH:7:LEU:HD12	31:RH:65:HIS:CE1	2.47	0.50
44:RY:73:ARG:HH21	44:RY:82:PRO:HD3	1.77	0.50
1:XA:530:G:O2'	24:XY:70:ALA:N	2.39	0.50
13:XM:9:ILE:HG12	13:XM:10:PRO:HD2	1.91	0.50
13:XM:73:GLU:O	13:XM:77:ASN:N	2.43	0.50
18:XR:40:LEU:HB3	18:XR:79:LEU:HD11	1.93	0.50
25:YA:1854:A:H62	25:YA:1888:G:H8	1.60	0.50
25:YA:2059:A:H5'	25:YA:2060:A:OP2	2.11	0.50
28:YE:116:VAL:O	28:YE:117:MET:HB3	2.12	0.50
33:YN:26:LEU:O	33:YN:30:ILE:HG13	2.11	0.50
52:Y6:23:THR:OG1	54:Y8:34:TRP:O	2.29	0.50
1:QA:1034:G:H2'	1:QA:1035:A:C8	2.46	0.50
25:RA:1413:G:N2	25:RA:1414:G:N9	2.60	0.50
25:RA:1999:C:H5''	25:RA:2723:C:O2'	2.12	0.50
31:RH:54:ARG:H	31:RH:54:ARG:HD3	1.77	0.50
39:RT:20:PRO:HD2	39:RT:86:ILE:HG23	1.94	0.50
54:R8:34:TRP:O	54:R8:36:LYS:HG3	2.12	0.50
4:XD:162:LEU:HD13	4:XD:181:MET:HG2	1.92	0.50
11:XK:10:VAL:HG12	11:XK:11:LYS:HG2	1.94	0.50
25:YA:631:A:OP2	54:Y8:47:LYS:NZ	2.44	0.50
25:YA:1190:G:OP1	35:YP:30:THR:OG1	2.29	0.50
25:YA:1999:C:H5''	25:YA:2723:C:O2'	2.11	0.50
27:YD:267:SER:O	27:YD:269:PHE:N	2.45	0.50
28:YE:120:TRP:CD1	28:YE:155:LYS:HB3	2.47	0.50
33:YN:12:ARG:O	33:YN:50:ASP:HB2	2.11	0.50
40:YU:113:ALA:O	40:YU:117:GLN:HB2	2.12	0.50
19:QS:40:ILE:HG21	19:QS:66:MET:O	2.12	0.50
25:RA:511:U:H3'	25:RA:512:G:H5''	1.94	0.50
25:RA:1405:U:H2'	25:RA:1406:U:C6	2.47	0.50
30:RG:47:LYS:HG3	30:RG:82:LEU:HG	1.93	0.50
31:RH:10:PRO:O	31:RH:11:VAL:O	2.30	0.50
43:RX:63:LYS:H	43:RX:63:LYS:NZ	2.10	0.50
45:RZ:45:ASP:O	45:RZ:49:ARG:HG2	2.12	0.50
54:R8:6:THR:HG21	54:R8:63:PRO:HD3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:769:G:H4'	1:XA:1513:A:H4'	1.92	0.50
1:XA:1001:G:OP1	1:XA:1001:G:H4'	2.11	0.50
1:XA:1156:G:C3'	1:XA:1157:A:H5''	2.41	0.50
2:XB:17:PHE:HA	2:XB:204:ASN:OD1	2.12	0.50
7:XG:76:ARG:HD2	7:XG:89:MET:HG3	1.94	0.50
11:XK:48:ILE:HD11	11:XK:64:ALA:HA	1.94	0.50
19:XS:40:ILE:HG12	19:XS:69:HIS:O	2.12	0.50
25:YA:444:C:H2'	25:YA:445:C:H6	1.76	0.50
25:YA:491:G:H2'	25:YA:492:A:C8	2.47	0.50
25:YA:928:G:H3'	25:YA:929:G:H8	1.77	0.50
25:YA:1012:U:O4	33:YN:25:ARG:HA	2.12	0.50
25:YA:1394:U:H4'	25:YA:1603:A:H4'	1.93	0.50
25:YA:2067:G:O2'	25:YA:2069:G:H5''	2.12	0.50
25:YA:2109:U:H2'	25:YA:2110:G:H8	1.76	0.50
25:YA:2692:C:H2'	25:YA:2693:A:C8	2.45	0.50
27:YD:109:ASP:N	27:YD:196:VAL:O	2.44	0.50
27:YD:267:SER:C	27:YD:269:PHE:H	2.15	0.50
35:YP:52:GLU:HG2	35:YP:55:ARG:HH11	1.77	0.50
35:YP:60:MET:C	35:YP:61:ARG:HG2	2.32	0.50
35:YP:138:LEU:HD11	35:YP:144:GLU:HG2	1.94	0.50
1:QA:1032(B):G:O2'	25:YA:2115:G:OP1	2.29	0.50
1:QA:1204:A:C2'	1:QA:1205:U:O5'	2.60	0.50
25:RA:273(F):C:H3'	25:RA:274:G:H5''	1.93	0.50
25:RA:969:U:H2'	25:RA:970:C:C6	2.46	0.50
26:RB:73:A:H2	45:RZ:34:ASN:HD22	1.59	0.50
44:RY:75:ILE:CG1	44:RY:80:GLY:N	2.62	0.50
45:RZ:157:LEU:O	45:RZ:158:PRO:O	2.30	0.50
1:XA:129(A):G:C6	1:XA:188:U:H4'	2.47	0.50
10:XJ:38:ILE:HB	10:XJ:71:LEU:HB3	1.94	0.50
25:YA:451:C:H4'	29:YF:52:LYS:NZ	2.27	0.50
25:YA:746:A:C5	25:YA:2611:U:H5''	2.47	0.50
25:YA:999:U:C2'	25:YA:1000:A:H5''	2.42	0.50
25:YA:1711:C:H2'	25:YA:1712:C:C6	2.47	0.50
25:YA:1754:C:OP1	39:YT:96:ARG:NH1	2.45	0.50
26:YB:80:U:H2'	26:YB:81:G:N2	2.26	0.50
40:YU:92:ARG:HH22	41:YV:10:LYS:CA	2.25	0.50
44:YY:52:SER:HA	44:YY:56:PRO:HA	1.94	0.50
47:Y1:7:ILE:HD13	47:Y1:69:LYS:HB3	1.92	0.50
1:QA:1322:C:H5''	13:QM:100:GLY:HA3	1.94	0.49
2:QB:103:THR:HA	2:QB:180:LEU:HD11	1.93	0.49
25:RA:918:A:N3	26:RB:80:U:O2'	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:RG:43:LEU:HD22	30:RG:90:LEU:HD23	1.94	0.49
34:RO:104:ARG:HG2	34:RO:121:VAL:HG12	1.94	0.49
41:RV:2:PHE:CD2	41:RV:42:GLY:HA2	2.46	0.49
1:XA:714:G:H2'	1:XA:715:A:C8	2.47	0.49
4:XD:111:ALA:HB2	4:XD:120:LEU:HD12	1.94	0.49
6:XF:83:ASP:OD2	6:XF:83:ASP:N	2.45	0.49
25:YA:2210:G:H3'	25:YA:2211:G:C8	2.47	0.49
25:YA:2393:A:H2'	25:YA:2394:C:O4'	2.11	0.49
29:YF:83:PHE:O	29:YF:85:GLY:N	2.45	0.49
38:YS:71:ARG:HH12	38:YS:106:ARG:HH21	1.60	0.49
45:YZ:124:ILE:HD11	45:YZ:165:VAL:HG11	1.94	0.49
5:QE:79:GLU:HG3	5:QE:93:PRO:HD2	1.94	0.49
10:QJ:48:THR:HA	10:QJ:62:HIS:HB3	1.93	0.49
25:RA:654(R):C:HO2'	25:RA:654(S):G:P	2.35	0.49
25:RA:764:A:H5''	27:RD:210:GLY:HA2	1.93	0.49
26:RB:34:U:H5''	26:RB:35:U:OP1	2.12	0.49
31:RH:6:ARG:HB3	31:RH:54:ARG:HH12	1.77	0.49
31:RH:147:ASN:O	31:RH:151:ILE:HG12	2.12	0.49
45:RZ:165:VAL:HG13	45:RZ:166:SER:H	1.76	0.49
52:R6:15:GLU:OE1	52:R6:18:ARG:HB2	2.12	0.49
1:XA:413:G:N2	1:XA:428:G:H1'	2.27	0.49
1:XA:960:U:H4'	1:XA:961:U:C5'	2.42	0.49
1:XA:1299:A:N6	1:XA:1301:U:H3	2.10	0.49
2:XB:82:ARG:O	2:XB:86:GLU:HG2	2.12	0.49
2:XB:146:GLN:O	2:XB:150:SER:HB3	2.12	0.49
7:XG:20:ASP:OD1	7:XG:23:VAL:HB	2.12	0.49
25:YA:2183:C:H2'	25:YA:2184:G:C8	2.47	0.49
25:YA:2320:A:H2'	25:YA:2320:A:N3	2.27	0.49
25:YA:2591:C:H2'	25:YA:2592:G:C8	2.47	0.49
44:YY:62:GLU:CD	44:YY:63:LYS:H	2.15	0.49
45:YZ:126:VAL:HG12	45:YZ:163:LEU:HA	1.94	0.49
46:Y0:3:HIS:ND1	46:Y0:3:HIS:O	2.43	0.49
52:Y6:6:ARG:HG2	52:Y6:8:LYS:N	2.24	0.49
52:Y6:28:ARG:CB	52:Y6:31:PRO:HD2	2.41	0.49
1:QA:1278:U:H5'	1:QA:1279:A:O4'	2.13	0.49
5:QE:87:SER:HB3	5:QE:131:ILE:HD13	1.94	0.49
7:QG:113:GLU:HB2	7:QG:119:ARG:HG2	1.94	0.49
25:RA:460:A:H2'	25:RA:461:C:O4'	2.12	0.49
25:RA:636:G:N7	35:RP:113:LYS:NZ	2.42	0.49
28:RE:35:GLN:HG3	28:RE:64:LYS:HZ2	1.72	0.49
30:RG:114:ILE:HD11	30:RG:140:ILE:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:RG:135:LEU:HD23	30:RG:140:ILE:HD11	1.93	0.49
31:RH:153:LYS:HB3	31:RH:161:GLY:HA2	1.94	0.49
41:RV:76:LYS:HB3	41:RV:79:VAL:HG23	1.94	0.49
1:XA:502:G:OP1	12:XL:118:SER:HB3	2.12	0.49
1:XA:881:G:OP2	12:XL:12:ARG:NH2	2.41	0.49
25:YA:1141:U:H4'	25:YA:1142(A):A:O4'	2.12	0.49
25:YA:1149:G:H2'	25:YA:1150:C:C6	2.47	0.49
25:YA:2305:A:H2'	25:YA:2306:C:H5''	1.94	0.49
27:YD:65:ILE:HD11	27:YD:67:PHE:CZ	2.47	0.49
30:YG:145:THR:O	30:YG:147:ASP:N	2.43	0.49
31:YH:105:LEU:HD12	31:YH:113:VAL:HB	1.94	0.49
54:Y8:6:THR:OG1	54:Y8:6:THR:O	2.26	0.49
1:QA:345:C:O2'	1:QA:346:G:O5'	2.30	0.49
3:QC:116:VAL:HG21	3:QC:202:ILE:HD11	1.93	0.49
6:QF:42:GLU:OE2	6:QF:59:TYR:OH	2.29	0.49
25:RA:710:G:H2'	25:RA:711:G:H8	1.77	0.49
25:RA:907:U:OP1	36:RQ:24:GLY:N	2.34	0.49
25:RA:1645:G:H5''	25:RA:1646:C:H5'	1.94	0.49
25:RA:1754:C:P	39:RT:96:ARG:HH12	2.36	0.49
28:RE:32:PRO:HG3	28:RE:70:ALA:HB2	1.94	0.49
31:RH:94:TYR:CD2	31:RH:107:VAL:HG12	2.47	0.49
39:RT:26:ASP:CB	39:RT:91:ARG:HA	2.42	0.49
40:RU:92:ARG:HG3	40:RU:95:LEU:H	1.76	0.49
41:RV:48:GLY:O	41:RV:49:THR:O	2.30	0.49
53:R7:24:THR:HG23	53:R7:27:GLY:HA3	1.95	0.49
15:XO:39:LEU:HD12	15:XO:56:LEU:HB2	1.94	0.49
25:YA:990:A:C6	25:YA:1186:G:H1'	2.47	0.49
25:YA:2046:G:H5'	51:Y5:19:ARG:HG3	1.94	0.49
25:YA:2148:G:H2'	25:YA:2149:G:C8	2.48	0.49
25:YA:2887:U:H2'	25:YA:2888:C:H6	1.78	0.49
27:YD:43:ARG:HB3	27:YD:54:ARG:HB2	1.94	0.49
52:Y6:7:ILE:HD13	52:Y6:7:ILE:H	1.78	0.49
1:QA:6:G:H4'	1:QA:298:A:H4'	1.93	0.49
2:QB:112:VAL:HG22	2:QB:149:LEU:HD13	1.95	0.49
24:QY:41:THR:N	24:QY:45:GLU:OE1	2.41	0.49
28:RE:62:PRO:C	28:RE:64:LYS:H	2.15	0.49
37:RR:37:THR:HG22	37:RR:39:PRO:HD2	1.95	0.49
1:XA:321:A:C8	1:XA:328:C:C2	3.01	0.49
1:XA:404:U:H2'	1:XA:405:U:C6	2.48	0.49
1:XA:868:C:H2'	1:XA:869:G:O4'	2.12	0.49
19:XS:40:ILE:HG21	19:XS:66:MET:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:XV:20:U:H5'	22:XV:21:A:OP2	2.13	0.49
25:YA:740:U:H2'	25:YA:741:G:C8	2.47	0.49
25:YA:900:A:H3'	25:YA:901:A:H8	1.77	0.49
25:YA:1025:G:H8	25:YA:1025:G:OP1	1.95	0.49
25:YA:2690:C:OP2	37:YR:17:ARG:NH1	2.43	0.49
25:YA:2776:A:OP1	25:YA:2776:A:H3'	2.12	0.49
28:YE:36:ARG:HH21	28:YE:88:GLY:HA3	1.77	0.49
44:YY:87:LYS:HB3	44:YY:92:ASN:HB3	1.95	0.49
45:YZ:91:LEU:HD12	45:YZ:130:PRO:HB3	1.95	0.49
1:QA:1305:G:HO2'	1:QA:1306:A:H8	1.59	0.49
15:QO:16:ALA:HB1	15:QO:21:ASP:HB3	1.95	0.49
18:QR:23:LYS:HD2	18:QR:58:LEU:HB3	1.93	0.49
25:RA:2306:C:H3'	25:RA:2307:G:H5''	1.93	0.49
30:RG:120:LEU:N	30:RG:179:PRO:O	2.43	0.49
32:RI:2:LYS:HD2	32:RI:20:ASP:HB3	1.94	0.49
38:RS:24:LEU:HB2	38:RS:85:VAL:HG12	1.93	0.49
45:RZ:110:GLY:O	45:RZ:112:ARG:N	2.44	0.49
2:XB:24:TRP:CD1	2:XB:24:TRP:N	2.80	0.49
4:XD:7:PRO:HB2	4:XD:10:ARG:HD2	1.94	0.49
11:XK:13:GLN:NE2	11:XK:76:GLY:HA3	2.28	0.49
25:YA:1094:U:O2'	25:YA:1096:A:OP1	2.28	0.49
25:YA:2472:G:H5'	25:YA:2473:U:H5''	1.95	0.49
29:YF:24:LEU:HD13	29:YF:25:PRO:HD2	1.93	0.49
30:YG:9:ARG:O	30:YG:13:GLU:HG2	2.12	0.49
31:YH:107:VAL:HG23	31:YH:108:GLY:H	1.76	0.49
32:YI:8:PRO:HD3	32:YI:15:VAL:HG22	1.95	0.49
34:YO:71:ARG:NH1	39:YT:74:ARG:HH21	2.10	0.49
37:YR:42:LYS:HA	37:YR:45:ARG:HE	1.77	0.49
44:YY:20:TYR:CZ	44:YY:42:VAL:HA	2.47	0.49
50:Y4:55:ARG:HH21	50:Y4:56:VAL:HG12	1.77	0.49
1:QA:67:C:H2'	1:QA:68:G:C8	2.47	0.49
1:QA:263:A:OP2	20:QT:79:ARG:NH1	2.46	0.49
1:QA:973:G:H3'	1:QA:974:A:H5''	1.93	0.49
1:QA:1004:A:O2'	1:QA:1005:A:O5'	2.22	0.49
1:QA:1157:A:O2'	1:QA:1158:C:C2	2.60	0.49
3:QC:108:ASN:ND2	3:QC:144:SER:HB2	2.27	0.49
4:QD:79:PHE:HE1	4:QD:204:ILE:HD13	1.76	0.49
6:QF:42:GLU:HG2	6:QF:42:GLU:O	2.11	0.49
11:QK:21:ILE:HG12	11:QK:30:VAL:HG12	1.94	0.49
16:QP:52:ASP:OD2	16:QP:54:GLU:HG2	2.13	0.49
25:RA:2166:G:O2'	25:RA:2167:U:OP1	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:RT:16:ARG:NH2	39:RT:19:LEU:HD21	2.28	0.49
40:RU:81:HIS:CD2	40:RU:84:LYS:HD3	2.48	0.49
52:R6:12:GLU:HA	52:R6:24:GLU:HB3	1.94	0.49
1:XA:250:A:H4'	1:XA:251:G:O5'	2.12	0.49
1:XA:1218:C:H2'	1:XA:1219:U:C6	2.47	0.49
10:XJ:40:LEU:HG	10:XJ:41:PRO:HD2	1.94	0.49
25:YA:581:C:H2'	25:YA:582:G:C8	2.48	0.49
25:YA:928:G:H3'	25:YA:929:G:C8	2.46	0.49
25:YA:2563:U:H4'	34:YO:28:SER:HA	1.95	0.49
28:YE:128:SER:OG	28:YE:129:HIS:N	2.44	0.49
30:YG:104:GLU:HG2	50:Y4:23:GLU:HG3	1.94	0.49
31:YH:10:PRO:O	31:YH:11:VAL:O	2.30	0.49
34:YO:25:LEU:HB2	34:YO:38:VAL:HG23	1.93	0.49
1:QA:62:U:OP1	1:QA:385:C:O2'	2.30	0.49
1:QA:309:G:O2'	1:QA:607:A:N1	2.45	0.49
1:QA:1213:A:N6	1:QA:1215:G:N3	2.61	0.49
1:QA:1233:G:H2'	1:QA:1234:C:C6	2.47	0.49
9:QI:19:LEU:HB3	9:QI:59:PHE:HB3	1.94	0.49
10:QJ:46:ARG:HG2	10:QJ:64:GLU:HB3	1.94	0.49
15:QO:24:SER:OG	15:QO:25:THR:N	2.46	0.49
25:RA:1857:G:C6	25:RA:1858:G:N1	2.81	0.49
54:R8:34:TRP:C	54:R8:36:LYS:H	2.16	0.49
1:XA:811:C:O2'	1:XA:901:A:N1	2.42	0.49
1:XA:1314:C:OP2	19:XS:6:LYS:HD2	2.13	0.49
23:XX:14:A:C2'	23:XX:15:A:H5'	2.41	0.49
25:YA:54:G:O2'	53:Y7:35:ARG:HD3	2.11	0.49
25:YA:84:A:N1	25:YA:98:G:O2'	2.38	0.49
28:YE:134:ILE:HD12	28:YE:134:ILE:N	2.21	0.49
30:YG:97:ASP:O	30:YG:101:ILE:HG23	2.13	0.49
31:YH:54:ARG:NE	31:YH:57:ASP:OD1	2.42	0.49
1:QA:410:G:H4'	1:QA:411:A:OP1	2.13	0.49
4:QD:163:GLU:OE1	4:QD:166:LYS:NZ	2.45	0.49
9:QI:19:LEU:HD23	9:QI:61:ALA:HA	1.94	0.49
25:RA:1171:G:O2'	25:RA:1173:G:O5'	2.28	0.49
25:RA:2212:A:H4'	25:RA:2213:U:H5	1.77	0.49
25:RA:2887:U:H2'	25:RA:2888:C:H6	1.78	0.49
26:RB:14:U:H5''	26:RB:71:C:O4'	2.12	0.49
34:RO:98:VAL:CG1	34:RO:117:LEU:HB3	2.43	0.49
43:RX:36:LYS:HG3	43:RX:54:VAL:HB	1.95	0.49
44:RY:97:ARG:NH2	44:RY:98:VAL:HB	2.20	0.49
54:R8:34:TRP:O	54:R8:36:LYS:N	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:512:U:H2'	1:XA:513:C:C6	2.48	0.49
5:XE:72:GLN:O	5:XE:75:THR:HG22	2.12	0.49
10:XJ:8:LEU:HD22	10:XJ:20:ALA:HB2	1.94	0.49
25:YA:1657:C:H2'	25:YA:1658:C:C6	2.47	0.49
25:YA:2120:G:H1	25:YA:2178:C:H42	1.60	0.49
36:YQ:63:LYS:H	45:YZ:178:GLU:HG2	1.78	0.49
39:YT:26:ASP:CB	39:YT:91:ARG:HA	2.43	0.49
3:QC:148:GLY:HA3	3:QC:172:ARG:O	2.12	0.49
7:QG:13:GLN:O	7:QG:24:THR:HG21	2.13	0.49
26:RB:65:C:N4	26:RB:108:C:H2'	2.28	0.49
47:R1:85:LEU:HA	47:R1:87:PRO:HD2	1.94	0.49
1:XA:1157:A:H1'	1:XA:1158:C:C2	2.47	0.49
1:XA:1157:A:O2'	1:XA:1158:C:O5'	2.31	0.49
1:XA:1157:A:O2'	1:XA:1158:C:OP2	2.29	0.49
25:YA:389:G:H22	35:YP:72:PRO:HD3	1.76	0.49
25:YA:2679:A:H4'	28:YE:165:VAL:HG11	1.94	0.49
25:YA:2884:U:O2	51:Y5:52:TYR:OH	2.31	0.49
27:YD:71:ASP:HB3	27:YD:103:ARG:HH22	1.78	0.49
28:YE:38:THR:HG22	28:YE:40:GLU:H	1.77	0.49
29:YF:33:LEU:HD13	29:YF:112:MET:HE2	1.95	0.49
33:YN:36:GLY:H	33:YN:42:TRP:HZ3	1.60	0.49
43:YX:26:TYR:HB3	43:YX:92:LEU:HD12	1.94	0.49
1:QA:139:G:H2'	1:QA:140:A:C8	2.47	0.48
1:QA:620:C:H2'	1:QA:621:A:O4'	2.13	0.48
1:QA:643:C:H2'	1:QA:644:G:H8	1.78	0.48
1:QA:881:G:OP2	12:QL:12:ARG:NH2	2.46	0.48
1:QA:1137:C:H5'	1:QA:1138:G:C2	2.48	0.48
1:QA:1256:A:H1'	1:QA:1258:G:C6	2.48	0.48
3:QC:76:VAL:HG13	3:QC:84:ILE:HG13	1.94	0.48
13:QM:2:ALA:O	13:QM:4:ILE:N	2.46	0.48
25:RA:654(A):G:O2'	25:RA:654(B):C:O5'	2.30	0.48
25:RA:1561:G:H2'	25:RA:1562:A:H8	1.77	0.48
25:RA:1589:C:C2	25:RA:1590:U:C5	3.01	0.48
39:RT:106:SER:HA	39:RT:110:ILE:HG13	1.95	0.48
45:RZ:162:GLU:O	45:RZ:163:LEU:HB3	2.13	0.48
1:XA:1277:C:O2'	1:XA:1279:A:H1'	2.12	0.48
2:XB:129:GLU:HB3	2:XB:130:ARG:NH1	2.27	0.48
15:XO:17:ARG:HD3	15:XO:26:GLU:HG3	1.94	0.48
25:YA:2404:C:H1'	35:YP:67:MET:HE1	1.94	0.48
27:YD:196:VAL:HG12	27:YD:197:GLY:H	1.77	0.48
30:YG:166:ASP:OD1	30:YG:166:ASP:N	2.35	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:YP:64:LYS:CG	54:Y8:25:MET:HB2	2.42	0.48
36:YQ:27:VAL:HG13	45:YZ:81:ARG:HH22	1.78	0.48
40:YU:100:VAL:O	40:YU:101:ARG:HG2	2.13	0.48
46:Y0:50:ASN:HB3	46:Y0:63:VAL:HG22	1.94	0.48
1:QA:210:U:O2'	1:QA:216:G:O4'	2.29	0.48
1:QA:692:U:O2'	1:QA:694:A:N7	2.31	0.48
1:QA:1062:U:H2'	1:QA:1063:C:C6	2.48	0.48
1:QA:1431:C:H2'	1:QA:1432:G:O4'	2.12	0.48
22:QV:13:C:O2'	25:RA:1924:C:H4'	2.13	0.48
25:RA:362:U:H5'	25:RA:363:G:OP2	2.12	0.48
25:RA:1027:A:C2	25:RA:2488:A:H5'	2.48	0.48
25:RA:1375:C:H2'	25:RA:1376:C:H6	1.77	0.48
25:RA:1786:A:H1'	25:RA:1938:A:N6	2.28	0.48
25:RA:2037:G:H2'	25:RA:2038:G:C8	2.48	0.48
25:RA:2183:C:H2'	25:RA:2184:G:C8	2.48	0.48
26:RB:89(A):A:N7	26:RB:90:C:H1'	2.28	0.48
27:RD:10:THR:HG23	27:RD:13:ARG:HB2	1.94	0.48
28:RE:111:ARG:HA	37:RR:2:ARG:HH12	1.78	0.48
28:RE:176:ILE:HB	28:RE:181:LEU:HB2	1.94	0.48
37:RR:73:VAL:O	37:RR:76:VAL:HG12	2.13	0.48
1:XA:653:A:C8	8:XH:56:LYS:HG2	2.48	0.48
1:XA:1143:G:H2'	1:XA:1144:G:C8	2.47	0.48
1:XA:1166:G:N2	1:XA:1170:A:OP2	2.44	0.48
4:XD:194:LEU:HB3	4:XD:196:LEU:HD12	1.95	0.48
5:XE:11:ILE:HD11	5:XE:33:VAL:HG23	1.96	0.48
11:XK:44:SER:O	11:XK:48:ILE:HG12	2.14	0.48
13:XM:118:ALA:HB1	22:XV:28:C:O3'	2.13	0.48
25:YA:2144:U:H4'	25:YA:2145:C:OP1	2.13	0.48
25:YA:2228:G:OP1	27:YD:261:LYS:NZ	2.45	0.48
27:YD:30:GLU:HG3	27:YD:63:ARG:CZ	2.42	0.48
31:YH:10:PRO:O	31:YH:11:VAL:HG12	2.12	0.48
38:YS:74:ALA:HB1	38:YS:107:GLU:HB3	1.95	0.48
8:QH:85:ARG:HG2	8:QH:88:LYS:HG2	1.95	0.48
10:QJ:23:ILE:HG23	10:QJ:85:LEU:HD22	1.94	0.48
25:RA:654(T):C:H2'	25:RA:654(U):A:O4'	2.13	0.48
25:RA:657:U:H2'	25:RA:658:C:C6	2.47	0.48
25:RA:1310:G:OP2	53:R7:9:ARG:NE	2.42	0.48
25:RA:1653:G:C6	37:RR:9:LYS:HG3	2.49	0.48
33:RN:90:MET:HB3	33:RN:98:VAL:HG12	1.95	0.48
44:RY:95:LYS:HB2	44:RY:95:LYS:HZ3	1.78	0.48
2:XB:207:ALA:O	2:XB:211:ILE:HG13	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:XE:7:GLU:HG2	5:XE:112:LEU:HD22	1.95	0.48
6:XF:50:TYR:CE1	18:XR:77:GLY:HA2	2.48	0.48
7:XG:28:ASN:OD1	7:XG:36:LYS:NZ	2.46	0.48
25:YA:651:G:H5''	54:Y8:18:ALA:HB3	1.94	0.48
25:YA:2828:C:H2'	25:YA:2829:C:C6	2.48	0.48
39:YT:26:ASP:O	39:YT:49:VAL:HG12	2.13	0.48
44:YY:48:ALA:N	44:YY:59:GLY:O	2.45	0.48
47:Y1:58:ILE:HG23	47:Y1:87:PRO:HG3	1.95	0.48
55:Y9:9:ARG:NH1	55:Y9:14:CYS:O	2.47	0.48
12:QL:27:LEU:HD13	12:QL:33:ARG:HB2	1.95	0.48
25:RA:1190:G:H5'	35:RP:32:THR:HA	1.96	0.48
25:RA:1413:G:C2	25:RA:1414:G:N9	2.81	0.48
25:RA:2291:U:H2'	25:RA:2292:C:C6	2.48	0.48
25:RA:2298:A:H2'	25:RA:2299:G:O4'	2.13	0.48
29:RF:78:ILE:HA	29:RF:83:PHE:CD1	2.48	0.48
30:RG:104:GLU:HG2	50:R4:23:GLU:HG3	1.95	0.48
31:RH:52:VAL:HG12	31:RH:65:HIS:CD2	2.48	0.48
32:RI:84:GLY:O	32:RI:86:THR:N	2.46	0.48
35:RP:16:ARG:HA	35:RP:16:ARG:HE	1.78	0.48
36:RQ:116:GLU:O	36:RQ:120:ILE:HG12	2.13	0.48
1:XA:527:G:O2'	1:XA:535:A:N1	2.43	0.48
1:XA:957:U:H2'	1:XA:959:A:OP2	2.13	0.48
1:XA:1137:C:H5'	1:XA:1138:G:C4	2.47	0.48
2:XB:54:THR:HG21	2:XB:201:ILE:HD11	1.96	0.48
10:XJ:54:PHE:CD1	10:XJ:55:LYS:HG3	2.48	0.48
10:XJ:86:MET:HG2	10:XJ:87:THR:HG23	1.95	0.48
19:XS:67:VAL:HG13	19:XS:68:GLY:H	1.78	0.48
25:YA:1805:U:O2	27:YD:50:THR:HB	2.14	0.48
25:YA:2305:A:H5''	30:YG:134:GLY:HA3	1.95	0.48
28:YE:50:GLY:HA2	28:YE:74:PRO:HG3	1.94	0.48
54:Y8:31:HIS:CG	54:Y8:32:LEU:N	2.81	0.48
1:QA:691:G:OP2	11:QK:26:ASN:ND2	2.47	0.48
1:QA:769:G:H4'	1:QA:1513:A:H4'	1.96	0.48
1:QA:1005:A:H3'	1:QA:1006:C:O4'	2.13	0.48
1:QA:1093:A:N3	1:QA:1109:C:O2'	2.41	0.48
25:RA:463:G:N2	25:RA:466:A:OP2	2.40	0.48
25:RA:644:A:H4'	25:RA:645:C:H5	1.79	0.48
25:RA:1444:G:C2	25:RA:1548:C:C2	3.01	0.48
25:RA:1800:C:OP2	27:RD:183:ARG:NH2	2.42	0.48
25:RA:2711:A:H5''	25:RA:2712:U:H5''	1.96	0.48
26:RB:78:A:H2'	26:RB:79:C:O4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:RD:145:VAL:HB	27:RD:155:LEU:HB2	1.95	0.48
32:RI:57:ARG:HA	32:RI:60:GLU:HB3	1.95	0.48
44:RY:19:LYS:HD2	44:RY:67:LEU:HD11	1.96	0.48
45:RZ:118:GLN:HG2	45:RZ:172:ALA:HA	1.95	0.48
1:XA:392:G:H2'	1:XA:393:A:C8	2.48	0.48
1:XA:982:U:H4'	1:XA:983:A:O5'	2.13	0.48
15:XO:10:LYS:HA	15:XO:10:LYS:HD2	1.69	0.48
18:XR:22:VAL:O	18:XR:24:ALA:N	2.42	0.48
25:YA:265:A:N1	25:YA:427:U:O2'	2.40	0.48
25:YA:270(B):A:N7	25:YA:270(X):G:N2	2.60	0.48
25:YA:453:C:O2	25:YA:457:A:O2'	2.30	0.48
25:YA:1357:U:H4'	53:Y7:23:ARG:HH21	1.79	0.48
25:YA:2389:G:H5''	25:YA:2390:U:O4'	2.14	0.48
42:YW:64:MET:HE3	42:YW:109:GLU:HG3	1.96	0.48
44:YY:19:LYS:HB2	44:YY:20:TYR:H	1.34	0.48
52:Y6:34:LEU:HD11	52:Y6:50:ARG:HH21	1.78	0.48
1:QA:1182:G:H4'	1:QA:1183:A:H5'	1.95	0.48
1:QA:1280:A:H5'	1:QA:1281:U:OP2	2.14	0.48
1:QA:1306:A:N6	1:QA:1331:G:H1'	2.28	0.48
1:QA:1316:G:H4'	14:QN:18:VAL:HG11	1.95	0.48
19:QS:65:ASN:HA	50:R4:55:ARG:HD2	1.95	0.48
25:RA:372:G:O2'	25:RA:373:U:P	2.70	0.48
25:RA:1313:U:H3'	25:RA:1313:U:O2	2.14	0.48
34:RO:4:PRO:O	34:RO:5:GLN:HB2	2.13	0.48
41:RV:10:LYS:NZ	41:RV:23:GLU:OE1	2.46	0.48
44:RY:62:GLU:CD	44:RY:63:LYS:H	2.17	0.48
44:RY:84:ARG:NH2	44:RY:97:ARG:HB2	2.28	0.48
45:RZ:58:VAL:HG12	45:RZ:60:GLU:CG	2.44	0.48
1:XA:243:A:N6	1:XA:281:G:O2'	2.47	0.48
1:XA:356:A:N3	1:XA:368:U:O2'	2.34	0.48
1:XA:1392:G:N2	1:XA:1502:A:C8	2.80	0.48
13:XM:9:ILE:HG12	13:XM:10:PRO:CD	2.43	0.48
20:XT:14:LYS:HA	20:XT:17:ARG:HE	1.78	0.48
25:YA:1980:G:O2'	25:YA:1982:C:OP2	2.28	0.48
25:YA:2708:G:O2'	25:YA:2709:G:H5'	2.13	0.48
29:YF:7:TYR:HB3	29:YF:18:ARG:HB2	1.96	0.48
31:YH:124:GLU:HB2	31:YH:132:ARG:HG3	1.95	0.48
33:YN:30:ILE:HG21	33:YN:120:LEU:HD13	1.95	0.48
53:Y7:16:HIS:HB2	53:Y7:44:PRO:HG2	1.96	0.48
1:QA:28:G:O2'	1:QA:296:U:OP1	2.23	0.48
1:QA:37:U:O2'	1:QA:500:G:H4'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:QA:269:C:H2'	1:QA:270:A:C8	2.48	0.48
1:QA:957:U:H4'	19:QS:79:THR:OG1	2.14	0.48
1:QA:1148:U:H2'	1:QA:1149:C:O4'	2.13	0.48
1:QA:1320:C:C5	19:QS:36:ARG:HG2	2.48	0.48
19:QS:38:SER:O	19:QS:70:LYS:HB3	2.14	0.48
25:RA:39:C:O2	29:RF:46:ARG:NH2	2.46	0.48
25:RA:2129:C:H3'	25:RA:2130:U:C5'	2.44	0.48
25:RA:2130:U:O2	25:RA:2133:G:O2'	2.32	0.48
36:RQ:34:LEU:HD11	36:RQ:129:THR:HB	1.96	0.48
39:RT:26:ASP:HB2	39:RT:91:ARG:HA	1.96	0.48
41:RV:98:GLU:OE2	41:RV:100:ARG:NH1	2.47	0.48
1:XA:1125:U:H2'	1:XA:1126:U:H2'	1.96	0.48
3:XC:23:TYR:CD2	10:XJ:10:GLY:HA2	2.49	0.48
25:YA:832:G:H4'	35:YP:45:LEU:HD11	1.95	0.48
25:YA:1488:G:H5'	25:YA:1489:U:OP2	2.13	0.48
25:YA:1694:C:H4'	25:YA:1695:G:O5'	2.14	0.48
25:YA:2712:U:O2'	25:YA:2712(A):A:OP2	2.30	0.48
36:YQ:138:ASP:OD2	36:YQ:138:ASP:N	2.46	0.48
52:Y6:15:GLU:OE2	52:Y6:44:ARG:NH1	2.43	0.48
11:QK:30:VAL:HG21	11:QK:65:ALA:HA	1.94	0.48
20:QT:26:ASN:HB3	20:QT:71:THR:OG1	2.14	0.48
23:QX:12:A:H8	23:QX:13:A:H8	1.61	0.48
25:RA:861:A:N3	26:RB:79:C:O2'	2.47	0.48
25:RA:1025:G:C4	25:RA:1135:C:H1'	2.49	0.48
25:RA:2645:G:H3'	25:RA:2646:C:C5'	2.44	0.48
31:RH:7:LEU:HD22	31:RH:69:ARG:HG2	1.96	0.48
31:RH:9:ILE:O	31:RH:69:ARG:HD2	2.14	0.48
32:RI:98:ALA:HA	32:RI:109:ILE:HD11	1.95	0.48
39:RT:105:LEU:HD13	39:RT:109:GLU:HG3	1.95	0.48
1:XA:153:C:H42	1:XA:168:G:H1	1.61	0.48
1:XA:1152:A:H2'	1:XA:1153:C:C6	2.48	0.48
1:XA:1493:A:N1	25:YA:1913:A:H1'	2.29	0.48
2:XB:18:GLY:HA2	2:XB:40:HIS:O	2.13	0.48
25:YA:1270:C:H5''	25:YA:1271:G:H5'	1.95	0.48
25:YA:1935:G:H1'	25:YA:1964:G:N2	2.28	0.48
25:YA:2319:G:N7	38:YS:3:ARG:HB3	2.28	0.48
25:YA:2875:C:H4'	39:YT:5:ALA:HB2	1.94	0.48
26:YB:44:G:H1'	26:YB:47:C:N4	2.29	0.48
36:YQ:116:GLU:O	36:YQ:120:ILE:HG12	2.12	0.48
40:YU:50:ARG:HH11	41:YV:72:VAL:HG11	1.78	0.48
1:QA:539:A:H2'	1:QA:540:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:QA:1347:G:N2	1:QA:1373:G:H2'	2.29	0.48
3:QC:20:SER:HB2	3:QC:40:ARG:HH12	1.78	0.48
25:RA:1062:G:H2'	25:RA:1063:G:C8	2.49	0.48
25:RA:2144:U:H4'	25:RA:2145:C:OP1	2.14	0.48
31:RH:8:PRO:O	31:RH:9:ILE:CB	2.61	0.48
45:RZ:52:SER:O	45:RZ:54:HIS:N	2.46	0.48
1:XA:1299:A:C8	1:XA:1299:A:C3'	2.96	0.48
9:XI:20:ARG:O	9:XI:60:ASP:N	2.46	0.48
11:XK:34:ASP:HB3	11:XK:40:ILE:HD11	1.96	0.48
13:XM:10:PRO:O	13:XM:45:VAL:HG11	2.14	0.48
25:YA:957:A:N1	25:YA:2458:G:H4'	2.29	0.48
25:YA:1265:A:H8	25:YA:1265:A:OP1	1.97	0.48
28:YE:75:VAL:O	28:YE:77:ILE:N	2.47	0.48
29:YF:25:PRO:HD3	29:YF:115:ALA:HB1	1.96	0.48
37:YR:52:ILE:HD13	37:YR:79:LEU:HD21	1.95	0.48
39:YT:39:ARG:NH2	39:YT:41:ARG:HG2	2.28	0.48
1:QA:801:U:H2'	1:QA:802:A:C8	2.48	0.48
1:QA:920:U:H2'	1:QA:921:U:C6	2.48	0.48
1:QA:1004:A:HO2'	1:QA:1005:A:P	2.36	0.48
1:QA:1305:G:OP1	21:QU:2:GLY:HA2	2.14	0.48
1:QA:1346:A:N1	1:QA:1374:A:H5''	2.28	0.48
1:QA:1443:G:N2	25:RA:2863:C:O3'	2.47	0.48
3:QC:130:VAL:O	3:QC:134:ILE:HG12	2.13	0.48
16:QP:71:ARG:HG3	16:QP:80:PHE:CE1	2.47	0.48
25:RA:250:G:H2'	25:RA:251:A:C8	2.49	0.48
25:RA:884:C:N4	25:RA:890:A:H62	2.12	0.48
25:RA:1149:G:H2'	25:RA:1150:C:C6	2.49	0.48
25:RA:1805:U:O2	27:RD:50:THR:HB	2.13	0.48
25:RA:2017:U:O2	51:R5:10:LYS:HB2	2.14	0.48
27:RD:35:LYS:NZ	27:RD:64:ILE:O	2.43	0.48
41:RV:38:LEU:HD12	41:RV:55:ALA:HB1	1.95	0.48
41:RV:58:VAL:HB	41:RV:98:GLU:HB2	1.95	0.48
54:R8:33:ASN:OD1	54:R8:33:ASN:N	2.47	0.48
12:XL:53:ARG:NH2	12:XL:92:ASP:OD2	2.33	0.48
19:XS:36:ARG:NH2	19:XS:73:GLU:OE2	2.45	0.48
19:XS:44:MET:HG2	19:XS:47:HIS:NE2	2.28	0.48
22:XV:9:G:O2'	22:XV:10:G:N7	2.45	0.48
25:YA:607:U:OP1	29:YF:102:PRO:HA	2.14	0.48
25:YA:888:C:H4'	25:YA:889:C:H5	1.78	0.48
25:YA:2572:A:N7	28:YE:144:ARG:HD2	2.29	0.48
25:YA:2584:U:H4'	56:Z6:76:PPU:H92	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:YE:68:ALA:O	28:YE:70:ALA:N	2.47	0.48
3:QC:66:VAL:HG13	3:QC:101:LEU:HA	1.96	0.47
25:RA:588:U:H2'	25:RA:589:C:C6	2.49	0.47
25:RA:1412:A:H2'	25:RA:1413:G:C8	2.48	0.47
25:RA:2712:U:O2'	25:RA:2713:A:H5'	2.14	0.47
25:RA:2758:A:C4	31:RH:67:LEU:HD21	2.50	0.47
27:RD:35:LYS:HZ1	27:RD:65:ILE:HA	1.78	0.47
28:RE:116:VAL:O	28:RE:117:MET:HB3	2.14	0.47
31:RH:51:ARG:H	31:RH:51:ARG:HG3	1.32	0.47
34:RO:35:VAL:HG11	34:RO:103:ALA:HB3	1.96	0.47
44:RY:40:GLU:N	44:RY:40:GLU:OE2	2.46	0.47
1:XA:542:G:H5'	4:XD:41:GLY:HA3	1.94	0.47
1:XA:598:U:H4'	8:XH:94:TYR:CD2	2.49	0.47
1:XA:953:G:N7	13:XM:104:ARG:NH2	2.50	0.47
19:XS:66:MET:HA	19:XS:69:HIS:HD2	1.79	0.47
25:YA:2396:G:H4'	47:Y1:30:VAL:H	1.79	0.47
25:YA:2584:U:O2	25:YA:2585:U:C5	2.67	0.47
25:YA:2855:C:H2'	25:YA:2856:C:C6	2.46	0.47
28:YE:8:LYS:HB3	28:YE:193:GLY:N	2.28	0.47
28:YE:87:GLU:HG3	28:YE:89:ASP:H	1.78	0.47
29:YF:24:LEU:CD1	29:YF:25:PRO:HD2	2.44	0.47
39:YT:26:ASP:HB2	39:YT:90:GLN:O	2.14	0.47
4:QD:178:VAL:O	4:QD:180:GLY:N	2.45	0.47
8:QH:64:LYS:HG2	8:QH:79:VAL:HG21	1.96	0.47
33:RN:63:THR:O	33:RN:66:LYS:HG3	2.13	0.47
43:RX:43:VAL:HG23	43:RX:51:VAL:HG21	1.97	0.47
1:XA:1302:U:OP1	13:XM:13:LYS:HE2	2.14	0.47
1:XA:1411:C:H2'	1:XA:1412:C:C6	2.49	0.47
9:XI:117:HIS:CD2	9:XI:123:PRO:HA	2.49	0.47
18:XR:26:LEU:HD22	18:XR:39:VAL:HG13	1.96	0.47
20:XT:53:LEU:HB3	20:XT:102:GLY:HA3	1.94	0.47
25:YA:247:G:H4'	25:YA:386:G:C5	2.49	0.47
25:YA:1230:C:H2'	25:YA:1231:G:C8	2.49	0.47
25:YA:1845:G:OP1	27:YD:258:LYS:NZ	2.46	0.47
25:YA:2647:U:H2'	25:YA:2648:C:C6	2.49	0.47
31:YH:38:SER:O	31:YH:40:GLU:N	2.47	0.47
33:YN:95:PRO:O	33:YN:98:VAL:HG22	2.14	0.47
50:Y4:14:ILE:HG23	50:Y4:21:VAL:HG23	1.96	0.47
1:QA:7:G:H5'	1:QA:298:A:O4'	2.15	0.47
1:QA:1008:C:H3'	1:QA:1009:G:H5''	1.95	0.47
4:QD:15:GLU:O	4:QD:17:VAL:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:QJ:51:ARG:HB2	10:QJ:60:ARG:HA	1.95	0.47
10:QJ:51:ARG:HE	10:QJ:61:GLU:HB2	1.78	0.47
25:RA:1225:C:O3'	41:RV:85:LYS:HD3	2.14	0.47
25:RA:1342:A:OP2	43:RX:36:LYS:NZ	2.47	0.47
25:RA:2705:A:H2	37:RR:64:ARG:NH1	2.12	0.47
27:RD:92:ILE:HD12	27:RD:104:TYR:CD2	2.49	0.47
27:RD:131:LEU:HB2	27:RD:136:ILE:HD11	1.97	0.47
36:RQ:21:THR:OG1	36:RQ:23:GLY:O	2.32	0.47
41:RV:64:HIS:CE1	41:RV:92:THR:HG1	2.31	0.47
43:RX:40:LYS:HG3	43:RX:51:VAL:HB	1.97	0.47
1:XA:612:C:O2	1:XA:629:G:N2	2.47	0.47
1:XA:1148:U:H2'	1:XA:1149:C:O4'	2.15	0.47
1:XA:1320:C:C6	19:XS:36:ARG:HG2	2.50	0.47
3:XC:32:LEU:HD22	3:XC:59:ARG:NH1	2.30	0.47
7:XG:18:TYR:HD2	7:XG:59:LEU:HD22	1.79	0.47
10:XJ:54:PHE:CG	10:XJ:55:LYS:N	2.82	0.47
13:XM:99:ARG:O	13:XM:101:GLN:N	2.47	0.47
25:YA:297:C:H5''	44:YY:85:VAL:HG11	1.95	0.47
25:YA:495:G:N3	42:YW:61:ASN:ND2	2.60	0.47
25:YA:518:G:H4'	42:YW:18:ARG:NH1	2.29	0.47
25:YA:722:A:H5'	25:YA:723:G:OP2	2.14	0.47
25:YA:1028:A:N6	25:YA:1125:G:H2'	2.29	0.47
25:YA:2467:C:H4'	36:YQ:123:HIS:ND1	2.28	0.47
28:YE:200:GLU:HG2	28:YE:201:THR:H	1.80	0.47
37:YR:78:LYS:HE2	37:YR:83:ILE:HD11	1.95	0.47
41:YV:29:PRO:HA	41:YV:61:VAL:HG13	1.96	0.47
45:YZ:48:PHE:HE2	45:YZ:71:VAL:HG21	1.80	0.47
45:YZ:51:ALA:HB1	45:YZ:57:ILE:HD11	1.97	0.47
45:YZ:103:ARG:HB3	45:YZ:104:PHE:H	1.47	0.47
50:Y4:58:ARG:NH2	50:Y4:62:ARG:HG3	2.29	0.47
1:QA:422:C:HO2'	1:QA:423:G:N2	2.11	0.47
1:QA:662:G:H2'	1:QA:663:A:H8	1.78	0.47
1:QA:737:A:H5''	6:QF:92:LYS:HG3	1.95	0.47
1:QA:814:A:H2'	1:QA:816:A:H5''	1.95	0.47
1:QA:877:C:H5''	8:QH:88:LYS:HD2	1.95	0.47
1:QA:977:A:O2'	1:QA:981:U:N3	2.39	0.47
1:QA:1028(A):C:H2'	1:QA:1028(B):C:C6	2.49	0.47
1:QA:1226:C:H4'	19:QS:80:TYR:CZ	2.49	0.47
1:QA:1491:G:H2'	1:QA:1492:A:C8	2.49	0.47
11:QK:22:HIS:HB3	11:QK:29:ILE:HG12	1.96	0.47
19:QS:45:VAL:O	19:QS:62:ILE:HB	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:RA:1329:U:H5'	25:RA:1330:C:C5	2.49	0.47
35:RP:59:LEU:HG	35:RP:59:LEU:O	2.14	0.47
1:XA:160:A:H2'	1:XA:161:A:O4'	2.14	0.47
1:XA:1314:C:H2'	1:XA:1315:U:C6	2.49	0.47
1:XA:1316:G:N1	1:XA:1319:A:OP2	2.40	0.47
3:XC:116:VAL:HG21	3:XC:202:ILE:HD11	1.96	0.47
10:XJ:27:ALA:HB2	10:XJ:85:LEU:HD11	1.95	0.47
24:XY:26:ASP:OD1	24:XY:69:ARG:NE	2.31	0.47
25:YA:17:G:H4'	40:YU:25:TRP:CH2	2.49	0.47
25:YA:909:A:H2'	25:YA:912:C:C5	2.50	0.47
25:YA:1587:A:H8	25:YA:1587:A:C5'	2.19	0.47
38:YS:30:ARG:HH21	38:YS:92:TYR:HD1	1.62	0.47
48:Y2:15:LYS:HE3	48:Y2:67:LYS:HE2	1.95	0.47
1:QA:985:C:H2'	1:QA:986:A:C8	2.50	0.47
12:QL:127:GLU:O	12:QL:129:ALA:N	2.48	0.47
25:RA:807:U:OP2	35:RP:41:ARG:NH1	2.47	0.47
25:RA:2679:A:H4'	28:RE:165:VAL:HG11	1.97	0.47
32:RI:2:LYS:HB2	32:RI:39:ALA:HB3	1.97	0.47
36:RQ:83:MET:HB2	46:R0:7:LEU:HD13	1.96	0.47
38:RS:108:GLY:O	38:RS:110:LEU:N	2.48	0.47
1:XA:973:G:OP1	10:XJ:57:LYS:HE2	2.14	0.47
10:XJ:30:SER:OG	10:XJ:81:THR:HG22	2.15	0.47
23:XX:19:A2M:H4'	23:XX:20:OMC:O4'	2.15	0.47
25:YA:826:U:H2'	25:YA:828:U:O4'	2.15	0.47
25:YA:835:A:OP1	54:Y8:52:LYS:HG2	2.14	0.47
25:YA:1419:A:C8	25:YA:1421:G:C6	3.03	0.47
25:YA:2729:G:H2'	25:YA:2730:C:C6	2.48	0.47
28:YE:120:TRP:CD2	28:YE:155:LYS:HD3	2.48	0.47
29:YF:4:VAL:HG11	29:YF:17:ARG:HE	1.78	0.47
29:YF:157:VAL:HB	29:YF:194:MET:HB3	1.97	0.47
38:YS:3:ARG:HD3	38:YS:4:LEU:HB2	1.96	0.47
38:YS:7:TYR:CZ	38:YS:91:PRO:HG3	2.49	0.47
46:Y0:4:LYS:HB2	46:Y0:5:LYS:HA	1.96	0.47
1:QA:148:G:H2'	1:QA:149:A:H8	1.80	0.47
1:QA:1118:C:OP1	9:QI:104:ARG:NH1	2.47	0.47
1:QA:1516:G:N1	1:QA:1519:A:OP2	2.47	0.47
10:QJ:54:PHE:CG	10:QJ:55:LYS:N	2.83	0.47
33:RN:39:ARG:HH21	33:RN:41:ASP:CB	2.27	0.47
41:RV:85:LYS:HG3	41:RV:87:HIS:N	2.29	0.47
48:R2:47:ASN:HB2	48:R2:48:HIS:H	1.56	0.47
52:R6:9:LEU:HD22	52:R6:10:LEU:H	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:522:C:H41	12:XL:53:ARG:NH2	2.13	0.47
1:XA:890:G:O2'	1:XA:906:G:O6	2.21	0.47
1:XA:946:A:H2'	1:XA:947:G:C8	2.49	0.47
1:XA:951:G:OP2	13:XM:102:ARG:NH2	2.47	0.47
21:XU:9:ARG:HH21	21:XU:10:ARG:HH21	1.61	0.47
25:YA:1766:U:H2'	25:YA:1767:C:H6	1.80	0.47
25:YA:2406:U:H2'	25:YA:2406:U:OP2	2.14	0.47
30:YG:15:VAL:HG21	30:YG:176:LEU:HD23	1.96	0.47
30:YG:107:LEU:HD11	30:YG:178:PHE:CE1	2.49	0.47
33:YN:93:THR:HB	33:YN:94:HIS:CE1	2.50	0.47
35:YP:84:ASN:HA	35:YP:115:LEU:O	2.14	0.47
41:YV:85:LYS:HD2	41:YV:86:GLY:H	1.79	0.47
45:YZ:127:LYS:O	45:YZ:162:GLU:HG2	2.14	0.47
52:Y6:42:TRP:HD1	52:Y6:44:ARG:HG2	1.79	0.47
56:Z7:76:PPU:H93	56:Z7:76:PPU:N7	2.28	0.47
1:QA:103:C:P	20:QT:17:ARG:HH21	2.38	0.47
1:QA:428:G:H4'	1:QA:429:U:O5'	2.14	0.47
1:QA:1106:G:H5''	3:QC:172:ARG:HG2	1.96	0.47
1:QA:1493:A:H2'	1:QA:1494:G:H5'	1.97	0.47
2:QB:97:TRP:CH2	2:QB:173:ALA:HA	2.50	0.47
5:QE:101:ILE:HD11	5:QE:119:LEU:HD23	1.97	0.47
8:QH:102:ARG:H	8:QH:102:ARG:HG3	1.42	0.47
9:QI:28:VAL:HG22	9:QI:29:ASN:N	2.30	0.47
10:QJ:49:VAL:HG22	14:QN:41:ARG:HB2	1.95	0.47
17:QQ:59:ILE:HG23	17:QQ:71:PHE:HB3	1.97	0.47
25:RA:138:G:H22	43:RX:44:GLU:CD	2.17	0.47
25:RA:1568:G:P	27:RD:63:ARG:HH12	2.37	0.47
25:RA:1688:U:O2	25:RA:1700:A:H5'	2.15	0.47
25:RA:1790:C:H5''	25:RA:1791:A:OP1	2.15	0.47
25:RA:2466:C:H5''	55:R9:6:SER:HB2	1.96	0.47
25:RA:2689:U:H5''	25:RA:2713:A:C2	2.50	0.47
27:RD:260:ARG:NH1	27:RD:267:SER:OG	2.47	0.47
28:RE:111:ARG:HA	37:RR:2:ARG:NH1	2.30	0.47
30:RG:94:LEU:HD12	30:RG:99:MET:HA	1.95	0.47
31:RH:32:GLU:HG2	31:RH:34:GLU:H	1.80	0.47
31:RH:76:VAL:O	31:RH:79:VAL:HG22	2.15	0.47
35:RP:57:THR:O	35:RP:60:MET:HG3	2.14	0.47
45:RZ:130:PRO:O	45:RZ:133:ILE:HD11	2.14	0.47
49:R3:38:GLU:HB3	49:R3:40:THR:HG23	1.97	0.47
1:XA:1183:A:O2'	1:XA:1184:G:P	2.73	0.47
2:XB:21:ARG:HA	2:XB:39:ILE:H	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:XB:82:ARG:HB3	2:XB:94:ASN:ND2	2.29	0.47
3:XC:76:VAL:HG13	3:XC:84:ILE:HG13	1.97	0.47
5:XE:80:ILE:HD11	5:XE:138:ALA:HB1	1.96	0.47
7:XG:47:CYS:HB3	7:XG:58:PRO:HG3	1.95	0.47
9:XI:28:VAL:HG22	9:XI:29:ASN:H	1.78	0.47
9:XI:28:VAL:HG11	9:XI:63:ILE:H	1.79	0.47
10:XJ:48:THR:HG22	10:XJ:60:ARG:HD2	1.97	0.47
22:XV:75:C:H5''	22:XV:76:A:OP2	2.15	0.47
25:YA:673:C:H5''	29:YF:81:PRO:HD2	1.95	0.47
25:YA:1448:G:O2'	25:YA:1528:A:N6	2.48	0.47
26:YB:48:A:H4'	38:YS:95:HIS:HD2	1.80	0.47
27:YD:68:LYS:HB2	27:YD:70:TRP:CE2	2.49	0.47
31:YH:8:PRO:O	31:YH:9:ILE:CB	2.63	0.47
31:YH:54:ARG:HD3	31:YH:54:ARG:H	1.80	0.47
31:YH:150:ALA:O	31:YH:152:ARG:N	2.47	0.47
34:YO:87:ILE:HG21	34:YO:91:LEU:HD13	1.95	0.47
38:YS:10:ARG:O	38:YS:14:VAL:HG12	2.15	0.47
46:Y0:27:GLU:HB2	46:Y0:69:PHE:HD1	1.80	0.47
50:Y4:46:GLN:HE21	50:Y4:48:ARG:HD3	1.80	0.47
52:Y6:9:LEU:HD22	52:Y6:10:LEU:H	1.80	0.47
1:QA:728:A:H2'	1:QA:729:A:C8	2.49	0.47
5:QE:78:HIS:HD1	8:QH:104:ARG:HG3	1.78	0.47
9:QI:37:PHE:CE2	9:QI:70:LYS:HG3	2.50	0.47
25:RA:389:G:H22	35:RP:72:PRO:HD3	1.79	0.47
25:RA:2475:C:H5''	25:RA:2476:A:OP2	2.15	0.47
25:RA:2848:G:HO2'	25:RA:2849:U:P	2.38	0.47
28:RE:35:GLN:HE22	28:RE:37:ARG:NH2	2.12	0.47
34:RO:76:ALA:HB3	39:RT:75:ILE:HB	1.96	0.47
35:RP:52:GLU:HG2	35:RP:56:SER:O	2.15	0.47
40:RU:95:LEU:HD13	41:RV:4:ILE:HG13	1.96	0.47
45:RZ:118:GLN:HE21	45:RZ:174:VAL:HA	1.78	0.47
1:XA:1313:U:OP2	19:XS:6:LYS:HB3	2.15	0.47
7:XG:104:LEU:HD13	7:XG:104:LEU:HA	1.81	0.47
19:XS:45:VAL:O	19:XS:47:HIS:N	2.44	0.47
25:YA:528:A:O2'	25:YA:529:A:H5''	2.14	0.47
25:YA:1217:C:OP1	40:YU:15:LYS:HE3	2.15	0.47
25:YA:2336:A:H61	46:Y0:43:THR:CG2	2.28	0.47
25:YA:2365:G:N7	54:Y8:39:LYS:NZ	2.63	0.47
25:YA:2393:A:H4'	35:YP:62:LEU:N	2.30	0.47
25:YA:2414:G:H21	35:YP:67:MET:HE1	1.80	0.47
25:YA:2711:A:C8	25:YA:2714:G:O4'	2.68	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:YU:81:HIS:HD2	40:YU:84:LYS:HD3	1.79	0.47
42:YW:94:ASP:OD1	42:YW:94:ASP:N	2.47	0.47
45:YZ:111:VAL:O	45:YZ:113:ALA:N	2.42	0.47
50:Y4:23:GLU:O	50:Y4:25:TYR:N	2.47	0.47
50:Y4:39:CYS:O	50:Y4:40:HIS:ND1	2.48	0.47
10:QJ:50:ILE:HA	10:QJ:60:ARG:HB3	1.97	0.47
25:RA:270(F):U:H2'	25:RA:270(G):C:C6	2.50	0.47
25:RA:1817:G:OP1	27:RD:88:ARG:NH2	2.44	0.47
25:RA:2211:G:H3'	25:RA:2212:A:N3	2.29	0.47
25:RA:2572:A:N7	28:RE:144:ARG:HD2	2.30	0.47
25:RA:2750:A:OP2	31:RH:6:ARG:NH2	2.48	0.47
27:RD:44:ASN:HB2	27:RD:48:ARG:O	2.15	0.47
28:RE:63:LEU:HD22	28:RE:63:LEU:N	2.29	0.47
49:R3:40:THR:OG1	49:R3:43:ILE:HG12	2.15	0.47
1:XA:392:G:H2'	1:XA:393:A:H8	1.80	0.47
1:XA:452:A:HO2'	1:XA:453:A:H8	1.62	0.47
1:XA:1101:A:H4'	1:XA:1102:A:O5'	2.14	0.47
1:XA:1117:G:H4'	9:XI:104:ARG:HD2	1.96	0.47
1:XA:1316:G:N2	1:XA:1318:A:H3'	2.30	0.47
1:XA:1376:U:H2'	1:XA:1377:A:H8	1.80	0.47
9:XI:2:GLU:HG3	9:XI:3:GLN:H	1.79	0.47
14:XN:23:ARG:HD2	14:XN:28:GLY:O	2.14	0.47
18:XR:22:VAL:HG22	18:XR:23:LYS:H	1.80	0.47
25:YA:270(N):G:O2'	25:YA:270(O):U:H5'	2.15	0.47
25:YA:840:C:H2'	25:YA:841:A:C8	2.49	0.47
25:YA:1169:G:H1	25:YA:1180:C:H42	1.62	0.47
25:YA:2869:G:H2'	25:YA:2870:C:C6	2.49	0.47
28:YE:111:ARG:HA	37:YR:2:ARG:HH12	1.79	0.47
32:YI:69:LYS:HG2	32:YI:136:VAL:HB	1.97	0.47
33:YN:14:VAL:HA	33:YN:135:PRO:HD2	1.96	0.47
34:YO:98:VAL:HG22	34:YO:118:ALA:HA	1.96	0.47
35:YP:15:ARG:O	35:YP:17:LYS:N	2.48	0.47
45:YZ:119:GLU:OE1	45:YZ:122:ARG:NH2	2.44	0.47
47:Y1:51:VAL:HG11	47:Y1:74:VAL:HG21	1.97	0.47
1:QA:612:C:O2	1:QA:629:G:N2	2.48	0.47
1:QA:812:C:OP1	1:QA:902:G:N2	2.42	0.47
1:QA:960:U:O2'	1:QA:961:U:OP2	2.30	0.47
1:QA:979:C:H3'	1:QA:980:C:H5''	1.96	0.47
1:QA:1346:A:OP1	9:QI:120:ARG:NH1	2.44	0.47
17:QQ:40:LYS:HD3	17:QQ:42:TYR:CZ	2.50	0.47
19:QS:67:VAL:HG11	50:R4:55:ARG:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:QT:29:LYS:O	20:QT:33:ILE:HG12	2.15	0.47
25:RA:469:G:P	29:RF:60:SER:HB3	2.55	0.47
25:RA:921:G:H4'	25:RA:2269:A:C5	2.50	0.47
25:RA:1165:U:H2'	25:RA:1166:C:C6	2.49	0.47
25:RA:1429:G:H2'	25:RA:1430:C:C6	2.50	0.47
25:RA:1542:G:H3'	25:RA:1543:A:H5''	1.88	0.47
25:RA:1918:A:O2'	25:RA:1920:C:N4	2.47	0.47
29:RF:192:LEU:HD23	29:RF:193:VAL:N	2.29	0.47
35:RP:23:PRO:C	35:RP:25:SER:H	2.18	0.47
35:RP:65:ARG:HH22	54:R8:23:VAL:HG12	1.79	0.47
37:RR:55:ALA:HB2	37:RR:79:LEU:HD13	1.96	0.47
17:XQ:21:VAL:HG21	17:XQ:59:ILE:HD11	1.98	0.47
17:XQ:41:LYS:HB2	17:XQ:41:LYS:HE3	1.66	0.47
25:YA:389:G:N1	35:YP:71:VAL:HG12	2.29	0.47
27:YD:35:LYS:HD3	27:YD:63:ARG:HG3	1.97	0.47
27:YD:43:ARG:NH1	27:YD:44:ASN:HD21	2.13	0.47
32:YI:9:LEU:HD11	32:YI:12:LEU:HD22	1.97	0.47
35:YP:63:PRO:CA	54:Y8:13:ARG:CG	2.82	0.47
38:YS:71:ARG:NH1	38:YS:106:ARG:HH21	2.13	0.47
48:Y2:5:GLU:H	48:Y2:5:GLU:CD	2.18	0.47
1:QA:190:G:O2'	1:QA:191(A):G:P	2.73	0.46
1:QA:201:C:O2'	1:QA:208:U:OP1	2.33	0.46
1:QA:452:A:H2'	1:QA:453:A:C8	2.51	0.46
1:QA:511:C:HO2'	1:QA:512:U:H6	1.63	0.46
1:QA:677:U:H3	1:QA:713:G:H22	1.62	0.46
1:QA:748:C:H4'	1:QA:749:C:O5'	2.16	0.46
1:QA:1218:C:H2'	1:QA:1219:U:C6	2.49	0.46
13:QM:23:TYR:CG	13:QM:71:ARG:HD2	2.50	0.46
18:QR:32:ARG:HA	18:QR:69:THR:HG21	1.97	0.46
22:QV:50:U:H2'	22:QV:51:C:C6	2.49	0.46
25:RA:729:G:C6	27:RD:208:LYS:HB2	2.50	0.46
25:RA:876:C:H2'	25:RA:877:U:O4'	2.15	0.46
25:RA:1899:G:H2'	25:RA:1899:G:N3	2.30	0.46
25:RA:2645:G:H3'	25:RA:2646:C:H5'	1.96	0.46
28:RE:57:LYS:HZ1	28:RE:72:VAL:HG13	1.80	0.46
35:RP:65:ARG:HE	54:R8:15:LYS:HB2	1.80	0.46
42:RW:13:SER:HB3	42:RW:16:LYS:HD2	1.98	0.46
44:RY:19:LYS:HE3	44:RY:71:LYS:HZ1	1.80	0.46
1:XA:751:U:H4'	15:XO:24:SER:HA	1.97	0.46
8:XH:20:TYR:HE2	8:XH:75:ARG:HD2	1.80	0.46
9:XI:43:ALA:HA	9:XI:74:ILE:HD13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:XS:19:VAL:HG22	19:XS:44:MET:SD	2.55	0.46
25:YA:579:G:O2'	25:YA:2019:A:OP1	2.30	0.46
25:YA:1198:U:H2'	25:YA:1199:U:C6	2.50	0.46
1:QA:881:G:P	12:QL:12:ARG:HH22	2.38	0.46
1:QA:1139:G:H4'	1:QA:1140:C:O5'	2.14	0.46
3:QC:32:LEU:O	3:QC:36:ASP:HB2	2.15	0.46
25:RA:994:C:OP1	40:RU:53:ARG:NH2	2.48	0.46
25:RA:2097:C:H42	25:RA:2192:G:H1	1.63	0.46
26:RB:60:C:H2'	26:RB:61:G:C8	2.51	0.46
30:RG:142:PRO:HB2	50:R4:31:ILE:HD12	1.96	0.46
44:RY:81:LYS:HD3	44:RY:97:ARG:CZ	2.45	0.46
19:XS:44:MET:HG2	19:XS:47:HIS:CE1	2.50	0.46
23:XX:5:A:H2'	23:XX:6:G:C8	2.48	0.46
25:YA:848:G:N3	25:YA:933:A:H1'	2.30	0.46
25:YA:922:U:H1'	46:Y0:26:TYR:CD1	2.50	0.46
25:YA:959:A:N6	36:YQ:82:ARG:HH12	2.13	0.46
25:YA:1544:C:O2	25:YA:1544:C:H3'	2.14	0.46
25:YA:2772:C:H2'	25:YA:2773:C:C6	2.50	0.46
28:YE:11:MET:HA	28:YE:24:THR:HA	1.96	0.46
33:YN:9:VAL:HG11	33:YN:39:ARG:HH22	1.80	0.46
1:QA:412:A:C6	4:QD:35:ARG:HG2	2.50	0.46
1:QA:807:A:H2'	1:QA:808:C:C6	2.50	0.46
10:QJ:40:LEU:HB3	10:QJ:69:ASN:HB2	1.97	0.46
11:QK:34:ASP:HB3	11:QK:40:ILE:HD11	1.96	0.46
13:QM:93:ARG:HD3	13:QM:93:ARG:HA	1.53	0.46
25:RA:185:U:H4'	25:RA:218:A:H4'	1.97	0.46
25:RA:651:G:H5'	54:R8:18:ALA:HB3	1.98	0.46
25:RA:1484:G:H2'	25:RA:1485:G:H5''	1.98	0.46
25:RA:1930:G:O2'	25:RA:1968:G:O6	2.20	0.46
25:RA:2313:C:H2'	25:RA:2314:C:C6	2.50	0.46
28:RE:34:VAL:HG12	28:RE:64:LYS:HZ1	1.79	0.46
34:RO:120:GLU:OE1	39:RT:67:SER:OG	2.32	0.46
47:R1:70:VAL:O	47:R1:74:VAL:HG23	2.15	0.46
1:XA:335:C:H2'	1:XA:336:C:C6	2.49	0.46
1:XA:376:G:H5''	16:XP:5:ARG:HB2	1.97	0.46
1:XA:524:G:H2'	1:XA:525:C:C6	2.50	0.46
25:YA:26:G:H1'	25:YA:514:A:N6	2.30	0.46
25:YA:2012:G:OP1	42:YW:11:ARG:NH2	2.38	0.46
25:YA:2695:C:H2'	25:YA:2696:U:C6	2.50	0.46
29:YF:23:ASP:OD2	29:YF:203:GLN:NE2	2.47	0.46
30:YG:83:ARG:N	30:YG:86:MET:HG3	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:YI:7:GLU:HG3	32:YI:8:PRO:HD2	1.96	0.46
39:YT:74:ARG:HD3	39:YT:76:PHE:CE2	2.50	0.46
40:YU:90:VAL:HG21	41:YV:48:GLY:O	2.14	0.46
1:QA:485:G:HO2'	1:QA:486:U:P	2.38	0.46
1:QA:1072:G:H2'	1:QA:1073:U:C6	2.51	0.46
1:QA:1178:G:N2	1:QA:1181:G:N7	2.63	0.46
1:QA:1376:U:H2'	1:QA:1377:A:C8	2.51	0.46
25:RA:389:G:H1	35:RP:71:VAL:HG12	1.80	0.46
25:RA:854:G:H5'	25:RA:855:G:OP2	2.15	0.46
25:RA:1476:C:H2'	25:RA:1477:A:H8	1.80	0.46
25:RA:2468:G:N2	25:RA:2481:G:O2'	2.48	0.46
29:RF:122:LYS:HD2	29:RF:191:ARG:HG2	1.97	0.46
31:RH:7:LEU:HD13	31:RH:69:ARG:CB	2.45	0.46
40:RU:92:ARG:HH22	41:RV:11:GLN:N	2.14	0.46
43:RX:63:LYS:H	43:RX:63:LYS:CE	2.28	0.46
44:RY:4:LYS:HE2	44:RY:4:LYS:HA	1.96	0.46
1:XA:1190:G:OP1	3:XC:5:ILE:HG23	2.14	0.46
1:XA:1494:G:HO2'	25:YA:1912:A:HO2'	1.59	0.46
4:XD:18:LYS:HE2	4:XD:20:TYR:CE2	2.51	0.46
25:YA:498:G:N3	44:YY:47:LYS:NZ	2.57	0.46
25:YA:519:U:H2'	25:YA:520:G:H8	1.81	0.46
27:YD:43:ARG:HD2	27:YD:44:ASN:OD1	2.15	0.46
28:YE:14:ILE:HD11	28:YE:173:VAL:HG11	1.97	0.46
36:YQ:35:VAL:CG1	36:YQ:130:LYS:HB3	2.45	0.46
41:YV:35:LEU:HB2	41:YV:37:VAL:HG13	1.96	0.46
1:QA:5:U:H4'	1:QA:6:G:O5'	2.15	0.46
1:QA:833:U:H2'	1:QA:834:C:H6	1.80	0.46
1:QA:1152:A:H2'	1:QA:1153:C:C6	2.51	0.46
2:QB:194:PRO:O	2:QB:197:VAL:N	2.48	0.46
3:QC:157:ILE:HD12	3:QC:164:ARG:HB3	1.97	0.46
19:QS:5:LEU:H	19:QS:5:LEU:HD12	1.80	0.46
20:QT:26:ASN:HB2	20:QT:71:THR:HG23	1.98	0.46
25:RA:335:C:O5'	25:RA:335:C:H6	1.98	0.46
25:RA:1105:U:H2'	25:RA:1106:G:H8	1.80	0.46
25:RA:2529:G:OP2	25:RA:2530:A:H8	1.98	0.46
34:RO:8:LEU:HB2	34:RO:19:ILE:HG13	1.96	0.46
47:R1:94:LEU:HD23	47:R1:94:LEU:H	1.81	0.46
1:XA:689:C:H2'	1:XA:690:G:O4'	2.16	0.46
6:XF:61:LEU:HB3	6:XF:63:TYR:HE2	1.79	0.46
25:YA:363:G:H5'	25:YA:363(A):A:OP2	2.15	0.46
25:YA:394:A:N6	25:YA:395:U:O4	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:YA:1932:A:H2'	25:YA:1933:G:O4'	2.15	0.46
25:YA:2074:U:H2'	25:YA:2075:U:C6	2.50	0.46
25:YA:2183:C:H2'	25:YA:2184:G:H8	1.81	0.46
30:YG:171:ALA:O	30:YG:175:LEU:HG	2.15	0.46
35:YP:46:LYS:HG2	35:YP:51:PHE:CG	2.50	0.46
35:YP:64:LYS:CB	54:Y8:25:MET:HE2	2.44	0.46
40:YU:24:TYR:HB2	40:YU:29:SER:HB3	1.97	0.46
52:Y6:27:LYS:HE2	52:Y6:27:LYS:HB2	1.23	0.46
1:QA:279:A:C4	17:QQ:98:LEU:HD13	2.51	0.46
1:QA:781:A:H4'	1:QA:1522:U:O2'	2.16	0.46
1:QA:960:U:O2	1:QA:960:U:O4'	2.30	0.46
1:QA:1286:A:C8	1:QA:1287:A:H4'	2.51	0.46
1:QA:1336:C:O2'	1:QA:1337:G:OP2	2.28	0.46
2:QB:91:PRO:HA	2:QB:154:LEU:HD11	1.97	0.46
19:QS:36:ARG:NH1	19:QS:73:GLU:H	2.14	0.46
25:RA:1856:G:C2'	25:RA:1857:G:H5'	2.45	0.46
25:RA:2092:U:H4'	32:RI:24:GLY:HA3	1.97	0.46
25:RA:2275:C:O2	36:RQ:83:MET:HG3	2.16	0.46
25:RA:2876:G:O5'	39:RT:3:ARG:HA	2.16	0.46
32:RI:76:THR:H	32:RI:77:LEU:HD23	1.81	0.46
35:RP:98:GLU:HA	35:RP:101:VAL:HG12	1.98	0.46
41:RV:30:GLY:H	41:RV:61:VAL:CG1	2.29	0.46
54:R8:16:ILE:HD11	54:R8:60:LEU:HD12	1.98	0.46
54:R8:54:GLU:O	54:R8:57:ARG:N	2.40	0.46
1:XA:482:A:H5'	1:XA:483:C:OP2	2.16	0.46
1:XA:662:G:H2'	1:XA:663:A:C8	2.51	0.46
25:YA:524:U:H2'	25:YA:525:U:C6	2.51	0.46
27:YD:27:THR:O	27:YD:28:GLU:HB2	2.15	0.46
46:Y0:12:ASN:HA	46:Y0:14:ARG:HH21	1.79	0.46
1:QA:1391:U:H2'	1:QA:1392:G:C8	2.51	0.46
12:QL:47:LYS:HB3	12:QL:48:PRO:CD	2.44	0.46
25:RA:1394:U:H4'	25:RA:1603:A:H4'	1.97	0.46
25:RA:1688:U:H1'	25:RA:1701:A:C6	2.51	0.46
25:RA:1792:G:H5'	27:RD:205:VAL:HG13	1.98	0.46
25:RA:2286:A:H4'	25:RA:2287:A:O4'	2.15	0.46
27:RD:77:ALA:HB2	27:RD:97:TYR:CD2	2.50	0.46
28:RE:55:ASN:HA	28:RE:56:PRO:HD3	1.81	0.46
40:RU:92:ARG:HH22	41:RV:10:LYS:HA	1.79	0.46
1:XA:719:C:O2'	18:XR:49:LYS:HB3	2.16	0.46
1:XA:1008:C:H4'	1:XA:1008:C:OP1	2.16	0.46
17:XQ:58:GLU:O	17:XQ:74:LEU:N	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:YA:270(I):G:H1	25:YA:270(Q):C:H42	1.62	0.46
25:YA:871:U:H2'	25:YA:872:A:C8	2.51	0.46
25:YA:964:C:O2'	25:YA:2273:A:N3	2.47	0.46
25:YA:1573:G:H2'	25:YA:1574:C:H5'	1.98	0.46
25:YA:2102:U:H2'	25:YA:2103:C:C6	2.50	0.46
25:YA:2306:C:H5'	25:YA:2307:G:H2'	1.96	0.46
34:YO:88:ASN:OD1	34:YO:92:GLU:N	2.49	0.46
35:YP:57:THR:HG23	35:YP:60:MET:HB2	1.97	0.46
42:YW:58:ALA:HB1	42:YW:64:MET:HB2	1.98	0.46
47:Y1:92:LYS:HE2	47:Y1:92:LYS:HB3	1.78	0.46
53:Y7:5:TRP:NE1	53:Y7:7:PRO:HG3	2.31	0.46
1:QA:277:C:H2'	1:QA:278:G:H8	1.81	0.46
1:QA:701:C:OP1	1:QA:701:C:H4'	2.16	0.46
1:QA:1101:A:H4'	1:QA:1102:A:O5'	2.16	0.46
1:QA:1356:G:H2'	1:QA:1357:A:C8	2.50	0.46
4:QD:22:LYS:O	4:QD:113:SER:HB2	2.16	0.46
25:RA:729:G:C8	27:RD:208:LYS:HD2	2.50	0.46
31:RH:38:SER:O	31:RH:40:GLU:N	2.49	0.46
34:RO:2:ILE:HG21	34:RO:8:LEU:HD21	1.98	0.46
35:RP:65:ARG:O	35:RP:68:GLN:NE2	2.41	0.46
50:R4:58:ARG:O	50:R4:62:ARG:N	2.49	0.46
1:XA:960:U:HO2'	1:XA:961:U:P	2.39	0.46
13:XM:14:ARG:HA	13:XM:43:THR:O	2.16	0.46
17:XQ:59:ILE:HG22	17:XQ:71:PHE:CD1	2.51	0.46
25:YA:289:A:H5'	25:YA:290:G:OP2	2.16	0.46
25:YA:729:G:C6	27:YD:208:LYS:HB2	2.51	0.46
25:YA:990:A:H5'	25:YA:990:A:H8	1.79	0.46
25:YA:1109:C:N3	25:YA:1110:G:N2	2.64	0.46
25:YA:1542:G:O6	25:YA:1543:A:N6	2.49	0.46
25:YA:2545:G:N3	25:YA:2565:A:H2	2.13	0.46
32:YI:141:LYS:CD	32:YI:142:VAL:HG13	2.46	0.46
51:Y5:51:TYR:HB3	51:Y5:52:TYR:H	1.51	0.46
1:QA:1316:G:N2	1:QA:1319:A:OP2	2.44	0.46
3:QC:71:ALA:HB1	3:QC:109:PRO:HG3	1.97	0.46
7:QG:78:ARG:HB3	7:QG:79:ARG:H	1.57	0.46
25:RA:392:C:H5''	25:RA:409:C:H5''	1.97	0.46
25:RA:958:U:OP2	36:RQ:14:ARG:NH1	2.47	0.46
25:RA:2319:G:C2	25:RA:2320:A:N1	2.84	0.46
25:RA:2481:G:O2'	25:RA:2482:G:P	2.74	0.46
38:RS:26:LEU:HD22	38:RS:87:PHE:HD1	1.81	0.46
44:RY:96:ILE:HD12	44:RY:98:VAL:HG12	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:RZ:150:LEU:O	45:RZ:155:LEU:HD21	2.16	0.46
1:XA:35:G:N3	12:XL:118:SER:OG	2.46	0.46
10:XJ:45:ARG:HB3	10:XJ:65:LEU:HB3	1.98	0.46
13:XM:73:GLU:OE1	13:XM:77:ASN:ND2	2.48	0.46
19:XS:38:SER:HB2	19:XS:39:THR:H	1.63	0.46
25:YA:1047:G:H2'	25:YA:1110:G:N1	2.31	0.46
25:YA:1429:G:H2'	25:YA:1430:C:C6	2.51	0.46
32:YI:12:LEU:HG	32:YI:19:VAL:HG11	1.97	0.46
35:YP:63:PRO:O	35:YP:64:LYS:C	2.54	0.46
38:YS:29:PHE:HB3	38:YS:36:TYR:HB2	1.98	0.46
38:YS:59:LYS:HD3	38:YS:60:GLY:H	1.81	0.46
40:YU:44:ASN:HD21	41:YV:75:PHE:HB3	1.80	0.46
1:QA:878:G:H5'	8:QH:89:PRO:HG2	1.98	0.46
1:QA:1376:U:H2'	1:QA:1377:A:H8	1.81	0.46
3:QC:62:ASP:HA	3:QC:97:LYS:HD2	1.96	0.46
6:QF:4:TYR:CE1	6:QF:92:LYS:HG2	2.51	0.46
19:QS:33:THR:OG1	19:QS:34:TRP:N	2.48	0.46
25:RA:1112:G:H2'	25:RA:1113:U:C6	2.51	0.46
28:RE:35:GLN:CG	28:RE:64:LYS:NZ	2.66	0.46
28:RE:144:ARG:HB3	28:RE:145:LYS:H	1.44	0.46
37:RR:78:LYS:O	37:RR:82:GLU:HB3	2.15	0.46
52:R6:9:LEU:N	52:R6:27:LYS:HA	2.29	0.46
54:R8:30:ARG:HG3	54:R8:31:HIS:HB2	1.96	0.46
8:XH:51:VAL:HG11	8:XH:60:ARG:HH11	1.80	0.46
11:XK:13:GLN:HE21	11:XK:76:GLY:HA3	1.81	0.46
25:YA:94:G:H2'	25:YA:95:G:O4'	2.16	0.46
25:YA:183:C:O2'	25:YA:432:A:N3	2.44	0.46
25:YA:486:C:H2'	25:YA:487:C:C6	2.50	0.46
25:YA:783:A:N3	25:YA:783:A:C2'	2.78	0.46
25:YA:1534:G:N2	25:YA:1537:C:N3	2.64	0.46
25:YA:2109:U:H2'	25:YA:2110:G:C8	2.51	0.46
27:YD:43:ARG:NH1	27:YD:44:ASN:ND2	2.64	0.46
44:YY:46:LYS:HD3	44:YY:63:LYS:HB3	1.97	0.46
52:Y6:8:LYS:CG	52:Y6:27:LYS:HG2	2.46	0.46
1:QA:455:C:H42	1:QA:477:G:H1	1.64	0.45
1:QA:718:G:H5'	11:QK:117:ASN:ND2	2.30	0.45
1:QA:974:A:H1'	14:QN:31:ARG:NE	2.31	0.45
1:QA:977:A:H2'	1:QA:978:A:H5'	1.98	0.45
1:QA:1033:G:O2'	1:QA:1034:G:OP1	2.23	0.45
1:QA:1347:G:C8	9:QI:107:ARG:HB3	2.51	0.45
1:QA:1483:A:H1'	25:RA:1948:G:H1'	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:QC:7:PRO:O	3:QC:11:ARG:NH1	2.49	0.45
9:QI:43:ALA:HA	9:QI:74:ILE:HD13	1.97	0.45
10:QJ:61:GLU:OE2	14:QN:45:ARG:NH1	2.49	0.45
17:QQ:92:ARG:HA	17:QQ:95:TYR:CE2	2.50	0.45
24:QY:33:ARG:O	24:QY:37:ILE:HG13	2.16	0.45
25:RA:94:G:H2'	25:RA:95:G:O4'	2.16	0.45
25:RA:760:G:H2'	25:RA:761:A:O4'	2.16	0.45
25:RA:1012:U:O4	33:RN:25:ARG:HA	2.16	0.45
25:RA:1449:A:C4	25:RA:1529:A:C2	3.04	0.45
25:RA:2319:G:C5	25:RA:2320:A:N6	2.84	0.45
25:RA:2441:C:OP2	25:RA:2586:C:O2'	2.34	0.45
28:RE:21:VAL:HA	28:RE:22:PRO:HD2	1.74	0.45
35:RP:37:GLY:O	35:RP:41:ARG:HG2	2.16	0.45
45:RZ:35:ARG:HH12	45:RZ:61:LEU:HD22	1.80	0.45
45:RZ:94:GLU:HG3	45:RZ:129:SER:OG	2.17	0.45
1:XA:377:G:OP1	16:XP:3:LYS:HD2	2.15	0.45
1:XA:1289:A:OP1	21:XU:9:ARG:NH2	2.49	0.45
1:XA:1499:A:H1'	1:XA:1520:G:H5'	1.99	0.45
3:XC:161:GLU:O	3:XC:162:GLN:HB2	2.15	0.45
25:YA:27:G:C2	25:YA:512:G:O2'	2.68	0.45
25:YA:774:A:H2'	25:YA:774:A:N3	2.32	0.45
25:YA:826:U:H4'	35:YP:55:ARG:HA	1.97	0.45
25:YA:1826:G:H4'	27:YD:242:ARG:NH2	2.32	0.45
31:YH:86:GLU:H	31:YH:86:GLU:CD	2.19	0.45
35:YP:64:LYS:HG2	54:Y8:25:MET:HE3	1.78	0.45
38:YS:4:LEU:HD23	38:YS:8:GLU:HG3	1.97	0.45
39:YT:51:ARG:HG2	39:YT:98:LYS:HE2	1.98	0.45
46:Y0:80:HIS:CD2	46:Y0:82:ARG:HH21	2.34	0.45
47:Y1:53:VAL:HB	47:Y1:58:ILE:HD12	1.98	0.45
1:QA:971:G:H21	1:QA:1233:G:H1'	1.79	0.45
8:QH:23:SER:HB3	8:QH:62:TYR:CD1	2.51	0.45
9:QI:5:TYR:HB3	9:QI:6:GLY:H	1.47	0.45
12:QL:87:GLY:HA2	12:QL:98:TYR:HD2	1.81	0.45
14:QN:23:ARG:HD2	14:QN:28:GLY:O	2.16	0.45
25:RA:634:C:H2'	25:RA:635:C:C6	2.52	0.45
25:RA:1414:G:C4	25:RA:1415:U:C6	3.04	0.45
25:RA:1542:G:C8	25:RA:1543:A:C8	3.04	0.45
25:RA:1819:A:H5''	27:RD:158:ALA:HB3	1.97	0.45
29:RF:4:VAL:HG13	29:RF:19:GLU:CD	2.36	0.45
35:RP:6:LEU:HD13	35:RP:6:LEU:HA	1.72	0.45
38:RS:39:ILE:HD12	38:RS:85:VAL:HG11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:RU:50:ARG:HH22	41:RV:72:VAL:HG23	1.80	0.45
42:RW:13:SER:HA	42:RW:14:PRO:HD3	1.84	0.45
45:RZ:110:GLY:H	45:RZ:142:SER:HB2	1.80	0.45
1:XA:58:C:O2'	1:XA:388:G:N7	2.38	0.45
1:XA:477:G:H2'	1:XA:478:A:O4'	2.16	0.45
1:XA:1033:G:H2'	1:XA:1034:G:C8	2.51	0.45
1:XA:1053:G:N7	1:XA:1199:U:H3'	2.31	0.45
9:XI:16:ARG:O	9:XI:63:ILE:HA	2.16	0.45
14:YN:6:LEU:HD23	14:YN:9:LYS:HD3	1.98	0.45
23:XX:17:U:O2'	23:XX:18:G:H5'	2.16	0.45
25:YA:270(N):G:O2'	25:YA:270(P):C:H5''	2.15	0.45
25:YA:1190:G:H5'	35:YP:32:THR:HA	1.98	0.45
25:YA:1441:G:O2'	25:YA:1442:G:H5'	2.16	0.45
30:YG:174:GLU:HG2	30:YG:180:PHE:HD1	1.81	0.45
31:YH:50:VAL:HG22	31:YH:52:VAL:H	1.81	0.45
41:YV:4:ILE:HB	41:YV:40:LEU:HB2	1.97	0.45
43:YX:67:GLY:O	43:YX:69:TYR:N	2.42	0.45
52:Y6:31:PRO:HB2	52:Y6:32:ASN:H	1.50	0.45
1:QA:398:C:H2'	1:QA:399:G:C8	2.52	0.45
1:QA:542:G:H5'	4:QD:41:GLY:HA3	1.97	0.45
1:QA:716:A:H2'	1:QA:717:C:O4'	2.17	0.45
1:QA:719:C:O2'	18:QR:49:LYS:HB3	2.17	0.45
1:QA:1086:U:O5'	1:QA:1086:U:H6	2.00	0.45
1:QA:1422:G:O3'	34:RO:49:ARG:NH1	2.47	0.45
2:QB:127:ILE:HD13	2:QB:127:ILE:HA	1.88	0.45
17:QQ:69:LYS:H	17:QQ:70:ARG:HD2	1.81	0.45
19:QS:11:VAL:HG13	19:QS:39:THR:H	1.81	0.45
25:RA:271:G:H2'	25:RA:272:G:C8	2.51	0.45
25:RA:882:G:H1	25:RA:894:C:H42	1.65	0.45
25:RA:1588:C:O2	25:RA:1588:C:H2'	2.17	0.45
25:RA:2343:C:H2'	25:RA:2344:U:C6	2.51	0.45
25:RA:2666:C:N3	31:RH:152:ARG:NH2	2.65	0.45
25:RA:2774:C:H2'	25:RA:2775:A:O4'	2.16	0.45
25:RA:2850:A:N7	25:RA:2868:A:O2'	2.45	0.45
29:RF:33:LEU:HD12	29:RF:33:LEU:HA	1.80	0.45
38:RS:61:ASN:O	38:RS:65:VAL:N	2.46	0.45
44:RY:28:LYS:O	44:RY:38:ILE:HG23	2.15	0.45
45:RZ:24:LEU:HD22	45:RZ:41:LEU:HD23	1.97	0.45
1:XA:570:G:H1'	1:XA:820:U:C4	2.52	0.45
2:XB:7:VAL:O	2:XB:217:ARG:NH2	2.48	0.45
2:XB:162:ILE:HD11	2:XB:184:VAL:HG22	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:XD:178:VAL:O	4:XD:180:GLY:N	2.42	0.45
7:XG:20:ASP:OD2	7:XG:22:LEU:N	2.49	0.45
16:XP:71:ARG:HG3	16:XP:80:PHE:CE1	2.51	0.45
25:YA:644:A:H4'	25:YA:645:C:H5	1.81	0.45
25:YA:848:G:H2'	25:YA:849:A:C8	2.52	0.45
25:YA:960:A:H61	36:YQ:82:ARG:NH2	2.14	0.45
25:YA:1000:A:C6	25:YA:1001:A:C6	3.05	0.45
25:YA:1049:C:N4	25:YA:2751:G:O6	2.49	0.45
25:YA:1171:G:H1	25:YA:1178:C:N4	2.11	0.45
25:YA:1281:G:H5'	25:YA:1282:U:OP2	2.16	0.45
25:YA:1427:A:H4'	25:YA:1428:C:O5'	2.17	0.45
25:YA:1709:U:H2'	25:YA:1710:C:C6	2.51	0.45
25:YA:1914:C:O2	25:YA:1914:C:O4'	2.29	0.45
25:YA:2015:A:H1'	51:Y5:2:ALA:HA	1.98	0.45
31:YH:7:LEU:HD12	31:YH:65:HIS:CE1	2.51	0.45
32:YI:40:THR:OG1	32:YI:43:ASN:OD1	2.33	0.45
45:YZ:52:SER:O	45:YZ:54:HIS:N	2.49	0.45
52:Y6:39:TYR:HB3	52:Y6:41:PRO:HD2	1.98	0.45
54:Y8:60:LEU:O	54:Y8:63:PRO:HD2	2.16	0.45
1:QA:116:A:H61	1:QA:313:A:H1'	1.82	0.45
1:QA:276:G:O3'	17:QQ:68:ARG:NH1	2.38	0.45
3:QC:177:THR:HG23	3:QC:180:ALA:HB2	1.98	0.45
25:RA:747:U:O2	25:RA:2014:A:H1'	2.17	0.45
25:RA:2286:A:C8	25:RA:2287:A:C6	3.05	0.45
25:RA:2420:C:OP1	54:R8:34:TRP:CB	2.58	0.45
25:RA:2485:G:H5''	36:RQ:46:GLN:HE21	1.82	0.45
25:RA:2811:G:OP1	28:RE:61:ARG:CG	2.64	0.45
28:RE:131:ALA:HB1	28:RE:135:HIS:CE1	2.51	0.45
31:RH:159:GLU:HG3	31:RH:170:ARG:NH1	2.31	0.45
35:RP:36:LYS:HB3	35:RP:37:GLY:HA2	1.97	0.45
42:RW:18:ARG:HD3	42:RW:76:VAL:CG1	2.44	0.45
50:R4:26:SER:OG	50:R4:27:THR:N	2.48	0.45
55:R9:1:MET:HB3	55:R9:4:ARG:CZ	2.46	0.45
1:XA:44:G:H2'	1:XA:45:U:O4'	2.15	0.45
1:XA:923:A:OP1	5:XE:21:ALA:HB2	2.16	0.45
1:XA:1308:U:H2'	1:XA:1309:G:C8	2.51	0.45
1:XA:1510:U:H2'	1:XA:1511:G:C8	2.50	0.45
9:XI:28:VAL:HG21	9:XI:63:ILE:H	1.81	0.45
20:XT:14:LYS:O	20:XT:18:GLN:HG3	2.16	0.45
25:YA:566:U:H2'	25:YA:567:A:O4'	2.17	0.45
25:YA:1070:A:H5'	25:YA:1071:G:H5''	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:YA:2562:U:H1'	34:YO:23:ARG:HH11	1.80	0.45
25:YA:2786:U:H2'	25:YA:2787:C:H6	1.82	0.45
31:YH:94:TYR:OH	31:YH:153:LYS:HE2	2.16	0.45
34:YO:75:SER:HB2	39:YT:74:ARG:HH12	1.81	0.45
44:YY:99:CYS:SG	44:YY:100:ALA:N	2.86	0.45
45:YZ:150:LEU:CB	45:YZ:171:ILE:H	2.29	0.45
52:Y6:28:ARG:CG	52:Y6:30:THR:H	2.29	0.45
1:QA:1322:C:H5'	13:QM:100:GLY:O	2.16	0.45
1:QA:1429:C:H2'	1:QA:1430:C:C6	2.52	0.45
6:QF:9:VAL:HB	6:QF:87:ARG:HB2	1.97	0.45
25:RA:1096:A:C5	25:RA:1097:U:H1'	2.52	0.45
25:RA:1226:G:P	41:RV:85:LYS:HD3	2.57	0.45
25:RA:1979:C:C2'	25:RA:1980:G:H5'	2.46	0.45
25:RA:2758:A:C2	25:RA:2759:G:H1'	2.52	0.45
25:RA:2823:A:OP1	28:RE:113:PHE:HB2	2.17	0.45
26:RB:24:G:O6	26:RB:56:G:O2'	2.34	0.45
28:RE:51:PHE:CE2	28:RE:52:LEU:HG	2.52	0.45
31:RH:3:ARG:HH11	31:RH:6:ARG:NE	2.14	0.45
32:RI:100:ALA:O	32:RI:102:SER:N	2.49	0.45
34:RO:64:ARG:HB2	34:RO:83:ALA:HB3	1.99	0.45
48:R2:25:VAL:O	48:R2:29:LYS:HG3	2.17	0.45
1:XA:31:G:O2'	1:XA:48:C:N4	2.49	0.45
7:XG:5:ARG:HH21	7:XG:7:ALA:HA	1.81	0.45
25:YA:764:A:O4'	27:YD:213:ARG:HG3	2.16	0.45
25:YA:815:C:H2'	25:YA:816:C:C6	2.50	0.45
25:YA:2811:G:OP2	25:YA:2811:G:H8	1.99	0.45
39:YT:104:ASN:O	39:YT:106:SER:N	2.50	0.45
41:YV:38:LEU:HD23	41:YV:38:LEU:HA	1.71	0.45
44:YY:84:ARG:CZ	44:YY:97:ARG:HB2	2.46	0.45
45:YZ:110:GLY:C	45:YZ:112:ARG:H	2.20	0.45
1:QA:1412:C:H2'	1:QA:1413:A:H8	1.80	0.45
1:QA:1502:A:H2	1:QA:1505:G:N1	1.98	0.45
2:QB:37:ASN:O	2:QB:37:ASN:ND2	2.49	0.45
5:QE:57:LYS:O	5:QE:61:TYR:HD2	1.99	0.45
19:QS:42:PRO:HG3	50:R4:60:GLN:HG3	1.98	0.45
25:RA:226:G:H21	25:RA:228:A:H62	1.64	0.45
25:RA:1795:C:O2	27:RD:255:LYS:HE3	2.17	0.45
27:RD:30:GLU:HG3	27:RD:63:ARG:CZ	2.47	0.45
28:RE:35:GLN:H	28:RE:48:GLN:HB2	1.81	0.45
32:RI:79:ILE:O	32:RI:142:VAL:CG2	2.52	0.45
1:XA:210:U:O2'	1:XA:216:G:O4'	2.33	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:1453:G:N1	20:XT:55:ILE:HD11	2.32	0.45
2:XB:172:ILE:H	2:XB:172:ILE:HD12	1.82	0.45
13:XM:15:VAL:HG12	13:XM:45:VAL:HG22	1.99	0.45
25:YA:817:C:H4'	25:YA:932:G:C6	2.52	0.45
31:YH:77:LYS:HD2	31:YH:77:LYS:HA	1.72	0.45
33:YN:63:THR:O	33:YN:66:LYS:HG3	2.17	0.45
36:YQ:65:PHE:O	36:YQ:104:PHE:HA	2.17	0.45
43:YX:64:LYS:HZ1	43:YX:73:ARG:NH2	2.15	0.45
1:QA:130:A:H1'	1:QA:263:A:O2'	2.15	0.45
1:QA:250:A:H5'	1:QA:252:U:O4'	2.17	0.45
1:QA:1068:G:N2	1:QA:1191:A:N3	2.58	0.45
3:QC:59:ARG:HG2	3:QC:64:VAL:HG12	1.99	0.45
3:QC:139:GLN:O	3:QC:143:GLU:N	2.49	0.45
5:QE:78:HIS:HA	8:QH:105:ARG:HG3	1.98	0.45
8:QH:51:VAL:HG11	8:QH:60:ARG:NH1	2.31	0.45
12:QL:58:VAL:O	12:QL:65:GLU:HA	2.16	0.45
25:RA:105:C:O2'	44:RY:2:ARG:NE	2.49	0.45
25:RA:971:C:H2'	25:RA:972:G:O4'	2.17	0.45
25:RA:2712:U:O2'	25:RA:2712(A):A:OP2	2.30	0.45
25:RA:2816:C:O2	25:RA:2883:A:O2'	2.33	0.45
28:RE:116:VAL:HG13	28:RE:122:PHE:HB2	1.97	0.45
48:R2:15:LYS:HD3	48:R2:67:LYS:HZ1	1.81	0.45
1:XA:374:A:C6	1:XA:375:U:C4	3.05	0.45
1:XA:1118:C:H2'	1:XA:1119:C:C6	2.52	0.45
1:XA:1227:A:C2	13:XM:117:VAL:HG11	2.52	0.45
1:XA:1289:A:H2'	1:XA:1290:G:H5'	1.97	0.45
4:XD:9:CYS:O	4:XD:13:ARG:HG3	2.16	0.45
7:XG:78:ARG:HB3	7:XG:79:ARG:H	1.50	0.45
10:XJ:3:LYS:N	10:XJ:74:ILE:O	2.50	0.45
11:XK:9:LYS:HB2	11:XK:9:LYS:HE2	1.75	0.45
25:YA:589:C:H2'	25:YA:590:A:C8	2.52	0.45
25:YA:667:U:O2	54:Y8:2:PRO:HD2	2.17	0.45
25:YA:910:A:N1	25:YA:2277:G:H1'	2.32	0.45
25:YA:1203:G:H5'	35:YP:3:LEU:HD12	1.97	0.45
49:Y3:7:LYS:HG2	49:Y3:9:VAL:HG13	1.97	0.45
1:QA:243:A:H4'	1:QA:244:U:O5'	2.16	0.45
1:QA:328:C:H4'	1:QA:329:A:H5'	1.98	0.45
1:QA:413:G:N2	1:QA:429:U:OP2	2.30	0.45
1:QA:429:U:H1'	1:QA:430:A:H5''	1.98	0.45
1:QA:484:G:H5'	1:QA:486:U:H1'	1.99	0.45
1:QA:1189:C:H5''	3:QC:5:ILE:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:QA:1288:A:H2'	1:QA:1289:A:C8	2.52	0.45
3:QC:119:ARG:HH22	3:QC:140:ARG:HG2	1.81	0.45
3:QC:180:ALA:HB1	3:QC:182:ILE:HG13	1.98	0.45
5:QE:11:ILE:O	5:QE:12:LEU:CB	2.34	0.45
25:RA:244:A:H4'	35:RP:74:GLU:HB2	1.99	0.45
25:RA:443:A:H5''	25:RA:444:C:OP1	2.17	0.45
25:RA:1043:C:O2	25:RA:1112:G:N2	2.30	0.45
25:RA:1856:G:H2'	25:RA:1857:G:C5'	2.47	0.45
27:RD:35:LYS:HD3	27:RD:63:ARG:HG3	1.99	0.45
27:RD:137:PRO:O	27:RD:140:THR:OG1	2.28	0.45
28:RE:67:PHE:O	28:RE:69:LYS:N	2.50	0.45
29:RF:136:THR:HG23	29:RF:170:LEU:HD11	1.99	0.45
36:RQ:78:PRO:O	36:RQ:79:LEU:HG	2.17	0.45
38:RS:27:SER:HA	38:RS:88:ASP:HB2	1.99	0.45
41:RV:67:GLY:O	41:RV:88:ARG:HD2	2.16	0.45
52:R6:41:PRO:HD2	52:R6:49:HIS:NE2	2.32	0.45
1:XA:1434:A:H2'	1:XA:1435:G:O4'	2.17	0.45
13:XM:3:ARG:HA	13:XM:8:GLU:HA	1.98	0.45
31:YH:10:PRO:HB2	31:YH:11:VAL:H	1.62	0.45
31:YH:151:ILE:O	31:YH:152:ARG:HG2	2.15	0.45
32:YI:74:ASN:HB2	32:YI:75:LEU:H	1.65	0.45
32:YI:76:THR:OG1	32:YI:140:LEU:HD12	2.17	0.45
35:YP:3:LEU:HA	35:YP:6:LEU:HD23	1.98	0.45
35:YP:64:LYS:HB3	35:YP:65:ARG:H	1.50	0.45
43:YX:49:VAL:HB	43:YX:83:VAL:HG23	1.98	0.45
1:QA:1323:G:O2'	1:QA:1324:A:H5'	2.17	0.45
2:QB:33:TYR:HB3	2:QB:41:ILE:O	2.16	0.45
14:QN:27:CYS:HB3	14:QN:28:GLY:H	1.44	0.45
17:QQ:81:ARG:HE	17:QQ:84:LEU:HD12	1.82	0.45
19:QS:70:LYS:HB2	19:QS:71:LEU:H	1.68	0.45
25:RA:271:G:H2'	25:RA:272:G:H8	1.81	0.45
25:RA:389:G:N1	35:RP:71:VAL:HG12	2.32	0.45
25:RA:394:A:C2'	25:RA:395:U:H5''	2.46	0.45
25:RA:526:A:O2'	25:RA:2043:C:O2	2.27	0.45
25:RA:576:U:H2'	25:RA:577:G:C8	2.52	0.45
25:RA:661:C:H1'	35:RP:12:ALA:HA	1.99	0.45
25:RA:885:C:H1'	25:RA:890:A:N6	2.32	0.45
25:RA:1281:G:H5'	25:RA:1282:U:OP2	2.17	0.45
25:RA:2696:U:H2'	25:RA:2697:G:C8	2.52	0.45
26:RB:11:C:OP2	46:R0:72:ARG:NH1	2.50	0.45
28:RE:58:ARG:CZ	28:RE:58:ARG:HA	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:RF:34:TRP:CE3	35:RP:8:PRO:HB3	2.51	0.45
29:RF:133:ASN:HB2	29:RF:138:GLU:OE1	2.17	0.45
40:RU:92:ARG:HH12	41:RV:11:GLN:H	1.64	0.45
41:RV:7:THR:HG23	41:RV:22:VAL:HG21	1.99	0.45
45:RZ:107:THR:OG1	45:RZ:108:PRO:HD3	2.17	0.45
1:XA:1293:G:H2'	1:XA:1294:G:H8	1.82	0.45
2:XB:97:TRP:CH2	2:XB:173:ALA:HA	2.52	0.45
7:XG:65:ALA:HB1	7:XG:127:ALA:HB3	1.98	0.45
8:XH:102:ARG:H	8:XH:102:ARG:HG3	1.66	0.45
25:YA:363(B):G:H2'	25:YA:363(C):G:C8	2.52	0.45
25:YA:581:C:H2'	25:YA:582:G:H8	1.80	0.45
25:YA:1054:A:H61	25:YA:1105:U:H3	1.64	0.45
25:YA:1084:A:H2	25:YA:1106:G:H1'	1.82	0.45
25:YA:1085:A:O2'	25:YA:1086:A:OP1	2.31	0.45
29:YF:127:GLU:O	29:YF:129:PHE:N	2.49	0.45
30:YG:16:ARG:O	30:YG:20:ILE:HG12	2.17	0.45
43:YX:26:TYR:O	43:YX:81:VAL:HG22	2.17	0.45
52:Y6:28:ARG:HG2	52:Y6:31:PRO:HD2	1.99	0.45
56:Z7:75:C:O5'	56:Z7:75:C:H6	1.99	0.45
1:QA:4:U:O4	8:QH:105:ARG:HD3	2.17	0.45
1:QA:518:C:H2'	1:QA:530:G:H8	1.82	0.45
1:QA:657:G:H4'	15:QO:28:GLN:HG2	1.99	0.45
1:QA:1493:A:O2'	24:QY:55:PRO:HD2	2.17	0.45
1:QA:1503:A:N3	23:QX:12:A:H2	2.15	0.45
13:QM:77:ASN:O	13:QM:80:ARG:HB2	2.16	0.45
18:QR:50:ILE:HD11	18:QR:70:ILE:HG21	1.98	0.45
20:QT:92:LEU:HD13	20:QT:92:LEU:HA	1.84	0.45
24:QY:37:ILE:HD11	24:QY:66:ILE:HD11	1.99	0.45
25:RA:264:C:O2'	25:RA:265:A:H2'	2.17	0.45
25:RA:465:G:H2'	25:RA:466:A:C8	2.52	0.45
25:RA:627:A:H4'	25:RA:628:G:H5'	1.97	0.45
25:RA:1047:G:H2'	25:RA:1110:G:N1	2.33	0.45
25:RA:1113:U:H2'	25:RA:1114:G:H8	1.81	0.45
25:RA:1169:G:H1	25:RA:1180:C:N4	2.12	0.45
25:RA:1339:G:H5''	43:RX:16:LYS:HD3	1.98	0.45
25:RA:1570:A:H2'	25:RA:1571:A:C8	2.52	0.45
25:RA:2019:A:O4'	40:RU:34:LYS:HD2	2.18	0.45
25:RA:2593:U:H2'	25:RA:2594:C:C6	2.51	0.45
25:RA:2887:U:H2'	25:RA:2888:C:C6	2.51	0.45
32:RI:56:LYS:HE3	32:RI:57:ARG:HG3	1.99	0.45
45:RZ:3:TYR:HB2	45:RZ:57:ILE:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:RZ:6:LYS:HE3	45:RZ:6:LYS:HB2	1.76	0.45
45:RZ:157:LEU:HB3	45:RZ:161:VAL:HG11	1.97	0.45
1:XA:197:A:H1'	1:XA:198:G:O4'	2.17	0.45
1:XA:1260:C:O5'	1:XA:1284:C:H4'	2.16	0.45
22:XV:61:C:H2'	22:XV:62:C:C6	2.52	0.45
25:YA:997:G:OP2	40:YU:58:ARG:NH1	2.50	0.45
25:YA:2887:U:H2'	25:YA:2888:C:C6	2.51	0.45
29:YF:25:PRO:HB2	29:YF:26:ALA:H	1.62	0.45
29:YF:46:ARG:HB3	29:YF:48:THR:HG23	1.98	0.45
29:YF:117:ARG:HD2	29:YF:190:GLU:O	2.16	0.45
49:Y3:43:ILE:O	49:Y3:47:VAL:HG23	2.17	0.45
1:QA:179:A:H2'	1:QA:180:U:C6	2.52	0.44
1:QA:458:C:H2'	1:QA:464:G:H8	1.82	0.44
1:QA:793:U:H5'	1:QA:794:A:O5'	2.17	0.44
1:QA:971:G:H4'	1:QA:972:C:H5''	2.00	0.44
1:QA:979:C:OP1	1:QA:1223:C:N4	2.50	0.44
1:QA:1348:U:OP2	1:QA:1348:U:C6	2.70	0.44
19:QS:32:LYS:HE2	19:QS:32:LYS:HB2	1.76	0.44
21:QU:8:THR:HG22	21:QU:10:ARG:H	1.82	0.44
25:RA:247:G:H4'	25:RA:386:G:C6	2.52	0.44
25:RA:352:G:O2'	25:RA:353:G:OP1	2.31	0.44
25:RA:654(S):G:O2'	25:RA:654(T):C:OP2	2.30	0.44
25:RA:1589:C:N3	25:RA:1590:U:C5	2.84	0.44
25:RA:1932:A:H2'	25:RA:1933:G:O4'	2.17	0.44
29:RF:34:TRP:CE2	35:RP:8:PRO:HD3	2.52	0.44
48:R2:50:ILE:HD12	48:R2:51:ARG:H	1.82	0.44
51:R5:3:LYS:HA	51:R5:3:LYS:HE3	1.99	0.44
52:R6:15:GLU:OE2	52:R6:44:ARG:NH1	2.49	0.44
1:XA:736:C:OP1	18:XR:68:LYS:NZ	2.41	0.44
1:XA:1028(B):C:H3'	1:XA:1029:G:H4'	1.99	0.44
7:XG:22:LEU:HG	7:XG:62:PHE:HE2	1.81	0.44
13:XM:102:ARG:HD3	13:XM:105:THR:OG1	2.17	0.44
25:YA:197:A:N6	25:YA:2430:A:H2'	2.33	0.44
25:YA:250:G:H2'	25:YA:251:A:C8	2.52	0.44
25:YA:686:G:N2	25:YA:788:A:H61	2.14	0.44
25:YA:1225:C:O2'	41:YV:85:LYS:N	2.44	0.44
25:YA:1922:G:H2'	25:YA:1923:U:O4'	2.17	0.44
25:YA:2291:U:H2'	25:YA:2292:C:C6	2.52	0.44
25:YA:2365:G:H4'	46:Y0:60:PHE:CZ	2.52	0.44
26:YB:24:G:H5''	26:YB:25:A:OP1	2.17	0.44
28:YE:4:ILE:HD13	28:YE:95:ILE:HD13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:YU:98:LEU:C	40:YU:100:VAL:H	2.19	0.44
41:YV:61:VAL:HA	41:YV:94:LEU:HD22	1.99	0.44
50:Y4:5:ILE:HD12	50:Y4:5:ILE:HA	1.88	0.44
52:Y6:40:CYS:N	52:Y6:41:PRO:HD2	2.32	0.44
1:QA:858:G:O6	1:QA:869:G:H3'	2.17	0.44
1:QA:1314:C:H2'	1:QA:1315:U:C6	2.52	0.44
4:QD:13:ARG:HB3	4:QD:14:ARG:H	1.51	0.44
25:RA:1006:C:C2	25:RA:1138:G:N2	2.85	0.44
25:RA:1879:C:H2'	25:RA:1880:C:O4'	2.17	0.44
29:RF:128:ALA:O	29:RF:142:TRP:NE1	2.49	0.44
31:RH:54:ARG:NE	31:RH:57:ASP:OD1	2.50	0.44
40:RU:76:TYR:CZ	40:RU:80:ILE:HG13	2.51	0.44
48:R2:4:SER:HB2	48:R2:5:GLU:H	1.45	0.44
50:R4:60:GLN:HB3	50:R4:61:ARG:NH2	2.32	0.44
1:XA:792:A:H4'	1:XA:793:U:O5'	2.17	0.44
2:XB:178:ARG:NH2	8:XH:74:PRO:HB3	2.32	0.44
9:XI:65:VAL:HG21	9:XI:73:GLN:HB3	1.99	0.44
18:XR:32:ARG:HA	18:XR:69:THR:HG21	1.99	0.44
25:YA:414:C:H2'	25:YA:415:A:C8	2.53	0.44
25:YA:2693:A:H2'	25:YA:2694:G:C8	2.52	0.44
25:YA:2774:C:H2'	25:YA:2775:A:O4'	2.17	0.44
31:YH:52:VAL:O	31:YH:65:HIS:NE2	2.42	0.44
31:YH:144:VAL:O	31:YH:148:ILE:HG12	2.17	0.44
36:YQ:103:MET:H	36:YQ:103:MET:HG3	1.53	0.44
39:YT:26:ASP:HB2	39:YT:91:ARG:HA	1.98	0.44
40:YU:88:ILE:HG22	41:YV:49:THR:O	2.17	0.44
45:YZ:29:TYR:CE2	45:YZ:87:ASP:HB2	2.52	0.44
7:QG:26:PHE:O	7:QG:30:ILE:HG12	2.17	0.44
9:QI:48:GLU:N	9:QI:49:PRO:HD2	2.32	0.44
9:QI:85:LEU:O	9:QI:89:ASN:HB2	2.17	0.44
20:QT:14:LYS:HB2	20:QT:17:ARG:NH2	2.32	0.44
25:RA:530:G:N1	25:RA:2023:G:OP1	2.42	0.44
25:RA:1496:A:H8	25:RA:1577:C:O2'	1.99	0.44
25:RA:2318:G:H8	25:RA:2318:G:O5'	2.01	0.44
26:RB:30:C:H1'	26:RB:57:A:H61	1.81	0.44
31:RH:90:LYS:NZ	31:RH:159:GLU:OE1	2.48	0.44
33:RN:17:ASP:OD2	33:RN:56:ASN:ND2	2.29	0.44
37:RR:38:VAL:HB	37:RR:39:PRO:HD3	1.99	0.44
38:RS:14:VAL:HG21	38:RS:89:ARG:HD3	1.99	0.44
44:RY:7:VAL:HG21	44:RY:37:VAL:HG11	1.99	0.44
44:RY:17:SER:HB2	44:RY:71:LYS:HB3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:1183:A:HO2'	1:XA:1184:G:P	2.40	0.44
3:XC:179:ARG:NH1	3:XC:207:VAL:HG22	2.33	0.44
8:XH:4:ASP:OD2	8:XH:89:PRO:HD3	2.18	0.44
11:XK:111:ASP:OD2	18:XR:84:LYS:HD2	2.17	0.44
12:XL:45:PRO:HG2	12:XL:49:ASN:O	2.17	0.44
19:XS:6:LYS:HG2	19:XS:7:LYS:H	1.81	0.44
25:YA:729:G:C5	27:YD:208:LYS:HB2	2.52	0.44
25:YA:910:A:H2'	25:YA:911:A:C8	2.52	0.44
25:YA:1445:C:H2'	25:YA:1446:C:C6	2.50	0.44
25:YA:1568:G:H4'	27:YD:59:LYS:HB3	1.98	0.44
25:YA:1686:C:H2'	25:YA:1687:G:O4'	2.18	0.44
25:YA:2522:U:O4	25:YA:2541:A:H2	2.00	0.44
25:YA:2688:U:OP1	25:YA:2713:A:N6	2.50	0.44
27:YD:43:ARG:CB	27:YD:54:ARG:HB2	2.48	0.44
27:YD:69:ARG:NH1	27:YD:128:GLY:O	2.46	0.44
29:YF:149:ASP:OD1	29:YF:149:ASP:N	2.43	0.44
32:YI:12:LEU:HD12	32:YI:12:LEU:HA	1.79	0.44
32:YI:114:LEU:HA	32:YI:130:TYR:HB2	1.98	0.44
34:YO:87:ILE:HG22	34:YO:88:ASN:O	2.18	0.44
36:YQ:55:VAL:HG23	36:YQ:64:ILE:HD11	1.98	0.44
40:YU:50:ARG:HH11	41:YV:72:VAL:CG1	2.31	0.44
42:YW:46:PHE:O	42:YW:50:VAL:HG12	2.17	0.44
1:QA:1472:U:H2'	1:QA:1473:A:C8	2.52	0.44
2:QB:189:ASP:O	2:QB:191:ASP:N	2.50	0.44
3:QC:71:ALA:HB2	3:QC:115:LEU:HD13	1.99	0.44
6:QF:44:GLY:O	6:QF:60:PHE:N	2.47	0.44
8:QH:29:SER:HB3	8:QH:32:LYS:HG3	1.99	0.44
8:QH:83:ILE:HB	8:QH:137:VAL:HG13	1.99	0.44
9:QI:128:ARG:NH2	22:QV:33:U:OP2	2.48	0.44
20:QT:32:ALA:O	20:QT:36:LEU:HB2	2.18	0.44
24:QY:50:ILE:HG13	24:QY:51:TYR:CD1	2.52	0.44
25:RA:197:A:N6	25:RA:2430:A:H2'	2.32	0.44
25:RA:483:A:C5'	44:RY:49:VAL:HA	2.48	0.44
25:RA:635:C:O2'	25:RA:639:U:OP1	2.32	0.44
25:RA:773:U:O2'	27:RD:48:ARG:HD3	2.17	0.44
25:RA:2529:G:H5'	25:RA:2530:A:O5'	2.17	0.44
25:RA:2563:U:H4'	34:RO:28:SER:HA	1.99	0.44
28:RE:34:VAL:HG12	28:RE:64:LYS:HE2	1.98	0.44
28:RE:57:LYS:HZ2	28:RE:57:LYS:H	1.66	0.44
47:R1:40:ARG:NH2	47:R1:42:GLN:HG2	2.32	0.44
1:XA:45:U:H2'	1:XA:46:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:1181:G:O2'	1:XA:1182:G:C8	2.70	0.44
2:XB:80:ILE:HD13	2:XB:212:GLN:HA	1.99	0.44
8:XH:21:LYS:O	8:XH:65:TYR:OH	2.21	0.44
20:XT:10:LEU:HD22	20:XT:11:SER:N	2.32	0.44
25:YA:631:A:H2'	25:YA:632:A:O4'	2.17	0.44
25:YA:670:A:H5'	35:YP:42:SER:O	2.18	0.44
25:YA:1183:G:O3'	49:Y3:29:ARG:NH2	2.43	0.44
25:YA:1578:U:C2'	25:YA:1579:A:H5'	2.48	0.44
25:YA:1899:G:H2'	25:YA:1899:G:N3	2.33	0.44
25:YA:1952:A:C2	34:YO:22:ILE:HG23	2.52	0.44
25:YA:2150:U:H2'	25:YA:2151:G:C8	2.52	0.44
25:YA:2396:G:O2'	47:Y1:29:GLY:HA3	2.18	0.44
25:YA:2836:U:H2'	25:YA:2837:G:C8	2.52	0.44
27:YD:144:ALA:HB3	27:YD:192:THR:HG23	2.00	0.44
29:YF:18:ARG:HG2	29:YF:19:GLU:H	1.82	0.44
31:YH:20:ALA:O	31:YH:22:GLY:N	2.51	0.44
35:YP:64:LYS:CG	54:Y8:25:MET:HE2	2.46	0.44
35:YP:66:GLY:O	35:YP:67:MET:CB	2.65	0.44
51:Y5:36:CYS:HB3	51:Y5:37:LYS:H	1.67	0.44
56:Z6:75:C:H2'	56:Z6:76:PPU:N9	2.32	0.44
1:QA:110:C:O2'	16:QP:25:ARG:O	2.32	0.44
1:QA:1352:C:OP1	21:QU:3:LYS:NZ	2.35	0.44
2:QB:21:ARG:NH2	2:QB:38:GLY:HA3	2.32	0.44
2:QB:87:ARG:NH2	2:QB:233:SER:HB2	2.33	0.44
10:QJ:99:LYS:HD3	10:QJ:100:THR:H	1.83	0.44
15:QO:26:GLU:OE2	15:QO:77:ARG:HD2	2.18	0.44
25:RA:593:G:O4'	54:R8:4:MET:HE1	2.18	0.44
25:RA:877:U:O2'	25:RA:878:A:OP1	2.34	0.44
25:RA:1400:G:H2'	25:RA:1401:G:C8	2.52	0.44
25:RA:2529:G:H22	55:R9:31:LYS:NZ	2.15	0.44
27:RD:4:LYS:NZ	27:RD:20:ASP:HA	2.32	0.44
27:RD:97:TYR:HE1	27:RD:103:ARG:HG3	1.83	0.44
13:XM:93:ARG:HA	13:XM:93:ARG:HD3	1.64	0.44
25:YA:196:A:O4'	35:YP:46:LYS:HE2	2.17	0.44
25:YA:345:A:O2'	25:YA:346:A:N7	2.49	0.44
25:YA:997:G:H5''	40:YU:58:ARG:HH12	1.83	0.44
25:YA:1418:G:O5'	25:YA:1418:G:H8	2.00	0.44
25:YA:1761:C:N3	25:YA:1762:A:N6	2.65	0.44
25:YA:2357:U:OP1	46:Y0:20:ARG:NH1	2.50	0.44
25:YA:2772:C:H2'	25:YA:2773:C:H6	1.83	0.44
26:YB:11:C:OP2	46:Y0:72:ARG:NH1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:YO:47:ILE:HG13	34:YO:48:PRO:HD2	1.98	0.44
45:YZ:40:ASP:HB3	45:YZ:43:GLU:HG3	2.00	0.44
50:Y4:13:ARG:N	50:Y4:24:THR:OG1	2.51	0.44
1:QA:974:A:H1'	14:QN:31:ARG:HE	1.81	0.44
1:QA:1145:C:H4'	1:QA:1146:A:H8	1.80	0.44
2:QB:163:PHE:HA	2:QB:185:ILE:HG13	1.98	0.44
2:QB:184:VAL:HG12	2:QB:197:VAL:HG13	2.00	0.44
5:QE:92:LYS:HA	5:QE:93:PRO:HD2	1.89	0.44
6:QF:82:ARG:HB2	6:QF:85:VAL:HG22	2.00	0.44
25:RA:322:A:OP2	29:RF:169:ASN:HB2	2.18	0.44
25:RA:755:C:H2'	25:RA:756:C:H6	1.81	0.44
25:RA:1255:U:H5''	25:RA:1256:G:H5''	2.00	0.44
25:RA:1268:A:H2'	25:RA:1269:A:O4'	2.18	0.44
25:RA:1358:G:O2'	25:RA:1359:A:H5''	2.17	0.44
25:RA:1625:C:H2'	25:RA:1626:G:O4'	2.17	0.44
25:RA:1923:U:H2'	25:RA:1924:C:C6	2.53	0.44
25:RA:2468:G:H2'	25:RA:2476:A:C2	2.52	0.44
26:RB:87:G:H2'	26:RB:88:C:H5''	2.00	0.44
29:RF:140:LEU:HD13	29:RF:170:LEU:HD21	1.98	0.44
32:RI:12:LEU:HG	32:RI:19:VAL:HG11	2.00	0.44
34:RO:68:GLU:HB3	34:RO:78:ARG:HB2	1.98	0.44
40:RU:99:ALA:HB2	40:RU:106:PHE:CD1	2.52	0.44
40:RU:100:VAL:O	40:RU:101:ARG:HG2	2.17	0.44
42:RW:29:LEU:HD21	42:RW:33:ARG:NH2	2.32	0.44
55:R9:1:MET:SD	55:R9:1:MET:N	2.89	0.44
1:XA:553:A:H5''	12:XL:24:VAL:HG21	1.99	0.44
1:XA:625:G:H2'	1:XA:626:U:C6	2.53	0.44
1:XA:1015:A:H2'	1:XA:1016:A:C8	2.53	0.44
2:XB:15:VAL:HG21	2:XB:209:ARG:HB3	1.99	0.44
3:XC:52:LEU:HD23	3:XC:52:LEU:H	1.82	0.44
6:XF:69:GLU:H	6:XF:69:GLU:CD	2.21	0.44
8:XH:42:GLU:HG3	8:XH:109:ILE:HD12	2.00	0.44
25:YA:479:A:HO2'	25:YA:481:G:H8	1.63	0.44
25:YA:2191:G:O2'	25:YA:2192:G:OP1	2.30	0.44
28:YE:11:MET:SD	28:YE:24:THR:HG22	2.58	0.44
34:YO:8:LEU:HB2	34:YO:19:ILE:HG13	2.00	0.44
34:YO:104:ARG:NE	39:YT:34:VAL:HG11	2.32	0.44
44:YY:97:ARG:NH2	44:YY:98:VAL:HB	2.24	0.44
45:YZ:135:GLU:H	45:YZ:135:GLU:HG2	1.60	0.44
53:Y7:9:ARG:HH12	53:Y7:47:ARG:HH12	1.65	0.44
1:QA:222:U:H2'	1:QA:223:U:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:QA:706:A:O4'	11:QK:29:ILE:HD11	2.18	0.44
1:QA:1347:G:C8	9:QI:11:LYS:HE3	2.52	0.44
4:QD:9:CYS:SG	4:QD:32:ALA:HB2	2.58	0.44
12:QL:41:ARG:HB3	12:QL:42:THR:H	1.56	0.44
25:RA:27:G:N2	25:RA:512:G:H1'	2.33	0.44
25:RA:1728:G:H8	25:RA:1732:A:N6	2.15	0.44
25:RA:2109:U:H2'	25:RA:2110:G:C8	2.53	0.44
27:RD:108:PRO:HA	27:RD:196:VAL:HA	1.99	0.44
29:RF:34:TRP:HB2	35:RP:6:LEU:HD12	1.99	0.44
44:RY:75:ILE:CG1	44:RY:76:CYS:N	2.80	0.44
6:XF:97:PHE:HD2	18:XR:31:LEU:HD11	1.83	0.44
13:XM:9:ILE:CG1	13:XM:10:PRO:N	2.81	0.44
15:XO:70:LEU:HD11	15:XO:77:ARG:HG3	1.98	0.44
16:XP:34:GLU:OE2	16:XP:55:ARG:HD3	2.17	0.44
25:YA:394:A:C6	25:YA:395:U:C4	3.05	0.44
25:YA:2370:G:C6	25:YA:2371:G:C6	3.06	0.44
25:YA:2633:G:H1'	28:YE:62:PRO:HG3	2.00	0.44
25:YA:2839:G:H5'	37:YR:46:GLY:HA2	2.00	0.44
30:YG:55:LYS:O	30:YG:59:GLU:HB2	2.17	0.44
32:YI:95:LYS:HE2	32:YI:95:LYS:HB3	1.86	0.44
32:YI:141:LYS:CB	32:YI:142:VAL:HG13	2.46	0.44
41:YV:71:LEU:H	41:YV:86:GLY:CA	2.30	0.44
44:YY:56:PRO:O	44:YY:57:GLN:HB2	2.17	0.44
47:Y1:93:GLU:HG2	47:Y1:98:LEU:HD11	1.99	0.44
1:QA:103:C:O2'	1:QA:172:A:N1	2.40	0.44
1:QA:1330:U:H3'	1:QA:1331:G:O4'	2.18	0.44
1:QA:1347:G:H4'	1:QA:1348:U:H6	1.82	0.44
2:QB:178:ARG:HH22	8:QH:74:PRO:HB3	1.83	0.44
12:QL:53:ARG:NH1	12:QL:92:ASP:OD2	2.40	0.44
12:QL:110:VAL:HG23	12:QL:120:TYR:HB3	2.00	0.44
20:QT:25:ARG:HG2	20:QT:29:LYS:NZ	2.33	0.44
25:RA:340:A:H2'	25:RA:341:G:O4'	2.17	0.44
25:RA:859:G:N2	25:RA:917:A:OP2	2.40	0.44
25:RA:1060:U:H3	25:RA:1088:A:H8	1.65	0.44
32:RI:92:VAL:HB	32:RI:120:ILE:HB	1.99	0.44
35:RP:97:PRO:HD3	35:RP:126:VAL:O	2.18	0.44
38:RS:110:LEU:HB3	38:RS:111:GLU:H	1.51	0.44
45:RZ:5:LEU:HB2	45:RZ:59:LEU:HA	1.99	0.44
54:R8:54:GLU:OE2	54:R8:55:ALA:N	2.50	0.44
1:XA:224:C:H2'	1:XA:225:C:C6	2.53	0.44
4:XD:111:ALA:HB1	4:XD:116:GLN:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:XF:86:ARG:O	6:XF:87:ARG:HG2	2.18	0.44
7:XG:97:GLN:HE21	7:XG:97:GLN:HB2	1.60	0.44
9:XI:29:ASN:HB3	9:XI:30:GLY:H	1.65	0.44
21:XU:2:GLY:O	21:XU:4:GLY:N	2.51	0.44
25:YA:709:U:H2'	25:YA:710:G:H8	1.82	0.44
25:YA:1889:A:N1	25:YA:2234:G:H1'	2.33	0.44
25:YA:2876:G:O5'	39:YT:3:ARG:HA	2.17	0.44
27:YD:260:ARG:NH1	27:YD:267:SER:OG	2.51	0.44
29:YF:28:ILE:O	29:YF:30:PRO:HD3	2.17	0.44
38:YS:62:LYS:HD3	38:YS:97:ARG:NH1	2.33	0.44
1:QA:181:G:O2'	1:QA:182:U:O5'	2.35	0.44
1:QA:1225:A:H2'	1:QA:1225:A:N3	2.33	0.44
4:QD:102:ASP:OD2	4:QD:103:ASN:N	2.51	0.44
6:QF:76:ALA:O	6:QF:80:ARG:HG3	2.17	0.44
12:QL:85:ILE:HD12	12:QL:85:ILE:HA	1.85	0.44
17:QQ:57:VAL:HG12	17:QQ:76:LEU:HA	2.00	0.44
23:QX:5:A:H2'	23:QX:6:G:C8	2.52	0.44
25:RA:620:G:N3	25:RA:620:G:H5'	2.33	0.44
25:RA:1213:A:N3	25:RA:1238:G:O2'	2.43	0.44
25:RA:1228:G:OP2	40:RU:16:LYS:NZ	2.31	0.44
25:RA:1668:A:H5''	34:RO:5:GLN:HG2	2.00	0.44
25:RA:2286:A:H8	25:RA:2287:A:N6	2.16	0.44
28:RE:8:LYS:O	28:RE:10:GLY:N	2.50	0.44
31:RH:86:GLU:OE1	31:RH:86:GLU:N	2.51	0.44
54:R8:34:TRP:CG	54:R8:35:GLN:N	2.83	0.44
1:XA:359:U:H2'	1:XA:360:A:C8	2.53	0.44
1:XA:779:C:H2'	1:XA:780:A:O4'	2.17	0.44
1:XA:986:A:H1'	19:XS:54:GLY:O	2.18	0.44
1:XA:1160:G:O6	1:XA:1181:G:C6	2.71	0.44
1:XA:1399:C:C2	1:XA:1502:A:N6	2.85	0.44
3:XC:164:ARG:HG2	3:XC:165:THR:H	1.83	0.44
9:XI:103:THR:HG22	9:XI:105:ASP:H	1.83	0.44
17:XQ:45:HIS:HB2	17:XQ:65:ILE:HD12	1.98	0.44
25:YA:1424:G:H2'	25:YA:1425:G:O4'	2.18	0.44
25:YA:1990:C:H2'	25:YA:1991:U:O4'	2.17	0.44
27:YD:206:LEU:HD23	27:YD:206:LEU:HA	1.82	0.44
29:YF:140:LEU:HD13	29:YF:170:LEU:HD21	1.99	0.44
35:YP:101:VAL:HG21	35:YP:108:LYS:HG2	1.99	0.44
51:Y5:16:ARG:NH1	51:Y5:17:ASP:OD1	2.51	0.44
52:Y6:12:GLU:HA	52:Y6:24:GLU:HG2	2.00	0.44
1:QA:530:G:N3	23:QX:21:A2M:H2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:QA:811:C:H4'	1:QA:900:A:N6	2.34	0.43
1:QA:922:G:N3	1:QA:1398:A:H2	2.15	0.43
1:QA:985:C:H2'	1:QA:986:A:H8	1.82	0.43
25:RA:2286:A:H8	25:RA:2287:A:C6	2.36	0.43
25:RA:2349:G:H5'	25:RA:2350:C:OP2	2.18	0.43
27:RD:142:VAL:HG23	27:RD:193:VAL:HA	1.99	0.43
28:RE:58:ARG:HA	28:RE:58:ARG:NH2	2.32	0.43
30:RG:86:MET:HA	30:RG:87:PRO:HD2	1.74	0.43
32:RI:48:GLU:HA	32:RI:51:ILE:HB	1.99	0.43
35:RP:39:LYS:HG3	35:RP:45:LEU:HD22	1.99	0.43
41:RV:40:LEU:HD23	41:RV:40:LEU:HA	1.86	0.43
45:RZ:171:ILE:HD13	45:RZ:172:ALA:N	2.33	0.43
46:R0:11:ARG:O	46:R0:14:ARG:NH1	2.37	0.43
7:XG:113:GLU:H	7:XG:113:GLU:HG2	1.57	0.43
9:XI:20:ARG:HB2	9:XI:60:ASP:HB2	1.99	0.43
10:XJ:57:LYS:HD3	10:XJ:57:LYS:HA	1.81	0.43
25:YA:27:G:HO2'	25:YA:28:A:P	2.40	0.43
25:YA:329:G:N7	44:YY:19:LYS:HG2	2.33	0.43
25:YA:771:G:OP1	53:Y7:10:ARG:NH1	2.49	0.43
25:YA:2208:U:O4'	27:YD:151:LYS:HE2	2.18	0.43
25:YA:2213:U:H2'	25:YA:2215:G:H5'	2.00	0.43
25:YA:2506:U:OP1	28:YE:144:ARG:NH2	2.51	0.43
25:YA:2715:C:H2'	25:YA:2716:U:O5'	2.18	0.43
32:YI:141:LYS:CB	32:YI:142:VAL:HG22	2.47	0.43
32:YI:144:VAL:C	32:YI:145:VAL:CG1	2.83	0.43
35:YP:66:GLY:O	35:YP:67:MET:HB3	2.18	0.43
38:YS:110:LEU:HB3	38:YS:111:GLU:H	1.52	0.43
42:YW:20:VAL:HG22	42:YW:47:VAL:HG21	2.00	0.43
48:Y2:47:ASN:HB2	48:Y2:48:HIS:H	1.54	0.43
51:Y5:4:HIS:CB	51:Y5:5:PRO:CD	2.85	0.43
54:Y8:25:MET:SD	54:Y8:47:LYS:HG2	2.58	0.43
1:QA:141:A:H1'	1:QA:182:U:O2	2.18	0.43
1:QA:501:C:H2'	1:QA:502:G:H8	1.83	0.43
1:QA:560:U:H4'	1:QA:561:U:H5''	2.00	0.43
1:QA:611:A:H61	1:QA:629:G:H1	1.66	0.43
1:QA:1189:C:P	10:QJ:51:ARG:HH22	2.42	0.43
1:QA:1479:C:H2'	1:QA:1480:G:H8	1.82	0.43
15:QO:23:GLY:O	15:QO:27:VAL:HB	2.18	0.43
25:RA:458:G:C8	53:R7:37:LYS:HG2	2.53	0.43
25:RA:593:G:C1'	54:R8:4:MET:HE1	2.49	0.43
25:RA:1810:A:H2'	25:RA:1811:G:O4'	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:RA:2292:C:OP2	38:RS:17:ARG:NH2	2.43	0.43
25:RA:2493:U:H2'	25:RA:2494:G:O4'	2.18	0.43
26:RB:30:C:H2'	26:RB:31:C:O4'	2.19	0.43
28:RE:52:LEU:HD12	28:RE:76:ARG:HD3	2.00	0.43
32:RI:2:LYS:HA	32:RI:20:ASP:HA	1.99	0.43
34:RO:10:VAL:HG22	34:RO:17:ARG:O	2.19	0.43
35:RP:52:GLU:OE1	35:RP:53:GLY:N	2.51	0.43
44:RY:17:SER:CB	44:RY:71:LYS:HB3	2.48	0.43
45:RZ:156:LYS:O	45:RZ:157:LEU:HB2	2.14	0.43
47:R1:62:VAL:HG23	47:R1:63:ALA:O	2.18	0.43
48:R2:42:GLY:O	48:R2:44:LEU:N	2.40	0.43
1:XA:922:G:H2'	1:XA:923:A:C8	2.54	0.43
1:XA:1072:G:H2'	1:XA:1073:U:C6	2.53	0.43
2:XB:93:VAL:HG11	2:XB:97:TRP:CD1	2.53	0.43
2:XB:135:GLN:HG3	2:XB:136:VAL:HG23	1.99	0.43
12:XL:47:LYS:HB3	12:XL:48:PRO:HD3	2.00	0.43
24:XY:41:THR:O	24:XY:81:GLY:HA2	2.18	0.43
25:YA:909:A:H2'	25:YA:912:C:H5	1.81	0.43
25:YA:2350:C:H2'	25:YA:2351:G:O4'	2.19	0.43
30:YG:53:LEU:HG	30:YG:90:LEU:HD21	2.01	0.43
32:YI:56:LYS:HA	32:YI:59:ALA:HB3	1.99	0.43
33:YN:46:VAL:HG13	33:YN:48:MET:HG3	2.00	0.43
37:YR:116:LEU:HD23	37:YR:116:LEU:HA	1.83	0.43
40:YU:52:ARG:HB3	40:YU:52:ARG:NH1	2.33	0.43
1:QA:939:G:H5''	7:QG:102:ARG:NH2	2.33	0.43
3:QC:7:PRO:O	3:QC:11:ARG:HG2	2.19	0.43
4:QD:171:GLY:HA2	4:QD:172:PRO:HD3	1.87	0.43
7:QG:16:LEU:HD21	9:QI:42:ARG:HA	2.00	0.43
12:QL:71:PRO:HD2	12:QL:102:ARG:HD2	2.00	0.43
19:QS:16:LEU:HA	19:QS:19:VAL:HG12	1.98	0.43
19:QS:71:LEU:O	19:QS:73:GLU:N	2.51	0.43
25:RA:324:A:N6	25:RA:338:G:O2'	2.49	0.43
25:RA:1614:A:N1	42:RW:93:ALA:HB2	2.33	0.43
28:RE:117:MET:O	28:RE:117:MET:HG2	2.19	0.43
29:RF:46:ARG:HG2	29:RF:46:ARG:HH11	1.83	0.43
29:RF:117:ARG:HA	29:RF:117:ARG:HD3	1.57	0.43
35:RP:52:GLU:HB2	35:RP:53:GLY:H	1.49	0.43
35:RP:126:VAL:HG22	35:RP:145:PRO:HG2	2.00	0.43
54:R8:38:GLY:O	54:R8:41:ILE:HG22	2.18	0.43
1:XA:1493:A:C6	25:YA:1913:A:N3	2.85	0.43
25:YA:6:A:O5'	25:YA:6:A:C8	2.70	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:YA:593:G:H1'	54:Y8:4:MET:HE1	1.99	0.43
25:YA:1430:C:H2'	25:YA:1431:U:C6	2.53	0.43
25:YA:2329:G:H2'	25:YA:2330:G:C8	2.53	0.43
25:YA:2496:C:P	36:YQ:81:VAL:HG13	2.58	0.43
35:YP:21:ARG:HB3	35:YP:22:GLY:H	1.66	0.43
1:QA:1064:G:H1'	1:QA:1066:C:C6	2.54	0.43
1:QA:1319:A:C5	1:QA:1323:G:C4	3.06	0.43
6:QF:35:ALA:HA	6:QF:67:MET:HB3	2.00	0.43
25:RA:631:A:OP2	54:R8:47:LYS:NZ	2.40	0.43
25:RA:1310:G:C2'	25:RA:1311:G:H5''	2.44	0.43
25:RA:1413:G:N2	25:RA:1414:G:H1'	2.31	0.43
25:RA:1414:G:H5'	25:RA:1415:U:OP2	2.18	0.43
25:RA:2848:G:O2'	25:RA:2849:U:P	2.76	0.43
28:RE:12:THR:HB	28:RE:13:ARG:H	1.59	0.43
29:RF:2:LYS:HE2	29:RF:2:LYS:HB3	1.31	0.43
29:RF:129:PHE:CG	29:RF:163:VAL:HG21	2.53	0.43
30:RG:82:LEU:HA	30:RG:86:MET:SD	2.57	0.43
46:R0:53:MET:HB2	46:R0:59:LEU:HD23	2.00	0.43
52:R6:14:THR:HG1	52:R6:15:GLU:H	1.61	0.43
1:XA:181:G:O2'	1:XA:182:U:O5'	2.25	0.43
1:XA:1087:G:H2'	1:XA:1088:G:C8	2.53	0.43
1:XA:1432:G:OP1	39:YT:107:ASP:HB2	2.17	0.43
3:XC:153:VAL:HG22	3:XC:198:VAL:HG22	1.99	0.43
8:XH:99:GLU:OE1	8:XH:99:GLU:N	2.51	0.43
18:XR:41:LYS:HE3	18:XR:41:LYS:HB3	1.84	0.43
25:YA:706:A:C2	25:YA:707:G:H1'	2.53	0.43
25:YA:1882:C:H5'	25:YA:1883:G:OP2	2.17	0.43
27:YD:10:THR:OG1	27:YD:13:ARG:HB2	2.18	0.43
28:YE:60:ASN:O	28:YE:62:PRO:HD3	2.18	0.43
35:YP:9:ASN:O	35:YP:10:PRO:C	2.56	0.43
41:YV:71:LEU:H	41:YV:86:GLY:HA3	1.83	0.43
44:YY:19:LYS:HE3	44:YY:71:LYS:NZ	2.28	0.43
45:YZ:150:LEU:HG	45:YZ:171:ILE:HG22	2.00	0.43
1:QA:485:G:O2'	1:QA:486:U:O5'	2.31	0.43
1:QA:918:A:H2'	1:QA:919:A:C8	2.53	0.43
1:QA:986:A:H1'	19:QS:54:GLY:O	2.18	0.43
1:QA:1037:C:H2'	1:QA:1038:C:C6	2.53	0.43
1:QA:1055:A:C6	1:QA:1206:G:C5	3.06	0.43
2:QB:135:GLN:HE21	2:QB:135:GLN:HB2	1.70	0.43
4:QD:199:ASN:O	4:QD:201:GLN:N	2.39	0.43
5:QE:35:GLY:HA3	5:QE:112:LEU:HB3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:QK:15:ALA:HB2	11:QK:76:GLY:O	2.19	0.43
15:QO:36:ILE:HG23	15:QO:56:LEU:HD11	2.00	0.43
24:QY:46:LEU:O	24:QY:53:LEU:HD22	2.18	0.43
25:RA:581:C:OP1	40:RU:33:ARG:HG3	2.18	0.43
25:RA:954:G:H5''	36:RQ:13:GLN:HB3	1.99	0.43
25:RA:1316:U:H2'	25:RA:1317:A:C8	2.53	0.43
25:RA:2359:C:H2'	25:RA:2360:A:O4'	2.19	0.43
25:RA:2543:G:H2'	25:RA:2544:G:C8	2.53	0.43
25:RA:2685:G:H1'	25:RA:2726:U:H5	1.83	0.43
26:RB:64:C:H2'	26:RB:65:C:C6	2.53	0.43
28:RE:154:LYS:HA	28:RE:154:LYS:HE3	1.99	0.43
31:RH:10:PRO:HB2	31:RH:11:VAL:H	1.61	0.43
35:RP:58:THR:CG2	35:RP:61:ARG:HH21	2.23	0.43
42:RW:5:ALA:HB3	42:RW:54:ALA:HB2	2.00	0.43
44:RY:95:LYS:O	44:RY:95:LYS:HD3	2.18	0.43
54:R8:22:VAL:HB	54:R8:50:LEU:HD12	1.99	0.43
1:XA:67:C:H2'	1:XA:68:G:C8	2.53	0.43
1:XA:413:G:O6	4:XD:35:ARG:NH2	2.52	0.43
1:XA:511:C:O2'	1:XA:512:U:H5''	2.19	0.43
1:XA:1273:G:H5'	1:XA:1274:G:OP2	2.18	0.43
2:XB:6:THR:HG23	2:XB:217:ARG:HB3	2.00	0.43
7:XG:47:CYS:O	7:XG:50:ILE:HB	2.19	0.43
10:XJ:33:GLN:H	10:XJ:75:ILE:HD11	1.83	0.43
13:XM:59:TYR:O	13:XM:63:THR:OG1	2.27	0.43
20:XT:77:ALA:O	20:XT:81:LYS:HB2	2.18	0.43
25:YA:947:G:N3	25:YA:984:A:H2	2.17	0.43
25:YA:1036:G:OP1	31:YH:59:ARG:HB2	2.18	0.43
26:YB:34:U:H5''	26:YB:35:U:OP1	2.18	0.43
28:YE:38:THR:O	28:YE:42:ASP:N	2.50	0.43
30:YG:114:ILE:HG12	30:YG:140:ILE:HD13	2.00	0.43
32:YI:4:ILE:HG12	32:YI:18:VAL:HG22	2.00	0.43
37:YR:38:VAL:HB	37:YR:39:PRO:HD3	2.00	0.43
44:YY:84:ARG:NH2	44:YY:97:ARG:HB2	2.33	0.43
46:Y0:3:HIS:O	46:Y0:4:LYS:HG3	2.19	0.43
1:QA:1028(B):C:N4	1:QA:1032(A):G:H1	2.16	0.43
1:QA:1241:G:H2'	1:QA:1242:C:C6	2.53	0.43
1:QA:1256:A:OP2	3:QC:26:LYS:NZ	2.31	0.43
3:QC:40:ARG:NH2	3:QC:55:VAL:O	2.51	0.43
13:QM:16:ASP:OD2	13:QM:16:ASP:N	2.50	0.43
16:QP:43:LYS:HG2	16:QP:48:TRP:CD2	2.53	0.43
19:QS:48:THR:HG22	19:QS:61:TYR:HD1	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:RA:38:A:H2'	25:RA:39:C:C6	2.53	0.43
25:RA:654(R):C:O2'	25:RA:654(S):G:O5'	2.37	0.43
25:RA:958:U:H5'	36:RQ:14:ARG:CD	2.48	0.43
25:RA:1306:C:H2'	25:RA:1307:A:H8	1.83	0.43
25:RA:1308:A:H2'	25:RA:1309:G:O4'	2.19	0.43
25:RA:1341:U:OP2	25:RA:1341:U:H6	2.01	0.43
25:RA:1820:U:C2	27:RD:202:LYS:HD2	2.53	0.43
25:RA:2811:G:P	28:RE:61:ARG:HG3	2.59	0.43
27:RD:35:LYS:HB3	27:RD:63:ARG:HA	2.01	0.43
31:RH:44:VAL:HG22	31:RH:51:ARG:NH1	2.33	0.43
36:RQ:81:VAL:HG23	46:R0:7:LEU:HD11	2.00	0.43
41:RV:2:PHE:HD2	41:RV:42:GLY:HA2	1.82	0.43
41:RV:5:VAL:HG23	41:RV:37:VAL:HG11	2.00	0.43
41:RV:89:GLN:HA	41:RV:90:PRO:HD3	1.89	0.43
1:XA:646:U:H2'	1:XA:647:C:C6	2.54	0.43
1:XA:736:C:H2'	1:XA:737:A:C8	2.52	0.43
1:XA:1278:U:H5'	1:XA:1279:A:O4'	2.18	0.43
19:XS:5:LEU:H	19:XS:5:LEU:HD12	1.84	0.43
19:XS:32:LYS:HE2	19:XS:32:LYS:HB2	1.60	0.43
20:XT:23:ARG:O	20:XT:27:LYS:HB2	2.18	0.43
25:YA:277:C:H3'	25:YA:278:A:H8	1.83	0.43
25:YA:1048:A:H2	25:YA:1112:G:H21	1.67	0.43
25:YA:1114:G:H2'	25:YA:1115:G:C8	2.54	0.43
25:YA:2655:G:O2'	25:YA:2656:U:H5	2.02	0.43
25:YA:2695:C:H2'	25:YA:2696:U:H6	1.83	0.43
29:YF:125:LEU:HD12	29:YF:196:LEU:HD23	2.00	0.43
35:YP:49:ARG:HD2	54:Y8:58:ILE:CG2	2.49	0.43
47:Y1:84:GLY:O	47:Y1:87:PRO:HD2	2.19	0.43
1:QA:192:U:H2'	1:QA:193:C:H6	1.83	0.43
1:QA:246:A:N6	1:QA:281:G:H1'	2.34	0.43
1:QA:369:C:OP2	1:QA:388:G:N2	2.47	0.43
1:QA:1204:A:C5'	1:QA:1204:A:H8	2.32	0.43
1:QA:1319:A:H2'	1:QA:1323:G:N7	2.34	0.43
25:RA:623:G:H2'	25:RA:624:C:C6	2.54	0.43
25:RA:1131:G:N2	25:RA:1132:A:N3	2.66	0.43
25:RA:1528:A:C8	25:RA:1545:A:N6	2.86	0.43
25:RA:1930:G:O2'	25:RA:1931:U:P	2.77	0.43
25:RA:2364:C:H2'	25:RA:2365:G:O4'	2.19	0.43
25:RA:2451:A:N3	56:Z7:76:PPU:HD2	2.33	0.43
35:RP:98:GLU:O	35:RP:101:VAL:HG12	2.18	0.43
39:RT:125:ARG:HA	39:RT:125:ARG:HD3	1.78	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:390:C:H2'	1:XA:391:G:C8	2.54	0.43
25:YA:674:G:O2'	29:YF:74:ARG:HG3	2.19	0.43
25:YA:1075:C:H2'	25:YA:1076:C:C6	2.53	0.43
25:YA:2039:C:H2'	25:YA:2040:C:H6	1.83	0.43
25:YA:2159:G:H2'	25:YA:2160:G:C8	2.54	0.43
39:YT:65:LYS:HE3	39:YT:67:SER:HB2	2.00	0.43
43:YX:8:ILE:O	48:Y2:36:ARG:NH2	2.52	0.43
46:Y0:40:GLN:OE1	46:Y0:44:ARG:N	2.51	0.43
1:QA:324:G:N2	1:QA:326:G:H3'	2.33	0.43
3:QC:22:TRP:CD1	3:QC:59:ARG:HD2	2.53	0.43
8:QH:37:ARG:O	8:QH:41:ARG:HB2	2.19	0.43
11:QK:29:ILE:HB	11:QK:44:SER:HB3	2.00	0.43
13:QM:4:ILE:HG23	13:QM:5:ALA:H	1.82	0.43
17:QQ:58:GLU:O	17:QQ:74:LEU:N	2.50	0.43
22:QV:56:C:O2	30:RG:78:SER:HB2	2.19	0.43
25:RA:57:C:H2'	25:RA:58:G:O4'	2.18	0.43
25:RA:1020:A:N1	25:RA:1141:U:H2'	2.34	0.43
25:RA:1278:A:OP1	37:RR:36:THR:HG22	2.17	0.43
25:RA:1751:C:H2'	25:RA:1752:C:C6	2.53	0.43
28:RE:32:PRO:O	28:RE:49:LEU:HA	2.18	0.43
31:RH:9:ILE:O	31:RH:69:ARG:CD	2.67	0.43
32:RI:142:VAL:HG22	32:RI:143:SER:N	2.33	0.43
33:RN:12:ARG:O	33:RN:50:ASP:HB2	2.18	0.43
34:RO:87:ILE:CG2	34:RO:91:LEU:HA	2.49	0.43
38:RS:19:LYS:O	38:RS:21:THR:N	2.50	0.43
40:RU:8:VAL:HG12	40:RU:11:ARG:NH2	2.34	0.43
52:R6:40:CYS:HB3	52:R6:46:HIS:CG	2.53	0.43
53:R7:47:ARG:HH11	53:R7:47:ARG:H	1.66	0.43
1:XA:313:A:H2'	1:XA:314:C:C6	2.54	0.43
1:XA:1366:C:H2'	1:XA:1367:C:C6	2.53	0.43
2:XB:17:PHE:CD2	2:XB:41:ILE:HG23	2.54	0.43
2:XB:163:PHE:HA	2:XB:185:ILE:HG13	2.01	0.43
5:XE:5:ASP:N	5:XE:5:ASP:OD1	2.52	0.43
7:XG:131:LYS:HB2	7:XG:131:LYS:HZ2	1.84	0.43
8:XH:121:ASP:OD2	8:XH:122:ARG:HG3	2.19	0.43
9:XI:37:PHE:CE2	9:XI:70:LYS:HG3	2.54	0.43
12:XL:58:VAL:O	12:XL:65:GLU:HA	2.18	0.43
23:XX:21:A2M:H8	24:XY:91:TYR:HE2	1.83	0.43
25:YA:709:U:H2'	25:YA:710:G:C8	2.52	0.43
25:YA:1357:U:H2'	25:YA:1358:G:O4'	2.18	0.43
25:YA:1665:A:H1'	34:YO:1:MET:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:YA:1948:G:H5'	25:YA:1949:G:OP2	2.19	0.43
39:YT:6:LEU:O	39:YT:10:VAL:HG23	2.19	0.43
39:YT:102:ILE:O	39:YT:106:SER:HB3	2.19	0.43
43:YX:25:LYS:NZ	43:YX:82:GLN:OE1	2.51	0.43
1:QA:540:G:H2'	1:QA:541:G:O4'	2.19	0.43
1:QA:564:C:O2'	8:QH:91:ARG:NH2	2.45	0.43
1:QA:923:A:OP1	5:QE:21:ALA:HB2	2.19	0.43
13:QM:99:ARG:O	13:QM:101:GLN:N	2.52	0.43
20:QT:55:ILE:HD13	20:QT:55:ILE:HA	1.87	0.43
24:QY:76:PHE:HB3	24:QY:86:LEU:HD13	1.99	0.43
25:RA:484:C:H2'	25:RA:485:C:C6	2.54	0.43
25:RA:878:A:N6	25:RA:899:A:O2'	2.51	0.43
25:RA:1239:G:H2'	25:RA:1240:U:O4'	2.17	0.43
25:RA:1589:C:C2'	25:RA:1590:U:H5'	2.49	0.43
25:RA:2451:A:C2	56:Z7:76:PPU:CD2	3.02	0.43
25:RA:2811:G:H22	25:RA:2891:G:H1'	1.83	0.43
25:RA:2855:C:H2'	25:RA:2856:C:H6	1.83	0.43
28:RE:34:VAL:HG11	28:RE:64:LYS:HD3	2.01	0.43
28:RE:52:LEU:O	28:RE:75:VAL:HG23	2.19	0.43
30:RG:112:PRO:HG2	50:R4:37:SER:CB	2.49	0.43
30:RG:143:GLU:HG2	50:R4:26:SER:HB2	2.01	0.43
36:RQ:2:LEU:H	36:RQ:2:LEU:HD12	1.83	0.43
36:RQ:65:PHE:O	36:RQ:104:PHE:HA	2.19	0.43
37:RR:103:ARG:HD3	37:RR:103:ARG:HA	1.82	0.43
40:RU:92:ARG:NH2	41:RV:11:GLN:HG3	2.34	0.43
44:RY:11:ASP:O	44:RY:27:VAL:HG23	2.19	0.43
50:R4:14:ILE:O	50:R4:21:VAL:HG23	2.19	0.43
1:XA:131:C:H2'	1:XA:132:C:C6	2.53	0.43
1:XA:197:A:C6	1:XA:221:C:H4'	2.54	0.43
1:XA:236:G:OP1	17:XQ:40:LYS:NZ	2.48	0.43
1:XA:345:C:H5'	39:YT:41:ARG:NH2	2.33	0.43
9:XI:18:PHE:HB2	9:XI:62:TYR:HB3	2.01	0.43
20:XT:58:LYS:HE2	20:XT:62:LEU:HD21	2.00	0.43
23:XX:14:A:HO2'	23:XX:15:A:H5'	1.81	0.43
25:YA:491:G:H2'	25:YA:492:A:H8	1.84	0.43
25:YA:570:G:H2'	25:YA:2030:A:C5	2.53	0.43
25:YA:836:G:C5	25:YA:837:C:C4	3.07	0.43
25:YA:1030:G:OP2	36:YQ:128:LYS:HE3	2.19	0.43
25:YA:1222:C:H2'	25:YA:1223:C:C6	2.54	0.43
25:YA:1385:G:HO2'	25:YA:1396:U:H6	1.65	0.43
25:YA:2111:C:N4	25:YA:2118:U:O2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:YE:3:GLY:HA2	28:YE:198:VAL:O	2.18	0.43
30:YG:10:LYS:HE2	30:YG:175:LEU:O	2.19	0.43
34:YO:104:ARG:HG2	34:YO:121:VAL:HG12	2.01	0.43
36:YQ:63:LYS:HD2	45:YZ:175:VAL:HG21	2.01	0.43
1:QA:490:G:H2'	1:QA:491:G:H8	1.84	0.43
1:QA:797:C:OP1	11:QK:124:LYS:HE2	2.19	0.43
1:QA:1070:U:OP1	5:QE:18:ARG:NH1	2.52	0.43
1:QA:1190:G:H5''	3:QC:176:HIS:NE2	2.34	0.43
2:QB:7:VAL:HG13	2:QB:8:LYS:H	1.84	0.43
10:QJ:4:ILE:HB	10:QJ:74:ILE:HG12	2.01	0.43
10:QJ:8:LEU:HD22	10:QJ:20:ALA:HB2	1.99	0.43
25:RA:598:G:C5'	35:RP:11:GLY:HA3	2.48	0.43
25:RA:746:A:H2'	25:RA:2612:C:H5''	2.01	0.43
25:RA:811:U:H3'	35:RP:22:GLY:HA2	2.01	0.43
25:RA:1341:U:OP1	25:RA:1397:U:N3	2.46	0.43
25:RA:1345:C:H2'	25:RA:1346:G:C8	2.54	0.43
25:RA:2031:A:N3	25:RA:2455:G:O2'	2.39	0.43
25:RA:2293:C:O3'	38:RS:89:ARG:NH2	2.48	0.43
27:RD:24:ILE:HD11	27:RD:84:TYR:HB2	2.01	0.43
35:RP:64:LYS:CB	54:R8:25:MET:HG2	2.48	0.43
50:R4:55:ARG:H	50:R4:55:ARG:NE	2.17	0.43
1:XA:222:U:H2'	1:XA:223:U:C6	2.54	0.43
1:XA:435:C:H2'	1:XA:436:C:H6	1.84	0.43
1:XA:1337:G:H5''	1:XA:1338:G:OP1	2.18	0.43
1:XA:1443:G:N2	25:YA:2863:C:O3'	2.51	0.43
13:XM:10:PRO:HD2	13:XM:18:ALA:HB1	2.00	0.43
25:YA:443:A:H1'	25:YA:1201:C:O4'	2.18	0.43
25:YA:626:U:H5'	25:YA:627:A:H5'	2.01	0.43
25:YA:635:C:O2'	25:YA:639:U:OP1	2.36	0.43
25:YA:723:G:H2'	25:YA:724:U:O4'	2.19	0.43
25:YA:839:U:H2'	25:YA:840:C:C6	2.54	0.43
25:YA:2304:G:H22	25:YA:2312:U:H3	1.67	0.43
25:YA:2359:C:H2'	25:YA:2360:A:C8	2.54	0.43
25:YA:2410:G:C2	25:YA:2411:A:H1'	2.54	0.43
25:YA:2729:G:H2'	25:YA:2730:C:H6	1.84	0.43
25:YA:2827:C:H5'	25:YA:2828:C:OP2	2.19	0.43
28:YE:23:VAL:HA	28:YE:184:VAL:O	2.19	0.43
30:YG:7:LEU:HB2	30:YG:104:GLU:OE1	2.18	0.43
40:YU:98:LEU:O	40:YU:99:ALA:HB3	2.19	0.43
1:QA:474:G:OP2	16:QP:75:ARG:NH1	2.52	0.42
1:QA:875:C:O2'	8:QH:14:ARG:NH1	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:QA:1347:G:N7	9:QI:11:LYS:CE	2.80	0.42
7:QG:46:ALA:O	7:QG:50:ILE:HG12	2.19	0.42
10:QJ:33:GLN:H	10:QJ:75:ILE:HG12	1.84	0.42
12:QL:39:VAL:HG12	12:QL:41:ARG:HG3	2.01	0.42
16:QP:5:ARG:NH2	16:QP:24:ALA:HA	2.34	0.42
16:QP:11:SER:HB2	16:QP:14:ASN:HB3	2.01	0.42
25:RA:297:C:H2'	25:RA:298:G:O4'	2.19	0.42
25:RA:528:A:HO2'	25:RA:2042:A:H2	1.64	0.42
25:RA:813:U:H2'	25:RA:814:C:C6	2.54	0.42
25:RA:1142(A):A:H4'	33:RN:25:ARG:HH22	1.83	0.42
25:RA:2307:G:H8	25:RA:2307:G:OP1	2.01	0.42
39:RT:26:ASP:HB3	39:RT:92:GLY:H	1.83	0.42
48:R2:53:LEU:O	48:R2:56:GLN:HB2	2.18	0.42
55:R9:32:HIS:O	55:R9:34:GLN:HG3	2.19	0.42
1:XA:237:C:OP2	17:XQ:40:LYS:NZ	2.51	0.42
1:XA:691:G:H2'	1:XA:692:U:C6	2.53	0.42
1:XA:1126:U:HO2'	1:XA:1127:G:H8	1.64	0.42
10:XJ:6:ILE:HG22	10:XJ:98:ILE:HA	2.00	0.42
12:XL:93:LEU:HA	12:XL:94:PRO:HD2	1.90	0.42
21:XU:15:ARG:HD3	21:XU:15:ARG:HA	1.82	0.42
25:YA:635:C:H2'	25:YA:636:G:O4'	2.19	0.42
25:YA:747:U:OP2	51:Y5:3:LYS:HD3	2.19	0.42
26:YB:48:A:H2'	26:YB:49:C:C6	2.54	0.42
27:YD:35:LYS:HZ1	27:YD:104:TYR:HB2	1.84	0.42
27:YD:108:PRO:HB3	27:YD:143:HIS:NE2	2.34	0.42
29:YF:117:ARG:HD3	29:YF:117:ARG:HA	1.71	0.42
32:YI:128:LEU:O	32:YI:138:ILE:N	2.52	0.42
41:YV:85:LYS:CG	41:YV:87:HIS:H	2.24	0.42
42:YW:9:TYR:H	42:YW:102:HIS:CE1	2.37	0.42
42:YW:18:ARG:NH1	42:YW:76:VAL:O	2.52	0.42
50:Y4:60:GLN:HB3	50:Y4:61:ARG:NH2	2.34	0.42
1:QA:707:C:H2'	1:QA:708:C:H6	1.83	0.42
1:QA:727:G:N2	1:QA:730:G:OP2	2.47	0.42
1:QA:1059:C:O2'	10:QJ:53:PRO:HD3	2.18	0.42
1:QA:1169:A:H2'	1:QA:1170:A:C8	2.53	0.42
1:QA:1175:G:H2'	1:QA:1176:A:C8	2.53	0.42
3:QC:19:GLU:HG2	3:QC:40:ARG:NH2	2.34	0.42
21:QU:9:ARG:O	21:QU:13:ILE:HG13	2.19	0.42
25:RA:46:C:H2'	25:RA:47:C:C6	2.54	0.42
25:RA:394:A:C6	25:RA:395:U:C4	3.07	0.42
25:RA:942:G:OP2	35:RP:39:LYS:NZ	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:RA:1151:G:H5''	40:RU:81:HIS:NE2	2.33	0.42
25:RA:1264:G:H3'	25:RA:1265:A:H5''	2.00	0.42
25:RA:1295:C:H2'	25:RA:1296:G:H8	1.84	0.42
26:RB:17:C:H2'	26:RB:18:G:O4'	2.20	0.42
28:RE:68:ALA:O	28:RE:71:GLY:N	2.51	0.42
29:RF:32:LEU:O	29:RF:36:VAL:HG23	2.19	0.42
30:RG:99:MET:HG3	30:RG:100:TRP:N	2.34	0.42
34:RO:34:THR:OG1	34:RO:35:VAL:N	2.52	0.42
38:RS:62:LYS:HD3	38:RS:97:ARG:NH1	2.35	0.42
47:R1:34:THR:HG22	47:R1:36:GLY:H	1.84	0.42
1:XA:176:C:H2'	1:XA:177:C:C6	2.53	0.42
1:XA:542:G:H2'	1:XA:543:C:H6	1.84	0.42
1:XA:686:U:O4	1:XA:703:G:H1'	2.18	0.42
1:XA:920:U:H2'	1:XA:921:U:C6	2.54	0.42
2:XB:133:LYS:HD2	2:XB:137:ARG:NH1	2.34	0.42
3:XC:34:LEU:HD13	14:XN:25:VAL:HG11	2.00	0.42
3:XC:179:ARG:HH11	3:XC:207:VAL:HG22	1.84	0.42
7:XG:20:ASP:O	7:XG:21:VAL:HG22	2.19	0.42
20:XT:67:ALA:HA	20:XT:73:HIS:N	2.31	0.42
25:YA:194:G:H2'	25:YA:195:A:O4'	2.19	0.42
25:YA:571:A:H1'	25:YA:573:G:H5''	2.01	0.42
25:YA:685:A:O2'	25:YA:773:U:O4	2.31	0.42
25:YA:1053:C:H42	25:YA:1106:G:H1	1.65	0.42
25:YA:2017:U:O2	51:Y5:10:LYS:HB2	2.19	0.42
25:YA:2811:G:O5'	28:YE:60:ASN:O	2.37	0.42
26:YB:15:A:H5'	26:YB:16:G:N7	2.34	0.42
29:YF:25:PRO:HB3	29:YF:28:ILE:HG12	2.01	0.42
34:YO:15:GLY:O	34:YO:47:ILE:N	2.47	0.42
35:YP:65:ARG:CZ	54:Y8:15:LYS:HB2	2.49	0.42
35:YP:146:VAL:HG13	35:YP:147:LEU:HD22	2.01	0.42
40:YU:100:VAL:C	40:YU:102:GLU:H	2.22	0.42
1:QA:277:C:H2'	1:QA:278:G:C8	2.55	0.42
1:QA:1007:C:H3'	1:QA:1008:C:H5''	1.99	0.42
25:RA:61:G:H1	25:RA:93:C:N4	2.15	0.42
25:RA:1021:A:N3	25:RA:1021:A:C3'	2.78	0.42
25:RA:1225:C:C4'	41:RV:85:LYS:HB2	2.34	0.42
29:RF:103:LYS:HG2	29:RF:106:ARG:NH2	2.34	0.42
29:RF:164:ARG:HG3	29:RF:175:THR:OG1	2.19	0.42
30:RG:11:TYR:HA	30:RG:15:VAL:HB	2.00	0.42
35:RP:14:LYS:C	35:RP:16:ARG:N	2.73	0.42
39:RT:91:ARG:HD2	39:RT:124:ASP:OD2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:RV:48:GLY:C	41:RV:49:THR:O	2.57	0.42
41:RV:68:LYS:HD3	41:RV:68:LYS:HA	1.87	0.42
44:RY:42:VAL:O	44:RY:65:ALA:N	2.38	0.42
1:XA:434:U:H2'	1:XA:435:C:C6	2.54	0.42
1:XA:1468:A:H2'	1:XA:1469:G:O4'	2.19	0.42
2:XB:102:LEU:HD23	2:XB:182:ILE:HD12	2.02	0.42
5:XE:69:VAL:HA	5:XE:70:PRO:HD2	1.90	0.42
8:XH:1:MET:SD	8:XH:1:MET:N	2.77	0.42
10:XJ:56:HIS:O	10:XJ:57:LYS:C	2.57	0.42
11:XK:98:LEU:HD23	11:XK:98:LEU:HA	1.87	0.42
13:XM:18:ALA:HB2	13:XM:45:VAL:HG21	2.01	0.42
13:XM:67:GLU:OE2	30:YG:115:ARG:NH2	2.52	0.42
16:XP:54:GLU:CD	16:XP:54:GLU:H	2.23	0.42
19:XS:79:THR:O	19:XS:81:ARG:N	2.52	0.42
25:YA:483:A:C5'	44:YY:49:VAL:HA	2.46	0.42
25:YA:978:G:C2	25:YA:986:C:C2	3.07	0.42
25:YA:1085:A:HO2'	25:YA:1086:A:P	2.41	0.42
25:YA:2165:G:H2'	25:YA:2166:G:C2	2.54	0.42
25:YA:2292:C:P	38:YS:17:ARG:HH21	2.42	0.42
28:YE:97:LYS:N	28:YE:100:GLU:OE1	2.48	0.42
31:YH:33:LEU:HD12	31:YH:33:LEU:HA	1.78	0.42
37:YR:104:ARG:HB3	37:YR:107:ASP:OD2	2.19	0.42
40:YU:83:LEU:HG	40:YU:88:ILE:HD11	2.01	0.42
44:YY:96:ILE:HD12	44:YY:98:VAL:HG12	2.00	0.42
46:Y0:24:LYS:C	46:Y0:25:ARG:HD2	2.40	0.42
47:Y1:86:SER:N	47:Y1:87:PRO:HD2	2.34	0.42
1:QA:1202:G:H2'	1:QA:1203:C:O4'	2.19	0.42
4:QD:92:VAL:O	4:QD:96:LEU:HD22	2.19	0.42
4:QD:96:LEU:HD12	4:QD:139:ARG:NH1	2.35	0.42
5:QE:127:ASN:HA	5:QE:128:PRO:HD3	1.86	0.42
9:QI:16:ARG:O	9:QI:63:ILE:HA	2.18	0.42
10:QJ:22:LYS:HB3	10:QJ:22:LYS:HE3	1.81	0.42
25:RA:909:A:H2'	25:RA:912:C:C5	2.55	0.42
25:RA:2432:A:N1	47:R1:35:THR:HG22	2.35	0.42
28:RE:23:VAL:O	28:RE:24:THR:OG1	2.22	0.42
31:RH:42:ARG:HA	31:RH:42:ARG:HD2	1.78	0.42
40:RU:50:ARG:O	40:RU:54:LYS:NZ	2.40	0.42
40:RU:92:ARG:HH22	41:RV:11:GLN:H	1.67	0.42
44:RY:65:ALA:HA	44:RY:66:PRO:HD3	1.90	0.42
48:R2:28:LYS:HD3	48:R2:28:LYS:HA	1.88	0.42
1:XA:932:C:H5''	7:XG:2:ALA:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:XC:8:ILE:HG23	3:XC:16:ARG:HG2	2.01	0.42
6:XF:23:LYS:HB3	6:XF:23:LYS:HE2	1.88	0.42
8:XH:86:ILE:HG12	8:XH:135:CYS:HA	2.01	0.42
13:XM:54:VAL:HG22	13:XM:57:ARG:NH2	2.34	0.42
25:YA:207:A:H2'	25:YA:208:C:O4'	2.19	0.42
25:YA:248:G:H5'	25:YA:250:G:N7	2.34	0.42
25:YA:748:G:OP1	25:YA:2612:C:N4	2.52	0.42
25:YA:1979:C:H2'	25:YA:1980:G:O5'	2.19	0.42
27:YD:92:ILE:HD12	27:YD:104:TYR:CD2	2.54	0.42
33:YN:34:LEU:HD22	33:YN:119:ARG:HB2	2.00	0.42
35:YP:63:PRO:C	54:Y8:13:ARG:HA	2.37	0.42
36:YQ:60:ARG:O	45:YZ:177:PRO:HB2	2.19	0.42
36:YQ:77:LYS:HG3	36:YQ:86:GLY:HA2	2.02	0.42
41:YV:70:ILE:HG13	41:YV:86:GLY:O	2.19	0.42
50:Y4:9:LEU:HD23	50:Y4:25:TYR:HB3	2.02	0.42
56:Z6:75:C:H6	56:Z6:75:C:O5'	2.02	0.42
1:QA:1189:C:OP1	10:QJ:51:ARG:NH2	2.52	0.42
1:QA:1352:C:H2'	1:QA:1353:G:C8	2.53	0.42
1:QA:1503:A:C4	23:QX:12:A:H2	2.38	0.42
7:QG:76:ARG:HH11	7:QG:78:ARG:HH12	1.67	0.42
12:QL:102:ARG:HE	12:QL:102:ARG:HB3	1.67	0.42
17:QQ:5:VAL:HG22	17:QQ:60:ILE:HG13	2.02	0.42
19:QS:35:SER:HB3	19:QS:37:ARG:HB2	2.01	0.42
25:RA:1424:G:OP1	27:RD:33:LEU:HD12	2.19	0.42
25:RA:1904:G:H2'	25:RA:1905:C:O4'	2.19	0.42
25:RA:2394:C:OP1	35:RP:63:PRO:CD	2.57	0.42
25:RA:2526:G:C6	25:RA:2527:C:C4	3.08	0.42
35:RP:86:LYS:HB3	35:RP:117:GLU:O	2.19	0.42
45:RZ:139:VAL:HG13	45:RZ:139:VAL:O	2.19	0.42
52:R6:18:ARG:HG3	52:R6:44:ARG:NH1	2.34	0.42
1:XA:197:A:H3'	1:XA:197:A:OP2	2.19	0.42
4:XD:190:ASP:OD1	4:XD:191:ARG:N	2.51	0.42
7:XG:20:ASP:CG	7:XG:23:VAL:HB	2.39	0.42
12:XL:46:LYS:HB3	12:XL:46:LYS:HE2	1.81	0.42
20:XT:58:LYS:O	20:XT:58:LYS:HD3	2.19	0.42
21:XU:9:ARG:O	21:XU:13:ILE:HG13	2.19	0.42
22:XV:17(A):U:H4'	22:XV:18:G:OP1	2.19	0.42
24:XY:34:LEU:HD23	24:XY:34:LEU:HA	1.90	0.42
25:YA:253:C:H2'	25:YA:254:G:O4'	2.18	0.42
25:YA:1329:U:H5''	25:YA:1330:C:H5	1.84	0.42
25:YA:1416:G:O2'	25:YA:1417:C:P	2.78	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:YA:2316:C:O2'	30:YG:128:ARG:NH1	2.53	0.42
25:YA:2786:U:H4'	28:YE:65:GLY:N	2.35	0.42
26:YB:29:A:H2'	26:YB:30:C:O4'	2.20	0.42
31:YH:78:GLY:HA2	31:YH:83:TYR:CE1	2.54	0.42
35:YP:39:LYS:HB2	35:YP:45:LEU:HD23	2.00	0.42
35:YP:101:VAL:HA	35:YP:105:LEU:O	2.20	0.42
40:YU:58:ARG:HA	40:YU:61:TRP:CE3	2.54	0.42
42:YW:82:LEU:HD23	42:YW:82:LEU:HA	1.89	0.42
48:Y2:50:ILE:HD12	48:Y2:51:ARG:H	1.85	0.42
51:Y5:9:LYS:HD3	51:Y5:9:LYS:HA	1.86	0.42
1:QA:436:C:H2'	1:QA:437:U:C6	2.54	0.42
1:QA:999:U:O4	1:QA:1000:A:N6	2.52	0.42
2:QB:186:ALA:O	2:QB:201:ILE:N	2.50	0.42
5:QE:82:VAL:HG21	5:QE:138:ALA:HA	2.02	0.42
6:QF:96:PRO:HB2	6:QF:98:LEU:HD23	2.02	0.42
8:QH:25:ASP:N	8:QH:25:ASP:OD1	2.52	0.42
19:QS:79:THR:O	19:QS:81:ARG:N	2.53	0.42
22:QV:76:A:H2'	25:RA:2602:A:N6	2.34	0.42
25:RA:26:G:H1'	25:RA:515:A:H61	1.85	0.42
25:RA:198:C:H5'	25:RA:2244:U:OP1	2.19	0.42
25:RA:372:G:O2'	25:RA:400:G:N1	2.52	0.42
25:RA:537:C:O2	33:RN:45:ASN:ND2	2.53	0.42
25:RA:1131:G:C2	25:RA:1132:A:C4	3.07	0.42
25:RA:1174:A:H62	25:RA:1177:A:H4'	1.85	0.42
25:RA:2291:U:O2'	25:RA:2374:C:O2	2.29	0.42
25:RA:2772:C:H2'	25:RA:2773:C:H6	1.83	0.42
36:RQ:43:THR:HG22	36:RQ:94:VAL:HG12	2.00	0.42
41:RV:71:LEU:HA	41:RV:71:LEU:HD12	1.63	0.42
1:XA:620:C:H2'	1:XA:621:A:O4'	2.20	0.42
1:XA:697:U:H5''	1:XA:698:G:OP2	2.19	0.42
1:XA:1028(A):C:H2'	1:XA:1028(B):C:C6	2.54	0.42
7:XG:14:PRO:HB2	7:XG:19:GLY:HA2	2.01	0.42
9:XI:20:ARG:O	9:XI:22:GLY:N	2.47	0.42
17:XQ:95:TYR:O	17:XQ:98:LEU:N	2.52	0.42
25:YA:263:C:H2'	25:YA:264:C:O4'	2.19	0.42
25:YA:1639:U:C2'	25:YA:1640:C:H5''	2.47	0.42
25:YA:2103:C:H2'	25:YA:2104:G:C8	2.54	0.42
25:YA:2838:G:H1'	37:YR:45:ARG:HH12	1.84	0.42
33:YN:127:ASP:OD1	33:YN:127:ASP:N	2.52	0.42
43:YX:14:SER:H	43:YX:17:ALA:HB3	1.84	0.42
44:YY:101:LYS:HE2	44:YY:101:LYS:HB3	1.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:QA:427:U:OP2	1:QA:428:G:O2'	2.30	0.42
1:QA:983:A:H5''	1:QA:984:C:OP2	2.20	0.42
1:QA:1343:G:H2'	1:QA:1344:C:C6	2.55	0.42
1:QA:1401:G:C2	1:QA:1402:C:H1'	2.55	0.42
2:QB:69:LEU:HA	2:QB:91:PRO:HG2	2.01	0.42
2:QB:213:LEU:HD21	2:QB:217:ARG:HH12	1.84	0.42
5:QE:48:ALA:HB2	5:QE:57:LYS:HD3	2.02	0.42
9:QI:11:LYS:CD	9:QI:107:ARG:O	2.57	0.42
14:QN:6:LEU:HD22	14:QN:23:ARG:HH22	1.83	0.42
25:RA:1857:G:C6	25:RA:1858:G:C6	3.08	0.42
25:RA:2091:U:H1'	47:R1:47:GLN:HE21	1.85	0.42
25:RA:2319:G:H2'	25:RA:2319:G:O5'	2.19	0.42
25:RA:2336:A:H61	46:R0:43:THR:CG2	2.32	0.42
28:RE:120:TRP:CE3	28:RE:155:LYS:HE3	2.54	0.42
29:RF:33:LEU:HD13	29:RF:112:MET:HE2	2.02	0.42
30:RG:27:ASN:HB3	30:RG:30:GLU:HG3	2.02	0.42
34:RO:63:VAL:HG12	34:RO:106:LEU:HD11	2.02	0.42
35:RP:56:SER:HB3	35:RP:57:THR:H	1.47	0.42
38:RS:5:THR:OG1	38:RS:8:GLU:HG2	2.19	0.42
45:RZ:74:VAL:HG22	45:RZ:86:VAL:HG13	2.01	0.42
45:RZ:103:ARG:HG3	45:RZ:104:PHE:H	1.85	0.42
46:R0:30:VAL:HG22	46:R0:66:VAL:HG22	2.02	0.42
49:R3:43:ILE:O	49:R3:47:VAL:HG23	2.19	0.42
1:XA:444:C:H2'	1:XA:445:G:H8	1.85	0.42
2:XB:200:ILE:HG22	2:XB:202:PRO:HD3	2.02	0.42
3:XC:134:ILE:HG22	3:XC:168:ALA:HB3	2.01	0.42
20:XT:14:LYS:HA	20:XT:17:ARG:NE	2.34	0.42
25:YA:1230:C:H2'	25:YA:1231:G:H8	1.83	0.42
25:YA:2370:G:H2'	25:YA:2371:G:C8	2.54	0.42
25:YA:2660:A:H2'	25:YA:2661:G:O4'	2.20	0.42
25:YA:2749:A:C6	25:YA:2750:A:N6	2.88	0.42
25:YA:2870:C:H5''	37:YR:65:LEU:HD21	2.01	0.42
30:YG:105:LYS:HD3	50:Y4:24:THR:O	2.19	0.42
31:YH:49:VAL:HG22	31:YH:50:VAL:H	1.85	0.42
36:YQ:88:GLY:O	36:YQ:90:VAL:N	2.52	0.42
38:YS:44:LYS:HB2	38:YS:44:LYS:HE3	1.84	0.42
44:YY:101:LYS:HE3	44:YY:101:LYS:O	2.20	0.42
55:Y9:11:CYS:SG	55:Y9:27:CYS:SG	3.17	0.42
1:QA:45:U:H2'	1:QA:46:G:C8	2.55	0.42
1:QA:1057:G:C4	1:QA:1204:A:C2	3.08	0.42
7:QG:116:ALA:O	7:QG:120:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:QV:2:G:H2'	22:QV:3:C:H6	1.84	0.42
25:RA:654(A):G:C6	25:RA:654(U):A:C2	3.07	0.42
25:RA:2591:C:H2'	25:RA:2592:G:C8	2.55	0.42
25:RA:2771:C:H2'	25:RA:2772:C:C6	2.55	0.42
39:RT:56:GLY:O	39:RT:59:THR:HG22	2.20	0.42
45:RZ:26:GLY:HA2	45:RZ:85:HIS:CD2	2.55	0.42
45:RZ:81:ARG:HE	45:RZ:81:ARG:HB2	1.44	0.42
53:R7:34:ARG:NH1	53:R7:41:ARG:O	2.53	0.42
1:XA:56:U:H2'	1:XA:57:G:H8	1.84	0.42
1:XA:243:A:H4'	1:XA:244:U:O5'	2.20	0.42
1:XA:391:G:P	16:XP:28:ARG:HH22	2.43	0.42
1:XA:410:G:H3'	4:XD:25:ARG:HH21	1.85	0.42
1:XA:667:G:H4'	15:XO:51:HIS:ND1	2.35	0.42
1:XA:743:U:H2'	1:XA:744:C:C6	2.55	0.42
1:XA:1057:G:H2'	1:XA:1058:G:O4'	2.18	0.42
7:XG:18:TYR:CD2	7:XG:59:LEU:HD22	2.55	0.42
17:XQ:63:ARG:HG2	17:XQ:64:PRO:HD2	2.02	0.42
25:YA:646:A:H2'	25:YA:647:G:O4'	2.20	0.42
25:YA:815:C:H2'	25:YA:816:C:H6	1.84	0.42
25:YA:1550:C:OP1	25:YA:1727:U:O2'	2.32	0.42
28:YE:143:ASN:HB2	28:YE:147:PRO:HD2	2.02	0.42
29:YF:61:GLY:C	29:YF:77:ASP:HB3	2.40	0.42
30:YG:121:ASN:HA	30:YG:122:PRO:HD2	1.92	0.42
33:YN:56:ASN:HA	33:YN:125:GLY:N	2.35	0.42
35:YP:70:GLN:HB3	35:YP:71:VAL:H	1.72	0.42
35:YP:134:ALA:O	35:YP:138:LEU:HD12	2.20	0.42
41:YV:21:ARG:HG2	41:YV:93:GLU:HG3	2.01	0.42
43:YX:49:VAL:HG23	43:YX:51:VAL:HG23	2.02	0.42
46:Y0:7:LEU:HD13	46:Y0:7:LEU:HA	1.93	0.42
49:Y3:35:ARG:HE	49:Y3:37:LEU:HD21	1.84	0.42
1:QA:345:C:H5''	1:QA:345:C:H6	1.85	0.42
1:QA:518:C:H2'	1:QA:530:G:C8	2.54	0.42
3:QC:152:ILE:HB	3:QC:199:LYS:HB2	2.02	0.42
4:QD:21:LEU:O	4:QD:23:GLY:N	2.53	0.42
16:QP:38:TYR:CZ	16:QP:50:LYS:HB3	2.55	0.42
20:QT:38:LYS:HB3	20:QT:38:LYS:HE2	1.73	0.42
25:RA:589:C:H2'	25:RA:590:A:C8	2.54	0.42
25:RA:1814:G:H4'	27:RD:51:VAL:HG21	2.00	0.42
25:RA:1889:A:H1'	25:RA:2087:G:O4'	2.19	0.42
25:RA:2271:G:OP1	46:R0:18:ALA:HB1	2.20	0.42
25:RA:2319:G:C5	25:RA:2320:A:C6	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:RA:2748:A:O2'	31:RH:66:GLY:HA3	2.20	0.42
27:RD:43:ARG:HB2	27:RD:54:ARG:HB2	2.00	0.42
30:RG:55:LYS:HD2	30:RG:58:GLN:NE2	2.34	0.42
31:RH:69:ARG:HG3	31:RH:70:THR:N	2.31	0.42
39:RT:80:SER:HB3	39:RT:83:ILE:HG13	2.00	0.42
44:RY:60:PHE:HD2	44:RY:60:PHE:H	1.66	0.42
52:R6:30:THR:HA	52:R6:31:PRO:C	2.40	0.42
1:XA:335:C:H2'	1:XA:336:C:H6	1.84	0.42
1:XA:1443:G:H22	25:YA:2864:G:P	2.42	0.42
4:XD:187:ARG:NH2	4:XD:193:ASP:OD1	2.53	0.42
23:XX:12:A:H5'	23:XX:13:A:P	2.60	0.42
25:YA:78:A:H2'	25:YA:79:G:C8	2.55	0.42
25:YA:242:G:O2'	25:YA:254:G:O6	2.29	0.42
25:YA:631:A:H5'	35:YP:65:ARG:HA	2.00	0.42
25:YA:648:G:H2'	25:YA:649:G:H8	1.85	0.42
25:YA:796:C:H2'	25:YA:797:C:C6	2.55	0.42
25:YA:1651:G:OP1	37:YR:40:LYS:HG3	2.20	0.42
25:YA:2155:G:H2'	25:YA:2156:G:O4'	2.20	0.42
25:YA:2347:C:H5	25:YA:2382:G:N9	2.18	0.42
25:YA:2488:A:H2'	25:YA:2489:G:O4'	2.19	0.42
44:YY:29:GLU:HB3	44:YY:38:ILE:HG23	2.02	0.42
44:YY:88:LYS:C	44:YY:90:LEU:H	2.21	0.42
1:QA:1237:C:N4	1:QA:1336:C:O2	2.52	0.42
1:QA:1251:A:H2'	1:QA:1252:A:C8	2.55	0.42
4:QD:200:GLU:O	4:QD:204:ILE:HG12	2.20	0.42
8:QH:6:ILE:H	8:QH:6:ILE:HD12	1.85	0.42
8:QH:50:ARG:HA	8:QH:59:LEU:HD23	2.01	0.42
11:QK:120:ARG:HA	11:QK:121:PRO:HD3	1.91	0.42
25:RA:311:A:C6	25:RA:328:U:C4	3.08	0.42
25:RA:372:G:H2'	25:RA:400:G:O6	2.20	0.42
25:RA:1351:C:H2'	25:RA:1352:U:C6	2.55	0.42
25:RA:1632:A:C6	25:RA:1633:G:C6	3.08	0.42
25:RA:2015:A:H5'	42:RW:92:ARG:HH21	1.84	0.42
27:RD:25:THR:HG21	27:RD:82:ILE:H	1.84	0.42
27:RD:133:LEU:HD12	27:RD:189:CYS:HB2	2.01	0.42
28:RE:103:ASP:OD1	28:RE:201:THR:HG23	2.19	0.42
29:RF:34:TRP:CZ3	35:RP:8:PRO:HB3	2.55	0.42
30:RG:111:LEU:HD13	30:RG:120:LEU:HD21	2.01	0.42
35:RP:144:GLU:OE1	35:RP:144:GLU:N	2.52	0.42
42:RW:31:GLU:O	42:RW:35:ILE:HG13	2.20	0.42
45:RZ:24:LEU:HB2	45:RZ:41:LEU:HG	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:321:A:N7	1:XA:328:C:C2	2.88	0.42
1:XA:865:A:H2	1:XA:918:A:H4'	1.84	0.42
1:XA:1157:A:C2'	1:XA:1158:C:OP2	2.68	0.42
1:XA:1347:G:N2	1:XA:1373:G:H2'	2.35	0.42
2:XB:34:ALA:O	2:XB:41:ILE:HB	2.20	0.42
2:XB:108:ILE:HD13	2:XB:108:ILE:HA	1.80	0.42
3:XC:112:SER:O	3:XC:116:VAL:HG23	2.20	0.42
4:XD:50:ARG:HA	4:XD:51:PRO:HD3	1.76	0.42
11:XK:124:LYS:HE2	11:XK:124:LYS:HB3	1.71	0.42
15:XO:21:ASP:OD1	15:XO:24:SER:HB2	2.20	0.42
25:YA:2451:A:C6	56:Z6:76:PPU:HE2	2.54	0.42
25:YA:2584:U:H5'	56:Z6:76:PPU:H103	2.01	0.42
28:YE:10:GLY:HA3	39:YT:8:LYS:HD2	2.02	0.42
31:YH:22:GLY:C	31:YH:37:VAL:HB	2.39	0.42
35:YP:63:PRO:O	54:Y8:13:ARG:HA	2.20	0.42
35:YP:124:LYS:HA	35:YP:143:GLY:O	2.19	0.42
39:YT:88:ILE:O	39:YT:88:ILE:HG13	2.20	0.42
46:Y0:72:ARG:HB2	46:Y0:75:LEU:HB2	2.02	0.42
55:Y9:4:ARG:O	55:Y9:36:GLN:HA	2.20	0.42
1:QA:269:C:H2'	1:QA:270:A:H8	1.84	0.41
1:QA:437:U:H5'	4:QD:155:LEU:HD21	2.01	0.41
1:QA:764:C:H2'	1:QA:765:G:O4'	2.20	0.41
1:QA:1190:G:OP1	3:QC:5:ILE:HG23	2.20	0.41
5:QE:71:LEU:HD11	5:QE:114:GLY:HA3	2.01	0.41
5:QE:112:LEU:HD23	5:QE:112:LEU:HA	1.86	0.41
7:QG:65:ALA:O	7:QG:69:VAL:HG23	2.20	0.41
9:QI:31:GLN:HB3	9:QI:32:ASP:H	1.52	0.41
20:QT:26:ASN:O	20:QT:30:LYS:HB2	2.19	0.41
24:QY:67:THR:HG23	24:QY:73:ARG:NH1	2.35	0.41
25:RA:601:C:O2'	25:RA:605:C:H5''	2.20	0.41
25:RA:1388:G:HO2'	25:RA:1525:G:HO2'	1.60	0.41
25:RA:2098:U:H3	25:RA:2191:G:H1	1.67	0.41
35:RP:79:ARG:NE	35:RP:109:GLY:HA3	2.35	0.41
39:RT:6:LEU:HD12	39:RT:6:LEU:HA	1.95	0.41
42:RW:17:VAL:O	42:RW:20:VAL:HG22	2.20	0.41
44:RY:75:ILE:HD11	44:RY:79:CYS:HA	2.02	0.41
45:RZ:7:ALA:HB2	45:RZ:59:LEU:CG	2.50	0.41
48:R2:13:ALA:HB1	48:R2:21:LEU:HD21	2.02	0.41
54:R8:32:LEU:HA	54:R8:33:ASN:HA	1.88	0.41
55:R9:2:LYS:HD2	55:R9:33:LYS:O	2.20	0.41
1:XA:191:G:H1'	20:XT:104:LEU:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:XA:224:C:H2'	1:XA:225:C:H6	1.85	0.41
1:XA:512:U:H2'	1:XA:513:C:H6	1.85	0.41
1:XA:1309:G:OP1	13:XM:88:ARG:NH1	2.53	0.41
1:XA:1429:C:H2'	1:XA:1430:C:C6	2.55	0.41
2:XB:22:LYS:HB3	2:XB:23:ARG:H	1.70	0.41
4:XD:3:ARG:HB2	4:XD:4:TYR:H	1.54	0.41
12:XL:33:ARG:HD3	12:XL:62:SER:OG	2.20	0.41
13:XM:50:GLU:O	13:XM:54:VAL:HG23	2.20	0.41
15:XO:12:ILE:HG12	15:XO:31:LEU:HD11	2.01	0.41
15:XO:43:LEU:HD11	15:XO:53:HIS:HA	2.01	0.41
19:XS:62:ILE:HA	19:XS:66:MET:HE1	2.01	0.41
24:XY:91:TYR:HD2	24:XY:91:TYR:HA	1.77	0.41
25:YA:519:U:H2'	25:YA:520:G:C8	2.54	0.41
25:YA:760:G:H2'	25:YA:761:A:O4'	2.19	0.41
25:YA:2080:G:H5'	47:Y1:19:GLN:HG3	2.00	0.41
25:YA:2145:C:H5''	25:YA:2146:C:C5	2.55	0.41
25:YA:2360:A:H2'	25:YA:2361:A:O4'	2.19	0.41
25:YA:2676:C:OP1	34:YO:31:LYS:NZ	2.51	0.41
25:YA:2781:A:H5''	25:YA:2782:G:H5'	2.02	0.41
25:YA:2816:C:O2	25:YA:2883:A:O2'	2.32	0.41
27:YD:34:VAL:C	27:YD:35:LYS:HG3	2.40	0.41
27:YD:102:LYS:C	27:YD:103:ARG:HG2	2.41	0.41
27:YD:165:ILE:H	27:YD:165:ILE:HG12	1.61	0.41
28:YE:144:ARG:HB3	28:YE:145:LYS:H	1.42	0.41
29:YF:46:ARG:HH11	29:YF:46:ARG:HG2	1.83	0.41
29:YF:116:ASP:OD1	29:YF:119:ARG:NH2	2.53	0.41
30:YG:111:LEU:HB2	30:YG:112:PRO:HD3	2.02	0.41
31:YH:159:GLU:HB3	31:YH:160:LYS:H	1.55	0.41
35:YP:144:GLU:HA	35:YP:145:PRO:HD3	1.80	0.41
38:YS:5:THR:OG1	38:YS:8:GLU:HG2	2.20	0.41
38:YS:62:LYS:HB3	38:YS:97:ARG:CD	2.49	0.41
44:YY:89:PHE:O	44:YY:90:LEU:HD22	2.20	0.41
1:QA:109:A:C6	1:QA:326:G:C6	3.08	0.41
1:QA:382:A:H2'	1:QA:383:A:H8	1.83	0.41
2:QB:97:TRP:CE2	2:QB:101:MET:HG3	2.56	0.41
5:QE:51:VAL:O	5:QE:55:VAL:HG23	2.19	0.41
7:QG:76:ARG:O	7:QG:87:VAL:N	2.52	0.41
12:QL:57:LYS:HE3	12:QL:65:GLU:HG2	2.01	0.41
19:QS:36:ARG:HH22	19:QS:69:HIS:HA	1.85	0.41
25:RA:583:G:H5''	40:RU:10:ARG:HH12	1.85	0.41
25:RA:654(A):G:O2'	25:RA:654(B):C:P	2.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:RA:706:A:H2'	25:RA:707:G:O4'	2.20	0.41
25:RA:1341:U:O2'	25:RA:1342:A:P	2.79	0.41
25:RA:1681:G:OP2	25:RA:1681:G:H8	2.02	0.41
25:RA:2212:A:H1'	25:RA:2215:G:C5	2.55	0.41
25:RA:2243:U:H2'	25:RA:2244:U:C6	2.56	0.41
25:RA:2870:C:H2'	25:RA:2871:C:O4'	2.20	0.41
25:RA:2876:G:H1'	39:RT:3:ARG:CZ	2.50	0.41
27:RD:92:ILE:HD12	27:RD:104:TYR:CE2	2.55	0.41
30:RG:53:LEU:HD13	30:RG:87:PRO:HB2	2.01	0.41
32:RI:10:GLU:OE1	32:RI:11:ASN:N	2.53	0.41
38:RS:10:ARG:O	38:RS:14:VAL:HG12	2.20	0.41
41:RV:85:LYS:HG3	41:RV:87:HIS:HA	2.02	0.41
43:RX:60:ARG:O	43:RX:75:ASP:HB3	2.20	0.41
1:XA:164:U:H2'	1:XA:165:C:C6	2.55	0.41
1:XA:1251:A:N3	1:XA:1369:C:O2'	2.44	0.41
1:XA:1460:A:H2'	1:XA:1461:G:O4'	2.20	0.41
4:XD:20:TYR:CE2	4:XD:27:TYR:HA	2.55	0.41
4:XD:64:LEU:HD23	4:XD:75:PHE:HZ	1.85	0.41
21:XU:9:ARG:NH2	21:XU:10:ARG:HE	2.18	0.41
25:YA:106:C:HO2'	25:YA:294:A:HO2'	1.57	0.41
25:YA:1101:U:H2'	25:YA:1102:C:C6	2.56	0.41
25:YA:2607:G:H2'	25:YA:2608:G:O4'	2.19	0.41
28:YE:81:ILE:HG21	28:YE:84:PHE:CD1	2.55	0.41
32:YI:1:MET:HB3	32:YI:21:VAL:O	2.21	0.41
36:YQ:81:VAL:HG12	36:YQ:82:ARG:HG2	2.03	0.41
38:YS:93:LYS:HE3	38:YS:93:LYS:HB2	1.75	0.41
41:YV:79:VAL:O	41:YV:80:GLN:HB2	2.19	0.41
44:YY:43:ASN:HB3	44:YY:64:GLU:HA	2.03	0.41
44:YY:88:LYS:HA	44:YY:88:LYS:HD3	1.93	0.41
1:QA:500:G:H2'	1:QA:501:C:C6	2.55	0.41
1:QA:1118:C:H1'	1:QA:1179:A:C4	2.56	0.41
1:QA:1306:A:H61	1:QA:1331:G:H1'	1.83	0.41
5:QE:70:PRO:O	5:QE:72:GLN:NE2	2.53	0.41
9:QI:2:GLU:O	9:QI:20:ARG:NH1	2.53	0.41
12:QL:45:PRO:HD3	12:QL:51:ALA:O	2.20	0.41
13:QM:86:CYS:HB2	19:QS:73:GLU:HB3	2.02	0.41
25:RA:69:C:O2	25:RA:69:C:C5'	2.65	0.41
25:RA:224:G:H2'	25:RA:225:A:O4'	2.20	0.41
25:RA:1488:G:H5'	25:RA:1489:U:OP2	2.20	0.41
25:RA:1694:C:O5'	25:RA:1694:C:H6	2.04	0.41
29:RF:53:THR:HG22	29:RF:56:GLU:HG3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:RI:73:GLU:OE1	32:RI:137:PRO:HD2	2.21	0.41
36:RQ:137:TYR:CE1	45:RZ:83:PRO:HG3	2.55	0.41
38:RS:93:LYS:HE3	38:RS:93:LYS:HB2	1.90	0.41
40:RU:28:ARG:NH1	40:RU:38:THR:OG1	2.45	0.41
47:R1:81:LYS:HE3	47:R1:81:LYS:HB3	1.50	0.41
47:R1:91:LYS:C	47:R1:93:GLU:H	2.23	0.41
51:R5:25:LEU:HD23	51:R5:25:LEU:HA	1.88	0.41
1:XA:336:C:H2'	1:XA:337:C:C6	2.55	0.41
1:XA:1429:C:H2'	1:XA:1430:C:H6	1.85	0.41
2:XB:93:VAL:HG11	2:XB:97:TRP:HD1	1.85	0.41
4:XD:9:CYS:SG	4:XD:32:ALA:HB2	2.60	0.41
4:XD:104:VAL:O	4:XD:108:LEU:HB2	2.21	0.41
4:XD:107:ARG:HH21	4:XD:194:LEU:HD12	1.85	0.41
7:XG:76:ARG:HB3	7:XG:78:ARG:HH11	1.84	0.41
19:XS:35:SER:HB3	19:XS:37:ARG:HB2	2.02	0.41
25:YA:184:C:H2'	25:YA:185:U:H6	1.82	0.41
25:YA:376:C:H2'	25:YA:377:C:C6	2.55	0.41
25:YA:1113:U:H2'	25:YA:1114:G:C8	2.55	0.41
25:YA:1419:A:N7	25:YA:1421:G:C6	2.88	0.41
25:YA:2404:C:O3'	35:YP:77:ARG:NH2	2.53	0.41
25:YA:2741:A:H2'	25:YA:2742:C:O4'	2.21	0.41
25:YA:2847:U:H2'	25:YA:2848:G:H5'	2.02	0.41
25:YA:2869:G:H2'	25:YA:2870:C:H6	1.85	0.41
28:YE:60:ASN:O	28:YE:62:PRO:CD	2.68	0.41
32:YI:77:LEU:HB2	32:YI:141:LYS:CB	2.33	0.41
36:YQ:134:ARG:HH21	45:YZ:122:ARG:NH1	2.18	0.41
37:YR:5:LYS:HE2	37:YR:5:LYS:HB3	1.83	0.41
50:Y4:58:ARG:O	50:Y4:62:ARG:HG2	2.20	0.41
1:QA:1347:G:N7	9:QI:11:LYS:HD2	2.35	0.41
1:QA:1512:U:H2'	1:QA:1513:A:C8	2.55	0.41
2:QB:221:LEU:HA	2:QB:224:GLN:HB2	2.00	0.41
5:QE:69:VAL:HA	5:QE:70:PRO:HD2	1.92	0.41
9:QI:118:LYS:O	9:QI:120:ARG:N	2.53	0.41
25:RA:207:A:H2'	25:RA:208:C:O4'	2.20	0.41
25:RA:1710:C:H2'	25:RA:1711:C:C6	2.56	0.41
25:RA:1971:A:C4	27:RD:241:PRO:HD3	2.55	0.41
25:RA:1991:U:H2'	25:RA:1992:G:H5''	2.01	0.41
25:RA:2514:U:H2'	25:RA:2515:C:C6	2.56	0.41
25:RA:2819:G:H1	25:RA:2827:C:H42	1.66	0.41
30:RG:76:SER:OG	30:RG:83:ARG:HA	2.19	0.41
31:RH:136:ILE:O	31:RH:137:ASP:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:RH:170:ARG:HB3	31:RH:171:LEU:H	1.57	0.41
40:RU:98:LEU:C	40:RU:100:VAL:N	2.74	0.41
41:RV:1:MET:N	41:RV:16:PRO:HD3	2.36	0.41
41:RV:41:GLY:H	41:RV:46:VAL:HG13	1.85	0.41
48:R2:15:LYS:HA	48:R2:15:LYS:HD3	1.93	0.41
1:XA:5:U:H5''	1:XA:6:G:C8	2.54	0.41
1:XA:42:G:H2'	1:XA:43:C:C6	2.56	0.41
1:XA:171:A:H2'	1:XA:172:A:C8	2.55	0.41
1:XA:531:U:O4	24:XY:29:ARG:NH2	2.46	0.41
1:XA:692:U:H1'	1:XA:695:A:N7	2.35	0.41
2:XB:17:PHE:HD2	2:XB:41:ILE:HG23	1.85	0.41
4:XD:199:ASN:O	4:XD:199:ASN:ND2	2.37	0.41
13:XM:66:LEU:HA	13:XM:70:LEU:HD12	2.02	0.41
13:XM:108:ARG:HA	13:XM:108:ARG:HD2	1.89	0.41
17:XQ:19:VAL:HG23	17:XQ:44:ALA:HB3	2.03	0.41
18:XR:51:LEU:HD23	18:XR:51:LEU:HA	1.92	0.41
25:YA:270(E):G:H1	25:YA:270(U):C:H42	1.67	0.41
25:YA:439:G:H2'	25:YA:440:G:C8	2.54	0.41
25:YA:612:G:N2	25:YA:616:A:O2'	2.53	0.41
25:YA:2162:G:O2'	25:YA:2173:A:OP2	2.24	0.41
25:YA:2306:C:H3'	25:YA:2307:G:C8	2.55	0.41
25:YA:2579:C:H2'	25:YA:2580:U:O4'	2.21	0.41
26:YB:95:U:C2	26:YB:96:G:C8	3.08	0.41
27:YD:201:HIS:O	27:YD:204:ILE:HG12	2.21	0.41
28:YE:114:ALA:HB3	28:YE:160:TYR:HB3	2.02	0.41
29:YF:7:TYR:HA	29:YF:125:LEU:O	2.21	0.41
29:YF:32:LEU:O	29:YF:36:VAL:HG23	2.21	0.41
34:YO:68:GLU:HB3	34:YO:78:ARG:HB2	2.02	0.41
35:YP:12:ALA:C	35:YP:14:LYS:H	2.23	0.41
44:YY:95:LYS:NZ	44:YY:95:LYS:HB2	2.35	0.41
45:YZ:53:ILE:HA	45:YZ:71:VAL:HG13	2.02	0.41
50:Y4:40:HIS:H	50:Y4:41:PRO:CD	2.31	0.41
1:QA:17:U:H2'	1:QA:18:C:C6	2.56	0.41
1:QA:60:A:H4'	1:QA:61:G:O5'	2.21	0.41
1:QA:674:G:H2'	1:QA:675:A:H8	1.85	0.41
3:QC:47:LEU:HD21	3:QC:68:VAL:HG11	2.02	0.41
7:QG:104:LEU:HD13	7:QG:104:LEU:HA	1.91	0.41
10:QJ:27:ALA:HB2	10:QJ:85:LEU:HD11	2.03	0.41
24:QY:31:ASN:O	24:QY:35:GLN:HG2	2.20	0.41
24:QY:49:GLN:O	24:QY:52:LYS:HE3	2.20	0.41
25:RA:93:C:H5'	25:RA:94:G:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:RA:541:C:H2'	25:RA:542:C:H6	1.85	0.41
25:RA:614:U:H4'	25:RA:615:G:H5''	2.03	0.41
25:RA:674:G:H2'	25:RA:804:A:H61	1.86	0.41
25:RA:2224:G:H4'	25:RA:2226:C:C2	2.55	0.41
27:RD:108:PRO:HB3	27:RD:143:HIS:NE2	2.35	0.41
31:RH:103:LEU:HD13	31:RH:123:PHE:HB3	2.02	0.41
34:RO:1:MET:HB2	34:RO:32:TYR:HB3	2.02	0.41
35:RP:6:LEU:HB3	35:RP:7:ARG:H	1.61	0.41
39:RT:118:ARG:HA	39:RT:121:ILE:HD12	2.02	0.41
1:XA:186(F):C:H2'	1:XA:187:C:O4'	2.21	0.41
1:XA:429:U:H1'	1:XA:430:A:H5''	2.02	0.41
1:XA:708:C:H2'	1:XA:709:G:H8	1.85	0.41
1:XA:865:A:C2	1:XA:918:A:H4'	2.56	0.41
2:XB:29:ALA:HB1	2:XB:30:ARG:HH21	1.85	0.41
2:XB:55:PHE:CE1	2:XB:218:ALA:HA	2.56	0.41
2:XB:126:GLU:O	2:XB:130:ARG:NH1	2.53	0.41
10:XJ:54:PHE:CG	10:XJ:55:LYS:HG3	2.55	0.41
25:YA:78:A:H2'	25:YA:79:G:H8	1.83	0.41
25:YA:92:G:H2'	25:YA:93:C:C6	2.56	0.41
25:YA:481:G:C4	25:YA:507:A:C2	3.09	0.41
25:YA:588:U:H2'	25:YA:589:C:C6	2.55	0.41
25:YA:1592:C:H2'	25:YA:1593:G:H8	1.86	0.41
25:YA:1913:A:OP2	25:YA:1913:A:C4'	2.58	0.41
25:YA:2298:A:H2'	25:YA:2299:G:O4'	2.21	0.41
25:YA:2751:G:H5''	25:YA:2752:C:OP2	2.21	0.41
27:YD:145:VAL:HG12	27:YD:146:GLU:O	2.20	0.41
35:YP:6:LEU:HD13	35:YP:6:LEU:HA	1.78	0.41
38:YS:11:LYS:HD3	38:YS:91:PRO:HD3	2.02	0.41
39:YT:27:THR:CG2	39:YT:90:GLN:HB3	2.50	0.41
39:YT:33:LYS:O	39:YT:82:LEU:HD23	2.20	0.41
41:YV:38:LEU:HD12	41:YV:55:ALA:HB1	2.03	0.41
48:Y2:21:LEU:HD11	48:Y2:63:VAL:HG12	2.03	0.41
52:Y6:14:THR:HG22	52:Y6:50:ARG:O	2.20	0.41
1:QA:197:A:H3'	1:QA:197:A:OP2	2.20	0.41
1:QA:531:U:OP2	24:QY:69:ARG:NH1	2.50	0.41
1:QA:812:C:H4'	1:QA:813:U:O5'	2.21	0.41
1:QA:1127:G:H1'	1:QA:1280:A:C6	2.56	0.41
1:QA:1229:A:H2'	1:QA:1230:C:C6	2.56	0.41
1:QA:1347:G:N7	9:QI:11:LYS:CD	2.83	0.41
3:QC:12:LEU:HD23	3:QC:12:LEU:HA	1.89	0.41
9:QI:56:LEU:HD23	9:QI:56:LEU:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:QI:83:ARG:HH21	9:QI:102:LEU:HD21	1.86	0.41
11:QK:110:ASP:HB3	18:QR:85:LEU:HG	2.02	0.41
13:QM:23:TYR:CD2	13:QM:70:LEU:HD11	2.56	0.41
13:QM:99:ARG:O	13:QM:101:GLN:HG3	2.21	0.41
14:QN:10:ALA:HB2	14:QN:23:ARG:HE	1.84	0.41
15:QO:29:VAL:HG11	15:QO:67:LEU:HD21	2.02	0.41
16:QP:34:GLU:OE2	16:QP:55:ARG:HD3	2.21	0.41
18:QR:22:VAL:CG1	18:QR:56:THR:HA	2.48	0.41
19:QS:36:ARG:HD2	19:QS:71:LEU:N	2.21	0.41
25:RA:140:A:H8	25:RA:1408:C:O2'	2.02	0.41
25:RA:141:A:C8	25:RA:1408:C:H1'	2.55	0.41
25:RA:709:U:H2'	25:RA:710:G:C8	2.54	0.41
25:RA:2142:C:H2'	25:RA:2143:C:C6	2.56	0.41
25:RA:2159:G:H2'	25:RA:2160:G:C8	2.55	0.41
27:RD:35:LYS:HD2	27:RD:104:TYR:CD1	2.55	0.41
28:RE:61:ARG:O	28:RE:63:LEU:N	2.50	0.41
29:RF:125:LEU:HD23	29:RF:125:LEU:N	2.36	0.41
33:RN:111:PRO:HA	33:RN:114:ARG:NH1	2.35	0.41
38:RS:14:VAL:HG21	38:RS:89:ARG:HB3	2.02	0.41
38:RS:14:VAL:HG11	38:RS:90:GLY:O	2.20	0.41
38:RS:78:LEU:HD11	38:RS:107:GLU:HG3	2.02	0.41
45:RZ:15:PRO:O	45:RZ:19:ARG:HB2	2.21	0.41
47:R1:15:ALA:O	47:R1:40:ARG:HG3	2.21	0.41
47:R1:97:LEU:HD13	47:R1:97:LEU:HA	1.91	0.41
52:R6:14:THR:OG1	52:R6:19:ARG:HA	2.19	0.41
1:XA:1494:G:O2'	25:YA:1912:A:O2'	2.33	0.41
2:XB:37:ASN:O	2:XB:37:ASN:ND2	2.47	0.41
2:XB:217:ARG:HA	2:XB:220:ASP:HB2	2.02	0.41
4:XD:39:PRO:HA	4:XD:40:PRO:HD3	1.90	0.41
8:XH:13:ILE:O	8:XH:17:THR:HG23	2.21	0.41
8:XH:49:GLU:HG2	8:XH:62:TYR:HE2	1.85	0.41
11:XK:29:ILE:HD13	11:XK:29:ILE:HG21	1.80	0.41
25:YA:311:A:C6	25:YA:328:U:C4	3.09	0.41
25:YA:526:A:O2'	25:YA:2043:C:O2	2.33	0.41
25:YA:1162:G:H1'	41:YV:23:GLU:OE2	2.21	0.41
25:YA:1541:U:H2'	25:YA:1542:G:O4'	2.20	0.41
25:YA:1788:C:H2'	25:YA:1789:A:O4'	2.21	0.41
25:YA:2740:A:C6	25:YA:2741:A:C6	3.09	0.41
30:YG:114:ILE:HG12	30:YG:140:ILE:HG21	2.02	0.41
32:YI:140:LEU:C	32:YI:141:LYS:HG3	2.41	0.41
41:YV:71:LEU:N	41:YV:86:GLY:HA2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:QA:860:A:H2'	1:QA:861:G:O4'	2.21	0.41
1:QA:950:U:H2'	1:QA:951:G:C8	2.56	0.41
1:QA:1432:G:OP1	39:RT:107:ASP:HB2	2.21	0.41
2:QB:228:GLY:O	2:QB:230:VAL:HG23	2.21	0.41
3:QC:186:PHE:HA	3:QC:198:VAL:O	2.21	0.41
6:QF:12:PRO:HD3	6:QF:58:GLY:HA2	2.03	0.41
19:QS:36:ARG:CZ	19:QS:73:GLU:HB2	2.51	0.41
19:QS:64:GLU:C	19:QS:66:MET:H	2.22	0.41
25:RA:137(A):G:C6	25:RA:139:G:H2'	2.56	0.41
25:RA:404:C:H4'	25:RA:405:U:H5'	2.03	0.41
25:RA:778:G:C5	25:RA:779:U:C4	3.09	0.41
25:RA:1312:U:OP2	43:RX:63:LYS:HE2	2.20	0.41
25:RA:1665:A:C2'	25:RA:1666:G:H5'	2.50	0.41
25:RA:1812:A:O2'	27:RD:45:ASN:HB2	2.21	0.41
25:RA:2070:G:H2'	25:RA:2071:A:H8	1.84	0.41
25:RA:2562:U:H1'	34:RO:23:ARG:HH11	1.85	0.41
26:RB:45:A:OP1	30:RG:96:ARG:HD2	2.20	0.41
27:RD:71:ASP:OD2	27:RD:103:ARG:NH2	2.52	0.41
28:RE:77:ILE:HG22	28:RE:78:LEU:HG	2.03	0.41
29:RF:195:ASP:OD1	29:RF:196:LEU:N	2.54	0.41
1:XA:1181:G:O2'	1:XA:1182:G:P	2.79	0.41
1:XA:1319:A:H2'	1:XA:1323:G:N7	2.35	0.41
1:XA:1411:C:H2'	1:XA:1412:C:H6	1.86	0.41
3:XC:206:GLU:HB3	3:XC:207:VAL:H	1.64	0.41
6:XF:91:VAL:HG12	6:XF:92:LYS:O	2.20	0.41
8:XH:38:ILE:HD12	8:XH:118:VAL:HG12	2.02	0.41
9:XI:48:GLU:N	9:XI:49:PRO:HD2	2.35	0.41
10:XJ:20:ALA:O	10:XJ:24:VAL:HG23	2.21	0.41
25:YA:1778:U:H2'	25:YA:1784:A:N6	2.36	0.41
25:YA:1946:U:H2'	25:YA:1947:C:C6	2.56	0.41
27:YD:27:THR:C	27:YD:29:PRO:HD2	2.40	0.41
30:YG:38:VAL:HG13	30:YG:158:ALA:HB3	2.03	0.41
41:YV:33:VAL:N	41:YV:59:ALA:O	2.54	0.41
41:YV:44:LYS:O	41:YV:46:VAL:N	2.54	0.41
42:YW:4:LYS:HB3	42:YW:106:ILE:HG22	2.03	0.41
1:QA:4:U:N3	8:QH:102:ARG:HD2	2.35	0.41
1:QA:188:U:O2'	1:QA:189:U:H5'	2.20	0.41
1:QA:547:A:OP2	4:QD:2:GLY:HA2	2.20	0.41
1:QA:1177:G:N2	1:QA:1181:G:O6	2.54	0.41
2:QB:156:LYS:HD2	2:QB:156:LYS:HA	1.92	0.41
17:QQ:52:LYS:HE3	17:QQ:52:LYS:HB3	1.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:RA:329:G:N7	44:RY:19:LYS:HE2	2.36	0.41
25:RA:864:G:C6	25:RA:865:C:N4	2.89	0.41
25:RA:1203:G:C6	25:RA:1204:A:N6	2.89	0.41
25:RA:1309:G:H4'	53:R7:7:PRO:HB2	2.03	0.41
25:RA:1796:U:H2'	25:RA:1797:C:C6	2.56	0.41
28:RE:203:LYS:HE3	28:RE:203:LYS:HB2	1.80	0.41
29:RF:140:LEU:HA	29:RF:140:LEU:HD12	1.78	0.41
31:RH:86:GLU:H	31:RH:86:GLU:CD	2.24	0.41
38:RS:15:ARG:HD3	38:RS:15:ARG:HA	1.93	0.41
38:RS:106:ARG:HB3	38:RS:110:LEU:HD21	2.03	0.41
41:RV:64:HIS:CE1	41:RV:92:THR:OG1	2.74	0.41
1:XA:710:G:OP1	6:XF:54:LYS:HE2	2.21	0.41
5:XE:127:ASN:HA	5:XE:128:PRO:HD3	1.93	0.41
19:XS:12:ASP:H	19:XS:38:SER:HB3	1.85	0.41
25:YA:2191:G:HO2'	25:YA:2192:G:P	2.42	0.41
25:YA:2749:A:H4'	31:YH:62:LYS:HD3	2.02	0.41
26:YB:8:U:H5'	38:YS:15:ARG:HH12	1.85	0.41
27:YD:142:VAL:HG12	27:YD:163:ALA:HB3	2.03	0.41
31:YH:30:LYS:HB3	31:YH:136:ILE:HG21	2.02	0.41
31:YH:51:ARG:H	31:YH:51:ARG:HG3	1.41	0.41
31:YH:109:PHE:CG	31:YH:110:SER:N	2.88	0.41
44:YY:15:VAL:HG12	44:YY:17:SER:OG	2.21	0.41
48:Y2:46:GLN:HB2	48:Y2:49:LYS:NZ	2.34	0.41
50:Y4:46:GLN:NE2	50:Y4:48:ARG:HD3	2.36	0.41
1:QA:381:C:H2'	1:QA:382:A:O4'	2.21	0.41
1:QA:444:C:H2'	1:QA:445:G:H8	1.85	0.41
1:QA:960:U:HO2'	1:QA:961:U:P	2.41	0.41
2:QB:16:HIS:HB2	2:QB:17:PHE:CD2	2.55	0.41
3:QC:174:PRO:O	3:QC:177:THR:HG22	2.21	0.41
4:QD:61:LYS:HE3	4:QD:61:LYS:HB3	1.89	0.41
4:QD:73:ARG:HD2	4:QD:73:ARG:HA	1.86	0.41
7:QG:94:ARG:NH1	7:QG:98:SER:OG	2.54	0.41
7:QG:115:ARG:O	7:QG:118:VAL:HG22	2.21	0.41
11:QK:93:GLN:OE1	11:QK:96:ARG:NH1	2.54	0.41
13:QM:9:ILE:H	13:QM:9:ILE:HG12	1.60	0.41
20:QT:104:LEU:HB3	20:QT:105:SER:H	1.51	0.41
22:QV:50:U:H2'	22:QV:51:C:H6	1.86	0.41
22:QV:53:G:H2'	22:QV:54:U:C6	2.56	0.41
25:RA:65:C:H2'	25:RA:66:C:H6	1.86	0.41
25:RA:86:C:H4'	25:RA:104:U:H1'	2.02	0.41
25:RA:459:U:H2'	25:RA:460:A:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:RA:686:G:H1'	53:R7:6:GLN:O	2.21	0.41
25:RA:754:C:H2'	25:RA:755:C:H6	1.85	0.41
25:RA:826:U:H2'	25:RA:828:U:O4'	2.20	0.41
25:RA:909:A:H2'	25:RA:912:C:H5	1.85	0.41
25:RA:1417:C:H2'	25:RA:1418:G:O4'	2.21	0.41
25:RA:1790:C:H2'	25:RA:1791:A:C5	2.55	0.41
25:RA:2062:A:O2'	25:RA:2063:C:P	2.78	0.41
25:RA:2074:U:H2'	25:RA:2075:U:C6	2.56	0.41
25:RA:2191:G:HO2'	25:RA:2192:G:P	2.44	0.41
25:RA:2211:G:H3'	25:RA:2212:A:C2	2.56	0.41
25:RA:2321:G:N2	25:RA:2322:A:O4'	2.50	0.41
25:RA:2607:G:H2'	25:RA:2608:G:O4'	2.21	0.41
25:RA:2805:G:H2'	25:RA:2807:G:C8	2.55	0.41
25:RA:2848:G:H2'	25:RA:2867:G:N2	2.36	0.41
30:RG:38:VAL:HG13	30:RG:158:ALA:HB3	2.03	0.41
31:RH:80:SER:OG	31:RH:81:GLU:N	2.53	0.41
31:RH:89:ILE:HD11	31:RH:129:THR:HG22	2.03	0.41
39:RT:50:ILE:HD12	39:RT:50:ILE:HA	1.88	0.41
40:RU:37:GLU:HA	40:RU:40:PHE:CD1	2.56	0.41
48:R2:16:LEU:O	48:R2:20:GLU:HB2	2.21	0.41
48:R2:32:LEU:HD21	48:R2:54:LYS:HG2	2.03	0.41
48:R2:44:LEU:HD23	48:R2:44:LEU:HA	1.93	0.41
1:XA:412:A:C6	4:XD:35:ARG:HG2	2.55	0.41
1:XA:947:G:H2'	1:XA:948:C:O4'	2.21	0.41
1:XA:950:U:H2'	1:XA:951:G:C8	2.56	0.41
1:XA:960:U:O2'	1:XA:961:U:P	2.78	0.41
1:XA:1308:U:H2'	1:XA:1309:G:H8	1.85	0.41
3:XC:23:TYR:HE1	10:XJ:92:THR:HG23	1.86	0.41
4:XD:149:ALA:O	4:XD:153:ARG:HG2	2.21	0.41
9:XI:53:VAL:HG13	9:XI:95:LYS:HE3	2.03	0.41
20:XT:65:LYS:O	20:XT:68:LYS:HG2	2.21	0.41
20:XT:97:ALA:O	20:XT:99:LEU:N	2.53	0.41
21:XU:8:THR:HB	21:XU:11:GLY:H	1.86	0.41
25:YA:147:U:H2'	25:YA:148:C:C6	2.55	0.41
25:YA:434:U:H1'	25:YA:435:C:H5	1.86	0.41
25:YA:607:U:H5	25:YA:619:G:C5	2.39	0.41
25:YA:797:C:H2'	25:YA:798:G:O4'	2.21	0.41
25:YA:1114:G:H2'	25:YA:1115:G:H8	1.85	0.41
25:YA:1375:C:H2'	25:YA:1376:C:H6	1.86	0.41
25:YA:2177:C:H2'	25:YA:2178:C:C6	2.56	0.41
25:YA:2356:C:H4'	46:Y0:20:ARG:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:YB:28:C:H2'	26:YB:29:A:O4'	2.21	0.41
27:YD:224:ALA:HA	27:YD:233:HIS:O	2.21	0.41
28:YE:36:ARG:HH21	28:YE:88:GLY:CA	2.32	0.41
30:YG:105:LYS:NZ	50:Y4:26:SER:HB3	2.35	0.41
31:YH:59:ARG:C	31:YH:61:HIS:H	2.23	0.41
31:YH:85:LYS:HD2	31:YH:85:LYS:HA	1.62	0.41
33:YN:34:LEU:HD11	33:YN:120:LEU:HB2	2.02	0.41
35:YP:1:MET:HE1	35:YP:6:LEU:HD13	2.02	0.41
35:YP:98:GLU:H	35:YP:98:GLU:HG3	1.34	0.41
35:YP:100:LEU:HD23	35:YP:100:LEU:HA	1.92	0.41
37:YR:67:LEU:HD13	37:YR:76:VAL:HG21	2.03	0.41
39:YT:11:GLU:OE1	39:YT:11:GLU:N	2.53	0.41
41:YV:28:GLU:HA	41:YV:29:PRO:HD3	1.88	0.41
41:YV:61:VAL:O	41:YV:63:GLY:N	2.54	0.41
44:YY:96:ILE:HG12	44:YY:101:LYS:HG3	2.03	0.41
50:Y4:26:SER:OG	50:Y4:27:THR:N	2.50	0.41
3:QC:68:VAL:HG12	3:QC:70:VAL:HG23	2.03	0.41
3:QC:134:ILE:HG22	3:QC:168:ALA:HB3	2.02	0.41
4:QD:108:LEU:HD12	4:QD:108:LEU:HA	1.77	0.41
23:QX:13:A:H3'	23:QX:14:A:H5''	2.01	0.41
25:RA:84:A:OP2	44:RY:8:LYS:HD3	2.21	0.41
25:RA:835:A:OP1	54:R8:52:LYS:HG2	2.21	0.41
28:RE:4:ILE:HG21	28:RE:92:THR:O	2.21	0.41
31:RH:3:ARG:HD3	31:RH:6:ARG:HH21	1.85	0.41
39:RT:60:THR:HG22	39:RT:77:PRO:HA	2.02	0.41
41:RV:38:LEU:HD21	41:RV:57:VAL:HG23	2.03	0.41
41:RV:62:LEU:HB3	41:RV:93:GLU:O	2.21	0.41
42:RW:47:VAL:HA	42:RW:50:VAL:HG12	2.03	0.41
44:RY:101:LYS:HE3	44:RY:101:LYS:HB3	1.93	0.41
45:RZ:148:ASP:OD2	45:RZ:148:ASP:N	2.53	0.41
47:R1:58:ILE:HG23	47:R1:87:PRO:HG3	2.03	0.41
50:R4:46:GLN:HE21	50:R4:48:ARG:HD3	1.85	0.41
1:XA:293:G:C6	1:XA:294:U:C4	3.08	0.41
1:XA:1007:C:N3	1:XA:1022:G:N2	2.60	0.41
1:XA:1417:G:C6	1:XA:1482:G:C6	3.09	0.41
9:XI:20:ARG:HA	9:XI:21:PRO:HD3	1.85	0.41
11:XK:127:LYS:HD3	11:XK:127:LYS:HA	1.92	0.41
15:XO:75:PRO:HB2	15:XO:79:ARG:HH21	1.86	0.41
25:YA:211:A:H2'	25:YA:212:G:O4'	2.21	0.41
25:YA:817:C:H4'	25:YA:932:G:C5	2.55	0.41
25:YA:910:A:C6	25:YA:911:A:C6	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:YA:1544:C:O2	25:YA:1544:C:C3'	2.69	0.41
33:YN:43:THR:HB	33:YN:46:VAL:HG12	2.03	0.41
45:YZ:182:LYS:HB3	45:YZ:182:LYS:HE3	1.95	0.41
47:Y1:85:LEU:HD23	47:Y1:85:LEU:HA	1.90	0.41
52:Y6:12:GLU:CD	52:Y6:12:GLU:H	2.25	0.41
1:QA:882:C:O2'	1:QA:883:C:H5'	2.21	0.40
11:QK:44:SER:O	11:QK:48:ILE:HG12	2.21	0.40
25:RA:347:A:H2'	25:RA:348:G:H8	1.85	0.40
25:RA:439:G:H2'	25:RA:440:G:C8	2.56	0.40
25:RA:559:G:H22	40:RU:49:HIS:CE1	2.38	0.40
25:RA:658:C:H2'	25:RA:659:C:C6	2.56	0.40
25:RA:894:C:H5'	25:RA:895:U:OP2	2.21	0.40
25:RA:1105:U:H2'	25:RA:1106:G:C8	2.56	0.40
25:RA:1184:G:C6	25:RA:1185:C:C4	3.09	0.40
25:RA:2056:G:N2	51:R5:4:HIS:O	2.54	0.40
25:RA:2875:C:O2'	39:RT:5:ALA:HB3	2.22	0.40
28:RE:6:GLY:HA2	28:RE:51:PHE:CZ	2.56	0.40
30:RG:47:LYS:HE3	30:RG:47:LYS:HB2	1.91	0.40
30:RG:97:ASP:O	30:RG:101:ILE:HG23	2.22	0.40
35:RP:45:LEU:HD12	35:RP:45:LEU:HA	1.83	0.40
40:RU:58:ARG:HA	40:RU:61:TRP:CE3	2.56	0.40
49:R3:8:LEU:CD1	49:R3:31:LEU:HD12	2.51	0.40
1:XA:745:C:OP1	1:XA:851:G:O2'	2.39	0.40
1:XA:1313:U:OP2	19:XS:6:LYS:HD3	2.21	0.40
3:XC:174:PRO:O	3:XC:177:THR:HG22	2.21	0.40
5:XE:7:GLU:HB3	5:XE:35:GLY:O	2.21	0.40
18:XR:66:LEU:O	18:XR:70:ILE:HG13	2.21	0.40
25:YA:336:C:HO2'	44:YY:35:TYR:HH	1.59	0.40
25:YA:467:G:OP1	53:Y7:33:ARG:NH1	2.48	0.40
25:YA:755:C:H2'	25:YA:756:C:C6	2.55	0.40
25:YA:897:C:H6	25:YA:897:C:P	2.44	0.40
25:YA:1024:G:C3'	25:YA:1025:G:H5''	2.47	0.40
25:YA:2420:C:N4	54:Y8:31:HIS:HA	2.36	0.40
25:YA:2684:U:H1'	34:YO:70:LYS:HD2	2.03	0.40
25:YA:2828:C:H2'	25:YA:2829:C:H6	1.84	0.40
28:YE:52:LEU:HB3	28:YE:75:VAL:HG23	2.03	0.40
31:YH:35:VAL:HG11	31:YH:72:ILE:HG13	2.03	0.40
31:YH:116:GLU:HA	31:YH:117:PRO:HD3	1.90	0.40
32:YI:72:LEU:HD21	32:YI:107:VAL:HG11	2.03	0.40
32:YI:77:LEU:CG	32:YI:142:VAL:HG22	2.49	0.40
34:YO:4:PRO:O	34:YO:5:GLN:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:YO:73:ASP:OD1	39:YT:32:TYR:OH	2.30	0.40
41:YV:35:LEU:HD23	41:YV:37:VAL:HG21	2.03	0.40
49:Y3:46:ASN:O	49:Y3:50:VAL:HG22	2.21	0.40
50:Y4:2:LYS:HB2	50:Y4:2:LYS:HE3	1.84	0.40
53:Y7:48:LYS:HB2	53:Y7:49:ARG:H	1.62	0.40
8:QH:20:TYR:HE2	8:QH:75:ARG:HD2	1.86	0.40
10:QJ:54:PHE:HE1	10:QJ:55:LYS:HZ2	1.68	0.40
15:QO:21:ASP:OD2	15:QO:24:SER:HB2	2.21	0.40
25:RA:69:C:H6	25:RA:73:A:O2'	2.04	0.40
25:RA:485:C:H2'	25:RA:486:C:C6	2.56	0.40
25:RA:646:A:H2'	25:RA:647:G:O4'	2.21	0.40
25:RA:775:G:C5	25:RA:794:G:C8	3.09	0.40
25:RA:883:G:H4'	25:RA:884:C:OP2	2.21	0.40
25:RA:1778:U:H2'	25:RA:1784:A:N6	2.36	0.40
25:RA:1831:G:H2'	25:RA:1832:C:H6	1.84	0.40
25:RA:2210:G:N3	25:RA:2210:G:H2'	2.36	0.40
25:RA:2748:A:H8	31:RH:63:SER:HB3	1.86	0.40
28:RE:117:MET:HG3	28:RE:122:PHE:O	2.20	0.40
30:RG:143:GLU:OE1	30:RG:143:GLU:N	2.50	0.40
31:RH:108:GLY:HA3	31:RH:152:ARG:NH2	2.36	0.40
35:RP:3:LEU:HD23	35:RP:3:LEU:HA	1.95	0.40
39:RT:6:LEU:O	39:RT:10:VAL:HG23	2.21	0.40
42:RW:9:TYR:H	42:RW:102:HIS:CE1	2.39	0.40
42:RW:92:ARG:NH1	42:RW:94:ASP:OD2	2.54	0.40
44:RY:84:ARG:HG3	44:RY:84:ARG:O	2.21	0.40
1:XA:321:A:C8	1:XA:328:C:O2	2.74	0.40
2:XB:25:ASN:C	2:XB:27:LYS:H	2.24	0.40
3:XC:68:VAL:HG12	3:XC:70:VAL:HG23	2.03	0.40
11:XK:62:GLN:OE1	11:XK:93:GLN:NE2	2.54	0.40
11:XK:120:ARG:HA	11:XK:121:PRO:HD3	1.86	0.40
18:XR:22:VAL:HG13	18:XR:23:LYS:N	2.36	0.40
20:XT:17:ARG:HA	20:XT:20:LEU:HD12	2.03	0.40
20:XT:104:LEU:HB3	20:XT:105:SER:H	1.53	0.40
25:YA:540:G:H2'	25:YA:541:C:C6	2.56	0.40
25:YA:1062:G:H2'	25:YA:1063:G:H8	1.86	0.40
25:YA:1278:A:H5''	37:YR:36:THR:HG22	2.02	0.40
25:YA:1418:G:N1	25:YA:1579:A:OP2	2.37	0.40
25:YA:1653:G:C6	37:YR:11:ASN:OD1	2.75	0.40
25:YA:2241:A:H2'	25:YA:2242:G:C8	2.56	0.40
25:YA:2716:U:O2'	25:YA:2717:G:H5'	2.21	0.40
28:YE:105:THR:HB	28:YE:197:ILE:HG12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:YI:122:GLU:HB3	32:YI:126:TYR:OH	2.21	0.40
34:YO:71:ARG:NE	34:YO:105:GLU:OE2	2.55	0.40
35:YP:45:LEU:HD22	35:YP:45:LEU:HA	1.78	0.40
35:YP:126:VAL:HG22	35:YP:145:PRO:HG2	2.02	0.40
37:YR:34:ILE:HD13	37:YR:34:ILE:HA	1.81	0.40
41:YV:77:ALA:O	41:YV:79:VAL:HG22	2.21	0.40
45:YZ:156:LYS:HB3	45:YZ:157:LEU:H	1.63	0.40
50:Y4:8:LYS:O	50:Y4:9:LEU:HD12	2.20	0.40
1:QA:580:U:H2'	1:QA:581:G:O4'	2.21	0.40
1:QA:1005:A:O2'	1:QA:1037:C:H1'	2.21	0.40
1:QA:1371:G:C6	1:QA:1372:U:C4	3.10	0.40
3:QC:86:VAL:O	3:QC:90:GLU:N	2.55	0.40
11:QK:11:LYS:HB2	11:QK:12:ARG:H	1.63	0.40
25:RA:839:U:H2'	25:RA:840:C:H6	1.81	0.40
25:RA:1057:A:N6	25:RA:1087:G:OP2	2.54	0.40
25:RA:1342:A:H2	25:RA:1396:U:O2'	2.02	0.40
25:RA:1375:C:H2'	25:RA:1376:C:C6	2.56	0.40
26:RB:44:G:H5''	26:RB:45:A:OP1	2.21	0.40
27:RD:95:LEU:HD22	27:RD:117:VAL:HG11	2.02	0.40
29:RF:10:PRO:HA	29:RF:127:GLU:HB3	2.03	0.40
31:RH:156:ALA:HB3	31:RH:159:GLU:O	2.21	0.40
32:RI:123:LEU:HD21	32:RI:144:VAL:CG1	2.45	0.40
38:RS:67:ARG:O	38:RS:71:ARG:HG3	2.21	0.40
38:RS:74:ALA:HB1	38:RS:107:GLU:CB	2.50	0.40
47:R1:88:LYS:O	47:R1:91:LYS:HB2	2.21	0.40
1:XA:381:C:H2'	1:XA:382:A:O4'	2.20	0.40
1:XA:973:G:OP1	10:XJ:57:LYS:NZ	2.52	0.40
1:XA:1280:A:H5'	1:XA:1281:U:OP2	2.20	0.40
2:XB:221:LEU:HA	2:XB:224:GLN:HB2	2.02	0.40
4:XD:9:CYS:SG	4:XD:26:CYS:SG	3.12	0.40
13:XM:40:ASN:HB3	13:XM:43:THR:HG23	2.04	0.40
19:XS:29:ARG:HB2	19:XS:48:THR:OG1	2.22	0.40
19:XS:39:THR:HA	19:XS:70:LYS:HA	2.02	0.40
25:YA:598:G:H2'	25:YA:599:G:O4'	2.20	0.40
25:YA:1228:G:OP2	40:YU:16:LYS:NZ	2.52	0.40
25:YA:1264:G:H2'	25:YA:2014:A:N6	2.37	0.40
25:YA:1517:G:C6	25:YA:1518:C:C4	3.10	0.40
25:YA:1999:C:H4'	25:YA:2723:C:O2	2.22	0.40
25:YA:2115:G:H5''	25:YA:2167:U:C4	2.57	0.40
25:YA:2238:G:H2'	25:YA:2238:G:N3	2.36	0.40
25:YA:2557:G:H2'	25:YA:2558:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:YA:2804:C:H2'	25:YA:2805:G:O4'	2.22	0.40
25:YA:2817:G:OP1	37:YR:99:LYS:HE2	2.21	0.40
26:YB:89:G:C6	26:YB:89(A):A:C6	3.10	0.40
26:YB:114:G:H2'	26:YB:115:G:H8	1.85	0.40
29:YF:118:ALA:HB2	29:YF:123:LEU:HD22	2.03	0.40
35:YP:63:PRO:N	54:Y8:13:ARG:HG2	2.36	0.40
36:YQ:80:GLU:HG2	36:YQ:81:VAL:N	2.35	0.40
42:YW:71:VAL:HA	42:YW:107:LEU:HD12	2.03	0.40
44:YY:17:SER:CB	44:YY:71:LYS:HB3	2.50	0.40
1:QA:123:C:OP1	1:QA:312:C:H5'	2.21	0.40
1:QA:1285:A:O2'	1:QA:1286:A:H5''	2.21	0.40
2:QB:121:LEU:HA	2:QB:124:SER:HB3	2.04	0.40
3:QC:69:HIS:HA	3:QC:104:GLN:HB2	2.03	0.40
12:QL:126:LYS:O	12:QL:128:ALA:N	2.54	0.40
25:RA:78:A:H2'	25:RA:79:G:H8	1.86	0.40
25:RA:90:U:H1'	25:RA:91:A:C8	2.57	0.40
25:RA:413:C:H4'	25:RA:1880:C:O2'	2.21	0.40
25:RA:2593:U:H2'	25:RA:2594:C:H6	1.85	0.40
26:RB:5:C:O2'	26:RB:27:C:O2	2.39	0.40
26:RB:89:G:OP2	26:RB:89:G:H8	2.04	0.40
27:RD:102:LYS:C	27:RD:103:ARG:HG2	2.41	0.40
28:RE:35:GLN:HE22	28:RE:37:ARG:HH21	1.69	0.40
28:RE:69:LYS:HE2	28:RE:69:LYS:HA	2.04	0.40
29:RF:63:LYS:HE2	29:RF:67:GLN:HB2	2.02	0.40
31:RH:90:LYS:HE2	31:RH:90:LYS:HB3	1.92	0.40
35:RP:47:ASP:OD1	35:RP:50:ARG:NH1	2.55	0.40
39:RT:102:ILE:O	39:RT:106:SER:HB3	2.21	0.40
45:RZ:69:THR:HG22	45:RZ:90:VAL:HG22	2.04	0.40
46:R0:82:ARG:HA	46:R0:82:ARG:HD3	1.89	0.40
47:R1:85:LEU:HA	47:R1:85:LEU:HD23	1.83	0.40
50:R4:58:ARG:NH2	50:R4:62:ARG:HG3	2.36	0.40
50:R4:58:ARG:HG3	50:R4:59:PHE:N	2.37	0.40
52:R6:40:CYS:N	52:R6:41:PRO:HD3	2.36	0.40
1:XA:116:A:H2'	1:XA:117:G:O4'	2.22	0.40
1:XA:859:A:OP2	1:XA:869:G:N1	2.44	0.40
1:XA:975:A:O2'	14:XN:32:SER:HB3	2.21	0.40
1:XA:1426:C:H2'	1:XA:1427:U:C6	2.57	0.40
10:XJ:10:GLY:HA3	10:XJ:16:LEU:CD2	2.51	0.40
22:XV:21:A:N6	22:XV:46:G:H2'	2.37	0.40
25:YA:1418:G:OP1	25:YA:1588:C:O2'	2.37	0.40
25:YA:1586:A:C2'	25:YA:1587:A:C5'	2.95	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:YB:37:C:H2'	26:YB:38:C:O4'	2.22	0.40
27:YD:184:LYS:HE3	27:YD:269:PHE:HA	2.02	0.40
30:YG:82:LEU:HA	30:YG:86:MET:SD	2.62	0.40
32:YI:76:THR:HG21	32:YI:138:ILE:HD11	2.02	0.40
40:YU:17:ILE:HG23	40:YU:39:LEU:HD12	2.03	0.40
48:Y2:21:LEU:HA	48:Y2:21:LEU:HD23	1.82	0.40
2:QB:29:ALA:HB1	2:QB:30:ARG:NH2	2.32	0.40
4:QD:111:ALA:HA	4:QD:161:ASN:ND2	2.37	0.40
6:QF:69:GLU:O	6:QF:72:VAL:HG12	2.21	0.40
7:QG:75:VAL:HG13	7:QG:145:ALA:HA	2.02	0.40
7:QG:155:ARG:HB3	7:QG:156:TRP:H	1.54	0.40
8:QH:36:LEU:HD23	8:QH:36:LEU:HA	1.97	0.40
14:QN:26:ARG:HD3	14:QN:43:CYS:HB3	2.02	0.40
19:QS:63:THR:H	19:QS:66:MET:CE	2.34	0.40
24:QY:79:ILE:HG22	24:QY:84:TYR:CE2	2.57	0.40
25:RA:380:U:O3'	47:R1:16:ASN:HB2	2.21	0.40
25:RA:550:G:O2'	25:RA:1220:A:N3	2.38	0.40
25:RA:1889:A:N1	25:RA:2234:G:H1'	2.36	0.40
25:RA:2322:A:H2'	25:RA:2323:G:O4'	2.21	0.40
29:RF:2:LYS:CB	29:RF:24:LEU:HD12	2.47	0.40
31:RH:33:LEU:HD12	31:RH:33:LEU:HA	1.97	0.40
35:RP:30:THR:O	35:RP:33:ARG:HB2	2.22	0.40
35:RP:62:LEU:CD2	54:R8:25:MET:HB3	2.48	0.40
39:RT:50:ILE:HG22	39:RT:62:THR:OG1	2.21	0.40
43:RX:63:LYS:HZ2	43:RX:63:LYS:N	2.16	0.40
45:RZ:100:VAL:HG11	45:RZ:134:PRO:HB2	2.02	0.40
46:R0:25:ARG:HB3	46:R0:67:VAL:HG21	2.03	0.40
1:XA:149:A:H2'	1:XA:150:C:C6	2.57	0.40
1:XA:619:U:N3	4:XD:134:ASP:OD2	2.38	0.40
1:XA:892:A:O2'	1:XA:1415:G:H4'	2.21	0.40
1:XA:973:G:OP1	10:XJ:57:LYS:CE	2.70	0.40
1:XA:1442:G:O6	1:XA:1446:A:N6	2.54	0.40
5:XE:152:ARG:NH2	8:XH:107:LEU:O	2.54	0.40
11:XK:84:VAL:HG23	11:XK:110:ASP:HA	2.04	0.40
13:XM:44:ARG:C	13:XM:46:LYS:H	2.25	0.40
19:XS:36:ARG:HH12	19:XS:73:GLU:HB2	1.82	0.40
22:XV:50:U:H2'	22:XV:51:C:C6	2.55	0.40
25:YA:76:C:H1'	48:Y2:62:THR:HG21	2.04	0.40
25:YA:444:C:H2'	25:YA:445:C:C6	2.55	0.40
25:YA:828:U:H4'	25:YA:831:G:N1	2.37	0.40
25:YA:945:A:C4	25:YA:2448:A:C2	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:YA:1049:C:O2	25:YA:1113:U:O2'	2.26	0.40
25:YA:1069:A:O2'	25:YA:1072:C:OP2	2.33	0.40
25:YA:1273:U:O2'	25:YA:1275:A:OP1	2.34	0.40
25:YA:2009:G:N3	37:YR:107:ASP:HA	2.36	0.40
27:YD:165:ILE:HD13	27:YD:175:LEU:HD21	2.02	0.40
28:YE:203:LYS:HE3	28:YE:203:LYS:HB2	1.75	0.40
30:YG:41:GLN:HG2	30:YG:154:GLY:O	2.21	0.40
30:YG:41:GLN:HB3	30:YG:43:LEU:HD13	2.02	0.40
32:YI:1:MET:HG3	32:YI:23:PRO:HG3	2.03	0.40
35:YP:83:VAL:CG1	35:YP:112:LEU:HD21	2.50	0.40
39:YT:130:ALA:HA	39:YT:133:GLU:HG2	2.03	0.40
43:YX:36:LYS:HD2	43:YX:54:VAL:O	2.22	0.40
45:YZ:158:PRO:HB2	45:YZ:161:VAL:HG23	2.03	0.40

There are no symmetry-related clashes.

## 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	
2	QB	234/256 (91%)	186 (80%)	29 (12%)	19 (8%)	1	5
2	XB	234/256 (91%)	189 (81%)	27 (12%)	18 (8%)	1	5
3	QC	204/239 (85%)	161 (79%)	27 (13%)	16 (8%)	1	5
3	XC	204/239 (85%)	160 (78%)	31 (15%)	13 (6%)	1	8
4	QD	206/209 (99%)	169 (82%)	26 (13%)	11 (5%)	2	12
4	XD	206/209 (99%)	168 (82%)	22 (11%)	16 (8%)	1	5
5	QE	152/162 (94%)	135 (89%)	12 (8%)	5 (3%)	4	21
5	XE	152/162 (94%)	137 (90%)	9 (6%)	6 (4%)	3	18
6	QF	99/101 (98%)	89 (90%)	10 (10%)	0	100	100
6	XF	99/101 (98%)	95 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	QG	153/156 (98%)	136 (89%)	13 (8%)	4 (3%)	5	26
7	XG	153/156 (98%)	133 (87%)	15 (10%)	5 (3%)	4	21
8	QH	136/138 (99%)	126 (93%)	7 (5%)	3 (2%)	6	29
8	XH	136/138 (99%)	123 (90%)	10 (7%)	3 (2%)	6	29
9	QI	126/128 (98%)	94 (75%)	24 (19%)	8 (6%)	1	8
9	XI	126/128 (98%)	97 (77%)	22 (18%)	7 (6%)	2	11
10	QJ	97/105 (92%)	80 (82%)	13 (13%)	4 (4%)	3	16
10	XJ	97/105 (92%)	81 (84%)	11 (11%)	5 (5%)	2	12
11	QK	119/129 (92%)	102 (86%)	13 (11%)	4 (3%)	3	21
11	XK	119/129 (92%)	105 (88%)	10 (8%)	4 (3%)	3	21
12	QL	123/132 (93%)	99 (80%)	16 (13%)	8 (6%)	1	8
12	XL	123/132 (93%)	97 (79%)	18 (15%)	8 (6%)	1	8
13	QM	116/126 (92%)	88 (76%)	17 (15%)	11 (10%)	0	3
13	XM	116/126 (92%)	88 (76%)	17 (15%)	11 (10%)	0	3
14	QN	58/61 (95%)	51 (88%)	4 (7%)	3 (5%)	2	12
14	XN	58/61 (95%)	51 (88%)	4 (7%)	3 (5%)	2	12
15	QO	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
15	XO	86/89 (97%)	79 (92%)	7 (8%)	0	100	100
16	QP	82/88 (93%)	72 (88%)	10 (12%)	0	100	100
16	XP	82/88 (93%)	76 (93%)	6 (7%)	0	100	100
17	QQ	98/105 (93%)	90 (92%)	7 (7%)	1 (1%)	15	49
17	XQ	98/105 (93%)	89 (91%)	7 (7%)	2 (2%)	7	31
18	QR	69/88 (78%)	61 (88%)	8 (12%)	0	100	100
18	XR	69/88 (78%)	62 (90%)	6 (9%)	1 (1%)	11	40
19	QS	80/93 (86%)	52 (65%)	18 (22%)	10 (12%)	0	1
19	XS	80/93 (86%)	52 (65%)	18 (22%)	10 (12%)	0	1
20	QT	97/106 (92%)	79 (81%)	15 (16%)	3 (3%)	4	23
20	XT	97/106 (92%)	80 (82%)	14 (14%)	3 (3%)	4	23
21	QU	23/25 (92%)	16 (70%)	6 (26%)	1 (4%)	2	16
21	XU	23/25 (92%)	18 (78%)	3 (13%)	2 (9%)	1	4
24	QY	89/117 (76%)	80 (90%)	9 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	XY	89/117 (76%)	83 (93%)	6 (7%)	0	100	100
27	RD	270/276 (98%)	224 (83%)	38 (14%)	8 (3%)	4	23
27	YD	270/276 (98%)	228 (84%)	32 (12%)	10 (4%)	3	19
28	RE	203/206 (98%)	137 (68%)	38 (19%)	28 (14%)	0	1
28	YE	203/206 (98%)	134 (66%)	39 (19%)	30 (15%)	0	0
29	RF	206/210 (98%)	167 (81%)	26 (13%)	13 (6%)	1	8
29	YF	206/210 (98%)	168 (82%)	22 (11%)	16 (8%)	1	5
30	RG	179/182 (98%)	141 (79%)	26 (14%)	12 (7%)	1	7
30	YG	179/182 (98%)	147 (82%)	21 (12%)	11 (6%)	1	9
31	RH	168/180 (93%)	104 (62%)	37 (22%)	27 (16%)	0	0
31	YH	168/180 (93%)	98 (58%)	42 (25%)	28 (17%)	0	0
32	RI	144/148 (97%)	109 (76%)	28 (19%)	7 (5%)	2	14
32	YI	144/148 (97%)	116 (81%)	24 (17%)	4 (3%)	5	25
33	RN	136/140 (97%)	116 (85%)	13 (10%)	7 (5%)	2	13
33	YN	136/140 (97%)	110 (81%)	19 (14%)	7 (5%)	2	13
34	RO	120/122 (98%)	110 (92%)	9 (8%)	1 (1%)	19	54
34	YO	120/122 (98%)	109 (91%)	10 (8%)	1 (1%)	19	54
35	RP	148/150 (99%)	97 (66%)	23 (16%)	28 (19%)	0	0
35	YP	148/150 (99%)	102 (69%)	22 (15%)	24 (16%)	0	0
36	RQ	138/141 (98%)	110 (80%)	17 (12%)	11 (8%)	1	5
36	YQ	137/141 (97%)	111 (81%)	15 (11%)	11 (8%)	1	5
37	RR	115/118 (98%)	107 (93%)	4 (4%)	4 (4%)	3	20
37	YR	115/118 (98%)	109 (95%)	3 (3%)	3 (3%)	5	26
38	RS	109/112 (97%)	84 (77%)	17 (16%)	8 (7%)	1	6
38	YS	109/112 (97%)	85 (78%)	13 (12%)	11 (10%)	0	3
39	RT	135/146 (92%)	109 (81%)	24 (18%)	2 (2%)	10	39
39	YT	135/146 (92%)	113 (84%)	17 (13%)	5 (4%)	3	19
40	RU	115/118 (98%)	107 (93%)	6 (5%)	2 (2%)	9	36
40	YU	115/118 (98%)	103 (90%)	9 (8%)	3 (3%)	5	26
41	RV	99/101 (98%)	72 (73%)	12 (12%)	15 (15%)	0	0
41	YV	99/101 (98%)	71 (72%)	15 (15%)	13 (13%)	0	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	RW	111/113 (98%)	107 (96%)	1 (1%)	3 (3%)	5	25
42	YW	111/113 (98%)	104 (94%)	3 (3%)	4 (4%)	3	20
43	RX	90/96 (94%)	76 (84%)	12 (13%)	2 (2%)	6	29
43	YX	90/96 (94%)	77 (86%)	11 (12%)	2 (2%)	6	29
44	RY	100/110 (91%)	56 (56%)	28 (28%)	16 (16%)	0	0
44	YY	100/110 (91%)	57 (57%)	27 (27%)	16 (16%)	0	0
45	RZ	174/206 (84%)	117 (67%)	33 (19%)	24 (14%)	0	1
45	YZ	181/206 (88%)	122 (67%)	42 (23%)	17 (9%)	0	3
46	R0	81/85 (95%)	73 (90%)	5 (6%)	3 (4%)	3	19
46	Y0	81/85 (95%)	67 (83%)	11 (14%)	3 (4%)	3	19
47	R1	95/98 (97%)	71 (75%)	12 (13%)	12 (13%)	0	1
47	Y1	95/98 (97%)	76 (80%)	13 (14%)	6 (6%)	1	8
48	R2	67/72 (93%)	54 (81%)	8 (12%)	5 (8%)	1	6
48	Y2	67/72 (93%)	56 (84%)	5 (8%)	6 (9%)	1	4
49	R3	57/60 (95%)	51 (90%)	6 (10%)	0	100	100
49	Y3	57/60 (95%)	51 (90%)	6 (10%)	0	100	100
50	R4	68/71 (96%)	43 (63%)	12 (18%)	13 (19%)	0	0
50	Y4	68/71 (96%)	38 (56%)	15 (22%)	15 (22%)	0	0
51	R5	57/60 (95%)	46 (81%)	9 (16%)	2 (4%)	3	20
51	Y5	55/60 (92%)	48 (87%)	4 (7%)	3 (6%)	2	11
52	R6	46/54 (85%)	22 (48%)	15 (33%)	9 (20%)	0	0
52	Y6	46/54 (85%)	16 (35%)	17 (37%)	13 (28%)	0	0
53	R7	47/49 (96%)	47 (100%)	0	0	100	100
53	Y7	47/49 (96%)	44 (94%)	3 (6%)	0	100	100
54	R8	62/65 (95%)	48 (77%)	7 (11%)	7 (11%)	0	2
54	Y8	62/65 (95%)	49 (79%)	6 (10%)	7 (11%)	0	2
55	R9	35/37 (95%)	34 (97%)	0	1 (3%)	4	24
55	Y9	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
All	All	11647/12358 (94%)	9391 (81%)	1489 (13%)	767 (7%)	1	7

All (767) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
2	QB	29	ALA
2	QB	165	VAL
2	QB	195	ASP
2	QB	238	LEU
3	QC	64	VAL
3	QC	77	ILE
4	QD	13	ARG
4	QD	14	ARG
4	QD	24	GLU
4	QD	34	GLU
4	QD	150	GLU
5	QE	7	GLU
5	QE	12	LEU
5	QE	115	VAL
7	QG	80	VAL
9	QI	34	ASN
9	QI	35	GLU
10	QJ	75	ILE
12	QL	47	LYS
12	QL	79	GLU
13	QM	12	ASN
13	QM	14	ARG
13	QM	47	ASP
13	QM	83	ASP
17	QQ	69	LYS
19	QS	37	ARG
19	QS	67	VAL
19	QS	70	LYS
19	QS	72	GLY
27	RD	28	GLU
28	RE	59	VAL
28	RE	61	ARG
28	RE	78	LEU
29	RF	2	LYS
29	RF	3	GLU
29	RF	25	PRO
29	RF	132	VAL
30	RG	97	ASP
31	RH	9	ILE
31	RH	10	PRO
31	RH	12	PRO
31	RH	15	VAL
31	RH	49	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
31	RH	80	SER
31	RH	152	ARG
31	RH	153	LYS
31	RH	164	TYR
31	RH	168	PRO
32	RI	144	VAL
33	RN	131	GLN
34	RO	48	PRO
35	RP	6	LEU
35	RP	10	PRO
35	RP	15	ARG
35	RP	27	HIS
35	RP	29	LYS
35	RP	42	SER
35	RP	56	SER
35	RP	64	LYS
35	RP	98	GLU
36	RQ	78	PRO
36	RQ	90	VAL
36	RQ	133	ARG
38	RS	89	ARG
41	RV	49	THR
44	RY	76	CYS
44	RY	79	CYS
44	RY	85	VAL
44	RY	89	PHE
45	RZ	53	ILE
45	RZ	59	LEU
45	RZ	157	LEU
45	RZ	158	PRO
45	RZ	159	PRO
46	R0	47	PRO
47	R1	30	VAL
47	R1	45	ASN
48	R2	47	ASN
50	R4	39	CYS
50	R4	40	HIS
51	R5	4	HIS
52	R6	19	ARG
52	R6	31	PRO
54	R8	32	LEU
54	R8	34	TRP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
55	R9	2	LYS
2	XB	15	VAL
2	XB	29	ALA
2	XB	165	VAL
2	XB	190	THR
2	XB	238	LEU
3	XC	12	LEU
3	XC	64	VAL
4	XD	14	ARG
4	XD	24	GLU
4	XD	26	CYS
4	XD	110	PHE
5	XE	115	VAL
7	XG	3	ARG
7	XG	80	VAL
9	XI	118	LYS
10	XJ	54	PHE
10	XJ	57	LYS
10	XJ	75	ILE
12	XL	127	GLU
13	XM	3	ARG
13	XM	14	ARG
13	XM	47	ASP
13	XM	83	ASP
14	XN	15	LYS
18	XR	20	ALA
19	XS	37	ARG
19	XS	38	SER
19	XS	70	LYS
27	YD	26	LYS
27	YD	28	GLU
28	YE	54	GLN
28	YE	61	ARG
28	YE	64	LYS
28	YE	78	LEU
28	YE	132	HIS
29	YF	25	PRO
29	YF	67	GLN
29	YF	123	LEU
29	YF	124	LEU
31	YH	9	ILE
31	YH	10	PRO

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
31	YH	12	PRO
31	YH	15	VAL
31	YH	49	VAL
31	YH	84	SER
31	YH	109	PHE
31	YH	152	ARG
31	YH	153	LYS
31	YH	168	PRO
33	YN	17	ASP
33	YN	18	ALA
34	YO	48	PRO
35	YP	6	LEU
35	YP	15	ARG
35	YP	16	ARG
35	YP	27	HIS
35	YP	45	LEU
35	YP	56	SER
35	YP	65	ARG
36	YQ	18	LYS
36	YQ	59	ARG
36	YQ	78	PRO
36	YQ	133	ARG
38	YS	89	ARG
38	YS	107	GLU
41	YV	50	PRO
41	YV	85	LYS
44	YY	77	PRO
44	YY	78	ALA
44	YY	89	PHE
45	YZ	53	ILE
45	YZ	111	VAL
45	YZ	141	VAL
45	YZ	154	ASP
46	Y0	47	PRO
47	Y1	30	VAL
47	Y1	93	GLU
48	Y2	43	GLN
48	Y2	47	ASN
50	Y4	6	HIS
50	Y4	40	HIS
51	Y5	4	HIS
52	Y6	28	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
52	Y6	31	PRO
54	Y8	30	ARG
54	Y8	33	ASN
54	Y8	51	ALA
54	Y8	61	LEU
2	QB	16	HIS
2	QB	20	GLU
2	QB	39	ILE
2	QB	194	PRO
3	QC	12	LEU
3	QC	78	GLY
3	QC	85	ARG
3	QC	160	ALA
3	QC	162	GLN
7	QG	17	VAL
8	QH	99	GLU
9	QI	119	ALA
9	QI	124	GLN
10	QJ	54	PHE
11	QK	10	VAL
11	QK	15	ALA
12	QL	45	PRO
12	QL	127	GLU
13	QM	3	ARG
13	QM	48	LEU
13	QM	63	THR
13	QM	100	GLY
13	QM	116	THR
14	QN	14	PRO
14	QN	15	LYS
19	QS	38	SER
19	QS	41	VAL
19	QS	80	TYR
27	RD	25	THR
27	RD	33	LEU
27	RD	159	ALA
27	RD	196	VAL
27	RD	239	ARG
28	RE	54	GLN
28	RE	63	LEU
28	RE	65	GLY
28	RE	68	ALA

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
28	RE	69	LYS
28	RE	71	GLY
29	RF	28	ILE
29	RF	67	GLN
29	RF	123	LEU
29	RF	124	LEU
31	RH	11	VAL
31	RH	45	VAL
31	RH	55	PRO
31	RH	109	PHE
31	RH	151	ILE
32	RI	77	LEU
33	RN	18	ALA
35	RP	12	ALA
35	RP	21	ARG
35	RP	24	GLY
35	RP	57	THR
35	RP	147	LEU
36	RQ	80	GLU
36	RQ	134	ARG
36	RQ	135	ASP
36	RQ	136	ALA
38	RS	4	LEU
38	RS	44	LYS
38	RS	88	ASP
38	RS	94	TYR
39	RT	86	ILE
40	RU	92	ARG
41	RV	72	VAL
41	RV	80	GLN
41	RV	84	LYS
41	RV	85	LYS
41	RV	87	HIS
41	RV	98	GLU
42	RW	63	ASP
43	RX	67	GLY
44	RY	61	ILE
44	RY	63	LYS
44	RY	99	CYS
45	RZ	51	ALA
45	RZ	115	GLY
45	RZ	119	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
45	RZ	142	SER
45	RZ	151	HIS
45	RZ	165	VAL
47	R1	27	GLU
47	R1	82	LEU
47	R1	92	LYS
47	R1	93	GLU
48	R2	48	HIS
50	R4	5	ILE
50	R4	48	ARG
50	R4	51	ASP
52	R6	14	THR
54	R8	30	ARG
54	R8	55	ALA
54	R8	61	LEU
2	XB	191	ASP
3	XC	84	ILE
3	XC	160	ALA
3	XC	162	GLN
4	XD	20	TYR
4	XD	23	GLY
4	XD	27	TYR
4	XD	29	PRO
7	XG	21	VAL
8	XH	99	GLU
9	XI	124	GLN
12	XL	19	ARG
12	XL	92	ASP
12	XL	128	ALA
13	XM	100	GLY
14	XN	14	PRO
14	XN	16	PHE
17	XQ	69	LYS
19	XS	25	LYS
19	XS	80	TYR
21	XU	25	LYS
27	YD	33	LEU
27	YD	196	VAL
27	YD	238	GLY
27	YD	267	SER
28	YE	9	VAL
28	YE	25	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
28	YE	59	VAL
28	YE	69	LYS
28	YE	71	GLY
28	YE	76	ARG
28	YE	77	ILE
28	YE	118	LYS
29	YF	3	GLU
29	YF	84	VAL
30	YG	14	GLU
30	YG	96	ARG
30	YG	97	ASP
31	YH	55	PRO
31	YH	80	SER
32	YI	102	SER
32	YI	145	VAL
33	YN	126	PRO
35	YP	29	LYS
35	YP	57	THR
36	YQ	81	VAL
36	YQ	86	GLY
36	YQ	90	VAL
36	YQ	134	ARG
36	YQ	135	ASP
36	YQ	136	ALA
38	YS	19	LYS
38	YS	88	ASP
38	YS	94	TYR
38	YS	96	GLY
39	YT	84	GLN
39	YT	107	ASP
40	YU	90	VAL
40	YU	101	ARG
41	YV	44	LYS
41	YV	45	THR
41	YV	62	LEU
41	YV	72	VAL
41	YV	80	GLN
42	YW	63	ASP
42	YW	93	ALA
44	YY	61	ILE
44	YY	63	LYS
44	YY	99	CYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
45	YZ	60	GLU
45	YZ	142	SER
45	YZ	146	ILE
48	Y2	70	GLN
50	Y4	11	PRO
50	Y4	22	ILE
50	Y4	23	GLU
50	Y4	24	THR
50	Y4	39	CYS
50	Y4	42	PHE
50	Y4	48	ARG
50	Y4	51	ASP
51	Y5	55	ARG
52	Y6	19	ARG
52	Y6	27	LYS
52	Y6	29	ASN
52	Y6	30	THR
52	Y6	32	ASN
54	Y8	7	HIS
54	Y8	55	ALA
2	QB	8	LYS
2	QB	28	PHE
2	QB	88	ALA
2	QB	133	LYS
2	QB	191	ASP
2	QB	239	VAL
3	QC	15	THR
4	QD	22	LYS
4	QD	32	ALA
5	QE	19	MET
8	QH	2	LEU
9	QI	21	PRO
9	QI	29	ASN
10	QJ	59	SER
12	QL	25	PRO
12	QL	128	ALA
14	QN	16	PHE
20	QT	97	ALA
20	QT	103	GLY
21	QU	25	LYS
28	RE	2	LYS
28	RE	25	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
28	RE	32	PRO
28	RE	66	HIS
28	RE	76	ARG
28	RE	92	THR
28	RE	204	ALA
29	RF	21	ALA
30	RG	82	LEU
30	RG	96	ARG
30	RG	116	ASP
31	RH	27	LYS
31	RH	47	GLU
31	RH	85	LYS
31	RH	160	LYS
32	RI	85	GLU
32	RI	102	SER
33	RN	17	ASP
35	RP	58	THR
35	RP	103	ALA
35	RP	141	ALA
37	RR	107	ASP
38	RS	106	ARG
39	RT	107	ASP
40	RU	98	LEU
41	RV	44	LYS
41	RV	62	LEU
41	RV	71	LEU
44	RY	3	VAL
44	RY	17	SER
44	RY	19	LYS
44	RY	53	PRO
45	RZ	13	GLU
46	R0	83	PRO
47	R1	55	GLY
47	R1	96	LYS
48	R2	43	GLN
50	R4	24	THR
50	R4	42	PHE
50	R4	52	THR
52	R6	49	HIS
54	R8	51	ALA
2	XB	16	HIS
2	XB	20	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	XB	26	PRO
2	XB	39	ILE
2	XB	133	LYS
3	XC	15	THR
3	XC	51	GLY
3	XC	53	ALA
3	XC	77	ILE
4	XD	25	ARG
4	XD	34	GLU
4	XD	150	GLU
5	XE	3	GLU
5	XE	7	GLU
5	XE	39	GLY
8	XH	2	LEU
10	XJ	91	PRO
11	XK	15	ALA
13	XM	82	MET
13	XM	116	THR
17	XQ	74	LEU
19	XS	67	VAL
20	XT	10	LEU
20	XT	103	GLY
21	XU	3	LYS
27	YD	25	THR
27	YD	159	ALA
28	YE	2	LYS
28	YE	48	GLN
28	YE	51	PHE
28	YE	187	ALA
28	YE	204	ALA
29	YF	9	ILE
29	YF	17	ARG
29	YF	62	ARG
29	YF	128	ALA
29	YF	133	ASN
30	YG	5	VAL
31	YH	21	PRO
31	YH	47	GLU
31	YH	90	LYS
31	YH	130	ARG
32	YI	77	LEU
33	YN	127	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
33	YN	131	GLN
35	YP	5	ASP
35	YP	47	ASP
35	YP	62	LEU
35	YP	107	LYS
35	YP	141	ALA
38	YS	12	PHE
38	YS	44	LYS
39	YT	86	ILE
40	YU	92	ARG
42	YW	110	LYS
44	YY	53	PRO
44	YY	58	GLY
45	YZ	6	LYS
45	YZ	13	GLU
45	YZ	73	GLN
45	YZ	136	PHE
45	YZ	150	LEU
45	YZ	173	ALA
46	Y0	83	PRO
47	Y1	79	GLY
47	Y1	96	LYS
48	Y2	48	HIS
50	Y4	34	GLU
50	Y4	52	THR
52	Y6	11	LEU
52	Y6	49	HIS
2	QB	131	PRO
2	QB	234	PRO
3	QC	13	GLY
3	QC	16	ARG
3	QC	206	GLU
4	QD	149	ALA
7	QG	7	ALA
8	QH	100	ILE
9	QI	19	LEU
11	QK	16	SER
12	QL	19	ARG
13	QM	82	MET
19	QS	43	GLU
19	QS	65	ASN
27	RD	3	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
28	RE	9	VAL
28	RE	33	VAL
28	RE	45	THR
28	RE	51	PHE
28	RE	77	ILE
28	RE	86	PRO
28	RE	90	THR
28	RE	129	HIS
28	RE	200	GLU
29	RF	17	ARG
29	RF	133	ASN
30	RG	5	VAL
30	RG	14	GLU
30	RG	36	LYS
30	RG	86	MET
31	RH	7	LEU
31	RH	34	GLU
31	RH	39	PRO
31	RH	111	HIS
31	RH	169	VAL
32	RI	117	GLU
32	RI	132	PRO
33	RN	126	PRO
33	RN	127	ASP
35	RP	111	ARG
36	RQ	59	ARG
36	RQ	104	PHE
37	RR	82	GLU
44	RY	57	GLN
44	RY	58	GLY
44	RY	73	ARG
44	RY	80	GLY
45	RZ	6	LYS
45	RZ	118	GLN
45	RZ	136	PHE
46	R0	49	LYS
48	R2	16	LEU
50	R4	46	GLN
50	R4	50	VAL
51	R5	49	CYS
52	R6	22	ALA
54	R8	7	HIS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	XB	95	GLN
2	XB	122	PHE
2	XB	226	ARG
3	XC	3	ASN
3	XC	79	ARG
4	XD	4	TYR
4	XD	16	GLY
4	XD	149	ALA
5	XE	19	MET
7	XG	7	ALA
8	XH	100	ILE
9	XI	19	LEU
11	XK	12	ARG
12	XL	47	LYS
13	XM	45	VAL
13	XM	63	THR
27	YD	46	GLN
27	YD	239	ARG
28	YE	32	PRO
28	YE	66	HIS
28	YE	90	THR
29	YF	21	ALA
29	YF	89	VAL
30	YG	36	LYS
30	YG	82	LEU
30	YG	109	VAL
30	YG	116	ASP
30	YG	117	PHE
31	YH	4	ILE
31	YH	11	VAL
31	YH	30	LYS
31	YH	39	PRO
31	YH	85	LYS
31	YH	160	LYS
32	YI	132	PRO
35	YP	10	PRO
35	YP	21	ARG
35	YP	63	PRO
35	YP	111	ARG
35	YP	147	LEU
36	YQ	104	PHE
37	YR	82	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
37	YR	107	ASP
38	YS	4	LEU
38	YS	57	LYS
39	YT	105	LEU
41	YV	79	VAL
41	YV	98	GLU
42	YW	65	LEU
44	YY	50	ARG
44	YY	73	ARG
44	YY	96	ILE
45	YZ	157	LEU
46	Y0	49	LYS
47	Y1	92	LYS
50	Y4	46	GLN
51	Y5	49	CYS
52	Y6	25	LYS
52	Y6	44	ARG
2	QB	150	SER
3	QC	3	ASN
3	QC	45	LYS
3	QC	84	ILE
3	QC	98	ASN
4	QD	5	ILE
4	QD	26	CYS
4	QD	39	PRO
7	QG	19	GLY
9	QI	107	ARG
10	QJ	37	PRO
11	QK	11	LYS
12	QL	92	ASP
13	QM	45	VAL
27	RD	191	ALA
28	RE	73	GLU
28	RE	82	ARG
29	RF	9	ILE
29	RF	66	PRO
30	RG	117	PHE
31	RH	46	GLU
31	RH	52	VAL
32	RI	145	VAL
33	RN	125	GLY
33	RN	129	PRO

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
35	RP	16	ARG
35	RP	47	ASP
35	RP	63	PRO
36	RQ	81	VAL
37	RR	103	ARG
37	RR	106	GLY
38	RS	19	LYS
38	RS	87	PHE
41	RV	99	ILE
42	RW	93	ALA
43	RX	51	VAL
45	RZ	73	GLN
45	RZ	146	ILE
45	RZ	173	ALA
47	R1	81	LYS
50	R4	11	PRO
50	R4	23	GLU
52	R6	20	ASN
52	R6	27	LYS
2	XB	131	PRO
2	XB	231	GLU
2	XB	234	PRO
2	XB	239	VAL
3	XC	16	ARG
3	XC	99	VAL
4	XD	3	ARG
4	XD	5	ILE
12	XL	17	LYS
12	XL	79	GLU
19	XS	41	VAL
28	YE	44	TYR
28	YE	45	THR
28	YE	47	VAL
28	YE	62	PRO
28	YE	73	GLU
28	YE	82	ARG
29	YF	27	GLU
29	YF	28	ILE
30	YG	86	MET
31	YH	7	LEU
31	YH	52	VAL
31	YH	87	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
31	YH	111	HIS
31	YH	169	VAL
33	YN	8	GLN
33	YN	129	PRO
35	YP	19	VAL
35	YP	106	LEU
38	YS	87	PHE
39	YT	97	ALA
41	YV	29	PRO
41	YV	36	PRO
41	YV	99	ILE
43	YX	51	VAL
44	YY	16	ALA
44	YY	85	VAL
45	YZ	156	LYS
48	Y2	16	LEU
48	Y2	44	LEU
50	Y4	50	VAL
50	Y4	57	GLU
20	QT	98	PRO
36	RQ	63	LYS
41	RV	37	VAL
41	RV	50	PRO
42	RW	65	LEU
45	RZ	67	LEU
47	R1	31	GLY
47	R1	86	SER
52	R6	11	LEU
9	XI	30	GLY
11	XK	10	VAL
11	XK	105	VAL
12	XL	65	GLU
19	XS	9	VAL
19	XS	72	GLY
30	YG	146	TYR
31	YH	151	ILE
35	YP	64	LYS
35	YP	67	MET
44	YY	41	GLY
45	YZ	59	LEU
45	YZ	165	VAL
47	Y1	27	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
52	Y6	22	ALA
54	Y8	32	LEU
2	QB	231	GLU
5	QE	39	GLY
30	RG	87	PRO
35	RP	23	PRO
35	RP	122	PRO
41	RV	79	VAL
45	RZ	141	VAL
47	R1	28	GLY
28	YE	81	ILE
41	YV	37	VAL
43	YX	67	GLY
52	Y6	41	PRO
35	RP	43	GLY
35	RP	97	PRO
41	RV	29	PRO
45	RZ	108	PRO
45	RZ	139	VAL
45	RZ	161	VAL
52	R6	41	PRO
9	XI	53	VAL
13	XM	9	ILE
28	YE	52	LEU
35	YP	7	ARG
37	YR	106	GLY
44	YY	80	GLY
3	QC	51	GLY
30	RG	109	VAL
35	RP	19	VAL
44	RY	77	PRO
45	RZ	134	PRO
50	R4	22	ILE
5	XE	70	PRO
9	XI	21	PRO
10	XJ	37	PRO
13	XM	4	ILE
19	XS	46	GLY
20	XT	97	ALA
28	YE	7	VAL
44	YY	49	VAL
2	QB	26	PRO

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Mol	Chain	Res	Type
28	RE	7	VAL
30	RG	85	GLY
31	RH	4	ILE
35	RP	11	GLY
7	XG	17	VAL
9	XI	28	VAL
19	QS	9	VAL
35	RP	146	VAL
29	YF	132	VAL
48	R2	18	PRO

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	QB	204/220 (93%)	174 (85%)	30 (15%)	3	13
2	XB	204/220 (93%)	176 (86%)	28 (14%)	3	16
3	QC	160/188 (85%)	142 (89%)	18 (11%)	6	23
3	XC	160/188 (85%)	141 (88%)	19 (12%)	5	20
4	QD	180/181 (99%)	157 (87%)	23 (13%)	4	18
4	XD	180/181 (99%)	155 (86%)	25 (14%)	3	15
5	QE	119/123 (97%)	101 (85%)	18 (15%)	3	12
5	XE	119/123 (97%)	106 (89%)	13 (11%)	6	25
6	QF	90/90 (100%)	85 (94%)	5 (6%)	21	52
6	XF	90/90 (100%)	77 (86%)	13 (14%)	3	14
7	QG	126/127 (99%)	112 (89%)	14 (11%)	6	24
7	XG	126/127 (99%)	109 (86%)	17 (14%)	4	16
8	QH	119/119 (100%)	109 (92%)	10 (8%)	11	38
8	XH	119/119 (100%)	106 (89%)	13 (11%)	6	25
9	QI	99/99 (100%)	79 (80%)	20 (20%)	1	5
9	XI	99/99 (100%)	80 (81%)	19 (19%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	QJ	89/92 (97%)	77 (86%)	12 (14%)	4	16
10	XJ	89/92 (97%)	75 (84%)	14 (16%)	2	11
11	QK	92/99 (93%)	82 (89%)	10 (11%)	6	25
11	XK	92/99 (93%)	84 (91%)	8 (9%)	10	36
12	QL	104/109 (95%)	89 (86%)	15 (14%)	3	14
12	XL	104/109 (95%)	87 (84%)	17 (16%)	2	10
13	QM	94/101 (93%)	80 (85%)	14 (15%)	3	13
13	XM	94/101 (93%)	82 (87%)	12 (13%)	4	18
14	QN	49/50 (98%)	48 (98%)	1 (2%)	55	80
14	XN	49/50 (98%)	44 (90%)	5 (10%)	7	27
15	QO	79/80 (99%)	74 (94%)	5 (6%)	18	48
15	XO	79/80 (99%)	74 (94%)	5 (6%)	18	48
16	QP	72/74 (97%)	64 (89%)	8 (11%)	6	24
16	XP	72/74 (97%)	64 (89%)	8 (11%)	6	24
17	QQ	95/97 (98%)	90 (95%)	5 (5%)	22	54
17	XQ	95/97 (98%)	88 (93%)	7 (7%)	13	42
18	QR	62/77 (80%)	56 (90%)	6 (10%)	8	30
18	XR	62/77 (80%)	54 (87%)	8 (13%)	4	18
19	QS	71/80 (89%)	54 (76%)	17 (24%)	0	2
19	XS	71/80 (89%)	58 (82%)	13 (18%)	1	7
20	QT	76/82 (93%)	62 (82%)	14 (18%)	1	7
20	XT	76/82 (93%)	66 (87%)	10 (13%)	4	17
21	QU	20/20 (100%)	18 (90%)	2 (10%)	7	28
21	XU	20/20 (100%)	18 (90%)	2 (10%)	7	28
24	QY	78/102 (76%)	75 (96%)	3 (4%)	33	66
24	XY	78/102 (76%)	74 (95%)	4 (5%)	24	56
27	RD	214/218 (98%)	178 (83%)	36 (17%)	2	9
27	YD	214/218 (98%)	179 (84%)	35 (16%)	2	10
28	RE	165/166 (99%)	137 (83%)	28 (17%)	2	9
28	YE	165/166 (99%)	138 (84%)	27 (16%)	2	10
29	RF	165/166 (99%)	139 (84%)	26 (16%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	YF	165/166 (99%)	142 (86%)	23 (14%)	3	15
30	RG	155/156 (99%)	147 (95%)	8 (5%)	23	55
30	YG	155/156 (99%)	138 (89%)	17 (11%)	6	25
31	RH	142/148 (96%)	123 (87%)	19 (13%)	4	16
31	YH	142/148 (96%)	115 (81%)	27 (19%)	1	6
32	RI	122/124 (98%)	98 (80%)	24 (20%)	1	6
32	YI	122/124 (98%)	99 (81%)	23 (19%)	1	6
33	RN	117/119 (98%)	107 (92%)	10 (8%)	10	37
33	YN	117/119 (98%)	104 (89%)	13 (11%)	6	24
34	RO	100/100 (100%)	91 (91%)	9 (9%)	9	34
34	YO	100/100 (100%)	90 (90%)	10 (10%)	7	28
35	RP	116/116 (100%)	81 (70%)	35 (30%)	0	0
35	YP	116/116 (100%)	83 (72%)	33 (28%)	0	1
36	RQ	110/111 (99%)	93 (84%)	17 (16%)	2	11
36	YQ	110/111 (99%)	93 (84%)	17 (16%)	2	11
37	RR	100/101 (99%)	82 (82%)	18 (18%)	1	7
37	YR	100/101 (99%)	87 (87%)	13 (13%)	4	18
38	RS	87/88 (99%)	80 (92%)	7 (8%)	12	40
38	YS	87/88 (99%)	73 (84%)	14 (16%)	2	10
39	RT	120/127 (94%)	100 (83%)	20 (17%)	2	9
39	YT	120/127 (94%)	98 (82%)	22 (18%)	1	7
40	RU	93/94 (99%)	85 (91%)	8 (9%)	10	37
40	YU	93/94 (99%)	85 (91%)	8 (9%)	10	37
41	RV	82/82 (100%)	66 (80%)	16 (20%)	1	6
41	YV	82/82 (100%)	63 (77%)	19 (23%)	1	3
42	RW	92/92 (100%)	82 (89%)	10 (11%)	6	25
42	YW	92/92 (100%)	79 (86%)	13 (14%)	3	15
43	RX	74/78 (95%)	65 (88%)	9 (12%)	5	19
43	YX	74/78 (95%)	68 (92%)	6 (8%)	11	39
44	RY	85/91 (93%)	63 (74%)	22 (26%)	0	1
44	YY	85/91 (93%)	61 (72%)	24 (28%)	0	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	RZ	155/179 (87%)	129 (83%)	26 (17%)	2	9
45	YZ	162/179 (90%)	134 (83%)	28 (17%)	2	9
46	R0	66/67 (98%)	62 (94%)	4 (6%)	18	49
46	Y0	66/67 (98%)	58 (88%)	8 (12%)	5	20
47	R1	82/83 (99%)	68 (83%)	14 (17%)	2	9
47	Y1	82/83 (99%)	72 (88%)	10 (12%)	5	19
48	R2	64/67 (96%)	52 (81%)	12 (19%)	1	6
48	Y2	64/67 (96%)	57 (89%)	7 (11%)	6	25
49	R3	51/52 (98%)	44 (86%)	7 (14%)	3	16
49	Y3	51/52 (98%)	47 (92%)	4 (8%)	12	40
50	R4	62/63 (98%)	47 (76%)	15 (24%)	0	2
50	Y4	62/63 (98%)	44 (71%)	18 (29%)	0	1
51	R5	51/52 (98%)	40 (78%)	11 (22%)	1	4
51	Y5	49/52 (94%)	42 (86%)	7 (14%)	3	14
52	R6	47/52 (90%)	32 (68%)	15 (32%)	0	0
52	Y6	47/52 (90%)	30 (64%)	17 (36%)	0	0
53	R7	42/42 (100%)	35 (83%)	7 (17%)	2	9
53	Y7	42/42 (100%)	35 (83%)	7 (17%)	2	9
54	R8	54/55 (98%)	43 (80%)	11 (20%)	1	5
54	Y8	54/55 (98%)	44 (82%)	10 (18%)	1	7
55	R9	34/34 (100%)	32 (94%)	2 (6%)	19	50
55	Y9	33/34 (97%)	33 (100%)	0	100	100
All	All	9854/10266 (96%)	8438 (86%)	1416 (14%)	3	14

All (1416) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	QB	10	LEU
2	QB	11	LEU
2	QB	16	HIS
2	QB	17	PHE
2	QB	23	ARG
2	QB	24	TRP
2	QB	30	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	QB	31	TYR
2	QB	32	ILE
2	QB	42	ILE
2	QB	44	LEU
2	QB	80	ILE
2	QB	101	MET
2	QB	114	ARG
2	QB	135	GLN
2	QB	154	LEU
2	QB	158	LEU
2	QB	165	VAL
2	QB	178	ARG
2	QB	185	ILE
2	QB	187	LEU
2	QB	191	ASP
2	QB	196	LEU
2	QB	204	ASN
2	QB	208	ILE
2	QB	221	LEU
2	QB	226	ARG
2	QB	233	SER
2	QB	238	LEU
2	QB	240	GLN
3	QC	5	ILE
3	QC	16	ARG
3	QC	27	LYS
3	QC	28	GLN
3	QC	29	TYR
3	QC	36	ASP
3	QC	46	GLU
3	QC	52	LEU
3	QC	66	VAL
3	QC	75	VAL
3	QC	83	ARG
3	QC	84	ILE
3	QC	140	ARG
3	QC	161	GLU
3	QC	165	THR
3	QC	188	LEU
3	QC	196	LEU
3	QC	206	GLU
4	QD	12	CYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	QD	13	ARG
4	QD	19	LEU
4	QD	24	GLU
4	QD	27	TYR
4	QD	31	CYS
4	QD	34	GLU
4	QD	45	GLN
4	QD	58	LEU
4	QD	84	LYS
4	QD	86	LYS
4	QD	96	LEU
4	QD	108	LEU
4	QD	119	GLN
4	QD	122	ARG
4	QD	127	THR
4	QD	135	LEU
4	QD	160	GLN
4	QD	178	VAL
4	QD	187	ARG
4	QD	191	ARG
4	QD	196	LEU
4	QD	200	GLU
5	QE	6	PHE
5	QE	7	GLU
5	QE	8	GLU
5	QE	12	LEU
5	QE	13	ILE
5	QE	25	ARG
5	QE	41	VAL
5	QE	47	LYS
5	QE	51	VAL
5	QE	60	TYR
5	QE	68	GLU
5	QE	72	GLN
5	QE	78	HIS
5	QE	79	GLU
5	QE	101	ILE
5	QE	126	ARG
5	QE	147	ASP
5	QE	152	ARG
6	QF	28	ARG
6	QF	54	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
6	QF	78	GLU
6	QF	83	ASP
6	QF	98	LEU
7	QG	3	ARG
7	QG	4	ARG
7	QG	8	GLU
7	QG	11	GLN
7	QG	57	GLU
7	QG	75	VAL
7	QG	78	ARG
7	QG	84	ASN
7	QG	94	ARG
7	QG	104	LEU
7	QG	136	LYS
7	QG	137	LYS
7	QG	151	TYR
7	QG	156	TRP
8	QH	1	MET
8	QH	25	ASP
8	QH	26	VAL
8	QH	37	ARG
8	QH	41	ARG
8	QH	56	LYS
8	QH	91	ARG
8	QH	102	ARG
8	QH	109	ILE
8	QH	137	VAL
9	QI	1	MET
9	QI	3	GLN
9	QI	10	ARG
9	QI	11	LYS
9	QI	12	GLU
9	QI	25	LYS
9	QI	38	GLN
9	QI	40	LEU
9	QI	56	LEU
9	QI	65	VAL
9	QI	88	TYR
9	QI	95	LYS
9	QI	102	LEU
9	QI	104	ARG
9	QI	110	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
9	QI	112	LYS
9	QI	114	TYR
9	QI	117	HIS
9	QI	121	ARG
9	QI	127	LYS
10	QJ	16	LEU
10	QJ	17	ASP
10	QJ	22	LYS
10	QJ	42	THR
10	QJ	47	PHE
10	QJ	57	LYS
10	QJ	60	ARG
10	QJ	62	HIS
10	QJ	74	ILE
10	QJ	79	ARG
10	QJ	80	LYS
10	QJ	96	ILE
11	QK	13	GLN
11	QK	14	VAL
11	QK	18	ARG
11	QK	29	ILE
11	QK	30	VAL
11	QK	50	TYR
11	QK	81	ASP
11	QK	84	VAL
11	QK	87	THR
11	QK	105	VAL
12	QL	8	ASN
12	QL	18	VAL
12	QL	20	LYS
12	QL	23	LYS
12	QL	24	VAL
12	QL	28	LYS
12	QL	33	ARG
12	QL	42	THR
12	QL	84	LEU
12	QL	85	ILE
12	QL	91	LYS
12	QL	92	ASP
12	QL	111	LYS
12	QL	124	LYS
12	QL	126	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
13	QM	9	ILE
13	QM	23	TYR
13	QM	27	LYS
13	QM	46	LYS
13	QM	48	LEU
13	QM	49	THR
13	QM	64	TRP
13	QM	66	LEU
13	QM	70	LEU
13	QM	71	ARG
13	QM	77	ASN
13	QM	81	LEU
13	QM	93	ARG
13	QM	108	ARG
14	QN	15	LYS
15	QO	3	ILE
15	QO	4	THR
15	QO	26	GLU
15	QO	82	ILE
15	QO	87	ILE
16	QP	18	ARG
16	QP	21	VAL
16	QP	27	LYS
16	QP	45	THR
16	QP	54	GLU
16	QP	55	ARG
16	QP	67	THR
16	QP	72	ARG
17	QQ	52	LYS
17	QQ	63	ARG
17	QQ	73	VAL
17	QQ	74	LEU
17	QQ	78	GLU
18	QR	19	LYS
18	QR	31	LEU
18	QR	58	LEU
18	QR	82	THR
18	QR	85	LEU
18	QR	87	ARG
19	QS	5	LEU
19	QS	6	LYS
19	QS	7	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
19	QS	10	PHE
19	QS	11	VAL
19	QS	12	ASP
19	QS	13	ASP
19	QS	19	VAL
19	QS	25	LYS
19	QS	27	GLU
19	QS	31	ILE
19	QS	34	TRP
19	QS	40	ILE
19	QS	56	GLN
19	QS	63	THR
19	QS	69	HIS
19	QS	83	HIS
20	QT	10	LEU
20	QT	14	LYS
20	QT	24	LEU
20	QT	29	LYS
20	QT	36	LEU
20	QT	72	LEU
20	QT	73	HIS
20	QT	74	LYS
20	QT	75	ASN
20	QT	83	ARG
20	QT	84	LEU
20	QT	92	LEU
20	QT	93	GLU
20	QT	105	SER
21	QU	9	ARG
21	QU	15	ARG
24	QY	6	LYS
24	QY	48	ARG
24	QY	49	GLN
27	RD	10	THR
27	RD	20	ASP
27	RD	27	THR
27	RD	34	VAL
27	RD	43	ARG
27	RD	49	ILE
27	RD	65	ILE
27	RD	72	LYS
27	RD	94	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
27	RD	95	LEU
27	RD	98	VAL
27	RD	103	ARG
27	RD	104	TYR
27	RD	106	ILE
27	RD	111	LEU
27	RD	138	VAL
27	RD	150	LYS
27	RD	155	LEU
27	RD	157	ARG
27	RD	165	ILE
27	RD	166	GLN
27	RD	168	ARG
27	RD	171	ASP
27	RD	173	VAL
27	RD	192	THR
27	RD	193	VAL
27	RD	211	ARG
27	RD	212	SER
27	RD	242	ARG
27	RD	244	ARG
27	RD	255	LYS
27	RD	257	LEU
27	RD	260	ARG
27	RD	268	ARG
27	RD	271	ILE
27	RD	273	ARG
28	RE	4	ILE
28	RE	37	ARG
28	RE	60	ASN
28	RE	61	ARG
28	RE	63	LEU
28	RE	66	HIS
28	RE	69	LYS
28	RE	78	LEU
28	RE	79	ARG
28	RE	82	ARG
28	RE	85	ASN
28	RE	89	ASP
28	RE	95	ILE
28	RE	113	PHE
28	RE	116	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
28	RE	118	LYS
28	RE	119	ARG
28	RE	134	ILE
28	RE	144	ARG
28	RE	154	LYS
28	RE	171	GLU
28	RE	179	GLU
28	RE	181	LEU
28	RE	184	VAL
28	RE	188	VAL
28	RE	197	ILE
28	RE	202	LYS
28	RE	203	LYS
29	RF	2	LYS
29	RF	7	TYR
29	RF	8	GLN
29	RF	19	GLU
29	RF	20	LEU
29	RF	23	ASP
29	RF	24	LEU
29	RF	28	ILE
29	RF	33	LEU
29	RF	38	ARG
29	RF	53	THR
29	RF	57	VAL
29	RF	60	SER
29	RF	62	ARG
29	RF	70	THR
29	RF	74	ARG
29	RF	88	VAL
29	RF	96	ASP
29	RF	110	LEU
29	RF	125	LEU
29	RF	158	THR
29	RF	165	ARG
29	RF	175	THR
29	RF	183	VAL
29	RF	201	VAL
29	RF	205	ARG
30	RG	34	LEU
30	RG	60	LEU
30	RG	63	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
30	RG	88	ILE
30	RG	94	LEU
30	RG	115	ARG
30	RG	133	LEU
30	RG	159	VAL
31	RH	3	ARG
31	RH	9	ILE
31	RH	17	VAL
31	RH	24	VAL
31	RH	27	LYS
31	RH	46	GLU
31	RH	49	VAL
31	RH	51	ARG
31	RH	54	ARG
31	RH	69	ARG
31	RH	83	TYR
31	RH	85	LYS
31	RH	89	ILE
31	RH	101	ARG
31	RH	104	GLU
31	RH	125	VAL
31	RH	130	ARG
31	RH	157	TYR
31	RH	158	HIS
32	RI	1	MET
32	RI	3	VAL
32	RI	10	GLU
32	RI	38	LEU
32	RI	56	LYS
32	RI	62	LYS
32	RI	74	ASN
32	RI	77	LEU
32	RI	81	VAL
32	RI	82	ARG
32	RI	85	GLU
32	RI	99	GLU
32	RI	101	LEU
32	RI	105	HIS
32	RI	109	ILE
32	RI	110	ASP
32	RI	114	LEU
32	RI	117	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
32	RI	122	GLU
32	RI	125	GLU
32	RI	130	TYR
32	RI	136	VAL
32	RI	141	LYS
32	RI	143	SER
33	RN	1	MET
33	RN	32	THR
33	RN	43	THR
33	RN	48	MET
33	RN	56	ASN
33	RN	87	LEU
33	RN	93	THR
33	RN	94	HIS
33	RN	98	VAL
33	RN	137	LYS
34	RO	23	ARG
34	RO	29	ASN
34	RO	47	ILE
34	RO	49	ARG
34	RO	80	ASP
34	RO	94	ARG
34	RO	98	VAL
34	RO	108	GLU
34	RO	117	LEU
35	RP	5	ASP
35	RP	6	LEU
35	RP	9	ASN
35	RP	14	LYS
35	RP	15	ARG
35	RP	16	ARG
35	RP	19	VAL
35	RP	21	ARG
35	RP	29	LYS
35	RP	45	LEU
35	RP	52	GLU
35	RP	56	SER
35	RP	57	THR
35	RP	62	LEU
35	RP	64	LYS
35	RP	67	MET
35	RP	75	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
35	RP	81	GLN
35	RP	83	VAL
35	RP	98	GLU
35	RP	101	VAL
35	RP	102	ARG
35	RP	106	LEU
35	RP	110	TYR
35	RP	114	ILE
35	RP	115	LEU
35	RP	117	GLU
35	RP	125	VAL
35	RP	135	LEU
35	RP	136	GLU
35	RP	138	LEU
35	RP	144	GLU
35	RP	147	LEU
35	RP	148	LEU
35	RP	149	GLU
36	RQ	1	MET
36	RQ	45	GLN
36	RQ	56	ARG
36	RQ	59	ARG
36	RQ	63	LYS
36	RQ	64	ILE
36	RQ	66	ILE
36	RQ	80	GLU
36	RQ	81	VAL
36	RQ	82	ARG
36	RQ	83	MET
36	RQ	109	VAL
36	RQ	110	THR
36	RQ	112	GLU
36	RQ	113	GLN
36	RQ	115	MET
36	RQ	134	ARG
37	RR	2	ARG
37	RR	4	LEU
37	RR	6	SER
37	RR	9	LYS
37	RR	15	SER
37	RR	17	ARG
37	RR	28	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
37	RR	29	LEU
37	RR	37	THR
37	RR	54	LEU
37	RR	65	LEU
37	RR	67	LEU
37	RR	71	GLN
37	RR	76	VAL
37	RR	79	LEU
37	RR	99	LYS
37	RR	104	ARG
37	RR	105	ARG
38	RS	4	LEU
38	RS	20	ARG
38	RS	52	SER
38	RS	56	LEU
38	RS	98	VAL
38	RS	106	ARG
38	RS	110	LEU
39	RT	8	LYS
39	RT	9	LEU
39	RT	23	ARG
39	RT	27	THR
39	RT	29	ARG
39	RT	30	VAL
39	RT	35	LYS
39	RT	41	ARG
39	RT	50	ILE
39	RT	58	ASN
39	RT	59	THR
39	RT	74	ARG
39	RT	78	LEU
39	RT	86	ILE
39	RT	87	ASP
39	RT	88	ILE
39	RT	93	ARG
39	RT	98	LYS
39	RT	99	LEU
39	RT	137	LYS
40	RU	31	SER
40	RU	37	GLU
40	RU	74	LEU
40	RU	83	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
40	RU	92	ARG
40	RU	104	GLN
40	RU	114	LYS
40	RU	117	GLN
41	RV	5	VAL
41	RV	15	GLU
41	RV	19	LYS
41	RV	22	VAL
41	RV	32	THR
41	RV	35	LEU
41	RV	66	ARG
41	RV	70	ILE
41	RV	76	LYS
41	RV	78	LYS
41	RV	79	VAL
41	RV	80	GLN
41	RV	81	TYR
41	RV	87	HIS
41	RV	95	LEU
41	RV	98	GLU
42	RW	11	ARG
42	RW	17	VAL
42	RW	69	LEU
42	RW	76	VAL
42	RW	88	ARG
42	RW	96	ILE
42	RW	100	THR
42	RW	106	ILE
42	RW	107	LEU
42	RW	113	LYS
43	RX	14	SER
43	RX	27	THR
43	RX	36	LYS
43	RX	48	LYS
43	RX	50	LYS
43	RX	63	LYS
43	RX	66	LEU
43	RX	76	ARG
43	RX	80	ILE
44	RY	5	MET
44	RY	9	LYS
44	RY	14	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
44	RY	17	SER
44	RY	19	LYS
44	RY	28	LYS
44	RY	33	LYS
44	RY	38	ILE
44	RY	50	ARG
44	RY	55	TYR
44	RY	60	PHE
44	RY	61	ILE
44	RY	62	GLU
44	RY	63	LYS
44	RY	76	CYS
44	RY	79	CYS
44	RY	86	ARG
44	RY	89	PHE
44	RY	95	LYS
44	RY	96	ILE
44	RY	97	ARG
44	RY	102	CYS
45	RZ	4	ARG
45	RZ	5	LEU
45	RZ	33	LEU
45	RZ	61	LEU
45	RZ	70	LEU
45	RZ	76	LEU
45	RZ	81	ARG
45	RZ	87	ASP
45	RZ	91	LEU
45	RZ	92	SER
45	RZ	104	PHE
45	RZ	112	ARG
45	RZ	118	GLN
45	RZ	120	ILE
45	RZ	121	HIS
45	RZ	128	VAL
45	RZ	135	GLU
45	RZ	136	PHE
45	RZ	138	GLU
45	RZ	140	ASP
45	RZ	141	VAL
45	RZ	144	LEU
45	RZ	148	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
45	RZ	156	LYS
45	RZ	171	ILE
45	RZ	175	VAL
46	R0	3	HIS
46	R0	20	ARG
46	R0	36	ILE
46	R0	53	MET
47	R1	3	LYS
47	R1	4	VAL
47	R1	38	SER
47	R1	40	ARG
47	R1	41	ARG
47	R1	57	GLU
47	R1	78	LYS
47	R1	80	LEU
47	R1	81	LYS
47	R1	82	LEU
47	R1	90	ILE
47	R1	94	LEU
47	R1	97	LEU
47	R1	98	LEU
48	R2	4	SER
48	R2	24	LEU
48	R2	25	VAL
48	R2	35	LEU
48	R2	47	ASN
48	R2	48	HIS
48	R2	50	ILE
48	R2	53	LEU
48	R2	57	ILE
48	R2	60	LEU
48	R2	62	THR
48	R2	67	LYS
49	R3	8	LEU
49	R3	24	LYS
49	R3	31	LEU
49	R3	32	GLN
49	R3	40	THR
49	R3	54	VAL
49	R3	56	VAL
50	R4	8	LYS
50	R4	10	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
50	R4	16	CYS
50	R4	21	VAL
50	R4	31	ILE
50	R4	34	GLU
50	R4	35	VAL
50	R4	43	TYR
50	R4	50	VAL
50	R4	55	ARG
50	R4	59	PHE
50	R4	61	ARG
50	R4	63	TYR
50	R4	67	TYR
50	R4	69	LYS
51	R5	3	LYS
51	R5	4	HIS
51	R5	6	VAL
51	R5	11	THR
51	R5	23	HIS
51	R5	26	THR
51	R5	36	CYS
51	R5	48	GLU
51	R5	49	CYS
51	R5	51	TYR
51	R5	52	TYR
52	R6	7	ILE
52	R6	8	LYS
52	R6	10	LEU
52	R6	12	GLU
52	R6	16	CYS
52	R6	21	TYR
52	R6	24	GLU
52	R6	28	ARG
52	R6	30	THR
52	R6	33	LYS
52	R6	37	ARG
52	R6	38	LYS
52	R6	39	TYR
52	R6	45	LYS
52	R6	47	THR
53	R7	1	MET
53	R7	12	ARG
53	R7	24	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
53	R7	43	THR
53	R7	47	ARG
53	R7	48	LYS
53	R7	49	ARG
54	R8	14	VAL
54	R8	31	HIS
54	R8	32	LEU
54	R8	33	ASN
54	R8	40	GLU
54	R8	41	ILE
54	R8	52	LYS
54	R8	54	GLU
54	R8	58	ILE
54	R8	61	LEU
54	R8	64	TYR
55	R9	1	MET
55	R9	17	ILE
2	XB	11	LEU
2	XB	17	PHE
2	XB	23	ARG
2	XB	24	TRP
2	XB	30	ARG
2	XB	31	TYR
2	XB	37	ASN
2	XB	42	ILE
2	XB	44	LEU
2	XB	49	GLU
2	XB	69	LEU
2	XB	108	ILE
2	XB	114	ARG
2	XB	122	PHE
2	XB	127	ILE
2	XB	144	ARG
2	XB	145	LEU
2	XB	153	ARG
2	XB	154	LEU
2	XB	156	LYS
2	XB	165	VAL
2	XB	185	ILE
2	XB	196	LEU
2	XB	208	ILE
2	XB	209	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	XB	226	ARG
2	XB	238	LEU
2	XB	240	GLN
3	XC	4	LYS
3	XC	5	ILE
3	XC	27	LYS
3	XC	36	ASP
3	XC	46	GLU
3	XC	66	VAL
3	XC	75	VAL
3	XC	83	ARG
3	XC	84	ILE
3	XC	94	LEU
3	XC	108	ASN
3	XC	119	ARG
3	XC	131	ARG
3	XC	140	ARG
3	XC	143	GLU
3	XC	161	GLU
3	XC	188	LEU
3	XC	196	LEU
3	XC	204	LEU
4	XD	3	ARG
4	XD	8	VAL
4	XD	10	ARG
4	XD	14	ARG
4	XD	18	LYS
4	XD	19	LEU
4	XD	24	GLU
4	XD	26	CYS
4	XD	31	CYS
4	XD	45	GLN
4	XD	58	LEU
4	XD	76	ARG
4	XD	84	LYS
4	XD	86	LYS
4	XD	96	LEU
4	XD	122	ARG
4	XD	127	THR
4	XD	135	LEU
4	XD	163	GLU
4	XD	168	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	XD	170	VAL
4	XD	187	ARG
4	XD	191	ARG
4	XD	194	LEU
4	XD	199	ASN
5	XE	6	PHE
5	XE	9	LYS
5	XE	12	LEU
5	XE	13	ILE
5	XE	41	VAL
5	XE	47	LYS
5	XE	51	VAL
5	XE	60	TYR
5	XE	72	GLN
5	XE	78	HIS
5	XE	79	GLU
5	XE	101	ILE
5	XE	155	GLU
6	XF	7	ASN
6	XF	15	ASP
6	XF	16	GLN
6	XF	21	LEU
6	XF	28	ARG
6	XF	38	GLU
6	XF	55	ASP
6	XF	64	GLN
6	XF	70	ASP
6	XF	72	VAL
6	XF	83	ASP
6	XF	85	VAL
6	XF	98	LEU
7	XG	3	ARG
7	XG	8	GLU
7	XG	16	LEU
7	XG	21	VAL
7	XG	78	ARG
7	XG	80	VAL
7	XG	84	ASN
7	XG	97	GLN
7	XG	104	LEU
7	XG	113	GLU
7	XG	114	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
7	XG	118	VAL
7	XG	136	LYS
7	XG	137	LYS
7	XG	151	TYR
7	XG	155	ARG
7	XG	156	TRP
8	XH	1	MET
8	XH	3	THR
8	XH	23	SER
8	XH	24	THR
8	XH	25	ASP
8	XH	26	VAL
8	XH	37	ARG
8	XH	41	ARG
8	XH	56	LYS
8	XH	60	ARG
8	XH	102	ARG
8	XH	112	LEU
8	XH	133	LEU
9	XI	1	MET
9	XI	10	ARG
9	XI	25	LYS
9	XI	31	GLN
9	XI	35	GLU
9	XI	38	GLN
9	XI	47	LEU
9	XI	56	LEU
9	XI	60	ASP
9	XI	70	LYS
9	XI	88	TYR
9	XI	95	LYS
9	XI	96	LEU
9	XI	102	LEU
9	XI	104	ARG
9	XI	114	TYR
9	XI	117	HIS
9	XI	121	ARG
9	XI	125	TYR
10	XJ	16	LEU
10	XJ	17	ASP
10	XJ	22	LYS
10	XJ	40	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
10	XJ	47	PHE
10	XJ	62	HIS
10	XJ	70	ARG
10	XJ	74	ILE
10	XJ	78	ASN
10	XJ	79	ARG
10	XJ	80	LYS
10	XJ	96	ILE
10	XJ	97	GLU
10	XJ	98	ILE
11	XK	13	GLN
11	XK	14	VAL
11	XK	18	ARG
11	XK	29	ILE
11	XK	30	VAL
11	XK	84	VAL
11	XK	114	VAL
11	XK	120	ARG
12	XL	18	VAL
12	XL	20	LYS
12	XL	23	LYS
12	XL	24	VAL
12	XL	27	LEU
12	XL	28	LYS
12	XL	33	ARG
12	XL	42	THR
12	XL	54	LYS
12	XL	62	SER
12	XL	83	VAL
12	XL	84	LEU
12	XL	85	ILE
12	XL	111	LYS
12	XL	116	SER
12	XL	124	LYS
12	XL	126	LYS
13	XM	4	ILE
13	XM	14	ARG
13	XM	35	GLU
13	XM	47	ASP
13	XM	48	LEU
13	XM	56	LEU
13	XM	64	TRP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
13	XM	66	LEU
13	XM	70	LEU
13	XM	93	ARG
13	XM	99	ARG
13	XM	108	ARG
14	XN	15	LYS
14	XN	18	VAL
14	XN	26	ARG
14	XN	32	SER
14	XN	58	LYS
15	XO	3	ILE
15	XO	39	LEU
15	XO	82	ILE
15	XO	84	LYS
15	XO	87	ILE
16	XP	2	VAL
16	XP	21	VAL
16	XP	27	LYS
16	XP	45	THR
16	XP	53	VAL
16	XP	54	GLU
16	XP	67	THR
16	XP	82	GLN
17	XQ	52	LYS
17	XQ	63	ARG
17	XQ	65	ILE
17	XQ	73	VAL
17	XQ	74	LEU
17	XQ	81	ARG
17	XQ	92	ARG
18	XR	19	LYS
18	XR	28	GLU
18	XR	31	LEU
18	XR	37	VAL
18	XR	58	LEU
18	XR	82	THR
18	XR	85	LEU
18	XR	87	ARG
19	XS	5	LEU
19	XS	6	LYS
19	XS	7	LYS
19	XS	10	PHE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
19	XS	19	VAL
19	XS	25	LYS
19	XS	27	GLU
19	XS	31	ILE
19	XS	32	LYS
19	XS	34	TRP
19	XS	40	ILE
19	XS	60	VAL
19	XS	64	GLU
20	XT	10	LEU
20	XT	14	LYS
20	XT	35	THR
20	XT	72	LEU
20	XT	73	HIS
20	XT	74	LYS
20	XT	75	ASN
20	XT	81	LYS
20	XT	84	LEU
20	XT	93	GLU
21	XU	9	ARG
21	XU	15	ARG
24	XY	26	ASP
24	XY	47	ASN
24	XY	85	ILE
24	XY	91	TYR
27	YD	18	VAL
27	YD	24	ILE
27	YD	25	THR
27	YD	33	LEU
27	YD	34	VAL
27	YD	43	ARG
27	YD	44	ASN
27	YD	61	LEU
27	YD	65	ILE
27	YD	71	ASP
27	YD	75	ILE
27	YD	88	ARG
27	YD	92	ILE
27	YD	94	LEU
27	YD	95	LEU
27	YD	99	ASP
27	YD	103	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
27	YD	104	TYR
27	YD	106	ILE
27	YD	111	LEU
27	YD	142	VAL
27	YD	150	LYS
27	YD	154	LYS
27	YD	157	ARG
27	YD	166	GLN
27	YD	168	ARG
27	YD	192	THR
27	YD	193	VAL
27	YD	211	ARG
27	YD	242	ARG
27	YD	244	ARG
27	YD	257	LEU
27	YD	268	ARG
27	YD	271	ILE
27	YD	273	ARG
28	YE	4	ILE
28	YE	12	THR
28	YE	35	GLN
28	YE	37	ARG
28	YE	47	VAL
28	YE	63	LEU
28	YE	66	HIS
28	YE	75	VAL
28	YE	78	LEU
28	YE	79	ARG
28	YE	82	ARG
28	YE	111	ARG
28	YE	116	VAL
28	YE	118	LYS
28	YE	119	ARG
28	YE	134	ILE
28	YE	144	ARG
28	YE	152	LYS
28	YE	154	LYS
28	YE	179	GLU
28	YE	181	LEU
28	YE	184	VAL
28	YE	185	LYS
28	YE	188	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
28	YE	201	THR
28	YE	202	LYS
28	YE	203	LYS
29	YF	2	LYS
29	YF	6	VAL
29	YF	7	TYR
29	YF	8	GLN
29	YF	20	LEU
29	YF	24	LEU
29	YF	33	LEU
29	YF	45	ARG
29	YF	53	THR
29	YF	57	VAL
29	YF	60	SER
29	YF	74	ARG
29	YF	83	PHE
29	YF	88	VAL
29	YF	110	LEU
29	YF	125	LEU
29	YF	136	THR
29	YF	140	LEU
29	YF	153	SER
29	YF	158	THR
29	YF	164	ARG
29	YF	183	VAL
29	YF	192	LEU
30	YG	4	ASP
30	YG	7	LEU
30	YG	26	GLN
30	YG	34	LEU
30	YG	35	GLU
30	YG	38	VAL
30	YG	60	LEU
30	YG	79	ASN
30	YG	80	PHE
30	YG	88	ILE
30	YG	101	ILE
30	YG	113	ARG
30	YG	114	ILE
30	YG	118	ARG
30	YG	123	ASN
30	YG	159	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
30	YG	164	GLU
31	YH	9	ILE
31	YH	16	SER
31	YH	17	VAL
31	YH	27	LYS
31	YH	32	GLU
31	YH	34	GLU
31	YH	45	VAL
31	YH	49	VAL
31	YH	51	ARG
31	YH	54	ARG
31	YH	59	ARG
31	YH	69	ARG
31	YH	77	LYS
31	YH	85	LYS
31	YH	89	ILE
31	YH	103	LEU
31	YH	105	LEU
31	YH	106	THR
31	YH	107	VAL
31	YH	109	PHE
31	YH	125	VAL
31	YH	130	ARG
31	YH	136	ILE
31	YH	143	GLN
31	YH	157	TYR
31	YH	158	HIS
31	YH	167	GLU
32	YI	1	MET
32	YI	2	LYS
32	YI	5	LEU
32	YI	9	LEU
32	YI	20	ASP
32	YI	38	LEU
32	YI	40	THR
32	YI	52	ARG
32	YI	54	GLN
32	YI	56	LYS
32	YI	62	LYS
32	YI	74	ASN
32	YI	77	LEU
32	YI	81	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
32	YI	87	LYS
32	YI	101	LEU
32	YI	105	HIS
32	YI	109	ILE
32	YI	114	LEU
32	YI	117	GLU
32	YI	122	GLU
32	YI	130	TYR
32	YI	142	VAL
33	YN	1	MET
33	YN	14	VAL
33	YN	41	ASP
33	YN	48	MET
33	YN	67	LEU
33	YN	87	LEU
33	YN	88	GLU
33	YN	93	THR
33	YN	94	HIS
33	YN	99	LEU
33	YN	120	LEU
33	YN	127	ASP
33	YN	137	LYS
34	YO	1	MET
34	YO	29	ASN
34	YO	47	ILE
34	YO	48	PRO
34	YO	49	ARG
34	YO	73	ASP
34	YO	80	ASP
34	YO	97	ARG
34	YO	108	GLU
34	YO	117	LEU
35	YP	6	LEU
35	YP	14	LYS
35	YP	15	ARG
35	YP	19	VAL
35	YP	21	ARG
35	YP	27	HIS
35	YP	40	SER
35	YP	45	LEU
35	YP	52	GLU
35	YP	56	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
35	YP	58	THR
35	YP	59	LEU
35	YP	61	ARG
35	YP	62	LEU
35	YP	64	LYS
35	YP	65	ARG
35	YP	67	MET
35	YP	75	ILE
35	YP	81	GLN
35	YP	85	LEU
35	YP	87	ASP
35	YP	98	GLU
35	YP	110	TYR
35	YP	112	LEU
35	YP	114	ILE
35	YP	115	LEU
35	YP	117	GLU
35	YP	136	GLU
35	YP	138	LEU
35	YP	144	GLU
35	YP	147	LEU
35	YP	148	LEU
35	YP	149	GLU
36	YQ	1	MET
36	YQ	10	ARG
36	YQ	27	VAL
36	YQ	45	GLN
36	YQ	52	VAL
36	YQ	56	ARG
36	YQ	64	ILE
36	YQ	66	ILE
36	YQ	79	LEU
36	YQ	80	GLU
36	YQ	81	VAL
36	YQ	82	ARG
36	YQ	83	MET
36	YQ	102	VAL
36	YQ	103	MET
36	YQ	134	ARG
36	YQ	138	ASP
37	YR	6	SER
37	YR	15	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
37	YR	18	LEU
37	YR	28	LEU
37	YR	29	LEU
37	YR	67	LEU
37	YR	74	LYS
37	YR	76	VAL
37	YR	79	LEU
37	YR	81	ASP
37	YR	104	ARG
37	YR	113	LEU
37	YR	117	VAL
38	YS	12	PHE
38	YS	20	ARG
38	YS	27	SER
38	YS	49	VAL
38	YS	52	SER
38	YS	54	LEU
38	YS	56	LEU
38	YS	58	LEU
38	YS	59	LYS
38	YS	69	VAL
38	YS	73	LEU
38	YS	89	ARG
38	YS	106	ARG
38	YS	110	LEU
39	YT	8	LYS
39	YT	23	ARG
39	YT	28	VAL
39	YT	30	VAL
39	YT	33	LYS
39	YT	35	LYS
39	YT	41	ARG
39	YT	50	ILE
39	YT	58	ASN
39	YT	59	THR
39	YT	62	THR
39	YT	74	ARG
39	YT	78	LEU
39	YT	88	ILE
39	YT	89	VAL
39	YT	91	ARG
39	YT	98	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
39	YT	99	LEU
39	YT	102	ILE
39	YT	107	ASP
39	YT	115	ARG
39	YT	137	LYS
40	YU	5	LYS
40	YU	27	LEU
40	YU	74	LEU
40	YU	88	ILE
40	YU	92	ARG
40	YU	93	LYS
40	YU	97	ASP
40	YU	114	LYS
41	YV	2	PHE
41	YV	5	VAL
41	YV	10	LYS
41	YV	18	LEU
41	YV	19	LYS
41	YV	32	THR
41	YV	35	LEU
41	YV	47	VAL
41	YV	51	VAL
41	YV	64	HIS
41	YV	66	ARG
41	YV	73	SER
41	YV	78	LYS
41	YV	79	VAL
41	YV	80	GLN
41	YV	81	TYR
41	YV	82	ARG
41	YV	98	GLU
41	YV	100	ARG
42	YW	11	ARG
42	YW	17	VAL
42	YW	20	VAL
42	YW	50	VAL
42	YW	63	ASP
42	YW	66	GLU
42	YW	76	VAL
42	YW	88	ARG
42	YW	94	ASP
42	YW	96	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
42	YW	106	ILE
42	YW	107	LEU
42	YW	113	LYS
43	YX	27	THR
43	YX	48	LYS
43	YX	50	LYS
43	YX	53	LYS
43	YX	66	LEU
43	YX	80	ILE
44	YY	2	ARG
44	YY	5	MET
44	YY	9	LYS
44	YY	13	VAL
44	YY	14	LEU
44	YY	28	LYS
44	YY	33	LYS
44	YY	38	ILE
44	YY	40	GLU
44	YY	50	ARG
44	YY	51	VAL
44	YY	55	TYR
44	YY	60	PHE
44	YY	61	ILE
44	YY	62	GLU
44	YY	71	LYS
44	YY	75	ILE
44	YY	76	CYS
44	YY	86	ARG
44	YY	87	LYS
44	YY	95	LYS
44	YY	96	ILE
44	YY	97	ARG
44	YY	101	LYS
45	YZ	4	ARG
45	YZ	9	TYR
45	YZ	19	ARG
45	YZ	28	MET
45	YZ	33	LEU
45	YZ	34	ASN
45	YZ	41	LEU
45	YZ	61	LEU
45	YZ	71	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
45	YZ	75	ASN
45	YZ	76	LEU
45	YZ	81	ARG
45	YZ	87	ASP
45	YZ	91	LEU
45	YZ	104	PHE
45	YZ	107	THR
45	YZ	111	VAL
45	YZ	116	VAL
45	YZ	120	ILE
45	YZ	121	HIS
45	YZ	122	ARG
45	YZ	128	VAL
45	YZ	135	GLU
45	YZ	141	VAL
45	YZ	148	ASP
45	YZ	150	LEU
45	YZ	162	GLU
45	YZ	171	ILE
46	Y0	5	LYS
46	Y0	7	LEU
46	Y0	9	SER
46	Y0	10	THR
46	Y0	20	ARG
46	Y0	36	ILE
46	Y0	49	LYS
46	Y0	55	ARG
47	Y1	4	VAL
47	Y1	21	ARG
47	Y1	30	VAL
47	Y1	46	LEU
47	Y1	51	VAL
47	Y1	75	GLU
47	Y1	78	LYS
47	Y1	92	LYS
47	Y1	97	LEU
47	Y1	98	LEU
48	Y2	24	LEU
48	Y2	44	LEU
48	Y2	48	HIS
48	Y2	50	ILE
48	Y2	53	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	Y2	64	LEU
48	Y2	67	LYS
49	Y3	8	LEU
49	Y3	32	GLN
49	Y3	40	THR
49	Y3	54	VAL
50	Y4	6	HIS
50	Y4	16	CYS
50	Y4	18	CYS
50	Y4	21	VAL
50	Y4	31	ILE
50	Y4	34	GLU
50	Y4	35	VAL
50	Y4	36	CYS
50	Y4	37	SER
50	Y4	43	TYR
50	Y4	50	VAL
50	Y4	51	ASP
50	Y4	55	ARG
50	Y4	59	PHE
50	Y4	61	ARG
50	Y4	63	TYR
50	Y4	67	TYR
50	Y4	69	LYS
51	Y5	3	LYS
51	Y5	4	HIS
51	Y5	11	THR
51	Y5	23	HIS
51	Y5	26	THR
51	Y5	29	THR
51	Y5	52	TYR
52	Y6	7	ILE
52	Y6	8	LYS
52	Y6	9	LEU
52	Y6	10	LEU
52	Y6	12	GLU
52	Y6	18	ARG
52	Y6	21	TYR
52	Y6	24	GLU
52	Y6	28	ARG
52	Y6	34	LEU
52	Y6	37	ARG

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Mol	Chain	Res	Type
52	Y6	38	LYS
52	Y6	39	TYR
52	Y6	40	CYS
52	Y6	44	ARG
52	Y6	45	LYS
52	Y6	47	THR
53	Y7	24	THR
53	Y7	33	ARG
53	Y7	43	THR
53	Y7	46	VAL
53	Y7	47	ARG
53	Y7	48	LYS
53	Y7	49	ARG
54	Y8	14	VAL
54	Y8	31	HIS
54	Y8	32	LEU
54	Y8	34	TRP
54	Y8	36	LYS
54	Y8	41	ILE
54	Y8	54	GLU
54	Y8	58	ILE
54	Y8	61	LEU
54	Y8	64	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
3	QC	63	ASN
3	QC	108	ASN
40	RU	81	HIS
45	RZ	118	GLN
3	XC	108	ASN
7	XG	97	GLN
9	XI	117	HIS
24	XY	54	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	QA	1509/1522 (99%)	309 (20%)	50 (3%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	XA	1506/1522 (98%)	306 (20%)	41 (2%)
22	QV	76/77 (98%)	16 (21%)	0
22	XV	76/77 (98%)	13 (17%)	1 (1%)
23	QX	19/24 (79%)	9 (47%)	2 (10%)
23	XX	19/24 (79%)	8 (42%)	0
25	RA	2888/2916 (99%)	599 (20%)	54 (1%)
25	YA	2872/2916 (98%)	584 (20%)	41 (1%)
26	RB	121/124 (97%)	23 (19%)	1 (0%)
26	YB	121/124 (97%)	24 (19%)	1 (0%)
56	Z6	1/3 (33%)	0	0
56	Z7	1/3 (33%)	0	0
All	All	9209/9332 (98%)	1891 (20%)	191 (2%)

All (1891) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	QA	4	U
1	QA	5	U
1	QA	6	G
1	QA	9	G
1	QA	22	G
1	QA	32	A
1	QA	39	G
1	QA	47	C
1	QA	48	C
1	QA	50	A
1	QA	51	A
1	QA	61	G
1	QA	64	G
1	QA	65	U
1	QA	66	G
1	QA	79	G
1	QA	80	G
1	QA	90	C
1	QA	92	G
1	QA	93	U
1	QA	101	A
1	QA	116	A
1	QA	121	C
1	QA	131	C
1	QA	182	U
1	QA	186	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	QA	188	U
1	QA	189	U
1	QA	190	G
1	QA	191(A)	G
1	QA	191(D)	U
1	QA	191(E)	G
1	QA	195	A
1	QA	197	A
1	QA	198	G
1	QA	201	C
1	QA	208	U
1	QA	209	U
1	QA	210	U
1	QA	216	G
1	QA	231	G
1	QA	244	U
1	QA	247	G
1	QA	251	G
1	QA	266	G
1	QA	267	C
1	QA	280	C
1	QA	281	G
1	QA	289	G
1	QA	321	A
1	QA	328	C
1	QA	329	A
1	QA	332	G
1	QA	345	C
1	QA	346	G
1	QA	347	G
1	QA	350	G
1	QA	351	G
1	QA	352	C
1	QA	353	A
1	QA	354	G
1	QA	356	A
1	QA	367	U
1	QA	372	C
1	QA	373	A
1	QA	384	G
1	QA	397	A
1	QA	398	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	QA	406	G
1	QA	411	A
1	QA	412	A
1	QA	422	C
1	QA	423	G
1	QA	424	G
1	QA	429	U
1	QA	430	A
1	QA	439	A
1	QA	442	C
1	QA	443	C
1	QA	452	A
1	QA	466	C
1	QA	478	A
1	QA	482	A
1	QA	485	G
1	QA	486	U
1	QA	494	U
1	QA	495	A
1	QA	497	U
1	QA	505	G
1	QA	511	C
1	QA	518	C
1	QA	519	C
1	QA	527	G
1	QA	531	U
1	QA	532	A
1	QA	533	A
1	QA	545	C
1	QA	547	A
1	QA	548	G
1	QA	559	A
1	QA	561	U
1	QA	562	C
1	QA	572	A
1	QA	573	A
1	QA	576	G
1	QA	577	G
1	QA	579	G
1	QA	594	G
1	QA	595	G
1	QA	596	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	QA	607	A
1	QA	623	C
1	QA	630	G
1	QA	653	A
1	QA	665	A
1	QA	666	G
1	QA	687	A
1	QA	688	G
1	QA	701	C
1	QA	702	A
1	QA	703	G
1	QA	704	A
1	QA	721	G
1	QA	722	A
1	QA	724	G
1	QA	731	G
1	QA	749	C
1	QA	755	G
1	QA	760	G
1	QA	777	A
1	QA	792	A
1	QA	793	U
1	QA	794	A
1	QA	813	U
1	QA	817	C
1	QA	828	A
1	QA	841	U
1	QA	842	C
1	QA	843	U
1	QA	848	C
1	QA	859	A
1	QA	870	U
1	QA	871	U
1	QA	872	A
1	QA	874	G
1	QA	914	A
1	QA	926	G
1	QA	927	G
1	QA	934	C
1	QA	935	A
1	QA	960	U
1	QA	961	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	QA	966	G
1	QA	969	A
1	QA	971	G
1	QA	974	A
1	QA	975	A
1	QA	976	G
1	QA	977	A
1	QA	978	A
1	QA	980	C
1	QA	983	A
1	QA	991	U
1	QA	992	U
1	QA	993	G
1	QA	999	U
1	QA	1000	A
1	QA	1001	G
1	QA	1003	G
1	QA	1005	A
1	QA	1006	C
1	QA	1007	C
1	QA	1008	C
1	QA	1009	G
1	QA	1020	U
1	QA	1021	G
1	QA	1024	G
1	QA	1025	U
1	QA	1026	G
1	QA	1029	G
1	QA	1031	G
1	QA	1032	A
1	QA	1032(A)	G
1	QA	1033	G
1	QA	1034	G
1	QA	1036	G
1	QA	1038	C
1	QA	1039	C
1	QA	1042	G
1	QA	1053	G
1	QA	1054	C
1	QA	1055	A
1	QA	1064	G
1	QA	1065	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	QA	1066	C
1	QA	1067	A
1	QA	1068	G
1	QA	1081	G
1	QA	1086	U
1	QA	1094	G
1	QA	1095	U
1	QA	1101	A
1	QA	1117	G
1	QA	1118	C
1	QA	1124	G
1	QA	1125	U
1	QA	1129	C
1	QA	1136	U
1	QA	1137	C
1	QA	1138	G
1	QA	1139	G
1	QA	1140	C
1	QA	1146	A
1	QA	1152	A
1	QA	1157	A
1	QA	1158	C
1	QA	1159	U
1	QA	1160	G
1	QA	1176	A
1	QA	1177	G
1	QA	1178	G
1	QA	1181	G
1	QA	1183	A
1	QA	1190	G
1	QA	1193	G
1	QA	1196	U
1	QA	1197	G
1	QA	1199	U
1	QA	1200	C
1	QA	1202	G
1	QA	1203	C
1	QA	1204	A
1	QA	1205	U
1	QA	1211	U
1	QA	1212	U
1	QA	1213	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	QA	1225	A
1	QA	1226	C
1	QA	1238	A
1	QA	1240	U
1	QA	1241	G
1	QA	1256	A
1	QA	1257	U
1	QA	1258	G
1	QA	1273	G
1	QA	1278	U
1	QA	1280	A
1	QA	1281	U
1	QA	1285	A
1	QA	1286	A
1	QA	1287	A
1	QA	1288	A
1	QA	1290	G
1	QA	1296	C
1	QA	1297	C
1	QA	1298	C
1	QA	1299	A
1	QA	1300	G
1	QA	1301	U
1	QA	1303	C
1	QA	1305	G
1	QA	1320	C
1	QA	1321	C
1	QA	1323	G
1	QA	1331	G
1	QA	1335	C
1	QA	1337	G
1	QA	1338	G
1	QA	1346	A
1	QA	1347	G
1	QA	1348	U
1	QA	1353	G
1	QA	1362(A)	C
1	QA	1363	A
1	QA	1364	U
1	QA	1365	G
1	QA	1370	G
1	QA	1379	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	QA	1398	A
1	QA	1406	U
1	QA	1419	G
1	QA	1442	G
1	QA	1446	A
1	QA	1450	U
1	QA	1451	A
1	QA	1452	C
1	QA	1453	G
1	QA	1454	G
1	QA	1487	G
1	QA	1492	A
1	QA	1493	A
1	QA	1497	G
1	QA	1499	A
1	QA	1502	A
1	QA	1504	G
1	QA	1505	G
1	QA	1506	U
1	QA	1517	G
1	QA	1519	A
1	QA	1520	G
1	QA	1529	G
1	QA	1530	G
1	QA	1532	U
1	QA	1533	C
1	QA	1534	A
1	QA	1536	C
1	QA	1540	U
1	QA	1541	U
1	QA	1542	U
22	QV	2	G
22	QV	3	C
22	QV	7	G
22	QV	9	G
22	QV	17(A)	U
22	QV	18	G
22	QV	19	G
22	QV	20	U
22	QV	21	A
22	QV	22	G
22	QV	47	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
22	QV	48	C
22	QV	49	G
22	QV	63	G
22	QV	65	C
22	QV	76	A
23	QX	10	G
23	QX	11	U
23	QX	12	A
23	QX	13	A
23	QX	14	A
23	QX	19	A2M
23	QX	20	OMC
23	QX	21	A2M
23	QX	22	U
25	RA	9	U
25	RA	12	U
25	RA	28	A
25	RA	34	C
25	RA	35	G
25	RA	46	C
25	RA	49	A
25	RA	58	G
25	RA	60	G
25	RA	69	C
25	RA	71	A
25	RA	74	A
25	RA	75	G
25	RA	90	U
25	RA	91	A
25	RA	93	C
25	RA	95	G
25	RA	101	G
25	RA	102	G
25	RA	113	G
25	RA	118	A
25	RA	119	A
25	RA	120	U
25	RA	123	G
25	RA	129	C
25	RA	138	G
25	RA	139	G
25	RA	140	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	141	A
25	RA	154	G
25	RA	155	C
25	RA	174	C
25	RA	175	G
25	RA	181	A
25	RA	182	A
25	RA	194	G
25	RA	196	A
25	RA	199	A
25	RA	215	G
25	RA	216	A
25	RA	221	A
25	RA	222	A
25	RA	225	A
25	RA	227	A
25	RA	228	A
25	RA	229	A
25	RA	233	A
25	RA	248	G
25	RA	249	C
25	RA	252	G
25	RA	260	G
25	RA	261	G
25	RA	267	C
25	RA	269	U
25	RA	270(K)	C
25	RA	270(L)	U
25	RA	270(M)	U
25	RA	270(O)	U
25	RA	270(P)	C
25	RA	270(Z)	U
25	RA	271(C)	U
25	RA	271	G
25	RA	273(D)	C
25	RA	274	G
25	RA	278	A
25	RA	279	C
25	RA	283	A
25	RA	284	U
25	RA	288	C
25	RA	289	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	311	A
25	RA	317	G
25	RA	324	A
25	RA	329	G
25	RA	330	A
25	RA	332	A
25	RA	335	C
25	RA	345	A
25	RA	352	G
25	RA	353	G
25	RA	356	G
25	RA	358	U
25	RA	362	U
25	RA	363	G
25	RA	363(E)	U
25	RA	363(F)	A
25	RA	364	C
25	RA	372	G
25	RA	373	U
25	RA	386	G
25	RA	388	G
25	RA	396	G
25	RA	405	U
25	RA	407	G
25	RA	411	G
25	RA	428	A
25	RA	443	A
25	RA	444	C
25	RA	448	U
25	RA	457	A
25	RA	470	A
25	RA	481	G
25	RA	493	G
25	RA	494	G
25	RA	505	A
25	RA	509	C
25	RA	512	G
25	RA	528	A
25	RA	530	G
25	RA	531	C
25	RA	532	A
25	RA	533	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	545	G
25	RA	549	G
25	RA	556	G
25	RA	561	G
25	RA	563	G
25	RA	573	G
25	RA	574	C
25	RA	575	A
25	RA	586	A
25	RA	587	C
25	RA	588	U
25	RA	593	G
25	RA	603	A
25	RA	604	G
25	RA	607	U
25	RA	609(A)	G
25	RA	613	U
25	RA	614	U
25	RA	615	G
25	RA	617	G
25	RA	627	A
25	RA	637	A
25	RA	645	C
25	RA	646	A
25	RA	651	G
25	RA	654	A
25	RA	654(A)	G
25	RA	654(B)	C
25	RA	654(F)	C
25	RA	654(G)	C
25	RA	654(O)	G
25	RA	654(Q)	C
25	RA	654(R)	C
25	RA	654(S)	G
25	RA	654(T)	C
25	RA	656	G
25	RA	657	U
25	RA	686	G
25	RA	708	C
25	RA	717	G
25	RA	722	A
25	RA	726	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	730	C
25	RA	753	C
25	RA	775	G
25	RA	782	A
25	RA	784	A
25	RA	785	G
25	RA	789	A
25	RA	792	G
25	RA	805	G
25	RA	812	C
25	RA	819	A
25	RA	827	U
25	RA	828	U
25	RA	845	G
25	RA	855	G
25	RA	856	C
25	RA	857	C
25	RA	859	G
25	RA	860	U
25	RA	863	A
25	RA	865	C
25	RA	866	A
25	RA	877	U
25	RA	878	A
25	RA	879	G
25	RA	881	G
25	RA	882	G
25	RA	883	G
25	RA	884	C
25	RA	885	C
25	RA	888	C
25	RA	889	C
25	RA	890	A
25	RA	894	C
25	RA	895	U
25	RA	896	A
25	RA	897	C
25	RA	900	A
25	RA	901	A
25	RA	906	G
25	RA	907	U
25	RA	910	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	917	A
25	RA	928	G
25	RA	932	G
25	RA	934	G
25	RA	941	A
25	RA	945	A
25	RA	946	G
25	RA	953	A
25	RA	961	C
25	RA	968	G
25	RA	974	G
25	RA	983	A
25	RA	990	A
25	RA	991	C
25	RA	996	A
25	RA	1010	A
25	RA	1011	G
25	RA	1012	U
25	RA	1013	C
25	RA	1017	G
25	RA	1022	G
25	RA	1025	G
25	RA	1026	U
25	RA	1027	A
25	RA	1033	U
25	RA	1034	G
25	RA	1044	G
25	RA	1045	A
25	RA	1046	A
25	RA	1047	G
25	RA	1049	C
25	RA	1060	U
25	RA	1061	U
25	RA	1070	A
25	RA	1086	A
25	RA	1087	G
25	RA	1088	A
25	RA	1089	G
25	RA	1095	A
25	RA	1096	A
25	RA	1099	G
25	RA	1105	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	1111	A
25	RA	1122	G
25	RA	1128	A
25	RA	1130	U
25	RA	1135	C
25	RA	1136	G
25	RA	1139	G
25	RA	1142	U
25	RA	1142(A)	A
25	RA	1155	A
25	RA	1173	G
25	RA	1174	A
25	RA	1175	U
25	RA	1176	G
25	RA	1177	A
25	RA	1178	C
25	RA	1180	C
25	RA	1195	G
25	RA	1220	A
25	RA	1221	C
25	RA	1236	G
25	RA	1244	G
25	RA	1250	G
25	RA	1253	A
25	RA	1254	A
25	RA	1255	U
25	RA	1256	G
25	RA	1265	A
25	RA	1271	G
25	RA	1272	A
25	RA	1281	G
25	RA	1286	A
25	RA	1300	U
25	RA	1301	A
25	RA	1312	U
25	RA	1313	U
25	RA	1314	C
25	RA	1319	G
25	RA	1329	U
25	RA	1341	U
25	RA	1342	A
25	RA	1346	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	1359	A
25	RA	1360	A
25	RA	1365	A
25	RA	1368	G
25	RA	1379	A
25	RA	1380	G
25	RA	1384	A
25	RA	1385	G
25	RA	1406	U
25	RA	1407	C
25	RA	1416	G
25	RA	1420	U
25	RA	1421	G
25	RA	1428	C
25	RA	1432	C
25	RA	1437	C
25	RA	1444(A)	A
25	RA	1449	A
25	RA	1449(A)	G
25	RA	1453	A
25	RA	1455	G
25	RA	1459	G
25	RA	1460	A
25	RA	1461	G
25	RA	1467	C
25	RA	1471	A
25	RA	1475	G
25	RA	1476	C
25	RA	1477	A
25	RA	1482	U
25	RA	1483	G
25	RA	1485	G
25	RA	1488	G
25	RA	1490	A
25	RA	1493	C
25	RA	1494	A
25	RA	1505	C
25	RA	1509	C
25	RA	1510	A
25	RA	1515	C
25	RA	1522	G
25	RA	1534	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	1535	U
25	RA	1536	A
25	RA	1537	C
25	RA	1538	G
25	RA	1543	A
25	RA	1544	C
25	RA	1545	A
25	RA	1547	C
25	RA	1554	A
25	RA	1558	A
25	RA	1566	A
25	RA	1569	A
25	RA	1578	U
25	RA	1581	G
25	RA	1585	C
25	RA	1586	A
25	RA	1588	C
25	RA	1589	C
25	RA	1598	C
25	RA	1608	A
25	RA	1648	C
25	RA	1654	A
25	RA	1667	G
25	RA	1674	G
25	RA	1695	G
25	RA	1696	G
25	RA	1700	A
25	RA	1725	G
25	RA	1728	G
25	RA	1729	A
25	RA	1735	C
25	RA	1743	G
25	RA	1750	G
25	RA	1756	G
25	RA	1758	G
25	RA	1763	G
25	RA	1764	G
25	RA	1773	A
25	RA	1780	A
25	RA	1791	A
25	RA	1800	C
25	RA	1801	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	1816	G
25	RA	1820	U
25	RA	1829	A
25	RA	1835	G
25	RA	1838	C
25	RA	1847	A
25	RA	1848	A
25	RA	1860	G
25	RA	1869	G
25	RA	1872	A
25	RA	1878	G
25	RA	1880	C
25	RA	1882	C
25	RA	1889	A
25	RA	1900	A
25	RA	1903	G
25	RA	1906	G
25	RA	1912	A
25	RA	1913	A
25	RA	1916	A
25	RA	1929	G
25	RA	1930	G
25	RA	1931	U
25	RA	1936	A
25	RA	1938	A
25	RA	1948	G
25	RA	1955	U
25	RA	1967	C
25	RA	1970	A
25	RA	1971	A
25	RA	1972	A
25	RA	1980	G
25	RA	1981	A
25	RA	1982	C
25	RA	1992	G
25	RA	1993	U
25	RA	2020	A
25	RA	2022	U
25	RA	2023	G
25	RA	2027	G
25	RA	2031	A
25	RA	2032	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	2033	A
25	RA	2043	C
25	RA	2052	G
25	RA	2055	C
25	RA	2056	G
25	RA	2059	A
25	RA	2060	A
25	RA	2061	G
25	RA	2062	A
25	RA	2063	C
25	RA	2069	G
25	RA	2071	A
25	RA	2093	G
25	RA	2095	C
25	RA	2096	U
25	RA	2099	U
25	RA	2108	C
25	RA	2111	C
25	RA	2112	G
25	RA	2113	U
25	RA	2114	A
25	RA	2116	G
25	RA	2117	A
25	RA	2120	G
25	RA	2123	G
25	RA	2128	C
25	RA	2130	U
25	RA	2131	G
25	RA	2132	U
25	RA	2140	C
25	RA	2145	C
25	RA	2147	G
25	RA	2148	G
25	RA	2165	G
25	RA	2167	U
25	RA	2168	G
25	RA	2169	A
25	RA	2171	A
25	RA	2173	A
25	RA	2178	C
25	RA	2190	G
25	RA	2192	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	2198	A
25	RA	2210	G
25	RA	2211	G
25	RA	2212	A
25	RA	2213	U
25	RA	2215	G
25	RA	2225	A
25	RA	2226	C
25	RA	2238	G
25	RA	2239	G
25	RA	2246	G
25	RA	2275	C
25	RA	2276	G
25	RA	2279	G
25	RA	2283	C
25	RA	2287	A
25	RA	2305	A
25	RA	2307	G
25	RA	2308	G
25	RA	2309	A
25	RA	2312	U
25	RA	2316	C
25	RA	2318	G
25	RA	2319	G
25	RA	2320	A
25	RA	2321	G
25	RA	2325	G
25	RA	2334	G
25	RA	2335	A
25	RA	2336	A
25	RA	2347	C
25	RA	2350	C
25	RA	2354	G
25	RA	2355	C
25	RA	2382	G
25	RA	2383	G
25	RA	2385	C
25	RA	2394	C
25	RA	2402	C
25	RA	2406	U
25	RA	2410	G
25	RA	2419	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	2422	A
25	RA	2423	U
25	RA	2424	C
25	RA	2425	A
25	RA	2429	G
25	RA	2430	A
25	RA	2435	A
25	RA	2439	A
25	RA	2440	C
25	RA	2441	C
25	RA	2445	G
25	RA	2447	G
25	RA	2448	A
25	RA	2460	U
25	RA	2465	C
25	RA	2468	G
25	RA	2469	A
25	RA	2470	G
25	RA	2471	C
25	RA	2474	C
25	RA	2475	C
25	RA	2476	A
25	RA	2481	G
25	RA	2482	G
25	RA	2483	C
25	RA	2484	G
25	RA	2491	U
25	RA	2494	G
25	RA	2502	G
25	RA	2505	G
25	RA	2518	A
25	RA	2519	U
25	RA	2529	G
25	RA	2535	G
25	RA	2542	A
25	RA	2543	G
25	RA	2554	U
25	RA	2566	A
25	RA	2567	G
25	RA	2569	G
25	RA	2573	C
25	RA	2582	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	2602	A
25	RA	2609	U
25	RA	2610	C
25	RA	2611	U
25	RA	2612	C
25	RA	2615	U
25	RA	2629	A
25	RA	2630	G
25	RA	2632	A
25	RA	2641	G
25	RA	2646	C
25	RA	2654	A
25	RA	2655	G
25	RA	2665	A
25	RA	2673	G
25	RA	2675	A
25	RA	2682	U
25	RA	2689	U
25	RA	2690	C
25	RA	2691	C
25	RA	2702	U
25	RA	2703	C
25	RA	2712(A)	A
25	RA	2713	A
25	RA	2714	G
25	RA	2725	A
25	RA	2726	U
25	RA	2730	C
25	RA	2733	A
25	RA	2744	G
25	RA	2748	A
25	RA	2752	C
25	RA	2758	A
25	RA	2762	G
25	RA	2765	A
25	RA	2766	G
25	RA	2770	G
25	RA	2777	G
25	RA	2778	A
25	RA	2790	A
25	RA	2791	C
25	RA	2792	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	2807	G
25	RA	2808	U
25	RA	2818	G
25	RA	2820	A
25	RA	2821	A
25	RA	2827	C
25	RA	2833	G
25	RA	2834	G
25	RA	2835	A
25	RA	2836	U
25	RA	2845	G
25	RA	2848	G
25	RA	2849	U
25	RA	2850	A
25	RA	2860	A
25	RA	2867	G
25	RA	2868	A
25	RA	2872	G
25	RA	2876	G
25	RA	2877	G
25	RA	2879	C
25	RA	2880	C
25	RA	2893	G
25	RA	2894	G
25	RA	2896	C
26	RB	0	A
26	RB	3	C
26	RB	8	U
26	RB	13	A
26	RB	14	U
26	RB	15	A
26	RB	25	A
26	RB	27	C
26	RB	33	G
26	RB	35	U
26	RB	40	U
26	RB	42	C
26	RB	44	G
26	RB	45	A
26	RB	52	A
26	RB	53	A
26	RB	59	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
26	RB	67	G
26	RB	73	A
26	RB	88	C
26	RB	89	G
26	RB	108	C
26	RB	109	G
1	XA	4	U
1	XA	5	U
1	XA	6	G
1	XA	9	G
1	XA	22	G
1	XA	32	A
1	XA	39	G
1	XA	47	C
1	XA	48	C
1	XA	51	A
1	XA	54	C
1	XA	61	G
1	XA	66	G
1	XA	75	C
1	XA	76	G
1	XA	79	G
1	XA	93	U
1	XA	101	A
1	XA	116	A
1	XA	121	C
1	XA	127	G
1	XA	131	C
1	XA	146	G
1	XA	151	A
1	XA	163	C
1	XA	169	C
1	XA	182	U
1	XA	185	A
1	XA	186(F)	C
1	XA	189	U
1	XA	190	G
1	XA	191(A)	G
1	XA	191(D)	U
1	XA	191(E)	G
1	XA	195	A
1	XA	197	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	XA	198	G
1	XA	208	U
1	XA	209	U
1	XA	210	U
1	XA	216	G
1	XA	231	G
1	XA	240	C
1	XA	244	U
1	XA	247	G
1	XA	251	G
1	XA	266	G
1	XA	267	C
1	XA	280	C
1	XA	281	G
1	XA	289	G
1	XA	316	G
1	XA	321	A
1	XA	328	C
1	XA	329	A
1	XA	332	G
1	XA	345	C
1	XA	346	G
1	XA	347	G
1	XA	350	G
1	XA	351	G
1	XA	352	C
1	XA	353	A
1	XA	354	G
1	XA	356	A
1	XA	367	U
1	XA	368	U
1	XA	372	C
1	XA	384	G
1	XA	397	A
1	XA	398	C
1	XA	406	G
1	XA	411	A
1	XA	412	A
1	XA	413	G
1	XA	422	C
1	XA	423	G
1	XA	429	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	XA	430	A
1	XA	439	A
1	XA	442	C
1	XA	452	A
1	XA	453	A
1	XA	465	A
1	XA	466	C
1	XA	467	G
1	XA	478	A
1	XA	482	A
1	XA	485	G
1	XA	486	U
1	XA	494	U
1	XA	495	A
1	XA	496	A
1	XA	497	U
1	XA	505	G
1	XA	511	C
1	XA	518	C
1	XA	527	G
1	XA	531	U
1	XA	532	A
1	XA	533	A
1	XA	545	C
1	XA	547	A
1	XA	548	G
1	XA	559	A
1	XA	562	C
1	XA	564	C
1	XA	572	A
1	XA	573	A
1	XA	576	G
1	XA	577	G
1	XA	579	G
1	XA	595	G
1	XA	596	C
1	XA	618	C
1	XA	630	G
1	XA	653	A
1	XA	665	A
1	XA	687	A
1	XA	688	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	XA	697	U
1	XA	702	A
1	XA	703	G
1	XA	704	A
1	XA	721	G
1	XA	723	U
1	XA	724	G
1	XA	731	G
1	XA	733	A
1	XA	749	C
1	XA	755	G
1	XA	760	G
1	XA	773	G
1	XA	777	A
1	XA	792	A
1	XA	793	U
1	XA	794	A
1	XA	801	U
1	XA	813	U
1	XA	817	C
1	XA	818	G
1	XA	819	A
1	XA	820	U
1	XA	821	G
1	XA	828	A
1	XA	841	U
1	XA	842	C
1	XA	843	U
1	XA	848	C
1	XA	859	A
1	XA	870	U
1	XA	874	G
1	XA	887	G
1	XA	914	A
1	XA	919	A
1	XA	926	G
1	XA	927	G
1	XA	934	C
1	XA	935	A
1	XA	960	U
1	XA	961	U
1	XA	966	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	XA	968	A
1	XA	969	A
1	XA	971	G
1	XA	972	C
1	XA	975	A
1	XA	977	A
1	XA	980	C
1	XA	983	A
1	XA	991	U
1	XA	992	U
1	XA	993	G
1	XA	1000	A
1	XA	1001	G
1	XA	1005	A
1	XA	1006	C
1	XA	1007	C
1	XA	1008	C
1	XA	1009	G
1	XA	1020	U
1	XA	1024	G
1	XA	1025	U
1	XA	1026	G
1	XA	1028(A)	C
1	XA	1029	G
1	XA	1031	G
1	XA	1032	A
1	XA	1032(A)	G
1	XA	1033	G
1	XA	1034	G
1	XA	1036	G
1	XA	1038	C
1	XA	1039	C
1	XA	1042	G
1	XA	1053	G
1	XA	1054	C
1	XA	1055	A
1	XA	1066	C
1	XA	1068	G
1	XA	1081	G
1	XA	1086	U
1	XA	1094	G
1	XA	1095	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	XA	1101	A
1	XA	1118	C
1	XA	1124	G
1	XA	1125	U
1	XA	1136	U
1	XA	1137	C
1	XA	1138	G
1	XA	1139	G
1	XA	1145	C
1	XA	1146	A
1	XA	1147	C
1	XA	1157	A
1	XA	1158	C
1	XA	1159	U
1	XA	1160	G
1	XA	1176	A
1	XA	1178	G
1	XA	1181	G
1	XA	1182	G
1	XA	1183	A
1	XA	1184	G
1	XA	1187	G
1	XA	1190	G
1	XA	1191	A
1	XA	1192	C
1	XA	1196	U
1	XA	1197	G
1	XA	1212	U
1	XA	1213	A
1	XA	1225	A
1	XA	1226	C
1	XA	1238	A
1	XA	1240	U
1	XA	1241	G
1	XA	1250	A
1	XA	1256	A
1	XA	1257	U
1	XA	1258	G
1	XA	1270	C
1	XA	1273	G
1	XA	1278	U
1	XA	1280	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	XA	1285	A
1	XA	1286	A
1	XA	1287	A
1	XA	1296	C
1	XA	1298	C
1	XA	1299	A
1	XA	1300	G
1	XA	1302	U
1	XA	1303	C
1	XA	1305	G
1	XA	1317	C
1	XA	1319	A
1	XA	1320	C
1	XA	1322	C
1	XA	1323	G
1	XA	1326	C
1	XA	1331	G
1	XA	1334	G
1	XA	1338	G
1	XA	1346	A
1	XA	1347	G
1	XA	1353	G
1	XA	1362(A)	C
1	XA	1363	A
1	XA	1364	U
1	XA	1370	G
1	XA	1397	C
1	XA	1398	A
1	XA	1406	U
1	XA	1419	G
1	XA	1422	G
1	XA	1442	G
1	XA	1446	A
1	XA	1447	G
1	XA	1450	U
1	XA	1451	A
1	XA	1452	C
1	XA	1453	G
1	XA	1454	G
1	XA	1487	G
1	XA	1492	A
1	XA	1493	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	XA	1494	G
1	XA	1497	G
1	XA	1499	A
1	XA	1502	A
1	XA	1504	G
1	XA	1505	G
1	XA	1506	U
1	XA	1517	G
1	XA	1520	G
1	XA	1529	G
1	XA	1530	G
1	XA	1532	U
1	XA	1533	C
1	XA	1534	A
1	XA	1536	C
1	XA	1540	U
1	XA	1541	U
1	XA	1542	U
22	XV	13	C
22	XV	17(A)	U
22	XV	18	G
22	XV	19	G
22	XV	20	U
22	XV	21	A
22	XV	22	G
22	XV	47	U
22	XV	48	C
22	XV	54	U
22	XV	63	G
22	XV	65	C
22	XV	76	A
23	XX	5	A
23	XX	11	U
23	XX	12	A
23	XX	13	A
23	XX	14	A
23	XX	19	A2M
23	XX	20	OMC
23	XX	21	A2M
25	YA	9	U
25	YA	34	C
25	YA	46	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	YA	51	G
25	YA	55	G
25	YA	58	G
25	YA	60	G
25	YA	69	C
25	YA	71	A
25	YA	74	A
25	YA	75	G
25	YA	82	G
25	YA	83	G
25	YA	87	C
25	YA	95	G
25	YA	102	G
25	YA	118	A
25	YA	119	A
25	YA	120	U
25	YA	125	G
25	YA	139	G
25	YA	140	A
25	YA	141	A
25	YA	149	A
25	YA	154	G
25	YA	175	G
25	YA	181	A
25	YA	182	A
25	YA	196	A
25	YA	199	A
25	YA	201	C
25	YA	215	G
25	YA	216	A
25	YA	221	A
25	YA	222	A
25	YA	227	A
25	YA	229	A
25	YA	232	G
25	YA	233	A
25	YA	245	G
25	YA	248	G
25	YA	249	C
25	YA	250	G
25	YA	252	G
25	YA	270(B)	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	YA	270(C)	C
25	YA	270(K)	C
25	YA	270(M)	U
25	YA	270(O)	U
25	YA	270(P)	C
25	YA	270(Z)	U
25	YA	271(C)	U
25	YA	271	G
25	YA	273(D)	C
25	YA	274	G
25	YA	278	A
25	YA	279	C
25	YA	283	A
25	YA	289	A
25	YA	311	A
25	YA	317	G
25	YA	324	A
25	YA	329	G
25	YA	330	A
25	YA	332	A
25	YA	345	A
25	YA	346	A
25	YA	352	G
25	YA	356	G
25	YA	361	G
25	YA	363	G
25	YA	363(E)	U
25	YA	363(F)	A
25	YA	386	G
25	YA	396	G
25	YA	407	G
25	YA	411	G
25	YA	412	A
25	YA	428	A
25	YA	444	C
25	YA	448	U
25	YA	454	A
25	YA	456	C
25	YA	457	A
25	YA	470	A
25	YA	481	G
25	YA	494	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	YA	505	A
25	YA	509	C
25	YA	512	G
25	YA	525	U
25	YA	528	A
25	YA	529	A
25	YA	530	G
25	YA	531	C
25	YA	532	A
25	YA	533	G
25	YA	561	G
25	YA	563	G
25	YA	571	A
25	YA	573	G
25	YA	574	C
25	YA	575	A
25	YA	588	U
25	YA	593	G
25	YA	603	A
25	YA	607	U
25	YA	613	U
25	YA	614	U
25	YA	615	G
25	YA	617	G
25	YA	622	G
25	YA	623	G
25	YA	624	C
25	YA	625	G
25	YA	627	A
25	YA	637	A
25	YA	645	C
25	YA	646	A
25	YA	647	G
25	YA	652	C
25	YA	668	G
25	YA	670	A
25	YA	686	G
25	YA	708	C
25	YA	717	G
25	YA	722	A
25	YA	730	C
25	YA	753	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	YA	764	A
25	YA	775	G
25	YA	776	G
25	YA	777	A
25	YA	782	A
25	YA	784	A
25	YA	785	G
25	YA	788	A
25	YA	792	G
25	YA	805	G
25	YA	812	C
25	YA	818	G
25	YA	819	A
25	YA	827	U
25	YA	828	U
25	YA	832	G
25	YA	848	G
25	YA	856	C
25	YA	857	C
25	YA	859	G
25	YA	860	U
25	YA	862	G
25	YA	866	A
25	YA	878	A
25	YA	879	G
25	YA	881	G
25	YA	882	G
25	YA	883	G
25	YA	884	C
25	YA	886	C
25	YA	889	C
25	YA	890	A
25	YA	893	C
25	YA	894	C
25	YA	896	A
25	YA	897	C
25	YA	901	A
25	YA	906	G
25	YA	907	U
25	YA	910	A
25	YA	917	A
25	YA	919	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	YA	928	G
25	YA	932	G
25	YA	938	G
25	YA	941	A
25	YA	945	A
25	YA	946	G
25	YA	953	A
25	YA	959	A
25	YA	961	C
25	YA	974	G
25	YA	983	A
25	YA	989	G
25	YA	990	A
25	YA	991	C
25	YA	996	A
25	YA	997	G
25	YA	1000	A
25	YA	1010	A
25	YA	1011	G
25	YA	1012	U
25	YA	1013	C
25	YA	1022	G
25	YA	1023	U
25	YA	1025	G
25	YA	1026	U
25	YA	1031	G
25	YA	1033	U
25	YA	1044	G
25	YA	1045	A
25	YA	1046	A
25	YA	1047	G
25	YA	1049	C
25	YA	1050	A
25	YA	1051	G
25	YA	1060	U
25	YA	1061	U
25	YA	1070	A
25	YA	1086	A
25	YA	1087	G
25	YA	1088	A
25	YA	1095	A
25	YA	1096	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	YA	1122	G
25	YA	1128	A
25	YA	1135	C
25	YA	1136	G
25	YA	1139	G
25	YA	1143	A
25	YA	1155	A
25	YA	1169	G
25	YA	1173	G
25	YA	1174	A
25	YA	1175	U
25	YA	1176	G
25	YA	1177	A
25	YA	1178	C
25	YA	1180	C
25	YA	1195	G
25	YA	1218	C
25	YA	1220	A
25	YA	1236	G
25	YA	1253	A
25	YA	1255	U
25	YA	1256	G
25	YA	1262	A
25	YA	1265	A
25	YA	1269	A
25	YA	1271	G
25	YA	1272	A
25	YA	1281	G
25	YA	1289	C
25	YA	1294	U
25	YA	1300	U
25	YA	1301	A
25	YA	1314	C
25	YA	1319	G
25	YA	1329	U
25	YA	1341	U
25	YA	1352	U
25	YA	1359	A
25	YA	1360	A
25	YA	1365	A
25	YA	1368	G
25	YA	1380	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	YA	1384	A
25	YA	1385	G
25	YA	1387	C
25	YA	1389	G
25	YA	1406	U
25	YA	1407	C
25	YA	1416	G
25	YA	1417	C
25	YA	1419	A
25	YA	1420	U
25	YA	1421	G
25	YA	1428	C
25	YA	1437	C
25	YA	1444(A)	A
25	YA	1449	A
25	YA	1449(A)	G
25	YA	1451	C
25	YA	1453	A
25	YA	1455	G
25	YA	1458	C
25	YA	1459	G
25	YA	1460	A
25	YA	1461	G
25	YA	1467	C
25	YA	1471	A
25	YA	1475	G
25	YA	1476	C
25	YA	1477	A
25	YA	1480	G
25	YA	1482	U
25	YA	1483	G
25	YA	1485	G
25	YA	1488	G
25	YA	1490	A
25	YA	1493	C
25	YA	1497	U
25	YA	1499	C
25	YA	1501	C
25	YA	1502	C
25	YA	1505	C
25	YA	1508	A
25	YA	1509	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	YA	1510	A
25	YA	1514	U
25	YA	1515	C
25	YA	1519	G
25	YA	1522	G
25	YA	1526	G
25	YA	1534	G
25	YA	1535	U
25	YA	1536	A
25	YA	1537	C
25	YA	1543	A
25	YA	1545	A
25	YA	1547	C
25	YA	1549	C
25	YA	1554	A
25	YA	1558	A
25	YA	1559	G
25	YA	1566	A
25	YA	1569	A
25	YA	1575	C
25	YA	1578	U
25	YA	1579	A
25	YA	1581	G
25	YA	1585	C
25	YA	1586	A
25	YA	1587	A
25	YA	1588	C
25	YA	1592	C
25	YA	1598	C
25	YA	1608	A
25	YA	1609	A
25	YA	1610	A
25	YA	1616	A
25	YA	1618	A
25	YA	1639	U
25	YA	1640	C
25	YA	1648	C
25	YA	1654	A
25	YA	1667	G
25	YA	1674	G
25	YA	1675	C
25	YA	1681	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	YA	1695	G
25	YA	1696	G
25	YA	1700	A
25	YA	1701	A
25	YA	1703	G
25	YA	1725	G
25	YA	1729	A
25	YA	1733	G
25	YA	1735	C
25	YA	1742	C
25	YA	1743	G
25	YA	1750	G
25	YA	1754	C
25	YA	1756	G
25	YA	1762	A
25	YA	1763	G
25	YA	1764	G
25	YA	1773	A
25	YA	1780	A
25	YA	1791	A
25	YA	1800	C
25	YA	1816	G
25	YA	1820	U
25	YA	1829	A
25	YA	1835	G
25	YA	1838	C
25	YA	1847	A
25	YA	1848	A
25	YA	1858	G
25	YA	1869	G
25	YA	1870	C
25	YA	1872	A
25	YA	1878	G
25	YA	1881	C
25	YA	1882	C
25	YA	1888	G
25	YA	1889	A
25	YA	1896	G
25	YA	1900	A
25	YA	1903	G
25	YA	1905	C
25	YA	1906	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	YA	1912	A
25	YA	1913	A
25	YA	1914	C
25	YA	1916	A
25	YA	1929	G
25	YA	1930	G
25	YA	1931	U
25	YA	1938	A
25	YA	1946	U
25	YA	1948	G
25	YA	1955	U
25	YA	1963	U
25	YA	1967	C
25	YA	1970	A
25	YA	1971	A
25	YA	1972	A
25	YA	1982	C
25	YA	1991	U
25	YA	1992	G
25	YA	1993	U
25	YA	2020	A
25	YA	2021	C
25	YA	2023	G
25	YA	2027	G
25	YA	2031	A
25	YA	2032	G
25	YA	2033	A
25	YA	2043	C
25	YA	2055	C
25	YA	2056	G
25	YA	2059	A
25	YA	2060	A
25	YA	2061	G
25	YA	2062	A
25	YA	2069	G
25	YA	2099	U
25	YA	2108	C
25	YA	2111	C
25	YA	2112	G
25	YA	2113	U
25	YA	2114	A
25	YA	2116	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	YA	2117	A
25	YA	2120	G
25	YA	2126	A
25	YA	2128	C
25	YA	2130	U
25	YA	2131	G
25	YA	2132	U
25	YA	2134	A
25	YA	2140	C
25	YA	2145	C
25	YA	2148	G
25	YA	2161	C
25	YA	2167	U
25	YA	2168	G
25	YA	2169	A
25	YA	2170	A
25	YA	2171	A
25	YA	2173	A
25	YA	2186	G
25	YA	2190	G
25	YA	2191	G
25	YA	2192	G
25	YA	2198	A
25	YA	2210	G
25	YA	2211	G
25	YA	2212	A
25	YA	2213	U
25	YA	2215	G
25	YA	2225	A
25	YA	2226	C
25	YA	2235	G
25	YA	2238	G
25	YA	2239	G
25	YA	2246	G
25	YA	2268	A
25	YA	2275	C
25	YA	2283	C
25	YA	2287	A
25	YA	2305	A
25	YA	2306	C
25	YA	2307	G
25	YA	2308	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	YA	2309	A
25	YA	2312	U
25	YA	2319	G
25	YA	2320	A
25	YA	2325	G
25	YA	2327	A
25	YA	2336	A
25	YA	2345	G
25	YA	2347	C
25	YA	2350	C
25	YA	2354	G
25	YA	2383	G
25	YA	2385	C
25	YA	2391	G
25	YA	2394	C
25	YA	2402	C
25	YA	2406	U
25	YA	2410	G
25	YA	2411	A
25	YA	2422	A
25	YA	2423	U
25	YA	2425	A
25	YA	2429	G
25	YA	2430	A
25	YA	2431	U
25	YA	2434	A
25	YA	2435	A
25	YA	2439	A
25	YA	2440	C
25	YA	2441	C
25	YA	2445	G
25	YA	2448	A
25	YA	2450	A
25	YA	2465	C
25	YA	2469	A
25	YA	2470	G
25	YA	2472	G
25	YA	2475	C
25	YA	2476	A
25	YA	2478	A
25	YA	2484	G
25	YA	2491	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	YA	2494	G
25	YA	2502	G
25	YA	2505	G
25	YA	2518	A
25	YA	2525	G
25	YA	2529	G
25	YA	2535	G
25	YA	2554	U
25	YA	2562	U
25	YA	2566	A
25	YA	2567	G
25	YA	2569	G
25	YA	2573	C
25	YA	2578	G
25	YA	2586	C
25	YA	2602	A
25	YA	2609	U
25	YA	2611	U
25	YA	2612	C
25	YA	2629	A
25	YA	2630	G
25	YA	2634	G
25	YA	2646	C
25	YA	2654	A
25	YA	2655	G
25	YA	2665	A
25	YA	2673	G
25	YA	2689	U
25	YA	2691	C
25	YA	2703	C
25	YA	2712(A)	A
25	YA	2713	A
25	YA	2714	G
25	YA	2725	A
25	YA	2726	U
25	YA	2732	G
25	YA	2733	A
25	YA	2748	A
25	YA	2750	A
25	YA	2751	G
25	YA	2752	C
25	YA	2754	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	YA	2758	A
25	YA	2762	G
25	YA	2766	G
25	YA	2777	G
25	YA	2778	A
25	YA	2779	U
25	YA	2780	G
25	YA	2787	C
25	YA	2790	A
25	YA	2791	C
25	YA	2792	G
25	YA	2807	G
25	YA	2818	G
25	YA	2820	A
25	YA	2821	A
25	YA	2827	C
25	YA	2828	C
25	YA	2833	G
25	YA	2834	G
25	YA	2835	A
25	YA	2846	G
25	YA	2849	U
25	YA	2850	A
25	YA	2860	A
25	YA	2866	U
25	YA	2872	G
25	YA	2874	C
25	YA	2875	C
25	YA	2879	C
25	YA	2880	C
25	YA	2892	A
25	YA	2893	G
25	YA	2894	G
25	YA	2896	C
25	YA	2897	U
26	YB	7	G
26	YB	13	A
26	YB	14	U
26	YB	15	A
26	YB	16	G
26	YB	25	A
26	YB	32	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
26	YB	35	U
26	YB	40	U
26	YB	41	U
26	YB	42	C
26	YB	44	G
26	YB	45	A
26	YB	56	G
26	YB	67	G
26	YB	73	A
26	YB	81	G
26	YB	82	G
26	YB	88	C
26	YB	101	A
26	YB	108	C
26	YB	109	G
26	YB	118	G
26	YB	119	A

All (191) RNA pucker outliers are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	QA	5	U
1	QA	31	G
1	QA	60	A
1	QA	64	G
1	QA	115	G
1	QA	181	G
1	QA	190	G
1	QA	197	A
1	QA	201	C
1	QA	208	U
1	QA	243	A
1	QA	250	A
1	QA	279	A
1	QA	328	C
1	QA	345	C
1	QA	410	G
1	QA	428	G
1	QA	429	U
1	QA	484	G
1	QA	485	G
1	QA	496	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	QA	518	C
1	QA	547	A
1	QA	560	U
1	QA	687	A
1	QA	748	C
1	QA	792	A
1	QA	812	C
1	QA	841	U
1	QA	913	A
1	QA	960	U
1	QA	991	U
1	QA	992	U
1	QA	1004	A
1	QA	1033	G
1	QA	1038	C
1	QA	1054	C
1	QA	1065	U
1	QA	1067	A
1	QA	1137	C
1	QA	1139	G
1	QA	1182	G
1	QA	1297	C
1	QA	1300	G
1	QA	1346	A
1	QA	1347	G
1	QA	1491	G
1	QA	1498	U
1	QA	1528	U
1	QA	1532	U
23	QX	9	G
23	QX	11	U
25	RA	90	U
25	RA	119	A
25	RA	128	C
25	RA	195	A
25	RA	196	A
25	RA	227	A
25	RA	270(L)	U
25	RA	352	G
25	RA	372	G
25	RA	387	U
25	RA	395	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	404	C
25	RA	529	A
25	RA	587	C
25	RA	603	A
25	RA	614	U
25	RA	752	A
25	RA	859	G
25	RA	877	U
25	RA	883	G
25	RA	1085	A
25	RA	1171	G
25	RA	1300	U
25	RA	1301	A
25	RA	1311	G
25	RA	1341	U
25	RA	1427	A
25	RA	1653	G
25	RA	1694	C
25	RA	1819	A
25	RA	1912	A
25	RA	1992	G
25	RA	2022	U
25	RA	2062	A
25	RA	2092	U
25	RA	2144	U
25	RA	2166	G
25	RA	2191	G
25	RA	2211	G
25	RA	2275	C
25	RA	2320	A
25	RA	2405	G
25	RA	2422	A
25	RA	2439	A
25	RA	2447	G
25	RA	2481	G
25	RA	2518	A
25	RA	2610	C
25	RA	2689	U
25	RA	2776	A
25	RA	2848	G
25	RA	2849	U
25	RA	2859	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
25	RA	2867	G
26	RB	66	A
1	XA	5	U
1	XA	31	G
1	XA	60	A
1	XA	92	G
1	XA	115	G
1	XA	181	G
1	XA	197	A
1	XA	201	C
1	XA	243	A
1	XA	250	A
1	XA	279	A
1	XA	315	A
1	XA	328	C
1	XA	410	G
1	XA	428	G
1	XA	429	U
1	XA	485	G
1	XA	547	A
1	XA	595	G
1	XA	687	A
1	XA	703	G
1	XA	748	C
1	XA	792	A
1	XA	812	C
1	XA	818	G
1	XA	913	A
1	XA	960	U
1	XA	992	U
1	XA	1004	A
1	XA	1033	G
1	XA	1038	C
1	XA	1054	C
1	XA	1065	U
1	XA	1067	A
1	XA	1137	C
1	XA	1157	A
1	XA	1181	G
1	XA	1182	G
1	XA	1319	A
1	XA	1498	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	XA	1532	U
22	XV	17(A)	U
25	YA	74	A
25	YA	101	G
25	YA	119	A
25	YA	196	A
25	YA	528	A
25	YA	587	C
25	YA	752	A
25	YA	764	A
25	YA	856	C
25	YA	859	G
25	YA	877	U
25	YA	883	G
25	YA	1022	G
25	YA	1085	A
25	YA	1171	G
25	YA	1300	U
25	YA	1379	A
25	YA	1416	G
25	YA	1427	A
25	YA	1558	A
25	YA	1694	C
25	YA	1762	A
25	YA	1819	A
25	YA	1912	A
25	YA	1930	G
25	YA	1992	G
25	YA	2144	U
25	YA	2166	G
25	YA	2191	G
25	YA	2211	G
25	YA	2225	A
25	YA	2238	G
25	YA	2422	A
25	YA	2439	A
25	YA	2447	G
25	YA	2610	C
25	YA	2726	U
25	YA	2776	A
25	YA	2848	G
25	YA	2849	U

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Mol	Chain	Res	Type
25	YA	2859	G
26	YB	66	A

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

8 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
56	PPU	Z6	76	56,25	32,40,41	0.90	1 (3%)	33,57,60	1.73	7 (21%)
23	A2M	QX	19	23,22	18,25,26	1.05	1 (5%)	18,36,39	1.53	4 (22%)
56	PPU	Z7	76	56,25	32,40,41	0.93	1 (3%)	33,57,60	1.46	8 (24%)
23	A2M	QX	21	23,1	18,25,26	1.13	2 (11%)	18,36,39	1.40	2 (11%)
23	A2M	XX	21	23,1	18,25,26	1.07	1 (5%)	18,36,39	1.42	2 (11%)
23	OMC	XX	20	23	19,22,23	0.82	0	26,31,34	0.94	1 (3%)
23	OMC	QX	20	23	19,22,23	0.84	0	26,31,34	0.96	1 (3%)
23	A2M	XX	19	23,22	18,25,26	0.88	0	18,36,39	1.59	4 (22%)

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
56	PPU	Z6	76	56,25	-	1/21/43/44	0/4/4/4
23	A2M	QX	19	23,22	-	0/5/27/28	0/3/3/3
56	PPU	Z7	76	56,25	-	3/21/43/44	0/4/4/4
23	A2M	QX	21	23,1	-	4/5/27/28	0/3/3/3
23	A2M	XX	21	23,1	-	3/5/27/28	0/3/3/3
23	OMC	XX	20	23	-	2/9/27/28	0/2/2/2
23	OMC	QX	20	23	-	3/9/27/28	0/2/2/2
23	A2M	XX	19	23,22	-	1/5/27/28	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	QX	21	A2M	C5-C4	2.68	1.48	1.40
23	XX	21	A2M	C5-C4	2.64	1.47	1.40
23	QX	19	A2M	C5-C4	2.56	1.47	1.40
56	Z7	76	PPU	C5-C4	2.11	1.46	1.40
56	Z6	76	PPU	C5-C4	2.04	1.46	1.40
23	QX	21	A2M	O4'-C1'	2.01	1.43	1.41

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	Z6	76	PPU	N1-C6-N6	6.33	123.72	117.06
56	Z7	76	PPU	N1-C6-N6	3.89	121.15	117.06
23	XX	19	A2M	N3-C2-N1	-3.75	122.82	128.68
56	Z6	76	PPU	C9-N6-C6	-3.58	108.68	119.51
23	QX	19	A2M	N3-C2-N1	-3.45	123.29	128.68
56	Z7	76	PPU	N3-C2-N1	-3.25	123.60	128.68
56	Z6	76	PPU	N3-C2-N1	-3.13	123.78	128.68
23	XX	19	A2M	C4-C5-N7	-3.12	106.15	109.40
23	QX	21	A2M	N3-C2-N1	-3.07	123.88	128.68
56	Z7	76	PPU	C4-C5-N7	-2.83	106.45	109.40
23	QX	21	A2M	C4-C5-N7	-2.78	106.50	109.40
23	QX	19	A2M	CM'-O2'-C2'	-2.74	107.34	114.52
23	XX	21	A2M	N3-C2-N1	-2.73	124.41	128.68
56	Z7	76	PPU	C10-N6-C6	-2.63	111.55	119.51
23	XX	21	A2M	C4-C5-N7	-2.50	106.80	109.40
56	Z6	76	PPU	C4-C5-N7	-2.45	106.84	109.40
56	Z7	76	PPU	C10-N6-C9	-2.35	108.56	116.12
23	QX	19	A2M	C4-C5-N7	-2.27	107.03	109.40
56	Z6	76	PPU	C10-N6-C6	-2.26	112.68	119.51
56	Z7	76	PPU	C9-N6-C6	-2.23	112.77	119.51
23	QX	19	A2M	C2-N1-C6	2.17	122.47	118.75
23	XX	20	OMC	CM2-O2'-C2'	-2.17	108.84	114.52
56	Z6	76	PPU	C3'-N3'-C	-2.16	119.96	123.21
23	XX	19	A2M	C1'-N9-C4	-2.15	122.86	126.64
23	XX	19	A2M	O3'-C3'-C2'	-2.15	105.07	111.17
56	Z6	76	PPU	C10-N6-C9	-2.13	109.27	116.12
56	Z7	76	PPU	CM-OC-CZ	2.10	122.06	117.51
56	Z7	76	PPU	C3'-N3'-C	-2.02	120.16	123.21
23	QX	20	OMC	N4-C4-N3	2.01	121.49	117.97

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	QX	21	A2M	C3'-C2'-O2'-CM'
23	XX	21	A2M	C3'-C4'-C5'-O5'
23	XX	21	A2M	C3'-C2'-O2'-CM'
56	Z7	76	PPU	C5-C6-N6-C9
56	Z7	76	PPU	C5-C6-N6-C10
23	QX	20	OMC	O4'-C4'-C5'-O5'
23	QX	21	A2M	O4'-C4'-C5'-O5'
23	QX	20	OMC	C3'-C4'-C5'-O5'
23	QX	21	A2M	C3'-C4'-C5'-O5'
23	XX	21	A2M	O4'-C4'-C5'-O5'
56	Z7	76	PPU	N1-C6-N6-C10
56	Z6	76	PPU	C5-C6-N6-C9
23	XX	20	OMC	C3'-C4'-C5'-O5'
23	XX	19	A2M	C3'-C2'-O2'-CM'
23	QX	21	A2M	C4'-C5'-O5'-P
23	XX	20	OMC	O4'-C4'-C5'-O5'
23	QX	20	OMC	C4'-C5'-O5'-P

There are no ring outliers.

8 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	Z6	76	PPU	7	0
23	QX	19	A2M	1	0
56	Z7	76	PPU	9	0
23	QX	21	A2M	1	0
23	XX	21	A2M	4	0
23	XX	20	OMC	1	0
23	QX	20	OMC	1	0
23	XX	19	A2M	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 1350 ligands modelled in this entry, 1350 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

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

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

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	QA	1511/1522 (99%)	0.84	178 (11%) 4 2	34, 73, 167, 323	0
1	XA	1508/1522 (99%)	0.70	110 (7%) 15 6	27, 64, 152, 309	0
2	QB	236/256 (92%)	1.63	86 (36%) 0 0	56, 114, 192, 239	0
2	XB	236/256 (92%)	1.13	49 (20%) 1 0	51, 99, 182, 208	0
3	QC	206/239 (86%)	0.16	5 (2%) 59 37	42, 97, 183, 230	0
3	XC	206/239 (86%)	0.23	11 (5%) 26 12	48, 84, 156, 235	0
4	QD	208/209 (99%)	0.25	6 (2%) 51 28	37, 65, 105, 184	0
4	XD	208/209 (99%)	0.30	13 (6%) 20 8	39, 67, 113, 170	0
5	QE	154/162 (95%)	0.08	4 (2%) 56 33	38, 64, 127, 212	0
5	XE	154/162 (95%)	0.07	3 (1%) 66 46	33, 60, 127, 229	0
6	QF	101/101 (100%)	0.34	3 (2%) 50 27	51, 87, 129, 142	0
6	XF	101/101 (100%)	0.12	2 (1%) 65 44	34, 64, 107, 165	0
7	QG	155/156 (99%)	0.96	31 (20%) 1 0	71, 109, 182, 224	0
7	XG	155/156 (99%)	0.66	23 (14%) 2 1	49, 89, 156, 201	0
8	QH	138/138 (100%)	-0.00	3 (2%) 62 41	48, 72, 106, 156	0
8	XH	138/138 (100%)	0.24	3 (2%) 62 41	41, 64, 110, 142	0
9	QI	128/128 (100%)	1.67	42 (32%) 0 0	69, 127, 198, 231	0
9	XI	128/128 (100%)	1.20	24 (18%) 1 0	46, 97, 172, 248	0
10	QJ	99/105 (94%)	1.57	33 (33%) 0 0	67, 123, 200, 249	0
10	XJ	99/105 (94%)	1.44	32 (32%) 0 0	45, 109, 178, 237	0
11	QK	121/129 (93%)	0.98	13 (10%) 6 2	42, 85, 170, 226	0
11	XK	121/129 (93%)	0.31	8 (6%) 18 7	33, 65, 157, 195	0
12	QL	125/132 (94%)	0.12	1 (0%) 86 72	34, 58, 110, 215	0
12	XL	125/132 (94%)	0.26	2 (1%) 72 51	28, 55, 96, 205	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
13	QM	118/126 (93%)	0.79	16 (13%) 3 1	66, 113, 181, 242	0
13	XM	118/126 (93%)	0.86	13 (11%) 5 2	52, 97, 150, 259	0
14	QN	60/61 (98%)	0.55	4 (6%) 17 7	63, 95, 133, 188	0
14	XN	60/61 (98%)	0.38	3 (5%) 28 13	50, 77, 123, 190	0
15	QO	88/89 (98%)	0.73	10 (11%) 5 2	42, 75, 119, 154	0
15	XO	88/89 (98%)	0.68	5 (5%) 23 11	30, 63, 104, 120	0
16	QP	84/88 (95%)	0.36	3 (3%) 42 22	46, 66, 101, 182	0
16	XP	84/88 (95%)	0.35	4 (4%) 30 14	50, 70, 104, 198	0
17	QQ	100/105 (95%)	0.36	3 (3%) 50 27	44, 74, 105, 120	0
17	XQ	100/105 (95%)	0.06	1 (1%) 82 67	41, 67, 103, 183	0
18	QR	71/88 (80%)	0.85	10 (14%) 2 1	59, 91, 157, 210	0
18	XR	71/88 (80%)	0.23	3 (4%) 36 18	36, 63, 144, 203	0
19	QS	82/93 (88%)	1.38	25 (30%) 0 0	64, 120, 198, 256	0
19	XS	82/93 (88%)	1.80	34 (41%) 0 0	52, 100, 182, 224	0
20	QT	99/106 (93%)	1.41	23 (23%) 0 0	47, 80, 163, 206	0
20	XT	99/106 (93%)	0.47	4 (4%) 38 19	47, 80, 163, 198	0
21	QU	25/25 (100%)	3.11	16 (64%) 0 0	68, 98, 172, 193	0
21	XU	25/25 (100%)	3.49	21 (84%) 0 0	65, 95, 117, 174	0
22	QV	77/77 (100%)	0.78	8 (10%) 6 2	29, 71, 129, 189	0
22	XV	77/77 (100%)	0.42	4 (5%) 27 12	29, 68, 106, 175	0
23	QX	17/24 (70%)	4.93	13 (76%) 0 0	51, 206, 281, 292	0
23	XX	17/24 (70%)	4.33	12 (70%) 0 0	37, 216, 350, 357	0
24	QY	91/117 (77%)	0.07	3 (3%) 46 24	53, 81, 111, 140	0
24	XY	91/117 (77%)	0.31	6 (6%) 18 7	50, 78, 103, 123	0
25	RA	2891/2916 (99%)	0.91	285 (9%) 7 2	21, 50, 223, 352	0
25	YA	2875/2916 (98%)	0.97	282 (9%) 7 2	19, 45, 231, 375	0
26	RB	122/124 (98%)	0.63	9 (7%) 14 5	40, 82, 126, 193	0
26	YB	122/124 (98%)	0.67	9 (7%) 14 5	41, 72, 121, 208	0
27	RD	272/276 (98%)	0.07	6 (2%) 62 41	16, 46, 89, 168	0
27	YD	272/276 (98%)	-0.00	2 (0%) 87 75	10, 36, 80, 191	0
28	RE	205/206 (99%)	0.34	11 (5%) 25 12	26, 63, 143, 241	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
28	YE	205/206 (99%)	0.41	11 (5%) 25 12	23, 58, 148, 254	0
29	RF	208/210 (99%)	0.23	10 (4%) 30 14	18, 44, 142, 240	0
29	YF	208/210 (99%)	0.73	23 (11%) 5 2	21, 51, 167, 229	0
30	RG	181/182 (99%)	0.43	8 (4%) 34 17	56, 92, 150, 174	0
30	YG	181/182 (99%)	1.00	31 (17%) 1 0	45, 81, 134, 169	0
31	RH	170/180 (94%)	1.70	50 (29%) 0 0	53, 125, 218, 256	0
31	YH	170/180 (94%)	1.14	27 (15%) 1 1	54, 104, 201, 250	0
32	RI	146/148 (98%)	0.88	26 (17%) 1 0	46, 96, 156, 246	0
32	YI	146/148 (98%)	0.49	12 (8%) 11 4	30, 84, 153, 224	0
33	RN	138/140 (98%)	0.17	3 (2%) 62 41	30, 65, 114, 163	0
33	YN	138/140 (98%)	-0.04	2 (1%) 75 56	30, 61, 121, 149	0
34	RO	122/122 (100%)	-0.06	0 100 100	32, 55, 86, 131	0
34	YO	122/122 (100%)	-0.11	0 100 100	25, 46, 77, 97	0
35	RP	150/150 (100%)	0.64	11 (7%) 15 6	17, 63, 133, 211	0
35	YP	150/150 (100%)	0.45	12 (8%) 12 5	19, 54, 139, 202	0
36	RQ	140/141 (99%)	0.22	3 (2%) 63 43	28, 59, 104, 202	0
36	YQ	139/141 (98%)	0.08	4 (2%) 51 28	31, 55, 114, 204	0
37	RR	117/118 (99%)	0.20	3 (2%) 56 33	24, 56, 91, 123	0
37	YR	117/118 (99%)	0.31	3 (2%) 56 33	25, 51, 87, 124	0
38	RS	111/112 (99%)	1.40	35 (31%) 0 0	50, 83, 148, 217	0
38	YS	111/112 (99%)	0.89	17 (15%) 2 1	38, 67, 122, 171	0
39	RT	137/146 (93%)	0.23	5 (3%) 42 22	34, 67, 146, 241	0
39	YT	137/146 (93%)	0.22	7 (5%) 28 13	29, 59, 155, 214	0
40	RU	117/118 (99%)	0.39	6 (5%) 28 13	24, 48, 105, 151	0
40	YU	117/118 (99%)	0.31	5 (4%) 35 17	29, 54, 101, 169	0
41	RV	101/101 (100%)	0.24	6 (5%) 22 10	20, 65, 123, 222	0
41	YV	101/101 (100%)	0.67	11 (10%) 5 2	28, 75, 133, 247	0
42	RW	113/113 (100%)	0.11	1 (0%) 84 69	24, 49, 94, 175	0
42	YW	113/113 (100%)	0.03	0 100 100	25, 46, 99, 194	0
43	RX	92/96 (95%)	0.26	3 (3%) 46 24	39, 62, 87, 135	0
43	YX	92/96 (95%)	0.16	0 100 100	16, 47, 89, 103	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
44	RY	102/110 (92%)	1.14	20 (19%) 1 0	40, 75, 179, 238	0
44	YY	102/110 (92%)	1.28	21 (20%) 1 0	33, 79, 184, 214	0
45	RZ	176/206 (85%)	1.11	39 (22%) 0 0	49, 93, 187, 286	0
45	YZ	183/206 (88%)	0.71	19 (10%) 6 2	41, 92, 163, 211	0
46	R0	83/85 (97%)	0.06	1 (1%) 79 61	27, 50, 94, 200	0
46	Y0	83/85 (97%)	0.30	5 (6%) 21 10	24, 50, 81, 189	0
47	R1	97/98 (98%)	0.51	6 (6%) 20 9	29, 58, 172, 241	0
47	Y1	97/98 (98%)	0.28	5 (5%) 27 12	22, 46, 176, 235	0
48	R2	69/72 (95%)	0.30	4 (5%) 23 10	39, 79, 141, 190	0
48	Y2	69/72 (95%)	0.50	5 (7%) 15 6	29, 60, 106, 196	0
49	R3	59/60 (98%)	0.11	0 100 100	33, 53, 103, 126	0
49	Y3	59/60 (98%)	0.28	0 100 100	35, 61, 112, 167	0
50	R4	70/71 (98%)	2.04	26 (37%) 0 0	79, 165, 243, 284	0
50	Y4	70/71 (98%)	1.80	20 (28%) 0 0	79, 143, 226, 269	0
51	R5	59/60 (98%)	0.56	7 (11%) 4 2	23, 53, 179, 237	0
51	Y5	57/60 (95%)	0.31	5 (8%) 10 4	21, 53, 161, 284	0
52	R6	48/54 (88%)	3.82	32 (66%) 0 0	73, 134, 213, 253	0
52	Y6	48/54 (88%)	3.20	30 (62%) 0 0	73, 129, 207, 245	0
53	R7	49/49 (100%)	0.18	2 (4%) 37 18	21, 33, 127, 192	0
53	Y7	49/49 (100%)	0.08	1 (2%) 65 44	18, 29, 82, 193	0
54	R8	64/65 (98%)	0.59	5 (7%) 13 5	19, 47, 122, 180	0
54	Y8	64/65 (98%)	0.61	5 (7%) 13 5	16, 44, 72, 174	0
55	R9	37/37 (100%)	2.77	21 (56%) 0 0	52, 78, 134, 165	0
55	Y9	36/37 (97%)	0.93	4 (11%) 5 2	36, 76, 110, 130	0
56	Z6	2/3 (66%)	0.14	0 100 100	29, 29, 29, 38	0
56	Z7	2/3 (66%)	0.23	0 100 100	30, 30, 30, 43	0
All	All	21068/21690 (97%)	0.72	2151 (10%) 6 2	10, 65, 171, 375	0

All (2151) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
25	YA	1087	G	23.1
31	YH	2	SER	22.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
25	YA	2138	C	22.0
20	QT	106	ALA	18.7
25	YA	2137	C	18.6
25	YA	2114	A	17.5
25	YA	2157	G	17.4
23	QX	4	A	16.7
25	RA	2119	A	16.5
25	RA	2174	C	16.1
1	QA	88	C	16.0
25	RA	2156	G	15.9
25	RA	2117	A	15.9
25	YA	2134	A	15.8
25	RA	2157	G	15.5
25	YA	2136	C	15.2
31	RH	28	GLY	15.1
25	RA	2127	G	14.8
25	RA	2120	G	14.8
25	RA	2110	G	14.7
25	YA	2117	A	14.6
25	YA	1068	G	14.4
11	QK	9	LYS	14.2
25	YA	2110	G	14.1
25	YA	2127	G	14.1
25	YA	1070	A	14.1
11	QK	10	VAL	14.0
25	YA	2123	G	13.9
28	YE	204	ALA	13.8
25	YA	2174	C	13.7
52	R6	41	PRO	13.7
25	YA	2159	G	13.7
31	RH	2	SER	13.6
25	YA	2160	G	13.3
23	XX	3	C	13.2
25	YA	2121	G	13.2
25	RA	2169	A	13.1
25	YA	2115	G	13.1
25	YA	2112	G	13.0
25	YA	1057	A	12.8
41	YV	45	THR	12.8
23	QX	3	C	12.7
25	YA	2139	C	12.6
25	RA	1089	G	12.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
25	YA	2894	G	12.5
25	RA	1055	G	12.4
25	RA	1057	A	12.3
25	YA	2135	A	12.3
25	YA	1061	U	12.2
28	YE	205	ALA	12.2
25	RA	2111	C	12.2
25	YA	2120	G	12.2
25	RA	2801	A	12.2
25	RA	2173	A	12.1
25	YA	1079	C	12.1
7	XG	85	TYR	12.1
1	QA	1004	A	11.9
25	YA	2119	A	11.8
25	YA	2178	C	11.7
1	XA	1540	U	11.7
11	QK	129	SER	11.6
25	YA	1058	G	11.6
25	YA	2109	U	11.6
25	RA	2165	G	11.6
25	YA	1060	U	11.6
25	RA	2129	C	11.5
25	YA	2801	A	11.5
25	YA	2158	A	11.5
25	RA	2135	A	11.4
50	R4	63	TYR	11.3
25	YA	2122	U	11.2
25	YA	2130	U	11.2
25	YA	2177	C	11.2
25	YA	2140	C	11.1
25	RA	2112	G	11.0
25	YA	2116	G	11.0
25	YA	1089	G	11.0
47	R1	96	LYS	10.9
25	RA	2118	U	10.9
20	QT	101	GLY	10.9
25	RA	2128	C	10.9
52	Y6	40	CYS	10.8
25	RA	2799	A	10.8
25	YA	1096	A	10.7
44	RY	48	ALA	10.7
25	RA	2158	A	10.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
55	R9	37	GLY	10.6
20	QT	102	GLY	10.6
25	YA	1093	G	10.6
25	RA	1061	U	10.5
25	YA	2173	A	10.5
25	RA	2136	C	10.4
25	YA	1099	G	10.4
25	YA	2892	A	10.4
25	RA	2133	G	10.4
1	QA	1450	U	10.4
28	RE	205	ALA	10.4
25	RA	2134	A	10.3
25	YA	2179	C	10.3
25	RA	2130	U	10.3
25	YA	1088	A	10.3
52	Y6	43	CYS	10.3
25	YA	1078	U	10.3
25	YA	2111	C	10.2
23	XX	4	A	10.2
50	R4	53	GLU	10.2
25	RA	2155	G	10.2
25	YA	2802	G	10.1
25	YA	1059	G	10.1
25	YA	2104	G	10.1
25	RA	1062	G	10.0
25	YA	2129	C	10.0
55	R9	1	MET	9.9
25	RA	2148	G	9.9
25	YA	2133	G	9.9
44	RY	49	VAL	9.9
25	YA	2141	G	9.9
29	YF	1	MET	9.9
25	YA	2124	G	9.8
44	YY	91	GLU	9.7
25	RA	2116	G	9.7
25	RA	2167	U	9.7
25	RA	2125	G	9.7
28	YE	59	VAL	9.6
25	RA	2137	C	9.6
25	RA	2168	G	9.6
1	QA	1027	C	9.6
25	YA	2108	C	9.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
13	XM	47	ASP	9.5
25	YA	2169	A	9.5
25	RA	2126	A	9.5
25	YA	2156	G	9.5
25	YA	2168	G	9.5
25	YA	2792	G	9.4
31	RH	43	VAL	9.4
25	YA	2176	A	9.3
20	QT	98	PRO	9.3
25	YA	2155	G	9.3
31	RH	99	VAL	9.2
1	QA	1532	U	9.2
31	RH	32	GLU	9.2
25	RA	1060	U	9.1
25	RA	2146	C	9.1
25	RA	1066	U	9.1
25	RA	1056	G	9.1
11	XK	129	SER	9.1
1	QA	1026	G	9.1
25	RA	2144	U	9.1
25	RA	2181	G	9.1
25	YA	2165	G	9.0
47	R1	97	LEU	9.0
25	RA	2180	U	9.0
25	RA	2114	A	9.0
25	YA	1067	A	9.0
25	YA	2799	A	9.0
25	RA	2149	G	9.0
25	RA	2172	U	8.9
25	RA	1063	G	8.9
25	YA	2181	G	8.9
25	RA	1064	C	8.9
7	XG	153	HIS	8.8
25	YA	2154	G	8.8
45	RZ	153	SER	8.8
21	QU	18	TYR	8.8
1	XA	1026	G	8.8
25	YA	1080	C	8.7
25	RA	2171	A	8.7
25	YA	1103	A	8.7
25	RA	1077	A	8.6
1	XA	1004	A	8.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
25	RA	1078	U	8.5
25	RA	2179	C	8.5
52	R6	19	ARG	8.5
25	RA	1065	U	8.4
25	YA	2172	U	8.4
31	YH	3	ARG	8.4
25	YA	2893	G	8.4
25	RA	1068	G	8.4
52	Y6	41	PRO	8.4
50	Y4	66	SER	8.4
25	RA	2170	A	8.3
52	R6	40	CYS	8.3
25	RA	2164	C	8.3
20	XT	106	ALA	8.3
25	RA	2145	C	8.3
25	RA	2131	G	8.2
13	QM	119	GLY	8.2
25	RA	2175	C	8.2
25	RA	2109	U	8.2
25	YA	1066	U	8.2
44	YY	49	VAL	8.2
52	R6	21	TYR	8.2
25	RA	1099	G	8.2
29	YF	11	VAL	8.2
25	YA	2161	C	8.1
44	YY	48	ALA	8.1
25	YA	2151	G	8.1
25	RA	2113	U	8.1
25	YA	2152	G	8.1
25	YA	2189	U	8.1
25	YA	1069	A	8.1
14	QN	2	ALA	8.1
25	YA	2113	U	8.1
7	QG	3	ARG	8.0
44	RY	50	ARG	8.0
1	QA	1024	G	8.0
25	RA	2162	G	8.0
25	YA	2153	G	8.0
25	YA	2126	A	7.9
1	XA	1003	G	7.9
25	YA	1063	G	7.9
25	YA	1097	U	7.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
25	YA	2143	C	7.9
51	Y5	54	GLY	7.9
25	RA	1071	G	7.9
25	YA	1098	A	7.9
23	QX	5	A	7.9
25	YA	2790	A	7.8
25	RA	1076	C	7.8
23	QX	11	U	7.8
52	R6	20	ASN	7.8
25	YA	2166	G	7.8
25	RA	2121	G	7.8
25	RA	1096	A	7.8
1	XA	1024	G	7.7
52	R6	23	THR	7.7
25	YA	2793	G	7.7
25	RA	1075	C	7.7
40	RU	91	ASP	7.7
23	XX	6	G	7.7
21	QU	9	ARG	7.7
38	RS	108	GLY	7.6
50	R4	52	THR	7.6
14	XN	2	ALA	7.6
28	RE	204	ALA	7.6
25	RA	883	G	7.6
25	RA	2115	G	7.6
25	YA	1056	G	7.6
1	XA	1001	G	7.6
25	RA	2124	G	7.6
25	RA	2160	G	7.6
25	YA	2170	A	7.5
25	RA	1058	G	7.5
29	YF	133	ASN	7.5
25	YA	2795	G	7.5
25	RA	1087	G	7.5
25	YA	1092	C	7.5
45	RZ	9	TYR	7.5
1	QA	1003	G	7.5
1	QA	1542	U	7.5
25	RA	1059	G	7.4
35	RP	150	ALA	7.4
25	YA	2102	U	7.4
44	YY	90	LEU	7.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
25	YA	1073	A	7.4
46	Y0	85	ALA	7.4
25	RA	2159	G	7.4
25	YA	1086	A	7.4
25	YA	2144	U	7.4
25	YA	2791	C	7.3
23	XX	12	A	7.3
25	YA	1055	G	7.3
25	YA	11	G	7.3
29	YF	12	LEU	7.3
25	RA	2132	U	7.3
25	YA	1104	C	7.3
25	YA	2175	C	7.2
10	QJ	77	PRO	7.2
25	YA	1065	U	7.2
25	RA	2161	C	7.2
1	XA	1025	U	7.2
25	RA	2143	C	7.2
54	Y8	65	GLU	7.1
21	XU	26	LYS	7.1
25	YA	1064	C	7.1
25	RA	2178	C	7.1
31	RH	33	LEU	7.1
25	RA	1088	A	7.1
52	R6	14	THR	7.1
23	XX	11	U	7.1
52	R6	22	ALA	7.1
25	YA	1062	G	7.1
25	RA	2176	A	7.0
25	YA	2128	C	7.0
31	YH	33	LEU	7.0
25	YA	2150	U	7.0
50	Y4	47	GLN	7.0
50	Y4	52	THR	7.0
52	Y6	47	THR	7.0
25	RA	2123	G	7.0
38	YS	111	GLU	7.0
25	RA	1070	A	7.0
11	QK	128	ALA	7.0
47	R1	95	LEU	7.0
21	QU	2	GLY	6.9
25	YA	2182	G	6.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
25	YA	2167	U	6.9
50	Y4	40	HIS	6.9
25	RA	2803	C	6.9
31	RH	34	GLU	6.9
25	RA	2177	C	6.8
25	RA	2147	G	6.8
25	YA	2101	G	6.8
52	R6	38	LYS	6.8
25	YA	2803	C	6.8
2	QB	6	THR	6.8
2	QB	188	ALA	6.8
25	YA	1071	G	6.8
12	QL	129	ALA	6.8
25	RA	2892	A	6.8
25	RA	2795	G	6.7
39	RT	2	ASN	6.7
25	YA	2180	U	6.7
25	YA	2171	A	6.7
52	Y6	37	ARG	6.7
25	YA	2162	G	6.7
29	YF	2	LYS	6.7
25	RA	2804	C	6.7
52	Y6	45	LYS	6.7
7	QG	2	ALA	6.7
50	R4	66	SER	6.7
25	RA	1072	C	6.7
2	XB	232	PRO	6.6
45	RZ	107	THR	6.6
25	YA	2163	C	6.6
25	YA	1094	U	6.6
25	YA	2798	C	6.6
25	YA	2131	G	6.6
9	QI	15	ALA	6.6
2	XB	5	ILE	6.6
25	YA	2142	C	6.5
50	Y4	24	THR	6.5
50	R4	60	GLN	6.5
38	RS	109	GLY	6.5
1	XA	1450	U	6.5
11	XK	128	ALA	6.5
1	XA	1006	C	6.5
1	QA	1033	G	6.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
25	RA	2163	C	6.5
25	YA	1072	C	6.5
52	Y6	39	TYR	6.4
1	QA	1002	G	6.4
25	RA	2104	G	6.4
10	QJ	31	GLY	6.4
25	RA	1067	A	6.4
25	YA	1100	C	6.4
20	QT	99	LEU	6.4
18	QR	20	ALA	6.4
25	RA	2802	G	6.4
2	XB	123	ALA	6.3
10	XJ	35	SER	6.3
39	YT	2	ASN	6.3
16	XP	84	ALA	6.3
1	XA	1542	U	6.3
45	RZ	140	ASP	6.3
7	QG	85	TYR	6.3
52	R6	53	LYS	6.3
25	YA	362	U	6.3
13	QM	47	ASP	6.3
25	YA	1074	G	6.3
10	XJ	93	GLY	6.3
1	XA	1036	G	6.3
25	YA	2105	C	6.3
2	XB	233	SER	6.3
38	RS	111	GLU	6.3
25	RA	1079	C	6.2
9	XI	23	ASN	6.2
52	R6	43	CYS	6.2
25	YA	2895	U	6.2
53	R7	49	ARG	6.2
30	YG	26	GLN	6.2
2	XB	229	VAL	6.2
25	RA	2166	G	6.2
1	XA	1541	U	6.2
31	RH	104	GLU	6.2
25	RA	2107	C	6.2
47	R1	98	LEU	6.2
1	XA	1451	A	6.1
40	RU	90	VAL	6.1
1	QA	1034	G	6.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
25	YA	1090	U	6.1
9	XI	1	MET	6.1
25	RA	2805	G	6.1
31	RH	98	LEU	6.1
45	RZ	154	ASP	6.1
25	YA	2807	G	6.1
44	RY	52	SER	6.1
25	YA	1095	A	6.1
25	RA	2792	G	6.1
1	XA	208	U	6.1
25	YA	2125	G	6.0
31	RH	21	PRO	6.0
1	QA	1001	G	6.0
25	YA	2148	G	6.0
25	RA	895	U	6.0
52	Y6	21	TYR	6.0
25	RA	2139	C	6.0
48	Y2	71	ASN	6.0
25	RA	2151	G	6.0
52	R6	39	TYR	6.0
25	YA	1081	U	6.0
1	XA	1030	C	6.0
1	QA	1032	A	5.9
1	QA	1032(B)	G	5.9
1	QA	1039	C	5.9
25	RA	2896	C	5.9
25	YA	2188	C	5.9
44	YY	58	GLY	5.9
20	QT	100	ILE	5.8
44	RY	47	LYS	5.8
11	QK	127	LYS	5.8
1	XA	1041	A	5.8
31	RH	3	ARG	5.8
45	YZ	148	ASP	5.7
25	YA	1102	C	5.7
1	QA	1451	A	5.7
25	YA	2804	C	5.7
2	QB	163	PHE	5.7
9	QI	5	TYR	5.7
55	R9	9	ARG	5.7
25	RA	1098	A	5.6
25	YA	2805	G	5.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
31	YH	81	GLU	5.6
50	Y4	63	TYR	5.6
54	Y8	64	TYR	5.6
25	RA	2101	G	5.6
25	RA	894	C	5.6
51	R5	58	LEU	5.6
7	XG	82	GLY	5.6
19	XS	18	LYS	5.6
25	RA	2797	U	5.6
7	QG	81	GLY	5.6
1	QA	1533	C	5.5
8	XH	1	MET	5.5
25	YA	1085	A	5.5
21	XU	4	GLY	5.5
2	QB	136	VAL	5.5
2	QB	30	ARG	5.5
25	RA	2103	C	5.5
1	QA	1534	A	5.5
25	YA	1176	G	5.5
25	RA	897	C	5.5
25	RA	2138	C	5.5
25	YA	275	G	5.5
25	YA	1101	U	5.5
55	R9	17	ILE	5.5
19	XS	33	THR	5.5
1	XA	1005	A	5.5
25	RA	2154	G	5.4
9	QI	1	MET	5.4
1	XA	92	G	5.4
10	QJ	83	GLU	5.4
25	YA	1536	A	5.4
25	RA	2798	C	5.4
46	R0	85	ALA	5.4
1	QA	1138	G	5.4
25	RA	1103	A	5.4
25	RA	2108	C	5.4
1	XA	1031	G	5.4
21	XU	2	GLY	5.3
23	QX	12	A	5.3
25	RA	2893	G	5.3
44	RY	103	GLY	5.3
52	R6	13	CYS	5.3

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Mol	Chain	Res	Type	RSRZ
51	R5	53	ALA	5.3
25	YA	2164	C	5.3
21	XU	18	TYR	5.3
2	XB	235	SER	5.3
21	QU	10	ARG	5.3
1	QA	1036	G	5.3
31	RH	50	VAL	5.3
1	XA	1145	C	5.3
21	XU	14	TRP	5.3
7	XG	76	ARG	5.3
1	QA	1040	U	5.3
1	XA	466	C	5.3
25	RA	1097	U	5.2
25	YA	2118	U	5.2
1	QA	64	G	5.2
25	RA	2794	C	5.2
3	QC	79	ARG	5.2
52	Y6	42	TRP	5.2
1	XA	1032(A)	G	5.2
25	RA	2894	G	5.2
2	QB	140	HIS	5.2
52	Y6	46	HIS	5.2
25	RA	1084	A	5.2
8	QH	1	MET	5.2
35	RP	64	LYS	5.2
9	QI	7	THR	5.2
52	R6	51	GLU	5.1
9	QI	17	VAL	5.1
52	R6	45	LYS	5.1
1	QA	1031	G	5.1
1	XA	1032(B)	G	5.1
19	XS	36	ARG	5.1
25	RA	2106	G	5.1
44	YY	103	GLY	5.1
25	RA	2153	G	5.1
10	XJ	72	VAL	5.1
1	QA	1029	G	5.0
35	RP	13	ASN	5.0
25	RA	1045	A	5.0
25	RA	1093	G	5.0
21	XU	24	ARG	5.0
25	RA	1085	A	5.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
20	XT	9	ASN	5.0
1	XA	1539	C	5.0
50	Y4	53	GLU	5.0
39	RT	135	ALA	5.0
21	XU	9	ARG	5.0
31	RH	103	LEU	5.0
23	QX	6	G	5.0
10	QJ	54	PHE	5.0
51	R5	59	GLU	5.0
1	QA	1028(A)	C	5.0
52	Y6	38	LYS	5.0
25	YA	1077	A	5.0
13	QM	9	ILE	5.0
55	Y9	37	GLY	5.0
31	RH	109	PHE	5.0
7	XG	152	ALA	5.0
31	YH	15	VAL	5.0
52	R6	37	ARG	4.9
23	QX	7	G	4.9
31	RH	44	VAL	4.9
51	R5	60	VAL	4.9
25	YA	1091	G	4.9
31	RH	6	ARG	4.9
25	RA	2122	U	4.9
32	RI	76	THR	4.9
25	RA	1544	C	4.9
20	QT	9	ASN	4.9
29	RF	14	PRO	4.9
36	RQ	140	ALA	4.9
1	XA	1023	G	4.9
25	RA	1105	U	4.9
31	RH	102	ALA	4.9
23	XX	13	A	4.9
25	RA	1053	C	4.8
25	RA	2182	G	4.8
9	QI	8	GLY	4.8
52	Y6	20	ASN	4.8
28	RE	59	VAL	4.8
45	RZ	108	PRO	4.8
23	XX	5	A	4.8
2	QB	165	VAL	4.8
2	QB	5	ILE	4.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	XB	30	ARG	4.8
1	QA	1006	C	4.8
7	XG	78	ARG	4.8
9	QI	88	TYR	4.8
2	QB	202	PRO	4.8
39	YT	1	MET	4.8
1	QA	1032(A)	G	4.8
21	QU	26	LYS	4.8
1	QA	1025	U	4.8
1	QA	1042	G	4.8
55	R9	34	GLN	4.8
2	QB	80	ILE	4.8
9	QI	16	ARG	4.8
52	R6	46	HIS	4.8
44	RY	46	LYS	4.8
44	YY	47	LYS	4.8
23	QX	13	A	4.8
25	RA	881	G	4.8
2	QB	135	GLN	4.7
25	YA	276	A	4.7
25	RA	1044	G	4.7
45	RZ	174	VAL	4.7
1	QA	65	U	4.7
7	QG	5	ARG	4.7
25	RA	1080	C	4.7
9	QI	4	TYR	4.7
22	QV	47	U	4.7
2	QB	70	PHE	4.7
7	XG	32	ARG	4.7
2	QB	232	PRO	4.7
38	RS	112	PHE	4.7
11	QK	11	LYS	4.7
19	XS	49	ILE	4.7
40	YU	91	ASP	4.7
1	XA	1042	G	4.7
7	QG	82	GLY	4.7
9	QI	3	GLN	4.6
9	QI	65	VAL	4.6
25	YA	896	A	4.6
25	RA	2105	C	4.6
1	QA	1041	A	4.6
1	XA	1000	A	4.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
28	RE	69	LYS	4.6
1	QA	1028(B)	C	4.6
25	YA	1174	A	4.6
25	RA	896	A	4.6
1	QA	1137	C	4.6
50	Y4	39	CYS	4.6
9	QI	14	VAL	4.6
2	QB	9	GLU	4.6
45	RZ	144	LEU	4.6
25	RA	1094	U	4.6
25	RA	1104	C	4.6
23	QX	10	G	4.6
38	RS	51	ALA	4.6
20	XT	98	PRO	4.6
25	YA	1177	A	4.6
9	QI	66	ARG	4.6
45	RZ	148	ASP	4.6
7	XG	79	ARG	4.6
18	XR	18	ARG	4.6
25	RA	893	C	4.5
1	QA	220	G	4.5
32	RI	50	ARG	4.5
25	RA	882	G	4.5
54	R8	65	GLU	4.5
52	Y6	36	LEU	4.5
10	QJ	84	GLN	4.5
25	RA	2150	U	4.5
25	RA	2895	U	4.5
52	R6	49	HIS	4.5
47	Y1	96	LYS	4.5
55	R9	8	LYS	4.5
2	QB	218	ALA	4.5
25	RA	362	U	4.5
25	RA	2807	G	4.5
10	QJ	28	ARG	4.5
9	XI	12	GLU	4.5
25	RA	1069	A	4.5
45	RZ	104	PHE	4.5
2	QB	192	SER	4.5
29	YF	128	ALA	4.5
35	YP	13	ASN	4.5
50	Y4	42	PHE	4.5

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Mol	Chain	Res	Type	RSRZ
32	YI	57	ARG	4.5
19	QS	5	LEU	4.5
1	QA	1028	C	4.5
25	RA	884	C	4.4
25	RA	2808	U	4.4
25	YA	1171	G	4.4
25	YA	2132	U	4.4
47	Y1	97	LEU	4.4
9	QI	9	ARG	4.4
30	YG	137	GLU	4.4
25	YA	1082	U	4.4
40	YU	90	VAL	4.4
25	YA	2103	C	4.4
25	YA	2629	A	4.4
38	YS	110	LEU	4.4
1	XA	1034	G	4.4
19	QS	21	GLU	4.4
25	YA	2147	G	4.4
50	R4	64	GLY	4.4
2	QB	201	ILE	4.3
25	RA	1054	A	4.3
25	RA	2833	G	4.3
45	YZ	9	TYR	4.3
36	YQ	91	GLU	4.3
55	R9	4	ARG	4.3
50	R4	24	THR	4.3
2	QB	214	ILE	4.3
19	XS	30	LEU	4.3
35	YP	63	PRO	4.3
25	RA	885	C	4.3
25	RA	1074	G	4.3
9	XI	7	THR	4.2
25	RA	2793	G	4.2
1	QA	1000	A	4.2
25	YA	2794	C	4.2
2	QB	217	ARG	4.2
52	Y6	50	ARG	4.2
9	XI	3	GLN	4.2
21	QU	17	THR	4.2
25	YA	1083	U	4.2
2	XB	9	GLU	4.2
22	QV	16	C	4.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
14	QN	18	VAL	4.2
44	RY	99	CYS	4.2
25	RA	270(O)	U	4.2
10	QJ	40	LEU	4.2
1	XA	1032	A	4.2
19	XS	31	ILE	4.2
9	QI	11	LYS	4.2
25	YA	1537	C	4.2
25	YA	277	C	4.2
25	RA	1081	U	4.2
10	XJ	38	ILE	4.2
38	RS	35	ILE	4.2
52	Y6	13	CYS	4.1
31	RH	97	ARG	4.1
50	R4	69	LYS	4.1
19	QS	52	TYR	4.1
52	Y6	49	HIS	4.1
1	QA	1136	U	4.1
5	XE	2	PRO	4.1
45	RZ	151	HIS	4.1
2	XB	29	ALA	4.1
48	Y2	43	GLN	4.1
20	QT	105	SER	4.1
7	QG	80	VAL	4.1
30	YG	182	LYS	4.1
31	RH	136	ILE	4.1
25	YA	1498	C	4.1
7	XG	5	ARG	4.1
30	RG	74	LYS	4.1
9	QI	64	THR	4.1
55	R9	36	GLN	4.1
20	QT	50	GLU	4.1
32	YI	112	LYS	4.1
9	QI	18	PHE	4.1
45	RZ	2	GLU	4.1
1	QA	1023	G	4.1
21	XU	6	ARG	4.1
25	RA	278	A	4.1
25	YA	1535	U	4.1
22	QV	48	C	4.1
25	RA	2100	G	4.1
13	XM	119	GLY	4.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
25	RA	1086	A	4.1
55	R9	6	SER	4.1
1	QA	1140	C	4.1
2	QB	211	ILE	4.1
25	RA	2152	G	4.1
21	XU	25	LYS	4.0
1	QA	984	C	4.0
28	YE	203	LYS	4.0
2	XB	228	GLY	4.0
25	RA	1535	U	4.0
29	YF	25	PRO	4.0
31	RH	27	LYS	4.0
39	YT	137	LYS	4.0
1	QA	1141	C	4.0
2	QB	29	ALA	4.0
25	RA	1100	C	4.0
2	QB	193	ASP	4.0
25	YA	2797	U	4.0
1	QA	1269	A	4.0
1	QA	68	G	4.0
1	XA	79	G	4.0
9	QI	23	ASN	4.0
1	QA	1043	C	4.0
25	YA	2145	C	4.0
31	RH	20	ALA	4.0
46	Y0	84	LEU	4.0
50	R4	55	ARG	4.0
25	YA	1075	C	4.0
10	QJ	32	ALA	4.0
9	QI	63	ILE	4.0
21	XU	5	ASP	4.0
10	XJ	34	VAL	4.0
10	XJ	92	THR	4.0
19	QS	72	GLY	3.9
45	RZ	59	LEU	3.9
19	XS	71	LEU	3.9
1	XA	1029	G	3.9
19	XS	14	HIS	3.9
2	XB	230	VAL	3.9
7	QG	34	GLY	3.9
52	R6	12	GLU	3.9
38	RS	33	LYS	3.9

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Mol	Chain	Res	Type	RSRZ
51	R5	56	LYS	3.9
7	QG	53	LYS	3.9
1	QA	1135	U	3.9
1	QA	1283	G	3.9
1	XA	1124	G	3.9
25	RA	2897	U	3.9
50	R4	62	ARG	3.9
2	QB	207	ALA	3.9
19	XS	48	THR	3.9
25	YA	654(V)	A	3.9
1	QA	1005	A	3.9
19	XS	52	TYR	3.9
7	QG	33	ASP	3.9
51	Y5	58	LEU	3.9
1	QA	1139	G	3.9
23	XX	22	U	3.8
32	YI	142	VAL	3.8
47	Y1	98	LEU	3.8
44	RY	55	TYR	3.8
10	QJ	30	SER	3.8
7	QG	124	LEU	3.8
21	QU	8	THR	3.8
11	QK	40	ILE	3.8
32	RI	60	GLU	3.8
7	QG	32	ARG	3.8
1	QA	999	U	3.8
25	RA	280	C	3.8
1	XA	1021	G	3.8
31	RH	116	GLU	3.8
41	RV	45	THR	3.8
2	QB	236	TYR	3.8
25	YA	2896	C	3.8
7	XG	156	TRP	3.8
13	XM	26	GLY	3.8
32	YI	76	THR	3.8
52	Y6	48	VAL	3.8
25	RA	645	C	3.8
52	Y6	35	GLU	3.8
1	XA	1022	G	3.8
10	QJ	79	ARG	3.8
25	YA	2149	G	3.8
41	YV	86	GLY	3.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
9	XI	11	LYS	3.8
25	RA	2477	C	3.8
38	RS	52	SER	3.8
25	RA	1083	U	3.8
1	QA	663	A	3.8
45	YZ	107	THR	3.8
45	RZ	139	VAL	3.8
29	YF	165	ARG	3.7
2	XB	215	LEU	3.7
25	YA	2106	G	3.7
21	XU	10	ARG	3.7
55	R9	18	ARG	3.7
25	YA	1733	G	3.7
1	XA	1035	A	3.7
50	R4	22	ILE	3.7
13	XM	102	ARG	3.7
25	YA	1076	C	3.7
30	YG	178	PHE	3.7
31	RH	78	GLY	3.7
45	RZ	28	MET	3.7
10	QJ	27	ALA	3.7
9	XI	14	VAL	3.7
19	XS	72	GLY	3.7
44	RY	54	LYS	3.7
2	QB	73	THR	3.7
2	QB	81	VAL	3.7
2	XB	8	LYS	3.7
25	RA	1102	C	3.7
25	RA	2142	C	3.7
2	QB	187	LEU	3.7
35	RP	65	ARG	3.7
1	XA	1040	U	3.7
2	QB	189	ASP	3.7
52	R6	52	VAL	3.7
1	QA	746	A	3.7
45	RZ	50	GLN	3.7
48	R2	51	ARG	3.7
1	QA	93	U	3.6
10	XJ	54	PHE	3.6
25	RA	2402	C	3.6
26	RB	4	C	3.6
52	R6	48	VAL	3.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	XB	128	GLU	3.6
31	RH	128	PRO	3.6
2	XB	68	ILE	3.6
31	YH	155	SER	3.6
35	YP	65	ARG	3.6
2	XB	81	VAL	3.6
2	XB	231	GLU	3.6
9	QI	104	ARG	3.6
3	QC	78	GLY	3.6
44	RY	86	ARG	3.6
25	YA	1913	A	3.6
11	XK	9	LYS	3.6
9	XI	5	TYR	3.6
3	XC	80	GLY	3.6
19	XS	32	LYS	3.6
25	YA	2190	G	3.6
9	QI	92	TYR	3.6
25	RA	2629	A	3.6
52	Y6	14	THR	3.6
38	RS	34	HIS	3.6
1	XA	391	G	3.6
25	RA	1537	C	3.6
1	QA	1302	U	3.6
1	XA	93	U	3.6
38	RS	37	ALA	3.6
2	XB	220	ASP	3.6
23	QX	9	G	3.6
25	RA	880	G	3.6
25	RA	1106	G	3.6
54	Y8	63	PRO	3.6
50	R4	65	ASP	3.6
25	RA	1536	A	3.6
1	QA	66	G	3.6
23	XX	10	G	3.6
15	XO	7	GLU	3.6
54	R8	40	GLU	3.6
50	R4	39	CYS	3.6
20	QT	103	GLY	3.6
38	RS	110	LEU	3.6
47	R1	94	LEU	3.6
31	YH	4	ILE	3.5
30	YG	34	LEU	3.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
41	YV	85	LYS	3.5
44	RY	60	PHE	3.5
25	RA	2099	U	3.5
15	QO	69	TYR	3.5
23	QX	8	A	3.5
25	YA	2402	C	3.5
1	QA	1148	U	3.5
3	XC	62	ASP	3.5
25	RA	279	C	3.5
9	QI	106	ALA	3.5
25	YA	270(Z)	U	3.5
20	QT	64	ASP	3.5
25	RA	11	G	3.5
10	XJ	40	LEU	3.5
38	YS	2	ALA	3.5
45	RZ	8	TYR	3.5
1	QA	993	G	3.5
35	RP	145	PRO	3.5
5	QE	155	GLU	3.5
28	YE	60	ASN	3.5
45	RZ	150	LEU	3.5
19	QS	25	LYS	3.5
1	QA	1371	G	3.5
25	RA	277	C	3.5
25	YA	1106	G	3.5
13	QM	118	ALA	3.5
45	RZ	63	ASP	3.5
1	QA	1540	U	3.5
2	XB	71	VAL	3.5
2	XB	96	ARG	3.5
2	XB	217	ARG	3.5
24	XY	49	GLN	3.4
28	YE	54	GLN	3.4
48	R2	43	GLN	3.4
9	XI	88	TYR	3.4
25	RA	361	G	3.4
41	YV	1	MET	3.4
1	QA	221	C	3.4
25	RA	1498	C	3.4
1	XA	1033	G	3.4
10	XJ	17	ASP	3.4
52	R6	42	TRP	3.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
38	RS	105	ALA	3.4
25	RA	654(S)	G	3.4
44	YY	17	SER	3.4
27	RD	26	LYS	3.4
2	QB	16	HIS	3.4
10	QJ	85	LEU	3.4
1	XA	999	U	3.4
21	XU	21	TYR	3.4
32	RI	54	GLN	3.4
13	XM	84	ILE	3.4
7	XG	87	VAL	3.4
26	YB	81	G	3.4
52	Y6	44	ARG	3.4
29	RF	208	GLY	3.4
1	XA	3	G	3.4
25	RA	363	G	3.4
25	YA	1053	C	3.4
13	QM	17	VAL	3.4
2	QB	108	ILE	3.4
38	RS	27	SER	3.4
18	QR	19	LYS	3.4
25	YA	1105	U	3.4
50	R4	58	ARG	3.4
53	Y7	49	ARG	3.4
30	YG	97	ASP	3.4
25	RA	1091	G	3.4
1	XA	182	U	3.3
25	RA	1913	A	3.3
16	XP	13	HIS	3.3
19	XS	9	VAL	3.3
45	YZ	108	PRO	3.3
10	XJ	73	ASP	3.3
41	YV	70	ILE	3.3
15	XO	74	ASP	3.3
45	RZ	117	LEU	3.3
10	QJ	101	VAL	3.3
30	YG	37	VAL	3.3
2	XB	222	ILE	3.3
7	XG	3	ARG	3.3
19	QS	75	ALA	3.3
31	RH	101	ARG	3.3
4	XD	156	GLU	3.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
25	YA	2630	G	3.3
20	QT	49	ALA	3.3
50	R4	40	HIS	3.3
45	RZ	145	GLU	3.3
1	QA	1038	C	3.3
25	YA	1734	C	3.3
2	XB	122	PHE	3.3
19	XS	75	ALA	3.3
2	QB	99	GLY	3.3
19	QS	4	SER	3.3
32	YI	79	ILE	3.3
50	Y4	12	ALA	3.3
1	QA	95	G	3.3
25	YA	2100	G	3.3
52	R6	47	THR	3.3
2	QB	41	ILE	3.3
30	RG	88	ILE	3.3
21	XU	15	ARG	3.3
11	XK	10	VAL	3.3
21	XU	8	THR	3.3
2	XB	87	ARG	3.3
31	YH	124	GLU	3.3
7	XG	154	TYR	3.3
2	QB	40	HIS	3.3
25	RA	1112	G	3.3
44	YY	102	CYS	3.3
21	QU	5	ASP	3.3
52	R6	36	LEU	3.3
31	RH	29	PRO	3.2
51	R5	54	GLY	3.2
25	YA	10	G	3.2
55	R9	7	VAL	3.2
30	RG	2	PRO	3.2
25	RA	1095	A	3.2
50	Y4	44	THR	3.2
35	RP	61	ARG	3.2
25	RA	2141	G	3.2
10	XJ	39	PRO	3.2
51	Y5	53	ALA	3.2
7	QG	125	MET	3.2
2	QB	209	ARG	3.2
25	RA	2481	G	3.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	QB	109	SER	3.2
25	RA	2102	U	3.2
18	XR	88	LYS	3.2
35	YP	64	LYS	3.2
9	XI	20	ARG	3.2
28	RE	76	ARG	3.2
1	XA	95	G	3.2
25	YA	2373	G	3.2
32	YI	78	THR	3.2
50	R4	3	GLU	3.2
13	XM	114	ARG	3.2
21	QU	22	ARG	3.2
25	RA	1463	C	3.2
51	Y5	57	VAL	3.2
27	RD	34	VAL	3.2
1	QA	1037	C	3.2
2	QB	196	LEU	3.2
44	YY	83	THR	3.2
19	XS	47	HIS	3.2
32	RI	66	GLU	3.2
1	QA	1259	C	3.2
1	XA	1028(B)	C	3.2
19	XS	34	TRP	3.2
44	RY	78	ALA	3.2
52	Y6	22	ALA	3.2
19	QS	38	SER	3.2
1	QA	1030	C	3.1
25	YA	1577	C	3.1
25	YA	2183	C	3.1
31	YH	109	PHE	3.1
4	QD	42	GLN	3.1
7	QG	84	ASN	3.1
11	QK	14	VAL	3.1
19	QS	53	ASN	3.1
20	QT	67	ALA	3.1
19	XS	69	HIS	3.1
54	R8	64	TYR	3.1
55	R9	20	HIS	3.1
1	QA	1261	A	3.1
1	XA	181	G	3.1
22	QV	1	C	3.1
25	YA	2664	G	3.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
10	QJ	33	GLN	3.1
31	YH	46	GLU	3.1
10	XJ	78	ASN	3.1
2	QB	213	LEU	3.1
29	YF	10	PRO	3.1
1	XA	1493	A	3.1
21	XU	3	LYS	3.1
25	RA	1047	G	3.1
25	RA	1092	C	3.1
38	RS	68	GLN	3.1
2	QB	101	MET	3.1
50	R4	18	CYS	3.1
7	QG	64	GLN	3.1
25	YA	1496	A	3.1
1	XA	1027	C	3.1
1	XA	1149	C	3.1
2	QB	139	LYS	3.1
1	QA	961	U	3.1
1	QA	1020	U	3.1
25	YA	2837	G	3.1
2	QB	229	VAL	3.1
5	XE	5	ASP	3.1
45	YZ	87	ASP	3.1
9	QI	96	LEU	3.1
25	RA	2791	C	3.1
25	YA	270(K)	C	3.1
50	R4	71	ARG	3.1
1	QA	69	G	3.1
1	QA	1126	U	3.1
1	XA	951	G	3.1
2	QB	215	LEU	3.1
2	XB	216	SER	3.1
19	QS	78	ARG	3.1
50	R4	59	PHE	3.1
1	XA	1538	C	3.1
52	R6	24	GLU	3.1
1	XA	1532	U	3.1
55	R9	24	TYR	3.1
16	XP	12	LYS	3.1
10	QJ	86	MET	3.1
1	QA	983	A	3.1
13	QM	99	ARG	3.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
31	YH	170	ARG	3.1
32	YI	75	LEU	3.1
41	YV	44	LYS	3.0
18	QR	18	ARG	3.0
25	RA	360	G	3.0
2	XB	125	PRO	3.0
25	RA	1049	C	3.0
25	YA	2146	C	3.0
3	XC	98	ASN	3.0
9	QI	126	SER	3.0
27	RD	30	GLU	3.0
1	QA	1541	U	3.0
13	XM	105	THR	3.0
44	YY	50	ARG	3.0
7	QG	101	LEU	3.0
1	QA	1035	A	3.0
10	XJ	94	VAL	3.0
25	RA	1048	A	3.0
25	YA	1509	C	3.0
7	QG	62	PHE	3.0
45	RZ	152	ALA	3.0
41	YV	53	GLU	3.0
44	RY	53	PRO	3.0
10	QJ	29	ARG	3.0
44	YY	86	ARG	3.0
25	YA	883	G	3.0
25	YA	895	U	3.0
21	QU	3	LYS	3.0
10	XJ	98	ILE	3.0
1	QA	1159	U	3.0
1	QA	1313	U	3.0
25	RA	2140	C	3.0
25	YA	270(L)	U	3.0
29	RF	11	VAL	3.0
1	QA	92	G	3.0
25	RA	1042	G	3.0
25	YA	1054	A	3.0
2	QB	235	SER	3.0
38	RS	53	SER	3.0
1	QA	75	C	3.0
54	Y8	40	GLU	3.0
2	QB	233	SER	3.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
3	QC	161	GLU	3.0
31	RH	75	ALA	3.0
4	XD	35	ARG	3.0
31	RH	15	VAL	3.0
19	QS	57	HIS	3.0
19	XS	50	ALA	3.0
25	RA	2183	C	3.0
30	YG	108	ASN	3.0
32	YI	143	SER	3.0
35	RP	74	GLU	3.0
25	RA	1082	U	2.9
25	YA	12	U	2.9
31	YH	153	LYS	2.9
3	XC	161	GLU	2.9
19	QS	37	ARG	2.9
19	QS	15	LEU	2.9
32	RI	45	LYS	2.9
25	RA	1448	G	2.9
10	QJ	5	ARG	2.9
1	QA	1314	C	2.9
2	QB	228	GLY	2.9
1	QA	1312	G	2.9
2	XB	90	MET	2.9
25	YA	1173	G	2.9
4	XD	26	CYS	2.9
28	YE	69	LYS	2.9
28	YE	77	ILE	2.9
45	RZ	34	ASN	2.9
13	QM	20	THR	2.9
25	RA	1052	C	2.9
1	QA	152	A	2.9
1	QA	1288	A	2.9
10	XJ	8	LEU	2.9
44	RY	84	ARG	2.9
1	QA	190	G	2.9
2	QB	166	ASP	2.9
2	QB	208	ILE	2.9
25	YA	2891	G	2.9
50	Y4	7	PRO	2.9
45	RZ	5	LEU	2.9
1	QA	222	U	2.9
2	QB	167	PRO	2.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
25	RA	1051	G	2.9
25	RA	1073	A	2.9
2	QB	185	ILE	2.9
52	Y6	17	LYS	2.9
2	QB	79	ASP	2.9
19	XS	17	GLU	2.9
25	YA	2347	C	2.9
9	QI	67	GLY	2.9
2	QB	190	THR	2.9
19	XS	15	LEU	2.9
31	YH	136	ILE	2.9
7	XG	2	ALA	2.9
19	XS	29	ARG	2.9
38	RS	20	ARG	2.9
32	RI	34	GLY	2.9
9	XI	56	LEU	2.9
31	RH	114	VAL	2.9
36	YQ	90	VAL	2.9
51	R5	57	VAL	2.9
29	YF	175	THR	2.9
1	QA	1453	G	2.9
33	YN	8	GLN	2.9
13	XM	16	ASP	2.9
55	R9	2	LYS	2.9
19	QS	26	GLY	2.9
20	QT	73	HIS	2.9
9	XI	64	THR	2.8
5	QE	60	TYR	2.8
25	RA	270(B)	A	2.8
25	YA	2834	G	2.8
29	YF	139	PHE	2.8
38	YS	41	ASP	2.8
2	QB	200	ILE	2.8
10	XJ	6	ILE	2.8
1	XA	1286	A	2.8
25	RA	229	A	2.8
44	YY	88	LYS	2.8
2	QB	210	SER	2.8
25	RA	1107	G	2.8
29	YF	167	ALA	2.8
1	QA	1212	U	2.8
32	RI	6	LEU	2.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
4	QD	26	CYS	2.8
1	QA	1324	A	2.8
16	XP	11	SER	2.8
48	Y2	70	GLN	2.8
1	QA	836	G	2.8
1	QA	991	U	2.8
25	RA	1113	U	2.8
30	YG	156	ASP	2.8
1	QA	1452	C	2.8
11	QK	37	GLY	2.8
25	RA	1449	A	2.8
2	QB	231	GLU	2.8
31	RH	58	GLU	2.8
2	QB	33	TYR	2.8
48	Y2	55	ARG	2.8
11	XK	14	VAL	2.8
19	XS	73	GLU	2.8
25	RA	1529	A	2.8
35	RP	70	GLN	2.8
1	XA	91	C	2.8
36	RQ	90	VAL	2.8
38	RS	40	ILE	2.8
33	RN	1	MET	2.8
10	XJ	55	LYS	2.8
27	YD	38	LYS	2.8
44	RY	2	ARG	2.8
1	XA	209	U	2.8
38	YS	18	ILE	2.8
1	QA	1242	C	2.8
8	QH	102	ARG	2.8
19	XS	21	GLU	2.8
29	RF	18	ARG	2.8
2	QB	69	LEU	2.8
30	YG	82	LEU	2.8
25	RA	1090	U	2.8
25	RA	1587	A	2.8
25	RA	2790	A	2.8
29	RF	133	ASN	2.8
41	RV	38	LEU	2.8
1	QA	1222	G	2.8
25	YA	273	G	2.8
31	RH	152	ARG	2.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
31	RH	64	LEU	2.8
32	YI	101	LEU	2.8
39	YT	106	SER	2.8
50	R4	17	GLY	2.8
1	QA	67	C	2.8
1	QA	381	C	2.8
1	XA	590	C	2.8
18	QR	68	LYS	2.8
25	RA	888	C	2.8
30	RG	87	PRO	2.8
45	RZ	46	LYS	2.8
25	RA	1101	U	2.7
25	RA	2190	G	2.7
45	YZ	117	LEU	2.7
3	XC	23	TYR	2.7
20	QT	66	ALA	2.7
2	XB	211	ILE	2.7
10	XJ	37	PRO	2.7
37	RR	66	VAL	2.7
9	QI	2	GLU	2.7
1	QA	1243	C	2.7
25	YA	2343	C	2.7
19	QS	44	MET	2.7
1	XA	210	U	2.7
24	XY	52	LYS	2.7
2	XB	163	PHE	2.7
25	YA	270(I)	G	2.7
32	RI	49	ALA	2.7
38	RS	2	ALA	2.7
30	YG	39	ILE	2.7
44	YY	79	CYS	2.7
44	RY	59	GLY	2.7
25	RA	2891	G	2.7
50	Y4	6	HIS	2.7
55	R9	3	VAL	2.7
55	R9	5	ALA	2.7
25	RA	1499	C	2.7
25	YA	2185	C	2.7
25	YA	270(M)	U	2.7
27	RD	28	GLU	2.7
7	QG	56	GLN	2.7
11	QK	12	ARG	2.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
44	YY	54	LYS	2.7
50	R4	38	LYS	2.7
14	QN	61	TRP	2.7
25	RA	2732	G	2.7
25	YA	361	G	2.7
25	YA	1084	A	2.7
25	YA	2883	A	2.7
55	R9	23	VAL	2.7
45	RZ	33	LEU	2.7
29	YF	136	THR	2.7
7	QG	78	ARG	2.7
11	XK	11	LYS	2.7
21	QU	6	ARG	2.7
38	RS	36	TYR	2.7
25	RA	1530	G	2.7
25	YA	1470	G	2.7
54	R8	63	PRO	2.7
1	QA	1147	C	2.7
1	QA	1223	C	2.7
1	QA	1260	C	2.7
2	QB	105	PHE	2.7
25	RA	1497	U	2.7
44	RY	58	GLY	2.7
4	XD	3	ARG	2.7
41	RV	36	PRO	2.7
1	XA	41	G	2.7
25	RA	2184	G	2.7
25	YA	1497	U	2.7
25	YA	1578	U	2.7
1	QA	219	C	2.7
1	XA	1038	C	2.7
4	XD	5	ILE	2.7
10	XJ	4	ILE	2.7
2	QB	100	GLY	2.7
2	QB	131	PRO	2.7
1	QA	1319	A	2.7
9	QI	110	GLU	2.7
25	YA	2632	A	2.7
52	Y6	12	GLU	2.7
1	QA	992	U	2.7
2	XB	42	ILE	2.7
1	QA	1144	G	2.7

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Mol	Chain	Res	Type	RSRZ
1	QA	1443	G	2.7
9	QI	19	LEU	2.7
10	QJ	99	LYS	2.7
25	YA	2631	G	2.7
31	YH	44	VAL	2.7
1	XA	591	U	2.7
9	QI	105	ASP	2.7
24	XY	47	ASN	2.7
45	RZ	4	ARG	2.7
25	RA	1501	C	2.7
25	RA	270(Y)	G	2.7
25	YA	2655	G	2.7
4	XD	151	LYS	2.6
24	XY	53	LEU	2.6
14	XN	13	THR	2.6
19	XS	63	THR	2.6
1	QA	1146	A	2.6
25	RA	1489	U	2.6
25	YA	2836	U	2.6
1	QA	1119	C	2.6
15	XO	2	PRO	2.6
26	RB	28	C	2.6
32	RI	134	PRO	2.6
15	QO	70	LEU	2.6
55	R9	35	ARG	2.6
9	QI	33	PHE	2.6
30	YG	116	ASP	2.6
4	XD	42	GLN	2.6
32	YI	141	LYS	2.6
2	XB	92	TYR	2.6
7	QG	59	LEU	2.6
1	QA	186(A)	C	2.6
32	RI	143	SER	2.6
1	QA	104	G	2.6
25	RA	274	G	2.6
25	YA	2184	G	2.6
10	XJ	5	ARG	2.6
38	RS	21	THR	2.6
31	RH	153	LYS	2.6
31	YH	110	SER	2.6
2	XB	224	GLN	2.6
4	XD	134	ASP	2.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
19	QS	17	GLU	2.6
32	RI	135	GLU	2.6
52	Y6	29	ASN	2.6
52	Y6	34	LEU	2.6
1	QA	1442	G	2.6
1	XA	1136	U	2.6
25	YA	2833	G	2.6
52	R6	25	LYS	2.6
19	XS	28	LYS	2.6
38	RS	87	PHE	2.6
1	XA	388	G	2.6
1	XA	1094	G	2.6
25	RA	281	G	2.6
25	RA	2479	G	2.6
25	YA	1170	G	2.6
44	YY	70	SER	2.6
25	RA	1543	A	2.6
31	RH	105	LEU	2.6
2	XB	237	ALA	2.6
31	RH	39	PRO	2.6
25	RA	1026	U	2.6
39	RT	35	LYS	2.6
44	YY	46	LYS	2.6
9	XI	66	ARG	2.6
10	QJ	43	ARG	2.6
18	XR	20	ALA	2.6
32	RI	33	ARG	2.6
1	QA	1446	A	2.6
21	XU	23	PRO	2.6
13	XM	104	ARG	2.6
10	QJ	47	PHE	2.6
13	QM	2	ALA	2.6
38	RS	86	ALA	2.6
1	QA	73	G	2.6
4	QD	2	GLY	2.6
7	QG	129	GLU	2.6
2	XB	73	THR	2.6
10	XJ	10	GLY	2.6
25	YA	1521	G	2.6
23	XX	14	A	2.6
36	YQ	10	ARG	2.6
36	YQ	83	MET	2.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
11	QK	42	TRP	2.6
2	QB	17	PHE	2.6
7	QG	150	ALA	2.6
32	RI	63	ALA	2.6
19	XS	12	ASP	2.6
30	YG	27	ASN	2.6
30	RG	82	LEU	2.6
1	QA	1120	G	2.6
1	QA	1171	G	2.6
9	QI	31	GLN	2.6
22	QV	7	G	2.6
23	XX	9	G	2.6
25	RA	75	G	2.6
1	QA	979	C	2.6
1	XA	1148	U	2.6
25	RA	1033	U	2.6
18	QR	62	GLU	2.6
45	RZ	138	GLU	2.6
50	R4	8	LYS	2.6
6	QF	90	VAL	2.6
19	QS	36	ARG	2.6
10	QJ	71	LEU	2.6
19	QS	77	THR	2.6
9	XI	36	TYR	2.5
1	QA	1271	G	2.5
1	XA	589	C	2.5
1	XA	1002	G	2.5
1	XA	1037	C	2.5
1	XA	1212	U	2.5
25	YA	1863	G	2.5
38	YS	48	LEU	2.5
2	QB	162	ILE	2.5
2	XB	70	PHE	2.5
10	XJ	79	ARG	2.5
38	YS	38	GLN	2.5
2	QB	7	VAL	2.5
15	QO	23	GLY	2.5
1	QA	356	A	2.5
1	QA	1538	C	2.5
1	XA	90	C	2.5
25	YA	1484	G	2.5
29	YF	168	ARG	2.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
30	YG	93	THR	2.5
50	Y4	60	GLN	2.5
9	QI	79	LEU	2.5
30	RG	3	LEU	2.5
8	XH	30	ARG	2.5
1	QA	1326	C	2.5
25	RA	275	G	2.5
7	XG	72	ARG	2.5
1	XA	1537	U	2.5
31	YH	111	HIS	2.5
1	QA	1145	C	2.5
25	YA	1444(A)	A	2.5
26	RB	27	C	2.5
35	RP	84	ASN	2.5
2	XB	69	LEU	2.5
9	QI	121	ARG	2.5
1	XA	42	G	2.5
21	XU	13	ILE	2.5
25	RA	1173	G	2.5
45	YZ	104	PHE	2.5
35	RP	52	GLU	2.5
44	YY	19	LYS	2.5
19	QS	39	THR	2.5
21	XU	22	ARG	2.5
33	RN	42	TRP	2.5
1	XA	1039	C	2.5
25	RA	1111	A	2.5
25	YA	1467	C	2.5
1	QA	1290	G	2.5
13	QM	102	ARG	2.5
32	RI	133	HIS	2.5
7	XG	37	ASN	2.5
24	XY	71	ASN	2.5
25	RA	2809	A	2.5
41	YV	72	VAL	2.5
30	YG	106	LEU	2.5
54	R8	46	ARG	2.5
1	XA	1144	G	2.5
10	XJ	96	ILE	2.5
25	RA	226	G	2.5
28	RE	60	ASN	2.5
19	XS	27	GLU	2.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
20	QT	51	GLU	2.5
50	Y4	34	GLU	2.5
2	XB	209	ARG	2.5
55	R9	22	ARG	2.5
7	QG	83	ALA	2.5
25	YA	653	A	2.5
45	YZ	112	ARG	2.5
1	QA	631	G	2.5
1	XA	357	G	2.5
25	RA	1154	G	2.5
16	QP	40	ASP	2.5
25	RA	270(K)	C	2.5
31	YH	60	ARG	2.5
10	XJ	69	ASN	2.5
21	XU	17	THR	2.5
38	RS	55	ALA	2.5
1	QA	1142	G	2.5
7	QG	115	ARG	2.5
15	QO	26	GLU	2.5
25	RA	1500	G	2.5
25	YA	1524	G	2.5
31	YH	132	ARG	2.5
36	RQ	91	GLU	2.5
1	QA	1019	C	2.4
1	XA	483	C	2.4
26	YB	88	C	2.4
1	QA	171	A	2.4
1	XA	1236	A	2.4
7	XG	84	ASN	2.4
25	RA	270(A)	A	2.4
25	RA	1490	A	2.4
25	YA	1762	A	2.4
29	YF	61	GLY	2.4
35	YP	62	LEU	2.4
37	RR	93	GLY	2.4
1	QA	89	U	2.4
2	QB	237	ALA	2.4
19	XS	37	ARG	2.4
42	RW	63	ASP	2.4
19	QS	32	LYS	2.4
2	QB	203	GLY	2.4
25	YA	2372	G	2.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
13	QM	18	ALA	2.4
7	QG	79	ARG	2.4
13	XM	86	CYS	2.4
44	YY	92	ASN	2.4
45	RZ	173	ALA	2.4
52	Y6	16	CYS	2.4
10	XJ	77	PRO	2.4
19	QS	76	PRO	2.4
38	RS	39	ILE	2.4
2	QB	123	ALA	2.4
2	XB	218	ALA	2.4
10	QJ	46	ARG	2.4
1	XA	43	C	2.4
1	XA	588	G	2.4
2	QB	103	THR	2.4
2	XB	6	THR	2.4
2	QB	132	LYS	2.4
25	YA	2663	G	2.4
26	YB	23	G	2.4
28	YE	62	PRO	2.4
17	XQ	101	ARG	2.4
9	QI	70	LYS	2.4
52	Y6	26	ASN	2.4
19	XS	44	MET	2.4
1	QA	1289	A	2.4
8	XH	55	GLY	2.4
31	YH	6	ARG	2.4
38	YS	49	VAL	2.4
52	R6	6	ARG	2.4
52	R6	50	ARG	2.4
10	QJ	56	HIS	2.4
9	XI	37	PHE	2.4
10	QJ	55	LYS	2.4
14	XN	10	ALA	2.4
5	QE	3	GLU	2.4
15	XO	89	GLY	2.4
19	QS	68	GLY	2.4
7	QG	153	HIS	2.4
9	QI	37	PHE	2.4
25	YA	2374	C	2.4
25	YA	2789	C	2.4
44	RY	89	PHE	2.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
22	QV	49	G	2.4
25	RA	352	G	2.4
25	YA	102	G	2.4
25	YA	1107	G	2.4
26	YB	56	G	2.4
31	YH	104	GLU	2.4
32	RI	136	VAL	2.4
48	R2	47	ASN	2.4
52	R6	8	LYS	2.4
19	XS	40	ILE	2.4
30	YG	63	ILE	2.4
1	QA	662	G	2.4
1	XA	183	G	2.4
25	RA	1114	G	2.4
25	RA	1115	G	2.4
25	YA	1042	G	2.4
31	RH	93	GLY	2.4
38	YS	109	GLY	2.4
50	R4	20	ASN	2.4
9	XI	16	ARG	2.4
11	XK	12	ARG	2.4
1	QA	1282	C	2.4
2	XB	93	VAL	2.4
6	QF	91	VAL	2.4
15	QO	24	SER	2.4
25	RA	654(G)	C	2.4
25	RA	898	C	2.4
31	RH	67	LEU	2.4
35	RP	76	LYS	2.4
21	QU	15	ARG	2.4
20	XT	64	ASP	2.4
25	YA	1485	G	2.4
2	QB	102	LEU	2.4
25	YA	270(O)	U	2.4
29	RF	20	LEU	2.4
30	YG	55	LYS	2.4
45	YZ	70	LEU	2.4
10	QJ	24	VAL	2.4
2	QB	152	PHE	2.4
28	RE	54	GLN	2.4
30	YG	155	MET	2.4
33	YN	131	GLN	2.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
38	RS	50	SER	2.4
4	XD	47	ARG	2.4
48	R2	55	ARG	2.4
39	YT	105	LEU	2.4
1	QA	208	U	2.4
1	XA	843	U	2.4
2	QB	83	MET	2.4
13	QM	3	ARG	2.4
30	YG	41	GLN	2.4
48	Y2	51	ARG	2.4
1	QA	930	C	2.4
1	QA	1128	C	2.4
25	YA	2477	C	2.4
28	RE	44	TYR	2.4
28	YE	44	TYR	2.4
29	RF	21	ALA	2.4
29	YF	169	ASN	2.4
32	YI	105	HIS	2.4
1	QA	196	A	2.3
31	RH	107	VAL	2.3
10	XJ	41	PRO	2.3
13	XM	87	TYR	2.3
16	QP	41	PRO	2.3
25	YA	1466	G	2.3
1	QA	1277	C	2.3
1	QA	1539	C	2.3
3	XC	79	ARG	2.3
13	QM	45	VAL	2.3
21	QU	11	GLY	2.3
25	RA	1546	C	2.3
25	YA	1043	C	2.3
1	QA	1093	A	2.3
10	XJ	33	GLN	2.3
45	YZ	179	ASP	2.3
25	RA	1046	A	2.3
31	YH	159	GLU	2.3
9	XI	126	SER	2.3
2	QB	222	ILE	2.3
25	RA	270(Z)	U	2.3
9	XI	9	ARG	2.3
29	RF	17	ARG	2.3
55	Y9	35	ARG	2.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
30	YG	160	VAL	2.3
1	QA	3	G	2.3
22	QV	63	G	2.3
40	YU	118	GLY	2.3
1	QA	745	C	2.3
16	QP	83	GLU	2.3
45	YZ	118	GLN	2.3
10	XJ	74	ILE	2.3
31	YH	145	ALA	2.3
45	YZ	173	ALA	2.3
50	Y4	13	ARG	2.3
4	XD	40	PRO	2.3
5	QE	2	PRO	2.3
15	QO	2	PRO	2.3
31	RH	31	GLY	2.3
4	XD	154	ASN	2.3
52	R6	16	CYS	2.3
19	QS	50	ALA	2.3
26	RB	5	C	2.3
32	RI	35	LEU	2.3
19	XS	74	PHE	2.3
11	XK	117	ASN	2.3
18	QR	64	ARG	2.3
19	XS	53	ASN	2.3
30	RG	35	GLU	2.3
38	RS	107	GLU	2.3
43	RX	55	ASN	2.3
2	XB	43	ASP	2.3
7	XG	150	ALA	2.3
1	QA	744	C	2.3
1	QA	798	G	2.3
1	QA	1241	G	2.3
4	QD	40	PRO	2.3
20	QT	61	SER	2.3
31	YH	32	GLU	2.3
37	YR	102	GLU	2.3
1	QA	197	A	2.3
25	RA	1545(A)	A	2.3
29	YF	135	LYS	2.3
7	XG	33	ASP	2.3
7	XG	151	TYR	2.3
29	YF	170	LEU	2.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
38	YS	24	LEU	2.3
3	QC	80	GLY	2.3
1	QA	103	C	2.3
25	YA	1550	C	2.3
1	QA	1134	G	2.3
1	XA	1351	U	2.3
17	QQ	74	LEU	2.3
25	RA	12	U	2.3
20	QT	75	ASN	2.3
52	R6	11	LEU	2.3
25	YA	2835	A	2.3
26	YB	1(M)	A	2.3
35	YP	110	TYR	2.3
37	RR	73	VAL	2.3
38	RS	41	ASP	2.3
32	RI	48	GLU	2.3
39	RT	106	SER	2.3
2	XB	201	ILE	2.3
25	YA	1499	C	2.3
31	RH	111	HIS	2.3
13	QM	98	VAL	2.3
30	YG	102	PHE	2.3
31	RH	74	ASN	2.3
10	XJ	36	GLY	2.3
15	XO	73	GLU	2.3
25	YA	312	G	2.3
25	YA	2345	G	2.3
45	RZ	135	GLU	2.3
31	RH	36	PRO	2.3
20	QT	104	LEU	2.3
41	YV	87	HIS	2.3
1	XA	381	C	2.3
1	XA	1129	C	2.3
19	XS	51	VAL	2.3
25	YA	790	C	2.3
25	YA	2628	C	2.3
27	YD	236	GLY	2.3
1	QA	837	G	2.3
1	XA	1290	G	2.3
25	YA	1448	G	2.3
25	YA	1486	A	2.3
15	QO	52	SER	2.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
18	QR	65	ILE	2.3
28	RE	77	ILE	2.3
7	XG	75	VAL	2.3
54	Y8	31	HIS	2.3
2	XB	35	GLU	2.3
39	YT	133	GLU	2.3
1	QA	1118	C	2.3
1	QA	1284	C	2.3
25	RA	1108	U	2.3
45	RZ	146	ILE	2.3
23	QX	14	A	2.3
25	RA	2062	A	2.3
25	YA	1469	A	2.3
55	Y9	3	VAL	2.3
1	XA	64	G	2.2
1	XA	1138	G	2.2
45	RZ	147	GLY	2.2
1	XA	1150	U	2.2
40	RU	101	ARG	2.2
31	RH	4	ILE	2.2
31	RH	11	VAL	2.2
44	YY	89	PHE	2.2
10	XJ	9	ARG	2.2
1	XA	993	G	2.2
25	RA	1542	G	2.2
23	QX	22	U	2.2
25	RA	270(L)	U	2.2
2	XB	10	LEU	2.2
10	QJ	80	LYS	2.2
2	QB	197	VAL	2.2
45	RZ	141	VAL	2.2
1	QA	664	G	2.2
6	QF	77	ARG	2.2
7	XG	115	ARG	2.2
25	YA	1413	G	2.2
25	YA	1483	G	2.2
25	YA	1500	G	2.2
26	YB	61	G	2.2
18	QR	71	LYS	2.2
31	YH	140	LYS	2.2
25	RA	1043	C	2.2
25	YA	885	C	2.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
38	YS	112	PHE	2.2
9	QI	20	ARG	2.2
9	QI	90	PRO	2.2
1	QA	199	G	2.2
1	QA	1361	G	2.2
25	RA	363(B)	G	2.2
25	YA	1862	G	2.2
1	QA	1320	C	2.2
26	YB	28	C	2.2
28	RE	1	MET	2.2
32	RI	7	GLU	2.2
52	Y6	24	GLU	2.2
2	QB	34	ALA	2.2
30	RG	139	LEU	2.2
25	YA	2808	U	2.2
25	YA	2897	U	2.2
20	QT	85	MET	2.2
19	QS	9	VAL	2.2
35	YP	71	VAL	2.2
45	YZ	100	VAL	2.2
45	YZ	175	VAL	2.2
53	R7	48	LYS	2.2
55	R9	25	VAL	2.2
28	YE	73	GLU	2.2
1	QA	191	G	2.2
1	QA	1022	G	2.2
1	QA	1221	G	2.2
1	XA	266	G	2.2
9	XI	4	TYR	2.2
13	QM	21	TYR	2.2
25	YA	2817	G	2.2
30	YG	40	ASN	2.2
35	YP	148	LEU	2.2
41	YV	40	LEU	2.2
45	RZ	73	GLN	2.2
9	QI	111	ARG	2.2
2	QB	71	VAL	2.2
11	QK	16	SER	2.2
25	YA	1529	A	2.2
25	YA	1545(A)	A	2.2
1	QA	1008	C	2.2
1	XA	1260	C	2.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
18	QR	78	LEU	2.2
24	XY	90	ASP	2.2
29	RF	23	ASP	2.2
25	YA	1534	G	2.2
32	RI	67	ARG	2.2
10	QJ	34	VAL	2.2
17	QQ	59	ILE	2.2
41	RV	87	HIS	2.2
2	QB	50	GLU	2.2
12	XL	50	SER	2.2
29	YF	13	SER	2.2
25	RA	2476	A	2.2
5	XE	20	GLN	2.2
9	QI	102	LEU	2.2
10	QJ	66	ARG	2.2
52	Y6	53	LYS	2.2
55	Y9	4	ARG	2.2
25	YA	2107	C	2.2
31	RH	81	GLU	2.2
45	YZ	96	VAL	2.2
1	XA	484	G	2.2
21	QU	4	GLY	2.2
25	RA	408	G	2.2
25	RA	2838	G	2.2
25	RA	270(M)	U	2.2
35	YP	16	ARG	2.2
45	RZ	156	LYS	2.2
50	Y4	69	LYS	2.2
25	RA	1847	A	2.2
25	YA	2411	A	2.2
2	QB	68	ILE	2.2
4	QD	156	GLU	2.2
8	QH	132	GLU	2.2
13	XM	61	GLU	2.2
35	YP	117	GLU	2.2
38	RS	82	ILE	2.2
38	YS	43	GLU	2.2
41	RV	93	GLU	2.2
55	R9	16	VAL	2.2
1	XA	193	C	2.2
17	QQ	45	HIS	2.2
15	QO	17	ARG	2.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
25	RA	1577	C	2.2
15	QO	67	LEU	2.2
19	QS	18	LYS	2.2
51	Y5	51	TYR	2.2
22	XV	47	U	2.2
25	RA	818	G	2.2
25	YA	1449(A)	G	2.2
4	XD	9	CYS	2.2
29	RF	1	MET	2.2
38	RS	85	VAL	2.2
1	XA	382	A	2.2
13	QM	114	ARG	2.2
46	Y0	3	HIS	2.2
1	QA	1325	C	2.1
22	XV	48	C	2.1
25	YA	1386	C	2.1
25	YA	2881	C	2.1
26	YB	6	C	2.1
32	RI	46	ALA	2.1
45	RZ	172	ALA	2.1
38	YS	29	PHE	2.1
1	QA	960	U	2.1
25	RA	1012	U	2.1
2	QB	144	ARG	2.1
4	QD	10	ARG	2.1
45	RZ	119	GLU	2.1
50	Y4	55	ARG	2.1
25	YA	272	G	2.1
25	YA	1527	G	2.1
38	YS	108	GLY	2.1
31	YH	74	ASN	2.1
7	XG	83	ALA	2.1
25	RA	1729	A	2.1
26	RB	26	A	2.1
2	QB	240	GLN	2.1
38	RS	38	GLN	2.1
1	QA	186	C	2.1
3	XC	85	ARG	2.1
3	XC	86	VAL	2.1
25	RA	817	C	2.1
28	RE	200	GLU	2.1
37	YR	5	LYS	2.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
52	Y6	51	GLU	2.1
22	XV	60	U	2.1
45	RZ	157	LEU	2.1
44	YY	60	PHE	2.1
45	YZ	164	ALA	2.1
1	QA	1311	G	2.1
10	XJ	70	ARG	2.1
25	YA	1385	G	2.1
52	R6	35	GLU	2.1
1	QA	1536	C	2.1
25	RA	2658	C	2.1
45	YZ	140	ASP	2.1
11	QK	125	PHE	2.1
40	RU	76	TYR	2.1
32	RI	69	LYS	2.1
39	YT	129	ARG	2.1
47	R1	25	LYS	2.1
10	QJ	4	ILE	2.1
1	XA	348	G	2.1
2	XB	91	PRO	2.1
21	XU	19	GLY	2.1
25	RA	2290	G	2.1
25	RA	2661	G	2.1
25	YA	321	G	2.1
1	QA	1270	C	2.1
12	XL	115	LYS	2.1
21	QU	21	TYR	2.1
27	RD	35	LYS	2.1
2	QB	15	VAL	2.1
21	XU	11	GLY	2.1
29	YF	71	GLY	2.1
46	Y0	54	GLY	2.1
2	QB	91	PRO	2.1
31	RH	155	SER	2.1
1	XA	1531	A	2.1
25	YA	103	A	2.1
50	Y4	59	PHE	2.1
1	QA	1370	G	2.1
1	XA	1009	G	2.1
25	RA	2373	G	2.1
25	YA	75	G	2.1
26	RB	23	G	2.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
50	R4	12	ALA	2.1
1	XA	355	C	2.1
2	QB	32	ILE	2.1
2	QB	114	ARG	2.1
30	YG	118	ARG	2.1
35	YP	3	LEU	2.1
2	QB	77	ALA	2.1
1	QA	1268	A	2.1
1	XA	393	A	2.1
1	XA	1287	A	2.1
1	QA	1018	C	2.1
1	QA	1347	G	2.1
25	YA	271(B)	G	2.1
25	YA	919	G	2.1
25	YA	1423	G	2.1
25	YA	1505	C	2.1
25	YA	2375	G	2.1
38	RS	57	LYS	2.1
26	YB	5	C	2.1
47	Y1	26	ARG	2.1
9	XI	2	GLU	2.1
3	XC	97	LYS	2.1
9	QI	128	ARG	2.1
24	QY	8	LYS	2.1
30	YG	89	GLY	2.1
25	YA	9	U	2.1
30	YG	135	LEU	2.1
31	RH	60	ARG	2.1
1	QA	1279	A	2.1
25	RA	412	A	2.1
30	YG	71	THR	2.1
1	QA	91	C	2.1
1	QA	851	G	2.1
1	QA	1182	G	2.1
1	XA	220	G	2.1
1	XA	1043	C	2.1
2	QB	31	TYR	2.1
25	RA	273(A)	G	2.1
41	YV	43	GLU	2.1
7	QG	27	ILE	2.1
31	RH	110	SER	2.1
10	QJ	73	ASP	2.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
40	RU	92	ARG	2.1
43	RX	80	ILE	2.1
1	QA	1315	U	2.1
1	QA	412	A	2.1
32	RI	61	ARG	2.1
32	RI	65	ALA	2.1
32	YI	29	TYR	2.1
37	YR	45	ARG	2.1
44	RY	91	GLU	2.1
45	YZ	119	GLU	2.1
1	XA	63	C	2.1
25	YA	1504	C	2.1
4	XD	41	GLY	2.1
13	QM	16	ASP	2.1
25	YA	852	G	2.1
26	RB	61	G	2.1
30	YG	117	PHE	2.1
2	QB	8	LYS	2.1
9	XI	125	TYR	2.1
10	QJ	67	THR	2.1
13	XM	43	THR	2.1
29	YF	158	THR	2.1
45	RZ	43	GLU	2.1
2	QB	118	LEU	2.1
9	XI	85	LEU	2.1
32	RI	72	LEU	2.1
38	RS	26	LEU	2.1
38	RS	73	LEU	2.1
1	XA	1452	C	2.1
3	XC	4	LYS	2.0
15	QO	28	GLN	2.0
25	YA	2879	C	2.1
26	RB	3	C	2.1
40	RU	84	LYS	2.0
46	Y0	55	ARG	2.0
1	QA	357	G	2.0
7	QG	61	VAL	2.0
7	QG	154	TYR	2.0
25	RA	498	G	2.0
25	RA	1423	G	2.0
25	YA	859	G	2.0
25	YA	1522	G	2.0

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Mol	Chain	Res	Type	RSRZ
9	XI	106	ALA	2.0
50	R4	32	TYR	2.0
10	XJ	71	LEU	2.0
30	YG	133	LEU	2.0
32	RI	9	LEU	2.0
40	YU	109	LEU	2.0
1	XA	792	A	2.0
7	QG	4	ARG	2.0
9	QI	93	ARG	2.0
10	QJ	59	SER	2.0
19	XS	35	SER	2.0
23	XX	8	A	2.0
25	RA	363(A)	A	2.0
25	RA	878	A	2.0
33	RN	127	ASP	2.0
1	XA	1533	C	2.0
2	XB	84	GLU	2.0
38	RS	43	GLU	2.0
18	QR	31	LEU	2.0
30	YG	140	ILE	2.0
30	YG	176	LEU	2.0
39	RT	105	LEU	2.0
1	XA	371	G	2.0
1	XA	950	U	2.0
25	RA	1039	G	2.0
25	RA	2532	G	2.0
25	YA	2290	G	2.0
40	YU	7	GLY	2.0
20	QT	60	GLU	2.0
1	XA	482	A	2.0
26	RB	89(A)	A	2.0
1	QA	74	C	2.0
25	YA	1735	C	2.0
31	RH	162	ILE	2.0
38	YS	86	ALA	2.0
20	QT	68	LYS	2.0
31	YH	138	LYS	2.0
45	YZ	91	LEU	2.0
47	Y1	94	LEU	2.0
9	QI	83	ARG	2.0
50	R4	42	PHE	2.0
1	QA	113	G	2.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	QA	181	G	2.0
1	QA	666	G	2.0
1	QA	1276	G	2.0
1	XA	347	G	2.0
2	QB	191	ASP	2.0
22	QV	12	G	2.0
25	RA	1436	G	2.0
38	YS	64	GLU	2.0
31	RH	49	VAL	2.0
38	RS	80	LEU	2.0
38	YS	11	LYS	2.0
1	QA	172	A	2.0
2	XB	226	ARG	2.0
9	XI	10	ARG	2.0
1	QA	962	C	2.0
2	XB	234	PRO	2.0
22	XV	1	C	2.0
25	YA	2342	C	2.0
29	YF	129	PHE	2.0
6	XF	89	MET	2.0
2	XB	135	GLN	2.0
7	QG	57	GLU	2.0
24	QY	18	VAL	2.0
31	YH	114	VAL	2.0
3	QC	204	LEU	2.0
3	XC	60	ALA	2.0
30	YG	94	LEU	2.0
35	YP	15	ARG	2.0
41	RV	12	TYR	2.0
43	RX	6	ASP	2.0
10	QJ	74	ILE	2.0
21	QU	13	ILE	2.0
1	QA	1124	G	2.0
1	XA	426	G	2.0
24	QY	21	GLY	2.0
25	RA	2839	G	2.0
25	YA	1922	G	2.0
29	YF	134	GLY	2.0
50	Y4	41	PRO	2.0
1	QA	455	C	2.0
1	XA	40	C	2.0
6	XF	7	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
25	RA	74	A	2.0
25	RA	1444(A)	A	2.0
25	RA	2765	A	2.0
25	RA	2883	A	2.0
20	QT	65	LYS	2.0
27	RD	27	THR	2.0
14	QN	6	LEU	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
23	A2M	QX	21	23/24	0.74	0.36	44,130,130,130	0
23	A2M	XX	21	23/24	0.82	0.38	44,118,118,118	0
23	OMC	XX	20	21/22	0.92	0.21	44,74,74,74	0
23	OMC	QX	20	21/22	0.93	0.20	44,77,77,77	0
23	A2M	QX	19	23/24	0.94	0.20	39,73,73,73	0
23	A2M	XX	19	23/24	0.96	0.18	62,62,104,137	0
56	PPU	Z6	76	37/38	0.96	0.25	26,33,40,43	0
56	PPU	Z7	76	37/38	0.96	0.27	27,32,49,62	0

## 6.3 Carbohydrates [i](#)

There are no monosaccharides 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
57	MG	YA	3228	1/1	0.21	0.25	69,69,69,69	0
57	MG	YA	3448	1/1	0.30	0.76	82,82,82,82	0
57	MG	RA	3345	1/1	0.31	0.38	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YA	3294	1/1	0.34	0.32	45,45,45,45	0
57	MG	XA	1690	1/1	0.39	0.34	52,52,52,52	0
57	MG	QA	1720	1/1	0.40	0.30	67,67,67,67	0
57	MG	YA	3374	1/1	0.44	0.47	57,57,57,57	0
57	MG	RA	3414	1/1	0.47	0.12	42,42,42,42	0
57	MG	QA	1630	1/1	0.47	0.34	63,63,63,63	0
57	MG	RA	3075	1/1	0.48	0.55	42,42,42,42	0
57	MG	YA	3495	1/1	0.49	0.36	63,63,63,63	0
57	MG	XA	1743	1/1	0.50	0.24	56,56,56,56	0
57	MG	RA	3292	1/1	0.50	0.55	67,67,67,67	0
57	MG	YA	3186	1/1	0.51	0.49	48,48,48,48	0
57	MG	RA	3372	1/1	0.52	0.36	74,74,74,74	0
57	MG	XA	1763	1/1	0.53	0.33	59,59,59,59	0
57	MG	RA	3036	1/1	0.53	0.28	51,51,51,51	0
57	MG	YA	3335	1/1	0.53	0.29	52,52,52,52	0
57	MG	YA	3001	1/1	0.54	0.73	68,68,68,68	0
57	MG	RA	3371	1/1	0.55	0.36	70,70,70,70	0
57	MG	RA	3261	1/1	0.55	0.38	79,79,79,79	0
57	MG	YA	3104	1/1	0.56	0.42	76,76,76,76	0
57	MG	YA	3128	1/1	0.56	0.36	38,38,38,38	0
57	MG	RA	3366	1/1	0.56	0.19	71,71,71,71	0
57	MG	XA	1732	1/1	0.57	0.28	56,56,56,56	0
57	MG	RA	3397	1/1	0.57	0.21	52,52,52,52	0
57	MG	YA	3082	1/1	0.57	0.24	24,24,24,24	0
57	MG	RA	3083	1/1	0.58	0.28	30,30,30,30	0
57	MG	QA	1672	1/1	0.58	0.38	71,71,71,71	0
57	MG	QA	1637	1/1	0.58	0.34	74,74,74,74	0
57	MG	YA	3501	1/1	0.58	0.39	31,31,31,31	0
57	MG	YA	3287	1/1	0.59	0.46	58,58,58,58	0
57	MG	QA	1671	1/1	0.59	0.39	49,49,49,49	0
57	MG	YA	3394	1/1	0.59	0.34	56,56,56,56	0
57	MG	RA	3361	1/1	0.60	0.55	65,65,65,65	0
57	MG	RA	3102	1/1	0.60	0.54	28,28,28,28	0
57	MG	YA	3183	1/1	0.60	0.28	45,45,45,45	0
57	MG	YA	3392	1/1	0.60	0.37	51,51,51,51	0
57	MG	YA	3300	1/1	0.61	0.53	51,51,51,51	0
57	MG	XD	302	1/1	0.61	0.17	51,51,51,51	0
57	MG	YA	3362	1/1	0.61	0.47	61,61,61,61	0
57	MG	YA	3118	1/1	0.62	0.32	40,40,40,40	0
57	MG	RA	3198	1/1	0.62	0.34	50,50,50,50	0
57	MG	RA	3069	1/1	0.63	0.27	18,18,18,18	0
57	MG	YU	201	1/1	0.63	0.42	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	XA	1646	1/1	0.64	0.58	87,87,87,87	0
57	MG	QA	1734	1/1	0.64	0.28	55,55,55,55	0
57	MG	RA	3392	1/1	0.64	0.51	42,42,42,42	0
57	MG	YA	3488	1/1	0.64	0.36	53,53,53,53	0
57	MG	RA	3342	1/1	0.64	0.19	52,52,52,52	0
57	MG	YA	3371	1/1	0.64	0.51	64,64,64,64	0
57	MG	RA	3173	1/1	0.64	0.27	28,28,28,28	0
57	MG	YA	3398	1/1	0.65	0.20	67,67,67,67	0
57	MG	YA	3255	1/1	0.65	0.41	64,64,64,64	0
57	MG	YA	3451	1/1	0.65	0.27	66,66,66,66	0
57	MG	QA	1719	1/1	0.65	0.31	60,60,60,60	0
57	MG	RA	3431	1/1	0.65	0.35	53,53,53,53	0
57	MG	RA	3376	1/1	0.65	0.40	66,66,66,66	0
57	MG	YA	3120	1/1	0.65	0.24	41,41,41,41	0
57	MG	RA	3274	1/1	0.66	0.34	68,68,68,68	0
57	MG	RA	3387	1/1	0.66	0.43	56,56,56,56	0
57	MG	YA	3421	1/1	0.66	0.29	38,38,38,38	0
57	MG	YA	3444	1/1	0.66	0.43	48,48,48,48	0
57	MG	RA	3323	1/1	0.66	1.69	87,87,87,87	0
57	MG	RA	3210	1/1	0.67	0.51	64,64,64,64	0
57	MG	YA	3281	1/1	0.67	0.28	52,52,52,52	0
57	MG	RA	3449	1/1	0.67	0.33	32,32,32,32	0
57	MG	YO	201	1/1	0.67	0.24	66,66,66,66	0
57	MG	XA	1628	1/1	0.67	0.15	52,52,52,52	0
57	MG	YA	3470	1/1	0.68	0.23	50,50,50,50	0
57	MG	RA	3321	1/1	0.68	0.32	53,53,53,53	0
57	MG	YA	3493	1/1	0.68	0.33	63,63,63,63	0
57	MG	YA	3068	1/1	0.68	0.18	32,32,32,32	0
57	MG	RD	302	1/1	0.68	0.40	29,29,29,29	0
57	MG	RA	3333	1/1	0.68	0.11	55,55,55,55	0
57	MG	YA	3352	1/1	0.68	0.15	84,84,84,84	0
57	MG	XA	1744	1/1	0.69	0.31	33,33,33,33	0
57	MG	RA	3364	1/1	0.69	0.34	64,64,64,64	0
57	MG	XA	1634	1/1	0.69	0.19	41,41,41,41	0
57	MG	QA	1727	1/1	0.69	0.19	57,57,57,57	0
57	MG	YA	3215	1/1	0.69	0.49	33,33,33,33	0
57	MG	RA	3146	1/1	0.69	0.57	37,37,37,37	0
57	MG	XA	1723	1/1	0.69	0.31	55,55,55,55	0
57	MG	YA	3377	1/1	0.69	0.32	43,43,43,43	0
57	MG	YA	3268	1/1	0.69	0.42	55,55,55,55	0
57	MG	RA	3298	1/1	0.69	0.40	62,62,62,62	0
57	MG	R0	102	1/1	0.69	0.49	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
57	MG	XA	1624	1/1	0.70	0.24	39,39,39,39	0
57	MG	QV	103	1/1	0.70	0.28	52,52,52,52	0
57	MG	YA	3499	1/1	0.70	0.47	67,67,67,67	0
57	MG	QA	1722	1/1	0.70	0.34	57,57,57,57	0
57	MG	YA	3297	1/1	0.70	0.64	49,49,49,49	0
57	MG	QA	1741	1/1	0.70	0.18	46,46,46,46	0
57	MG	RB	205	1/1	0.71	0.32	59,59,59,59	0
57	MG	RA	3353	1/1	0.71	0.42	46,46,46,46	0
57	MG	YA	3437	1/1	0.71	0.24	37,37,37,37	0
57	MG	RA	3106	1/1	0.71	0.29	41,41,41,41	0
57	MG	R2	101	1/1	0.71	0.22	68,68,68,68	0
57	MG	YA	3348	1/1	0.71	0.47	77,77,77,77	0
57	MG	RA	3368	1/1	0.71	0.26	55,55,55,55	0
57	MG	XA	1700	1/1	0.72	0.24	47,47,47,47	0
57	MG	RA	3092	1/1	0.72	0.45	56,56,56,56	0
57	MG	RA	3300	1/1	0.72	0.45	37,37,37,37	0
57	MG	QA	1738	1/1	0.72	0.17	43,43,43,43	0
57	MG	QA	1693	1/1	0.72	0.34	63,63,63,63	0
57	MG	QA	1744	1/1	0.72	0.15	54,54,54,54	0
57	MG	YA	3147	1/1	0.72	0.48	25,25,25,25	0
57	MG	YA	3179	1/1	0.72	0.17	63,63,63,63	0
57	MG	XA	1685	1/1	0.72	0.54	62,62,62,62	0
57	MG	YB	206	1/1	0.72	0.29	49,49,49,49	0
57	MG	YA	3328	1/1	0.72	0.31	47,47,47,47	0
57	MG	QA	1669	1/1	0.72	0.25	53,53,53,53	0
57	MG	RA	3450	1/1	0.73	0.29	25,25,25,25	0
57	MG	XA	1756	1/1	0.73	0.48	45,45,45,45	0
57	MG	QA	1745	1/1	0.73	0.23	52,52,52,52	0
57	MG	XA	1712	1/1	0.73	0.12	61,61,61,61	0
57	MG	YA	3402	1/1	0.73	0.24	56,56,56,56	0
57	MG	RA	3214	1/1	0.73	0.38	57,57,57,57	0
57	MG	YA	3428	1/1	0.73	0.39	32,32,32,32	0
57	MG	RA	3438	1/1	0.73	0.51	58,58,58,58	0
57	MG	RA	3229	1/1	0.73	0.17	30,30,30,30	0
57	MG	YA	3100	1/1	0.73	0.43	20,20,20,20	0
57	MG	RA	3302	1/1	0.74	0.55	59,59,59,59	0
57	MG	QA	1631	1/1	0.74	0.33	55,55,55,55	0
57	MG	XA	1704	1/1	0.74	0.50	62,62,62,62	0
57	MG	YA	3452	1/1	0.74	0.30	49,49,49,49	0
57	MG	YA	3391	1/1	0.74	0.60	49,49,49,49	0
57	MG	RA	3351	1/1	0.74	0.60	58,58,58,58	0
57	MG	YA	3133	1/1	0.74	0.31	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3341	1/1	0.74	1.00	73,73,73,73	0
57	MG	YA	3158	1/1	0.74	0.18	30,30,30,30	0
57	MG	YA	3409	1/1	0.74	0.28	47,47,47,47	0
57	MG	YA	3160	1/1	0.74	0.31	37,37,37,37	0
57	MG	YH	202	1/1	0.74	0.26	47,47,47,47	0
57	MG	YA	3283	1/1	0.74	0.45	52,52,52,52	0
57	MG	YA	3365	1/1	0.74	0.48	39,39,39,39	0
57	MG	XA	1725	1/1	0.75	0.43	54,54,54,54	0
57	MG	QN	102	1/1	0.75	0.13	61,61,61,61	0
57	MG	QA	1743	1/1	0.75	0.20	52,52,52,52	0
57	MG	QA	1704	1/1	0.75	0.27	59,59,59,59	0
57	MG	XA	1656	1/1	0.75	0.17	65,65,65,65	0
57	MG	YA	3134	1/1	0.75	0.93	47,47,47,47	0
57	MG	YA	3387	1/1	0.75	0.24	71,71,71,71	0
57	MG	QA	1697	1/1	0.75	0.43	76,76,76,76	0
57	MG	YA	3291	1/1	0.75	0.29	54,54,54,54	0
57	MG	RA	3218	1/1	0.75	0.21	35,35,35,35	0
57	MG	RE	303	1/1	0.75	0.23	51,51,51,51	0
57	MG	YA	3502	1/1	0.75	0.47	32,32,32,32	0
57	MG	RA	3118	1/1	0.75	0.28	55,55,55,55	0
57	MG	QA	1751	1/1	0.75	0.49	84,84,84,84	0
57	MG	RA	3168	1/1	0.75	0.30	48,48,48,48	0
57	MG	YA	3197	1/1	0.75	0.77	38,38,38,38	0
57	MG	XA	1625	1/1	0.76	0.23	37,37,37,37	0
57	MG	QA	1713	1/1	0.76	0.17	58,58,58,58	0
57	MG	QD	303	1/1	0.76	0.11	48,48,48,48	0
57	MG	YA	3172	1/1	0.76	0.32	52,52,52,52	0
57	MG	YA	3231	1/1	0.76	0.28	35,35,35,35	0
57	MG	YA	3236	1/1	0.76	0.24	40,40,40,40	0
57	MG	YA	3249	1/1	0.76	0.27	42,42,42,42	0
57	MG	YA	3176	1/1	0.76	0.18	57,57,57,57	0
57	MG	RA	3277	1/1	0.76	0.31	57,57,57,57	0
57	MG	XA	1703	1/1	0.76	0.21	55,55,55,55	0
57	MG	RY	202	1/1	0.77	0.48	50,50,50,50	0
57	MG	RA	3442	1/1	0.77	0.38	41,41,41,41	0
57	MG	YA	3489	1/1	0.77	0.30	59,59,59,59	0
57	MG	XA	1682	1/1	0.77	0.33	42,42,42,42	0
57	MG	RA	3394	1/1	0.77	0.15	31,31,31,31	0
57	MG	RA	3143	1/1	0.77	0.25	61,61,61,61	0
57	MG	QA	1678	1/1	0.77	0.18	70,70,70,70	0
57	MG	QA	1686	1/1	0.77	0.24	43,43,43,43	0
57	MG	XA	1758	1/1	0.77	0.36	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YA	3265	1/1	0.77	0.30	45,45,45,45	0
57	MG	RA	3232	1/1	0.77	0.38	53,53,53,53	0
57	MG	YP	202	1/1	0.77	0.30	45,45,45,45	0
57	MG	YR	201	1/1	0.77	0.29	34,34,34,34	0
57	MG	YA	3457	1/1	0.77	0.27	24,24,24,24	0
57	MG	RY	201	1/1	0.78	0.18	37,37,37,37	0
57	MG	QA	1737	1/1	0.78	0.35	56,56,56,56	0
57	MG	XA	1748	1/1	0.78	0.40	62,62,62,62	0
57	MG	YA	3324	1/1	0.78	0.25	53,53,53,53	0
57	MG	RA	3182	1/1	0.78	0.49	78,78,78,78	0
57	MG	QA	1650	1/1	0.78	0.29	36,36,36,36	0
57	MG	RA	3358	1/1	0.78	0.15	46,46,46,46	0
57	MG	RA	3332	1/1	0.78	0.12	67,67,67,67	0
57	MG	RA	3294	1/1	0.78	0.33	63,63,63,63	0
57	MG	XA	1629	1/1	0.78	0.33	54,54,54,54	0
57	MG	RA	3205	1/1	0.78	0.20	30,30,30,30	0
57	MG	XA	1639	1/1	0.78	0.88	74,74,74,74	0
57	MG	QA	1684	1/1	0.78	0.37	54,54,54,54	0
57	MG	YA	3111	1/1	0.78	0.50	57,57,57,57	0
57	MG	XA	1752	1/1	0.79	0.31	56,56,56,56	0
57	MG	XA	1702	1/1	0.79	0.75	69,69,69,69	0
57	MG	RA	3041	1/1	0.79	0.21	23,23,23,23	0
57	MG	YA	3289	1/1	0.79	0.19	38,38,38,38	0
57	MG	YA	3198	1/1	0.79	0.12	54,54,54,54	0
57	MG	YA	3201	1/1	0.79	0.37	35,35,35,35	0
57	MG	YA	3490	1/1	0.79	0.69	63,63,63,63	0
57	MG	QA	1666	1/1	0.79	0.12	42,42,42,42	0
57	MG	RA	3336	1/1	0.79	0.16	33,33,33,33	0
57	MG	RA	3338	1/1	0.79	0.63	70,70,70,70	0
57	MG	XA	1669	1/1	0.79	0.48	48,48,48,48	0
57	MG	YA	3404	1/1	0.79	0.31	63,63,63,63	0
57	MG	RA	3422	1/1	0.79	0.21	41,41,41,41	0
57	MG	YA	3340	1/1	0.79	0.50	54,54,54,54	0
57	MG	QA	1668	1/1	0.79	0.20	44,44,44,44	0
57	MG	RA	3329	1/1	0.79	0.75	65,65,65,65	0
57	MG	YA	3353	1/1	0.79	0.59	53,53,53,53	0
57	MG	XA	1630	1/1	0.79	0.20	75,75,75,75	0
57	MG	RA	3399	1/1	0.80	0.24	40,40,40,40	0
57	MG	RA	3370	1/1	0.80	0.51	65,65,65,65	0
57	MG	YA	3467	1/1	0.80	0.20	43,43,43,43	0
57	MG	RA	3157	1/1	0.80	0.16	40,40,40,40	0
57	MG	XA	1708	1/1	0.80	0.14	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
57	MG	YA	3310	1/1	0.80	0.29	54,54,54,54	0
57	MG	RA	3357	1/1	0.80	0.88	61,61,61,61	0
57	MG	YA	3327	1/1	0.80	0.45	69,69,69,69	0
57	MG	YA	3152	1/1	0.80	0.39	43,43,43,43	0
57	MG	XA	1716	1/1	0.80	0.39	51,51,51,51	0
57	MG	YA	3059	1/1	0.80	0.18	28,28,28,28	0
57	MG	YA	3410	1/1	0.80	0.16	62,62,62,62	0
57	MG	RA	3433	1/1	0.80	0.31	49,49,49,49	0
57	MG	RA	3322	1/1	0.80	0.42	84,84,84,84	0
57	MG	RA	3188	1/1	0.80	0.40	58,58,58,58	0
57	MG	RA	3167	1/1	0.80	0.28	31,31,31,31	0
57	MG	RA	3176	1/1	0.80	0.44	57,57,57,57	0
57	MG	RA	3285	1/1	0.80	0.36	35,35,35,35	0
57	MG	Y0	101	1/1	0.80	0.36	52,52,52,52	0
57	MG	QA	1708	1/1	0.81	0.36	60,60,60,60	0
57	MG	RA	3315	1/1	0.81	0.23	27,27,27,27	0
57	MG	YA	3360	1/1	0.81	0.55	61,61,61,61	0
57	MG	QA	1735	1/1	0.81	0.34	73,73,73,73	0
57	MG	RA	3347	1/1	0.81	0.50	65,65,65,65	0
57	MG	RA	3014	1/1	0.81	0.35	17,17,17,17	0
57	MG	XA	1709	1/1	0.81	0.54	54,54,54,54	0
57	MG	YA	3476	1/1	0.81	0.14	53,53,53,53	0
57	MG	YA	3482	1/1	0.81	0.26	54,54,54,54	0
57	MG	RA	3383	1/1	0.81	0.12	75,75,75,75	0
57	MG	QA	1742	1/1	0.81	0.22	44,44,44,44	0
57	MG	RA	3291	1/1	0.81	0.62	48,48,48,48	0
57	MG	RD	301	1/1	0.81	0.30	28,28,28,28	0
57	MG	YA	3393	1/1	0.81	0.18	56,56,56,56	0
57	MG	YA	3498	1/1	0.81	0.55	57,57,57,57	0
57	MG	RA	3147	1/1	0.81	0.23	48,48,48,48	0
57	MG	YA	3308	1/1	0.81	0.71	54,54,54,54	0
57	MG	RA	3221	1/1	0.81	0.78	43,43,43,43	0
57	MG	YA	3218	1/1	0.81	0.63	40,40,40,40	0
57	MG	RA	3187	1/1	0.81	0.55	55,55,55,55	0
57	MG	RA	3408	1/1	0.81	0.27	38,38,38,38	0
57	MG	YA	3234	1/1	0.81	0.51	50,50,50,50	0
57	MG	YA	3425	1/1	0.81	0.12	33,33,33,33	0
57	MG	XA	1686	1/1	0.81	0.25	39,39,39,39	0
57	MG	QA	1633	1/1	0.81	0.37	57,57,57,57	0
57	MG	YA	3329	1/1	0.82	0.76	50,50,50,50	0
57	MG	YA	3142	1/1	0.82	0.67	65,65,65,65	0
57	MG	YA	3145	1/1	0.82	0.22	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	XA	1707	1/1	0.82	0.51	54,54,54,54	0
57	MG	YA	3149	1/1	0.82	0.42	34,34,34,34	0
57	MG	RA	3217	1/1	0.82	0.41	50,50,50,50	0
57	MG	YA	3461	1/1	0.82	0.31	39,39,39,39	0
57	MG	YA	3262	1/1	0.82	0.22	41,41,41,41	0
57	MG	XA	1666	1/1	0.82	0.36	52,52,52,52	0
57	MG	YA	3475	1/1	0.82	0.82	40,40,40,40	0
57	MG	RA	3446	1/1	0.82	0.50	33,33,33,33	0
57	MG	YA	3366	1/1	0.82	0.93	57,57,57,57	0
57	MG	YA	3272	1/1	0.82	0.22	48,48,48,48	0
57	MG	YA	3274	1/1	0.82	0.42	48,48,48,48	0
57	MG	YA	3162	1/1	0.82	0.28	46,46,46,46	0
57	MG	YA	3167	1/1	0.82	0.28	43,43,43,43	0
57	MG	YA	3285	1/1	0.82	0.17	52,52,52,52	0
57	MG	RA	3183	1/1	0.82	0.13	65,65,65,65	0
57	MG	XA	1684	1/1	0.82	0.26	55,55,55,55	0
57	MG	YA	3090	1/1	0.82	0.25	46,46,46,46	0
57	MG	QA	1679	1/1	0.82	0.25	37,37,37,37	0
57	MG	YA	3503	1/1	0.82	0.21	45,45,45,45	0
57	MG	RA	3111	1/1	0.82	0.17	45,45,45,45	0
57	MG	XA	1687	1/1	0.82	0.14	55,55,55,55	0
57	MG	QA	1680	1/1	0.82	0.40	58,58,58,58	0
57	MG	QA	1711	1/1	0.82	0.11	55,55,55,55	0
57	MG	RA	3093	1/1	0.82	0.34	38,38,38,38	0
57	MG	RA	3002	1/1	0.82	0.27	55,55,55,55	0
57	MG	RA	3319	1/1	0.82	0.24	51,51,51,51	0
57	MG	QA	1670	1/1	0.83	0.38	54,54,54,54	0
57	MG	YA	3140	1/1	0.83	0.11	32,32,32,32	0
57	MG	YA	3336	1/1	0.83	0.22	52,52,52,52	0
57	MG	XA	1761	1/1	0.83	0.20	53,53,53,53	0
57	MG	RA	3059	1/1	0.83	0.11	27,27,27,27	0
57	MG	RA	3254	1/1	0.83	0.09	47,47,47,47	0
57	MG	RA	3325	1/1	0.83	0.43	41,41,41,41	0
57	MG	YA	3354	1/1	0.83	0.20	41,41,41,41	0
57	MG	YA	3022	1/1	0.83	0.31	72,72,72,72	0
57	MG	YA	3031	1/1	0.83	0.28	19,19,19,19	0
57	MG	RA	3296	1/1	0.83	0.31	51,51,51,51	0
57	MG	YA	3063	1/1	0.83	0.21	21,21,21,21	0
57	MG	YA	3369	1/1	0.83	0.19	49,49,49,49	0
57	MG	RA	3356	1/1	0.83	0.71	46,46,46,46	0
57	MG	QA	1625	1/1	0.83	0.10	47,47,47,47	0
57	MG	YA	3173	1/1	0.83	0.36	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3388	1/1	0.83	0.14	56,56,56,56	0
57	MG	YA	3288	1/1	0.83	0.48	51,51,51,51	0
57	MG	YA	3097	1/1	0.83	0.25	20,20,20,20	0
57	MG	XA	1727	1/1	0.83	0.38	51,51,51,51	0
57	MG	RA	3447	1/1	0.83	0.20	32,32,32,32	0
57	MG	YA	3187	1/1	0.83	0.56	64,64,64,64	0
57	MG	YA	3110	1/1	0.83	0.33	42,42,42,42	0
57	MG	RA	3264	1/1	0.83	0.17	41,41,41,41	0
57	MG	YA	3406	1/1	0.83	0.37	49,49,49,49	0
57	MG	XA	1699	1/1	0.83	0.19	52,52,52,52	0
57	MG	RA	3128	1/1	0.83	0.18	35,35,35,35	0
57	MG	YQ	202	1/1	0.83	0.19	39,39,39,39	0
57	MG	YA	3420	1/1	0.83	0.29	65,65,65,65	0
57	MG	RA	3138	1/1	0.83	0.31	40,40,40,40	0
57	MG	YV	201	1/1	0.83	0.29	17,17,17,17	0
57	MG	QD	302	1/1	0.83	0.36	67,67,67,67	0
57	MG	QA	1640	1/1	0.84	0.71	60,60,60,60	0
57	MG	YA	3232	1/1	0.84	0.16	35,35,35,35	0
57	MG	YA	3471	1/1	0.84	0.27	44,44,44,44	0
57	MG	RA	3418	1/1	0.84	0.18	43,43,43,43	0
57	MG	RA	3148	1/1	0.84	0.39	19,19,19,19	0
57	MG	YA	3477	1/1	0.84	0.25	44,44,44,44	0
57	MG	YA	3480	1/1	0.84	0.22	50,50,50,50	0
57	MG	YA	3246	1/1	0.84	0.10	38,38,38,38	0
57	MG	RA	3426	1/1	0.84	0.13	56,56,56,56	0
57	MG	RA	3348	1/1	0.84	0.32	47,47,47,47	0
57	MG	YA	3399	1/1	0.84	0.20	47,47,47,47	0
57	MG	YA	3261	1/1	0.84	0.21	33,33,33,33	0
57	MG	RA	3211	1/1	0.84	0.18	31,31,31,31	0
57	MG	RQ	201	1/1	0.84	0.29	34,34,34,34	0
57	MG	XA	1728	1/1	0.84	0.57	59,59,59,59	0
57	MG	YA	3182	1/1	0.84	0.23	52,52,52,52	0
57	MG	QA	1749	1/1	0.84	0.33	57,57,57,57	0
57	MG	YA	3275	1/1	0.84	0.25	59,59,59,59	0
57	MG	YA	3136	1/1	0.84	0.37	33,33,33,33	0
57	MG	XA	1742	1/1	0.84	0.39	50,50,50,50	0
57	MG	YA	3361	1/1	0.84	0.35	48,48,48,48	0
57	MG	QA	1603	1/1	0.84	0.27	53,53,53,53	0
57	MG	XA	1657	1/1	0.84	0.37	37,37,37,37	0
57	MG	QA	1724	1/1	0.84	0.37	63,63,63,63	0
57	MG	QA	1677	1/1	0.84	0.15	50,50,50,50	0
57	MG	YA	3099	1/1	0.84	0.18	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YA	3155	1/1	0.84	0.34	44,44,44,44	0
57	MG	YA	3345	1/1	0.85	0.32	70,70,70,70	0
57	MG	YA	3443	1/1	0.85	0.22	43,43,43,43	0
57	MG	XA	1654	1/1	0.85	0.39	23,23,23,23	0
57	MG	RA	3327	1/1	0.85	0.28	67,67,67,67	0
57	MG	YA	3450	1/1	0.85	0.34	50,50,50,50	0
57	MG	QA	1723	1/1	0.85	0.20	74,74,74,74	0
57	MG	RE	301	1/1	0.85	0.37	41,41,41,41	0
57	MG	YA	3356	1/1	0.85	0.21	54,54,54,54	0
57	MG	YA	3458	1/1	0.85	0.39	28,28,28,28	0
57	MG	RA	3424	1/1	0.85	0.18	54,54,54,54	0
57	MG	YA	3466	1/1	0.85	0.43	48,48,48,48	0
57	MG	QA	1661	1/1	0.85	0.15	52,52,52,52	0
57	MG	YA	3273	1/1	0.85	0.34	50,50,50,50	0
57	MG	QA	1665	1/1	0.85	0.30	54,54,54,54	0
57	MG	XA	1736	1/1	0.85	0.19	56,56,56,56	0
57	MG	YA	3367	1/1	0.85	0.21	70,70,70,70	0
57	MG	XA	1739	1/1	0.85	0.18	48,48,48,48	0
57	MG	RA	3308	1/1	0.85	0.28	53,53,53,53	0
57	MG	RA	3434	1/1	0.85	0.31	46,46,46,46	0
57	MG	RA	3279	1/1	0.85	0.18	29,29,29,29	0
57	MG	YA	3384	1/1	0.85	0.28	65,65,65,65	0
57	MG	XA	1747	1/1	0.85	0.24	64,64,64,64	0
57	MG	XA	1620	1/1	0.85	0.14	27,27,27,27	0
57	MG	RA	3439	1/1	0.85	0.33	54,54,54,54	0
57	MG	RA	3441	1/1	0.85	0.77	59,59,59,59	0
57	MG	YA	3204	1/1	0.85	0.86	68,68,68,68	0
57	MG	YA	3207	1/1	0.85	0.21	20,20,20,20	0
57	MG	YA	3302	1/1	0.85	0.29	61,61,61,61	0
57	MG	XA	1757	1/1	0.85	0.16	68,68,68,68	0
57	MG	RA	3066	1/1	0.85	0.07	35,35,35,35	0
57	MG	YG	201	1/1	0.85	0.07	51,51,51,51	0
57	MG	QA	1688	1/1	0.85	0.14	56,56,56,56	0
57	MG	RA	3249	1/1	0.85	0.29	48,48,48,48	0
57	MG	RA	3401	1/1	0.85	0.26	58,58,58,58	0
57	MG	YQ	201	1/1	0.85	0.20	54,54,54,54	0
57	MG	XV	103	1/1	0.85	0.29	45,45,45,45	0
57	MG	YA	3148	1/1	0.85	0.38	59,59,59,59	0
57	MG	RA	3107	1/1	0.85	0.35	26,26,26,26	0
57	MG	QA	1648	1/1	0.85	0.12	56,56,56,56	0
57	MG	YA	3429	1/1	0.85	0.26	14,14,14,14	0
57	MG	RA	3334	1/1	0.86	0.97	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3097	1/1	0.86	0.92	53,53,53,53	0
57	MG	RA	3267	1/1	0.86	0.56	41,41,41,41	0
57	MG	RA	3309	1/1	0.86	0.17	60,60,60,60	0
57	MG	YA	3380	1/1	0.86	0.20	54,54,54,54	0
57	MG	QA	1696	1/1	0.86	0.20	58,58,58,58	0
57	MG	XK	201	1/1	0.86	0.31	37,37,37,37	0
57	MG	QA	1746	1/1	0.86	0.28	40,40,40,40	0
57	MG	YA	3309	1/1	0.86	0.65	73,73,73,73	0
57	MG	XA	1722	1/1	0.86	0.37	42,42,42,42	0
57	MG	YA	3323	1/1	0.86	0.19	42,42,42,42	0
57	MG	QA	1728	1/1	0.86	0.17	45,45,45,45	0
57	MG	RA	3003	1/1	0.86	0.39	22,22,22,22	0
57	MG	YA	3239	1/1	0.86	0.13	24,24,24,24	0
57	MG	XA	1677	1/1	0.86	0.34	65,65,65,65	0
57	MG	XA	1680	1/1	0.86	0.24	50,50,50,50	0
57	MG	RA	3158	1/1	0.86	0.40	57,57,57,57	0
57	MG	RA	3240	1/1	0.86	0.26	28,28,28,28	0
57	MG	YA	3088	1/1	0.86	0.35	21,21,21,21	0
57	MG	YA	3169	1/1	0.86	0.48	46,46,46,46	0
57	MG	YA	3349	1/1	0.86	0.25	62,62,62,62	0
57	MG	RA	3244	1/1	0.86	0.23	33,33,33,33	0
57	MG	R5	103	1/1	0.86	0.08	40,40,40,40	0
57	MG	QA	1639	1/1	0.86	0.27	76,76,76,76	0
57	MG	QA	1638	1/1	0.86	0.13	48,48,48,48	0
57	MG	RA	3398	1/1	0.86	0.14	24,24,24,24	0
57	MG	RA	3359	1/1	0.86	0.20	51,51,51,51	0
57	MG	XA	1749	1/1	0.86	0.34	52,52,52,52	0
57	MG	RA	3448	1/1	0.86	0.33	27,27,27,27	0
57	MG	XA	1755	1/1	0.86	0.15	58,58,58,58	0
57	MG	YA	3453	1/1	0.86	0.55	54,54,54,54	0
57	MG	QA	1707	1/1	0.86	0.61	45,45,45,45	0
57	MG	Y7	101	1/1	0.86	0.60	55,55,55,55	0
57	MG	YA	3192	1/1	0.87	0.34	34,34,34,34	0
57	MG	RA	3310	1/1	0.87	0.23	52,52,52,52	0
57	MG	YA	3370	1/1	0.87	0.93	50,50,50,50	0
57	MG	RA	3337	1/1	0.87	0.37	40,40,40,40	0
57	MG	RA	3362	1/1	0.87	0.10	56,56,56,56	0
57	MG	YA	3295	1/1	0.87	0.09	39,39,39,39	0
57	MG	RA	3108	1/1	0.87	0.28	56,56,56,56	0
57	MG	QA	1732	1/1	0.87	0.23	44,44,44,44	0
57	MG	RA	3412	1/1	0.87	0.21	41,41,41,41	0
57	MG	RA	3216	1/1	0.87	0.16	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3415	1/1	0.87	0.48	23,23,23,23	0
57	MG	XN	102	1/1	0.87	0.17	52,52,52,52	0
57	MG	RA	3117	1/1	0.87	0.67	39,39,39,39	0
57	MG	YA	3395	1/1	0.87	0.50	37,37,37,37	0
57	MG	YA	3396	1/1	0.87	0.23	48,48,48,48	0
57	MG	RA	3419	1/1	0.87	0.31	40,40,40,40	0
57	MG	YA	3010	1/1	0.87	0.49	22,22,22,22	0
57	MG	YA	3237	1/1	0.87	0.14	54,54,54,54	0
57	MG	YA	3019	1/1	0.87	0.33	21,21,21,21	0
57	MG	RA	3047	1/1	0.87	0.23	16,16,16,16	0
57	MG	YA	3408	1/1	0.87	0.36	47,47,47,47	0
57	MG	RA	3265	1/1	0.87	0.65	57,57,57,57	0
57	MG	RA	3126	1/1	0.87	0.25	34,34,34,34	0
57	MG	QA	1705	1/1	0.87	0.46	30,30,30,30	0
57	MG	RA	3354	1/1	0.87	0.17	65,65,65,65	0
57	MG	RA	3307	1/1	0.87	0.45	64,64,64,64	0
57	MG	RA	3091	1/1	0.87	0.31	24,24,24,24	0
57	MG	R5	102	1/1	0.87	0.26	40,40,40,40	0
57	MG	QA	1614	1/1	0.87	0.18	39,39,39,39	0
57	MG	XA	1617	1/1	0.87	0.19	42,42,42,42	0
57	MG	YA	3181	1/1	0.87	0.26	50,50,50,50	0
57	MG	RA	3440	1/1	0.87	0.37	53,53,53,53	0
57	MG	XA	1692	1/1	0.87	0.14	36,36,36,36	0
57	MG	XA	1694	1/1	0.87	0.20	43,43,43,43	0
57	MG	XA	1622	1/1	0.87	0.37	40,40,40,40	0
58	ZN	XD	301	1/1	0.87	0.41	60,60,60,60	0
57	MG	RA	3234	1/1	0.88	0.49	49,49,49,49	0
57	MG	RA	3303	1/1	0.88	0.14	42,42,42,42	0
57	MG	YA	3427	1/1	0.88	0.27	29,29,29,29	0
57	MG	XA	1724	1/1	0.88	0.60	54,54,54,54	0
57	MG	QA	1655	1/1	0.88	0.36	46,46,46,46	0
57	MG	YA	3433	1/1	0.88	0.35	46,46,46,46	0
57	MG	XA	1648	1/1	0.88	0.21	55,55,55,55	0
57	MG	YA	3439	1/1	0.88	0.33	42,42,42,42	0
57	MG	XA	1651	1/1	0.88	0.40	32,32,32,32	0
57	MG	RA	3349	1/1	0.88	0.20	41,41,41,41	0
57	MG	QV	105	1/1	0.88	0.34	31,31,31,31	0
57	MG	YA	3219	1/1	0.88	0.26	46,46,46,46	0
57	MG	RA	3186	1/1	0.88	0.22	54,54,54,54	0
57	MG	YA	3230	1/1	0.88	0.29	56,56,56,56	0
57	MG	QA	1681	1/1	0.88	0.21	68,68,68,68	0
57	MG	YA	3456	1/1	0.88	0.25	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	QA	1674	1/1	0.88	0.17	54,54,54,54	0
57	MG	XA	1676	1/1	0.88	0.22	33,33,33,33	0
57	MG	RA	3413	1/1	0.88	0.31	41,41,41,41	0
57	MG	RA	3191	1/1	0.88	0.14	24,24,24,24	0
57	MG	RA	3005	1/1	0.88	0.46	21,21,21,21	0
57	MG	YA	3244	1/1	0.88	0.54	57,57,57,57	0
57	MG	RV	201	1/1	0.88	0.27	14,14,14,14	0
57	MG	QA	1747	1/1	0.88	0.10	57,57,57,57	0
57	MG	RA	3272	1/1	0.88	0.23	26,26,26,26	0
57	MG	RA	3420	1/1	0.88	0.17	49,49,49,49	0
57	MG	RA	3206	1/1	0.88	0.20	18,18,18,18	0
57	MG	XA	1760	1/1	0.88	0.13	77,77,77,77	0
57	MG	YA	3266	1/1	0.88	0.40	31,31,31,31	0
57	MG	YA	3372	1/1	0.88	0.41	55,55,55,55	0
57	MG	XA	1691	1/1	0.88	0.20	46,46,46,46	0
57	MG	RA	3023	1/1	0.88	0.28	55,55,55,55	0
57	MG	QA	1610	1/1	0.88	0.10	76,76,76,76	0
57	MG	YA	3383	1/1	0.88	0.15	51,51,51,51	0
57	MG	XA	1608	1/1	0.88	0.41	47,47,47,47	0
57	MG	QA	1623	1/1	0.88	0.36	34,34,34,34	0
57	MG	XS	300	1/1	0.88	0.20	46,46,46,46	0
57	MG	RA	3288	1/1	0.88	0.17	61,61,61,61	0
57	MG	RA	3163	1/1	0.88	0.10	55,55,55,55	0
57	MG	YA	3005	1/1	0.88	0.44	24,24,24,24	0
57	MG	XA	1623	1/1	0.88	0.25	36,36,36,36	0
57	MG	YA	3175	1/1	0.88	0.12	27,27,27,27	0
57	MG	QA	1653	1/1	0.88	0.59	50,50,50,50	0
57	MG	YA	3292	1/1	0.88	0.26	32,32,32,32	0
57	MG	YA	3177	1/1	0.88	0.26	59,59,59,59	0
57	MG	QA	1710	1/1	0.88	0.19	50,50,50,50	0
57	MG	QA	1694	1/1	0.88	0.17	55,55,55,55	0
57	MG	YA	3038	1/1	0.88	0.22	45,45,45,45	0
57	MG	YW	201	1/1	0.88	0.33	32,32,32,32	0
57	MG	YA	3048	1/1	0.88	0.30	33,33,33,33	0
57	MG	Y5	102	1/1	0.88	0.29	50,50,50,50	0
57	MG	Y5	103	1/1	0.88	0.29	23,23,23,23	0
57	MG	RA	3175	1/1	0.88	0.16	31,31,31,31	0
57	MG	QV	101	1/1	0.88	0.29	15,15,15,15	0
57	MG	RA	3432	1/1	0.89	0.26	39,39,39,39	0
57	MG	QA	1706	1/1	0.89	0.23	47,47,47,47	0
57	MG	RA	3120	1/1	0.89	0.14	42,42,42,42	0
57	MG	RA	3343	1/1	0.89	0.63	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YA	3417	1/1	0.89	0.12	55,55,55,55	0
57	MG	YA	3418	1/1	0.89	0.28	24,24,24,24	0
57	MG	RA	3314	1/1	0.89	0.12	62,62,62,62	0
57	MG	RA	3385	1/1	0.89	0.25	57,57,57,57	0
57	MG	YA	3298	1/1	0.89	0.28	52,52,52,52	0
57	MG	YA	3013	1/1	0.89	0.57	27,27,27,27	0
57	MG	RA	3124	1/1	0.89	0.23	40,40,40,40	0
57	MG	RA	3230	1/1	0.89	0.22	42,42,42,42	0
57	MG	XA	1710	1/1	0.89	0.20	58,58,58,58	0
57	MG	YA	3035	1/1	0.89	0.23	39,39,39,39	0
57	MG	YA	3320	1/1	0.89	0.35	48,48,48,48	0
57	MG	XA	1633	1/1	0.89	0.37	28,28,28,28	0
57	MG	YA	3189	1/1	0.89	0.26	52,52,52,52	0
57	MG	YA	3326	1/1	0.89	0.67	46,46,46,46	0
57	MG	XA	1714	1/1	0.89	0.20	41,41,41,41	0
57	MG	QA	1729	1/1	0.89	0.17	30,30,30,30	0
57	MG	XA	1636	1/1	0.89	0.25	46,46,46,46	0
57	MG	YA	3199	1/1	0.89	0.45	54,54,54,54	0
57	MG	RA	3350	1/1	0.89	0.99	54,54,54,54	0
57	MG	QA	1731	1/1	0.89	0.27	45,45,45,45	0
57	MG	RA	3203	1/1	0.89	0.33	18,18,18,18	0
57	MG	RA	3324	1/1	0.89	0.44	40,40,40,40	0
57	MG	YA	3216	1/1	0.89	0.24	30,30,30,30	0
57	MG	YA	3091	1/1	0.89	0.30	40,40,40,40	0
57	MG	RA	3451	1/1	0.89	0.45	23,23,23,23	0
57	MG	YA	3226	1/1	0.89	0.36	48,48,48,48	0
57	MG	YA	3472	1/1	0.89	0.41	66,66,66,66	0
57	MG	RA	3133	1/1	0.89	0.50	59,59,59,59	0
57	MG	YA	3359	1/1	0.89	0.20	36,36,36,36	0
57	MG	XA	1734	1/1	0.89	0.21	16,16,16,16	0
57	MG	YA	3478	1/1	0.89	0.48	81,81,81,81	0
57	MG	RA	3172	1/1	0.89	0.17	47,47,47,47	0
57	MG	YA	3106	1/1	0.89	0.28	42,42,42,42	0
57	MG	XA	1738	1/1	0.89	0.24	43,43,43,43	0
57	MG	XA	1663	1/1	0.89	0.34	42,42,42,42	0
57	MG	YA	3114	1/1	0.89	0.35	26,26,26,26	0
57	MG	XA	1740	1/1	0.89	0.28	56,56,56,56	0
57	MG	RA	3134	1/1	0.89	0.85	46,46,46,46	0
57	MG	RA	3255	1/1	0.89	0.54	43,43,43,43	0
57	MG	QA	1627	1/1	0.89	0.14	42,42,42,42	0
57	MG	RF	301	1/1	0.89	0.15	34,34,34,34	0
57	MG	YA	3256	1/1	0.89	0.29	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
57	MG	QL	201	1/1	0.89	0.21	58,58,58,58	0
57	MG	YA	3382	1/1	0.89	0.28	55,55,55,55	0
57	MG	XA	1681	1/1	0.89	0.17	38,38,38,38	0
57	MG	RA	3416	1/1	0.89	0.25	44,44,44,44	0
57	MG	YA	3385	1/1	0.89	0.37	50,50,50,50	0
57	MG	RA	3051	1/1	0.89	0.35	26,26,26,26	0
57	MG	RA	3365	1/1	0.89	0.24	51,51,51,51	0
57	MG	QA	1699	1/1	0.89	0.28	58,58,58,58	0
57	MG	RA	3367	1/1	0.89	0.45	31,31,31,31	0
57	MG	RA	3270	1/1	0.89	0.45	42,42,42,42	0
57	MG	RA	3369	1/1	0.89	0.58	40,40,40,40	0
57	MG	XA	1762	1/1	0.89	0.09	33,33,33,33	0
57	MG	RA	3428	1/1	0.89	0.45	37,37,37,37	0
57	MG	Y5	101	1/1	0.89	0.28	27,27,27,27	0
57	MG	RA	3339	1/1	0.89	0.13	52,52,52,52	0
57	MG	YA	3400	1/1	0.89	0.13	42,42,42,42	0
57	MG	XA	1698	1/1	0.89	0.12	75,75,75,75	0
57	MG	YA	3168	1/1	0.89	0.24	31,31,31,31	0
57	MG	YA	3293	1/1	0.90	0.35	33,33,33,33	0
57	MG	YA	3061	1/1	0.90	0.51	27,27,27,27	0
57	MG	RA	3268	1/1	0.90	0.18	42,42,42,42	0
57	MG	QA	1673	1/1	0.90	0.12	60,60,60,60	0
57	MG	RA	3355	1/1	0.90	0.68	81,81,81,81	0
57	MG	RA	3094	1/1	0.90	0.42	43,43,43,43	0
57	MG	YA	3301	1/1	0.90	0.17	55,55,55,55	0
57	MG	YA	3188	1/1	0.90	0.37	38,38,38,38	0
57	MG	RA	3185	1/1	0.90	0.12	32,32,32,32	0
57	MG	XA	1671	1/1	0.90	0.39	41,41,41,41	0
57	MG	YA	3092	1/1	0.90	0.45	37,37,37,37	0
57	MG	YA	3313	1/1	0.90	0.59	37,37,37,37	0
57	MG	YA	3316	1/1	0.90	0.29	42,42,42,42	0
57	MG	YA	3095	1/1	0.90	0.36	42,42,42,42	0
57	MG	YA	3436	1/1	0.90	0.66	38,38,38,38	0
57	MG	XA	1675	1/1	0.90	0.33	47,47,47,47	0
57	MG	RA	3276	1/1	0.90	0.19	50,50,50,50	0
57	MG	RA	3222	1/1	0.90	0.46	50,50,50,50	0
57	MG	RA	3227	1/1	0.90	0.12	42,42,42,42	0
57	MG	RA	3283	1/1	0.90	0.35	36,36,36,36	0
57	MG	YA	3108	1/1	0.90	0.23	25,25,25,25	0
57	MG	RA	3151	1/1	0.90	0.21	54,54,54,54	0
57	MG	RA	3330	1/1	0.90	0.25	49,49,49,49	0
57	MG	RA	3331	1/1	0.90	0.66	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YA	3117	1/1	0.90	0.53	34,34,34,34	0
57	MG	QA	1613	1/1	0.90	0.28	53,53,53,53	0
57	MG	RA	3427	1/1	0.90	0.34	48,48,48,48	0
57	MG	YA	3459	1/1	0.90	0.22	24,24,24,24	0
57	MG	RA	3125	1/1	0.90	0.23	23,23,23,23	0
57	MG	XA	1613	1/1	0.90	0.14	24,24,24,24	0
57	MG	RA	3006	1/1	0.90	0.17	12,12,12,12	0
57	MG	YA	3355	1/1	0.90	0.51	33,33,33,33	0
57	MG	XA	1693	1/1	0.90	0.47	89,89,89,89	0
57	MG	RA	3237	1/1	0.90	0.45	34,34,34,34	0
57	MG	RA	3192	1/1	0.90	0.22	36,36,36,36	0
57	MG	YA	3245	1/1	0.90	0.49	40,40,40,40	0
57	MG	YA	3143	1/1	0.90	0.43	48,48,48,48	0
57	MG	YA	3363	1/1	0.90	0.56	59,59,59,59	0
57	MG	YA	3364	1/1	0.90	0.10	33,33,33,33	0
57	MG	YA	3481	1/1	0.90	0.46	53,53,53,53	0
57	MG	YA	3248	1/1	0.90	0.28	61,61,61,61	0
57	MG	YA	3483	1/1	0.90	0.20	51,51,51,51	0
57	MG	YA	3487	1/1	0.90	0.19	27,27,27,27	0
57	MG	RA	3242	1/1	0.90	0.09	40,40,40,40	0
57	MG	YA	3251	1/1	0.90	0.63	33,33,33,33	0
57	MG	RA	3435	1/1	0.90	0.27	57,57,57,57	0
57	MG	XA	1701	1/1	0.90	0.46	41,41,41,41	0
57	MG	RA	3166	1/1	0.90	0.14	27,27,27,27	0
57	MG	YA	3496	1/1	0.90	0.43	55,55,55,55	0
57	MG	RA	3301	1/1	0.90	0.28	34,34,34,34	0
57	MG	YA	3264	1/1	0.90	0.24	29,29,29,29	0
57	MG	YA	3153	1/1	0.90	0.47	41,41,41,41	0
57	MG	RA	3105	1/1	0.90	0.17	33,33,33,33	0
57	MG	YA	3157	1/1	0.90	0.15	34,34,34,34	0
57	MG	XA	1705	1/1	0.90	0.47	47,47,47,47	0
57	MG	QA	1609	1/1	0.90	0.45	61,61,61,61	0
57	MG	XA	1631	1/1	0.90	0.30	24,24,24,24	0
57	MG	RA	3170	1/1	0.90	0.23	47,47,47,47	0
57	MG	YA	3390	1/1	0.90	0.32	45,45,45,45	0
57	MG	YA	3276	1/1	0.90	0.39	43,43,43,43	0
57	MG	YA	3280	1/1	0.90	0.39	41,41,41,41	0
57	MG	QA	1739	1/1	0.90	0.30	52,52,52,52	0
57	MG	RA	3393	1/1	0.90	0.58	23,23,23,23	0
57	MG	QA	1715	1/1	0.90	0.28	33,33,33,33	0
57	MG	QA	1733	1/1	0.90	0.17	42,42,42,42	0
57	MG	YA	3397	1/1	0.90	0.25	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	XA	1719	1/1	0.90	0.22	43,43,43,43	0
57	MG	RA	3312	1/1	0.90	0.14	47,47,47,47	0
57	MG	QA	1601	1/1	0.90	0.29	39,39,39,39	0
57	MG	RB	203	1/1	0.90	0.31	45,45,45,45	0
57	MG	YA	3403	1/1	0.90	0.21	46,46,46,46	0
57	MG	YA	3286	1/1	0.91	0.49	56,56,56,56	0
57	MG	XA	1696	1/1	0.91	0.20	53,53,53,53	0
57	MG	RA	3049	1/1	0.91	0.31	23,23,23,23	0
57	MG	YA	3401	1/1	0.91	0.53	38,38,38,38	0
57	MG	RA	3305	1/1	0.91	0.32	41,41,41,41	0
57	MG	RA	3239	1/1	0.91	0.25	60,60,60,60	0
57	MG	QA	1643	1/1	0.91	0.09	40,40,40,40	0
57	MG	RA	3053	1/1	0.91	0.28	40,40,40,40	0
57	MG	QA	1683	1/1	0.91	0.35	59,59,59,59	0
57	MG	RA	3246	1/1	0.91	0.25	39,39,39,39	0
57	MG	YA	3029	1/1	0.91	0.28	33,33,33,33	0
57	MG	RA	3247	1/1	0.91	0.42	37,37,37,37	0
57	MG	XA	1626	1/1	0.91	0.32	37,37,37,37	0
57	MG	YA	3037	1/1	0.91	0.33	27,27,27,27	0
57	MG	QA	1647	1/1	0.91	0.32	60,60,60,60	0
57	MG	YA	3306	1/1	0.91	0.36	42,42,42,42	0
57	MG	YA	3040	1/1	0.91	0.27	26,26,26,26	0
57	MG	YA	3046	1/1	0.91	0.21	14,14,14,14	0
57	MG	YA	3047	1/1	0.91	0.51	18,18,18,18	0
57	MG	YA	3311	1/1	0.91	0.34	77,77,77,77	0
57	MG	RA	3316	1/1	0.91	0.86	40,40,40,40	0
57	MG	YA	3315	1/1	0.91	0.13	34,34,34,34	0
57	MG	YA	3438	1/1	0.91	0.16	26,26,26,26	0
57	MG	RA	3317	1/1	0.91	0.40	36,36,36,36	0
57	MG	YA	3193	1/1	0.91	0.45	43,43,43,43	0
57	MG	YA	3322	1/1	0.91	0.19	48,48,48,48	0
57	MG	RA	3253	1/1	0.91	0.47	53,53,53,53	0
57	MG	XA	1632	1/1	0.91	0.33	49,49,49,49	0
57	MG	QA	1662	1/1	0.91	0.17	27,27,27,27	0
57	MG	RA	3071	1/1	0.91	0.28	12,12,12,12	0
57	MG	QA	1687	1/1	0.91	0.10	52,52,52,52	0
57	MG	XA	1637	1/1	0.91	0.28	57,57,57,57	0
57	MG	YA	3333	1/1	0.91	0.18	53,53,53,53	0
57	MG	QA	1628	1/1	0.91	0.12	65,65,65,65	0
57	MG	RA	3137	1/1	0.91	0.16	55,55,55,55	0
57	MG	YA	3217	1/1	0.91	0.20	35,35,35,35	0
57	MG	YA	3343	1/1	0.91	0.51	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3444	1/1	0.91	0.14	52,52,52,52	0
57	MG	YA	3469	1/1	0.91	0.39	45,45,45,45	0
57	MG	RA	3445	1/1	0.91	0.54	18,18,18,18	0
57	MG	XA	1730	1/1	0.91	0.44	49,49,49,49	0
57	MG	YA	3350	1/1	0.91	0.37	55,55,55,55	0
57	MG	YA	3351	1/1	0.91	0.34	50,50,50,50	0
57	MG	QA	1690	1/1	0.91	0.24	49,49,49,49	0
57	MG	RA	3141	1/1	0.91	0.07	34,34,34,34	0
57	MG	YA	3105	1/1	0.91	0.19	56,56,56,56	0
57	MG	XA	1735	1/1	0.91	0.33	44,44,44,44	0
57	MG	YA	3107	1/1	0.91	0.18	33,33,33,33	0
57	MG	QA	1730	1/1	0.91	0.09	69,69,69,69	0
57	MG	QA	1619	1/1	0.91	0.44	31,31,31,31	0
57	MG	QA	1712	1/1	0.91	0.19	58,58,58,58	0
57	MG	QA	1651	1/1	0.91	0.30	39,39,39,39	0
57	MG	RA	3099	1/1	0.91	0.29	13,13,13,13	0
57	MG	RA	3278	1/1	0.91	0.27	39,39,39,39	0
57	MG	RA	3154	1/1	0.91	0.53	42,42,42,42	0
57	MG	RA	3156	1/1	0.91	0.13	42,42,42,42	0
57	MG	YA	3130	1/1	0.91	0.26	34,34,34,34	0
57	MG	YA	3132	1/1	0.91	0.15	29,29,29,29	0
57	MG	RA	3032	1/1	0.91	0.28	17,17,17,17	0
57	MG	YA	3500	1/1	0.91	0.35	71,71,71,71	0
57	MG	YA	3258	1/1	0.91	0.48	58,58,58,58	0
57	MG	QA	1642	1/1	0.91	0.15	50,50,50,50	0
57	MG	RA	3161	1/1	0.91	0.15	36,36,36,36	0
57	MG	YA	3376	1/1	0.91	0.34	63,63,63,63	0
57	MG	YE	301	1/1	0.91	0.20	40,40,40,40	0
57	MG	XA	1754	1/1	0.91	0.40	61,61,61,61	0
57	MG	XA	1683	1/1	0.91	0.17	38,38,38,38	0
57	MG	RA	3407	1/1	0.91	0.14	60,60,60,60	0
57	MG	RQ	202	1/1	0.91	0.11	58,58,58,58	0
57	MG	RA	3162	1/1	0.91	0.55	34,34,34,34	0
57	MG	XA	1759	1/1	0.91	0.71	60,60,60,60	0
57	MG	QA	1654	1/1	0.91	0.47	41,41,41,41	0
57	MG	YA	3388	1/1	0.91	0.12	52,52,52,52	0
57	MG	RA	3044	1/1	0.91	0.54	27,27,27,27	0
57	MG	RA	3046	1/1	0.91	0.38	16,16,16,16	0
57	MG	YA	3278	1/1	0.91	0.61	55,55,55,55	0
57	MG	QA	1736	1/1	0.91	0.13	47,47,47,47	0
57	MG	RA	3114	1/1	0.91	0.29	30,30,30,30	0
57	MG	RA	3171	1/1	0.91	0.71	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YA	3284	1/1	0.91	0.37	54,54,54,54	0
57	MG	XA	1695	1/1	0.91	0.30	40,40,40,40	0
57	MG	YA	3206	1/1	0.92	0.23	38,38,38,38	0
57	MG	YA	3411	1/1	0.92	0.35	67,67,67,67	0
57	MG	YA	3314	1/1	0.92	0.48	49,49,49,49	0
57	MG	RA	3252	1/1	0.92	0.21	43,43,43,43	0
57	MG	YA	3211	1/1	0.92	0.35	43,43,43,43	0
57	MG	YA	3212	1/1	0.92	0.12	28,28,28,28	0
57	MG	RA	3209	1/1	0.92	0.38	30,30,30,30	0
57	MG	XA	1745	1/1	0.92	0.19	36,36,36,36	0
57	MG	RA	3306	1/1	0.92	0.35	39,39,39,39	0
57	MG	YA	3109	1/1	0.92	0.49	40,40,40,40	0
57	MG	RA	3135	1/1	0.92	0.40	44,44,44,44	0
57	MG	YA	3224	1/1	0.92	0.31	35,35,35,35	0
57	MG	RA	3411	1/1	0.92	0.27	49,49,49,49	0
57	MG	YA	3227	1/1	0.92	0.44	51,51,51,51	0
57	MG	YA	3334	1/1	0.92	0.23	35,35,35,35	0
57	MG	YA	3442	1/1	0.92	0.30	61,61,61,61	0
57	MG	QA	1612	1/1	0.92	0.24	48,48,48,48	0
57	MG	YA	3229	1/1	0.92	0.33	29,29,29,29	0
57	MG	YA	3115	1/1	0.92	0.91	45,45,45,45	0
57	MG	RA	3256	1/1	0.92	0.60	67,67,67,67	0
57	MG	RA	3212	1/1	0.92	0.38	30,30,30,30	0
57	MG	RA	3262	1/1	0.92	0.17	40,40,40,40	0
57	MG	RA	3263	1/1	0.92	0.54	42,42,42,42	0
57	MG	RA	3018	1/1	0.92	0.48	20,20,20,20	0
57	MG	RA	3140	1/1	0.92	0.26	18,18,18,18	0
57	MG	YA	3242	1/1	0.92	0.22	25,25,25,25	0
57	MG	QE	201	1/1	0.92	0.13	42,42,42,42	0
57	MG	RA	3070	1/1	0.92	0.30	28,28,28,28	0
57	MG	YA	3135	1/1	0.92	0.26	31,31,31,31	0
57	MG	RA	3220	1/1	0.92	0.89	53,53,53,53	0
57	MG	QA	1721	1/1	0.92	0.28	52,52,52,52	0
57	MG	RA	3363	1/1	0.92	0.50	39,39,39,39	0
57	MG	RA	3033	1/1	0.92	0.52	25,25,25,25	0
57	MG	RA	3430	1/1	0.92	0.19	52,52,52,52	0
57	MG	YA	3473	1/1	0.92	0.24	39,39,39,39	0
57	MG	RA	3223	1/1	0.92	0.55	38,38,38,38	0
57	MG	QA	1700	1/1	0.92	0.56	51,51,51,51	0
57	MG	XV	104	1/1	0.92	0.21	15,15,15,15	0
57	MG	XA	1627	1/1	0.92	0.12	71,71,71,71	0
57	MG	YA	3479	1/1	0.92	0.09	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3087	1/1	0.92	0.19	31,31,31,31	0
57	MG	YA	3368	1/1	0.92	0.28	49,49,49,49	0
57	MG	RA	3328	1/1	0.92	0.55	61,61,61,61	0
57	MG	RA	3152	1/1	0.92	0.68	43,43,43,43	0
57	MG	YA	3484	1/1	0.92	0.18	47,47,47,47	0
57	MG	RA	3436	1/1	0.92	0.20	51,51,51,51	0
57	MG	RA	3437	1/1	0.92	0.29	52,52,52,52	0
57	MG	YA	3373	1/1	0.92	0.36	61,61,61,61	0
57	MG	RA	3281	1/1	0.92	0.27	53,53,53,53	0
57	MG	YA	3164	1/1	0.92	0.08	50,50,50,50	0
57	MG	YA	3166	1/1	0.92	0.18	41,41,41,41	0
57	MG	RA	3153	1/1	0.92	0.24	23,23,23,23	0
57	MG	YA	3497	1/1	0.92	0.11	55,55,55,55	0
57	MG	XA	1713	1/1	0.92	0.42	48,48,48,48	0
57	MG	RA	3119	1/1	0.92	0.35	23,23,23,23	0
57	MG	YA	3170	1/1	0.92	0.31	38,38,38,38	0
57	MG	RA	3374	1/1	0.92	0.79	44,44,44,44	0
57	MG	XA	1718	1/1	0.92	0.26	47,47,47,47	0
57	MG	YA	3041	1/1	0.92	0.40	23,23,23,23	0
57	MG	XA	1638	1/1	0.92	0.28	59,59,59,59	0
57	MG	RA	3375	1/1	0.92	0.60	61,61,61,61	0
57	MG	QA	1702	1/1	0.92	0.19	54,54,54,54	0
57	MG	RA	3380	1/1	0.92	0.36	15,15,15,15	0
57	MG	QA	1621	1/1	0.92	0.17	45,45,45,45	0
57	MG	XA	1726	1/1	0.92	0.26	54,54,54,54	0
57	MG	RA	3335	1/1	0.92	0.18	43,43,43,43	0
57	MG	QA	1629	1/1	0.92	0.29	53,53,53,53	0
57	MG	RA	3196	1/1	0.92	0.49	33,33,33,33	0
57	MG	RA	3391	1/1	0.92	0.12	24,24,24,24	0
57	MG	YA	3190	1/1	0.92	0.62	25,25,25,25	0
57	MG	QA	1675	1/1	0.92	0.37	48,48,48,48	0
57	MG	XA	1668	1/1	0.92	0.26	35,35,35,35	0
57	MG	RA	3245	1/1	0.92	0.20	34,34,34,34	0
57	MG	QA	1718	1/1	0.92	0.31	51,51,51,51	0
57	MG	XA	1672	1/1	0.92	0.14	52,52,52,52	0
57	MG	QA	1676	1/1	0.92	0.20	46,46,46,46	0
57	MG	QA	1740	1/1	0.92	0.53	46,46,46,46	0
57	MG	RA	3340	1/1	0.93	0.18	40,40,40,40	0
57	MG	YA	3412	1/1	0.93	0.20	25,25,25,25	0
57	MG	YA	3414	1/1	0.93	0.77	60,60,60,60	0
57	MG	XA	1602	1/1	0.93	0.31	32,32,32,32	0
57	MG	XA	1603	1/1	0.93	0.12	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3086	1/1	0.93	0.23	27,27,27,27	0
57	MG	YA	3213	1/1	0.93	0.22	14,14,14,14	0
57	MG	YA	3423	1/1	0.93	0.44	57,57,57,57	0
57	MG	QA	1691	1/1	0.93	0.25	38,38,38,38	0
57	MG	XA	1615	1/1	0.93	0.38	38,38,38,38	0
57	MG	RA	3378	1/1	0.93	0.09	49,49,49,49	0
57	MG	XA	1618	1/1	0.93	0.28	24,24,24,24	0
57	MG	YA	3431	1/1	0.93	0.08	31,31,31,31	0
57	MG	YA	3432	1/1	0.93	0.32	47,47,47,47	0
57	MG	YA	3119	1/1	0.93	0.32	32,32,32,32	0
57	MG	YA	3434	1/1	0.93	0.23	45,45,45,45	0
57	MG	RA	3144	1/1	0.93	0.42	44,44,44,44	0
57	MG	YA	3125	1/1	0.93	0.31	22,22,22,22	0
57	MG	RA	3381	1/1	0.93	0.79	43,43,43,43	0
57	MG	QA	1618	1/1	0.93	0.13	44,44,44,44	0
57	MG	YA	3440	1/1	0.93	0.34	49,49,49,49	0
57	MG	YA	3441	1/1	0.93	0.23	35,35,35,35	0
57	MG	RA	3384	1/1	0.93	0.24	28,28,28,28	0
57	MG	RA	3346	1/1	0.93	0.21	38,38,38,38	0
57	MG	RA	3241	1/1	0.93	0.18	35,35,35,35	0
57	MG	RA	3275	1/1	0.93	0.95	51,51,51,51	0
57	MG	QA	1703	1/1	0.93	0.33	86,86,86,86	0
57	MG	YA	3139	1/1	0.93	0.38	29,29,29,29	0
57	MG	RA	3243	1/1	0.93	0.29	48,48,48,48	0
57	MG	YA	3238	1/1	0.93	0.24	28,28,28,28	0
57	MG	RA	3318	1/1	0.93	0.34	51,51,51,51	0
57	MG	YA	3241	1/1	0.93	0.21	29,29,29,29	0
57	MG	YA	3002	1/1	0.93	0.49	11,11,11,11	0
57	MG	RA	3443	1/1	0.93	0.29	56,56,56,56	0
57	MG	RA	3029	1/1	0.93	0.27	28,28,28,28	0
57	MG	YA	3462	1/1	0.93	0.25	36,36,36,36	0
57	MG	RA	3030	1/1	0.93	0.34	15,15,15,15	0
57	MG	RA	3095	1/1	0.93	0.19	38,38,38,38	0
57	MG	YA	3468	1/1	0.93	0.21	41,41,41,41	0
57	MG	YA	3151	1/1	0.93	0.29	28,28,28,28	0
57	MG	QA	1748	1/1	0.93	0.12	46,46,46,46	0
57	MG	YA	3253	1/1	0.93	0.16	48,48,48,48	0
57	MG	RA	3067	1/1	0.93	0.18	32,32,32,32	0
57	MG	RA	3403	1/1	0.93	0.26	54,54,54,54	0
57	MG	YA	3156	1/1	0.93	0.23	29,29,29,29	0
57	MG	RA	3250	1/1	0.93	0.31	56,56,56,56	0
57	MG	QA	1646	1/1	0.93	0.09	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3409	1/1	0.93	0.40	43,43,43,43	0
57	MG	RB	204	1/1	0.93	0.07	47,47,47,47	0
57	MG	XA	1653	1/1	0.93	0.28	29,29,29,29	0
57	MG	RA	3360	1/1	0.93	0.12	32,32,32,32	0
57	MG	YA	3269	1/1	0.93	0.27	60,60,60,60	0
57	MG	YA	3271	1/1	0.93	0.38	42,42,42,42	0
57	MG	XA	1655	1/1	0.93	0.32	53,53,53,53	0
57	MG	QA	1664	1/1	0.93	0.19	39,39,39,39	0
57	MG	QA	1714	1/1	0.93	0.35	46,46,46,46	0
57	MG	QA	1620	1/1	0.93	0.16	40,40,40,40	0
57	MG	RA	3077	1/1	0.93	0.26	24,24,24,24	0
57	MG	RA	3299	1/1	0.93	0.35	49,49,49,49	0
57	MG	YA	3381	1/1	0.93	0.54	54,54,54,54	0
57	MG	YA	3069	1/1	0.93	0.27	19,19,19,19	0
57	MG	YA	3073	1/1	0.93	0.21	25,25,25,25	0
57	MG	YA	3282	1/1	0.93	0.32	31,31,31,31	0
57	MG	YA	3074	1/1	0.93	0.36	23,23,23,23	0
57	MG	YA	3076	1/1	0.93	0.29	27,27,27,27	0
57	MG	YA	3079	1/1	0.93	0.30	31,31,31,31	0
57	MG	YA	3389	1/1	0.93	0.35	51,51,51,51	0
57	MG	RP	201	1/1	0.93	0.20	31,31,31,31	0
57	MG	YB	203	1/1	0.93	0.25	31,31,31,31	0
57	MG	YA	3086	1/1	0.93	0.21	23,23,23,23	0
57	MG	YA	3184	1/1	0.93	0.20	46,46,46,46	0
57	MG	XA	1670	1/1	0.93	0.17	16,16,16,16	0
57	MG	YH	201	1/1	0.93	0.32	58,58,58,58	0
57	MG	RA	3257	1/1	0.93	0.23	42,42,42,42	0
57	MG	YN	201	1/1	0.93	0.24	38,38,38,38	0
57	MG	RA	3259	1/1	0.93	0.23	51,51,51,51	0
57	MG	XA	1674	1/1	0.93	0.24	43,43,43,43	0
57	MG	RA	3139	1/1	0.93	0.16	44,44,44,44	0
57	MG	RA	3165	1/1	0.93	0.12	57,57,57,57	0
57	MG	YA	3296	1/1	0.93	0.26	52,52,52,52	0
57	MG	RA	3197	1/1	0.93	0.29	24,24,24,24	0
57	MG	YA	3194	1/1	0.93	0.25	33,33,33,33	0
57	MG	R0	101	1/1	0.93	0.32	16,16,16,16	0
57	MG	RA	3425	1/1	0.93	0.34	46,46,46,46	0
57	MG	RA	3231	1/1	0.93	0.16	41,41,41,41	0
57	MG	YA	3305	1/1	0.93	0.36	34,34,34,34	0
57	MG	YA	3200	1/1	0.93	0.21	32,32,32,32	0
57	MG	R5	101	1/1	0.93	0.29	17,17,17,17	0
58	ZN	QD	301	1/1	0.93	0.39	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	QA	1658	1/1	0.93	0.50	34,34,34,34	0
57	MG	RA	3405	1/1	0.94	0.26	48,48,48,48	0
57	MG	XA	1697	1/1	0.94	0.15	62,62,62,62	0
57	MG	RA	3287	1/1	0.94	0.29	30,30,30,30	0
57	MG	RA	3251	1/1	0.94	0.11	24,24,24,24	0
57	MG	YA	3223	1/1	0.94	0.09	30,30,30,30	0
57	MG	XA	1764	1/1	0.94	0.07	45,45,45,45	0
57	MG	YA	3225	1/1	0.94	0.26	16,16,16,16	0
57	MG	RA	3181	1/1	0.94	0.12	56,56,56,56	0
57	MG	YA	3121	1/1	0.94	0.12	27,27,27,27	0
57	MG	RA	3410	1/1	0.94	0.19	43,43,43,43	0
57	MG	YA	3126	1/1	0.94	0.31	22,22,22,22	0
57	MG	XL	201	1/1	0.94	0.15	39,39,39,39	0
57	MG	RB	201	1/1	0.94	0.29	32,32,32,32	0
57	MG	RB	202	1/1	0.94	0.36	33,33,33,33	0
57	MG	RA	3127	1/1	0.94	0.39	60,60,60,60	0
57	MG	RA	3072	1/1	0.94	0.15	32,32,32,32	0
57	MG	RA	3017	1/1	0.94	0.23	16,16,16,16	0
57	MG	QA	1657	1/1	0.94	0.59	42,42,42,42	0
57	MG	YA	3445	1/1	0.94	0.20	38,38,38,38	0
57	MG	RA	3226	1/1	0.94	0.56	35,35,35,35	0
57	MG	RA	3022	1/1	0.94	0.52	22,22,22,22	0
57	MG	YA	3011	1/1	0.94	0.52	22,22,22,22	0
57	MG	XA	1647	1/1	0.94	0.09	45,45,45,45	0
57	MG	YA	3144	1/1	0.94	0.61	42,42,42,42	0
57	MG	RE	302	1/1	0.94	0.45	15,15,15,15	0
57	MG	YA	3247	1/1	0.94	0.47	47,47,47,47	0
57	MG	YA	3357	1/1	0.94	0.13	50,50,50,50	0
57	MG	RA	3260	1/1	0.94	0.32	45,45,45,45	0
57	MG	YA	3028	1/1	0.94	0.20	14,14,14,14	0
57	MG	QV	104	1/1	0.94	0.18	56,56,56,56	0
57	MG	RA	3109	1/1	0.94	0.30	25,25,25,25	0
57	MG	YA	3032	1/1	0.94	0.35	26,26,26,26	0
57	MG	QA	1602	1/1	0.94	0.32	33,33,33,33	0
57	MG	YA	3154	1/1	0.94	0.29	24,24,24,24	0
57	MG	RA	3423	1/1	0.94	0.20	51,51,51,51	0
57	MG	RR	201	1/1	0.94	0.36	33,33,33,33	0
57	MG	XA	1661	1/1	0.94	0.52	43,43,43,43	0
57	MG	RA	3164	1/1	0.94	0.17	41,41,41,41	0
57	MG	YA	3474	1/1	0.94	0.58	37,37,37,37	0
57	MG	RA	3089	1/1	0.94	0.30	21,21,21,21	0
57	MG	YA	3267	1/1	0.94	0.12	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
57	MG	RA	3235	1/1	0.94	0.22	48,48,48,48	0
57	MG	RA	3379	1/1	0.94	0.52	36,36,36,36	0
57	MG	YA	3049	1/1	0.94	0.41	13,13,13,13	0
57	MG	YA	3375	1/1	0.94	0.65	35,35,35,35	0
57	MG	YA	3052	1/1	0.94	0.57	9,9,9,9	0
57	MG	XA	1729	1/1	0.94	0.14	24,24,24,24	0
57	MG	YA	3060	1/1	0.94	0.50	12,12,12,12	0
57	MG	RA	3344	1/1	0.94	0.19	47,47,47,47	0
57	MG	YA	3485	1/1	0.94	0.18	52,52,52,52	0
57	MG	YA	3171	1/1	0.94	0.27	39,39,39,39	0
57	MG	YA	3277	1/1	0.94	0.14	44,44,44,44	0
57	MG	QA	1645	1/1	0.94	0.10	44,44,44,44	0
57	MG	XA	1733	1/1	0.94	0.24	18,18,18,18	0
57	MG	YA	3492	1/1	0.94	0.22	55,55,55,55	0
57	MG	YA	3386	1/1	0.94	0.37	58,58,58,58	0
57	MG	RA	3269	1/1	0.94	0.39	50,50,50,50	0
57	MG	YA	3070	1/1	0.94	0.32	28,28,28,28	0
57	MG	YA	3071	1/1	0.94	0.11	33,33,33,33	0
57	MG	RA	3202	1/1	0.94	0.08	49,49,49,49	0
57	MG	RA	3271	1/1	0.94	0.07	27,27,27,27	0
57	MG	XA	1737	1/1	0.94	0.38	34,34,34,34	0
57	MG	RA	3062	1/1	0.94	0.40	30,30,30,30	0
57	MG	QA	1652	1/1	0.94	0.22	34,34,34,34	0
57	MG	YA	3185	1/1	0.94	0.19	21,21,21,21	0
57	MG	YA	3083	1/1	0.94	0.31	30,30,30,30	0
57	MG	XA	1679	1/1	0.94	0.11	35,35,35,35	0
57	MG	YD	301	1/1	0.94	0.32	26,26,26,26	0
57	MG	XA	1606	1/1	0.94	0.38	18,18,18,18	0
57	MG	YF	301	1/1	0.94	0.17	27,27,27,27	0
57	MG	YF	302	1/1	0.94	0.26	35,35,35,35	0
57	MG	XA	1607	1/1	0.94	0.21	35,35,35,35	0
57	MG	RA	3390	1/1	0.94	0.35	19,19,19,19	0
57	MG	XA	1612	1/1	0.94	0.26	43,43,43,43	0
57	MG	XA	1746	1/1	0.94	0.26	46,46,46,46	0
57	MG	YA	3096	1/1	0.94	0.62	41,41,41,41	0
57	MG	QA	1615	1/1	0.94	0.30	38,38,38,38	0
57	MG	RA	3121	1/1	0.94	0.12	31,31,31,31	0
57	MG	QA	1634	1/1	0.94	0.22	45,45,45,45	0
57	MG	RA	3150	1/1	0.94	0.27	40,40,40,40	0
57	MG	XA	1753	1/1	0.94	0.18	51,51,51,51	0
57	MG	RA	3012	1/1	0.94	0.48	11,11,11,11	0
57	MG	QA	1622	1/1	0.94	0.52	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
57	MG	YA	3413	1/1	0.94	0.38	53,53,53,53	0
57	MG	RA	3282	1/1	0.94	0.24	36,36,36,36	0
57	MG	YA	3415	1/1	0.94	0.08	62,62,62,62	0
57	MG	RA	3177	1/1	0.94	0.35	44,44,44,44	0
57	MG	RA	3179	1/1	0.94	0.18	47,47,47,47	0
57	MG	Z7	101	1/1	0.94	0.31	35,35,35,35	0
57	MG	RA	3404	1/1	0.94	0.24	46,46,46,46	0
57	MG	YA	3112	1/1	0.94	0.18	19,19,19,19	0
57	MG	YA	3021	1/1	0.95	0.48	33,33,33,33	0
57	MG	YA	3321	1/1	0.95	0.19	67,67,67,67	0
57	MG	RA	3131	1/1	0.95	0.17	43,43,43,43	0
57	MG	YA	3131	1/1	0.95	0.20	40,40,40,40	0
57	MG	YA	3025	1/1	0.95	0.49	34,34,34,34	0
57	MG	YA	3325	1/1	0.95	0.50	51,51,51,51	0
57	MG	RA	3295	1/1	0.95	0.39	32,32,32,32	0
57	MG	XA	1601	1/1	0.95	0.33	36,36,36,36	0
57	MG	RA	3213	1/1	0.95	0.24	13,13,13,13	0
57	MG	RA	3050	1/1	0.95	0.28	12,12,12,12	0
57	MG	RA	3215	1/1	0.95	0.57	53,53,53,53	0
57	MG	YA	3036	1/1	0.95	0.45	21,21,21,21	0
57	MG	YA	3233	1/1	0.95	0.26	38,38,38,38	0
57	MG	QA	1611	1/1	0.95	0.44	31,31,31,31	0
57	MG	YA	3337	1/1	0.95	0.45	39,39,39,39	0
57	MG	YA	3339	1/1	0.95	0.13	31,31,31,31	0
57	MG	RA	3020	1/1	0.95	0.50	24,24,24,24	0
57	MG	YA	3039	1/1	0.95	0.41	11,11,11,11	0
57	MG	YA	3446	1/1	0.95	0.32	37,37,37,37	0
57	MG	XA	1611	1/1	0.95	0.18	43,43,43,43	0
57	MG	YA	3449	1/1	0.95	0.16	36,36,36,36	0
57	MG	YA	3346	1/1	0.95	0.37	47,47,47,47	0
57	MG	RA	3136	1/1	0.95	0.46	40,40,40,40	0
57	MG	QA	1682	1/1	0.95	0.26	49,49,49,49	0
57	MG	QA	1632	1/1	0.95	0.15	58,58,58,58	0
57	MG	YA	3455	1/1	0.95	0.22	52,52,52,52	0
57	MG	YA	3243	1/1	0.95	0.50	46,46,46,46	0
57	MG	RA	3064	1/1	0.95	0.30	26,26,26,26	0
57	MG	RA	3103	1/1	0.95	0.36	52,52,52,52	0
57	MG	XA	1619	1/1	0.95	0.32	28,28,28,28	0
57	MG	YA	3460	1/1	0.95	0.11	37,37,37,37	0
57	MG	YA	3056	1/1	0.95	0.35	5,5,5,5	0
57	MG	XA	1741	1/1	0.95	0.32	44,44,44,44	0
57	MG	YA	3465	1/1	0.95	0.27	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3028	1/1	0.95	0.44	12,12,12,12	0
57	MG	RA	3142	1/1	0.95	0.34	28,28,28,28	0
57	MG	RA	3400	1/1	0.95	0.32	44,44,44,44	0
57	MG	YA	3254	1/1	0.95	0.24	19,19,19,19	0
57	MG	XA	1689	1/1	0.95	0.18	46,46,46,46	0
57	MG	YA	3161	1/1	0.95	0.32	29,29,29,29	0
57	MG	YA	3257	1/1	0.95	0.34	29,29,29,29	0
57	MG	QA	1726	1/1	0.95	0.12	38,38,38,38	0
57	MG	YA	3259	1/1	0.95	0.26	35,35,35,35	0
57	MG	QA	1624	1/1	0.95	0.30	36,36,36,36	0
57	MG	YA	3165	1/1	0.95	0.25	14,14,14,14	0
57	MG	RA	3145	1/1	0.95	0.29	22,22,22,22	0
57	MG	QA	1604	1/1	0.95	0.24	33,33,33,33	0
57	MG	XA	1750	1/1	0.95	0.07	44,44,44,44	0
57	MG	RA	3406	1/1	0.95	0.10	50,50,50,50	0
57	MG	QA	1717	1/1	0.95	0.09	53,53,53,53	0
57	MG	YA	3080	1/1	0.95	0.59	21,21,21,21	0
57	MG	YA	3270	1/1	0.95	0.49	32,32,32,32	0
57	MG	RA	3035	1/1	0.95	0.27	21,21,21,21	0
57	MG	RA	3113	1/1	0.95	0.22	32,32,32,32	0
57	MG	YA	3379	1/1	0.95	0.07	42,42,42,42	0
57	MG	YA	3174	1/1	0.95	0.57	29,29,29,29	0
57	MG	YA	3084	1/1	0.95	0.15	20,20,20,20	0
57	MG	QA	1626	1/1	0.95	0.11	21,21,21,21	0
57	MG	YA	3491	1/1	0.95	0.31	37,37,37,37	0
57	MG	RA	3320	1/1	0.95	0.12	44,44,44,44	0
57	MG	YA	3178	1/1	0.95	0.19	18,18,18,18	0
57	MG	YA	3089	1/1	0.95	0.40	8,8,8,8	0
57	MG	RA	3116	1/1	0.95	0.43	20,20,20,20	0
57	MG	RA	3040	1/1	0.95	0.34	18,18,18,18	0
57	MG	RA	3078	1/1	0.95	0.54	22,22,22,22	0
57	MG	YA	3093	1/1	0.95	0.21	17,17,17,17	0
57	MG	RA	3079	1/1	0.95	0.58	26,26,26,26	0
57	MG	RA	3008	1/1	0.95	0.86	34,34,34,34	0
57	MG	XA	1643	1/1	0.95	0.50	35,35,35,35	0
57	MG	RA	3326	1/1	0.95	0.13	46,46,46,46	0
57	MG	YB	201	1/1	0.95	0.40	32,32,32,32	0
57	MG	YB	202	1/1	0.95	0.27	19,19,19,19	0
57	MG	RA	3085	1/1	0.95	0.12	15,15,15,15	0
57	MG	YB	204	1/1	0.95	0.11	69,69,69,69	0
57	MG	RA	3043	1/1	0.95	0.30	36,36,36,36	0
57	MG	RA	3011	1/1	0.95	0.42	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	XA	1652	1/1	0.95	0.43	46,46,46,46	0
57	MG	RA	3286	1/1	0.95	0.35	43,43,43,43	0
57	MG	XV	101	1/1	0.95	0.29	23,23,23,23	0
57	MG	RA	3248	1/1	0.95	0.52	33,33,33,33	0
57	MG	QA	1644	1/1	0.95	0.42	27,27,27,27	0
57	MG	XA	1717	1/1	0.95	0.15	37,37,37,37	0
57	MG	RA	3289	1/1	0.95	0.17	39,39,39,39	0
57	MG	YA	3003	1/1	0.95	0.39	14,14,14,14	0
57	MG	YA	3004	1/1	0.95	0.49	13,13,13,13	0
57	MG	RA	3290	1/1	0.95	0.10	52,52,52,52	0
57	MG	YA	3210	1/1	0.95	0.30	32,32,32,32	0
57	MG	YA	3006	1/1	0.95	0.36	17,17,17,17	0
57	MG	XA	1720	1/1	0.95	0.18	44,44,44,44	0
57	MG	QA	1709	1/1	0.95	0.34	36,36,36,36	0
57	MG	QA	1689	1/1	0.95	0.36	28,28,28,28	0
57	MG	YA	3122	1/1	0.95	0.39	19,19,19,19	0
57	MG	YA	3312	1/1	0.95	0.54	24,24,24,24	0
57	MG	YA	3124	1/1	0.95	0.32	27,27,27,27	0
57	MG	YA	3016	1/1	0.95	0.17	8,8,8,8	0
57	MG	RA	3293	1/1	0.95	0.44	25,25,25,25	0
57	MG	YA	3220	1/1	0.95	0.23	39,39,39,39	0
57	MG	YA	3422	1/1	0.95	0.39	29,29,29,29	0
57	MG	YA	3317	1/1	0.95	0.68	51,51,51,51	0
58	ZN	XN	101	1/1	0.95	0.17	69,69,69,69	0
57	MG	QA	1636	1/1	0.96	0.20	48,48,48,48	0
57	MG	RA	3088	1/1	0.96	0.31	23,23,23,23	0
57	MG	RA	3038	1/1	0.96	0.40	23,23,23,23	0
57	MG	RA	3065	1/1	0.96	0.53	31,31,31,31	0
57	MG	YA	3087	1/1	0.96	0.45	25,25,25,25	0
57	MG	RA	3352	1/1	0.96	0.49	44,44,44,44	0
57	MG	RA	3402	1/1	0.96	0.54	36,36,36,36	0
57	MG	RA	3180	1/1	0.96	0.50	23,23,23,23	0
57	MG	XE	201	1/1	0.96	0.37	32,32,32,32	0
57	MG	YA	3454	1/1	0.96	0.35	45,45,45,45	0
57	MG	XF	201	1/1	0.96	0.12	31,31,31,31	0
57	MG	QA	1616	1/1	0.96	0.19	45,45,45,45	0
57	MG	YA	3094	1/1	0.96	0.05	45,45,45,45	0
57	MG	RA	3224	1/1	0.96	0.22	31,31,31,31	0
57	MG	RA	3225	1/1	0.96	0.12	67,67,67,67	0
57	MG	RA	3019	1/1	0.96	0.35	20,20,20,20	0
57	MG	YA	3098	1/1	0.96	0.37	24,24,24,24	0
57	MG	RA	3042	1/1	0.96	0.35	14,14,14,14	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	XV	102	1/1	0.96	0.55	26,26,26,26	0
57	MG	XA	1640	1/1	0.96	0.20	36,36,36,36	0
57	MG	XA	1641	1/1	0.96	0.07	51,51,51,51	0
57	MG	XA	1642	1/1	0.96	0.10	61,61,61,61	0
57	MG	RA	3184	1/1	0.96	0.28	40,40,40,40	0
57	MG	YA	3378	1/1	0.96	0.22	56,56,56,56	0
57	MG	XA	1645	1/1	0.96	0.11	37,37,37,37	0
57	MG	RA	3122	1/1	0.96	0.41	29,29,29,29	0
57	MG	RA	3123	1/1	0.96	0.12	28,28,28,28	0
57	MG	QA	1659	1/1	0.96	0.43	43,43,43,43	0
57	MG	YA	3007	1/1	0.96	0.68	40,40,40,40	0
57	MG	YA	3113	1/1	0.96	0.28	34,34,34,34	0
57	MG	RA	3096	1/1	0.96	0.09	45,45,45,45	0
57	MG	RA	3189	1/1	0.96	0.40	18,18,18,18	0
57	MG	RA	3236	1/1	0.96	0.44	38,38,38,38	0
57	MG	RA	3190	1/1	0.96	0.47	18,18,18,18	0
57	MG	RA	3417	1/1	0.96	0.15	53,53,53,53	0
57	MG	RA	3280	1/1	0.96	0.28	24,24,24,24	0
57	MG	RA	3238	1/1	0.96	0.29	28,28,28,28	0
57	MG	RA	3155	1/1	0.96	0.24	30,30,30,30	0
57	MG	YA	3027	1/1	0.96	0.33	14,14,14,14	0
57	MG	YA	3486	1/1	0.96	0.17	38,38,38,38	0
57	MG	XA	1662	1/1	0.96	0.69	40,40,40,40	0
57	MG	YA	3304	1/1	0.96	0.28	47,47,47,47	0
57	MG	RA	3421	1/1	0.96	0.30	51,51,51,51	0
57	MG	QA	1641	1/1	0.96	0.20	33,33,33,33	0
57	MG	XA	1667	1/1	0.96	0.29	40,40,40,40	0
57	MG	YA	3221	1/1	0.96	0.45	32,32,32,32	0
57	MG	RA	3195	1/1	0.96	0.37	30,30,30,30	0
57	MG	QA	1698	1/1	0.96	0.32	47,47,47,47	0
57	MG	RA	3100	1/1	0.96	0.35	18,18,18,18	0
57	MG	RA	3160	1/1	0.96	0.16	30,30,30,30	0
57	MG	RA	3200	1/1	0.96	0.74	37,37,37,37	0
57	MG	YA	3405	1/1	0.96	0.32	57,57,57,57	0
57	MG	XA	1673	1/1	0.96	0.25	24,24,24,24	0
57	MG	RA	3377	1/1	0.96	0.17	38,38,38,38	0
57	MG	YA	3045	1/1	0.96	0.39	11,11,11,11	0
57	MG	YA	3141	1/1	0.96	0.57	37,37,37,37	0
57	MG	RA	3429	1/1	0.96	0.14	66,66,66,66	0
57	MG	QA	1606	1/1	0.96	0.23	19,19,19,19	0
57	MG	RA	3132	1/1	0.96	0.19	17,17,17,17	0
57	MG	YA	3235	1/1	0.96	0.55	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3076	1/1	0.96	0.23	25,25,25,25	0
57	MG	YA	3416	1/1	0.96	0.30	10,10,10,10	0
57	MG	YA	3050	1/1	0.96	0.23	23,23,23,23	0
57	MG	XA	1609	1/1	0.96	0.05	67,67,67,67	0
57	MG	YA	3419	1/1	0.96	0.11	37,37,37,37	0
57	MG	YA	3053	1/1	0.96	0.33	24,24,24,24	0
57	MG	RA	3104	1/1	0.96	0.40	28,28,28,28	0
57	MG	RA	3382	1/1	0.96	0.33	21,21,21,21	0
57	MG	RA	3208	1/1	0.96	0.39	32,32,32,32	0
57	MG	RA	3009	1/1	0.96	0.23	18,18,18,18	0
57	MG	YP	201	1/1	0.96	0.19	11,11,11,11	0
57	MG	YA	3426	1/1	0.96	0.78	23,23,23,23	0
57	MG	QA	1685	1/1	0.96	0.23	28,28,28,28	0
57	MG	YA	3066	1/1	0.96	0.21	33,33,33,33	0
57	MG	QA	1716	1/1	0.96	0.25	76,76,76,76	0
57	MG	QA	1750	1/1	0.96	0.07	45,45,45,45	0
57	MG	XA	1688	1/1	0.96	0.30	26,26,26,26	0
57	MG	RA	3084	1/1	0.96	0.41	33,33,33,33	0
57	MG	YA	3252	1/1	0.96	0.10	28,28,28,28	0
57	MG	YA	3347	1/1	0.96	0.19	40,40,40,40	0
57	MG	RA	3110	1/1	0.96	0.74	33,33,33,33	0
57	MG	RA	3016	1/1	0.96	0.38	15,15,15,15	0
57	MG	RA	3061	1/1	0.96	0.54	28,28,28,28	0
57	MG	YA	3077	1/1	0.96	0.43	16,16,16,16	0
57	MG	YA	3078	1/1	0.96	0.49	17,17,17,17	0
57	MG	RA	3304	1/1	0.96	0.09	45,45,45,45	0
57	MG	RA	3395	1/1	0.96	0.31	45,45,45,45	0
57	MG	XA	1604	1/1	0.97	0.27	36,36,36,36	0
57	MG	YA	3435	1/1	0.97	0.10	27,27,27,27	0
57	MG	XA	1711	1/1	0.97	0.09	27,27,27,27	0
57	MG	YA	3075	1/1	0.97	0.32	13,13,13,13	0
57	MG	XA	1605	1/1	0.97	0.33	18,18,18,18	0
57	MG	XA	1659	1/1	0.97	0.39	31,31,31,31	0
57	MG	YA	3342	1/1	0.97	0.33	27,27,27,27	0
57	MG	XA	1660	1/1	0.97	0.17	38,38,38,38	0
57	MG	YA	3344	1/1	0.97	0.70	28,28,28,28	0
57	MG	QA	1667	1/1	0.97	0.23	43,43,43,43	0
57	MG	RA	3174	1/1	0.97	0.56	19,19,19,19	0
57	MG	YA	3081	1/1	0.97	0.41	19,19,19,19	0
57	MG	QA	1635	1/1	0.97	0.26	29,29,29,29	0
57	MG	YA	3447	1/1	0.97	0.16	44,44,44,44	0
57	MG	YA	3163	1/1	0.97	0.18	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YA	3250	1/1	0.97	0.84	45,45,45,45	0
57	MG	RA	3004	1/1	0.97	0.42	17,17,17,17	0
57	MG	QA	1663	1/1	0.97	0.38	49,49,49,49	0
57	MG	XA	1721	1/1	0.97	0.22	32,32,32,32	0
57	MG	QA	1695	1/1	0.97	0.22	42,42,42,42	0
57	MG	RA	3098	1/1	0.97	0.54	44,44,44,44	0
57	MG	QA	1725	1/1	0.97	0.11	44,44,44,44	0
57	MG	RA	3284	1/1	0.97	0.21	38,38,38,38	0
57	MG	YA	3358	1/1	0.97	0.31	35,35,35,35	0
57	MG	RA	3045	1/1	0.97	0.54	19,19,19,19	0
57	MG	RA	3024	1/1	0.97	0.47	18,18,18,18	0
57	MG	YA	3260	1/1	0.97	0.40	49,49,49,49	0
57	MG	YA	3008	1/1	0.97	0.13	19,19,19,19	0
57	MG	RA	3027	1/1	0.97	0.34	9,9,9,9	0
57	MG	YA	3463	1/1	0.97	0.47	39,39,39,39	0
57	MG	YA	3464	1/1	0.97	0.24	43,43,43,43	0
57	MG	YA	3263	1/1	0.97	0.30	44,44,44,44	0
57	MG	RA	3130	1/1	0.97	0.17	28,28,28,28	0
57	MG	YA	3012	1/1	0.97	0.37	19,19,19,19	0
57	MG	RA	3219	1/1	0.97	0.21	20,20,20,20	0
57	MG	XA	1731	1/1	0.97	0.21	41,41,41,41	0
57	MG	YA	3017	1/1	0.97	0.28	16,16,16,16	0
57	MG	YA	3018	1/1	0.97	0.32	9,9,9,9	0
57	MG	YA	3101	1/1	0.97	0.44	35,35,35,35	0
57	MG	YA	3103	1/1	0.97	0.19	25,25,25,25	0
57	MG	QV	102	1/1	0.97	0.46	25,25,25,25	0
57	MG	XA	1678	1/1	0.97	0.14	28,28,28,28	0
57	MG	RA	3010	1/1	0.97	0.53	20,20,20,20	0
57	MG	YA	3024	1/1	0.97	0.40	18,18,18,18	0
57	MG	RA	3159	1/1	0.97	0.67	17,17,17,17	0
57	MG	QA	1608	1/1	0.97	0.24	39,39,39,39	0
57	MG	RA	3080	1/1	0.97	0.35	36,36,36,36	0
57	MG	YA	3279	1/1	0.97	0.40	20,20,20,20	0
57	MG	YA	3191	1/1	0.97	0.32	30,30,30,30	0
57	MG	RA	3373	1/1	0.97	0.24	49,49,49,49	0
57	MG	RA	3052	1/1	0.97	0.49	13,13,13,13	0
57	MG	QA	1660	1/1	0.97	0.25	32,32,32,32	0
57	MG	YA	3195	1/1	0.97	0.35	23,23,23,23	0
57	MG	YA	3196	1/1	0.97	0.39	24,24,24,24	0
57	MG	YA	3034	1/1	0.97	0.39	22,22,22,22	0
57	MG	RA	3297	1/1	0.97	0.12	27,27,27,27	0
57	MG	YA	3116	1/1	0.97	0.48	16,16,16,16	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3194	1/1	0.97	0.41	9,9,9,9	0
57	MG	RA	3228	1/1	0.97	0.36	27,27,27,27	0
57	MG	YA	3202	1/1	0.97	0.28	22,22,22,22	0
57	MG	YA	3203	1/1	0.97	0.43	35,35,35,35	0
57	MG	RA	3054	1/1	0.97	0.35	27,27,27,27	0
57	MG	YA	3205	1/1	0.97	0.35	21,21,21,21	0
57	MG	RP	202	1/1	0.97	0.18	28,28,28,28	0
57	MG	RA	3056	1/1	0.97	0.33	23,23,23,23	0
57	MG	YA	3208	1/1	0.97	0.51	35,35,35,35	0
57	MG	YA	3299	1/1	0.97	0.44	28,28,28,28	0
57	MG	YA	3209	1/1	0.97	0.09	14,14,14,14	0
57	MG	RA	3112	1/1	0.97	0.29	24,24,24,24	0
57	MG	YA	3123	1/1	0.97	0.26	30,30,30,30	0
57	MG	YA	3044	1/1	0.97	0.62	28,28,28,28	0
57	MG	RA	3266	1/1	0.97	0.29	37,37,37,37	0
57	MG	QA	1607	1/1	0.97	0.23	15,15,15,15	0
57	MG	YB	205	1/1	0.97	0.14	52,52,52,52	0
57	MG	YA	3307	1/1	0.97	0.40	68,68,68,68	0
57	MG	YA	3407	1/1	0.97	0.13	45,45,45,45	0
57	MG	RA	3233	1/1	0.97	0.27	38,38,38,38	0
57	MG	XA	1751	1/1	0.97	0.07	46,46,46,46	0
57	MG	RA	3060	1/1	0.97	0.28	9,9,9,9	0
57	MG	XA	1644	1/1	0.97	0.18	40,40,40,40	0
57	MG	RA	3201	1/1	0.97	0.44	27,27,27,27	0
57	MG	RA	3015	1/1	0.97	0.49	31,31,31,31	0
57	MG	YA	3222	1/1	0.97	0.54	32,32,32,32	0
57	MG	RA	3001	1/1	0.97	0.15	43,43,43,43	0
57	MG	YA	3057	1/1	0.97	0.19	17,17,17,17	0
57	MG	YA	3137	1/1	0.97	0.35	34,34,34,34	0
57	MG	RA	3273	1/1	0.97	0.39	41,41,41,41	0
57	MG	XA	1649	1/1	0.97	0.29	23,23,23,23	0
57	MG	XA	1650	1/1	0.97	0.45	23,23,23,23	0
57	MG	RA	3311	1/1	0.97	0.41	24,24,24,24	0
57	MG	RA	3204	1/1	0.97	0.58	39,39,39,39	0
57	MG	YA	3067	1/1	0.97	0.44	25,25,25,25	0
57	MG	XA	1706	1/1	0.97	0.28	31,31,31,31	0
57	MG	RA	3313	1/1	0.97	0.69	25,25,25,25	0
57	MG	RA	3037	1/1	0.97	0.48	10,10,10,10	0
57	MG	RA	3396	1/1	0.97	0.37	31,31,31,31	0
57	MG	YA	3331	1/1	0.97	0.57	18,18,18,18	0
57	MG	YA	3430	1/1	0.97	0.06	43,43,43,43	0
57	MG	YA	3332	1/1	0.97	0.13	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YA	3150	1/1	0.97	0.53	15,15,15,15	0
57	MG	YA	3072	1/1	0.97	0.26	19,19,19,19	0
57	MG	YA	3341	1/1	0.98	0.53	20,20,20,20	0
57	MG	RA	3193	1/1	0.98	0.45	16,16,16,16	0
57	MG	XA	1635	1/1	0.98	0.22	43,43,43,43	0
57	MG	YA	3009	1/1	0.98	0.60	17,17,17,17	0
57	MG	QA	1701	1/1	0.98	0.21	47,47,47,47	0
57	MG	RA	3073	1/1	0.98	0.24	22,22,22,22	0
57	MG	YA	3062	1/1	0.98	0.40	17,17,17,17	0
57	MG	QA	1656	1/1	0.98	0.51	41,41,41,41	0
57	MG	YA	3065	1/1	0.98	0.16	16,16,16,16	0
57	MG	RA	3169	1/1	0.98	0.39	19,19,19,19	0
57	MG	YA	3014	1/1	0.98	0.36	19,19,19,19	0
57	MG	YA	3015	1/1	0.98	0.51	13,13,13,13	0
57	MG	RA	3258	1/1	0.98	0.57	39,39,39,39	0
57	MG	YA	3290	1/1	0.98	0.16	38,38,38,38	0
57	MG	RA	3057	1/1	0.98	0.42	13,13,13,13	0
57	MG	RA	3199	1/1	0.98	0.29	23,23,23,23	0
57	MG	RA	3058	1/1	0.98	0.37	24,24,24,24	0
57	MG	YA	3180	1/1	0.98	0.55	11,11,11,11	0
57	MG	YA	3020	1/1	0.98	0.55	23,23,23,23	0
57	MG	YA	3424	1/1	0.98	0.12	1,1,1,1	0
57	MG	RA	3013	1/1	0.98	0.29	16,16,16,16	0
57	MG	RA	3031	1/1	0.98	0.54	10,10,10,10	0
57	MG	YA	3240	1/1	0.98	0.74	34,34,34,34	0
57	MG	YA	3127	1/1	0.98	0.18	41,41,41,41	0
57	MG	RA	3389	1/1	0.98	0.17	9,9,9,9	0
57	MG	XA	1610	1/1	0.98	0.34	33,33,33,33	0
57	MG	YA	3026	1/1	0.98	0.33	9,9,9,9	0
57	MG	YA	3303	1/1	0.98	0.07	41,41,41,41	0
57	MG	RA	3101	1/1	0.98	0.30	44,44,44,44	0
57	MG	RA	3149	1/1	0.98	0.58	21,21,21,21	0
57	MG	RA	3021	1/1	0.98	0.59	33,33,33,33	0
57	MG	YA	3030	1/1	0.98	0.55	15,15,15,15	0
57	MG	XA	1614	1/1	0.98	0.31	22,22,22,22	0
57	MG	YA	3504	1/1	0.98	0.40	18,18,18,18	0
57	MG	RA	3081	1/1	0.98	0.47	14,14,14,14	0
57	MG	YA	3138	1/1	0.98	0.20	39,39,39,39	0
57	MG	YA	3085	1/1	0.98	0.27	24,24,24,24	0
57	MG	YA	3033	1/1	0.98	0.37	16,16,16,16	0
57	MG	XA	1616	1/1	0.98	0.31	46,46,46,46	0
57	MG	RA	3207	1/1	0.98	0.59	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3178	1/1	0.98	0.28	15,15,15,15	0
57	MG	RA	3082	1/1	0.98	0.38	5,5,5,5	0
57	MG	YE	302	1/1	0.98	0.37	18,18,18,18	0
57	MG	RA	3007	1/1	0.98	0.46	19,19,19,19	0
57	MG	YA	3318	1/1	0.98	0.19	54,54,54,54	0
57	MG	YA	3319	1/1	0.98	0.26	57,57,57,57	0
57	MG	RA	3129	1/1	0.98	0.21	12,12,12,12	0
57	MG	RA	3063	1/1	0.98	0.34	10,10,10,10	0
57	MG	QA	1617	1/1	0.98	0.30	41,41,41,41	0
57	MG	YA	3042	1/1	0.98	0.19	23,23,23,23	0
57	MG	YA	3043	1/1	0.98	0.40	19,19,19,19	0
57	MG	RA	3048	1/1	0.98	0.54	13,13,13,13	0
57	MG	QA	1605	1/1	0.98	0.21	36,36,36,36	0
57	MG	RA	3025	1/1	0.98	0.42	19,19,19,19	0
57	MG	RA	3068	1/1	0.98	0.45	14,14,14,14	0
57	MG	RA	3090	1/1	0.98	0.38	11,11,11,11	0
57	MG	YA	3330	1/1	0.98	0.38	11,11,11,11	0
57	MG	YA	3102	1/1	0.98	0.44	40,40,40,40	0
57	MG	RA	3026	1/1	0.98	0.33	16,16,16,16	0
57	MG	YA	3214	1/1	0.98	0.50	19,19,19,19	0
57	MG	YA	3159	1/1	0.98	0.48	13,13,13,13	0
57	MG	RA	3039	1/1	0.98	0.24	34,34,34,34	0
57	MG	YA	3051	1/1	0.98	0.51	30,30,30,30	0
57	MG	RA	3115	1/1	0.98	0.56	52,52,52,52	0
57	MG	YA	3338	1/1	0.98	0.44	25,25,25,25	0
58	ZN	QN	101	1/1	0.98	0.17	79,79,79,79	0
57	MG	QA	1692	1/1	0.98	0.27	26,26,26,26	0
57	MG	YA	3055	1/1	0.98	0.34	14,14,14,14	0
57	MG	RA	3074	1/1	0.99	0.20	37,37,37,37	0
57	MG	QA	1649	1/1	0.99	0.41	32,32,32,32	0
57	MG	XA	1715	1/1	0.99	0.17	40,40,40,40	0
57	MG	YA	3054	1/1	0.99	0.53	20,20,20,20	0
57	MG	RA	3034	1/1	0.99	0.40	20,20,20,20	0
57	MG	RA	3055	1/1	0.99	0.52	25,25,25,25	0
57	MG	YA	3494	1/1	0.99	0.28	49,49,49,49	0
57	MG	YA	3023	1/1	0.99	0.40	14,14,14,14	0
57	MG	YA	3058	1/1	0.99	0.27	55,55,55,55	0
57	MG	YA	3129	1/1	0.99	0.20	19,19,19,19	0
57	MG	RA	3386	1/1	0.99	0.52	24,24,24,24	0
57	MG	YA	3146	1/1	0.99	0.45	29,29,29,29	0
57	MG	XA	1664	1/1	0.99	0.45	31,31,31,31	0
57	MG	XA	1665	1/1	0.99	0.28	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	XA	1621	1/1	0.99	0.41	46,46,46,46	0
57	MG	XA	1658	1/1	0.99	0.13	34,34,34,34	0
57	MG	YA	3064	1/1	0.99	0.53	26,26,26,26	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.