



Full wwPDB EM Validation Report ⓘ

Nov 20, 2022 – 01:03 am GMT

PDB ID : 5UMD
EMDB ID : EMD-8576
Title : Structure of the Plasmodium falciparum 80S ribosome bound to the antimalarial drug mefloquine
Authors : Wong, W.; Bai, X.-C.; Brown, A.; Scheres, S.; Baum, J.
Deposited on : 2017-01-27
Resolution : 3.20 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

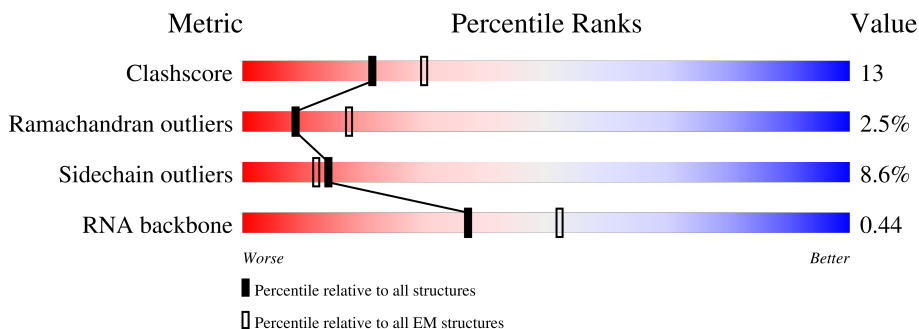
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	3788	
2	B	119	
3	C	159	
4	D	260	
5	E	386	
6	F	411	
7	G	173	

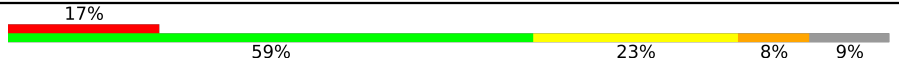

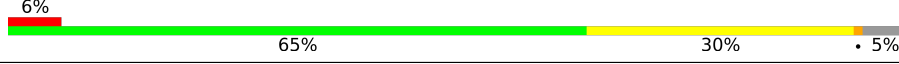
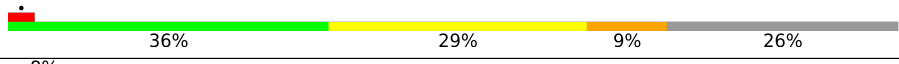

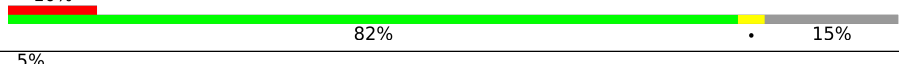
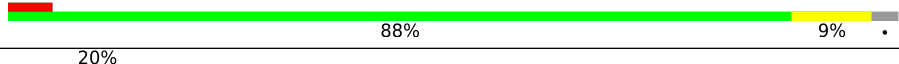

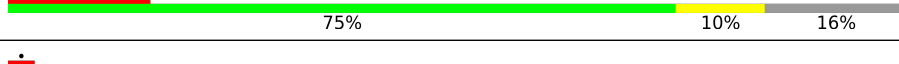


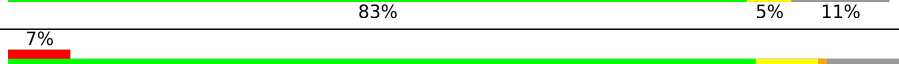

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Mol	Chain	Length	Quality of chain
8	H	190	8% 68% 23% 5% . .
9	I	221	10% 67% 25% 6%
10	J	283	18% 55% 19% 22%
11	K	202	10% 78% 19% .
12	L	215	10% 71% 21% 6% .
13	M	139	9% 68% 22% . . 5%
14	N	165	11% 51% 32% 5% 12%
15	O	148	5% 64% 33% . .
16	P	205	6% 60% 34% .
17	Q	219	9% 68% 17% . 14%
18	R	294	10% 62% 17% 6% 14%
19	S	187	5% 65% 32% . .
20	T	182	23% 73% 23% . .
21	U	184	7% 66% 29% . .
22	V	161	11% 76% 20% . .
23	W	203	6% 66% 16% . 16%
24	X	139	22% 51% 15% . 30%
25	Y	190	11% 40% 11% . 47%
26	Z	126	18% 67% 29% . .
27	0	162	7% 30% 8% 62%
28	1	146	18% 71% 19% 5% .
29	2	127	5% 69% 12% . 18%
30	3	124	7% 75% 19% . .
31	4	67	22% 73% 18% 7% .
32	5	257	6% 57% 26% . 13%

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Mol	Chain	Length	Quality of chain
33	6	108	
34	7	120	
35	8	131	
36	9	140	
37	a	150	
38	b	112	
39	c	92	
40	d	87	
41	e	51	
42	f	128	
43	g	39	
44	h	96	
45	i	104	

2 Entry composition [i](#)

There are 48 unique types of molecules in this entry. The entry contains 124502 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	3191	67935	30426	12044	22274	3191	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	821	C	U	conflict	GB 1013064538

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	118	2525	1128	461	818	118	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	23	A	C	conflict	GB 1016052399
B	24	U	C	conflict	GB 1016052399
B	119	G	U	conflict	GB 1016052399

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	C	151	3224	1444	589	1040	151	0	0

- Molecule 4 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	247	1866	1166	374	317	9	0	0

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	380	3061	1948	575	521	17	0	0

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	390	3094	1962	594	527	11	0	0

- Molecule 7 is a protein called 60S ribosomal protein L11a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	124	1010	636	197	171	6	0	0

- Molecule 8 is a protein called 60S ribosomal protein L6, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	185	1460	938	261	255	6	0	0

- Molecule 9 is a protein called 60S ribosomal protein L6-2, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	207	1684	1096	298	285	5	0	0

- Molecule 10 is a protein called 60S ribosomal protein L7-3, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	222	1813	1174	323	309	7	0	0

- Molecule 11 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	201	1659	1064	311	276	8	0	0

- Molecule 12 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	211	1756	1116	346	290	4	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	19	HIS	ARG	conflict	UNP Q8IAX6
L	20	ARG	HIS	conflict	UNP Q8IAX6
L	201	CYS	ARG	conflict	UNP Q8IAX6

- Molecule 13 is a protein called 60S ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	M	132	996	631	179	178	8	0	0

- Molecule 14 is a protein called 60S ribosomal protein L14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	N	146	1197	779	210	202	6	0	0

- Molecule 15 is a protein called 60S ribosomal protein L27a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	O	147	1172	747	232	189	4	0	0

- Molecule 16 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	P	204	1697	1075	351	267	4	0	0

- Molecule 17 is a protein called 60S ribosomal protein L10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	Q	189	1544	984	291	261	8	0	0

- Molecule 18 is a protein called 60S ribosomal protein L5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	R	252	2045	1298	384	357	6	0	0

- Molecule 19 is a protein called 60S ribosomal protein L18-2, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	S	186	1502	958	299	240	5	0	0

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	T	181	1505	949	308	244	4	0	0

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	U	180	1496	946	289	254	7	0	0

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	V	155	1275	814	241	214	6	0	0

- Molecule 23 is a protein called 60S ribosomal protein L17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	W	170	1318	824	266	221	7	0	0

- Molecule 24 is a protein called 60S ribosomal protein L22, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	X	97	824	548	135	139	2	0	0

- Molecule 25 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	101	Total	C	N	O	S	0	0
			796	502	144	144	6		

- Molecule 26 is a protein called 60S ribosomal protein L26, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	121	Total	C	N	O	S	0	0
			1000	626	206	165	3		

- Molecule 27 is a protein called 60S ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	0	62	Total	C	N	O	S	0	0
			521	336	97	87	1		

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	140	Total	C	N	O	S	0	0
			1134	736	204	191	3		

- Molecule 29 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	2	104	Total	C	N	O	S	0	0
			830	529	151	147	3		

- Molecule 30 is a protein called 60S ribosomal protein L35, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	3	119	Total	C	N	O	S	0	0
			994	635	194	163	2		

- Molecule 31 is a protein called 60S ribosomal protein L29, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 32 is a protein called 60S ribosomal protein L7, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 33 is a protein called 60S ribosomal protein L30e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	6	98	Total	C	N	O	S	0	0
			740	462	132	139	7		

- Molecule 34 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	7	96	Total	C	N	O	S	0	0
			793	508	151	129	5		

- Molecule 35 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	8	125	Total	C	N	O	S	0	0
			1036	660	206	163	7		

- Molecule 36 is a protein called 60S ribosomal protein L35Ae, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	9	103	Total	C	N	O	S	0	0
			844	543	163	135	3		

- Molecule 37 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	a	106	Total	C	N	O	S	0	0
			858	530	184	138	6		

- Molecule 38 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	b	95	Total	C	N	O	0	0
			756	477	150	129		

- Molecule 39 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	c	89	Total	C	N	O	S	0	0
			705	439	150	111	5		

- Molecule 40 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	d	72	Total	C	N	O	S	0	0
			603	395	107	99	2		

- Molecule 41 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	e	43	Total	C	N	O	S	0	0
			388	243	92	52	1		

- Molecule 42 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	f	51	Total	C	N	O	S	0	0
			413	255	87	66	5		

- Molecule 43 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	g	37	Total	C	N	O	S	0	0
			342	210	86	44	2		

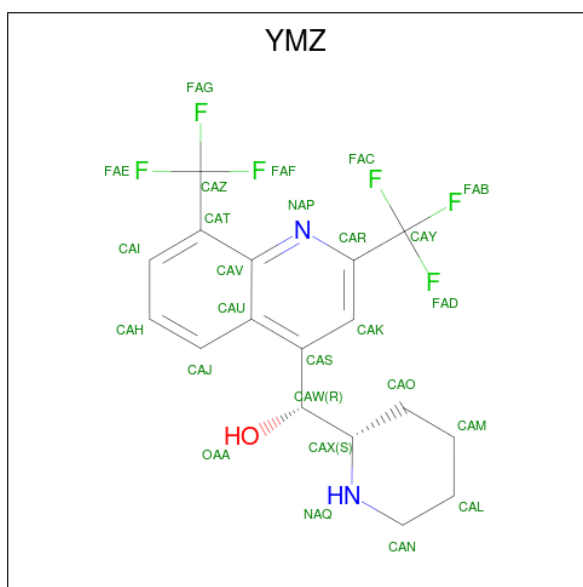
- Molecule 44 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	h	85	Total	C	N	O	S	0	0
			658	417	127	107	7		

- Molecule 45 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	i	95	Total	C	N	O	S	0	0
			778	490	152	127	9		

- Molecule 46 is Mefloquine (three-letter code: YMZ) (formula: C₁₇H₁₆F₆N₂O).



Mol	Chain	Residues	Atoms				AltConf	
46	A	1	Total	C	F	N	O	0
			26	17	6	2	1	
46	K	1	Total	C	F	N	O	0
			26	17	6	2	1	

- Molecule 47 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
47	A	155	Total	Mg	0
			155	155	
47	B	3	Total	Mg	0
			3	3	
47	C	5	Total	Mg	0
			5	5	
47	M	1	Total	Mg	0
			1	1	

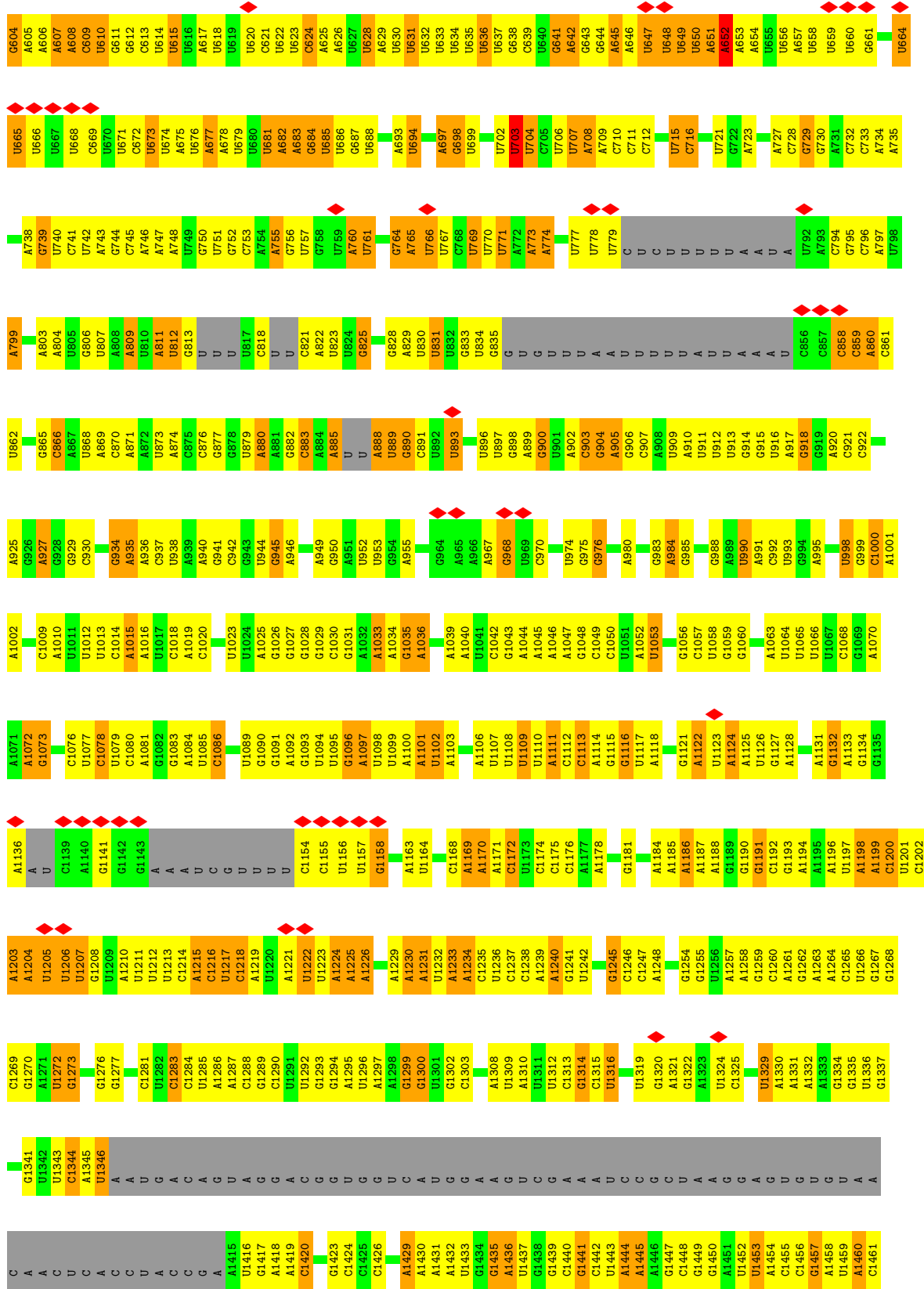
- Molecule 48 is ZINC ION (three-letter code: ZN) (formula: Zn).

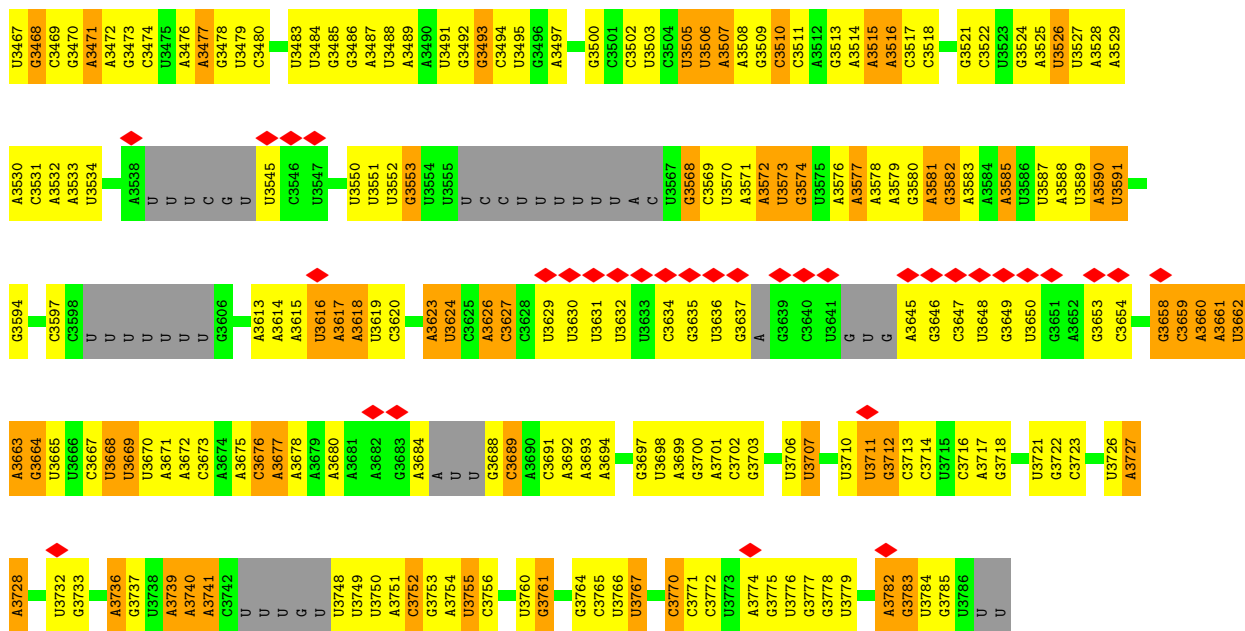
Mol	Chain	Residues	Atoms		AltConf
48	a	1	Total	Zn	0
			1	1	
48	c	1	Total	Zn	0
			1	1	
48	f	1	Total	Zn	0
			1	1	

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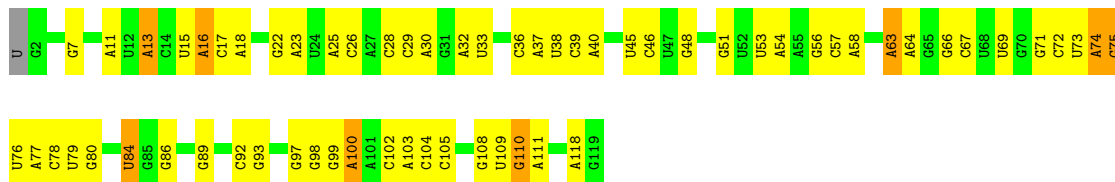
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Mol	Chain	Residues	Atoms		AltConf
48	h	1	Total 1	Zn 1	0
48	i	1	Total 1	Zn 1	0

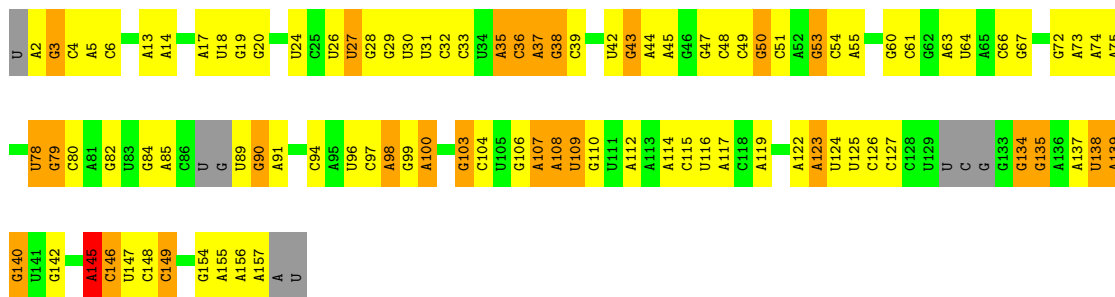




• Molecule 2: 5S ribosomal RNA

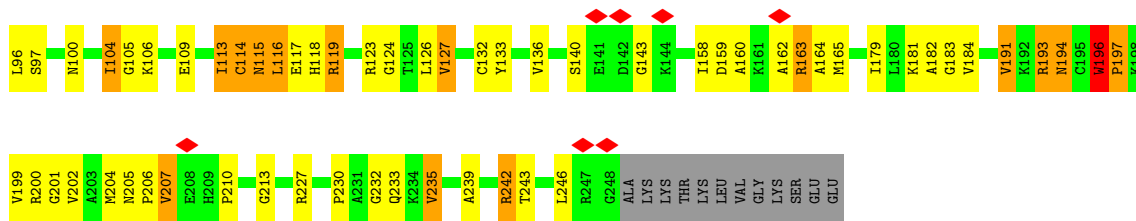


• Molecule 3: 5.8S ribosomal RNA

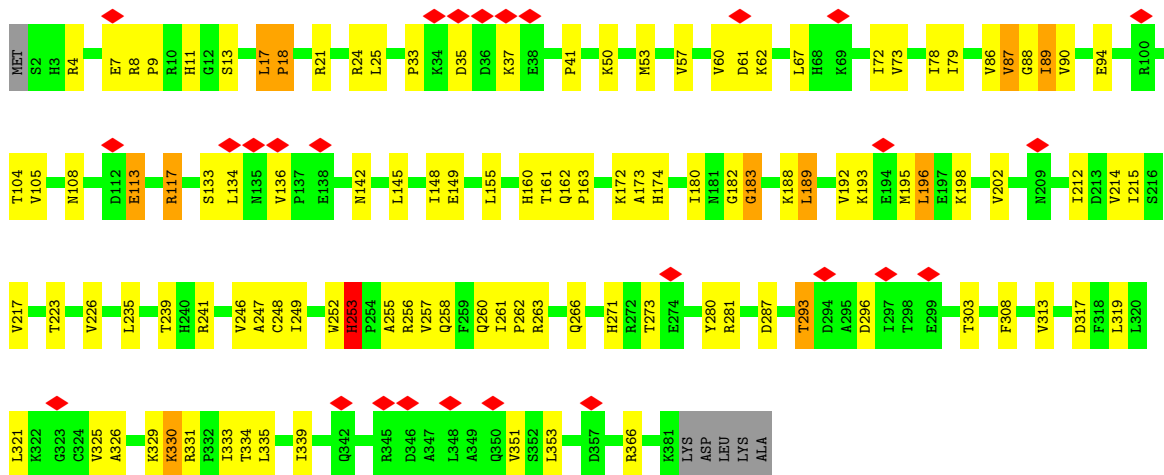


• Molecule 4: 60S ribosomal protein L2

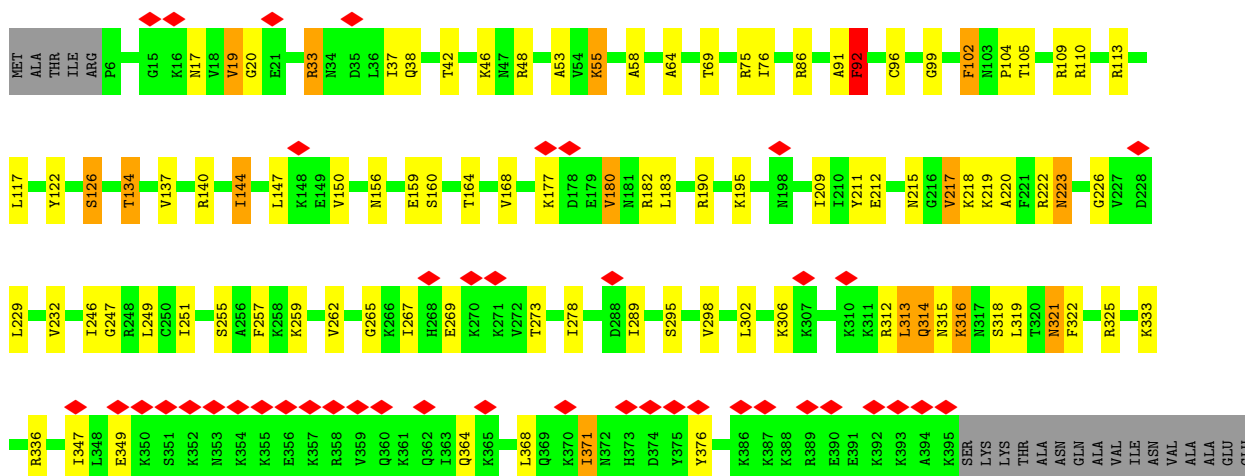




• Molecule 5: 60S ribosomal protein L3

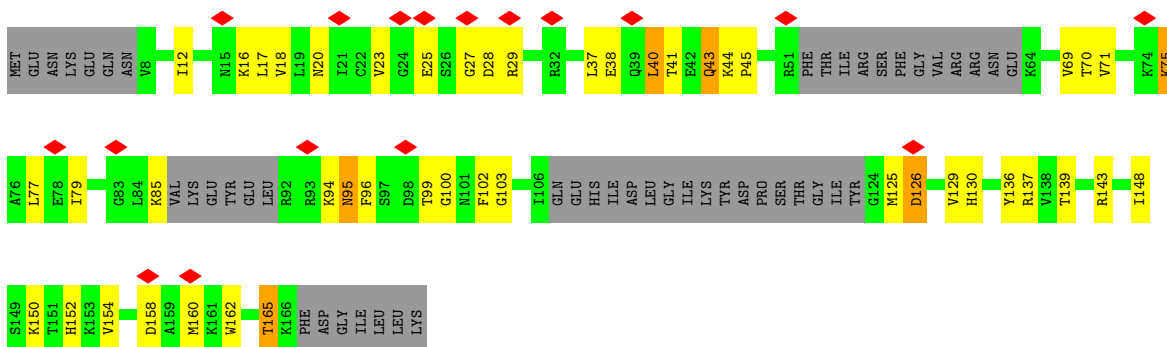


• Molecule 6: 60S ribosomal protein L4

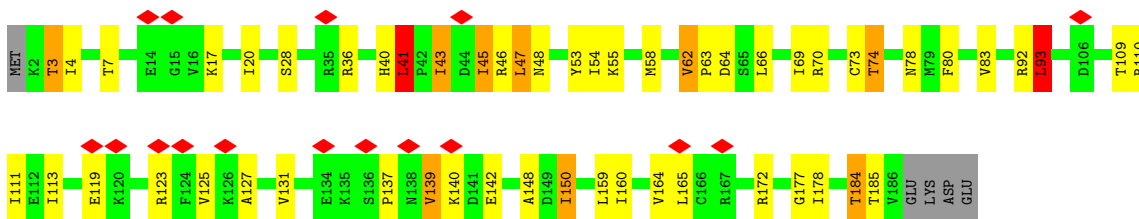


• Molecule 7: 60S ribosomal protein L11a, putative

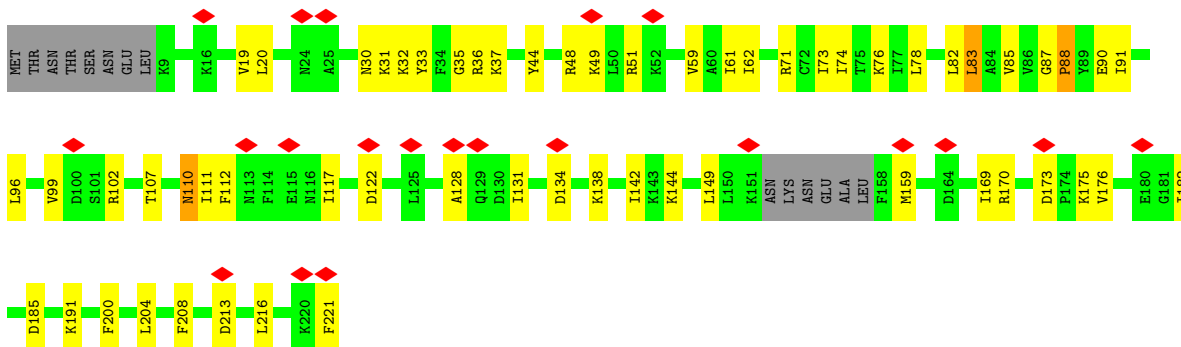




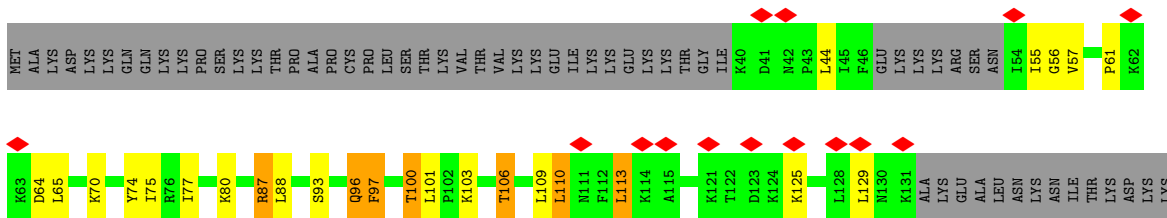
• Molecule 8: 60S ribosomal protein L6, putative

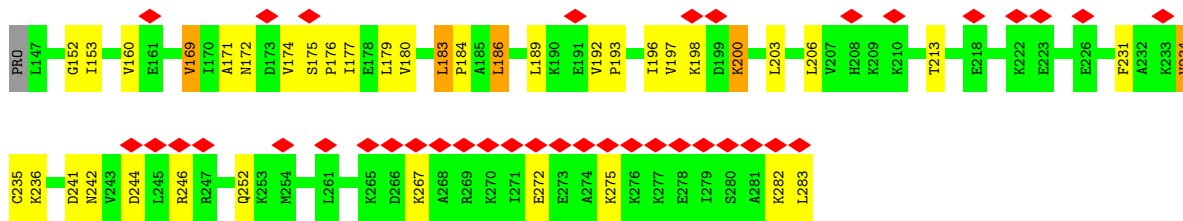


• Molecule 9: 60S ribosomal protein L6-2, putative

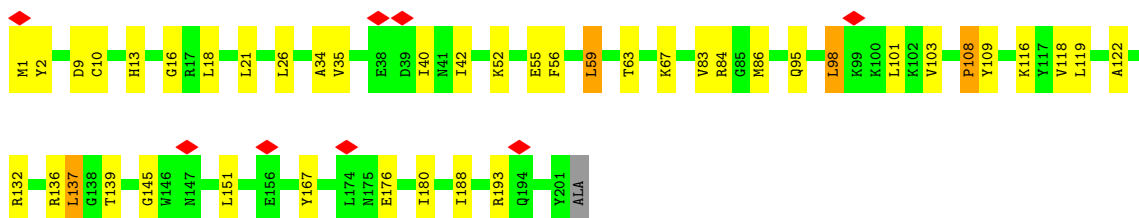
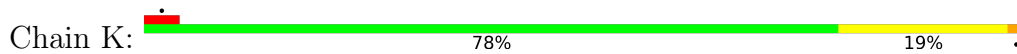


• Molecule 10: 60S ribosomal protein L7-3, putative

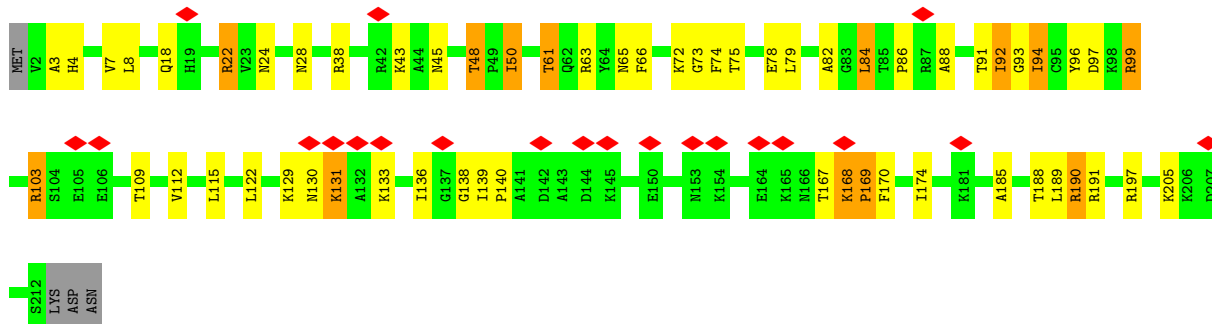




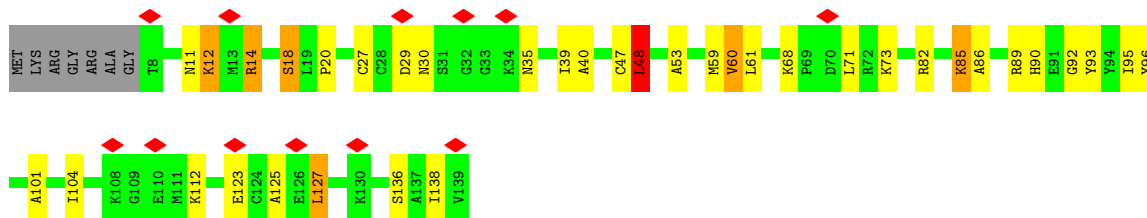
• Molecule 11: 60S ribosomal protein L13, putative



• Molecule 12: 60S ribosomal protein L13

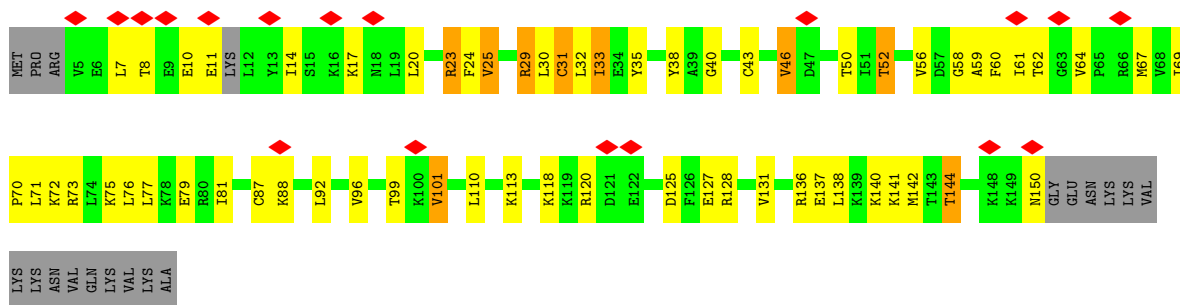


• Molecule 13: 60S ribosomal protein L23, putative

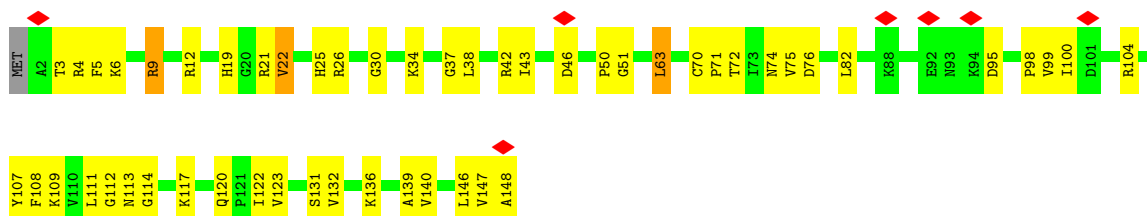


• Molecule 14: 60S ribosomal protein L14, putative

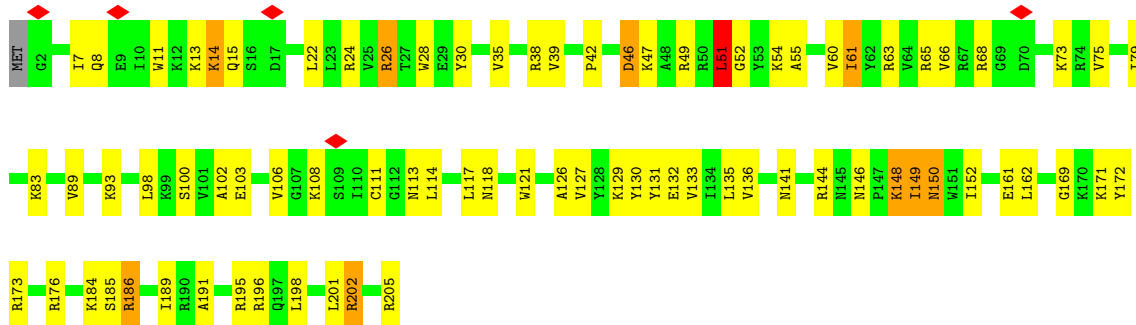




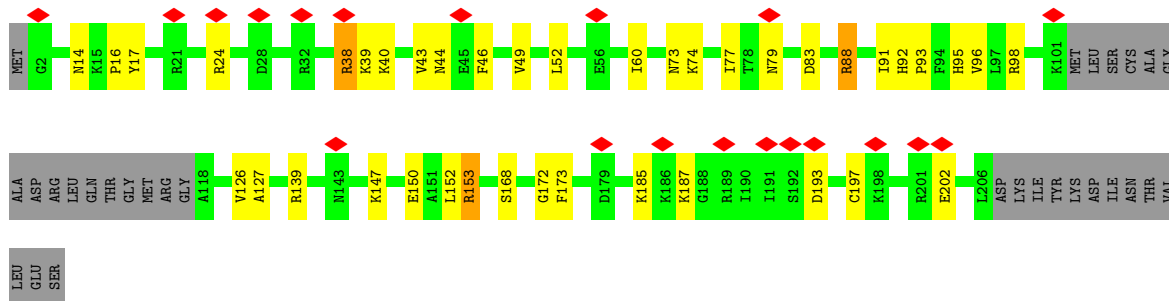
• Molecule 15: 60S ribosomal protein L27a, putative



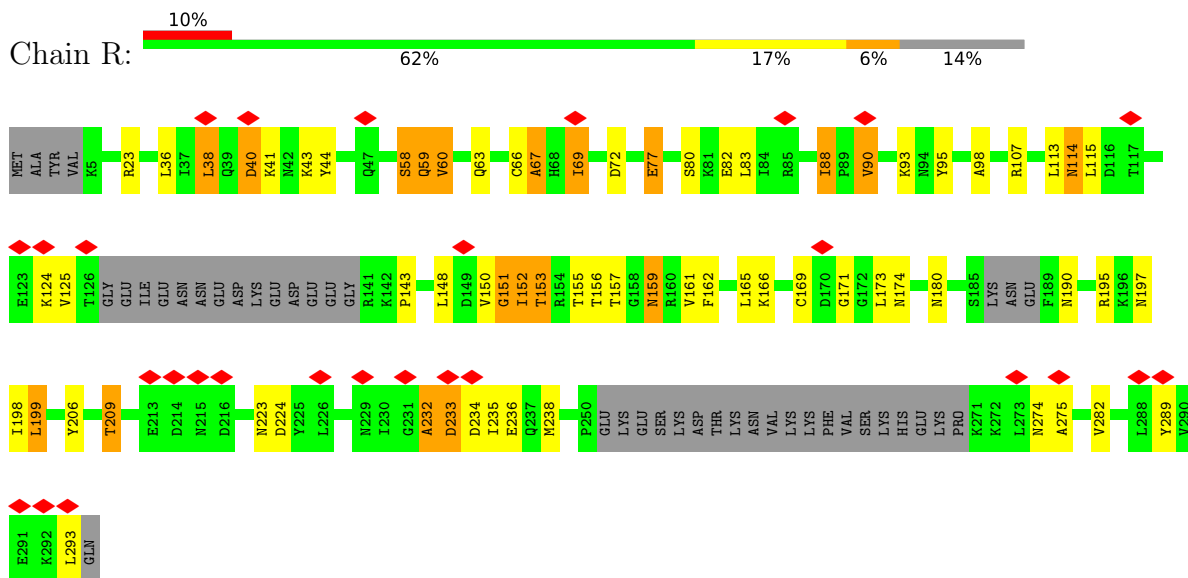
• Molecule 16: Ribosomal protein L15



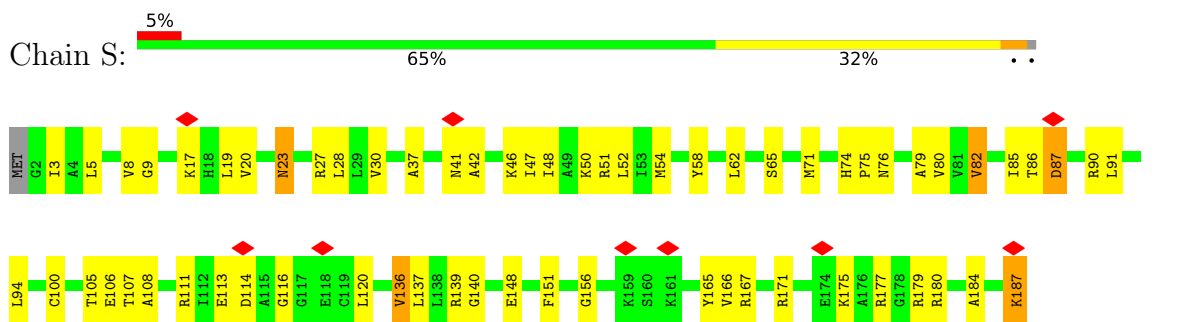
• Molecule 17: 60S ribosomal protein L10, putative



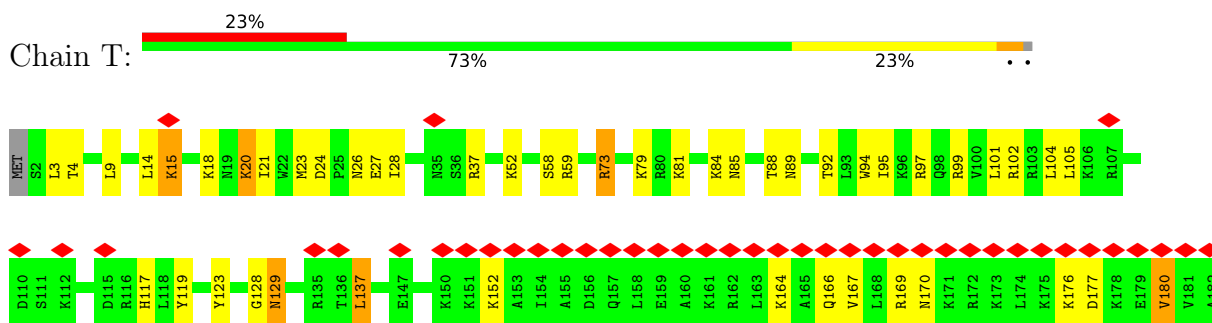
• Molecule 18: 60S ribosomal protein L5, putative



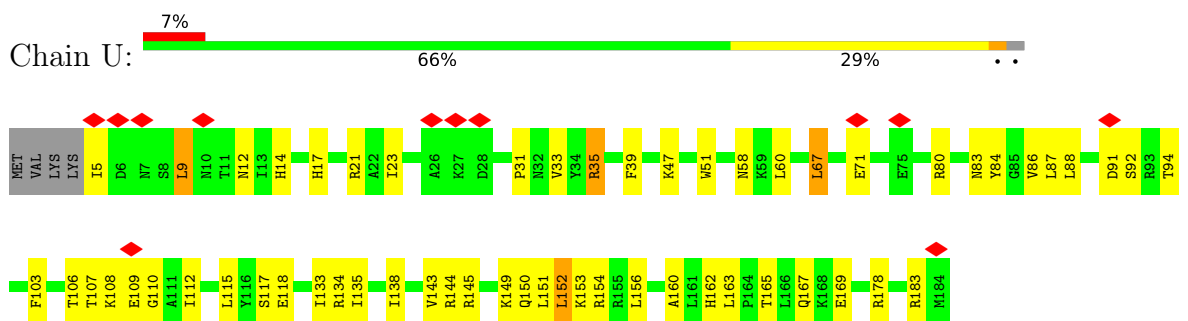
• Molecule 19: 60S ribosomal protein L18-2, putative



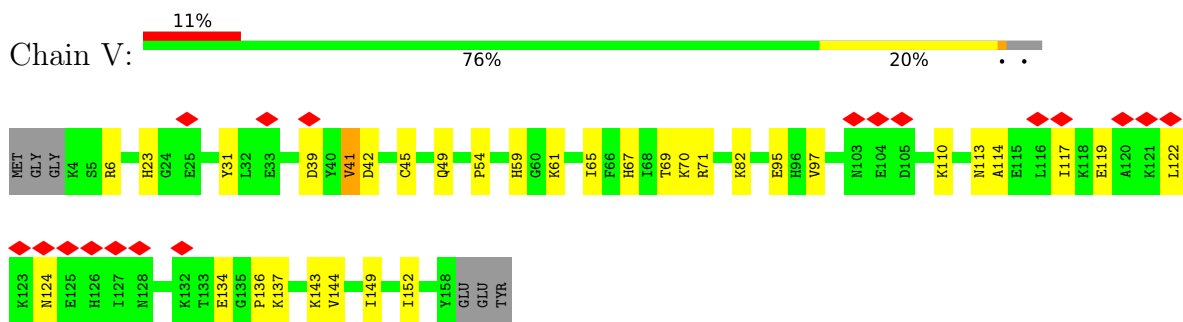
• Molecule 20: 60S ribosomal protein L19



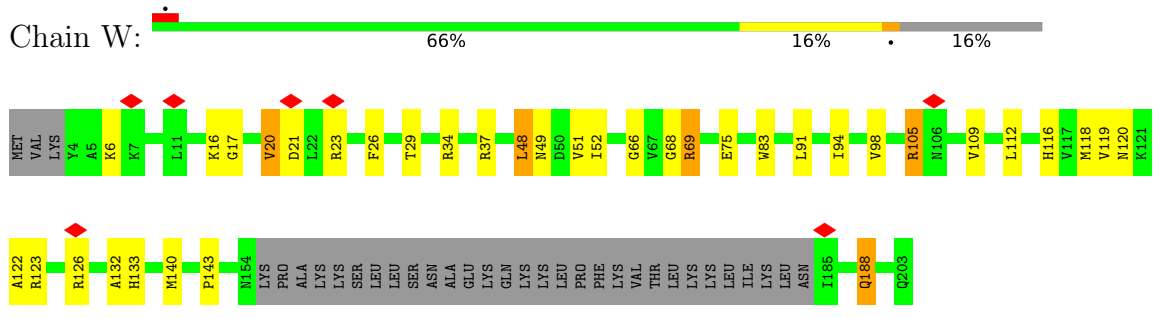
• Molecule 21: 60S ribosomal protein L18a



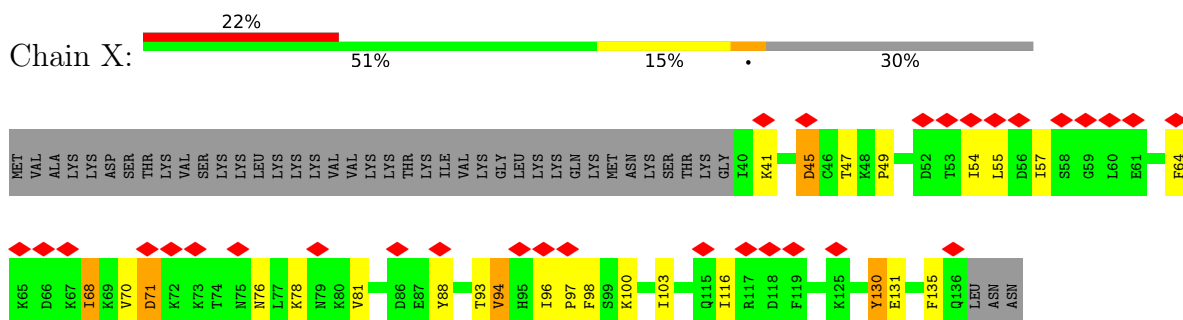
• Molecule 22: 60S ribosomal protein L21



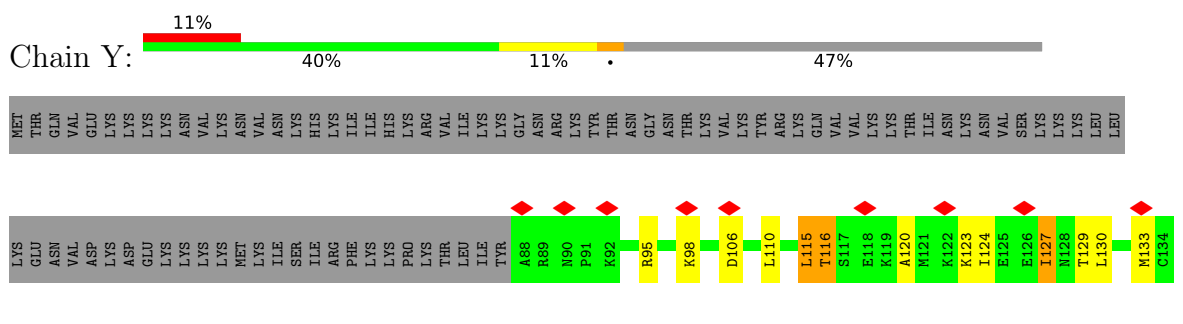
• Molecule 23: 60S ribosomal protein L17, putative



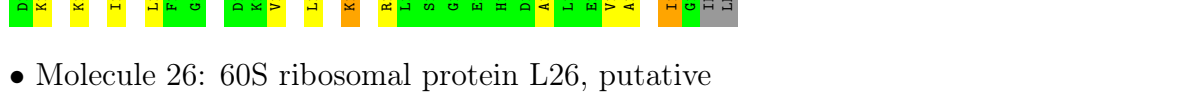
• Molecule 24: 60S ribosomal protein L22, putative

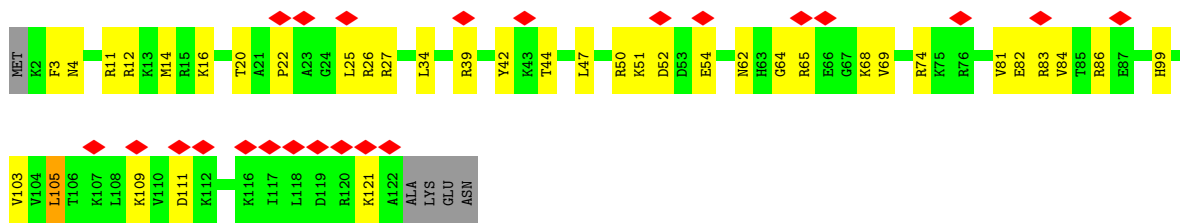


• Molecule 25: 60S ribosomal protein L23

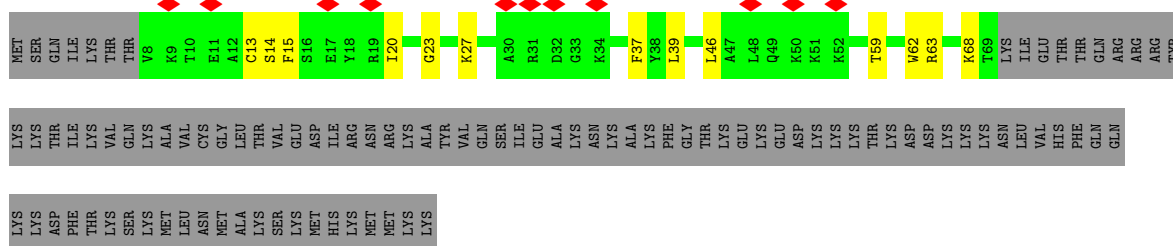


• Molecule 26: 60S ribosomal protein L26, putative

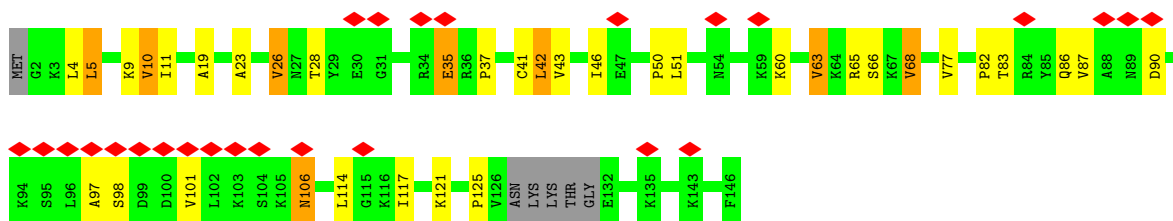




• Molecule 27: 60S ribosomal protein L24, putative



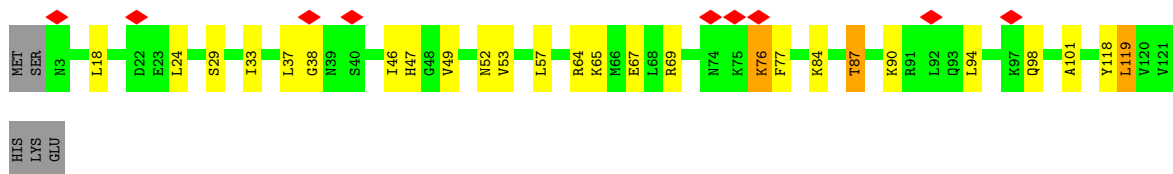
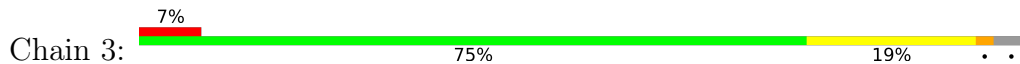
• Molecule 28: 60S ribosomal protein L27



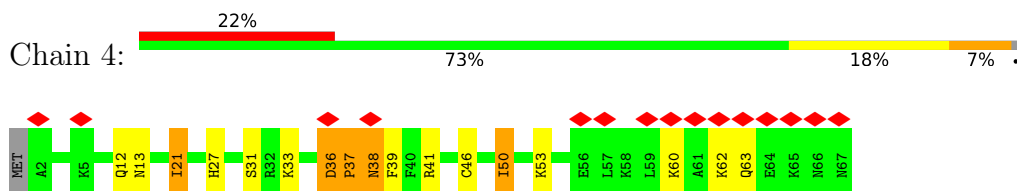
• Molecule 29: 60S ribosomal protein L28



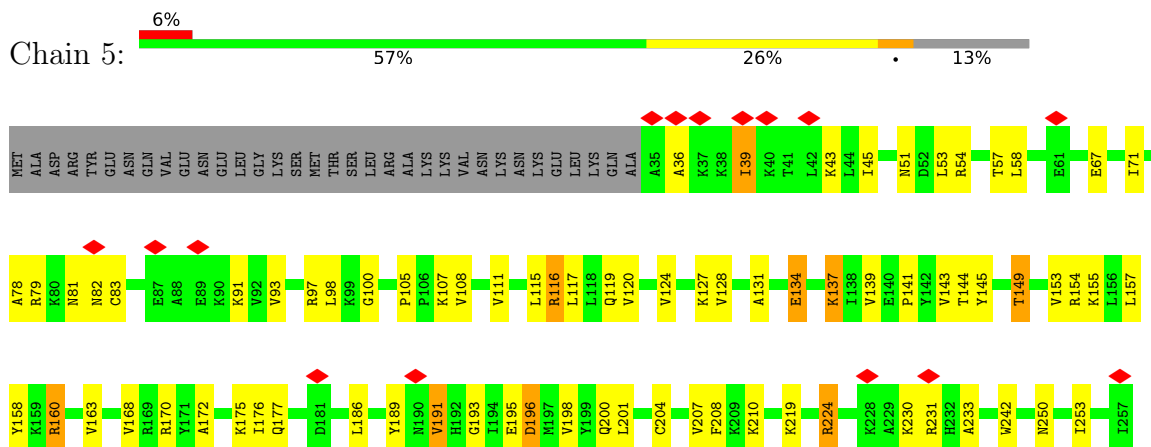
• Molecule 30: 60S ribosomal protein L35, putative



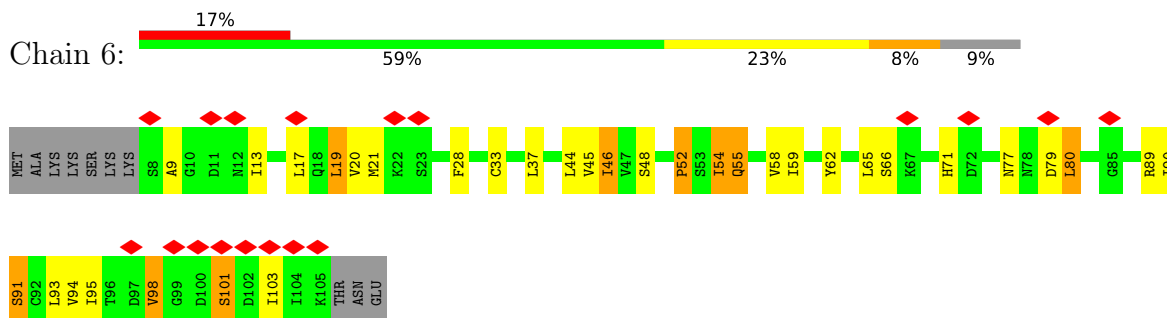
- Molecule 31: 60S ribosomal protein L29, putative



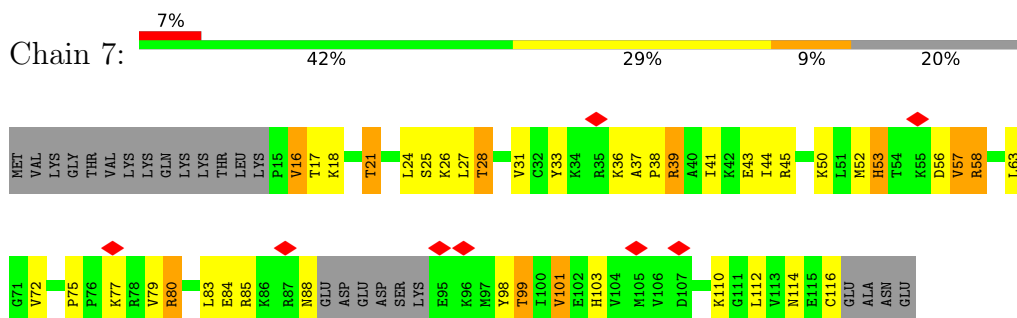
- Molecule 32: 60S ribosomal protein L7, putative



- Molecule 33: 60S ribosomal protein L30e, putative

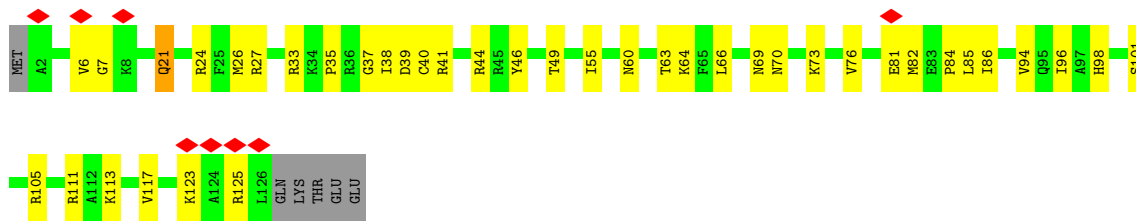


- Molecule 34: 60S ribosomal protein L31

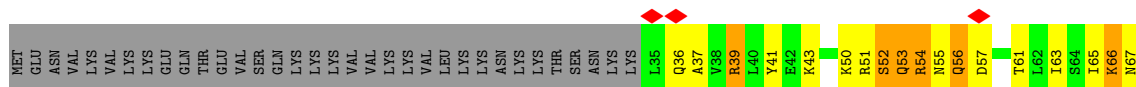


- Molecule 35: 60S ribosomal protein L32

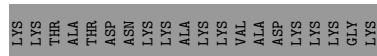
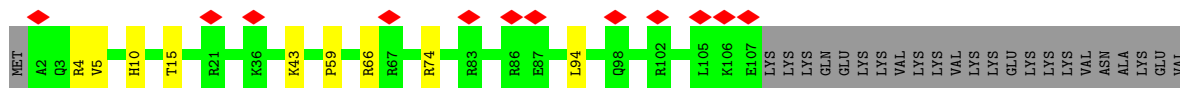




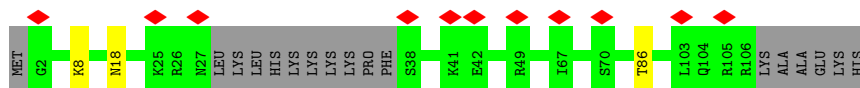
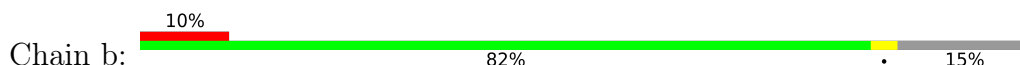
• Molecule 36: 60S ribosomal protein L35Ae, putative



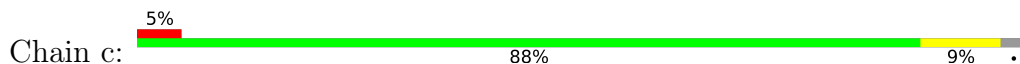
• Molecule 37: 60S ribosomal protein L34



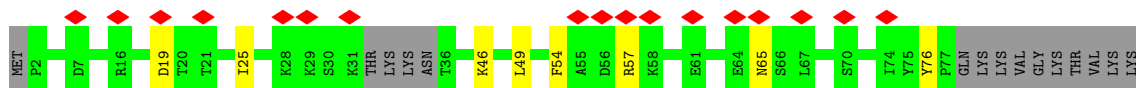
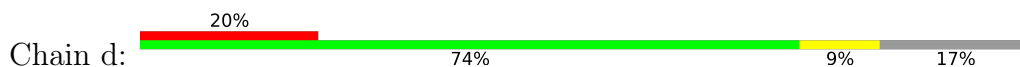
• Molecule 38: 60S ribosomal protein L36



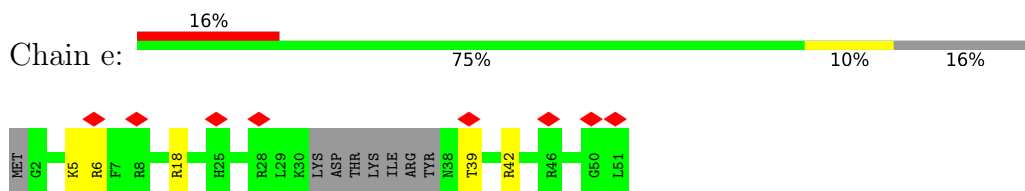
• Molecule 39: Ribosomal protein L37



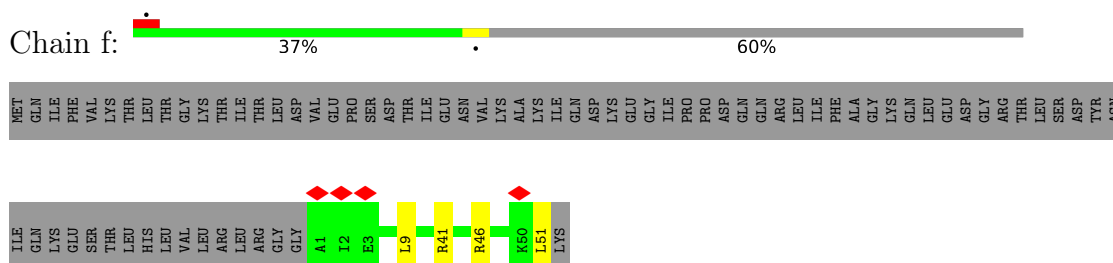
• Molecule 40: 60S ribosomal protein L38



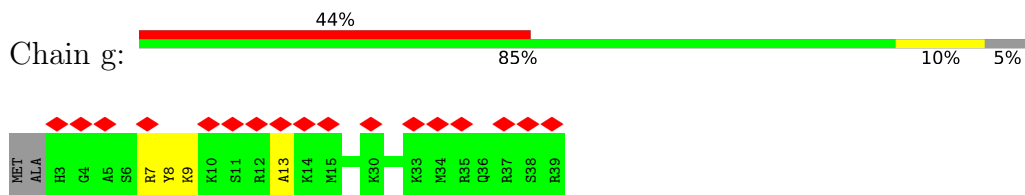
- Molecule 41: 60S ribosomal protein L39



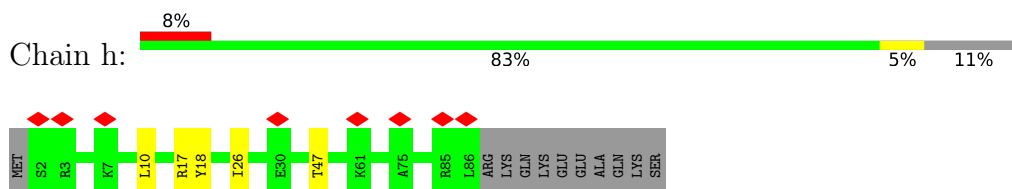
- Molecule 42: Ubiquitin-60S ribosomal protein L40



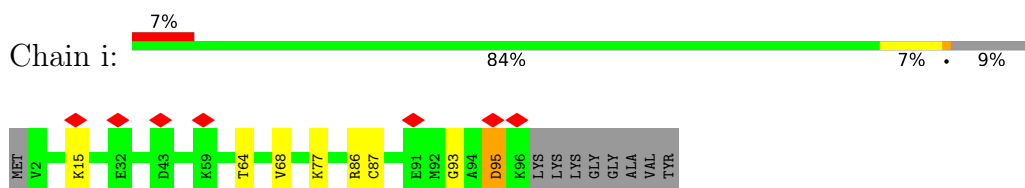
- Molecule 43: 60S ribosomal protein L41



- Molecule 44: 60S ribosomal protein L37a



- Molecule 45: 60S ribosomal protein L44



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	43184	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3800	Depositor
Magnification	104748	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.883	Depositor
Minimum map value	-0.507	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.034	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	603.0, 603.0, 603.0	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.03, 1.03, 1.03	Depositor

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: YMZ, ZN, MG

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	A	0.20	1/75982 (0.0%)	0.66	5/118263 (0.0%)
2	B	0.18	0/2826	0.64	0/4404
3	C	0.19	0/3608	0.66	2/5615 (0.0%)
4	D	0.37	0/1901	0.65	0/2544
5	E	0.32	0/3129	0.57	0/4195
6	F	0.32	0/3144	0.62	0/4205
7	G	0.33	0/1020	0.61	0/1349
8	H	0.31	0/1485	0.59	2/2009 (0.1%)
9	I	0.30	0/1707	0.58	0/2274
10	J	0.33	0/1840	0.63	0/2456
11	K	0.32	0/1689	0.64	0/2260
12	L	0.33	0/1788	0.62	0/2381
13	M	0.33	0/1012	0.60	0/1363
14	N	0.35	0/1213	0.64	0/1616
15	O	0.31	0/1199	0.58	0/1597
16	P	0.32	0/1735	0.60	0/2320
17	Q	0.31	0/1579	0.52	0/2113
18	R	0.33	0/2074	0.64	0/2772
19	S	0.32	0/1530	0.63	0/2040
20	T	0.35	0/1521	0.63	0/2012
21	U	0.33	0/1526	0.56	0/2043
22	V	0.27	0/1300	0.46	0/1732
23	W	0.30	0/1338	0.56	0/1793
24	X	0.35	0/841	0.59	0/1125
25	Y	0.34	0/805	0.61	0/1074
26	Z	0.28	0/1012	0.53	1/1339 (0.1%)
27	0	0.35	0/533	0.57	0/711
28	1	0.29	0/1151	0.53	0/1531
29	2	0.30	0/839	0.52	0/1114
30	3	0.34	0/1004	0.64	0/1329
31	4	0.34	0/564	0.63	0/737
32	5	0.33	0/1917	0.62	0/2562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	6	0.34	0/748	0.67	0/1001
34	7	0.34	0/805	0.64	0/1073
35	8	0.34	0/1053	0.60	0/1399
36	9	0.34	0/864	0.64	0/1160
37	a	0.28	0/871	0.53	0/1161
38	b	0.33	0/762	0.63	0/1008
39	c	0.33	0/718	0.60	0/946
40	d	0.34	0/611	0.64	0/812
41	e	0.35	0/396	0.59	0/521
42	f	0.36	0/418	0.63	0/556
43	g	0.35	0/347	0.60	0/448
44	h	0.29	0/667	0.52	0/887
45	i	0.32	0/788	0.57	0/1032
All	All	0.25	1/133860 (0.0%)	0.64	10/196882 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	D	0	1
5	E	0	2
33	6	0	1
36	9	0	1
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1475	G	O3'-P	-5.31	1.54	1.61

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1805	U	C2'-C3'-O3'	6.73	124.47	113.70
26	Z	105	LEU	CA-CB-CG	6.13	129.40	115.30
3	C	134	G	C2'-C3'-O3'	5.93	123.19	113.70
3	C	145	A	C2'-C3'-O3'	5.63	122.71	113.70
1	A	652	A	C2'-C3'-O3'	5.47	122.46	113.70
1	A	289	A	C2'-C3'-O3'	5.43	122.38	113.70
8	H	93	LEU	CA-CB-CG	5.34	127.58	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	215	C	C2'-C3'-O3'	5.26	122.12	113.70
8	H	41	LEU	CA-CB-CG	5.25	127.38	115.30
1	A	703	U	C2'-C3'-O3'	5.08	121.84	113.70

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	6	52	PRO	Peptide
36	9	136	TYR	Peptide
4	D	196	TRP	Peptide
5	E	17	LEU	Peptide
5	E	253	HIS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	67935	0	34198	1791	0
2	B	2525	0	1274	38	0
3	C	3224	0	1630	93	0
4	D	1866	0	1964	66	0
5	E	3061	0	3205	87	0
6	F	3094	0	3333	72	0
7	G	1010	0	1073	29	0
8	H	1460	0	1532	31	0
9	I	1684	0	1849	25	0
10	J	1813	0	1985	34	0
11	K	1659	0	1782	26	0
12	L	1756	0	1888	37	0
13	M	996	0	1044	20	0
14	N	1197	0	1312	46	0
15	O	1172	0	1230	37	0
16	P	1697	0	1802	55	0
17	Q	1544	0	1582	23	0
18	R	2045	0	2134	36	0
19	S	1502	0	1636	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	T	1505	0	1671	30	0
21	U	1496	0	1556	45	0
22	V	1275	0	1355	20	0
23	W	1318	0	1319	24	0
24	X	824	0	882	14	0
25	Y	796	0	850	18	0
26	Z	1000	0	1099	22	0
27	0	521	0	539	7	0
28	1	1134	0	1245	18	0
29	2	830	0	887	9	0
30	3	994	0	1121	10	0
31	4	555	0	599	12	0
32	5	1879	0	2005	54	0
33	6	740	0	763	15	0
34	7	793	0	869	32	0
35	8	1036	0	1139	26	0
36	9	844	0	886	37	0
37	a	858	0	911	0	0
38	b	756	0	842	0	0
39	c	705	0	755	0	0
40	d	603	0	686	0	0
41	e	388	0	421	0	0
42	f	413	0	450	0	0
43	g	342	0	388	0	0
44	h	658	0	725	0	0
45	i	778	0	858	0	0
46	A	26	0	0	3	0
46	K	26	0	0	0	0
47	A	155	0	0	0	0
47	B	3	0	0	0	0
47	C	5	0	0	0	0
47	M	1	0	0	0	0
48	a	1	0	0	0	0
48	c	1	0	0	0	0
48	f	1	0	0	0	0
48	h	1	0	0	0	0
48	i	1	0	0	0	0
All	All	124502	0	91274	2716	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 13.

All (2716) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1102:U:O4	1:A:1231:A:N1	1.59	1.34
1:A:3505:U:N3	1:A:3508:A:N6	1.77	1.33
1:A:2995:A:N6	1:A:3052:U:H3	1.26	1.32
1:A:1316:U:H3	1:A:1445:A:N6	1.28	1.29
1:A:78:U:H3	1:A:333:A:N6	1.28	1.26
1:A:440:A:H2'	1:A:441:A:C8	1.70	1.25
1:A:3122:A:N6	1:A:3137:U:H3	1.38	1.22
1:A:746:A:H2'	1:A:747:A:C8	1.75	1.19
1:A:912:U:H2'	1:A:913:U:C6	1.78	1.19
1:A:2703:U:O4	1:A:3160:A:N1	1.76	1.18
1:A:607:A:H2'	1:A:608:A:C8	1.79	1.16
1:A:1822:A:C2	1:A:2004:U:C5	2.33	1.15
1:A:1102:U:C4	1:A:1231:A:N1	2.19	1.10
1:A:3122:A:N1	1:A:3137:U:O4	1.83	1.10
1:A:78:U:O4	1:A:333:A:N1	1.85	1.08
1:A:2975:A:N6	1:A:2980:U:H3	1.52	1.08
1:A:684:G:H1'	6:F:314:GLN:HG2	1.32	1.06
1:A:1644:U:O4	1:A:2102:A:N1	1.91	1.02
1:A:2995:A:N1	1:A:3052:U:O4	1.93	1.01
1:A:3623:A:OP1	1:A:3623:A:H4'	1.58	1.01
1:A:3617:A:H4'	1:A:3618:A:OP1	1.60	1.00
1:A:2703:U:H3	1:A:3160:A:N6	1.58	0.99
1:A:1770:G:H1'	1:A:1797:A:H61	1.28	0.98
1:A:445:A:H2	1:A:702:U:C5	1.82	0.98
1:A:1644:U:C4	1:A:2102:A:N1	2.32	0.97
1:A:123:A:H3'	1:A:124:U:H5''	1.46	0.97
1:A:3505:U:C2	1:A:3508:A:N6	2.32	0.97
1:A:1822:A:H2	1:A:2004:U:C5	1.67	0.97
1:A:506:A:H2'	1:A:507:G:C8	1.99	0.96
1:A:1102:U:O4	1:A:1231:A:C2	2.17	0.96
21:U:88:LEU:HD11	21:U:115:LEU:HD11	1.48	0.95
8:H:66:LEU:O	8:H:69:ILE:HG22	1.66	0.95
1:A:1643:U:H1'	1:A:1644:U:H5	1.31	0.95
16:P:148:LYS:O	16:P:149:ILE:HG12	1.67	0.94
1:A:1615:G:N2	1:A:1659:A:H5''	1.82	0.94
1:A:525:U:H2'	1:A:526:U:C6	2.02	0.94
1:A:912:U:H2'	1:A:913:U:H6	1.23	0.94
3:C:30:U:H2'	3:C:31:U:C6	2.02	0.94
1:A:3122:A:N6	1:A:3137:U:N3	2.07	0.94
1:A:1122:A:H2	1:A:1169:A:H62	1.10	0.94
1:A:3505:U:N3	1:A:3508:A:C6	2.35	0.92
1:A:1630:A:O2'	1:A:2125:A:H1'	1.70	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:7:25:SER:HB2	34:7:77:LYS:HG3	1.48	0.92
1:A:606:A:H2'	1:A:607:A:C8	2.04	0.92
5:E:149:GLU:HG3	5:E:189:LEU:HD13	1.52	0.92
1:A:1206:U:H4'	1:A:1207:U:OP1	1.69	0.92
1:A:3505:U:C4	1:A:3508:A:N6	2.30	0.91
1:A:2703:U:N3	1:A:3160:A:N6	2.13	0.91
1:A:2506:A:H2'	1:A:2507:A:C8	2.06	0.91
1:A:344:A:H5''	1:A:344:A:H8	1.32	0.90
7:G:27:GLY:O	7:G:29:ARG:N	2.04	0.89
1:A:773:A:HO2'	1:A:774:A:H8	0.96	0.89
25:Y:116:THR:O	25:Y:120:ALA:HB3	1.73	0.89
1:A:440:A:H2'	1:A:441:A:H8	1.32	0.89
1:A:2703:U:H3	1:A:3160:A:H61	0.93	0.88
1:A:2995:A:N6	1:A:3052:U:N3	1.97	0.88
1:A:344:A:H2'	1:A:345:G:C8	2.09	0.88
18:R:83:LEU:HB3	18:R:88:ILE:HG23	1.56	0.87
1:A:664:U:H4'	1:A:665:U:OP1	1.73	0.86
1:A:2650:A:H2'	1:A:2651:A:C8	2.10	0.86
1:A:1476:A:N3	1:A:1476:A:H5''	1.91	0.86
1:A:3235:C:H1'	1:A:3311:G:N2	1.92	0.85
1:A:914:G:H2'	1:A:915:G:C8	2.11	0.85
1:A:3241:U:H2'	1:A:3242:U:C6	2.12	0.85
1:A:3495:U:N3	1:A:3505:U:O4	2.09	0.85
1:A:770:U:H3'	1:A:771:U:H5''	1.59	0.85
1:A:445:A:C2	1:A:702:U:C5	2.59	0.84
1:A:29:C:OP1	16:P:191:ALA:HB2	1.76	0.84
1:A:1316:U:O4	1:A:1445:A:N1	2.11	0.84
1:A:706:U:H2'	1:A:707:U:C6	2.12	0.83
4:D:196:TRP:CE3	4:D:197:PRO:HD3	2.13	0.83
1:A:2975:A:H61	1:A:2980:U:H3	0.82	0.82
1:A:1643:U:H1'	1:A:1644:U:C5	2.13	0.82
6:F:289:ILE:HD11	19:S:28:LEU:HG	1.58	0.82
1:A:624:C:H5'	1:A:625:A:H5'	1.62	0.82
1:A:773:A:O2'	1:A:774:A:H8	1.62	0.82
1:A:1103:A:H62	1:A:1230:A:H8	1.24	0.82
1:A:1109:U:H2'	1:A:1110:U:C6	2.15	0.82
1:A:1511:U:H2'	1:A:1512:A:C8	2.15	0.81
1:A:137:G:H8	1:A:140:A:H62	1.25	0.81
1:A:998:U:H4'	23:W:132:ALA:HB2	1.62	0.81
5:E:41:PRO:HA	5:E:182:GLY:HA3	1.62	0.81
1:A:1974:U:H2'	1:A:1975:A:C8	2.17	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:3:24:LEU:HB3	30:3:53:VAL:HG22	1.63	0.80
1:A:3648:U:H2'	1:A:3649:G:H8	1.46	0.80
36:9:50:LYS:O	36:9:56:GLN:O	1.97	0.80
1:A:453:A:N6	1:A:502:U:O2	2.13	0.80
1:A:345:G:N1	3:C:30:U:O2	2.15	0.80
1:A:526:U:H3	1:A:629:A:H2	1.28	0.80
1:A:202:C:H2'	1:A:203:A:C8	2.17	0.79
1:A:3402:A:H2'	1:A:3403:A:C8	2.16	0.79
5:E:188:LYS:O	5:E:192:VAL:HG23	1.82	0.79
14:N:59:ALA:O	14:N:61:ILE:N	2.15	0.79
1:A:3660:A:H2'	1:A:3661:A:C8	2.18	0.79
1:A:3195:C:H5	1:A:3211:C:H42	1.29	0.79
1:A:684:G:C1'	6:F:314:GLN:HG2	2.12	0.79
1:A:685:U:O2	1:A:685:U:H2'	1.81	0.79
18:R:60:VAL:HG21	18:R:98:ALA:HA	1.65	0.79
1:A:1110:U:H3	1:A:1184:A:H2	1.31	0.79
1:A:506:A:H2'	1:A:507:G:H8	1.42	0.78
14:N:96:VAL:HG23	14:N:101:VAL:HG12	1.65	0.78
1:A:3119:A:H5''	12:L:197:ARG:HG3	1.65	0.78
1:A:1794:U:O2	1:A:1794:U:H2'	1.81	0.78
26:Z:22:PRO:HD2	26:Z:25:LEU:HD12	1.66	0.78
1:A:3443:A:H2'	1:A:3444:G:H5'	1.63	0.78
1:A:190:G:N1	1:A:241:C:N4	2.32	0.78
35:8:81:GLU:O	35:8:84:PRO:HD2	1.81	0.78
15:O:21:ARG:HH22	35:8:37:GLY:HA2	1.49	0.78
1:A:404:U:H5'	26:Z:86:ARG:HH22	1.48	0.78
12:L:73:GLY:HA3	12:L:97:ASP:HB2	1.64	0.78
14:N:11:GLU:O	14:N:14:ILE:HG13	1.83	0.77
1:A:921:C:H5	15:O:25:HIS:HD1	1.32	0.77
1:A:2975:A:N1	1:A:2980:U:O4	2.18	0.77
2:B:63:A:H1'	18:R:282:VAL:HG11	1.65	0.77
17:Q:38:ARG:HE	17:Q:83:ASP:HB2	1.50	0.77
1:A:746:A:H2'	1:A:747:A:H8	1.47	0.77
1:A:1575:C:H5'	6:F:42:THR:HG21	1.66	0.77
8:H:20:ILE:HG12	8:H:47:LEU:HD23	1.65	0.76
1:A:2112:G:H5'	1:A:2113:C:H5'	1.67	0.76
1:A:2020:A:H2'	1:A:2021:A:C8	2.20	0.76
16:P:7:ILE:HD11	16:P:46:ASP:HB3	1.67	0.76
1:A:261:A:H2'	1:A:262:A:C8	2.21	0.76
1:A:3130:U:H4'	1:A:3131:A:H5'	1.66	0.76
16:P:121:TRP:O	16:P:130:TYR:O	2.04	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:88:LEU:HD21	21:U:115:LEU:HD21	1.68	0.76
1:A:3632:U:H3	1:A:3653:G:H1	1.34	0.75
16:P:136:VAL:HG11	16:P:152:ILE:HG21	1.68	0.75
1:A:526:U:H2'	1:A:527:A:O4'	1.86	0.75
1:A:3626:A:H3'	1:A:3627:C:H5''	1.68	0.75
16:P:73:LYS:HB3	16:P:89:VAL:HG12	1.67	0.75
1:A:1670:G:H21	1:A:2102:A:H1'	1.52	0.75
4:D:51:ASP:HB2	4:D:58:LEU:HD11	1.68	0.75
33:6:44:LEU:HB3	33:6:95:ILE:HD11	1.68	0.75
1:A:190:G:H1	1:A:241:C:N4	1.85	0.75
1:A:744:G:N2	1:A:915:G:N2	2.34	0.75
7:G:18:VAL:HG12	7:G:70:THR:HG22	1.68	0.75
13:M:18:SER:HB2	13:M:85:LYS:HG3	1.68	0.74
32:5:57:THR:HG23	32:5:195:GLU:HG2	1.68	0.74
1:A:746:A:N1	1:A:913:U:O4	2.21	0.74
1:A:1643:U:C1'	1:A:1644:U:C5	2.71	0.74
34:7:41:ILE:HD11	34:7:68:TRP:HE1	1.52	0.74
36:9:136:TYR:HB2	36:9:137:PRO:HD2	1.70	0.74
1:A:465:A:H2'	1:A:466:A:C8	2.23	0.74
1:A:703:U:H2'	1:A:704:U:C6	2.23	0.74
1:A:3025:U:H2'	1:A:3026:G:O4'	1.88	0.74
1:A:645:A:OP1	9:I:31:LYS:HG3	1.88	0.74
1:A:3314:U:C5	1:A:3336:G:N2	2.56	0.73
1:A:3022:U:H2'	1:A:3023:C:C6	2.23	0.73
1:A:3776:U:H2'	1:A:3777:G:C8	2.22	0.73
20:T:18:LYS:HA	20:T:21:ILE:HD12	1.70	0.73
24:X:47:THR:HG22	24:X:88:TYR:HB3	1.70	0.73
1:A:594:C:O2	1:A:594:C:H2'	1.87	0.73
1:A:2695:A:H5''	6:F:69:THR:HB	1.68	0.73
14:N:70:PRO:HD2	14:N:73:ARG:HD2	1.70	0.73
1:A:582:U:H2'	1:A:583:U:H6	1.54	0.73
1:A:3648:U:H2'	1:A:3649:G:C8	2.24	0.73
1:A:1316:U:N3	1:A:1445:A:N6	2.12	0.73
1:A:1476:A:H4'	1:A:1476:A:OP1	1.87	0.73
1:A:2442:A:H4'	4:D:179:ILE:O	1.88	0.73
14:N:24:PHE:O	14:N:29:ARG:HG3	1.89	0.73
1:A:1895:U:H2'	1:A:1896:C:C6	2.24	0.72
1:A:2091:U:H3'	1:A:2092:G:H5'	1.71	0.72
34:7:41:ILE:HD11	34:7:68:TRP:NE1	2.03	0.72
1:A:2181:A:N3	1:A:2413:A:H2'	2.04	0.72
12:L:189:LEU:HG	15:O:146:LEU:HD21	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:7:28:THR:CG2	34:7:36:LYS:HG3	2.20	0.72
1:A:3441:A:H2	1:A:3471:A:H62	1.35	0.72
18:R:143:PRO:HB2	18:R:174:ASN:HB2	1.71	0.72
1:A:1210:A:H2'	1:A:1211:U:C6	2.25	0.72
1:A:2650:A:H2'	1:A:2651:A:H8	1.52	0.72
8:H:164:VAL:HG11	8:H:178:ILE:H	1.52	0.72
1:A:582:U:H2'	1:A:583:U:C6	2.24	0.72
1:A:606:A:H2'	1:A:607:A:H8	1.50	0.72
1:A:746:A:C2	1:A:913:U:N3	2.58	0.72
32:5:139:VAL:O	32:5:139:VAL:HG12	1.90	0.72
34:7:28:THR:HG22	34:7:36:LYS:HG3	1.72	0.72
1:A:1537:G:H5''	1:A:1537:G:H8	1.53	0.72
8:H:62:VAL:HB	8:H:63:PRO:HD2	1.72	0.72
20:T:128:GLY:O	20:T:129:ASN:HB2	1.89	0.72
1:A:195:A:C8	1:A:216:C:O2'	2.42	0.72
1:A:588:C:C2	1:A:604:G:N2	2.58	0.71
1:A:3508:A:HO2'	8:H:40:HIS:HD1	1.36	0.71
1:A:3740:A:O2'	1:A:3741:A:H5''	1.90	0.71
4:D:52:PRO:HB3	4:D:191:VAL:HG11	1.72	0.71
5:E:113:GLU:HG2	5:E:163:PRO:HD2	1.70	0.71
1:A:2525:A:H2'	1:A:2526:A:C8	2.24	0.71
35:8:21:GLN:HG3	35:8:24:ARG:HB2	1.71	0.71
1:A:2107:C:H3'	1:A:2108:A:H5''	1.70	0.71
1:A:3553:G:H21	1:A:3572:A:H8	1.37	0.71
2:B:17:C:H5''	7:G:150:LYS:HD2	1.70	0.71
1:A:99:A:OP1	16:P:196:ARG:HD2	1.91	0.71
1:A:2473:A:H2'	1:A:2474:C:C6	2.25	0.71
36:9:56:GLN:HA	36:9:56:GLN:HE21	1.55	0.71
1:A:456:A:H2'	1:A:457:A:C8	2.26	0.71
1:A:3443:A:C2'	1:A:3444:G:H5'	2.20	0.71
1:A:2832:A:N3	1:A:2832:A:H2'	2.06	0.70
1:A:3587:U:H2'	1:A:3588:A:H8	1.56	0.70
1:A:2008:G:H2'	1:A:2009:A:C8	2.26	0.70
1:A:2981:A:H2'	1:A:2982:A:C8	2.26	0.70
1:A:3658:G:H4'	1:A:3659:C:OP1	1.90	0.70
18:R:113:LEU:HD22	18:R:115:LEU:HB2	1.73	0.70
1:A:929:G:H2'	1:A:930:C:C6	2.26	0.70
1:A:1331:A:H2'	1:A:1332:A:C8	2.26	0.70
1:A:2107:C:H3'	1:A:2108:A:C5'	2.21	0.70
3:C:44:A:H2'	3:C:45:A:C8	2.26	0.70
1:A:1316:U:H3	1:A:1445:A:H61	0.70	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1992:U:H2'	1:A:1993:A:C8	2.26	0.70
1:A:2400:A:H2	1:A:3736:A:C8	2.09	0.70
1:A:1102:U:N3	1:A:1231:A:N6	2.39	0.70
1:A:1574:C:O2'	1:A:1575:C:O5'	2.08	0.70
1:A:1704:U:O2	1:A:1704:U:H2'	1.91	0.70
5:E:215:ILE:HG12	5:E:273:THR:HG22	1.74	0.70
1:A:885:A:N7	1:A:3111:U:H5	1.90	0.69
5:E:303:THR:HG21	5:E:313:VAL:HG13	1.73	0.69
1:A:1102:U:O4	1:A:1231:A:C6	2.43	0.69
1:A:1112:C:H2'	1:A:1113:C:O4'	1.92	0.69
28:1:11:ILE:HG22	28:1:82:PRO:HA	1.73	0.69
1:A:3075:A:H2'	1:A:3076:G:O4'	1.93	0.69
21:U:87:LEU:HB3	21:U:133:ILE:O	1.92	0.69
3:C:31:U:H2'	3:C:32:C:C6	2.27	0.69
7:G:12:ILE:HG13	7:G:12:ILE:O	1.92	0.69
8:H:43:ILE:HD11	8:H:69:ILE:HG13	1.74	0.69
17:Q:150:GLU:O	17:Q:153:ARG:HG3	1.92	0.69
36:9:53:GLN:O	36:9:54:ARG:HG2	1.93	0.69
20:T:14:LEU:O	20:T:15:LYS:HB2	1.92	0.69
33:6:17:LEU:O	33:6:20:VAL:HG22	1.93	0.69
1:A:1216:C:H2'	1:A:1217:U:H5'	1.75	0.69
1:A:2163:A:O2'	1:A:3439:G:H4'	1.91	0.69
10:J:74:TYR:O	10:J:75:ILE:HG13	1.93	0.69
14:N:128:ARG:O	14:N:131:VAL:HG22	1.91	0.69
6:F:212:GLU:HG2	6:F:259:LYS:HD2	1.75	0.69
31:4:37:PRO:O	31:4:39:PHE:N	2.24	0.69
35:8:69:ASN:O	35:8:70:ASN:HB2	1.93	0.69
1:A:1822:A:H2'	1:A:1823:C:C6	2.28	0.69
1:A:2735:G:H1	1:A:2814:U:H3	1.39	0.69
15:O:70:CYS:HA	15:O:108:PHE:HB2	1.74	0.69
1:A:829:A:H2	19:S:137:LEU:O	1.76	0.68
1:A:1644:U:C4	1:A:2102:A:C2	2.81	0.68
1:A:209:G:H2'	1:A:210:C:C6	2.28	0.68
1:A:2590:U:O2	1:A:2590:U:H2'	1.93	0.68
1:A:3507:A:H2'	1:A:3508:A:H8	1.58	0.68
6:F:144:ILE:HG12	6:F:147:LEU:HD12	1.75	0.68
25:Y:183:VAL:O	25:Y:187:ILE:HG22	1.93	0.68
1:A:1126:U:H2'	1:A:1127:G:O4'	1.93	0.68
1:A:3587:U:H2'	1:A:3588:A:C8	2.26	0.68
3:C:31:U:H2'	3:C:32:C:H6	1.58	0.68
10:J:175:SER:HB3	10:J:176:PRO:HD3	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:125:ALA:HB2	13:M:138:ILE:HD11	1.76	0.68
1:A:906:G:H2'	1:A:907:C:C6	2.29	0.68
1:A:1534:U:O2'	1:A:1535:G:O5'	2.10	0.68
1:A:3361:U:H4'	1:A:3362:A:OP2	1.92	0.68
1:A:3414:G:H2'	1:A:3415:A:C8	2.28	0.68
6:F:38:GLN:O	6:F:42:THR:HG23	1.92	0.68
1:A:162:U:H4'	1:A:163:G:O5'	1.92	0.68
1:A:742:U:OP1	6:F:110:ARG:HG2	1.94	0.68
1:A:609:C:H3'	1:A:610:U:H5'	1.76	0.68
1:A:694:U:OP1	23:W:188:GLN:HA	1.94	0.68
24:X:49:PRO:HG2	24:X:55:LEU:HD12	1.76	0.68
1:A:1257:A:H2'	1:A:1258:A:C8	2.28	0.68
1:A:1851:A:H62	1:A:1969:A:H2	1.40	0.68
1:A:1794:U:O2	1:A:1794:U:C2'	2.42	0.68
19:S:30:VAL:HG12	19:S:52:LEU:HB3	1.75	0.68
1:A:338:U:H2'	1:A:339:G:H8	1.58	0.67
1:A:3726:U:H4'	1:A:3727:A:H5''	1.74	0.67
6:F:55:LYS:HG3	6:F:58:ALA:HB2	1.76	0.67
1:A:146:U:HO2'	1:A:147:C:H6	1.41	0.67
1:A:859:C:H2'	1:A:860:A:C8	2.30	0.67
1:A:1068:C:O2'	1:A:1090:G:H5''	1.95	0.67
1:A:3257:G:C8	1:A:3257:G:O5'	2.48	0.67
14:N:81:ILE:HG21	14:N:99:THR:HG21	1.75	0.67
1:A:2685:C:O2'	5:E:263:ARG:NH2	2.28	0.67
1:A:876:C:C2	1:A:900:G:N2	2.63	0.67
1:A:2696:G:H4'	1:A:2697:A:OP1	1.93	0.67
1:A:3443:A:C3'	1:A:3444:G:H5'	2.24	0.67
3:C:35:A:H2'	3:C:36:C:O4'	1.95	0.67
7:G:27:GLY:C	7:G:29:ARG:H	1.96	0.67
1:A:344:A:H5''	1:A:344:A:C8	2.22	0.67
16:P:106:VAL:HG11	16:P:133:VAL:HG21	1.77	0.67
1:A:3713:C:H2'	1:A:3714:C:C6	2.30	0.67
3:C:125:U:H2'	3:C:126:C:C6	2.30	0.67
5:E:217:VAL:O	5:E:331:ARG:HD3	1.94	0.67
1:A:1064:U:H2'	1:A:1065:U:C6	2.29	0.67
1:A:1530:G:C2	1:A:1575:C:C2	2.82	0.67
1:A:3353:A:N7	1:A:3526:U:H5	1.92	0.67
27:O:13:CYS:O	27:O:15:PHE:N	2.27	0.67
1:A:2723:G:H2'	1:A:2724:C:C6	2.29	0.67
19:S:28:LEU:HD12	29:2:11:GLU:HG3	1.77	0.67
1:A:2699:C:H2'	1:A:2700:C:C6	2.30	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:765:A:H3'	1:A:766:U:H5''	1.77	0.66
1:A:1110:U:C4	1:A:1111:A:N7	2.63	0.66
1:A:1822:A:C2	1:A:2004:U:H5	2.10	0.66
1:A:2450:G:H4'	1:A:2451:A:H5'	1.77	0.66
1:A:2936:A:H2'	1:A:2937:G:H8	1.60	0.66
1:A:3348:U:H2'	1:A:3349:G:O4'	1.96	0.66
1:A:1465:G:H2'	1:A:1466:C:C6	2.30	0.66
1:A:1331:A:H2'	1:A:1332:A:H8	1.60	0.66
1:A:1992:U:H2'	1:A:1993:A:H8	1.61	0.66
5:E:41:PRO:CA	5:E:182:GLY:HA3	2.25	0.66
1:A:344:A:H8	1:A:344:A:C5'	2.05	0.66
1:A:750:G:H5'	19:S:20:VAL:HG13	1.77	0.66
3:C:13:A:H2'	3:C:14:A:C8	2.31	0.66
1:A:308:U:HO2'	1:A:309:G:H8	1.44	0.66
1:A:742:U:H5'	6:F:109:ARG:HA	1.76	0.66
1:A:1588:U:H2'	1:A:1589:G:C8	2.31	0.66
1:A:1321:A:H2'	1:A:1322:G:C8	2.31	0.66
19:S:71:MET:SD	19:S:79:ALA:HB2	2.36	0.66
1:A:929:G:H2'	1:A:930:C:H6	1.61	0.66
4:D:227:ARG:HG2	4:D:239:ALA:HB2	1.78	0.66
1:A:1779:A:H4'	1:A:1780:G:O5'	1.94	0.66
1:A:3036:A:H2'	1:A:3037:G:C8	2.30	0.66
1:A:3235:C:H1'	1:A:3311:G:H22	1.60	0.66
1:A:1533:U:H4'	29:2:18:CYS:SG	2.36	0.65
6:F:156:ASN:HD21	6:F:255:SER:H	1.42	0.65
9:I:74:ILE:HD11	9:I:83:LEU:HG	1.78	0.65
1:A:594:C:O2	1:A:594:C:C2'	2.44	0.65
6:F:190:ARG:O	6:F:195:LYS:HE2	1.95	0.65
35:8:6:VAL:HG13	35:8:7:GLY:H	1.61	0.65
1:A:1435:G:H4'	1:A:1436:A:O5'	1.96	0.65
12:L:61:THR:HG23	12:L:63:ARG:H	1.60	0.65
18:R:125:VAL:HG13	18:R:198:ILE:HD11	1.79	0.65
21:U:17:HIS:CE1	21:U:35:ARG:HG3	2.30	0.65
35:8:35:PRO:HB2	35:8:40:CYS:SG	2.36	0.65
1:A:78:U:N3	1:A:333:A:N6	2.09	0.65
1:A:422:G:H21	23:W:118:MET:CE	2.09	0.65
1:A:2208:G:H21	1:A:3754:A:H8	1.43	0.65
1:A:3241:U:H2'	1:A:3242:U:H6	1.62	0.65
1:A:2144:U:H5''	1:A:2145:A:O4'	1.96	0.65
1:A:1615:G:H21	1:A:1659:A:H5''	1.62	0.65
7:G:162:TRP:O	7:G:165:THR:HG22	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3243:C:O2	1:A:3298:G:C2	2.50	0.65
6:F:222:ARG:O	6:F:223:ASN:HB2	1.94	0.65
1:A:635:U:H2'	1:A:636:U:O4'	1.96	0.65
1:A:949:A:H2	1:A:983:G:H21	1.43	0.65
1:A:1465:G:H2'	1:A:1466:C:H6	1.62	0.65
1:A:2937:G:H2'	1:A:2938:C:C6	2.31	0.65
4:D:118:HIS:HB3	4:D:126:LEU:HD11	1.79	0.65
1:A:11:A:H5''	1:A:11:A:H8	1.62	0.65
1:A:744:G:H1	1:A:915:G:H1	1.45	0.65
1:A:1537:G:H8	1:A:1537:G:C5'	2.09	0.65
1:A:3036:A:H2'	1:A:3037:G:H8	1.60	0.65
12:L:79:LEU:HD23	12:L:86:PRO:HA	1.77	0.65
1:A:1511:U:H2'	1:A:1512:A:H8	1.60	0.65
6:F:144:ILE:O	6:F:144:ILE:CG2	2.45	0.65
12:L:79:LEU:CD2	12:L:86:PRO:HA	2.27	0.65
1:A:1170:A:H2'	1:A:1171:A:C8	2.32	0.64
7:G:154:VAL:O	7:G:158:ASP:HB3	1.97	0.64
12:L:167:THR:O	12:L:168:LYS:HB2	1.96	0.64
14:N:136:ARG:O	14:N:140:LYS:HG3	1.96	0.64
3:C:42:U:H3'	3:C:43:G:H5'	1.79	0.64
1:A:3635:G:H4'	14:N:150:ASN:HB3	1.78	0.64
5:E:133:SER:O	5:E:136:VAL:HG22	1.97	0.64
20:T:128:GLY:O	20:T:129:ASN:CB	2.45	0.64
1:A:733:C:H2'	1:A:734:A:H8	1.63	0.64
1:A:1670:G:N2	1:A:2102:A:H1'	2.13	0.64
1:A:740:U:H2'	1:A:741:C:C6	2.33	0.64
1:A:745:C:O2'	1:A:746:A:H5'	1.98	0.64
1:A:1646:C:H2'	1:A:1647:U:C6	2.32	0.64
16:P:66:VAL:HG21	16:P:102:ALA:HB2	1.79	0.64
1:A:525:U:H2'	1:A:526:U:C5	2.32	0.64
1:A:1094:U:H2'	1:A:1095:U:C6	2.32	0.64
4:D:242:ARG:HH11	4:D:246:LEU:HA	1.62	0.64
1:A:579:C:H4'	1:A:580:A:OP1	1.98	0.64
1:A:1974:U:H2'	1:A:1975:A:H8	1.59	0.64
35:8:40:CYS:O	35:8:41:ARG:HB3	1.98	0.64
1:A:1205:U:H4'	1:A:1206:U:O5'	1.98	0.64
1:A:1681:C:C2	1:A:1734:G:C2	2.84	0.64
1:A:94:G:H2'	1:A:95:A:C8	2.33	0.64
1:A:733:C:H2'	1:A:734:A:C8	2.32	0.64
1:A:825:G:O6	1:A:870:C:N3	2.31	0.64
1:A:1102:U:H3	1:A:1231:A:N6	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3172:A:H2'	1:A:3173:G:O4'	1.98	0.64
1:A:3767:U:H5''	1:A:3770:C:H5	1.63	0.64
1:A:2703:U:C4	1:A:3160:A:N1	2.62	0.63
6:F:134:THR:HA	6:F:150:VAL:HG11	1.81	0.63
8:H:127:ALA:HB1	8:H:131:VAL:HG13	1.80	0.63
1:A:2034:G:H1	1:A:2075:U:H3	1.45	0.63
1:A:2672:U:H2'	1:A:2673:U:C6	2.32	0.63
1:A:3784:U:H2'	1:A:3785:G:C8	2.33	0.63
1:A:752:G:H2'	1:A:753:C:O4'	1.98	0.63
1:A:1752:C:H2'	1:A:1753:U:C6	2.33	0.63
1:A:3382:U:O2	1:A:3382:U:H2'	1.97	0.63
1:A:3418:A:H2'	1:A:3419:U:H6	1.63	0.63
1:A:1178:A:H5''	2:B:98:G:O2'	1.98	0.63
1:A:2135:G:H2'	1:A:2136:C:C6	2.34	0.63
1:A:3532:A:H2'	1:A:3533:A:C8	2.34	0.63
3:C:13:A:H2'	3:C:14:A:H8	1.64	0.63
34:7:27:LEU:HB3	34:7:43:GLU:HG2	1.81	0.63
1:A:868:U:H2'	1:A:869:A:H8	1.64	0.63
1:A:1574:C:O2'	1:A:1575:C:H6	1.82	0.63
3:C:154:G:H2'	3:C:155:A:H8	1.63	0.63
26:Z:52:ASP:HB2	26:Z:109:LYS:HD3	1.81	0.63
1:A:209:G:H2'	1:A:210:C:H6	1.63	0.63
25:Y:180:ALA:HA	25:Y:183:VAL:HG22	1.81	0.63
1:A:744:G:N2	1:A:915:G:H22	1.95	0.63
1:A:3635:G:H1	1:A:3650:U:H3	1.47	0.63
5:E:214:VAL:HG11	5:E:325:VAL:HG13	1.80	0.63
6:F:46:LYS:HD2	6:F:113:ARG:HG3	1.80	0.63
1:A:1537:G:H4'	1:A:1537:G:OP1	1.97	0.63
1:A:3243:C:C2	1:A:3298:G:N1	2.67	0.63
11:K:10:CYS:HB3	11:K:40:ILE:HG12	1.80	0.63
32:5:186:LEU:HB3	32:5:191:VAL:HG23	1.80	0.63
1:A:2723:G:H2'	1:A:2724:C:H6	1.63	0.63
1:A:3577:A:H3'	1:A:3581:A:N6	2.14	0.63
1:A:643:G:H1'	1:A:684:G:N2	2.14	0.62
1:A:746:A:H2	1:A:913:U:N3	1.97	0.62
1:A:1472:A:H5'	32:5:170:ARG:HG2	1.81	0.62
3:C:145:A:H2'	3:C:146:C:C6	2.34	0.62
16:P:60:VAL:HG23	16:P:135:LEU:HB2	1.80	0.62
19:S:47:ILE:O	19:S:51:ARG:HG2	1.98	0.62
36:9:52:SER:HB2	36:9:55:ASN:HB2	1.80	0.62
1:A:803:A:H2'	1:A:804:A:O4'	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1329:U:O4	1:A:3216:C:H5''	1.99	0.62
1:A:2707:G:H2'	1:A:2708:C:O4'	2.00	0.62
2:B:45:U:H2'	2:B:46:C:C6	2.34	0.62
8:H:62:VAL:HB	8:H:63:PRO:CD	2.29	0.62
21:U:33:VAL:HG21	22:V:144:VAL:HG11	1.79	0.62
1:A:2486:U:H5'	1:A:2487:G:H5'	1.79	0.62
3:C:44:A:H2'	3:C:45:A:H8	1.62	0.62
7:G:38:GLU:O	7:G:41:THR:O	2.16	0.62
1:A:2182:G:O2'	20:T:81:LYS:O	2.18	0.62
1:A:3693:A:H2'	1:A:3694:A:C8	2.34	0.62
1:A:2209:C:H42	1:A:2400:A:H61	1.47	0.62
1:A:3493:G:C2	1:A:3511:C:C2	2.87	0.62
1:A:3634:C:H2'	1:A:3635:G:H8	1.64	0.62
21:U:160:ALA:HB1	21:U:162:HIS:CE1	2.34	0.62
23:W:91:LEU:O	23:W:94:ILE:HG22	1.98	0.62
1:A:1141:G:H1	1:A:1156:U:H3	1.46	0.62
1:A:2128:G:O2'	1:A:3451:G:H5''	1.99	0.62
1:A:78:U:C4	1:A:333:A:N1	2.68	0.62
1:A:906:G:H2'	1:A:907:C:H6	1.64	0.62
1:A:3140:U:H4'	1:A:3141:G:OP1	1.99	0.62
9:I:102:ARG:HB3	36:9:137:PRO:HD3	1.81	0.62
28:1:5:LEU:HD13	28:1:28:THR:HG21	1.81	0.62
1:A:2021:A:H2'	1:A:2022:A:C8	2.34	0.62
2:B:45:U:H5''	18:R:159:ASN:HD21	1.64	0.62
5:E:329:LYS:O	5:E:330:LYS:HB2	1.99	0.62
16:P:100:SER:O	16:P:103:GLU:HG2	1.99	0.62
34:7:58:ARG:HD3	34:7:98:TYR:CD1	2.34	0.62
24:X:41:LYS:HG2	24:X:93:THR:HG22	1.82	0.62
28:1:11:ILE:HD11	28:1:43:VAL:HG11	1.80	0.62
1:A:1752:C:H5''	25:Y:173:ARG:HH21	1.63	0.62
1:A:2510:U:H2'	1:A:2511:G:C8	2.34	0.62
5:E:94:GLU:HB3	11:K:151:LEU:HD11	1.80	0.62
1:A:765:A:C3'	1:A:766:U:H5''	2.30	0.61
1:A:868:U:H2'	1:A:869:A:C8	2.35	0.61
1:A:1543:G:H2'	1:A:1544:C:O4'	2.00	0.61
20:T:101:LEU:HD22	20:T:137:LEU:HD12	1.82	0.61
22:V:143:LYS:HA	32:5:83:CYS:HB3	1.81	0.61
1:A:157:G:H5''	16:P:55:ALA:HB2	1.82	0.61
1:A:500:A:H4'	1:A:501:U:OP1	2.00	0.61
1:A:1064:U:H2'	1:A:1065:U:H6	1.63	0.61
1:A:1217:U:H4'	1:A:1218:C:OP1	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3242:U:H2'	1:A:3243:C:C6	2.35	0.61
4:D:104:ILE:HG13	4:D:162:ALA:O	2.01	0.61
14:N:136:ARG:HG2	14:N:140:LYS:HE3	1.82	0.61
1:A:2506:A:H2'	1:A:2507:A:H8	1.58	0.61
36:9:65:ILE:HB	36:9:68:VAL:HG13	1.82	0.61
1:A:1909:U:H3	1:A:1960:U:H3	1.48	0.61
1:A:909:U:H2'	1:A:910:A:C8	2.36	0.61
1:A:1277:G:N2	1:A:1283:C:C2	2.69	0.61
1:A:1801:G:H2'	1:A:2030:G:N2	2.15	0.61
7:G:41:THR:HG21	7:G:71:VAL:HG11	1.83	0.61
1:A:488:A:O2'	1:A:489:U:C6	2.50	0.61
1:A:1184:A:C6	1:A:1185:A:N6	2.68	0.61
1:A:2932:A:H4'	1:A:2933:C:O5'	1.99	0.61
1:A:2473:A:H2'	1:A:2474:C:H6	1.66	0.61
1:A:3289:G:H2'	1:A:3290:C:C6	2.35	0.61
7:G:20:ASN:HB3	7:G:126:ASP:HB2	1.83	0.61
14:N:70:PRO:HD3	21:U:9:LEU:HD21	1.81	0.61
1:A:3160:A:O2'	1:A:3161:A:H2'	2.01	0.61
3:C:146:C:H2'	3:C:147:U:H6	1.66	0.61
5:E:226:VAL:HG11	5:E:246:VAL:HG23	1.82	0.61
16:P:26:ARG:HG2	16:P:30:TYR:CZ	2.36	0.61
16:P:66:VAL:CG2	16:P:102:ALA:HB2	2.30	0.61
1:A:2937:G:H2'	1:A:2938:C:H6	1.66	0.61
5:E:117:ARG:O	5:E:117:ARG:HD3	2.00	0.61
14:N:137:GLU:HA	14:N:140:LYS:HD2	1.83	0.61
1:A:3122:A:N1	1:A:3137:U:C4	2.68	0.60
11:K:40:ILE:O	11:K:137:LEU:HB2	2.00	0.60
1:A:3636:U:H3	1:A:3649:G:H1	1.49	0.60
1:A:3707:U:OP1	5:E:117:ARG:NH1	2.34	0.60
10:J:231:PHE:O	10:J:234:VAL:HG12	2.01	0.60
15:O:21:ARG:NH2	35:8:37:GLY:HA2	2.15	0.60
1:A:348:C:C2	3:C:29:G:N2	2.69	0.60
1:A:890:G:H2'	1:A:891:C:H6	1.67	0.60
1:A:1818:C:H5''	20:T:95:ILE:HD13	1.84	0.60
1:A:2019:A:H2'	1:A:2020:A:C8	2.35	0.60
1:A:3197:A:H4'	17:Q:74:LYS:HD2	1.83	0.60
2:B:104:C:H2'	2:B:105:C:C6	2.36	0.60
6:F:144:ILE:HD11	6:F:249:LEU:HD13	1.83	0.60
7:G:45:PRO:HA	7:G:69:VAL:HG23	1.83	0.60
30:3:87:THR:HG23	30:3:90:LYS:HB2	1.84	0.60
1:A:3623:A:OP1	1:A:3623:A:C4'	2.43	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:607:A:H2'	1:A:608:A:H8	1.53	0.60
1:A:708:A:H8	1:A:708:A:H5''	1.66	0.60
1:A:2816:U:H2'	1:A:2817:U:C6	2.37	0.60
1:A:287:U:O2	1:A:289:A:H3'	2.02	0.60
1:A:703:U:H2'	1:A:704:U:H6	1.67	0.60
1:A:2708:C:OP1	4:D:2:GLY:HA2	2.01	0.60
8:H:58:MET:HB2	8:H:69:ILE:HD12	1.84	0.60
10:J:64:ASP:O	10:J:65:LEU:HB2	2.01	0.60
16:P:11:TRP:O	16:P:14:LYS:HG3	2.01	0.60
22:V:45:CYS:H	22:V:59:HIS:HD2	1.50	0.60
1:A:1586:C:O2'	6:F:76:ILE:HD11	2.00	0.60
3:C:110:G:H4'	3:C:145:A:H5'	1.84	0.60
19:S:23:ASN:C	19:S:23:ASN:HD22	2.05	0.60
1:A:338:U:H2'	1:A:339:G:C8	2.37	0.60
1:A:746:A:H2	1:A:913:U:H3	1.45	0.60
23:W:29:THR:HG23	23:W:119:VAL:HG11	1.81	0.60
33:6:45:VAL:HG22	33:6:94:VAL:HG22	1.83	0.60
1:A:261:A:H2'	1:A:262:A:H8	1.66	0.60
2:B:66:G:C6	2:B:67:C:N3	2.70	0.60
1:A:158:U:H5''	16:P:54:LYS:HG3	1.83	0.60
1:A:1102:U:C4	1:A:1231:A:C6	2.88	0.60
1:A:2732:A:H2'	1:A:2733:A:C8	2.37	0.60
1:A:3486:G:H2'	1:A:3487:A:C8	2.37	0.60
3:C:53:G:OP1	30:3:47:HIS:HB2	2.01	0.60
18:R:63:GLN:HG2	18:R:77:GLU:HG2	1.84	0.60
1:A:379:G:H4'	1:A:406:A:N1	2.16	0.59
14:N:33:ILE:HD12	14:N:38:TYR:HB2	1.82	0.59
31:4:21:ILE:HD13	31:4:21:ILE:H	1.66	0.59
1:A:1302:G:H2'	1:A:1303:C:C6	2.37	0.59
4:D:51:ASP:HB2	4:D:58:LEU:CD1	2.31	0.59
5:E:41:PRO:HA	5:E:182:GLY:CA	2.32	0.59
12:L:92:ILE:HG22	12:L:93:GLY:H	1.67	0.59
18:R:151:GLY:O	18:R:152:ILE:HG22	2.01	0.59
1:A:65:A:H61	1:A:331:A:H62	1.49	0.59
1:A:192:G:C6	1:A:193:C:C4	2.90	0.59
1:A:684:G:H1'	6:F:314:GLN:CG	2.20	0.59
1:A:2135:G:C2	1:A:2136:C:C2	2.90	0.59
1:A:3573:U:H4'	1:A:3574:G:OP1	2.01	0.59
21:U:107:THR:HG23	21:U:110:GLY:H	1.66	0.59
1:A:1819:U:H5'	20:T:99:ARG:HH22	1.66	0.59
1:A:3517:C:H2'	1:A:3518:C:C6	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:8:ARG:HH21	5:E:11:HIS:CD2	2.20	0.59
9:I:221:PHE:HB2	14:N:125:ASP:HB2	1.85	0.59
24:X:94:VAL:HG11	24:X:98:PHE:HB2	1.84	0.59
1:A:404:U:H5'	26:Z:86:ARG:NH2	2.16	0.59
1:A:876:C:C2	1:A:900:G:C2	2.91	0.59
1:A:882:G:H2'	1:A:883:C:O4'	2.02	0.59
1:A:1977:U:H2'	1:A:1978:U:O4'	2.02	0.59
1:A:3253:G:C2	1:A:3267:C:C2	2.91	0.59
1:A:829:A:C2	19:S:137:LEU:O	2.55	0.59
5:E:161:THR:O	5:E:163:PRO:HD3	2.03	0.59
15:O:19:HIS:HB3	15:O:25:HIS:HB2	1.84	0.59
1:A:744:G:H22	1:A:915:G:N2	1.99	0.59
1:A:2689:G:N2	1:A:3344:C:C2	2.71	0.59
4:D:196:TRP:C	4:D:197:PRO:O	2.40	0.59
21:U:103:PHE:HE1	21:U:118:GLU:HG3	1.68	0.59
1:A:1210:A:H2'	1:A:1211:U:H6	1.68	0.59
1:A:3458:A:H2'	1:A:3459:A:O4'	2.02	0.59
6:F:222:ARG:O	6:F:223:ASN:CB	2.50	0.59
8:H:111:ILE:HG23	8:H:125:VAL:HG13	1.85	0.59
16:P:169:GLY:HA2	16:P:172:TYR:CE2	2.37	0.59
1:A:1089:U:H2'	1:A:1090:G:C8	2.38	0.59
1:A:2135:G:H2'	1:A:2136:C:H6	1.67	0.59
4:D:35:CYS:HB3	4:D:41:ILE:HG12	1.85	0.59
1:A:195:A:H8	1:A:216:C:O2'	1.83	0.58
1:A:708:A:H5''	1:A:708:A:C8	2.38	0.58
1:A:828:G:O6	1:A:865:G:O2'	2.20	0.58
1:A:3664:G:C2	9:I:138:LYS:HB3	2.38	0.58
1:A:101:C:H2'	1:A:102:A:O4'	2.03	0.58
23:W:20:VAL:HG13	23:W:21:ASP:H	1.68	0.58
32:5:100:GLY:HA2	32:5:120:VAL:HG12	1.85	0.58
1:A:1483:A:H2'	1:A:1484:A:C8	2.37	0.58
1:A:1801:G:H2'	1:A:2030:G:H22	1.69	0.58
1:A:715:U:H2'	1:A:716:C:C6	2.38	0.58
1:A:1212:U:H2'	1:A:1213:U:C6	2.38	0.58
1:A:1866:C:C2	1:A:1893:G:N2	2.72	0.58
1:A:328:G:N2	1:A:329:C:C2	2.71	0.58
1:A:614:U:H2'	1:A:615:U:O4'	2.03	0.58
1:A:650:U:H2'	1:A:651:A:H5'	1.86	0.58
1:A:1254:G:OP1	17:Q:98:ARG:NH1	2.37	0.58
1:A:1423:G:H2'	1:A:1424:C:C6	2.38	0.58
1:A:3022:U:H2'	1:A:3023:C:H6	1.66	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:63:A:C8	17:Q:202:GLU:HG3	2.39	0.58
16:P:13:LYS:O	16:P:15:GLN:N	2.34	0.58
34:7:63:LEU:HD23	34:7:103:HIS:HB2	1.85	0.58
1:A:588:C:N3	1:A:604:G:C2	2.72	0.58
1:A:1019:A:H2'	1:A:1020:C:C6	2.39	0.58
1:A:1092:A:H2'	1:A:1093:G:O4'	2.04	0.58
1:A:3362:A:H8	1:A:3362:A:H5''	1.67	0.58
1:A:3386:A:H2'	1:A:3387:U:C6	2.39	0.58
1:A:3388:U:H2'	1:A:3389:G:O4'	2.03	0.58
1:A:3617:A:C4'	1:A:3618:A:OP1	2.45	0.58
1:A:3645:A:H2'	1:A:3646:G:C8	2.39	0.58
1:A:422:G:H21	23:W:118:MET:HE1	1.69	0.58
12:L:185:ALA:HB1	15:O:146:LEU:HD13	1.85	0.58
20:T:20:LYS:HG3	20:T:52:LYS:HB2	1.86	0.58
28:1:23:ALA:HB1	28:1:43:VAL:HG12	1.85	0.58
36:9:61:THR:HG21	36:9:122:ILE:HG12	1.85	0.58
1:A:2510:U:H2'	1:A:2511:G:H8	1.67	0.58
21:U:103:PHE:CE1	21:U:118:GLU:HG3	2.39	0.58
1:A:1035:G:H5'	1:A:1036:A:OP1	2.03	0.58
1:A:1096:G:H21	1:A:1231:A:H1'	1.69	0.58
1:A:1763:G:H2'	1:A:1764:U:C6	2.38	0.58
1:A:2735:G:H2'	1:A:2736:A:C8	2.38	0.58
1:A:3198:G:N2	1:A:3199:C:C2	2.72	0.58
8:H:160:ILE:HG22	8:H:178:ILE:HG21	1.84	0.58
20:T:177:ASP:O	20:T:180:VAL:HG12	2.03	0.58
1:A:41:G:N2	1:A:3162:A:H62	2.02	0.58
1:A:1272:U:H1'	1:A:1273:G:C8	2.39	0.58
1:A:344:A:C8	1:A:344:A:C5'	2.83	0.57
1:A:647:U:H4'	1:A:648:U:O5'	2.04	0.57
1:A:1113:C:H42	1:A:1181:G:H1	1.52	0.57
1:A:1264:A:H5'	1:A:2980:U:O2	2.03	0.57
1:A:1299:G:H2'	1:A:1300:G:O4'	2.04	0.57
1:A:2709:U:H2'	1:A:2710:U:C6	2.39	0.57
1:A:3289:G:H2'	1:A:3290:C:H6	1.67	0.57
6:F:218:LYS:HA	6:F:229:LEU:HD13	1.85	0.57
13:M:39:ILE:HG13	13:M:61:LEU:O	2.03	0.57
35:8:63:THR:HG23	35:8:66:LEU:HD12	1.86	0.57
1:A:539:G:N2	1:A:540:C:C2	2.72	0.57
1:A:1753:U:H2'	1:A:1754:G:O4'	2.05	0.57
1:A:3114:G:H2'	1:A:3115:C:C6	2.39	0.57
1:A:3253:G:N2	1:A:3267:C:C2	2.72	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3306:G:OP2	1:A:3306:G:H4'	2.04	0.57
1:A:3626:A:H3'	1:A:3627:C:C5'	2.34	0.57
4:D:127:VAL:HG11	4:D:133:TYR:HA	1.86	0.57
1:A:1822:A:H2'	1:A:1823:C:H6	1.68	0.57
1:A:2090:U:H2'	1:A:2091:U:O4'	2.04	0.57
1:A:3468:G:H2'	1:A:3469:C:O4'	2.04	0.57
3:C:154:G:H2'	3:C:155:A:C8	2.40	0.57
1:A:88:A:H4'	15:O:63:LEU:HD23	1.86	0.57
1:A:193:C:H5''	26:Z:121:LYS:HA	1.86	0.57
1:A:1108:U:O2'	32:5:131:ALA:HA	2.04	0.57
1:A:1419:A:H2'	1:A:1420:C:O4'	2.05	0.57
3:C:100:A:H5'	30:3:65:LYS:HG3	1.86	0.57
16:P:52:GLY:HA3	16:P:117:LEU:HD22	1.85	0.57
1:A:1461:C:H2'	1:A:1462:C:C6	2.40	0.57
1:A:2219:A:O2'	1:A:2220:U:O5'	2.22	0.57
3:C:123:A:H2'	3:C:124:U:C6	2.39	0.57
10:J:160:VAL:HG13	10:J:192:VAL:HG11	1.87	0.57
27:0:63:ARG:HG3	27:0:68:LYS:HB3	1.86	0.57
28:1:50:PRO:HB3	28:1:66:SER:HA	1.86	0.57
1:A:155:U:O2	1:A:155:U:H2'	2.04	0.57
1:A:456:A:H2'	1:A:457:A:H8	1.69	0.57
1:A:944:U:H2'	1:A:945:G:O4'	2.04	0.57
1:A:1537:G:C5'	1:A:1537:G:C8	2.87	0.57
1:A:1607:U:H2'	1:A:1608:C:C6	2.40	0.57
5:E:149:GLU:CG	5:E:189:LEU:HD13	2.31	0.57
18:R:289:TYR:CE2	18:R:293:LEU:HD11	2.40	0.57
32:5:78:ALA:O	32:5:81:ASN:O	2.21	0.57
1:A:11:A:H5''	1:A:11:A:C8	2.39	0.57
1:A:685:U:O2	1:A:685:U:C2'	2.52	0.57
1:A:890:G:H2'	1:A:891:C:C6	2.40	0.57
1:A:1851:A:N7	1:A:1969:A:N1	2.52	0.57
28:1:4:LEU:HD22	33:6:65:LEU:HB3	1.86	0.57
32:5:157:LEU:HD21	32:5:201:LEU:HD13	1.86	0.57
1:A:650:U:C2'	1:A:651:A:H5'	2.35	0.57
1:A:681:U:C6	1:A:681:U:H5''	2.39	0.57
1:A:2836:G:C2	1:A:2918:C:C2	2.93	0.57
1:A:3085:A:H2'	1:A:3086:A:O4'	2.05	0.57
3:C:146:C:H2'	3:C:147:U:C6	2.39	0.57
6:F:37:ILE:HD11	6:F:126:SER:HB2	1.85	0.57
16:P:195:ARG:HA	16:P:198:LEU:HD12	1.87	0.57
1:A:78:U:H3	1:A:333:A:H61	0.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:276:G:N2	1:A:301:U:H2'	2.20	0.57
1:A:344:A:H2'	1:A:345:G:H8	1.62	0.57
1:A:3085:A:H1'	18:R:162:PHE:HE1	1.70	0.57
4:D:77:ILE:HD12	4:D:115:ASN:HD21	1.68	0.57
1:A:237:A:H5''	26:Z:3:PHE:HB2	1.87	0.57
1:A:2571:C:C2	1:A:2600:G:N2	2.73	0.57
1:A:3273:G:OP1	5:E:9:PRO:HB3	2.05	0.57
1:A:3645:A:H2'	1:A:3646:G:H8	1.70	0.57
5:E:89:ILE:HG23	5:E:192:VAL:HG11	1.87	0.57
11:K:52:LYS:O	11:K:55:GLU:HG2	2.05	0.57
1:A:374:A:H2'	1:A:375:A:O4'	2.04	0.56
1:A:3444:G:H2'	1:A:3445:C:H6	1.70	0.56
5:E:148:ILE:HG21	5:E:155:LEU:HD21	1.87	0.56
24:X:96:ILE:HG13	24:X:97:PRO:HD2	1.86	0.56
1:A:293:U:H2'	1:A:294:G:C8	2.40	0.56
1:A:436:G:H2'	1:A:437:A:C8	2.40	0.56
1:A:440:A:C2	1:A:707:U:N3	2.73	0.56
1:A:764:G:H4'	1:A:765:A:OP1	2.05	0.56
1:A:1207:U:H2'	1:A:1208:G:O4'	2.04	0.56
1:A:1618:C:H3'	1:A:1658:G:H22	1.70	0.56
1:A:2135:G:C5	1:A:2136:C:C4	2.94	0.56
1:A:2621:U:H2'	1:A:2622:C:C6	2.40	0.56
1:A:3277:G:N2	1:A:3288:C:C2	2.73	0.56
1:A:3619:U:H2'	1:A:3620:C:C6	2.40	0.56
3:C:149:C:OP1	16:P:38:ARG:HD3	2.04	0.56
7:G:94:LYS:O	7:G:96:PHE:N	2.37	0.56
33:6:48:SER:HB3	33:6:80:LEU:HD12	1.86	0.56
1:A:29:C:C2	1:A:56:G:C2	2.93	0.56
1:A:378:U:H4'	1:A:414:C:H5'	1.86	0.56
1:A:394:A:H2'	1:A:395:A:C8	2.39	0.56
1:A:764:G:H2'	1:A:765:A:C8	2.40	0.56
1:A:1058:U:H2'	1:A:1059:G:C8	2.40	0.56
1:A:1452:U:H2'	1:A:1453:U:O4'	2.05	0.56
1:A:2735:G:H2'	1:A:2736:A:H8	1.70	0.56
1:A:2947:G:O2'	16:P:79:ILE:HG12	2.05	0.56
1:A:3171:C:H2'	1:A:3172:A:C8	2.40	0.56
3:C:107:A:H2'	3:C:109:U:O4	2.05	0.56
8:H:139:VAL:HG22	8:H:140:LYS:H	1.69	0.56
11:K:40:ILE:HB	11:K:137:LEU:HD12	1.87	0.56
1:A:904:G:H5''	19:S:90:ARG:HH22	1.69	0.56
1:A:1184:A:N1	1:A:1185:A:C6	2.74	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1690:A:H2'	1:A:1691:G:O4'	2.05	0.56
1:A:2165:G:H2'	1:A:2166:G:O4'	2.05	0.56
1:A:2916:C:H2'	1:A:2917:C:H6	1.69	0.56
1:A:3739:A:HO2'	1:A:3740:A:H8	1.51	0.56
23:W:48:LEU:O	23:W:51:VAL:HG12	2.05	0.56
1:A:760:A:H2'	1:A:761:U:C6	2.40	0.56
1:A:876:C:N3	1:A:900:G:C2	2.74	0.56
1:A:2135:G:C6	1:A:2136:C:C4	2.94	0.56
1:A:2553:U:H2'	1:A:2554:G:O4'	2.04	0.56
1:A:3427:U:H2'	1:A:3428:U:C6	2.41	0.56
5:E:215:ILE:CG2	5:E:271:HIS:CE1	2.88	0.56
5:E:235:LEU:HD21	5:E:247:ALA:HB2	1.87	0.56
1:A:223:G:C5'	26:Z:11:ARG:HG3	2.36	0.56
1:A:709:A:C6	1:A:710:C:N4	2.74	0.56
1:A:723:A:N6	1:A:3228:U:OP1	2.33	0.56
1:A:2400:A:C2	1:A:3736:A:H8	2.23	0.56
1:A:3459:A:H4'	34:7:70:LYS:HE2	1.87	0.56
3:C:125:U:H2'	3:C:126:C:H6	1.71	0.56
1:A:63:A:OP1	16:P:173:ARG:NH2	2.37	0.56
1:A:812:U:H2'	15:O:139:ALA:HB1	1.87	0.56
1:A:2494:G:C6	1:A:2495:C:C4	2.93	0.56
1:A:2549:A:H2'	1:A:2549:A:N3	2.21	0.56
1:A:3235:C:C1'	1:A:3311:G:H22	2.19	0.56
1:A:3381:A:H4'	1:A:3382:U:OP1	2.06	0.56
1:A:3675:A:H2'	1:A:3676:C:O4'	2.06	0.56
1:A:3677:A:H2'	1:A:3678:A:C8	2.41	0.56
1:A:909:U:H2'	1:A:910:A:H8	1.69	0.56
1:A:1029:G:C6	1:A:1030:C:C4	2.94	0.56
1:A:3183:G:H2'	1:A:3184:C:C6	2.41	0.56
1:A:3699:A:H2'	1:A:3700:G:O4'	2.06	0.56
14:N:29:ARG:HH11	14:N:29:ARG:CG	2.18	0.56
18:R:90:VAL:HG11	18:R:224:ASP:HB3	1.88	0.56
28:1:60:LYS:O	28:1:63:VAL:HG12	2.06	0.56
1:A:1203:A:C2	18:R:113:LEU:HD21	2.41	0.56
1:A:1770:G:H21	1:A:1798:A:H8	1.53	0.56
1:A:1881:C:O2'	1:A:1882:U:C6	2.59	0.56
1:A:1965:U:O2	1:A:1965:U:O4'	2.23	0.56
1:A:2460:A:H2'	1:A:2461:A:C8	2.40	0.56
1:A:3028:A:N3	1:A:3028:A:H2'	2.21	0.56
6:F:105:THR:HG22	6:F:109:ARG:HH12	1.71	0.56
21:U:86:VAL:HG23	21:U:135:ILE:HG22	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:35:GLU:O	28:1:37:PRO:HD3	2.05	0.56
1:A:1461:C:H2'	1:A:1462:C:H6	1.71	0.56
1:A:3351:U:H1'	23:W:69:ARG:HH21	1.71	0.56
1:A:3688:G:H2'	1:A:3689:C:O4'	2.05	0.56
3:C:60:G:H2'	3:C:61:C:O4'	2.06	0.56
25:Y:136:LYS:HA	25:Y:168:LYS:HG3	1.86	0.56
1:A:155:U:O2	1:A:155:U:C2'	2.53	0.55
1:A:339:G:H2'	1:A:340:U:C6	2.41	0.55
1:A:654:A:H5''	6:F:333:LYS:HD2	1.88	0.55
1:A:1423:G:C6	1:A:1424:C:C4	2.93	0.55
1:A:2208:G:H2'	1:A:2209:C:O4'	2.06	0.55
1:A:3065:C:C5	1:A:3067:G:C4	2.94	0.55
13:M:12:LYS:HB2	13:M:127:LEU:HD11	1.88	0.55
14:N:81:ILE:CG2	14:N:99:THR:HG21	2.36	0.55
21:U:151:LEU:C	21:U:153:LYS:H	2.10	0.55
32:5:51:ASN:O	32:5:54:ARG:HG2	2.06	0.55
1:A:1185:A:C2	1:A:1225:A:N7	2.74	0.55
15:O:51:GLY:HA2	19:S:177:ARG:O	2.07	0.55
1:A:457:A:H61	1:A:458:A:N6	2.05	0.55
1:A:1262:G:O2'	1:A:2981:A:N3	2.33	0.55
4:D:82:MET:SD	4:D:88:ILE:HD11	2.45	0.55
5:E:256:ARG:HE	11:K:63:THR:HG21	1.71	0.55
5:E:293:THR:H	5:E:296:ASP:HB2	1.72	0.55
6:F:289:ILE:HD11	19:S:28:LEU:CG	2.35	0.55
1:A:457:A:N6	1:A:458:A:H62	2.05	0.55
1:A:1465:G:C6	1:A:1466:C:C4	2.95	0.55
1:A:1567:A:H5''	6:F:195:LYS:NZ	2.21	0.55
1:A:1598:A:H2'	1:A:1599:G:O4'	2.06	0.55
1:A:1895:U:H2'	1:A:1896:C:H6	1.68	0.55
5:E:215:ILE:CG2	5:E:271:HIS:HE1	2.20	0.55
6:F:219:LYS:HG2	6:F:222:ARG:HH21	1.72	0.55
15:O:136:LYS:O	15:O:140:VAL:HG23	2.07	0.55
1:A:112:U:HO2'	1:A:113:C:H6	1.54	0.55
1:A:239:U:O2	1:A:239:U:O4'	2.24	0.55
1:A:405:A:H2'	1:A:406:A:C8	2.42	0.55
1:A:795:G:C6	1:A:796:C:N3	2.75	0.55
1:A:3171:C:H2'	1:A:3172:A:H8	1.70	0.55
1:A:3713:C:H2'	1:A:3714:C:H6	1.71	0.55
1:A:889:U:O3'	1:A:890:G:H4'	2.06	0.55
1:A:1094:U:H2'	1:A:1095:U:H6	1.70	0.55
1:A:1833:G:H2'	1:A:1834:C:C6	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1866:C:C2	1:A:1893:G:C2	2.95	0.55
1:A:2527:G:C6	1:A:2528:C:C4	2.94	0.55
1:A:3711:U:H4'	1:A:3712:G:OP2	2.06	0.55
19:S:27:ARG:O	19:S:30:VAL:HG22	2.07	0.55
34:7:37:ALA:HB3	34:7:38:PRO:HD3	1.89	0.55
1:A:743:A:OP1	16:P:205:ARG:HD3	2.06	0.55
1:A:1297:A:C8	1:A:1457:G:N2	2.75	0.55
1:A:1686:G:C2	1:A:1728:C:C2	2.94	0.55
1:A:2400:A:C2	1:A:3736:A:C8	2.92	0.55
1:A:2707:G:C6	1:A:2708:C:C4	2.94	0.55
1:A:2714:U:H2'	1:A:2715:C:O4'	2.06	0.55
1:A:3343:C:H2'	1:A:3344:C:C6	2.42	0.55
32:5:154:ARG:O	32:5:158:TYR:HD1	1.90	0.55
1:A:197:G:C2	1:A:214:C:C2	2.95	0.55
1:A:706:U:H2'	1:A:707:U:O4'	2.05	0.55
1:A:1192:C:H42	1:A:1215:A:H61	1.54	0.55
1:A:1691:G:C6	1:A:1692:C:C4	2.95	0.55
1:A:3235:C:C2	1:A:3311:G:C2	2.95	0.55
1:A:3572:A:H2'	1:A:3572:A:N3	2.21	0.55
14:N:72:LYS:O	21:U:165:THR:HG22	2.07	0.55
21:U:21:ARG:HB3	21:U:33:VAL:HG12	1.89	0.55
1:A:320:C:H2'	1:A:321:A:C8	2.42	0.55
1:A:501:U:H2'	1:A:502:U:H6	1.71	0.55
1:A:2995:A:N1	1:A:3052:U:C4	2.73	0.55
34:7:24:LEU:O	34:7:28:THR:OG1	2.24	0.55
1:A:425:A:H2'	1:A:426:A:C8	2.42	0.54
1:A:1098:U:H4'	32:5:168:VAL:HG13	1.90	0.54
6:F:368:LEU:O	6:F:371:ILE:HG22	2.06	0.54
17:Q:43:VAL:HG21	17:Q:197:CYS:HB3	1.89	0.54
17:Q:49:VAL:HG13	17:Q:168:SER:HB2	1.89	0.54
18:R:83:LEU:HB3	18:R:88:ILE:CG2	2.34	0.54
34:7:36:LYS:HB3	34:7:72:VAL:O	2.07	0.54
1:A:30:G:C6	1:A:31:C:C4	2.95	0.54
1:A:345:G:N2	1:A:347:C:C2	2.75	0.54
1:A:746:A:N1	1:A:913:U:C4	2.75	0.54
1:A:1289:G:C2	1:A:1467:C:C2	2.95	0.54
1:A:3505:U:N3	1:A:3509:G:C6	2.75	0.54
36:9:136:TYR:HB2	36:9:137:PRO:CD	2.36	0.54
1:A:173:A:H3'	1:A:174:U:H5''	1.89	0.54
1:A:1995:C:H5''	1:A:1996:C:H5'	1.88	0.54
1:A:2177:A:H2'	1:A:2178:A:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3246:A:H2'	1:A:3246:A:N3	2.21	0.54
1:A:3334:U:H2'	1:A:3335:A:H8	1.73	0.54
2:B:66:G:C6	2:B:67:C:C4	2.96	0.54
1:A:156:U:OP2	10:J:152:GLY:HA2	2.08	0.54
1:A:1444:A:C4	21:U:163:LEU:HD11	2.41	0.54
1:A:3111:U:H5''	1:A:3111:U:O2	2.06	0.54
2:B:11:A:O2'	2:B:13:A:OP2	2.22	0.54
6:F:64:ALA:CB	6:F:91:ALA:HB2	2.37	0.54
14:N:32:LEU:HB2	14:N:77:LEU:HD21	1.88	0.54
1:A:642:A:N6	1:A:684:G:O2'	2.40	0.54
1:A:683:A:H4'	1:A:684:G:O5'	2.06	0.54
1:A:1302:G:H2'	1:A:1303:C:H6	1.72	0.54
1:A:1432:A:H61	1:A:3219:U:H5''	1.72	0.54
1:A:3473:G:C6	1:A:3474:C:C4	2.95	0.54
2:B:23:A:C2	2:B:118:A:O2'	2.56	0.54
3:C:148:C:H2'	3:C:149:C:C6	2.42	0.54
24:X:57:ILE:H	24:X:57:ILE:HD12	1.72	0.54
1:A:200:A:N1	1:A:211:U:O4	2.40	0.54
1:A:2802:U:H2'	1:A:2803:A:H8	1.73	0.54
1:A:2837:G:C2	1:A:2917:C:C2	2.95	0.54
1:A:3444:G:H2'	1:A:3445:C:C6	2.42	0.54
3:C:126:C:OP1	30:3:64:ARG:NH2	2.40	0.54
11:K:136:ARG:HE	11:K:139:THR:HG23	1.72	0.54
16:P:68:ARG:HD3	16:P:129:LYS:HG3	1.90	0.54
24:X:45:ASP:HB2	24:X:131:GLU:HG3	1.89	0.54
32:5:189:TYR:HB3	32:5:207:VAL:HG21	1.89	0.54
1:A:595:U:O2	1:A:595:U:O4'	2.25	0.54
1:A:629:A:H2'	1:A:630:U:C6	2.41	0.54
1:A:707:U:C2	1:A:708:A:C8	2.96	0.54
1:A:1476:A:H5''	1:A:1476:A:C4	2.43	0.54
1:A:2209:C:H42	1:A:2400:A:N6	2.05	0.54
1:A:2577:C:O4'	1:A:2577:C:O2	2.24	0.54
1:A:3306:G:N3	5:E:247:ALA:HB1	2.23	0.54
1:A:3521:G:C6	1:A:3522:C:N3	2.76	0.54
1:A:3706:U:H4'	5:E:25:LEU:HD12	1.89	0.54
3:C:106:G:OP2	3:C:108:A:O2'	2.26	0.54
28:1:46:ILE:HG23	28:1:68:VAL:HG23	1.90	0.54
34:7:38:PRO:HA	34:7:41:ILE:HD12	1.90	0.54
1:A:629:A:H2'	1:A:630:U:O4'	2.08	0.54
1:A:734:A:H2'	1:A:735:A:C8	2.43	0.54
1:A:1124:A:H2'	1:A:1125:A:H8	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1255:G:N2	1:A:1257:A:H3'	2.22	0.54
1:A:1312:U:H5''	14:N:70:PRO:HG2	1.90	0.54
1:A:2508:C:H2'	1:A:2509:U:O4'	2.08	0.54
1:A:3362:A:H5''	1:A:3362:A:C8	2.42	0.54
1:A:3402:A:H2'	1:A:3403:A:H8	1.69	0.54
3:C:37:A:O2'	3:C:38:G:H5''	2.08	0.54
14:N:32:LEU:HD11	14:N:40:GLY:HA2	1.89	0.54
34:7:27:LEU:HD13	34:7:43:GLU:HB3	1.89	0.54
35:8:21:GLN:HE21	35:8:24:ARG:HG3	1.73	0.54
1:A:428:A:O2'	1:A:708:A:OP1	2.24	0.54
1:A:1048:G:C6	1:A:1049:C:C4	2.96	0.54
1:A:2644:U:H2'	1:A:2645:A:H8	1.73	0.54
1:A:3468:G:H2'	1:A:3469:C:C6	2.42	0.54
4:D:127:VAL:O	4:D:127:VAL:HG12	2.08	0.54
36:9:56:GLN:HE21	36:9:56:GLN:CA	2.21	0.54
1:A:28:C:H2'	1:A:29:C:C6	2.43	0.54
1:A:807:U:H5'	12:L:190:ARG:HH21	1.72	0.54
1:A:990:U:H2'	1:A:991:A:C8	2.43	0.54
1:A:1462:C:O2'	32:5:160:ARG:NH1	2.41	0.54
1:A:1667:A:H2'	1:A:1668:G:O4'	2.08	0.54
1:A:2503:G:H2'	1:A:2504:U:O4'	2.08	0.54
1:A:3071:A:H2'	1:A:3072:A:C8	2.43	0.54
1:A:3343:C:H2'	1:A:3344:C:H6	1.73	0.54
1:A:3581:A:H3'	1:A:3582:G:C5'	2.38	0.54
1:A:3637:G:H1	1:A:3648:U:H3	1.56	0.54
3:C:27:U:H5'	26:Z:12:ARG:HG3	1.89	0.54
5:E:215:ILE:HB	5:E:334:THR:OG1	2.08	0.54
8:H:164:VAL:HG11	8:H:178:ILE:N	2.22	0.54
1:A:638:G:H2'	1:A:639:C:C6	2.44	0.53
1:A:1543:G:C6	1:A:1544:C:C4	2.96	0.53
1:A:1851:A:H2'	1:A:1852:C:C6	2.43	0.53
1:A:2654:A:H2'	1:A:2655:C:C6	2.43	0.53
1:A:2975:A:N6	1:A:2980:U:N3	2.25	0.53
5:E:155:LEU:HD11	5:E:189:LEU:HG	1.91	0.53
7:G:37:LEU:HD23	7:G:45:PRO:HB3	1.89	0.53
1:A:146:U:O2'	1:A:147:C:H6	1.90	0.53
1:A:2079:A:H2'	1:A:2080:C:C6	2.43	0.53
1:A:2083:U:H2'	1:A:2084:U:C6	2.43	0.53
4:D:196:TRP:O	4:D:197:PRO:O	2.27	0.53
12:L:88:ALA:O	12:L:92:ILE:HG13	2.07	0.53
19:S:175:LYS:O	19:S:180:ARG:NH1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:0:13:CYS:HA	27:0:20:ILE:HD11	1.89	0.53
1:A:882:G:C6	1:A:883:C:C4	2.96	0.53
1:A:1247:C:H2'	1:A:1248:A:C8	2.43	0.53
1:A:1483:A:H2'	1:A:1484:A:H8	1.73	0.53
1:A:2490:C:N4	1:A:2534:U:H2'	2.24	0.53
1:A:2494:G:C2	1:A:2495:C:C2	2.95	0.53
1:A:3065:C:N4	1:A:3067:G:C6	2.77	0.53
1:A:3431:G:H2'	1:A:3432:A:O4'	2.08	0.53
1:A:112:U:O2'	1:A:113:C:H5''	2.09	0.53
1:A:1316:U:C4	1:A:1445:A:N1	2.76	0.53
1:A:2547:U:H2'	1:A:2554:G:N2	2.23	0.53
13:M:86:ALA:HA	13:M:96:TYR:HB3	1.90	0.53
19:S:79:ALA:HA	19:S:136:VAL:HG23	1.90	0.53
19:S:187:LYS:HA	19:S:187:LYS:HE3	1.91	0.53
1:A:100:A:H2'	1:A:101:C:O2	2.09	0.53
1:A:770:U:C3'	1:A:771:U:H5''	2.36	0.53
1:A:1587:U:H2'	1:A:1588:U:C6	2.44	0.53
1:A:1597:U:H5'	23:W:66:GLY:HA3	1.89	0.53
1:A:3711:U:O2	1:A:3711:U:O4'	2.24	0.53
4:D:104:ILE:HD11	4:D:116:LEU:HD21	1.90	0.53
5:E:215:ILE:HG22	5:E:271:HIS:HE1	1.74	0.53
1:A:728:C:H2'	1:A:729:G:C8	2.43	0.53
1:A:858:C:H3'	1:A:859:C:H5''	1.90	0.53
1:A:1537:G:P	35:8:101:SER:H	2.32	0.53
1:A:2723:G:C6	1:A:2724:C:C4	2.96	0.53
2:B:29:C:H2'	2:B:30:A:H8	1.73	0.53
5:E:280:TYR:HB3	5:E:353:LEU:HD21	1.91	0.53
36:9:50:LYS:O	36:9:57:ASP:HB2	2.08	0.53
1:A:458:A:O2'	1:A:459:G:H5''	2.09	0.53
1:A:513:U:H3	1:A:685:U:H5	1.57	0.53
1:A:1447:G:H2'	1:A:1448:C:C6	2.44	0.53
1:A:1506:C:H2'	1:A:1507:U:C6	2.44	0.53
1:A:3509:G:C6	1:A:3510:C:C4	2.97	0.53
5:E:319:LEU:HD12	5:E:335:LEU:HD13	1.91	0.53
17:Q:73:ASN:O	17:Q:77:ILE:HG12	2.09	0.53
21:U:71:GLU:HG3	32:5:79:ARG:HH22	1.73	0.53
27:0:59:THR:HG23	27:0:62:TRP:H	1.74	0.53
34:7:83:LEU:HD23	34:7:101:VAL:HB	1.90	0.53
1:A:638:G:C6	1:A:639:C:C4	2.96	0.53
1:A:3334:U:H2'	1:A:3335:A:C8	2.43	0.53
1:A:3515:A:H2'	1:A:3515:A:N3	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3585:A:H1'	11:K:167:TYR:HB2	1.91	0.53
46:A:3801:YMZ:CAJ	46:A:3801:YMZ:CAX	2.86	0.53
6:F:164:THR:HA	6:F:220:ALA:O	2.09	0.53
1:A:1423:G:C5	1:A:1424:C:C4	2.97	0.53
1:A:2095:U:O2'	1:A:2096:G:OP2	2.23	0.53
1:A:2527:G:C2	1:A:2528:C:C2	2.97	0.53
1:A:2816:U:H2'	1:A:2817:U:H6	1.73	0.53
1:A:3243:C:N3	1:A:3298:G:C6	2.77	0.53
6:F:319:LEU:HD11	32:5:155:LYS:HG3	1.91	0.53
7:G:12:ILE:HG23	7:G:162:TRP:HD1	1.74	0.53
19:S:51:ARG:CZ	19:S:139:ARG:HD2	2.39	0.53
21:U:33:VAL:HG23	22:V:149:ILE:HA	1.91	0.53
1:A:888:A:H4'	1:A:889:U:O5'	2.10	0.53
1:A:952:U:OP1	20:T:85:ASN:HB2	2.09	0.53
1:A:1522:A:H2'	1:A:1523:A:C8	2.44	0.53
1:A:3399:U:H2'	1:A:3400:C:C6	2.44	0.53
5:E:366:ARG:HG3	27:0:39:LEU:HD11	1.91	0.53
13:M:47:CYS:O	13:M:48:LEU:C	2.47	0.53
1:A:524:U:H3	1:A:631:U:H3	1.57	0.52
1:A:588:C:C2	1:A:604:G:C2	2.97	0.52
1:A:752:G:C6	1:A:753:C:C4	2.97	0.52
1:A:917:A:H2'	1:A:918:G:O4'	2.09	0.52
1:A:1533:U:N3	1:A:1534:U:C4	2.78	0.52
1:A:1833:G:H2'	1:A:1834:C:H6	1.74	0.52
1:A:2208:G:C6	1:A:2209:C:C4	2.97	0.52
1:A:2221:U:H3	1:A:2386:A:N6	2.07	0.52
1:A:3574:G:H5''	36:9:89:THR:HG21	1.91	0.52
5:E:67:LEU:HD21	5:E:72:ILE:HD12	1.90	0.52
5:E:145:LEU:HD13	5:E:193:LYS:HE2	1.90	0.52
17:Q:79:ASN:HB3	17:Q:147:LYS:HD3	1.91	0.52
34:7:24:LEU:HD23	34:7:27:LEU:HD12	1.91	0.52
1:A:320:C:H2'	1:A:321:A:H8	1.74	0.52
1:A:1260:C:H2'	1:A:1261:A:H8	1.74	0.52
1:A:2158:U:H2'	1:A:2159:A:C8	2.44	0.52
1:A:2515:A:H2'	1:A:2516:A:C8	2.44	0.52
1:A:2621:U:H2'	1:A:2622:C:H6	1.74	0.52
2:B:72:C:H2'	2:B:73:U:H6	1.74	0.52
3:C:60:G:C6	3:C:61:C:C4	2.97	0.52
3:C:145:A:H2'	3:C:146:C:H6	1.73	0.52
7:G:17:LEU:HB3	7:G:71:VAL:HG23	1.90	0.52
10:J:183:LEU:N	10:J:184:PRO:HD2	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1314:G:C6	1:A:1315:C:C4	2.97	0.52
1:A:1752:C:H2'	1:A:1753:U:H6	1.73	0.52
1:A:2073:G:H2'	1:A:2074:C:H6	1.75	0.52
1:A:3266:U:C2	1:A:3267:C:C5	2.97	0.52
3:C:126:C:H2'	3:C:127:C:C6	2.45	0.52
1:A:328:G:N1	1:A:329:C:C4	2.77	0.52
1:A:465:A:H2'	1:A:466:A:H8	1.71	0.52
1:A:612:G:H2'	1:A:613:C:C6	2.44	0.52
1:A:1747:U:O2	1:A:1747:U:C2'	2.57	0.52
1:A:2708:C:H5'	4:D:207:VAL:HG13	1.92	0.52
1:A:3180:C:H42	1:A:3228:U:H3	1.57	0.52
1:A:3235:C:C2	1:A:3311:G:N1	2.78	0.52
1:A:3242:U:H2'	1:A:3243:C:H6	1.74	0.52
5:E:50:LYS:HB2	5:E:333:ILE:CD1	2.40	0.52
9:I:149:LEU:HD11	9:I:169:ILE:HD12	1.91	0.52
11:K:9:ASP:HB2	11:K:116:LYS:HB3	1.92	0.52
1:A:203:A:C2	1:A:207:A:C2	2.97	0.52
1:A:660:U:H3	1:A:673:U:H5	1.55	0.52
1:A:1222:U:H3	32:5:210:LYS:HE2	1.75	0.52
1:A:3002:G:C6	1:A:3003:C:C4	2.97	0.52
5:E:57:VAL:HG22	5:E:73:VAL:HG22	1.91	0.52
5:E:195:MET:O	5:E:198:LYS:HB2	2.10	0.52
16:P:146:ASN:O	16:P:150:ASN:HB2	2.10	0.52
1:A:28:C:H2'	1:A:29:C:H6	1.75	0.52
1:A:217:A:N6	6:F:168:VAL:HG21	2.24	0.52
1:A:521:U:O2'	1:A:522:A:O5'	2.21	0.52
1:A:1023:U:H5'	1:A:1685:G:O2'	2.09	0.52
1:A:3193:G:C6	1:A:3194:C:C4	2.98	0.52
1:A:3198:G:N1	1:A:3199:C:C4	2.78	0.52
2:B:66:G:N1	2:B:67:C:C2	2.77	0.52
35:8:44:ARG:HD3	35:8:46:TYR:HE2	1.74	0.52
1:A:195:A:N6	1:A:219:A:O2'	2.41	0.52
1:A:417:A:H4'	1:A:1545:G:H5'	1.92	0.52
1:A:441:A:C2	1:A:706:U:O2	2.63	0.52
1:A:609:C:C3'	1:A:610:U:H5'	2.40	0.52
1:A:612:G:C2	1:A:613:C:C2	2.97	0.52
1:A:1549:U:O2	1:A:1549:U:O4'	2.25	0.52
1:A:1880:A:P	20:T:102:ARG:HH22	2.31	0.52
1:A:2525:A:H2'	1:A:2526:A:H8	1.74	0.52
2:B:66:G:C2	2:B:67:C:C2	2.98	0.52
2:B:110:G:H2'	2:B:111:A:O4'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:163:ARG:HH21	4:D:163:ARG:HB2	1.74	0.52
9:I:76:LYS:HB2	9:I:128:ALA:HB1	1.92	0.52
18:R:235:ILE:O	18:R:238:MET:HG2	2.10	0.52
1:A:69:U:H2'	1:A:70:A:O4'	2.10	0.52
1:A:310:U:H6	1:A:310:U:H5''	1.73	0.52
1:A:608:A:H1'	1:A:610:U:O4	2.09	0.52
1:A:1212:U:H2'	1:A:1213:U:H6	1.75	0.52
1:A:1276:G:N2	1:A:1284:C:C2	2.78	0.52
1:A:1297:A:H4'	32:5:230:LYS:HE2	1.92	0.52
1:A:1441:G:O3'	11:K:16:GLY:HA3	2.10	0.52
6:F:371:ILE:HD13	32:5:79:ARG:HD3	1.92	0.52
7:G:136:TYR:HA	7:G:148:ILE:HD11	1.92	0.52
21:U:150:GLN:O	21:U:153:LYS:HB2	2.09	0.52
25:Y:116:THR:O	25:Y:120:ALA:CB	2.52	0.52
1:A:795:G:C5	1:A:796:C:C4	2.98	0.52
1:A:1090:G:H2'	1:A:1091:G:C8	2.45	0.52
1:A:1599:G:C6	1:A:1600:C:N4	2.77	0.52
1:A:2642:U:H2'	1:A:2643:C:C6	2.45	0.52
1:A:3568:G:C2	1:A:3569:C:C2	2.98	0.52
10:J:174:VAL:HG11	10:J:213:THR:HG23	1.90	0.52
12:L:22:ARG:HG3	16:P:198:LEU:HD22	1.90	0.52
15:O:71:PRO:HD2	15:O:108:PHE:CD2	2.45	0.52
32:5:98:LEU:HD11	32:5:144:THR:HG23	1.92	0.52
1:A:1154:C:H2'	1:A:1155:C:C6	2.45	0.52
1:A:1294:G:H2'	1:A:1295:A:C8	2.45	0.52
1:A:1852:C:H3'	1:A:1853:C:H6	1.75	0.52
1:A:2925:U:O2	1:A:2925:U:O4'	2.26	0.52
1:A:3088:G:C6	1:A:3089:C:C4	2.97	0.52
1:A:3143:G:C6	1:A:3144:C:C4	2.99	0.52
1:A:3489:A:N7	1:A:3513:G:N2	2.58	0.52
1:A:3505:U:C2	1:A:3508:A:C6	2.91	0.52
1:A:3505:U:C4	1:A:3509:G:C6	2.98	0.52
1:A:3688:G:C6	1:A:3689:C:C4	2.98	0.52
4:D:193:ARG:HH11	4:D:193:ARG:CG	2.23	0.52
1:A:580:A:O2'	1:A:581:C:O5'	2.26	0.51
1:A:922:C:C2	1:A:1060:G:N2	2.78	0.51
1:A:1216:C:N4	1:A:1217:U:C4	2.78	0.51
1:A:1481:A:HO2'	1:A:1482:A:H8	1.55	0.51
1:A:1666:A:H2'	1:A:1667:A:C8	2.44	0.51
1:A:1739:C:H2'	1:A:1740:A:H8	1.75	0.51
1:A:2208:G:C2	1:A:2209:C:C2	2.98	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3079:A:H3'	1:A:3080:A:H8	1.75	0.51
1:A:3386:A:H2'	1:A:3387:U:H6	1.75	0.51
1:A:3691:C:H2'	1:A:3692:A:O4'	2.10	0.51
8:H:164:VAL:HG11	8:H:177:GLY:CA	2.40	0.51
10:J:74:TYR:HA	10:J:77:ILE:HG12	1.93	0.51
11:K:84:ARG:HG3	11:K:98:LEU:HD11	1.92	0.51
14:N:31:CYS:SG	14:N:76:LEU:HD23	2.49	0.51
14:N:141:LYS:O	14:N:144:THR:HG22	2.10	0.51
19:S:179:ARG:HE	19:S:187:LYS:HZ1	1.55	0.51
1:A:23:C:O2'	3:C:45:A:H1'	2.11	0.51
1:A:293:U:H2'	1:A:294:G:H8	1.75	0.51
1:A:649:U:N3	1:A:684:G:OP2	2.42	0.51
1:A:755:A:OP2	19:S:105:THR:HG21	2.10	0.51
1:A:1029:G:C2	1:A:1030:C:C2	2.98	0.51
1:A:2073:G:H2'	1:A:2074:C:C6	2.45	0.51
1:A:3493:G:N1	1:A:3494:C:C4	2.79	0.51
1:A:3741:A:H61	1:A:3748:U:H3	1.58	0.51
8:H:17:LYS:HB3	8:H:28:SER:HB2	1.92	0.51
18:R:206:TYR:O	18:R:209:THR:HG22	2.11	0.51
1:A:1096:G:N2	1:A:1231:A:H1'	2.26	0.51
1:A:2417:G:C2	1:A:2623:C:C2	2.97	0.51
1:A:2456:C:H2'	1:A:2457:C:O4'	2.10	0.51
15:O:98:PRO:HG2	15:O:122:ILE:HD12	1.90	0.51
34:7:80:ARG:HD3	34:7:112:LEU:HD23	1.91	0.51
1:A:297:G:C6	1:A:298:C:C4	2.98	0.51
1:A:339:G:H2'	1:A:340:U:H6	1.74	0.51
1:A:512:A:H4'	9:I:48:ARG:HG3	1.92	0.51
1:A:922:C:C2	1:A:1060:G:C2	2.98	0.51
1:A:1101:A:H4'	1:A:1102:U:OP1	2.10	0.51
1:A:1816:G:H2'	1:A:1817:G:C8	2.45	0.51
1:A:3244:C:C2	1:A:3297:G:C2	2.97	0.51
3:C:60:G:C2	3:C:61:C:C2	2.97	0.51
3:C:148:C:H2'	3:C:149:C:H6	1.75	0.51
31:4:46:CYS:O	31:4:50:ILE:HD12	2.10	0.51
1:A:426:A:H2'	1:A:427:G:O4'	2.10	0.51
1:A:706:U:H2'	1:A:707:U:H6	1.72	0.51
1:A:1292:U:H2'	1:A:1293:G:C8	2.45	0.51
1:A:1875:A:H2'	1:A:1876:A:C8	2.46	0.51
1:A:3088:G:C2	1:A:3089:C:C2	2.99	0.51
1:A:3190:G:C6	1:A:3191:C:C4	2.99	0.51
1:A:3568:G:C6	1:A:3569:C:C4	2.98	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:72:C:H2'	2:B:73:U:C6	2.46	0.51
8:H:125:VAL:HG23	8:H:159:LEU:HD23	1.93	0.51
15:O:76:ASP:HB2	15:O:113:ASN:O	2.11	0.51
1:A:1756:G:C6	1:A:1757:C:C4	2.99	0.51
1:A:1829:G:C2	1:A:1997:G:N7	2.79	0.51
1:A:3243:C:C2	1:A:3298:G:C2	2.99	0.51
1:A:3443:A:H2	1:A:3470:G:H21	1.56	0.51
1:A:3668:U:H5''	36:9:101:TRP:HZ2	1.74	0.51
4:D:52:PRO:HB3	4:D:191:VAL:CG1	2.40	0.51
25:Y:130:LEU:HD11	25:Y:183:VAL:HG23	1.92	0.51
1:A:224:G:C2	1:A:233:C:C2	2.99	0.51
1:A:440:A:N1	1:A:707:U:O4	2.44	0.51
1:A:457:A:N6	1:A:458:A:N6	2.58	0.51
1:A:1449:G:H2'	1:A:1450:G:O4'	2.11	0.51
1:A:1543:G:C2	1:A:1544:C:C2	2.99	0.51
1:A:1762:A:H5'	1:A:1762:A:H8	1.76	0.51
1:A:2405:A:H4'	1:A:2406:A:H5'	1.92	0.51
1:A:3662:U:H3'	1:A:3663:A:H5'	1.93	0.51
5:E:281:ARG:HH21	5:E:353:LEU:HD12	1.76	0.51
6:F:134:THR:HB	6:F:150:VAL:HG21	1.93	0.51
16:P:26:ARG:HG2	16:P:30:TYR:OH	2.11	0.51
1:A:422:G:H21	23:W:118:MET:HE2	1.76	0.51
1:A:2418:A:H2'	1:A:2419:A:O4'	2.10	0.51
1:A:2644:U:H2'	1:A:2645:A:C8	2.46	0.51
1:A:3237:G:C6	1:A:3238:C:C4	2.99	0.51
1:A:3534:U:H4'	5:E:104:THR:OG1	2.11	0.51
6:F:144:ILE:O	6:F:144:ILE:HG23	2.10	0.51
8:H:113:ILE:HB	8:H:123:ARG:HB2	1.93	0.51
14:N:58:GLY:HA3	14:N:64:VAL:HG13	1.93	0.51
15:O:72:THR:HG22	15:O:109:LYS:HB3	1.92	0.51
16:P:161:GLU:HG2	16:P:162:LEU:HD22	1.93	0.51
24:X:100:LYS:HA	24:X:103:ILE:HD12	1.93	0.51
26:Z:81:VAL:HG12	26:Z:82:GLU:N	2.26	0.51
1:A:203:A:H2	1:A:207:A:C2	2.29	0.51
1:A:591:G:C6	1:A:594:C:C4	2.99	0.51
1:A:799:A:N6	1:A:809:A:OP2	2.39	0.51
1:A:1423:G:OP1	21:U:92:SER:HB2	2.11	0.51
1:A:1465:G:C2	1:A:1466:C:C2	2.99	0.51
1:A:1739:C:H2'	1:A:1740:A:C8	2.46	0.51
1:A:3237:G:H2'	1:A:3238:C:O4'	2.11	0.51
1:A:3502:C:H2'	1:A:3503:U:O4'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:28:LYS:HD2	4:D:123:ARG:HB3	1.93	0.51
7:G:94:LYS:C	7:G:96:PHE:H	2.14	0.51
23:W:34:ARG:O	23:W:37:ARG:HG2	2.10	0.51
1:A:382:A:N3	1:A:385:G:H5'	2.26	0.51
1:A:544:C:H42	1:A:582:U:H5''	1.76	0.51
1:A:612:G:C6	1:A:613:C:C4	2.99	0.51
1:A:2916:C:H2'	1:A:2917:C:C6	2.46	0.51
4:D:6:ARG:CB	4:D:6:ARG:HH11	2.24	0.51
4:D:28:LYS:HB3	4:D:123:ARG:HD3	1.93	0.51
10:J:88:LEU:HD21	16:P:24:ARG:HE	1.76	0.51
28:1:10:VAL:HG22	28:1:83:THR:OG1	2.10	0.51
34:7:28:THR:HG21	34:7:36:LYS:HG3	1.93	0.51
1:A:425:A:H2'	1:A:426:A:H8	1.75	0.50
1:A:440:A:C2'	1:A:441:A:C8	2.66	0.50
1:A:990:U:H2'	1:A:991:A:H8	1.75	0.50
1:A:1072:A:H4'	1:A:1073:G:H21	1.76	0.50
1:A:1725:U:H2'	1:A:1726:C:C6	2.47	0.50
1:A:3271:G:H1'	1:A:3516:A:H5'	1.93	0.50
1:A:3493:G:C6	1:A:3494:C:C4	2.99	0.50
11:K:176:GLU:O	11:K:180:ILE:HG13	2.11	0.50
24:X:81:VAL:HG22	24:X:94:VAL:HG13	1.92	0.50
29:2:55:THR:HG22	29:2:68:VAL:HG13	1.94	0.50
33:6:55:GLN:O	33:6:59:ILE:HG12	2.10	0.50
36:9:61:THR:CG2	36:9:122:ILE:HG12	2.40	0.50
36:9:65:ILE:HB	36:9:68:VAL:CG1	2.40	0.50
1:A:192:G:C2	1:A:193:C:C2	2.99	0.50
1:A:708:A:H3'	1:A:709:A:H8	1.76	0.50
1:A:1881:C:O2'	1:A:1882:U:O5'	2.24	0.50
1:A:3507:A:H2'	1:A:3508:A:C8	2.42	0.50
1:A:3590:A:H4'	14:N:20:LEU:HD21	1.93	0.50
23:W:49:ASN:O	23:W:52:ILE:HG12	2.10	0.50
1:A:344:A:C2	3:C:31:U:N3	2.75	0.50
1:A:1083:G:H2'	1:A:1084:A:C8	2.46	0.50
1:A:1224:A:H4'	1:A:1225:A:OP2	2.09	0.50
1:A:1691:G:C2	1:A:1692:C:C2	2.99	0.50
1:A:1875:A:OP1	20:T:117:HIS:HA	2.10	0.50
1:A:3477:A:H8	1:A:3477:A:OP1	1.93	0.50
2:B:75:G:N2	2:B:99:G:H2'	2.27	0.50
3:C:103:G:N2	3:C:104:C:C2	2.79	0.50
13:M:40:ALA:O	13:M:60:VAL:HG12	2.12	0.50
22:V:136:PRO:HG3	32:5:91:LYS:HG3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1506:C:H2'	1:A:1507:U:H6	1.75	0.50
4:D:179:ILE:HG23	4:D:184:VAL:HG12	1.93	0.50
5:E:72:ILE:HA	13:M:90:HIS:O	2.11	0.50
11:K:13:HIS:CE1	11:K:119:LEU:H	2.29	0.50
12:L:8:LEU:HB3	15:O:34:LYS:HE2	1.92	0.50
14:N:14:ILE:O	14:N:17:LYS:HG2	2.12	0.50
26:Z:54:GLU:HA	26:Z:68:LYS:HA	1.94	0.50
32:5:157:LEU:HG	32:5:198:VAL:HG22	1.94	0.50
1:A:578:U:C4	1:A:579:C:N4	2.80	0.50
1:A:1155:C:H2'	1:A:1156:U:C6	2.45	0.50
1:A:1476:A:O2'	46:A:3801:YMZ:OAA	2.18	0.50
1:A:1762:A:O2'	1:A:1763:G:C8	2.59	0.50
1:A:1791:A:N6	1:A:1798:A:H2'	2.26	0.50
1:A:3123:C:H5''	12:L:205:LYS:NZ	2.26	0.50
1:A:3493:G:N2	1:A:3511:C:C2	2.80	0.50
1:A:3619:U:H2'	1:A:3620:C:H6	1.76	0.50
9:I:90:GLU:HG3	9:I:191:LYS:HD2	1.93	0.50
14:N:7:LEU:HB3	14:N:10:GLU:HB2	1.94	0.50
16:P:148:LYS:O	16:P:149:ILE:CG1	2.52	0.50
28:1:9:LYS:HA	28:1:86:GLN:HA	1.94	0.50
34:7:17:THR:HG22	34:7:84:GLU:HG2	1.93	0.50
1:A:11:A:H61	3:C:154:G:H1	1.59	0.50
1:A:599:G:H2'	1:A:600:U:O4'	2.12	0.50
1:A:1335:G:C2	1:A:1426:C:C2	2.99	0.50
1:A:2429:U:H2'	1:A:2435:A:N6	2.27	0.50
1:A:2950:U:H2'	1:A:2951:U:C6	2.46	0.50
1:A:3114:G:H2'	1:A:3115:C:H6	1.73	0.50
1:A:3427:U:H2'	1:A:3428:U:H6	1.77	0.50
1:A:3430:A:H4'	5:E:13:SER:HB3	1.94	0.50
3:C:53:G:C6	3:C:54:C:C4	2.99	0.50
8:H:109:THR:HG22	8:H:110:ARG:H	1.77	0.50
10:J:171:ALA:HB2	10:J:203:LEU:HD12	1.93	0.50
12:L:129:LYS:O	12:L:131:LYS:N	2.44	0.50
13:M:92:GLY:HA3	27:0:23:GLY:HA2	1.93	0.50
1:A:63:A:H4'	16:P:186:ARG:O	2.11	0.50
1:A:74:A:H5''	12:L:103:ARG:HH21	1.76	0.50
1:A:1416:U:H2'	1:A:1417:G:H8	1.77	0.50
1:A:2176:A:H2'	1:A:2177:A:C8	2.47	0.50
1:A:3193:G:C2	1:A:3194:C:C2	3.00	0.50
1:A:3433:C:H5'	5:E:326:ALA:HA	1.94	0.50
1:A:3577:A:H5''	1:A:3581:A:H61	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:278:ILE:HD13	19:S:106:GLU:HG2	1.94	0.50
7:G:75:LYS:O	7:G:79:ILE:HG12	2.12	0.50
14:N:30:LEU:O	14:N:43:CYS:O	2.30	0.50
1:A:79:U:H2'	1:A:80:C:C6	2.47	0.50
1:A:297:G:C2	1:A:298:C:C2	3.00	0.50
1:A:440:A:C2'	1:A:441:A:H8	2.15	0.50
1:A:1233:A:H2'	1:A:1234:A:C8	2.47	0.50
1:A:1242:U:H5''	15:O:22:VAL:HG13	1.93	0.50
1:A:1245:G:C6	1:A:1246:C:C4	2.99	0.50
1:A:1285:U:O2'	1:A:1297:A:N3	2.44	0.50
1:A:1462:C:H5''	32:5:219:LYS:HB3	1.94	0.50
1:A:1465:G:C4	1:A:1466:C:C5	3.00	0.50
1:A:1968:C:H2'	1:A:1969:A:C2	2.47	0.50
1:A:1979:C:H42	1:A:1989:A:H61	1.57	0.50
1:A:2817:U:H2'	1:A:2818:U:C6	2.47	0.50
1:A:3002:G:C2	1:A:3003:C:C2	3.00	0.50
3:C:90:G:H2'	3:C:90:G:N3	2.27	0.50
10:J:174:VAL:HG23	10:J:177:ILE:HA	1.93	0.50
14:N:72:LYS:HA	21:U:162:HIS:CD2	2.47	0.50
22:V:119:GLU:HA	22:V:122:LEU:HD12	1.94	0.50
32:5:134:GLU:HA	32:5:137:LYS:HD2	1.94	0.50
1:A:153:A:H2'	1:A:154:A:O4'	2.11	0.50
1:A:921:C:H2'	1:A:922:C:C6	2.47	0.50
1:A:1276:G:C2	1:A:1284:C:C2	2.99	0.50
1:A:1445:A:H2'	1:A:1445:A:N3	2.25	0.50
1:A:1648:U:H2'	1:A:1649:G:O4'	2.12	0.50
1:A:2540:G:C6	1:A:2541:C:C4	2.99	0.50
1:A:2645:A:H5''	23:W:83:TRP:O	2.12	0.50
4:D:116:LEU:HG	4:D:164:ALA:HB2	1.93	0.50
8:H:78:ASN:HB3	8:H:150:ILE:HG21	1.93	0.50
16:P:39:VAL:CG1	16:P:63:ARG:HB2	2.42	0.50
26:Z:27:ARG:HB2	26:Z:74:ARG:HE	1.77	0.50
1:A:995:A:H5''	1:A:2158:U:H5''	1.93	0.49
1:A:1132:G:H4'	17:Q:40:LYS:HG2	1.94	0.49
1:A:1277:G:C2	1:A:1283:C:C2	3.00	0.49
1:A:1294:G:C2	1:A:1462:C:C2	3.00	0.49
1:A:3136:C:H5''	12:L:191:ARG:HH11	1.77	0.49
1:A:3263:G:H2'	1:A:3264:U:C6	2.46	0.49
1:A:3305:A:H2'	1:A:3341:A:N7	2.27	0.49
3:C:72:G:H2'	3:C:73:A:O4'	2.12	0.49
18:R:58:SER:HA	18:R:93:LYS:HG3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:97:ARG:O	20:T:101:LEU:HG	2.11	0.49
36:9:78:VAL:O	36:9:104:VAL:O	2.30	0.49
1:A:79:U:OP1	16:P:186:ARG:HG3	2.12	0.49
1:A:191:A:C4	1:A:241:C:N4	2.80	0.49
1:A:203:A:C2	1:A:207:A:H2	2.30	0.49
1:A:360:A:N1	1:A:373:A:H5''	2.27	0.49
1:A:573:U:H2'	1:A:574:G:C8	2.47	0.49
1:A:915:G:H4'	12:L:3:ALA:HB3	1.93	0.49
1:A:1214:C:H3'	1:A:1215:A:H5''	1.94	0.49
1:A:1683:A:H2'	1:A:1684:A:C8	2.47	0.49
1:A:2547:U:H2'	1:A:2554:G:H22	1.76	0.49
1:A:2710:U:H3'	1:A:2945:G:H21	1.76	0.49
1:A:629:A:H2'	1:A:630:U:H6	1.76	0.49
1:A:638:G:C2	1:A:639:C:C2	3.00	0.49
1:A:739:G:C5	1:A:921:C:C6	3.00	0.49
1:A:1234:A:H5''	1:A:1234:A:H8	1.77	0.49
1:A:1550:A:H2'	1:A:1551:C:C6	2.48	0.49
1:A:1677:G:C6	1:A:1678:C:C4	3.00	0.49
1:A:1784:G:C2	1:A:1788:C:C2	3.00	0.49
1:A:1823:C:C2	1:A:1824:A:C8	3.00	0.49
1:A:2719:U:C2	1:A:2720:C:C5	3.01	0.49
1:A:3065:C:C2	1:A:3067:G:C2	3.00	0.49
3:C:47:G:C6	3:C:48:C:C4	3.00	0.49
8:H:109:THR:HG23	8:H:127:ALA:HB3	1.94	0.49
14:N:30:LEU:HB2	14:N:79:GLU:HB2	1.95	0.49
1:A:752:G:C2	1:A:753:C:C2	3.00	0.49
1:A:1441:G:C2	1:A:1442:C:C2	3.00	0.49
1:A:1607:U:H2'	1:A:1608:C:H6	1.74	0.49
1:A:2005:A:H2'	1:A:2006:A:C8	2.47	0.49
1:A:2832:A:H5''	10:J:70:LYS:HG3	1.94	0.49
7:G:40:LEU:HG	7:G:125:MET:HE2	1.94	0.49
15:O:37:GLY:O	15:O:38:LEU:CB	2.60	0.49
19:S:114:ASP:C	19:S:116:GLY:H	2.16	0.49
32:5:105:PRO:O	32:5:108:VAL:HG22	2.12	0.49
33:6:19:LEU:HB3	33:6:101:SER:OG	2.13	0.49
1:A:501:U:H2'	1:A:502:U:C6	2.47	0.49
1:A:739:G:C6	1:A:921:C:C5	3.00	0.49
1:A:1727:U:H2'	1:A:1728:C:H6	1.78	0.49
1:A:2029:G:C6	1:A:2030:G:N1	2.81	0.49
1:A:2736:A:H2'	1:A:2737:C:C6	2.47	0.49
1:A:2825:U:O4	1:A:2930:A:N1	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3437:U:H2'	1:A:3438:G:O4'	2.13	0.49
1:A:3754:A:H2'	1:A:3755:U:O4'	2.12	0.49
12:L:45:ASN:O	12:L:48:THR:HG23	2.13	0.49
26:Z:39:ARG:O	26:Z:42:TYR:O	2.30	0.49
1:A:190:G:C6	1:A:241:C:N4	2.80	0.49
1:A:446:G:C2	1:A:702:U:C4	3.00	0.49
1:A:687:G:H2'	1:A:688:U:C6	2.48	0.49
1:A:1192:C:N4	1:A:1215:A:H61	2.10	0.49
1:A:1447:G:H2'	1:A:1448:C:H6	1.78	0.49
1:A:1467:C:H5'	35:8:60:ASN:HA	1.95	0.49
1:A:1817:G:C6	1:A:1818:C:C4	3.00	0.49
1:A:2984:G:C6	1:A:2985:C:C4	3.00	0.49
1:A:3634:C:H2'	1:A:3635:G:C8	2.44	0.49
12:L:84:LEU:HA	12:L:138:GLY:HA3	1.95	0.49
20:T:94:TRP:HZ3	20:T:129:ASN:HD22	1.59	0.49
1:A:26:A:H2'	1:A:27:U:C6	2.48	0.49
1:A:270:U:H4'	1:A:271:G:H5'	1.95	0.49
1:A:697:A:H4'	1:A:698:G:O5'	2.12	0.49
1:A:902:A:H5''	1:A:903:C:H5'	1.94	0.49
1:A:1874:C:H2'	1:A:1875:A:C8	2.48	0.49
1:A:3244:C:C2	1:A:3297:G:N2	2.80	0.49
1:A:3401:C:H2'	1:A:3402:A:C8	2.48	0.49
1:A:3663:A:O2'	1:A:3664:G:P	2.70	0.49
3:C:126:C:H2'	3:C:127:C:H6	1.77	0.49
4:D:97:SER:H	4:D:100:ASN:HD22	1.61	0.49
5:E:60:VAL:HG12	5:E:61:ASP:H	1.78	0.49
5:E:108:ASN:O	5:E:134:LEU:HG	2.12	0.49
10:J:100:THR:HG23	10:J:196:ILE:HG12	1.94	0.49
28:1:26:VAL:HG11	28:1:97:ALA:HB3	1.94	0.49
32:5:141:PRO:HA	32:5:242:TRP:CD2	2.47	0.49
1:A:156:U:H5'	10:J:153:ILE:HG12	1.95	0.49
1:A:204:G:N2	1:A:206:A:H3'	2.27	0.49
1:A:510:A:H2'	1:A:511:C:C6	2.48	0.49
1:A:511:C:C2	1:A:512:A:C8	3.01	0.49
1:A:612:G:H2'	1:A:613:C:H6	1.77	0.49
1:A:638:G:H2'	1:A:639:C:H6	1.77	0.49
1:A:942:C:H5'	4:D:19:HIS:CE1	2.47	0.49
1:A:1423:G:C2	1:A:1424:C:C2	3.00	0.49
1:A:1560:U:OP1	35:8:105:ARG:NH2	2.45	0.49
1:A:1725:U:H2'	1:A:1726:C:H6	1.78	0.49
1:A:1843:U:H2'	1:A:1844:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1905:C:H2'	1:A:1906:A:C8	2.48	0.49
1:A:2990:G:H5''	1:A:2991:U:O4'	2.13	0.49
7:G:12:ILE:HG23	7:G:162:TRP:CD1	2.48	0.49
23:W:6:LYS:HG3	23:W:116:HIS:HB2	1.95	0.49
32:5:139:VAL:O	32:5:139:VAL:CG1	2.61	0.49
1:A:348:C:C2	3:C:29:G:C2	3.00	0.49
1:A:631:U:H2'	1:A:632:U:C6	2.48	0.49
1:A:641:G:H21	1:A:685:U:H5''	1.78	0.49
1:A:1157:U:H2'	1:A:1158:G:O4'	2.12	0.49
1:A:1200:C:H2'	1:A:1201:U:C6	2.47	0.49
1:A:1237:C:H2'	1:A:1238:C:C6	2.48	0.49
1:A:1800:U:H3	1:A:2032:A:H61	1.61	0.49
1:A:2098:G:C6	1:A:2099:C:C4	3.00	0.49
1:A:2105:A:H5''	1:A:2106:A:OP1	2.12	0.49
1:A:2651:A:H3'	1:A:2652:C:C6	2.48	0.49
1:A:2720:C:C2	1:A:2942:G:C2	3.01	0.49
1:A:3532:A:H2'	1:A:3533:A:H8	1.76	0.49
1:A:3672:A:H2'	1:A:3673:C:C6	2.48	0.49
5:E:94:GLU:HB3	11:K:151:LEU:CD1	2.43	0.49
21:U:17:HIS:HB3	21:U:71:GLU:HB2	1.95	0.49
36:9:63:ILE:HB	36:9:114:ILE:HG13	1.94	0.49
1:A:628:U:O2	1:A:628:U:H2'	2.13	0.49
1:A:1073:G:H1'	31:4:12:GLN:CD	2.32	0.49
1:A:1169:A:H2'	1:A:1172:C:H5	1.78	0.49
1:A:2178:A:H2'	1:A:2179:A:C8	2.47	0.49
1:A:3085:A:C5	18:R:155:THR:HG21	2.48	0.49
2:B:108:G:P	18:R:275:ALA:HB2	2.53	0.49
6:F:298:VAL:O	6:F:302:LEU:HG	2.13	0.49
30:3:64:ARG:O	30:3:67:GLU:HG2	2.12	0.49
1:A:179:G:H2'	1:A:180:C:C6	2.48	0.48
1:A:512:A:OP1	9:I:102:ARG:HD2	2.13	0.48
1:A:1089:U:H2'	1:A:1090:G:H8	1.78	0.48
1:A:1768:A:C2'	1:A:1769:U:H5'	2.42	0.48
1:A:1833:G:C2	1:A:1834:C:C2	3.00	0.48
1:A:2659:C:C2	1:A:2675:G:C2	3.01	0.48
1:A:2672:U:H2'	1:A:2673:U:H6	1.76	0.48
1:A:3065:C:O2	1:A:3065:C:O4'	2.30	0.48
10:J:87:ARG:O	10:J:252:GLN:HA	2.13	0.48
15:O:9:ARG:HB3	15:O:9:ARG:HH11	1.77	0.48
1:A:141:A:C2	1:A:142:C:C2	3.02	0.48
1:A:489:U:H1'	1:A:490:U:C6	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:651:A:H2'	1:A:652:A:O4'	2.13	0.48
1:A:893:U:H1'	1:A:1199:A:H2	1.78	0.48
1:A:1470:A:H2'	1:A:1471:A:O4'	2.12	0.48
1:A:1691:G:H2'	1:A:1692:C:O4'	2.13	0.48
1:A:1844:G:C6	1:A:1845:C:C4	3.01	0.48
1:A:3209:G:HO2'	1:A:3210:A:H8	1.60	0.48
1:A:3257:G:OP2	1:A:3258:C:H5'	2.14	0.48
1:A:3473:G:C2	1:A:3474:C:C2	3.01	0.48
1:A:3727:A:H2'	1:A:3728:A:C8	2.48	0.48
6:F:102:PHE:O	6:F:104:PRO:HD3	2.13	0.48
11:K:2:TYR:CZ	36:9:66:LYS:HA	2.47	0.48
12:L:82:ALA:HB2	12:L:115:LEU:HD13	1.94	0.48
1:A:101:C:O2	1:A:101:C:O4'	2.29	0.48
1:A:209:G:C2	1:A:210:C:C2	3.01	0.48
1:A:530:U:H4'	6:F:368:LEU:HD13	1.94	0.48
1:A:1740:A:H2'	1:A:1741:G:C8	2.48	0.48
1:A:1861:C:H2'	1:A:1862:A:H8	1.77	0.48
1:A:2021:A:H2'	1:A:2022:A:H8	1.74	0.48
1:A:2652:C:H4'	1:A:2692:A:H4'	1.94	0.48
1:A:2708:C:O3'	4:D:206:PRO:HB2	2.12	0.48
1:A:3045:G:C6	1:A:3046:C:C4	3.01	0.48
1:A:3215:G:C2	1:A:3216:C:C2	3.01	0.48
2:B:36:C:H2'	2:B:37:A:C8	2.47	0.48
6:F:37:ILE:HD12	6:F:246:ILE:HG22	1.94	0.48
10:J:169:VAL:HG22	10:J:203:LEU:HD21	1.94	0.48
13:M:93:TYR:HE1	13:M:95:ILE:HD11	1.78	0.48
22:V:49:GLN:HG3	22:V:95:GLU:HG2	1.94	0.48
1:A:331:A:H2'	1:A:332:A:C8	2.48	0.48
1:A:711:C:H2'	1:A:712:C:O4'	2.13	0.48
1:A:890:G:C2	1:A:891:C:C2	3.01	0.48
1:A:1058:U:H2'	1:A:1059:G:H8	1.78	0.48
1:A:1567:A:H5''	6:F:195:LYS:HZ1	1.77	0.48
1:A:1906:A:H2'	1:A:1907:A:O4'	2.13	0.48
1:A:2707:G:C2	1:A:2708:C:C2	3.01	0.48
1:A:3401:C:H2'	1:A:3402:A:H8	1.78	0.48
1:A:3509:G:H2'	1:A:3510:C:O4'	2.14	0.48
5:E:33:PRO:HA	5:E:339:ILE:HG23	1.95	0.48
5:E:235:LEU:HB3	5:E:239:THR:HG21	1.96	0.48
6:F:160:SER:HA	6:F:215:ASN:O	2.13	0.48
8:H:41:LEU:HD23	8:H:43:ILE:HB	1.95	0.48
10:J:179:LEU:HD11	10:J:213:THR:HG21	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:9:92:HIS:C	36:9:94:GLY:H	2.17	0.48
1:A:171:C:H5'	12:L:133:LYS:HD3	1.94	0.48
1:A:204:G:H22	1:A:207:A:H5''	1.78	0.48
1:A:608:A:N3	1:A:610:U:O4	2.46	0.48
1:A:1132:G:H22	1:A:1163:A:H2	1.61	0.48
1:A:1234:A:C8	1:A:1234:A:H5''	2.48	0.48
1:A:1727:U:H2'	1:A:1728:C:C6	2.48	0.48
1:A:2033:C:H4'	1:A:2034:G:OP1	2.13	0.48
1:A:2098:G:C2	1:A:2099:C:C2	3.01	0.48
1:A:3002:G:H2'	1:A:3003:C:O4'	2.13	0.48
1:A:3468:G:C6	1:A:3469:C:C4	3.01	0.48
3:C:79:G:C2	3:C:80:C:C2	3.02	0.48
4:D:4:VAL:HG13	4:D:8:GLN:HB2	1.96	0.48
10:J:97:PHE:CZ	10:J:180:VAL:HG13	2.48	0.48
13:M:125:ALA:HB2	13:M:138:ILE:CD1	2.42	0.48
19:S:51:ARG:HB3	19:S:82:VAL:HG21	1.96	0.48
35:8:35:PRO:CB	35:8:40:CYS:SG	3.02	0.48
36:9:56:GLN:HA	36:9:56:GLN:NE2	2.23	0.48
1:A:22:G:C6	1:A:23:C:C4	3.01	0.48
1:A:399:G:H2'	1:A:401:A:C8	2.48	0.48
1:A:1225:A:C2	1:A:1226:A:C8	3.02	0.48
1:A:3579:A:H3'	36:9:39:ARG:HD3	1.95	0.48
1:A:3717:A:H2'	1:A:3718:G:C8	2.49	0.48
18:R:95:TYR:CD1	18:R:197:ASN:HB3	2.49	0.48
24:X:64:PHE:O	24:X:68:ILE:HG13	2.14	0.48
1:A:53:G:N2	1:A:54:C:C2	2.82	0.48
1:A:223:G:H5'	26:Z:11:ARG:HG3	1.96	0.48
1:A:297:G:H5''	16:P:98:LEU:HD13	1.94	0.48
1:A:546:C:H2'	1:A:547:C:O4'	2.12	0.48
1:A:992:C:H4'	1:A:2176:A:H5'	1.94	0.48
1:A:1264:A:N6	1:A:1265:C:N4	2.62	0.48
1:A:2221:U:H3	1:A:2386:A:H61	1.62	0.48
1:A:2471:A:H5''	4:D:132:CYS:SG	2.53	0.48
1:A:3418:A:H2'	1:A:3419:U:C6	2.46	0.48
2:B:39:C:H2'	2:B:40:A:C8	2.49	0.48
20:T:9:LEU:HD22	20:T:37:ARG:HD3	1.94	0.48
1:A:276:G:H5'	16:P:121:TRP:CD2	2.49	0.48
1:A:391:A:H2'	1:A:392:G:O4'	2.14	0.48
1:A:732:C:H2'	1:A:733:C:H6	1.79	0.48
1:A:1289:G:C6	1:A:1290:C:C4	3.02	0.48
1:A:2079:A:H2'	1:A:2080:C:H6	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2103:C:O2'	1:A:2109:A:N1	2.38	0.48
1:A:2508:C:H42	1:A:2523:U:H3	1.60	0.48
1:A:2825:U:H3	1:A:2930:A:H2	1.61	0.48
1:A:3721:U:H2'	1:A:3722:G:O4'	2.13	0.48
21:U:86:VAL:HG11	21:U:115:LEU:HD13	1.95	0.48
1:A:177:A:H61	1:A:253:U:H3	1.62	0.48
1:A:268:C:O2'	1:A:269:A:H8	1.97	0.48
1:A:739:G:C6	1:A:921:C:C4	3.02	0.48
1:A:934:G:H5''	1:A:934:G:H8	1.78	0.48
1:A:1588:U:H2'	1:A:1589:G:H8	1.78	0.48
1:A:1622:G:H5'	20:T:23:MET:O	2.13	0.48
1:A:1833:G:C6	1:A:1834:C:C4	3.01	0.48
1:A:2712:A:H2'	1:A:2713:C:C6	2.49	0.48
1:A:3590:A:H4'	1:A:3591:U:O5'	2.14	0.48
5:E:180:ILE:HD13	5:E:192:VAL:HG22	1.94	0.48
5:E:317:ASP:N	5:E:317:ASP:OD1	2.46	0.48
6:F:33:ARG:NH2	6:F:33:ARG:HB3	2.28	0.48
8:H:93:LEU:HA	8:H:178:ILE:HA	1.96	0.48
16:P:63:ARG:HG3	16:P:132:GLU:HG3	1.95	0.48
18:R:150:VAL:HG22	18:R:153:THR:HG23	1.96	0.48
23:W:122:ALA:HB3	23:W:143:PRO:HB2	1.96	0.48
23:W:126:ARG:HA	23:W:140:MET:HG2	1.96	0.48
28:1:98:SER:HB2	28:1:101:VAL:HG23	1.95	0.48
1:A:10:G:O2'	1:A:11:A:OP1	2.24	0.48
1:A:155:U:C4'	1:A:156:U:OP2	2.62	0.48
1:A:583:U:H2'	1:A:584:U:C6	2.49	0.48
1:A:1484:A:H2'	1:A:1485:A:C8	2.49	0.48
1:A:1485:A:H2'	1:A:1486:A:O4'	2.14	0.48
1:A:3517:C:H2'	1:A:3518:C:H6	1.79	0.48
1:A:3653:G:H4'	14:N:140:LYS:HB3	1.95	0.48
1:A:3706:U:H2'	1:A:3707:U:O4'	2.14	0.48
1:A:3722:G:C6	1:A:3723:C:C4	3.02	0.48
4:D:206:PRO:HD3	4:D:213:GLY:HA3	1.96	0.48
5:E:215:ILE:HG22	5:E:271:HIS:CE1	2.49	0.48
6:F:269:GLU:H	6:F:273:THR:HG23	1.78	0.48
9:I:131:ILE:HG12	9:I:182:ILE:HG21	1.94	0.48
11:K:26:LEU:HD11	11:K:101:LEU:HB2	1.96	0.48
14:N:38:TYR:HH	21:U:5:ILE:N	2.11	0.48
14:N:92:LEU:O	14:N:96:VAL:HG12	2.13	0.48
19:S:51:ARG:HD3	19:S:54:MET:HE2	1.94	0.48
31:4:60:LYS:O	31:4:63:GLN:HG2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:G:H2'	1:A:206:A:C8	2.49	0.47
1:A:205:G:N2	1:A:380:A:C8	2.82	0.47
1:A:660:U:H2'	1:A:661:G:C8	2.49	0.47
1:A:929:G:C4	1:A:930:C:C5	3.01	0.47
1:A:1096:G:H2'	1:A:1097:A:C8	2.49	0.47
1:A:1910:C:H2'	1:A:1911:A:H8	1.79	0.47
1:A:2616:G:O2'	1:A:2618:G:OP2	2.29	0.47
1:A:3261:A:H2'	1:A:3262:A:O4'	2.14	0.47
1:A:3468:G:H2'	1:A:3469:C:H6	1.78	0.47
1:A:3623:A:O2'	1:A:3624:U:OP1	2.27	0.47
17:Q:16:PRO:HA	17:Q:95:HIS:HD2	1.78	0.47
34:7:41:ILE:CD1	34:7:68:TRP:HE1	2.24	0.47
35:8:81:GLU:C	35:8:84:PRO:HD2	2.35	0.47
1:A:1439:G:C2	1:A:1440:C:C2	3.02	0.47
1:A:1481:A:O2'	1:A:1482:A:H8	1.96	0.47
1:A:1819:U:H5'	20:T:99:ARG:NH2	2.29	0.47
1:A:3143:G:C2	1:A:3144:C:C2	3.02	0.47
1:A:3282:U:H2'	1:A:3283:U:C6	2.50	0.47
1:A:3306:G:C2	5:E:247:ALA:HB1	2.49	0.47
1:A:3384:G:H2'	1:A:3385:U:O4'	2.14	0.47
1:A:3712:G:H3'	1:A:3713:C:H6	1.78	0.47
4:D:45:VAL:HG22	4:D:61:VAL:HG22	1.96	0.47
5:E:86:VAL:HB	5:E:196:LEU:O	2.15	0.47
17:Q:49:VAL:HB	17:Q:172:GLY:HA2	1.96	0.47
26:Z:44:THR:HG21	26:Z:47:LEU:HG	1.96	0.47
1:A:308:U:O2'	1:A:309:G:H8	1.97	0.47
1:A:456:A:N6	1:A:500:A:N6	2.63	0.47
1:A:1047:A:H2'	1:A:1048:G:C8	2.49	0.47
1:A:1117:U:H2'	1:A:1118:A:H8	1.79	0.47
1:A:2603:U:H2'	1:A:2604:G:C8	2.49	0.47
1:A:2837:G:N2	1:A:2917:C:C2	2.82	0.47
1:A:3009:G:H2'	1:A:3010:A:C8	2.50	0.47
1:A:3653:G:C6	1:A:3654:C:C4	3.01	0.47
1:A:3750:U:H2'	1:A:3751:A:O4'	2.15	0.47
3:C:28:G:H2'	3:C:29:G:O4'	2.13	0.47
12:L:72:LYS:HG3	12:L:72:LYS:O	2.13	0.47
1:A:405:A:H2'	1:A:406:A:H8	1.79	0.47
1:A:1644:U:O4	1:A:2102:A:C6	2.62	0.47
1:A:2571:C:N3	1:A:2600:G:C2	2.83	0.47
1:A:2637:U:H2'	1:A:2638:G:H8	1.79	0.47
1:A:2975:A:H2'	1:A:2975:A:N3	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3237:G:C2	1:A:3238:C:C2	3.01	0.47
1:A:3516:A:H2'	1:A:3516:A:N3	2.29	0.47
1:A:3688:G:C2	1:A:3689:C:C2	3.03	0.47
1:A:3760:U:H4'	1:A:3761:G:H5'	1.95	0.47
3:C:53:G:C2	3:C:54:C:C2	3.02	0.47
6:F:322:PHE:HE1	6:F:336:ARG:HD3	1.78	0.47
17:Q:52:LEU:HB2	17:Q:152:LEU:HD22	1.96	0.47
19:S:85:ILE:HG13	19:S:85:ILE:O	2.14	0.47
1:A:579:C:H1'	1:A:580:A:H5'	1.97	0.47
1:A:913:U:C2	1:A:914:G:C8	3.02	0.47
1:A:1169:A:H2'	1:A:1172:C:C5	2.49	0.47
1:A:1441:G:C6	1:A:1442:C:C4	3.02	0.47
1:A:1767:U:O4	1:A:1768:A:N6	2.47	0.47
1:A:1852:C:H3'	1:A:1853:C:C6	2.50	0.47
1:A:3253:G:C2	1:A:3267:C:N3	2.83	0.47
1:A:3468:G:C2	1:A:3469:C:C2	3.02	0.47
1:A:3552:U:H2'	1:A:3553:G:O4'	2.15	0.47
15:O:99:VAL:HA	15:O:123:VAL:HB	1.97	0.47
16:P:103:GLU:HG3	16:P:161:GLU:HB2	1.95	0.47
1:A:185:A:H2'	1:A:186:A:O4'	2.14	0.47
1:A:753:C:O2'	1:A:757:U:H5''	2.14	0.47
1:A:1018:C:H2'	1:A:1019:A:H8	1.79	0.47
1:A:1203:A:H2'	1:A:1204:A:C8	2.49	0.47
1:A:1756:G:C2	1:A:1757:C:C2	3.02	0.47
1:A:1961:U:H2'	1:A:1962:U:C6	2.50	0.47
1:A:2937:G:C2	1:A:2938:C:C2	3.02	0.47
1:A:3198:G:C6	1:A:3199:C:C4	3.02	0.47
1:A:3473:G:H2'	1:A:3474:C:C6	2.49	0.47
3:C:19:G:C6	3:C:20:G:N1	2.83	0.47
3:C:47:G:C2	3:C:48:C:C2	3.02	0.47
1:A:223:G:H5''	26:Z:11:ARG:HG3	1.96	0.47
1:A:227:A:N7	1:A:1538:U:H2'	2.30	0.47
1:A:421:C:H2'	1:A:422:G:H8	1.80	0.47
1:A:441:A:N1	1:A:706:U:O2	2.48	0.47
1:A:580:A:H2'	1:A:581:C:C6	2.50	0.47
1:A:651:A:H4'	32:5:43:LYS:HE2	1.97	0.47
1:A:715:U:H2'	1:A:716:C:C5	2.50	0.47
1:A:906:G:C2	1:A:907:C:C2	3.02	0.47
1:A:929:G:C6	1:A:930:C:C4	3.03	0.47
1:A:941:G:C6	1:A:942:C:C4	3.03	0.47
1:A:984:A:H3'	1:A:985:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1033:A:C2	4:D:204:MET:SD	3.08	0.47
1:A:1245:G:C2	1:A:1246:C:C2	3.03	0.47
1:A:1439:G:C6	1:A:1440:C:C4	3.02	0.47
1:A:1455:C:H2'	1:A:1456:C:C6	2.50	0.47
1:A:1473:A:N6	1:A:1474:A:C6	2.82	0.47
1:A:2002:G:H1'	1:A:2003:G:N7	2.30	0.47
1:A:3055:U:H2'	1:A:3056:U:H6	1.78	0.47
1:A:3198:G:C2	1:A:3199:C:C6	3.02	0.47
1:A:3653:G:C2	1:A:3654:C:C2	3.02	0.47
1:A:3727:A:H5'	1:A:3727:A:H8	1.80	0.47
2:B:57:C:H2'	2:B:58:A:H8	1.80	0.47
3:C:3:G:C2	3:C:4:C:C2	3.03	0.47
3:C:79:G:C6	3:C:80:C:C4	3.03	0.47
5:E:163:PRO:HG3	5:E:173:ALA:HA	1.97	0.47
10:J:93:SER:O	10:J:96:GLN:HG3	2.14	0.47
12:L:94:ILE:HD12	12:L:115:LEU:HD21	1.96	0.47
17:Q:17:TYR:H	17:Q:95:HIS:CD2	2.33	0.47
17:Q:88:ARG:HG3	17:Q:173:PHE:CE2	2.49	0.47
18:R:60:VAL:CG2	18:R:80:SER:HB2	2.44	0.47
1:A:53:G:C6	1:A:54:C:C4	3.03	0.47
1:A:437:A:H61	1:A:709:A:N6	2.13	0.47
1:A:1268:G:C2	1:A:1269:C:C2	3.03	0.47
1:A:1423:G:C5	1:A:1424:C:C5	3.02	0.47
1:A:1455:C:H2'	1:A:1456:C:H6	1.80	0.47
1:A:3190:G:C2	1:A:3191:C:C2	3.03	0.47
6:F:211:TYR:HE2	6:F:229:LEU:HB3	1.80	0.47
36:9:85:VAL:HG12	36:9:99:CYS:HB2	1.97	0.47
1:A:544:C:O2	1:A:544:C:O4'	2.30	0.47
1:A:743:A:C6	1:A:744:G:C6	3.03	0.47
1:A:911:U:O2'	1:A:912:U:H5'	2.14	0.47
1:A:921:C:H2'	1:A:922:C:H6	1.79	0.47
1:A:1190:G:N1	1:A:1218:C:C2	2.83	0.47
1:A:1260:C:H2'	1:A:1261:A:C8	2.50	0.47
1:A:1268:G:C4	1:A:1269:C:C5	3.02	0.47
1:A:1537:G:C6	1:A:1567:A:N6	2.82	0.47
1:A:2540:G:C2	1:A:2541:C:C2	3.03	0.47
1:A:2637:U:H2'	1:A:2638:G:C8	2.49	0.47
1:A:3180:C:N4	1:A:3228:U:H3	2.13	0.47
1:A:3479:U:H2'	1:A:3480:C:C6	2.50	0.47
1:A:3521:G:C6	1:A:3522:C:C4	3.03	0.47
3:C:31:U:H4'	6:F:53:ALA:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:50:G:C6	3:C:51:C:C4	3.03	0.47
5:E:182:GLY:H	5:E:188:LYS:HE2	1.79	0.47
13:M:82:ARG:HD3	13:M:101:ALA:HB3	1.96	0.47
16:P:35:VAL:HG23	16:P:65:ARG:HD2	1.96	0.47
19:S:80:VAL:HG12	19:S:100:CYS:HB3	1.95	0.47
1:A:579:C:C2	1:A:580:A:C8	3.03	0.47
1:A:985:G:O6	1:A:1012:U:C2	2.68	0.47
1:A:1198:A:H1'	31:4:46:CYS:SG	2.55	0.47
1:A:1791:A:C6	1:A:1798:A:H2'	2.50	0.47
1:A:2184:U:H5''	20:T:84:LYS:HG3	1.96	0.47
1:A:2937:G:C4	1:A:2938:C:C5	3.03	0.47
1:A:3045:G:C4	1:A:3046:C:C5	3.03	0.47
1:A:3444:G:C6	1:A:3445:C:C4	3.03	0.47
1:A:3578:A:H2'	1:A:3579:A:C8	2.50	0.47
6:F:33:ARG:HB3	6:F:33:ARG:CZ	2.45	0.47
11:K:118:VAL:HG11	21:U:178:ARG:HG3	1.97	0.47
14:N:127:GLU:O	14:N:131:VAL:HG13	2.14	0.47
18:R:66:CYS:O	18:R:67:ALA:HB3	2.14	0.47
25:Y:106:ASP:O	25:Y:110:LEU:HB2	2.15	0.47
1:A:192:G:C5	1:A:193:C:C5	3.02	0.46
1:A:739:G:C2	1:A:921:C:C2	3.03	0.46
1:A:1155:C:H2'	1:A:1156:U:H6	1.81	0.46
1:A:2175:C:O2	1:A:2175:C:H2'	2.14	0.46
1:A:2183:A:H2'	1:A:2184:U:C6	2.50	0.46
1:A:2540:G:H2'	1:A:2541:C:O4'	2.15	0.46
1:A:3289:G:C6	1:A:3290:C:C4	3.03	0.46
1:A:3414:G:H2'	1:A:3415:A:H8	1.76	0.46
1:A:3589:U:H4'	1:A:3590:A:O5'	2.15	0.46
15:O:71:PRO:HG2	15:O:107:TYR:HA	1.97	0.46
1:A:611:G:H5''	14:N:88:LYS:HG2	1.97	0.46
1:A:818:C:H5	19:S:91:LEU:HA	1.79	0.46
1:A:1447:G:C2	1:A:1448:C:C2	3.04	0.46
1:A:1646:C:H2'	1:A:1647:U:H6	1.75	0.46
1:A:2651:A:H3'	1:A:2652:C:H6	1.80	0.46
1:A:3175:G:HO2'	1:A:3228:U:H5	1.63	0.46
1:A:3262:A:H2'	1:A:3263:G:O4'	2.15	0.46
1:A:3277:G:C2	1:A:3288:C:C2	3.04	0.46
3:C:37:A:HO2'	3:C:38:G:C5'	2.27	0.46
3:C:78:U:O2	3:C:78:U:O4'	2.33	0.46
9:I:59:VAL:HG23	9:I:107:THR:OG1	2.15	0.46
10:J:172:ASN:HA	10:J:196:ILE:HD11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:62:LEU:HD23	19:S:140:GLY:HA2	1.97	0.46
22:V:41:VAL:HG11	22:V:97:VAL:HG13	1.96	0.46
23:W:109:VAL:HA	23:W:112:LEU:HD12	1.96	0.46
29:2:68:VAL:HB	29:2:79:GLN:HB2	1.98	0.46
1:A:365:C:C2	1:A:371:G:C2	3.04	0.46
1:A:929:G:C2	1:A:930:C:C2	3.04	0.46
1:A:1048:G:C2	1:A:1049:C:C2	3.04	0.46
1:A:1666:A:H2'	1:A:1667:A:H8	1.80	0.46
1:A:1677:G:C2	1:A:1678:C:C2	3.03	0.46
1:A:2660:A:H2'	1:A:2661:A:C8	2.50	0.46
16:P:141:ASN:HA	16:P:144:ARG:HB2	1.97	0.46
25:Y:123:LYS:HB3	25:Y:129:THR:OG1	2.16	0.46
1:A:38:U:H2'	1:A:39:A:O4'	2.14	0.46
1:A:277:U:H2'	1:A:278:C:H6	1.81	0.46
1:A:1204:A:H5''	1:A:1204:A:H8	1.80	0.46
1:A:1255:G:H22	1:A:1257:A:H3'	1.78	0.46
1:A:2651:A:H2'	1:A:2652:C:O4'	2.16	0.46
1:A:3286:C:H2'	1:A:3287:C:C6	2.50	0.46
4:D:92:THR:O	4:D:106:LYS:HD3	2.14	0.46
19:S:105:THR:HG23	19:S:108:ALA:H	1.80	0.46
1:A:929:G:C2	1:A:1050:C:C2	3.03	0.46
1:A:975:G:C6	1:A:976:G:N1	2.84	0.46
1:A:1216:C:C2'	1:A:1217:U:H5'	2.43	0.46
1:A:1268:G:H2'	1:A:1269:C:C6	2.50	0.46
1:A:2005:A:H2'	1:A:2006:A:H8	1.81	0.46
1:A:3551:U:H2'	1:A:3552:U:C6	2.49	0.46
1:A:3570:U:H3	3:C:2:A:H61	1.63	0.46
3:C:32:C:H2'	3:C:33:C:H6	1.80	0.46
5:E:255:ALA:O	5:E:256:ARG:HG3	2.15	0.46
8:H:4:ILE:HD13	21:U:156:LEU:HD11	1.96	0.46
15:O:75:VAL:HG22	15:O:112:GLY:HA2	1.97	0.46
16:P:111:CYS:HB3	16:P:114:LEU:HD12	1.97	0.46
17:Q:88:ARG:HG3	17:Q:173:PHE:HE2	1.81	0.46
1:A:32:C:H2'	1:A:33:G:O4'	2.15	0.46
1:A:109:A:H4'	1:A:110:G:OP1	2.15	0.46
1:A:644:G:H5''	9:I:32:LYS:HD2	1.98	0.46
1:A:755:A:N1	1:A:797:A:O2'	2.43	0.46
1:A:1747:U:O2	1:A:1747:U:H2'	2.14	0.46
1:A:2494:G:C5	1:A:2495:C:C4	3.03	0.46
1:A:2527:G:H2'	1:A:2528:C:O4'	2.16	0.46
1:A:2640:U:H2'	1:A:2641:A:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2689:G:C2	1:A:3344:C:C2	3.04	0.46
1:A:2949:G:H2'	1:A:2950:U:O4'	2.16	0.46
1:A:3045:G:N2	1:A:3046:C:C2	2.83	0.46
1:A:3289:G:C2	1:A:3290:C:C2	3.04	0.46
1:A:3470:G:O3'	1:A:3471:A:H8	1.99	0.46
8:H:3:THR:HA	21:U:150:GLN:HE22	1.80	0.46
18:R:40:ASP:HA	22:V:70:LYS:O	2.16	0.46
18:R:169:CYS:HA	18:R:173:LEU:O	2.16	0.46
26:Z:16:LYS:O	26:Z:20:THR:HG22	2.15	0.46
28:1:4:LEU:HD21	33:6:66:SER:OG	2.15	0.46
1:A:1085:U:H1'	15:O:43:ILE:CD1	2.45	0.46
1:A:1439:G:H2'	1:A:1440:C:O4'	2.16	0.46
1:A:2068:G:C6	1:A:2069:C:C4	3.04	0.46
1:A:2975:A:N1	1:A:2980:U:C4	2.84	0.46
1:A:3023:C:H2'	1:A:3024:U:C6	2.51	0.46
1:A:3206:A:H1'	1:A:3256:C:O2'	2.16	0.46
1:A:3616:U:H3'	1:A:3617:A:H5''	1.97	0.46
17:Q:17:TYR:H	17:Q:95:HIS:HD2	1.62	0.46
20:T:26:ASN:O	20:T:27:GLU:HB2	2.15	0.46
32:5:115:LEU:O	32:5:116:ARG:HB2	2.15	0.46
1:A:345:G:C6	1:A:347:C:N4	2.84	0.46
1:A:859:C:H2'	1:A:860:A:H8	1.80	0.46
1:A:882:G:C2	1:A:883:C:C2	3.04	0.46
1:A:921:C:H5	15:O:25:HIS:ND1	2.06	0.46
1:A:1268:G:C6	1:A:1269:C:C4	3.04	0.46
1:A:1270:G:OP2	1:A:1272:U:H2'	2.16	0.46
1:A:1313:C:O2	21:U:117:SER:HB3	2.16	0.46
1:A:1314:G:C2	1:A:1315:C:C2	3.04	0.46
1:A:1751:C:C2	1:A:1752:C:C5	3.04	0.46
1:A:2073:G:C2	1:A:2074:C:C2	3.04	0.46
4:D:12:ARG:HG2	4:D:12:ARG:HH11	1.81	0.46
10:J:80:LYS:HB3	16:P:28:TRP:HH2	1.80	0.46
19:S:87:ASP:HB2	19:S:111:ARG:HD3	1.98	0.46
22:V:67:HIS:CD2	31:4:36:ASP:H	2.34	0.46
1:A:80:C:H2'	1:A:81:C:C6	2.50	0.46
1:A:328:G:C6	1:A:329:C:C4	3.04	0.46
1:A:490:U:H2'	1:A:491:C:O4'	2.15	0.46
1:A:539:G:C6	1:A:540:C:N4	2.84	0.46
1:A:1302:G:C6	1:A:1303:C:C4	3.03	0.46
1:A:1440:C:O2	11:K:86:MET:HG2	2.16	0.46
1:A:1456:C:H2'	1:A:1457:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2004:U:O2	1:A:2004:U:O4'	2.32	0.46
1:A:2441:U:O2'	4:D:182:ALA:HB2	2.16	0.46
1:A:2494:G:C5	1:A:2495:C:C5	3.04	0.46
1:A:2827:C:C2	1:A:2929:G:C2	3.04	0.46
1:A:3420:U:H2'	1:A:3421:A:C8	2.51	0.46
1:A:3524:G:H2'	1:A:3525:A:O4'	2.16	0.46
13:M:104:ILE:HD12	13:M:112:LYS:HD3	1.96	0.46
15:O:117:LYS:HD3	15:O:120:GLN:HG3	1.97	0.46
15:O:147:VAL:HG22	15:O:148:ALA:H	1.81	0.46
20:T:92:THR:HA	20:T:95:ILE:HD12	1.98	0.46
25:Y:124:ILE:HG12	25:Y:130:LEU:HD23	1.98	0.46
1:A:22:G:C2	1:A:23:C:C2	3.04	0.46
1:A:209:G:C6	1:A:210:C:C4	3.04	0.46
1:A:634:U:H2'	1:A:635:U:C6	2.50	0.46
1:A:890:G:C6	1:A:891:C:C4	3.03	0.46
1:A:952:U:H2'	1:A:953:U:O4'	2.15	0.46
1:A:1086:C:H5''	1:A:1086:C:H6	1.81	0.46
1:A:1185:A:C2	1:A:1225:A:C5	3.04	0.46
1:A:1302:G:C2	1:A:1303:C:C2	3.04	0.46
1:A:3035:A:H3'	1:A:3036:A:C8	2.50	0.46
1:A:3035:A:H3'	1:A:3036:A:H8	1.81	0.46
1:A:3764:G:C6	1:A:3765:C:C4	3.04	0.46
5:E:8:ARG:HD3	13:M:48:LEU:HD12	1.97	0.46
9:I:87:GLY:O	9:I:88:PRO:C	2.55	0.46
1:A:209:G:C4	1:A:210:C:C5	3.04	0.45
1:A:297:G:H2'	1:A:298:C:C6	2.50	0.45
1:A:612:G:H2'	1:A:613:C:O4'	2.16	0.45
1:A:1762:A:O2'	1:A:1763:G:H8	2.00	0.45
1:A:2487:G:C2	1:A:2488:C:C2	3.04	0.45
1:A:3306:G:C2	1:A:3307:C:C2	3.03	0.45
1:A:3497:A:OP1	8:H:74:THR:HG21	2.16	0.45
1:A:3646:G:C2	1:A:3647:C:C2	3.04	0.45
3:C:32:C:H2'	3:C:33:C:C6	2.51	0.45
19:S:86:THR:HA	19:S:105:THR:HG22	1.99	0.45
19:S:156:GLY:HA2	19:S:187:LYS:O	2.16	0.45
34:7:52:MET:O	34:7:53:HIS:HB2	2.16	0.45
1:A:25:A:H2'	1:A:25:A:N3	2.31	0.45
1:A:33:G:N2	1:A:50:U:C4	2.84	0.45
1:A:588:C:C4	1:A:604:G:N1	2.84	0.45
1:A:921:C:H41	15:O:25:HIS:HB3	1.81	0.45
1:A:1190:G:C2	1:A:1218:C:O2	2.69	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1979:C:H2'	1:A:1980:G:O4'	2.15	0.45
1:A:2090:U:H6	1:A:2090:U:H5''	1.81	0.45
1:A:2135:G:C4	1:A:2136:C:C5	3.05	0.45
1:A:3752:C:N4	1:A:3753:G:C6	2.84	0.45
2:B:15:U:H2'	2:B:16:A:C8	2.51	0.45
6:F:76:ILE:HG21	6:F:96:CYS:SG	2.56	0.45
12:L:74:PHE:O	12:L:78:GLU:HB2	2.16	0.45
12:L:84:LEU:HD23	12:L:138:GLY:HA3	1.98	0.45
14:N:23:ARG:HA	14:N:29:ARG:CZ	2.46	0.45
19:S:148:GLU:HA	19:S:151:PHE:CD2	2.51	0.45
1:A:912:U:C2	1:A:913:U:C5	3.04	0.45
1:A:1474:A:H5''	6:F:306:LYS:HB2	1.98	0.45
1:A:1481:A:O2'	1:A:1482:A:H5''	2.16	0.45
1:A:1516:G:HO2'	1:A:1517:U:H6	1.61	0.45
1:A:2004:U:C4	1:A:2005:A:C5	3.05	0.45
1:A:2487:G:H2'	1:A:2488:C:C6	2.51	0.45
1:A:2690:A:H8	1:A:3300:A:N1	2.14	0.45
1:A:3114:G:C2	1:A:3115:C:C2	3.05	0.45
1:A:3145:A:H2'	1:A:3146:U:O4'	2.16	0.45
1:A:3306:G:N2	1:A:3307:C:C2	2.84	0.45
1:A:3353:A:H3'	1:A:3354:A:H8	1.80	0.45
3:C:3:G:C6	3:C:4:C:C4	3.05	0.45
3:C:49:C:H2'	3:C:50:G:O4'	2.16	0.45
3:C:103:G:C2	3:C:104:C:C2	3.05	0.45
4:D:32:LEU:HD23	4:D:37:LYS:HE3	1.97	0.45
29:2:118:LEU:HD11	35:8:86:ILE:HD12	1.97	0.45
1:A:95:A:H5''	15:O:34:LYS:HB2	1.98	0.45
1:A:289:A:H2'	1:A:293:U:C6	2.51	0.45
1:A:345:G:C6	1:A:347:C:C4	3.04	0.45
1:A:871:A:H5'	31:4:31:SER:HB3	1.99	0.45
1:A:1910:C:H2'	1:A:1911:A:C8	2.52	0.45
1:A:2822:U:H4'	1:A:2823:U:OP1	2.17	0.45
1:A:2937:G:N2	1:A:2938:C:C2	2.85	0.45
1:A:3215:G:C6	1:A:3216:C:C4	3.04	0.45
1:A:3377:A:OP1	1:A:3377:A:H4'	2.16	0.45
1:A:3473:G:H2'	1:A:3474:C:H6	1.82	0.45
1:A:3509:G:C2	1:A:3510:C:C2	3.05	0.45
3:C:149:C:H5''	16:P:60:VAL:HG11	1.98	0.45
5:E:249:ILE:HG21	5:E:257:VAL:HG22	1.97	0.45
8:H:184:THR:HG22	8:H:185:THR:H	1.81	0.45
22:V:113:ASN:O	22:V:117:ILE:HG13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:48:LEU:HA	23:W:51:VAL:HG12	1.98	0.45
26:Z:81:VAL:HG12	26:Z:82:GLU:H	1.82	0.45
32:5:115:LEU:O	32:5:116:ARG:CB	2.65	0.45
1:A:463:G:C2	1:A:493:C:C2	3.05	0.45
1:A:507:G:H2'	1:A:508:A:C8	2.51	0.45
1:A:520:U:O2'	36:9:75:GLN:HG2	2.17	0.45
1:A:1015:A:H5''	4:D:183:GLY:HA3	1.98	0.45
1:A:1296:U:H5''	1:A:1457:G:O6	2.17	0.45
1:A:2209:C:N4	1:A:2400:A:H61	2.11	0.45
1:A:2217:A:H2'	1:A:2218:C:O4'	2.17	0.45
1:A:2836:G:N2	1:A:2918:C:C2	2.85	0.45
1:A:3393:C:H2'	1:A:3394:A:H8	1.80	0.45
1:A:3444:G:C2	1:A:3445:C:C2	3.04	0.45
1:A:3646:G:N2	1:A:3647:C:C2	2.84	0.45
2:B:102:C:H2'	2:B:103:A:O4'	2.16	0.45
7:G:102:PHE:CE2	7:G:129:VAL:HG21	2.50	0.45
25:Y:115:LEU:CD2	25:Y:133:MET:HB2	2.46	0.45
32:5:157:LEU:HD21	32:5:201:LEU:CD1	2.47	0.45
1:A:65:A:H61	1:A:331:A:N6	2.14	0.45
1:A:65:A:H4'	1:A:66:A:OP2	2.16	0.45
1:A:204:G:H22	1:A:206:A:H3'	1.82	0.45
1:A:584:U:C2	1:A:586:U:C5	3.04	0.45
1:A:756:G:H2'	1:A:757:U:O4'	2.16	0.45
1:A:1247:C:H2'	1:A:1248:A:H8	1.81	0.45
1:A:1289:G:C2	1:A:1290:C:C2	3.04	0.45
1:A:1302:G:C6	1:A:1303:C:N4	2.85	0.45
1:A:1463:A:N6	1:A:1464:A:N6	2.65	0.45
1:A:1614:A:H2'	1:A:1615:G:C8	2.52	0.45
1:A:2527:G:C5	1:A:2528:C:C5	3.05	0.45
1:A:2737:C:H2'	1:A:2738:U:C6	2.51	0.45
1:A:3613:A:H2'	1:A:3614:A:O4'	2.17	0.45
1:A:3646:G:H2'	1:A:3647:C:H6	1.82	0.45
3:C:50:G:C2	3:C:51:C:C2	3.04	0.45
3:C:127:C:C2	3:C:135:G:C2	3.05	0.45
4:D:113:ILE:HG22	4:D:165:MET:C	2.37	0.45
1:A:176:A:H2'	1:A:177:A:C8	2.52	0.45
1:A:505:A:H61	1:A:693:A:H61	1.64	0.45
1:A:1264:A:C6	1:A:1265:C:N4	2.85	0.45
1:A:3285:A:H2'	1:A:3286:C:C6	2.51	0.45
1:A:3550:U:H2'	1:A:3551:U:C6	2.51	0.45
1:A:3646:G:C6	1:A:3647:C:C4	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:74:A:H61	2:B:100:A:H3'	1.82	0.45
4:D:109:GLU:HA	4:D:136:VAL:HG12	1.99	0.45
5:E:37:LYS:HA	5:E:183:GLY:HA2	1.99	0.45
19:S:37:ALA:HB1	19:S:46:LYS:HG2	1.98	0.45
1:A:30:G:C2	1:A:31:C:C2	3.05	0.45
1:A:1018:C:H2'	1:A:1019:A:C8	2.52	0.45
1:A:1101:A:H2'	1:A:1102:U:C6	2.52	0.45
1:A:1978:U:H2'	1:A:1979:C:C6	2.52	0.45
1:A:2655:C:H2'	1:A:2656:A:O4'	2.17	0.45
1:A:2937:G:C6	1:A:2938:C:C4	3.04	0.45
46:A:3801:YMZ:FAF	29:2:44:PRO:HB2	2.07	0.45
3:C:103:G:C6	3:C:104:C:C4	3.05	0.45
5:E:87:VAL:CG2	5:E:160:HIS:HD2	2.30	0.45
11:K:180:ILE:CG2	14:N:142:MET:HG3	2.46	0.45
18:R:69:ILE:HD13	18:R:69:ILE:H	1.82	0.45
18:R:157:THR:HG22	18:R:180:ASN:O	2.16	0.45
19:S:86:THR:HA	19:S:105:THR:CG2	2.47	0.45
1:A:685:U:HO2'	1:A:686:U:H6	1.64	0.45
1:A:796:C:O2'	1:A:907:C:H5''	2.17	0.45
1:A:1029:G:C5	1:A:1030:C:C4	3.05	0.45
1:A:1053:U:H2'	1:A:1053:U:O2	2.16	0.45
1:A:1111:A:H2'	1:A:1112:C:O4'	2.16	0.45
1:A:1191:G:C6	1:A:1192:C:N4	2.85	0.45
1:A:1844:G:C2	1:A:1845:C:C2	3.05	0.45
1:A:1866:C:N3	1:A:1893:G:C2	2.85	0.45
1:A:2210:U:H2'	1:A:2211:C:O4'	2.17	0.45
1:A:2571:C:C2	1:A:2600:G:C2	3.05	0.45
1:A:2723:G:C2	1:A:2724:C:C2	3.04	0.45
1:A:3505:U:C4	1:A:3509:G:O6	2.69	0.45
5:E:142:ASN:HA	5:E:145:LEU:HD12	1.97	0.45
7:G:27:GLY:C	7:G:29:ARG:N	2.61	0.45
9:I:30:ASN:HA	9:I:36:ARG:HG2	1.98	0.45
12:L:168:LYS:N	12:L:169:PRO:HD2	2.32	0.45
16:P:68:ARG:HH21	16:P:126:ALA:HA	1.82	0.45
20:T:14:LEU:O	20:T:15:LYS:CB	2.63	0.45
25:Y:123:LYS:HA	25:Y:127:ILE:HD11	1.99	0.45
33:6:95:ILE:HD12	33:6:98:VAL:HG13	1.99	0.45
1:A:746:A:C2'	1:A:747:A:C8	2.70	0.45
1:A:830:U:H2'	1:A:831:U:O4'	2.17	0.45
1:A:1116:G:N2	1:A:1176:C:H2'	2.31	0.45
1:A:1268:G:N2	1:A:1269:C:C2	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3306:G:C6	1:A:3307:C:C4	3.05	0.45
1:A:3426:G:H5''	13:M:14:ARG:HB3	1.99	0.45
1:A:3568:G:H2'	1:A:3569:C:H6	1.81	0.45
4:D:117:GLU:HG2	4:D:124:GLY:H	1.82	0.45
12:L:109:THR:O	12:L:112:VAL:HG22	2.17	0.45
1:A:29:C:C2	1:A:56:G:N2	2.85	0.44
1:A:51:A:H2'	1:A:52:A:O4'	2.17	0.44
1:A:906:G:C6	1:A:907:C:C4	3.05	0.44
1:A:1184:A:H2'	1:A:1185:A:C8	2.52	0.44
1:A:1284:C:H1'	2:B:84:U:H5	1.82	0.44
1:A:1423:G:H2'	1:A:1424:C:O4'	2.17	0.44
1:A:1523:A:H2'	1:A:1524:U:O4'	2.16	0.44
1:A:2401:C:H1'	1:A:3736:A:C8	2.52	0.44
1:A:2630:C:H2'	1:A:2631:C:C6	2.51	0.44
1:A:3676:C:H2'	1:A:3677:A:C8	2.52	0.44
4:D:5:ILE:HG22	4:D:6:ARG:H	1.82	0.44
4:D:117:GLU:HB3	4:D:119:ARG:O	2.17	0.44
5:E:21:ARG:HG3	5:E:266:GLN:HG3	1.98	0.44
17:Q:46:PHE:HB2	17:Q:139:ARG:HG2	1.99	0.44
1:A:53:G:C2	1:A:54:C:C2	3.05	0.44
1:A:657:A:H2'	1:A:658:U:O4'	2.16	0.44
1:A:949:A:N6	1:A:983:G:O2'	2.50	0.44
1:A:1009:C:H2'	1:A:1010:A:H8	1.82	0.44
1:A:1019:A:H1'	1:A:1732:A:N6	2.32	0.44
1:A:1031:G:H2'	1:A:1033:A:N7	2.32	0.44
1:A:1078:C:H2'	1:A:2703:U:N3	2.32	0.44
1:A:1090:G:H2'	1:A:1091:G:H8	1.80	0.44
1:A:1175:C:H2'	1:A:1176:C:O4'	2.16	0.44
1:A:1302:G:C4	1:A:1303:C:C5	3.05	0.44
1:A:2073:G:N2	1:A:2074:C:C2	2.86	0.44
1:A:2098:G:H2'	1:A:2099:C:C6	2.52	0.44
4:D:114:CYS:SG	4:D:115:ASN:N	2.90	0.44
5:E:79:ILE:HD12	5:E:321:LEU:HD12	1.99	0.44
5:E:280:TYR:CE1	5:E:351:VAL:HG21	2.52	0.44
11:K:10:CYS:HA	11:K:13:HIS:HD2	1.83	0.44
11:K:21:LEU:HD12	11:K:122:ALA:HB2	1.98	0.44
32:5:81:ASN:O	32:5:83:CYS:N	2.50	0.44
1:A:184:U:H3'	1:A:185:A:H5''	1.98	0.44
1:A:1875:A:H2'	1:A:1876:A:H8	1.81	0.44
1:A:2683:A:H2'	1:A:2684:G:O4'	2.17	0.44
1:A:2984:G:C2	1:A:2985:C:C2	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:37:A:O2'	3:C:38:G:C5'	2.65	0.44
10:J:160:VAL:HG11	10:J:186:LEU:HD13	1.98	0.44
12:L:92:ILE:HD11	12:L:139:ILE:HG12	1.99	0.44
13:M:20:PRO:HA	13:M:53:ALA:HA	1.98	0.44
13:M:68:LYS:HB3	13:M:71:LEU:HD23	1.99	0.44
23:W:48:LEU:O	23:W:52:ILE:HG23	2.16	0.44
25:Y:184:ALA:HA	25:Y:187:ILE:HG23	1.99	0.44
32:5:97:ARG:HB2	32:5:117:LEU:HD23	1.99	0.44
1:A:281:G:H2'	1:A:282:U:O4'	2.18	0.44
1:A:904:G:H5''	19:S:90:ARG:NH2	2.33	0.44
1:A:1432:A:N6	1:A:3219:U:H5''	2.32	0.44
1:A:1447:G:C6	1:A:1448:C:C4	3.05	0.44
1:A:2739:U:H2'	1:A:2740:A:H8	1.83	0.44
14:N:35:TYR:HB3	14:N:73:ARG:HG2	2.00	0.44
16:P:68:ARG:HA	16:P:98:LEU:HD21	1.99	0.44
32:5:67:GLU:O	32:5:71:ILE:HG12	2.17	0.44
32:5:115:LEU:HB3	32:5:117:LEU:HD13	2.00	0.44
32:5:127:LYS:HB2	32:5:208:PHE:CE2	2.52	0.44
1:A:113:C:O2	1:A:113:C:H2'	2.16	0.44
1:A:123:A:H3'	1:A:124:U:C5'	2.31	0.44
1:A:192:G:N1	1:A:193:C:C2	2.86	0.44
1:A:941:G:C2	1:A:942:C:C2	3.05	0.44
1:A:1435:G:H1'	1:A:1436:A:C8	2.52	0.44
1:A:3509:G:C6	1:A:3510:C:C5	3.05	0.44
2:B:57:C:H2'	2:B:58:A:C8	2.53	0.44
10:J:100:THR:HG21	10:J:198:LYS:HA	1.99	0.44
11:K:83:VAL:HG11	11:K:101:LEU:HD22	1.99	0.44
18:R:232:ALA:O	18:R:234:ASP:N	2.50	0.44
34:7:66:PHE:HE2	34:7:79:VAL:HG12	1.83	0.44
36:9:87:ARG:HG3	36:9:97:ILE:HG12	2.00	0.44
1:A:18:G:N2	3:C:149:C:C2	2.85	0.44
1:A:388:C:H2'	1:A:389:U:C6	2.51	0.44
1:A:453:A:H2'	1:A:454:G:O4'	2.18	0.44
1:A:1029:G:H2'	1:A:1030:C:O4'	2.17	0.44
1:A:1758:C:H2'	1:A:1759:A:C8	2.53	0.44
1:A:1817:G:C2	1:A:1818:C:C2	3.05	0.44
1:A:1913:A:N6	1:A:1956:U:H3	2.16	0.44
1:A:2487:G:N2	1:A:2488:C:C2	2.85	0.44
1:A:2681:U:O2	1:A:2681:U:H2'	2.16	0.44
1:A:2802:U:H2'	1:A:2803:A:C8	2.50	0.44
1:A:3748:U:H2'	1:A:3749:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:230:PRO:HD2	4:D:233:GLN:HB2	2.00	0.44
6:F:177:LYS:O	6:F:180:VAL:HG12	2.18	0.44
11:K:108:PRO:HB2	11:K:109:TYR:H	1.57	0.44
12:L:74:PHE:H	12:L:96:TYR:HA	1.82	0.44
12:L:92:ILE:HG22	12:L:93:GLY:N	2.32	0.44
19:S:28:LEU:CD1	29:2:11:GLU:HG3	2.46	0.44
21:U:151:LEU:O	21:U:153:LYS:N	2.50	0.44
36:9:109:GLY:O	36:9:111:SER:N	2.41	0.44
1:A:310:U:H5''	1:A:310:U:C6	2.53	0.44
1:A:600:U:H2'	1:A:601:G:C8	2.53	0.44
1:A:821:C:O2	1:A:821:C:H2'	2.18	0.44
1:A:897:U:P	31:4:33:LYS:HZ1	2.41	0.44
1:A:1876:A:H4'	1:A:1889:A:H4'	2.00	0.44
1:A:2028:G:H2'	1:A:2029:G:O4'	2.17	0.44
1:A:2487:G:C6	1:A:2488:C:C4	3.05	0.44
1:A:3038:G:C2	1:A:3095:C:C2	3.06	0.44
1:A:3646:G:H2'	1:A:3647:C:C6	2.53	0.44
1:A:3722:G:N2	1:A:3723:C:C2	2.86	0.44
5:E:17:LEU:HB3	5:E:18:PRO:CD	2.48	0.44
6:F:134:THR:HG22	6:F:150:VAL:HB	1.99	0.44
6:F:262:VAL:O	6:F:273:THR:HG22	2.17	0.44
7:G:43:GLN:N	7:G:43:GLN:HE21	2.16	0.44
10:J:193:PRO:HG3	10:J:236:LYS:HE3	1.98	0.44
10:J:203:LEU:HD23	10:J:206:LEU:HD12	2.00	0.44
16:P:171:LYS:HG2	16:P:176:ARG:HG3	2.00	0.44
34:7:21:THR:HB	34:7:80:ARG:HD2	1.99	0.44
1:A:730:G:O6	1:A:2654:A:C8	2.71	0.44
1:A:760:A:H2'	1:A:761:U:H6	1.83	0.44
1:A:807:U:O2'	1:A:877:G:H5''	2.18	0.44
1:A:1190:G:C2	1:A:1218:C:C2	3.06	0.44
1:A:1331:A:N3	1:A:3214:A:O2'	2.41	0.44
1:A:1429:A:H4'	1:A:1430:A:O5'	2.17	0.44
1:A:1587:U:H5'	6:F:76:ILE:HD12	1.98	0.44
1:A:1697:A:H2'	1:A:1698:A:O4'	2.18	0.44
1:A:2122:U:H2'	1:A:2123:C:C6	2.53	0.44
1:A:2954:A:H2'	1:A:2955:C:O4'	2.18	0.44
1:A:3008:A:H2'	1:A:3009:G:C8	2.53	0.44
1:A:3070:C:H2'	1:A:3071:A:O4'	2.18	0.44
1:A:3726:U:H4'	1:A:3727:A:C5'	2.47	0.44
4:D:32:LEU:HD11	4:D:163:ARG:HD3	1.99	0.44
4:D:201:GLY:HA2	4:D:204:MET:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:121:TRP:HA	16:P:131:TYR:CD2	2.53	0.44
19:S:100:CYS:HA	19:S:120:LEU:O	2.18	0.44
24:X:100:LYS:HE2	24:X:130:TYR:CD2	2.53	0.44
28:1:41:CYS:SG	28:1:77:VAL:HG12	2.58	0.44
32:5:97:ARG:HA	32:5:143:VAL:HG12	2.00	0.44
1:A:216:C:H2'	1:A:217:A:O4'	2.18	0.44
1:A:751:U:O3'	6:F:33:ARG:NH1	2.51	0.44
1:A:769:U:O2	1:A:769:U:O4'	2.36	0.44
1:A:2671:C:H2'	1:A:2672:U:C6	2.53	0.44
1:A:2707:G:C5	1:A:2708:C:C5	3.05	0.44
1:A:2938:C:H2'	1:A:2939:C:H6	1.83	0.44
1:A:3087:A:H1'	18:R:36:LEU:HD12	1.99	0.44
1:A:3782:A:H4'	1:A:3783:G:O5'	2.17	0.44
4:D:105:GLY:HA3	4:D:160:ALA:HB1	1.99	0.44
5:E:90:VAL:HG22	5:E:104:THR:HG22	1.99	0.44
5:E:148:ILE:HG22	5:E:189:LEU:HD11	2.00	0.44
9:I:173:ASP:HB3	9:I:176:VAL:HB	2.00	0.44
11:K:56:PHE:O	11:K:59:LEU:HG	2.18	0.44
1:A:249:U:H2'	1:A:250:U:H5'	1.99	0.43
1:A:795:G:C6	1:A:796:C:C4	3.06	0.43
1:A:876:C:C4	1:A:900:G:N1	2.86	0.43
1:A:1560:U:H2'	1:A:1561:C:C6	2.53	0.43
1:A:1863:A:H2'	1:A:1864:A:C8	2.53	0.43
1:A:3295:A:H2'	1:A:3296:G:C8	2.53	0.43
1:A:3531:C:H2'	1:A:3532:A:H8	1.83	0.43
1:A:3727:A:H5'	1:A:3727:A:C8	2.53	0.43
3:C:53:G:H2'	3:C:54:C:C6	2.52	0.43
3:C:138:U:H2'	3:C:139:A:H5''	2.00	0.43
10:J:169:VAL:CG2	10:J:203:LEU:HD21	2.48	0.43
16:P:7:ILE:HD11	16:P:46:ASP:CB	2.45	0.43
21:U:108:LYS:HB3	21:U:135:ILE:HD11	1.99	0.43
21:U:167:GLN:C	21:U:169:GLU:H	2.21	0.43
1:A:30:G:H2'	1:A:31:C:O4'	2.19	0.43
1:A:332:A:C6	1:A:333:A:N6	2.86	0.43
1:A:440:A:N1	1:A:707:U:C4	2.86	0.43
1:A:443:A:H2'	1:A:444:G:O4'	2.17	0.43
1:A:514:C:H6	1:A:514:C:H5''	1.83	0.43
1:A:539:G:N1	1:A:540:C:C4	2.85	0.43
1:A:1030:C:OP2	4:D:9:ARG:HG2	2.19	0.43
1:A:1441:G:H2'	1:A:1442:C:C6	2.54	0.43
1:A:1611:A:H2'	1:A:1612:U:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1691:G:C5	1:A:1692:C:C5	3.05	0.43
1:A:2489:C:C2	1:A:2540:G:C2	3.06	0.43
1:A:2717:A:H2'	1:A:2718:G:O4'	2.18	0.43
1:A:3268:A:H2'	1:A:3269:A:O4'	2.18	0.43
2:B:79:U:H2'	2:B:80:G:H8	1.83	0.43
4:D:158:ILE:HG22	4:D:159:ASP:N	2.33	0.43
8:H:45:ILE:HD11	8:H:54:ILE:HD12	2.00	0.43
8:H:92:ARG:HG2	8:H:142:GLU:HB3	1.99	0.43
1:A:348:C:N3	3:C:29:G:C2	2.87	0.43
1:A:365:C:C2	1:A:371:G:N2	2.86	0.43
1:A:1230:A:O2'	1:A:1231:A:C5'	2.67	0.43
1:A:1574:C:H4'	1:A:1575:C:OP1	2.18	0.43
1:A:1647:U:H2'	1:A:1648:U:C6	2.54	0.43
1:A:1696:A:H2'	1:A:1697:A:C8	2.53	0.43
1:A:1762:A:N1	1:A:2090:U:O4	2.52	0.43
1:A:1817:G:H2'	1:A:1818:C:C6	2.53	0.43
1:A:3393:C:H2'	1:A:3394:A:C8	2.53	0.43
1:A:3397:A:H4'	1:A:3398:A:H4'	2.00	0.43
1:A:3493:G:N2	1:A:3494:C:C2	2.86	0.43
7:G:100:GLY:HA3	7:G:154:VAL:HG23	2.00	0.43
33:6:90:ILE:O	33:6:91:SER:HB2	2.18	0.43
1:A:328:G:C2	1:A:329:C:C2	3.06	0.43
1:A:441:A:C2	1:A:442:G:C4	3.06	0.43
1:A:682:A:OP1	6:F:316:LYS:HD3	2.18	0.43
1:A:1078:C:H2'	1:A:2703:U:H3	1.83	0.43
1:A:1423:G:H2'	1:A:1424:C:H6	1.83	0.43
1:A:1621:U:H5'	20:T:3:LEU:HB2	1.99	0.43
1:A:2568:A:H2'	1:A:2569:G:O4'	2.19	0.43
1:A:3215:G:H2'	1:A:3216:C:C6	2.53	0.43
1:A:3653:G:C5'	14:N:140:LYS:HB3	2.48	0.43
1:A:3668:U:O4	36:9:95:VAL:HG11	2.19	0.43
1:A:3764:G:C2	1:A:3765:C:C2	3.07	0.43
2:B:40:A:H5'	7:G:43:GLN:HG3	2.00	0.43
2:B:63:A:N7	17:Q:202:GLU:HG3	2.34	0.43
3:C:36:C:C2'	3:C:37:A:H5'	2.48	0.43
3:C:43:G:OP2	3:C:43:G:H8	2.01	0.43
5:E:37:LYS:O	5:E:183:GLY:HA2	2.18	0.43
14:N:17:LYS:HG3	14:N:17:LYS:O	2.18	0.43
18:R:124:LYS:HB3	18:R:125:VAL:H	1.59	0.43
19:S:50:LYS:O	19:S:54:MET:HG3	2.19	0.43
21:U:39:PHE:CD2	21:U:112:ILE:HG13	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:5:36:ALA:O	32:5:39:ILE:HG22	2.17	0.43
35:8:76:VAL:HG11	35:8:82:MET:HG2	1.99	0.43
1:A:91:G:O2'	1:A:95:A:N6	2.52	0.43
1:A:596:A:H5'	8:H:7:THR:HG21	2.01	0.43
1:A:1568:C:OP1	3:C:24:U:H5''	2.17	0.43
1:A:2073:G:C6	1:A:2074:C:C4	3.05	0.43
1:A:2166:G:N2	1:A:2631:C:C2	2.86	0.43
1:A:2814:U:H2'	1:A:2815:G:H8	1.84	0.43
1:A:3006:A:H2'	1:A:3007:A:O4'	2.18	0.43
1:A:3045:G:C2	1:A:3046:C:C2	3.07	0.43
1:A:3114:G:C6	1:A:3115:C:C4	3.06	0.43
1:A:3195:C:H5	1:A:3211:C:N4	2.06	0.43
1:A:3195:C:O2	1:A:3195:C:O4'	2.35	0.43
1:A:3424:U:H2'	1:A:3425:G:O4'	2.18	0.43
1:A:3447:A:H2'	1:A:3448:U:O4'	2.19	0.43
1:A:3450:G:H2'	1:A:3451:G:O4'	2.18	0.43
1:A:3473:G:C5	1:A:3474:C:C5	3.06	0.43
1:A:3491:U:H2'	1:A:3492:G:C8	2.53	0.43
1:A:3668:U:H5''	36:9:101:TRP:CZ2	2.52	0.43
1:A:3677:A:H2'	1:A:3678:A:H8	1.82	0.43
1:A:3751:A:N6	1:A:3752:C:N4	2.66	0.43
4:D:182:ALA:HB1	4:D:196:TRP:HH2	1.84	0.43
18:R:148:LEU:HD13	18:R:165:LEU:HB2	2.01	0.43
22:V:70:LYS:HG2	22:V:71:ARG:HH11	1.83	0.43
32:5:139:VAL:O	32:5:143:VAL:HG22	2.19	0.43
1:A:31:C:O2	1:A:31:C:H2'	2.17	0.43
1:A:811:A:C8	15:O:136:LYS:HE2	2.53	0.43
1:A:1033:A:N7	4:D:199:VAL:HG21	2.33	0.43
1:A:1465:G:C5	1:A:1466:C:C5	3.06	0.43
1:A:1562:G:H2'	1:A:1563:U:O4'	2.18	0.43
1:A:1608:C:H2'	1:A:1609:A:C8	2.53	0.43
1:A:1805:U:H6	1:A:1805:U:H5''	1.84	0.43
1:A:2218:C:H2'	1:A:2219:A:H5'	2.01	0.43
1:A:2946:G:H4'	4:D:232:GLY:HA3	2.01	0.43
1:A:2948:A:H2'	1:A:2949:G:C8	2.54	0.43
2:B:45:U:H2'	2:B:46:C:O4'	2.18	0.43
3:C:18:U:C4	3:C:19:G:C6	3.06	0.43
3:C:103:G:C4	3:C:104:C:C5	3.06	0.43
7:G:95:ASN:HB2	7:G:103:GLY:O	2.17	0.43
16:P:185:SER:HB2	16:P:189:ILE:HG12	2.01	0.43
21:U:47:LYS:HE3	21:U:67:LEU:HD22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:384:A:H1'	26:Z:86:ARG:NH2	2.33	0.43
1:A:394:A:H2'	1:A:395:A:H8	1.84	0.43
1:A:1045:A:H2'	1:A:1046:A:O4'	2.18	0.43
1:A:1466:C:H2'	1:A:1467:C:H6	1.83	0.43
1:A:1642:G:H8	1:A:2102:A:H61	1.66	0.43
1:A:1768:A:H2'	1:A:1769:U:H5'	2.01	0.43
1:A:1827:C:H2'	1:A:1828:G:H8	1.83	0.43
1:A:2566:G:N2	1:A:2604:G:H2'	2.33	0.43
1:A:2657:G:H22	1:A:2689:G:H1'	1.83	0.43
1:A:3053:G:H4'	1:A:3054:A:H5''	1.99	0.43
1:A:3253:G:N1	1:A:3267:C:C4	2.87	0.43
3:C:109:U:H4'	3:C:110:G:H5''	2.01	0.43
4:D:5:ILE:HG22	4:D:6:ARG:N	2.34	0.43
32:5:93:VAL:HG21	32:5:145:TYR:HD2	1.82	0.43
35:8:96:ILE:HG21	35:8:105:ARG:HG2	2.00	0.43
36:9:77:TYR:HA	36:9:80:LYS:HD3	2.01	0.43
1:A:18:G:C2	3:C:149:C:C2	3.06	0.43
1:A:114:A:H2'	1:A:115:A:O4'	2.19	0.43
1:A:440:A:C2	1:A:441:A:C6	3.06	0.43
1:A:539:G:C4	1:A:540:C:C5	3.06	0.43
1:A:773:A:O2'	1:A:774:A:C8	2.43	0.43
1:A:882:G:H1	1:A:891:C:H42	1.65	0.43
1:A:1597:U:O2	1:A:1597:U:H2'	2.18	0.43
1:A:2034:G:O2'	1:A:2081:U:H5'	2.18	0.43
1:A:2123:C:H2'	1:A:2124:C:C6	2.53	0.43
1:A:2702:G:H3'	1:A:2703:U:H4'	1.99	0.43
1:A:2732:A:H2'	1:A:2733:A:H8	1.81	0.43
1:A:2937:G:C6	1:A:2938:C:N4	2.87	0.43
1:A:3509:G:C5	1:A:3510:C:C5	3.07	0.43
4:D:193:ARG:CG	4:D:193:ARG:NH1	2.82	0.43
10:J:282:LYS:O	10:J:283:LEU:HB2	2.19	0.43
18:R:150:VAL:HG23	18:R:161:VAL:HG21	2.01	0.43
28:1:87:VAL:HG13	28:1:90:ASP:HB2	2.00	0.43
1:A:136:U:O2	1:A:136:U:O4'	2.36	0.43
1:A:439:U:C2	1:A:440:A:C8	3.07	0.43
1:A:450:A:H5''	1:A:451:C:H5'	2.01	0.43
1:A:502:U:H3'	9:I:144:LYS:HZ1	1.84	0.43
1:A:507:G:H2'	1:A:508:A:H8	1.83	0.43
1:A:974:U:H2'	1:A:975:G:C8	2.54	0.43
1:A:1002:A:H5'	23:W:133:HIS:HA	2.01	0.43
1:A:1094:U:H4'	19:S:58:TYR:CE1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1845:C:H5'	20:T:58:SER:HA	2.01	0.43
1:A:2440:A:H2'	1:A:2441:U:O4'	2.19	0.43
1:A:2719:U:N3	1:A:2720:C:C5	2.87	0.43
1:A:2926:A:H2'	1:A:2927:U:C6	2.54	0.43
1:A:3065:C:H3'	1:A:3067:G:H21	1.84	0.43
1:A:3114:G:N2	1:A:3115:C:C2	2.86	0.43
1:A:3159:G:N7	15:O:42:ARG:NH1	2.67	0.43
1:A:3784:U:H2'	1:A:3785:G:H8	1.79	0.43
3:C:79:G:H2'	3:C:80:C:C6	2.54	0.43
11:K:34:ALA:HB3	11:K:103:VAL:HG12	2.00	0.43
26:Z:65:ARG:HH22	26:Z:83:ARG:HB3	1.84	0.43
1:A:30:G:C5	1:A:31:C:C5	3.07	0.43
1:A:81:C:C2	1:A:105:G:C2	3.07	0.43
1:A:125:C:H2'	1:A:126:C:C6	2.53	0.43
1:A:192:G:C4	1:A:193:C:C6	3.07	0.43
1:A:298:C:OP1	16:P:68:ARG:HD2	2.18	0.43
1:A:437:A:H61	1:A:709:A:H61	1.66	0.43
1:A:686:U:H2'	1:A:687:G:H8	1.82	0.43
1:A:732:C:H2'	1:A:733:C:C6	2.54	0.43
1:A:859:C:C3'	1:A:860:A:H8	2.32	0.43
1:A:1308:A:OP1	36:9:110:ASN:HB2	2.19	0.43
1:A:1474:A:H2'	1:A:1475:G:H8	1.84	0.43
1:A:1550:A:H2'	1:A:1551:C:H6	1.84	0.43
1:A:1643:U:O4'	1:A:1644:U:C5	2.72	0.43
1:A:1911:A:H2'	1:A:1912:A:C8	2.53	0.43
1:A:3493:G:C2	1:A:3511:C:N3	2.87	0.43
1:A:3521:G:N1	1:A:3522:C:C2	2.87	0.43
6:F:218:LYS:O	6:F:222:ARG:HG3	2.18	0.43
14:N:29:ARG:HG3	14:N:29:ARG:HH11	1.84	0.43
21:U:151:LEU:C	21:U:153:LYS:N	2.72	0.43
25:Y:140:LYS:O	25:Y:143:ILE:HG22	2.19	0.43
25:Y:183:VAL:O	25:Y:187:ILE:CG2	2.62	0.43
1:A:225:U:H4'	26:Z:99:HIS:CG	2.54	0.42
1:A:277:U:H2'	1:A:278:C:C6	2.54	0.42
1:A:416:G:H1'	3:C:20:G:N2	2.33	0.42
1:A:422:G:H5'	23:W:26:PHE:HZ	1.84	0.42
1:A:539:G:C2	1:A:540:C:C2	3.07	0.42
1:A:638:G:C5	1:A:639:C:C5	3.07	0.42
1:A:1235:C:H2'	1:A:1236:U:C6	2.53	0.42
1:A:1447:G:N2	1:A:1448:C:C2	2.87	0.42
1:A:1579:U:H2'	15:O:9:ARG:NH2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1886:A:C6	33:6:52:PRO:HD3	2.54	0.42
1:A:2084:U:H6	1:A:2084:U:H5''	1.83	0.42
1:A:2455:G:C5	1:A:2456:C:C4	3.07	0.42
1:A:2723:G:C4	1:A:2724:C:C5	3.07	0.42
2:B:86:G:C2	2:B:92:C:C2	3.07	0.42
5:E:89:ILE:HG22	5:E:155:LEU:HD22	2.01	0.42
6:F:314:GLN:HE21	6:F:314:GLN:HA	1.84	0.42
6:F:364:GLN:O	6:F:368:LEU:HG	2.18	0.42
14:N:61:ILE:H	14:N:61:ILE:HG13	1.66	0.42
15:O:76:ASP:HB2	15:O:114:GLY:HA3	2.01	0.42
19:S:166:VAL:HG12	19:S:167:ARG:H	1.84	0.42
24:X:70:VAL:O	24:X:71:ASP:C	2.56	0.42
30:3:49:VAL:O	30:3:53:VAL:HG23	2.19	0.42
1:A:517:U:H2'	1:A:518:G:O4'	2.18	0.42
1:A:519:A:H5''	32:5:224:ARG:HH21	1.83	0.42
1:A:583:U:C6	1:A:583:U:H5''	2.54	0.42
1:A:607:A:C2'	1:A:608:A:C8	2.74	0.42
1:A:684:G:H5''	6:F:313:LEU:HB3	2.01	0.42
1:A:1186:A:C6	22:V:110:LYS:HG2	2.54	0.42
1:A:1286:A:H4'	1:A:1460:A:H1'	2.00	0.42
1:A:1699:G:H2'	1:A:1700:U:O4'	2.19	0.42
1:A:2470:A:H4'	1:A:2473:A:H1'	2.00	0.42
1:A:2680:A:H2'	1:A:2681:U:O4'	2.19	0.42
1:A:3205:U:O2	1:A:3205:U:O4'	2.37	0.42
1:A:3722:G:C2	1:A:3723:C:C2	3.07	0.42
3:C:53:G:H2'	3:C:54:C:O4'	2.19	0.42
8:H:139:VAL:HG13	8:H:140:LYS:N	2.33	0.42
10:J:110:LEU:HD11	10:J:197:VAL:HG11	2.00	0.42
14:N:71:LEU:HG	21:U:162:HIS:CE1	2.54	0.42
36:9:36:GLN:O	36:9:37:ALA:HB3	2.19	0.42
1:A:224:G:N2	1:A:233:C:C2	2.87	0.42
1:A:299:A:H2'	1:A:300:C:O4'	2.20	0.42
1:A:542:A:N3	1:A:544:C:H1'	2.34	0.42
1:A:1191:G:H5''	1:A:1191:G:H8	1.84	0.42
1:A:1494:U:H2'	1:A:1495:U:C6	2.54	0.42
1:A:1503:A:H4'	1:A:1504:A:OP2	2.18	0.42
1:A:3215:G:N2	1:A:3216:C:C2	2.88	0.42
1:A:3252:G:H2'	1:A:3253:G:O4'	2.20	0.42
1:A:3550:U:H2'	1:A:3551:U:H6	1.84	0.42
1:A:3712:G:H3'	1:A:3713:C:C6	2.54	0.42
22:V:143:LYS:HA	32:5:83:CYS:CB	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:8:85:LEU:HD21	35:8:94:VAL:HG12	2.01	0.42
1:A:580:A:H2'	1:A:581:C:H6	1.84	0.42
1:A:734:A:H2'	1:A:735:A:H8	1.84	0.42
1:A:1513:U:H5''	19:S:3:ILE:HG21	2.01	0.42
1:A:2081:U:H2'	1:A:2082:C:O4'	2.19	0.42
1:A:2158:U:H2'	1:A:2159:A:H8	1.85	0.42
5:E:321:LEU:HD11	5:E:335:LEU:HD21	2.01	0.42
6:F:318:SER:HB2	32:5:158:TYR:HD2	1.84	0.42
9:I:31:LYS:HB2	9:I:35:GLY:O	2.19	0.42
20:T:3:LEU:HD21	20:T:28:ILE:HG23	2.02	0.42
21:U:21:ARG:HD2	21:U:31:PRO:HG2	2.02	0.42
21:U:88:LEU:HD11	21:U:115:LEU:CD1	2.34	0.42
32:5:107:LYS:O	32:5:111:VAL:HG23	2.19	0.42
36:9:108:HIS:O	36:9:113:VAL:HG23	2.19	0.42
1:A:178:U:H2'	1:A:179:G:H5'	2.01	0.42
1:A:539:G:H2'	1:A:540:C:C6	2.54	0.42
1:A:1530:G:H2'	1:A:1531:G:C8	2.55	0.42
1:A:2110:C:H2'	1:A:2111:C:C6	2.53	0.42
1:A:2185:C:H2'	1:A:2186:C:O4'	2.19	0.42
1:A:3094:C:H2'	1:A:3095:C:C6	2.54	0.42
1:A:3263:G:H2'	1:A:3264:U:H6	1.85	0.42
1:A:3306:G:H2'	1:A:3307:C:H6	1.85	0.42
1:A:3435:A:C8	5:E:53:MET:HE2	2.54	0.42
1:A:3702:C:H3'	1:A:3703:G:H21	1.84	0.42
1:A:3749:U:O5'	1:A:3749:U:H6	2.03	0.42
2:B:73:U:H5''	2:B:74:A:H2'	2.02	0.42
3:C:90:G:H4'	3:C:91:A:OP2	2.20	0.42
5:E:37:LYS:CA	5:E:183:GLY:HA2	2.50	0.42
7:G:148:ILE:HG23	7:G:152:HIS:HB3	1.99	0.42
19:S:65:SER:HA	19:S:91:LEU:HD11	2.00	0.42
30:3:94:LEU:HB3	30:3:98:GLN:HE21	1.84	0.42
32:5:149:THR:O	32:5:153:VAL:HG23	2.19	0.42
34:7:57:VAL:HG12	34:7:99:THR:HG23	2.00	0.42
1:A:107:C:H2'	1:A:108:C:O4'	2.19	0.42
1:A:393:G:H2'	1:A:394:A:O4'	2.19	0.42
1:A:733:C:C2	1:A:1590:G:N2	2.87	0.42
1:A:1057:C:H3'	15:O:26:ARG:HH12	1.84	0.42
1:A:1110:U:N3	1:A:1184:A:H2	2.09	0.42
1:A:1268:G:C6	1:A:1269:C:N4	2.88	0.42
1:A:1454:A:H2'	1:A:1455:C:O4'	2.20	0.42
1:A:2068:G:C2	1:A:2069:C:C2	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2137:C:OP1	1:A:3462:A:H4'	2.19	0.42
1:A:2218:C:H2'	1:A:2218:C:O2	2.19	0.42
1:A:2487:G:C4	1:A:2488:C:C5	3.07	0.42
1:A:2995:A:N6	1:A:3052:U:C2	2.79	0.42
1:A:3467:U:C2'	1:A:3468:G:H5'	2.50	0.42
9:I:61:ILE:HG21	9:I:208:PHE:HB3	2.01	0.42
9:I:142:ILE:H	9:I:142:ILE:HG13	1.69	0.42
10:J:55:ILE:O	10:J:57:VAL:N	2.52	0.42
16:P:136:VAL:HG11	16:P:152:ILE:CG2	2.44	0.42
22:V:45:CYS:SG	22:V:54:PRO:HG2	2.60	0.42
24:X:54:ILE:H	24:X:54:ILE:HG13	1.68	0.42
33:6:9:ALA:O	33:6:13:ILE:HG12	2.19	0.42
1:A:66:A:H5''	12:L:99:ARG:NH2	2.35	0.42
1:A:656:U:O4	1:A:657:A:N6	2.53	0.42
1:A:897:U:H2'	1:A:898:G:C8	2.55	0.42
1:A:940:A:H2'	1:A:941:G:H8	1.84	0.42
1:A:1045:A:H2'	1:A:1046:A:C8	2.55	0.42
1:A:1522:A:H2'	1:A:1523:A:H8	1.85	0.42
1:A:1817:G:H22	1:A:2009:A:H2	1.66	0.42
1:A:2112:G:H5'	1:A:2113:C:C5'	2.45	0.42
1:A:3065:C:C4	1:A:3067:G:C6	3.08	0.42
1:A:3088:G:C4	1:A:3089:C:C5	3.08	0.42
1:A:3258:C:O2'	1:A:3260:G:OP2	2.37	0.42
1:A:3373:A:H2'	1:A:3374:U:C6	2.54	0.42
1:A:3493:G:C5	1:A:3494:C:C5	3.08	0.42
1:A:3505:U:H5''	1:A:3506:U:H5'	2.01	0.42
3:C:97:C:O2'	3:C:98:A:H8	2.03	0.42
5:E:50:LYS:HB2	5:E:333:ILE:HD11	2.02	0.42
6:F:19:VAL:HB	6:F:20:GLY:H	1.70	0.42
15:O:3:THR:HA	15:O:6:LYS:HG3	2.01	0.42
18:R:125:VAL:CG1	18:R:195:ARG:HG3	2.50	0.42
36:9:41:TYR:HB3	36:9:134:LEU:HD13	2.01	0.42
1:A:63:A:H2	1:A:78:U:O2	2.03	0.42
1:A:297:G:H2'	1:A:298:C:H6	1.85	0.42
1:A:1277:G:C2	1:A:1283:C:N3	2.88	0.42
1:A:1674:G:C6	1:A:1675:C:N4	2.88	0.42
1:A:1827:C:H2'	1:A:1828:G:C8	2.54	0.42
1:A:2527:G:C4	1:A:2528:C:C6	3.07	0.42
1:A:3031:C:H2'	1:A:3032:U:O4'	2.20	0.42
1:A:3382:U:O2	1:A:3382:U:C2'	2.65	0.42
1:A:3493:G:C6	1:A:3494:C:C5	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:28:C:H5''	7:G:137:ARG:HD3	2.01	0.42
3:C:79:G:H2'	3:C:80:C:H6	1.85	0.42
14:N:110:LEU:O	14:N:113:LYS:HG2	2.20	0.42
19:S:74:HIS:HA	19:S:75:PRO:HD3	1.94	0.42
21:U:71:GLU:CG	32:5:79:ARG:HH22	2.33	0.42
35:8:98:HIS:HA	35:8:105:ARG:HH22	1.84	0.42
1:A:514:C:C2	1:A:515:A:C8	3.07	0.42
1:A:935:A:H1'	1:A:938:U:O4	2.20	0.42
1:A:1467:C:O2'	35:8:55:ILE:O	2.30	0.42
1:A:2177:A:H2'	1:A:2178:A:H8	1.83	0.42
1:A:2494:G:C4	1:A:2495:C:C6	3.08	0.42
1:A:2519:U:H2'	1:A:2520:C:O4'	2.20	0.42
1:A:3064:U:H4'	22:V:6:ARG:HD2	2.01	0.42
1:A:3077:A:H2'	1:A:3078:A:H8	1.84	0.42
1:A:3139:C:O2	1:A:3139:C:O4'	2.36	0.42
1:A:3247:U:C5	1:A:3269:A:C6	3.07	0.42
3:C:96:U:H2'	3:C:97:C:O4'	2.20	0.42
6:F:92:PHE:HA	6:F:99:GLY:HA2	2.02	0.42
6:F:316:LYS:H	32:5:177:GLN:NE2	2.17	0.42
10:J:176:PRO:HD2	10:J:179:LEU:HD23	2.02	0.42
17:Q:91:ILE:HG13	17:Q:127:ALA:HB1	2.02	0.42
21:U:23:ILE:HG23	22:V:137:LYS:HZ1	1.85	0.42
32:5:53:LEU:HD11	32:5:193:GLY:HA3	2.02	0.42
34:7:36:LYS:HG2	34:7:75:PRO:HD2	2.01	0.42
1:A:732:C:C2	1:A:733:C:C5	3.08	0.42
1:A:830:U:O2	1:A:830:U:O4'	2.38	0.42
1:A:866:C:O2	19:S:139:ARG:HD3	2.20	0.42
1:A:929:G:C6	1:A:930:C:N4	2.87	0.42
1:A:1103:A:C6	1:A:1231:A:C2	3.08	0.42
1:A:1289:G:N2	1:A:1467:C:C2	2.88	0.42
1:A:1314:G:H2'	1:A:1315:C:O4'	2.20	0.42
1:A:1476:A:N3	1:A:1476:A:C5'	2.73	0.42
1:A:1993:A:O2'	1:A:1994:U:H5'	2.20	0.42
1:A:3085:A:H1'	18:R:162:PHE:CE1	2.54	0.42
1:A:3493:G:C2	1:A:3494:C:C6	3.08	0.42
1:A:3700:G:H2'	1:A:3701:A:H5''	2.02	0.42
1:A:3717:A:H2'	1:A:3718:G:H8	1.83	0.42
3:C:17:A:O2'	23:W:120:ASN:HB3	2.19	0.42
14:N:25:VAL:HG11	14:N:71:LEU:HD21	2.02	0.42
24:X:55:LEU:HD23	24:X:55:LEU:HA	1.89	0.42
36:9:134:LEU:HG	36:9:136:TYR:CZ	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:721:U:H5''	1:A:1072:A:C2	2.54	0.41
1:A:1233:A:H2'	1:A:1234:A:H8	1.83	0.41
1:A:1484:A:H2'	1:A:1485:A:H8	1.85	0.41
1:A:3016:G:H2'	1:A:3018:A:C2	2.54	0.41
1:A:3065:C:C2	1:A:3067:G:N2	2.88	0.41
1:A:3296:G:H2'	1:A:3297:G:O4'	2.20	0.41
1:A:3630:U:H2'	1:A:3631:U:C6	2.55	0.41
2:B:74:A:N1	2:B:100:A:H5'	2.34	0.41
4:D:205:ASN:HB3	4:D:206:PRO:HD2	2.01	0.41
12:L:7:VAL:HG22	19:S:165:TYR:HB3	2.02	0.41
12:L:66:PHE:HE2	15:O:108:PHE:CZ	2.38	0.41
18:R:38:LEU:HD13	22:V:31:TYR:CD1	2.55	0.41
18:R:199:LEU:HD12	18:R:236:GLU:HG3	2.01	0.41
36:9:84:TYR:HB3	36:9:100:ILE:HG13	2.02	0.41
1:A:87:U:H2'	1:A:88:A:H8	1.85	0.41
1:A:546:C:N3	21:U:80:ARG:NH2	2.68	0.41
1:A:1346:U:O2	1:A:1346:U:H2'	2.19	0.41
1:A:1542:A:OP1	35:8:98:HIS:NE2	2.51	0.41
1:A:1543:G:C5	1:A:1544:C:C5	3.09	0.41
1:A:1681:C:C2	1:A:1734:G:N2	2.87	0.41
1:A:2017:U:H5''	1:A:2018:G:H5'	2.03	0.41
1:A:2716:U:H2'	1:A:2717:A:C8	2.54	0.41
1:A:2951:U:H2'	1:A:2952:U:O4'	2.21	0.41
1:A:3616:U:H3'	1:A:3617:A:C5'	2.49	0.41
3:C:60:G:C5	3:C:61:C:C5	3.08	0.41
9:I:110:ASN:HD22	9:I:112:PHE:H	1.67	0.41
15:O:82:LEU:HD21	15:O:100:ILE:HD11	2.01	0.41
20:T:73:ARG:HA	20:T:73:ARG:HD3	1.66	0.41
21:U:83:ASN:HD21	21:U:152:LEU:HD21	1.84	0.41
22:V:114:ALA:HA	22:V:117:ILE:HD12	2.02	0.41
34:7:16:VAL:H	34:7:85:ARG:HB3	1.85	0.41
1:A:209:G:C6	1:A:210:C:N4	2.88	0.41
1:A:1441:G:C4	1:A:1442:C:C5	3.08	0.41
1:A:1913:A:N1	1:A:1956:U:C2	2.88	0.41
1:A:1999:A:H2'	1:A:2000:G:C8	2.55	0.41
1:A:2703:U:O4	1:A:3160:A:C2	2.65	0.41
1:A:3045:G:H2'	1:A:3046:C:C6	2.55	0.41
1:A:3198:G:C2	1:A:3199:C:C2	3.08	0.41
7:G:16:LYS:O	7:G:129:VAL:O	2.38	0.41
10:J:109:LEU:O	10:J:113:LEU:HD22	2.19	0.41
12:L:7:VAL:CG2	19:S:165:TYR:HB3	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:5:233:ALA:HB2	32:5:242:TRP:CZ2	2.55	0.41
1:A:122:A:N7	1:A:155:U:H5	2.18	0.41
1:A:309:G:H2'	1:A:310:U:H6	1.85	0.41
1:A:356:A:N3	1:A:360:A:O2'	2.53	0.41
1:A:744:G:C5	1:A:745:C:C5	3.08	0.41
1:A:752:G:H2'	1:A:753:C:C6	2.55	0.41
1:A:1191:G:H1	1:A:1216:C:H42	1.68	0.41
1:A:1235:C:H2'	1:A:1236:U:H6	1.85	0.41
1:A:1245:G:H2'	1:A:1246:C:C6	2.54	0.41
1:A:2416:G:N2	1:A:2624:C:C2	2.89	0.41
1:A:2549:A:N3	1:A:2549:A:C2'	2.81	0.41
1:A:2934:A:H3'	1:A:2935:U:H6	1.86	0.41
1:A:3235:C:C1'	1:A:3311:G:N2	2.71	0.41
1:A:3306:G:H2'	1:A:3307:C:C6	2.55	0.41
1:A:3658:G:C4'	1:A:3659:C:OP1	2.65	0.41
9:I:111:ILE:HG12	9:I:200:PHE:HZ	1.86	0.41
10:J:103:LYS:O	10:J:106:THR:HG22	2.20	0.41
20:T:105:LEU:HB3	20:T:119:TYR:CE2	2.55	0.41
23:W:17:GLY:HA3	23:W:98:VAL:HG22	2.02	0.41
29:2:32:LEU:HD12	29:2:42:ASN:HA	2.03	0.41
31:4:38:ASN:O	31:4:41:ARG:HG2	2.21	0.41
1:A:328:G:C2	1:A:329:C:C6	3.08	0.41
1:A:328:G:N3	1:A:329:C:C6	2.89	0.41
1:A:501:U:O2'	1:A:502:U:P	2.79	0.41
1:A:1019:A:H2'	1:A:1020:C:H6	1.86	0.41
1:A:1184:A:C2	1:A:1185:A:C6	3.08	0.41
1:A:1230:A:O2'	1:A:1231:A:H5'	2.20	0.41
1:A:1722:C:H2'	1:A:1723:C:O4'	2.20	0.41
1:A:2677:A:H61	11:K:95:GLN:HE22	1.69	0.41
1:A:2950:U:H2'	1:A:2951:U:H6	1.85	0.41
1:A:3303:U:H1'	5:E:248:CYS:SG	2.60	0.41
2:B:56:G:H2'	2:B:56:G:N3	2.35	0.41
5:E:50:LYS:HB2	5:E:333:ILE:HD12	2.01	0.41
6:F:183:LEU:HD22	6:F:226:GLY:HA3	2.03	0.41
19:S:166:VAL:HG12	19:S:167:ARG:N	2.35	0.41
25:Y:143:ILE:HD12	25:Y:143:ILE:HA	1.83	0.41
31:4:21:ILE:O	31:4:21:ILE:HG12	2.20	0.41
33:6:37:LEU:HD13	33:6:62:TYR:HB3	2.02	0.41
36:9:53:GLN:O	36:9:54:ARG:CG	2.66	0.41
1:A:26:A:H2'	1:A:27:U:H6	1.85	0.41
1:A:498:U:O2	1:A:498:U:H2'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:603:G:H2'	1:A:604:G:O4'	2.20	0.41
1:A:607:A:H4'	1:A:608:A:OP1	2.20	0.41
1:A:860:A:H2'	1:A:861:C:H6	1.86	0.41
1:A:870:C:H4'	31:4:27:HIS:CG	2.56	0.41
1:A:1184:A:N1	1:A:1185:A:N6	2.69	0.41
1:A:1865:C:H2'	1:A:1866:C:H6	1.85	0.41
1:A:2832:A:N3	1:A:2832:A:C2'	2.80	0.41
1:A:3572:A:N3	1:A:3572:A:C2'	2.83	0.41
2:B:77:A:H2'	2:B:78:C:O4'	2.21	0.41
6:F:209:ILE:HG13	6:F:251:ILE:HB	2.03	0.41
13:M:95:ILE:HG12	27:0:27:LYS:HB3	2.02	0.41
14:N:30:LEU:HB3	14:N:77:LEU:HB2	2.03	0.41
21:U:51:TRP:CE3	21:U:51:TRP:HA	2.54	0.41
21:U:84:TYR:CE1	21:U:108:LYS:HG2	2.56	0.41
26:Z:50:ARG:HB3	26:Z:51:LYS:H	1.74	0.41
33:6:46:ILE:HD11	33:6:80:LEU:HD21	2.02	0.41
34:7:31:VAL:CG2	34:7:39:ARG:HD2	2.50	0.41
34:7:45:ARG:HG3	34:7:57:VAL:HG21	2.03	0.41
1:A:192:G:N2	1:A:193:C:H1'	2.36	0.41
1:A:422:G:H2'	1:A:423:U:C6	2.56	0.41
1:A:438:U:H2'	1:A:439:U:O4'	2.21	0.41
1:A:539:G:C6	1:A:540:C:C4	3.08	0.41
1:A:879:U:C2	1:A:880:A:C8	3.08	0.41
1:A:1029:G:C5	1:A:1030:C:C5	3.09	0.41
1:A:1462:C:H2'	1:A:1463:A:C8	2.56	0.41
1:A:1640:G:H2'	1:A:1641:G:O4'	2.20	0.41
1:A:1818:C:H5''	20:T:95:ILE:CD1	2.49	0.41
1:A:2208:G:N2	1:A:3754:A:C8	2.81	0.41
1:A:2494:G:H2'	1:A:2495:C:O4'	2.20	0.41
1:A:2689:G:C2	1:A:3344:C:N3	2.88	0.41
1:A:2717:A:H5'	16:P:89:VAL:CG2	2.51	0.41
1:A:2813:U:H2'	1:A:2814:U:C6	2.56	0.41
1:A:2943:U:O4	1:A:2944:G:C6	2.74	0.41
1:A:3114:G:C4	1:A:3115:C:C5	3.08	0.41
1:A:3190:G:H2'	1:A:3191:C:C6	2.56	0.41
1:A:3300:A:OP2	1:A:3300:A:H8	2.03	0.41
3:C:3:G:N2	3:C:4:C:C2	2.89	0.41
4:D:117:GLU:HG2	4:D:124:GLY:N	2.35	0.41
9:I:61:ILE:HD12	9:I:71:ARG:HG2	2.02	0.41
13:M:27:CYS:O	13:M:29:ASP:N	2.54	0.41
16:P:47:LYS:O	16:P:51:LEU:HD22	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:92:HIS:HA	17:Q:93:PRO:HD3	1.96	0.41
32:5:250:ASN:HA	32:5:253:ILE:HD12	2.03	0.41
35:8:85:LEU:HD13	35:8:117:VAL:HG21	2.03	0.41
1:A:539:G:C2	1:A:540:C:C4	3.08	0.41
1:A:589:C:H2'	1:A:590:C:C6	2.56	0.41
1:A:1191:G:C2	1:A:1192:C:N3	2.89	0.41
1:A:1240:A:H2'	1:A:1241:G:C8	2.55	0.41
1:A:2403:G:H5''	1:A:3756:C:H5'	2.02	0.41
1:A:2496:U:H2'	1:A:2497:U:C6	2.55	0.41
1:A:2990:G:H5''	1:A:2991:U:C1'	2.50	0.41
1:A:3045:G:C6	1:A:3046:C:N4	2.89	0.41
1:A:3307:C:H5'	5:E:241:ARG:HG3	2.03	0.41
1:A:3484:U:HO2'	1:A:3485:G:H8	1.67	0.41
3:C:103:G:N1	3:C:104:C:C4	2.88	0.41
19:S:51:ARG:HD2	19:S:82:VAL:HG21	2.01	0.41
1:A:79:U:H2'	1:A:80:C:H6	1.86	0.41
1:A:278:C:H2'	1:A:279:G:O4'	2.21	0.41
1:A:676:U:H2'	1:A:677:A:C8	2.56	0.41
1:A:822:A:H5''	1:A:823:U:H5'	2.03	0.41
1:A:905:A:H4'	1:A:906:G:H5'	2.03	0.41
1:A:967:A:C5	1:A:968:G:H1'	2.56	0.41
1:A:984:A:O2'	1:A:2134:A:H4'	2.20	0.41
1:A:1076:C:H2'	1:A:1077:U:O4'	2.21	0.41
1:A:1133:A:H2'	1:A:1134:G:C8	2.56	0.41
1:A:1266:U:H2'	1:A:1267:G:C8	2.56	0.41
1:A:1312:U:H3	1:A:1313:C:N4	2.19	0.41
1:A:1463:A:C5	1:A:1464:A:N7	2.89	0.41
1:A:1499:U:O2	1:A:1499:U:H2'	2.20	0.41
1:A:1843:U:H2'	1:A:1844:G:H8	1.86	0.41
1:A:2128:G:N2	1:A:2137:C:C2	2.89	0.41
1:A:2386:A:H2'	1:A:2387:A:C8	2.56	0.41
1:A:2642:U:C4	1:A:2643:C:N4	2.89	0.41
1:A:2719:U:H2'	1:A:2720:C:C6	2.56	0.41
1:A:2982:A:H2'	1:A:2984:G:O5'	2.21	0.41
1:A:3066:A:H3'	1:A:3067:G:H4'	2.03	0.41
1:A:3079:A:H3'	1:A:3080:A:C8	2.54	0.41
1:A:3131:A:H1'	1:A:3133:U:OP2	2.21	0.41
1:A:3198:G:N3	1:A:3199:C:C6	2.89	0.41
1:A:3282:U:H2'	1:A:3283:U:H6	1.84	0.41
1:A:3378:C:H6	1:A:3378:C:H2'	1.71	0.41
1:A:3545:U:C4	1:A:3684:A:C2	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3766:U:H2'	1:A:3770:C:N4	2.36	0.41
3:C:53:G:H2'	3:C:54:C:H6	1.86	0.41
3:C:74:A:H61	3:C:89:U:H3'	1.86	0.41
4:D:194:ASN:CG	4:D:194:ASN:O	2.59	0.41
4:D:210:PRO:HD2	4:D:235:VAL:HG21	2.02	0.41
5:E:78:ILE:HD13	5:E:308:PHE:HZ	1.85	0.41
5:E:117:ARG:HH11	5:E:172:LYS:HB3	1.85	0.41
5:E:226:VAL:HG13	5:E:262:PRO:HB2	2.02	0.41
19:S:114:ASP:C	19:S:116:GLY:N	2.74	0.41
20:T:164:LYS:O	20:T:167:VAL:HG12	2.21	0.41
28:1:51:LEU:HB2	28:1:65:ARG:HG2	2.02	0.41
30:3:29:SER:O	30:3:33:ILE:HG13	2.21	0.41
1:A:916:U:H2'	1:A:917:A:C8	2.56	0.41
1:A:1416:U:H2'	1:A:1417:G:C8	2.54	0.41
1:A:1466:C:H2'	1:A:1467:C:C6	2.56	0.41
1:A:1531:G:H1	1:A:1573:C:H5	1.65	0.41
1:A:1557:U:H2'	1:A:1558:U:O4'	2.21	0.41
1:A:2068:G:N2	1:A:2069:C:C2	2.89	0.41
1:A:2135:G:C5	1:A:2136:C:C5	3.09	0.41
4:D:140:SER:O	4:D:143:GLY:N	2.47	0.41
5:E:88:GLY:HA2	5:E:105:VAL:O	2.21	0.41
5:E:160:HIS:HA	5:E:174:HIS:O	2.21	0.41
5:E:249:ILE:CG2	5:E:257:VAL:HG13	2.51	0.41
8:H:80:PHE:HA	8:H:83:VAL:HG22	2.03	0.41
21:U:14:HIS:HA	21:U:109:GLU:HG2	2.03	0.41
22:V:39:ASP:HB2	22:V:65:ILE:HD12	2.03	0.41
28:1:90:ASP:HB3	28:1:121:LYS:HE2	2.03	0.41
32:5:196:ASP:O	32:5:200:GLN:HG2	2.21	0.41
1:A:34:A:OP1	1:A:34:A:H4'	2.21	0.40
1:A:227:A:H8	1:A:1538:U:C2	2.40	0.40
1:A:906:G:C4	1:A:907:C:C5	3.09	0.40
1:A:927:A:O2'	1:A:2706:A:H5'	2.21	0.40
1:A:1447:G:C4	1:A:1448:C:C5	3.09	0.40
1:A:1474:A:H2'	1:A:1475:G:C8	2.55	0.40
1:A:1576:U:H2'	1:A:1577:A:O4'	2.20	0.40
1:A:1595:A:N1	1:A:2649:A:H5''	2.36	0.40
1:A:1766:U:H2'	1:A:1767:U:O4'	2.21	0.40
1:A:2408:G:H22	1:A:2413:A:H1'	1.86	0.40
1:A:2945:G:H2'	1:A:2945:G:N3	2.36	0.40
1:A:3062:U:H2'	1:A:3063:U:C6	2.56	0.40
3:C:140:G:N3	3:C:140:G:H3'	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:200:ARG:HB3	4:D:202:VAL:HG12	2.04	0.40
6:F:159:GLU:HA	6:F:217:VAL:HG13	2.03	0.40
12:L:50:ILE:H	12:L:50:ILE:HG13	1.53	0.40
26:Z:51:LYS:O	26:Z:69:VAL:HB	2.21	0.40
34:7:37:ALA:N	34:7:38:PRO:CD	2.83	0.40
36:9:50:LYS:HG3	36:9:115:ARG:HH11	1.86	0.40
1:A:33:G:N2	1:A:50:U:C5	2.89	0.40
1:A:53:G:N1	1:A:54:C:C4	2.89	0.40
1:A:270:U:O2'	1:A:271:G:OP2	2.36	0.40
1:A:739:G:N1	1:A:921:C:C2	2.89	0.40
1:A:1508:U:H2'	1:A:1509:U:O4'	2.21	0.40
1:A:1657:U:H2'	1:A:1658:G:C8	2.55	0.40
1:A:2112:G:H3'	1:A:2116:C:H42	1.86	0.40
1:A:2533:G:H2'	1:A:2534:U:O4'	2.20	0.40
1:A:2716:U:C4	1:A:2944:G:C2	3.09	0.40
1:A:3669:U:H6	1:A:3669:U:O5'	2.05	0.40
2:B:104:C:H2'	2:B:105:C:H6	1.82	0.40
4:D:116:LEU:O	4:D:126:LEU:HD12	2.21	0.40
15:O:74:ASN:HD22	15:O:111:LEU:HB2	1.86	0.40
16:P:42:PRO:HG3	16:P:61:ILE:HG12	2.03	0.40
20:T:85:ASN:O	20:T:89:ASN:HA	2.22	0.40
30:3:118:TYR:O	30:3:119:LEU:C	2.59	0.40
33:6:54:ILE:O	33:6:58:VAL:HG23	2.21	0.40
34:7:18:LYS:HG2	34:7:116:CYS:HA	2.04	0.40
36:9:43:LYS:HB3	36:9:130:ARG:HH11	1.86	0.40
1:A:441:A:H2'	1:A:442:G:O4'	2.20	0.40
1:A:501:U:HO2'	1:A:502:U:P	2.43	0.40
1:A:543:U:O2	1:A:543:U:H2'	2.21	0.40
1:A:795:G:C2	1:A:796:C:C2	3.10	0.40
1:A:1000:C:H2'	1:A:1001:A:H8	1.86	0.40
1:A:1066:U:C5'	35:8:55:ILE:HB	2.51	0.40
1:A:1184:A:N6	1:A:1185:A:N6	2.69	0.40
1:A:1423:G:C4	1:A:1424:C:C6	3.09	0.40
1:A:1494:U:H2'	1:A:1495:U:H6	1.86	0.40
1:A:1867:U:H2'	1:A:1868:U:O4'	2.20	0.40
1:A:2019:A:H1'	4:D:21:HIS:CE1	2.56	0.40
1:A:2526:A:H2	1:A:2942:G:H1'	1.87	0.40
1:A:2723:G:C5	1:A:2724:C:C5	3.10	0.40
1:A:3215:G:H2'	1:A:3216:C:H6	1.86	0.40
1:A:3300:A:OP1	5:E:252:TRP:HB3	2.22	0.40
1:A:3462:A:N6	1:A:3465:G:C5	2.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3771:C:H2'	1:A:3772:C:C6	2.56	0.40
4:D:5:ILE:HD12	4:D:232:GLY:HA2	2.03	0.40
5:E:258:GLN:H	5:E:261:ILE:HD12	1.86	0.40
12:L:94:ILE:CD1	12:L:115:LEU:HD21	2.52	0.40
17:Q:44:ASN:HD21	17:Q:185:LYS:HE3	1.86	0.40
25:Y:143:ILE:HG21	25:Y:158:VAL:HG21	2.03	0.40
32:5:97:ARG:HD3	32:5:119:GLN:O	2.22	0.40
34:7:24:LEU:HD21	34:7:44:ILE:HG13	2.03	0.40
35:8:69:ASN:O	35:8:70:ASN:CB	2.67	0.40
1:A:625:A:H2'	1:A:626:A:O4'	2.21	0.40
1:A:632:U:H2'	1:A:633:U:O4'	2.21	0.40
1:A:660:U:H2'	1:A:661:G:H8	1.86	0.40
1:A:1154:C:H2'	1:A:1155:C:H6	1.86	0.40
1:A:1292:U:H2'	1:A:1293:G:H8	1.85	0.40
1:A:1302:G:N2	1:A:1303:C:C2	2.90	0.40
1:A:1999:A:H2'	1:A:2000:G:H8	1.86	0.40
1:A:3114:G:C6	1:A:3115:C:N4	2.89	0.40
1:A:3380:U:C2'	1:A:3381:A:H5'	2.52	0.40
1:A:3423:U:H2'	1:A:3424:U:C6	2.56	0.40
1:A:3509:G:C4	1:A:3510:C:C6	3.10	0.40
6:F:315:ASN:HB3	32:5:175:LYS:HD3	2.02	0.40
9:I:20:LEU:HB3	9:I:44:TYR:HB3	2.03	0.40
9:I:88:PRO:HB2	9:I:91:ILE:HD12	2.02	0.40
13:M:93:TYR:CE1	13:M:95:ILE:HD11	2.57	0.40
14:N:50:THR:HG23	14:N:52:THR:H	1.85	0.40
17:Q:202:GLU:HG2	17:Q:202:GLU:O	2.21	0.40
19:S:48:ILE:CD1	19:S:137:LEU:HD21	2.50	0.40
21:U:39:PHE:CG	21:U:112:ILE:HG13	2.56	0.40
21:U:143:VAL:HG13	21:U:149:LYS:HG2	2.03	0.40
1:A:156:U:O4	10:J:200:LYS:HE2	2.21	0.40
1:A:730:G:C6	1:A:2654:A:C8	3.09	0.40
1:A:748:A:N6	1:A:910:A:H61	2.20	0.40
1:A:882:G:C5	1:A:883:C:C5	3.10	0.40
1:A:1343:U:H2'	1:A:1344:C:O4'	2.21	0.40
1:A:1643:U:C4	25:Y:164:LEU:HD22	2.57	0.40
1:A:1740:A:H2'	1:A:1741:G:H8	1.87	0.40
1:A:1797:A:N3	1:A:2083:U:O2'	2.53	0.40
1:A:2189:A:H2'	1:A:2190:A:C8	2.57	0.40
1:A:2514:G:N2	1:A:2516:A:H3'	2.36	0.40
1:A:2938:C:H2'	1:A:2939:C:C6	2.56	0.40
1:A:3183:G:H2'	1:A:3184:C:H6	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3270:A:H4'	1:A:3271:G:C8	2.57	0.40
3:C:156:A:H2'	3:C:157:A:C8	2.56	0.40
6:F:137:VAL:HA	6:F:247:GLY:O	2.22	0.40
6:F:347:ILE:H	6:F:347:ILE:HG13	1.74	0.40
6:F:368:LEU:HD23	32:5:79:ARG:HD2	2.04	0.40
16:P:201:LEU:O	16:P:202:ARG:CB	2.70	0.40
19:S:3:ILE:HG12	19:S:5:LEU:HG	2.02	0.40
29:2:54:SER:H	29:2:69:LYS:HB2	1.85	0.40
34:7:28:THR:HG21	34:7:36:LYS:CG	2.51	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 PDB entries followed by that with respect to all EM entries.

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	
4	D	245/260 (94%)	224 (91%)	18 (7%)	3 (1%)	13	49
5	E	378/386 (98%)	340 (90%)	31 (8%)	7 (2%)	8	39
6	F	388/411 (94%)	363 (94%)	16 (4%)	9 (2%)	6	34
7	G	116/173 (67%)	101 (87%)	11 (10%)	4 (3%)	3	24
8	H	183/190 (96%)	158 (86%)	20 (11%)	5 (3%)	5	30
9	I	203/221 (92%)	174 (86%)	24 (12%)	5 (2%)	5	32
10	J	216/283 (76%)	198 (92%)	14 (6%)	4 (2%)	8	39
11	K	199/202 (98%)	181 (91%)	15 (8%)	3 (2%)	10	44
12	L	209/215 (97%)	183 (88%)	18 (9%)	8 (4%)	3	22
13	M	130/139 (94%)	117 (90%)	9 (7%)	4 (3%)	4	26
14	N	144/165 (87%)	137 (95%)	3 (2%)	4 (3%)	5	29
15	O	145/148 (98%)	131 (90%)	12 (8%)	2 (1%)	11	46
16	P	202/205 (98%)	184 (91%)	11 (5%)	7 (4%)	3	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	Q	185/219 (84%)	155 (84%)	27 (15%)	3 (2%)	9	43
18	R	244/294 (83%)	216 (88%)	18 (7%)	10 (4%)	3	21
19	S	184/187 (98%)	164 (89%)	14 (8%)	6 (3%)	4	25
20	T	179/182 (98%)	172 (96%)	4 (2%)	3 (2%)	9	42
21	U	178/184 (97%)	166 (93%)	8 (4%)	4 (2%)	6	35
22	V	153/161 (95%)	139 (91%)	10 (6%)	4 (3%)	5	31
23	W	166/203 (82%)	151 (91%)	11 (7%)	4 (2%)	6	34
24	X	95/139 (68%)	82 (86%)	9 (10%)	4 (4%)	3	20
25	Y	99/190 (52%)	91 (92%)	6 (6%)	2 (2%)	7	38
26	Z	119/126 (94%)	107 (90%)	10 (8%)	2 (2%)	9	42
27	0	60/162 (37%)	55 (92%)	4 (7%)	1 (2%)	9	42
28	1	136/146 (93%)	128 (94%)	3 (2%)	5 (4%)	3	22
29	2	96/127 (76%)	84 (88%)	11 (12%)	1 (1%)	15	54
30	3	117/124 (94%)	108 (92%)	4 (3%)	5 (4%)	2	20
31	4	64/67 (96%)	56 (88%)	5 (8%)	3 (5%)	2	17
32	5	221/257 (86%)	199 (90%)	17 (8%)	5 (2%)	6	34
33	6	96/108 (89%)	89 (93%)	4 (4%)	3 (3%)	4	26
34	7	92/120 (77%)	87 (95%)	5 (5%)	0	100	100
35	8	123/131 (94%)	110 (89%)	9 (7%)	4 (3%)	4	25
36	9	101/140 (72%)	87 (86%)	8 (8%)	6 (6%)	1	12
37	a	104/150 (69%)	96 (92%)	7 (7%)	1 (1%)	15	54
38	b	91/112 (81%)	84 (92%)	5 (6%)	2 (2%)	6	35
39	c	87/92 (95%)	72 (83%)	11 (13%)	4 (5%)	2	18
40	d	68/87 (78%)	65 (96%)	3 (4%)	0	100	100
41	e	39/51 (76%)	38 (97%)	1 (3%)	0	100	100
42	f	49/128 (38%)	46 (94%)	3 (6%)	0	100	100
43	g	35/39 (90%)	31 (89%)	2 (6%)	2 (6%)	1	14
44	h	83/96 (86%)	72 (87%)	10 (12%)	1 (1%)	13	49
45	i	93/104 (89%)	83 (89%)	5 (5%)	5 (5%)	2	14
All	All	6115/7124 (86%)	5524 (90%)	436 (7%)	155 (2%)	9	32

All (155) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	197	PRO
5	E	18	PRO
5	E	196	LEU
6	F	102	PHE
6	F	265	GLY
6	F	321	ASN
7	G	28	ASP
7	G	95	ASN
7	G	130	HIS
7	G	143	ARG
10	J	61	PRO
10	J	242	ASN
11	K	188	ILE
12	L	130	ASN
12	L	131	LYS
12	L	140	PRO
12	L	168	LYS
12	L	169	PRO
13	M	48	LEU
14	N	60	PHE
18	R	58	SER
18	R	90	VAL
18	R	232	ALA
19	S	8	VAL
20	T	129	ASN
21	U	154	ARG
23	W	105	ARG
31	4	38	ASN
32	5	116	ARG
33	6	71	HIS
35	8	64	LYS
35	8	123	LYS
36	9	66	LYS
39	c	24	ARG
39	c	28	ARG
39	c	68	ARG
4	D	13	GLY
5	E	183	GLY
6	F	223	ASN
6	F	267	ILE
8	H	53	TYR
8	H	148	ALA
9	I	88	PRO

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Mol	Chain	Res	Type
9	I	159	MET
9	I	213	ASP
10	J	56	GLY
11	K	108	PRO
13	M	12	LYS
13	M	18	SER
16	P	51	LEU
16	P	150	ASN
18	R	59	GLN
18	R	151	GLY
18	R	233	ASP
19	S	9	GLY
20	T	4	THR
20	T	15	LYS
21	U	152	LEU
22	V	134	GLU
23	W	68	GLY
27	0	14	SER
28	1	19	ALA
28	1	35	GLU
29	2	95	GLN
32	5	82	ASN
32	5	204	CYS
33	6	103	ILE
35	8	27	ARG
36	9	109	GLY
36	9	110	ASN
38	b	86	THR
43	g	8	TYR
45	i	68	VAL
45	i	93	GLY
45	i	95	ASP
6	F	17	ASN
6	F	19	VAL
12	L	92	ILE
13	M	136	SER
14	N	8	THR
16	P	14	LYS
16	P	108	LYS
16	P	186	ARG
17	Q	24	ARG
22	V	23	HIS

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Mol	Chain	Res	Type
23	W	188	GLN
24	X	76	ASN
24	X	78	LYS
24	X	135	PHE
30	3	76	LYS
32	5	172	ALA
33	6	91	SER
36	9	54	ARG
45	i	15	LYS
6	F	295	SER
9	I	19	VAL
9	I	49	LYS
17	Q	60	ILE
18	R	67	ALA
18	R	114	ASN
18	R	171	GLY
19	S	184	ALA
21	U	183	ARG
22	V	124	ASN
25	Y	116	THR
26	Z	64	GLY
30	3	38	GLY
30	3	84	LYS
30	3	101	ALA
30	3	119	LEU
31	4	36	ASP
35	8	39	ASP
6	F	92	PHE
8	H	62	VAL
10	J	101	LEU
12	L	4	HIS
12	L	75	THR
14	N	23	ARG
14	N	46	VAL
16	P	202	ARG
19	S	41	ASN
19	S	42	ALA
19	S	82	VAL
21	U	134	ARG
22	V	82	LYS
25	Y	98	LYS
28	1	42	LEU

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Mol	Chain	Res	Type
36	9	39	ARG
36	9	104	VAL
37	a	10	HIS
39	c	66	ARG
43	g	13	ALA
5	E	62	LYS
5	E	162	GLN
5	E	330	LYS
17	Q	14	ASN
26	Z	84	VAL
28	1	106	ASN
38	b	8	LYS
44	h	18	TYR
45	i	77	LYS
18	R	152	ILE
4	D	127	VAL
8	H	139	VAL
16	P	149	ILE
32	5	176	ILE
5	E	253	HIS
8	H	137	PRO
11	K	145	GLY
15	O	30	GLY
15	O	50	PRO
23	W	20	VAL
24	X	68	ILE
28	1	125	PRO
31	4	37	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 PDB entries followed by that with respect to all EM entries.

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	
4	D	191/202 (95%)	163 (85%)	28 (15%)	3	14
5	E	335/340 (98%)	319 (95%)	16 (5%)	25	61
6	F	336/352 (96%)	310 (92%)	26 (8%)	13	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	110/155 (71%)	97 (88%)	13 (12%)	5	23
8	H	164/173 (95%)	145 (88%)	19 (12%)	5	24
9	I	189/203 (93%)	169 (89%)	20 (11%)	6	27
10	J	204/260 (78%)	181 (89%)	23 (11%)	6	25
11	K	181/182 (100%)	171 (94%)	10 (6%)	21	57
12	L	190/194 (98%)	169 (89%)	21 (11%)	6	25
13	M	106/110 (96%)	94 (89%)	12 (11%)	6	25
14	N	134/152 (88%)	117 (87%)	17 (13%)	4	20
15	O	121/122 (99%)	110 (91%)	11 (9%)	9	34
16	P	179/180 (99%)	164 (92%)	15 (8%)	11	39
17	Q	165/190 (87%)	157 (95%)	8 (5%)	25	61
18	R	214/254 (84%)	189 (88%)	25 (12%)	5	23
19	S	158/159 (99%)	147 (93%)	11 (7%)	15	48
20	T	161/163 (99%)	146 (91%)	15 (9%)	9	33
21	U	162/166 (98%)	150 (93%)	12 (7%)	13	46
22	V	140/144 (97%)	135 (96%)	5 (4%)	35	69
23	W	128/178 (72%)	121 (94%)	7 (6%)	21	57
24	X	92/131 (70%)	87 (95%)	5 (5%)	22	58
25	Y	90/177 (51%)	84 (93%)	6 (7%)	16	50
26	Z	111/115 (96%)	103 (93%)	8 (7%)	14	47
27	0	53/146 (36%)	51 (96%)	2 (4%)	33	67
28	1	127/132 (96%)	118 (93%)	9 (7%)	14	47
29	2	97/118 (82%)	92 (95%)	5 (5%)	23	59
30	3	110/115 (96%)	101 (92%)	9 (8%)	11	41
31	4	60/61 (98%)	55 (92%)	5 (8%)	11	40
32	5	201/231 (87%)	187 (93%)	14 (7%)	15	48
33	6	83/92 (90%)	69 (83%)	14 (17%)	2	10
34	7	90/112 (80%)	72 (80%)	18 (20%)	1	6
35	8	114/120 (95%)	105 (92%)	9 (8%)	12	43
36	9	90/127 (71%)	78 (87%)	12 (13%)	4	18
37	a	89/128 (70%)	81 (91%)	8 (9%)	9	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	b	82/97 (84%)	81 (99%)	1 (1%)	71	88
39	c	73/77 (95%)	69 (94%)	4 (6%)	21	57
40	d	69/83 (83%)	61 (88%)	8 (12%)	5	24
41	e	40/48 (83%)	35 (88%)	5 (12%)	4	21
42	f	45/114 (40%)	41 (91%)	4 (9%)	9	35
43	g	34/35 (97%)	32 (94%)	2 (6%)	19	54
44	h	70/80 (88%)	66 (94%)	4 (6%)	20	56
45	i	87/93 (94%)	83 (95%)	4 (5%)	27	63
All	All	5475/6311 (87%)	5005 (91%)	470 (9%)	14	38

All (470) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	6	ARG
4	D	12	ARG
4	D	17	LYS
4	D	32	LEU
4	D	33	ASP
4	D	40	TYR
4	D	41	ILE
4	D	58	LEU
4	D	64	LYS
4	D	65	ARG
4	D	82	MET
4	D	96	LEU
4	D	104	ILE
4	D	113	ILE
4	D	114	CYS
4	D	115	ASN
4	D	116	LEU
4	D	119	ARG
4	D	163	ARG
4	D	181	LYS
4	D	191	VAL
4	D	193	ARG
4	D	194	ASN
4	D	196	TRP
4	D	207	VAL
4	D	235	VAL

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Mol	Chain	Res	Type
4	D	242	ARG
4	D	243	THR
5	E	4	ARG
5	E	7	GLU
5	E	24	ARG
5	E	35	ASP
5	E	87	VAL
5	E	89	ILE
5	E	113	GLU
5	E	117	ARG
5	E	189	LEU
5	E	202	VAL
5	E	212	ILE
5	E	223	THR
5	E	253	HIS
5	E	260	GLN
5	E	287	ASP
5	E	293	THR
6	F	33	ARG
6	F	48	ARG
6	F	55	LYS
6	F	75	ARG
6	F	86	ARG
6	F	92	PHE
6	F	117	LEU
6	F	122	TYR
6	F	126	SER
6	F	134	THR
6	F	140	ARG
6	F	144	ILE
6	F	180	VAL
6	F	182	ARG
6	F	217	VAL
6	F	232	VAL
6	F	257	PHE
6	F	312	ARG
6	F	313	LEU
6	F	314	GLN
6	F	316	LYS
6	F	321	ASN
6	F	325	ARG
6	F	349	GLU

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Mol	Chain	Res	Type
6	F	371	ILE
6	F	376	TYR
7	G	23	VAL
7	G	25	GLU
7	G	40	LEU
7	G	43	GLN
7	G	44	LYS
7	G	75	LYS
7	G	77	LEU
7	G	85	LYS
7	G	99	THR
7	G	126	ASP
7	G	139	THR
7	G	160	MET
7	G	165	THR
8	H	3	THR
8	H	36	ARG
8	H	41	LEU
8	H	43	ILE
8	H	45	ILE
8	H	46	ARG
8	H	47	LEU
8	H	48	ASN
8	H	55	LYS
8	H	64	ASP
8	H	70	ARG
8	H	73	CYS
8	H	74	THR
8	H	93	LEU
8	H	119	GLU
8	H	150	ILE
8	H	165	LEU
8	H	172	ARG
8	H	184	THR
9	I	33	TYR
9	I	37	LYS
9	I	51	ARG
9	I	62	ILE
9	I	73	ILE
9	I	78	LEU
9	I	82	LEU
9	I	83	LEU

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Mol	Chain	Res	Type
9	I	85	VAL
9	I	96	LEU
9	I	99	VAL
9	I	110	ASN
9	I	117	ILE
9	I	122	ASP
9	I	134	ASP
9	I	170	ARG
9	I	175	LYS
9	I	185	ASP
9	I	204	LEU
9	I	216	LEU
10	J	44	LEU
10	J	87	ARG
10	J	96	GLN
10	J	97	PHE
10	J	100	THR
10	J	106	THR
10	J	110	LEU
10	J	113	LEU
10	J	125	LYS
10	J	129	LEU
10	J	169	VAL
10	J	183	LEU
10	J	186	LEU
10	J	189	LEU
10	J	200	LYS
10	J	234	VAL
10	J	235	CYS
10	J	241	ASP
10	J	244	ASP
10	J	246	ARG
10	J	267	LYS
10	J	272	GLU
10	J	275	LYS
11	K	1	MET
11	K	18	LEU
11	K	35	VAL
11	K	42	ILE
11	K	59	LEU
11	K	67	LYS
11	K	98	LEU

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Mol	Chain	Res	Type
11	K	132	ARG
11	K	137	LEU
11	K	193	ARG
12	L	18	GLN
12	L	22	ARG
12	L	24	ASN
12	L	28	ASN
12	L	38	ARG
12	L	43	LYS
12	L	48	THR
12	L	50	ILE
12	L	61	THR
12	L	65	ASN
12	L	84	LEU
12	L	91	THR
12	L	94	ILE
12	L	99	ARG
12	L	103	ARG
12	L	122	LEU
12	L	136	ILE
12	L	170	PHE
12	L	174	ILE
12	L	188	THR
12	L	190	ARG
13	M	11	ASN
13	M	14	ARG
13	M	30	ASN
13	M	35	ASN
13	M	48	LEU
13	M	59	MET
13	M	60	VAL
13	M	73	LYS
13	M	85	LYS
13	M	89	ARG
13	M	123	GLU
13	M	127	LEU
14	N	25	VAL
14	N	29	ARG
14	N	31	CYS
14	N	33	ILE
14	N	46	VAL
14	N	52	THR

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Mol	Chain	Res	Type
14	N	56	VAL
14	N	62	THR
14	N	67	MET
14	N	69	ILE
14	N	75	LYS
14	N	87	CYS
14	N	101	VAL
14	N	118	LYS
14	N	120	ARG
14	N	138	LEU
14	N	144	THR
15	O	4	ARG
15	O	5	PHE
15	O	9	ARG
15	O	12	ARG
15	O	22	VAL
15	O	46	ASP
15	O	63	LEU
15	O	95	ASP
15	O	104	ARG
15	O	131	SER
15	O	132	VAL
16	P	8	GLN
16	P	22	LEU
16	P	26	ARG
16	P	46	ASP
16	P	49	ARG
16	P	51	LEU
16	P	61	ILE
16	P	75	VAL
16	P	83	LYS
16	P	93	LYS
16	P	113	ASN
16	P	118	ASN
16	P	127	VAL
16	P	148	LYS
16	P	184	LYS
17	Q	38	ARG
17	Q	39	LYS
17	Q	88	ARG
17	Q	96	VAL
17	Q	126	VAL

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Mol	Chain	Res	Type
17	Q	153	ARG
17	Q	187	LYS
17	Q	193	ASP
18	R	23	ARG
18	R	38	LEU
18	R	40	ASP
18	R	41	LYS
18	R	43	LYS
18	R	44	TYR
18	R	59	GLN
18	R	60	VAL
18	R	69	ILE
18	R	72	ASP
18	R	77	GLU
18	R	82	GLU
18	R	88	ILE
18	R	107	ARG
18	R	114	ASN
18	R	153	THR
18	R	156	THR
18	R	159	ASN
18	R	166	LYS
18	R	190	ASN
18	R	199	LEU
18	R	209	THR
18	R	223	ASN
18	R	233	ASP
18	R	274	ASN
19	S	17	LYS
19	S	19	LEU
19	S	23	ASN
19	S	76	ASN
19	S	87	ASP
19	S	94	LEU
19	S	107	THR
19	S	113	GLU
19	S	136	VAL
19	S	171	ARG
19	S	187	LYS
20	T	20	LYS
20	T	24	ASP
20	T	59	ARG

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Mol	Chain	Res	Type
20	T	73	ARG
20	T	79	LYS
20	T	88	THR
20	T	104	LEU
20	T	123	TYR
20	T	137	LEU
20	T	152	LYS
20	T	166	GLN
20	T	169	ARG
20	T	170	ASN
20	T	176	LYS
20	T	180	VAL
21	U	9	LEU
21	U	12	ASN
21	U	35	ARG
21	U	58	ASN
21	U	60	LEU
21	U	67	LEU
21	U	91	ASP
21	U	94	THR
21	U	106	THR
21	U	138	ILE
21	U	144	ARG
21	U	145	ARG
22	V	41	VAL
22	V	42	ASP
22	V	61	LYS
22	V	69	THR
22	V	152	ILE
23	W	16	LYS
23	W	23	ARG
23	W	48	LEU
23	W	69	ARG
23	W	75	GLU
23	W	105	ARG
23	W	123	ARG
24	X	45	ASP
24	X	71	ASP
24	X	94	VAL
24	X	116	ILE
24	X	130	TYR
25	Y	95	ARG

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Mol	Chain	Res	Type
25	Y	115	LEU
25	Y	127	ILE
25	Y	150	LEU
25	Y	168	LYS
25	Y	187	ILE
26	Z	4	ASN
26	Z	14	MET
26	Z	26	ARG
26	Z	34	LEU
26	Z	62	ASN
26	Z	103	VAL
26	Z	105	LEU
26	Z	111	ASP
27	0	37	PHE
27	0	46	LEU
28	1	5	LEU
28	1	10	VAL
28	1	26	VAL
28	1	42	LEU
28	1	63	VAL
28	1	68	VAL
28	1	106	ASN
28	1	114	LEU
28	1	117	ILE
29	2	23	ASN
29	2	24	LYS
29	2	37	ASN
29	2	96	HIS
29	2	118	LEU
30	3	18	LEU
30	3	37	LEU
30	3	46	ILE
30	3	52	ASN
30	3	57	LEU
30	3	69	ARG
30	3	76	LYS
30	3	77	PHE
30	3	87	THR
31	4	13	ASN
31	4	21	ILE
31	4	50	ILE
31	4	53	LYS

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Mol	Chain	Res	Type
31	4	62	LYS
32	5	39	ILE
32	5	45	ILE
32	5	58	LEU
32	5	124	VAL
32	5	128	VAL
32	5	134	GLU
32	5	137	LYS
32	5	149	THR
32	5	160	ARG
32	5	163	VAL
32	5	191	VAL
32	5	196	ASP
32	5	224	ARG
32	5	231	ARG
33	6	19	LEU
33	6	21	MET
33	6	28	PHE
33	6	33	CYS
33	6	46	ILE
33	6	54	ILE
33	6	55	GLN
33	6	77	ASN
33	6	79	ASP
33	6	80	LEU
33	6	89	ARG
33	6	93	LEU
33	6	98	VAL
33	6	101	SER
34	7	16	VAL
34	7	21	THR
34	7	26	LYS
34	7	28	THR
34	7	33	TYR
34	7	39	ARG
34	7	50	LYS
34	7	53	HIS
34	7	56	ASP
34	7	57	VAL
34	7	58	ARG
34	7	70	LYS
34	7	80	ARG

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Mol	Chain	Res	Type
34	7	88	ASN
34	7	99	THR
34	7	101	VAL
34	7	110	LYS
34	7	114	ASN
35	8	21	GLN
35	8	26	MET
35	8	33	ARG
35	8	38	ILE
35	8	49	THR
35	8	73	LYS
35	8	111	ARG
35	8	113	LYS
35	8	125	ARG
36	9	51	ARG
36	9	52	SER
36	9	53	GLN
36	9	56	GLN
36	9	67	ASN
36	9	68	VAL
36	9	69	ASN
36	9	71	LYS
36	9	81	ARG
36	9	113	VAL
36	9	131	VAL
36	9	132	ARG
37	a	4	ARG
37	a	5	VAL
37	a	15	THR
37	a	43	LYS
37	a	59	PRO
37	a	66	ARG
37	a	74	ARG
37	a	94	LEU
38	b	18	ASN
39	c	49	ARG
39	c	53	SER
39	c	60	ASN
39	c	73	LEU
40	d	19	ASP
40	d	25	ILE
40	d	46	LYS

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Mol	Chain	Res	Type
40	d	49	LEU
40	d	54	PHE
40	d	57	ARG
40	d	65	ASN
40	d	76	TYR
41	e	5	LYS
41	e	6	ARG
41	e	18	ARG
41	e	39	THR
41	e	42	ARG
42	f	9	LEU
42	f	41	ARG
42	f	46	ARG
42	f	51	LEU
43	g	7	ARG
43	g	9	LYS
44	h	10	LEU
44	h	17	ARG
44	h	26	ILE
44	h	47	THR
45	i	64	THR
45	i	86	ARG
45	i	87	CYS
45	i	95	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (102) such sidechains are listed below:

Mol	Chain	Res	Type
4	D	19	HIS
4	D	31	HIS
4	D	86	GLN
4	D	115	ASN
4	D	139	GLN
4	D	215	ASN
4	D	217	GLN
5	E	55	HIS
5	E	68	HIS
5	E	160	HIS
5	E	221	HIS
5	E	253	HIS
5	E	260	GLN
5	E	271	HIS

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Mol	Chain	Res	Type
5	E	310	HIS
6	F	156	ASN
6	F	314	GLN
6	F	317	ASN
6	F	321	ASN
7	G	15	ASN
7	G	20	ASN
7	G	43	GLN
7	G	152	HIS
8	H	21	ASN
8	H	115	ASN
9	I	12	ASN
9	I	110	ASN
9	I	217	HIS
10	J	96	GLN
11	K	13	HIS
12	L	18	GLN
12	L	24	ASN
12	L	65	ASN
12	L	153	ASN
12	L	204	GLN
13	M	11	ASN
13	M	49	ASN
15	O	74	ASN
15	O	118	HIS
15	O	143	GLN
16	P	15	GLN
16	P	145	ASN
16	P	180	HIS
16	P	197	GLN
17	Q	59	GLN
17	Q	95	HIS
18	R	42	ASN
18	R	45	ASN
18	R	118	GLN
18	R	190	ASN
18	R	202	HIS
18	R	223	ASN
18	R	274	ASN
19	S	23	ASN
19	S	76	ASN
19	S	150	HIS

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Mol	Chain	Res	Type
20	T	57	HIS
20	T	129	ASN
21	U	15	GLN
21	U	17	HIS
21	U	32	ASN
21	U	45	ASN
21	U	58	ASN
21	U	123	HIS
21	U	147	HIS
21	U	150	GLN
22	V	56	ASN
22	V	59	HIS
22	V	103	ASN
23	W	71	ASN
23	W	120	ASN
24	X	76	ASN
25	Y	159	ASN
25	Y	185	ASN
26	Z	90	ASN
28	1	32	GLN
28	1	79	HIS
30	3	52	ASN
30	3	61	ASN
30	3	93	GLN
30	3	98	GLN
31	4	13	ASN
31	4	17	HIS
32	5	119	GLN
32	5	177	GLN
32	5	254	ASN
33	6	77	ASN
34	7	29	HIS
34	7	64	ASN
35	8	21	GLN
35	8	78	ASN
36	9	56	GLN
36	9	73	HIS
36	9	108	HIS
37	a	12	HIS
38	b	87	HIS
38	b	98	GLN
39	c	51	ASN

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Mol	Chain	Res	Type
41	e	20	ASN
41	e	43	HIS
42	f	8	GLN
42	f	33	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3155/3788 (83%)	972 (30%)	177 (5%)
2	B	117/119 (98%)	24 (20%)	4 (3%)
3	C	148/159 (93%)	46 (31%)	9 (6%)
All	All	3420/4066 (84%)	1042 (30%)	190 (5%)

All (1042) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	A
1	A	13	G
1	A	14	U
1	A	16	A
1	A	18	G
1	A	25	A
1	A	26	A
1	A	30	G
1	A	32	C
1	A	40	A
1	A	43	A
1	A	44	U
1	A	45	A
1	A	49	U
1	A	57	A
1	A	59	G
1	A	60	A
1	A	66	A
1	A	73	U
1	A	75	U
1	A	78	U
1	A	85	A
1	A	87	U
1	A	92	G
1	A	105	G

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Mol	Chain	Res	Type
1	A	109	A
1	A	110	G
1	A	111	C
1	A	121	U
1	A	122	A
1	A	124	U
1	A	130	G
1	A	133	U
1	A	134	G
1	A	135	G
1	A	136	U
1	A	137	G
1	A	139	A
1	A	144	U
1	A	146	U
1	A	147	C
1	A	148	G
1	A	149	A
1	A	151	G
1	A	152	G
1	A	156	U
1	A	157	G
1	A	162	U
1	A	163	G
1	A	165	A
1	A	167	U
1	A	168	A
1	A	171	C
1	A	173	A
1	A	174	U
1	A	175	G
1	A	183	U
1	A	185	A
1	A	186	A
1	A	189	U
1	A	191	A
1	A	192	G
1	A	197	G
1	A	198	U
1	A	199	G
1	A	200	A
1	A	201	G

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Mol	Chain	Res	Type
1	A	207	A
1	A	208	U
1	A	211	U
1	A	215	C
1	A	216	C
1	A	218	U
1	A	219	A
1	A	220	G
1	A	221	A
1	A	226	G
1	A	227	A
1	A	228	A
1	A	229	A
1	A	231	G
1	A	235	A
1	A	239	U
1	A	241	C
1	A	246	U
1	A	247	A
1	A	250	U
1	A	251	U
1	A	255	C
1	A	263	U
1	A	265	U
1	A	268	C
1	A	269	A
1	A	271	G
1	A	274	G
1	A	276	G
1	A	290	G
1	A	291	A
1	A	292	U
1	A	293	U
1	A	302	A
1	A	303	A
1	A	304	U
1	A	306	C
1	A	307	G
1	A	308	U
1	A	309	G
1	A	310	U
1	A	313	U

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Mol	Chain	Res	Type
1	A	314	A
1	A	319	U
1	A	324	U
1	A	336	U
1	A	337	A
1	A	338	U
1	A	342	G
1	A	344	A
1	A	346	A
1	A	347	C
1	A	360	A
1	A	362	U
1	A	370	G
1	A	378	U
1	A	382	A
1	A	384	A
1	A	385	G
1	A	386	U
1	A	392	G
1	A	396	U
1	A	400	C
1	A	401	A
1	A	402	A
1	A	405	A
1	A	408	U
1	A	409	A
1	A	411	U
1	A	413	C
1	A	417	A
1	A	431	G
1	A	432	A
1	A	439	U
1	A	442	G
1	A	444	G
1	A	447	A
1	A	448	A
1	A	449	A
1	A	451	C
1	A	458	A
1	A	459	G
1	A	462	G
1	A	463	G

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Mol	Chain	Res	Type
1	A	489	U
1	A	490	U
1	A	495	U
1	A	497	U
1	A	498	U
1	A	499	U
1	A	500	A
1	A	501	U
1	A	502	U
1	A	503	A
1	A	504	A
1	A	505	A
1	A	506	A
1	A	509	A
1	A	514	C
1	A	521	U
1	A	522	A
1	A	523	A
1	A	530	U
1	A	531	U
1	A	532	C
1	A	534	A
1	A	536	A
1	A	538	A
1	A	539	G
1	A	542	A
1	A	543	U
1	A	545	C
1	A	546	C
1	A	547	C
1	A	549	G
1	A	573	U
1	A	579	C
1	A	580	A
1	A	581	C
1	A	582	U
1	A	583	U
1	A	585	C
1	A	586	U
1	A	592	C
1	A	593	A
1	A	594	C

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Mol	Chain	Res	Type
1	A	595	U
1	A	599	G
1	A	601	G
1	A	604	G
1	A	605	A
1	A	608	A
1	A	609	C
1	A	610	U
1	A	615	U
1	A	617	A
1	A	618	U
1	A	620	U
1	A	621	C
1	A	622	U
1	A	623	U
1	A	624	C
1	A	628	U
1	A	631	U
1	A	636	U
1	A	637	U
1	A	641	G
1	A	642	A
1	A	645	A
1	A	646	A
1	A	647	U
1	A	648	U
1	A	649	U
1	A	650	U
1	A	651	A
1	A	653	A
1	A	659	U
1	A	665	U
1	A	666	U
1	A	668	U
1	A	669	C
1	A	671	U
1	A	672	C
1	A	673	U
1	A	674	U
1	A	675	A
1	A	677	A
1	A	678	A

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Mol	Chain	Res	Type
1	A	679	U
1	A	681	U
1	A	682	A
1	A	683	A
1	A	684	G
1	A	685	U
1	A	694	U
1	A	697	A
1	A	698	G
1	A	699	U
1	A	704	U
1	A	707	U
1	A	708	A
1	A	715	U
1	A	716	C
1	A	727	A
1	A	729	G
1	A	738	A
1	A	755	A
1	A	760	A
1	A	761	U
1	A	765	A
1	A	766	U
1	A	767	U
1	A	769	U
1	A	771	U
1	A	773	A
1	A	774	A
1	A	778	U
1	A	779	U
1	A	794	C
1	A	799	A
1	A	806	G
1	A	809	A
1	A	811	A
1	A	812	U
1	A	813	G
1	A	825	G
1	A	831	U
1	A	833	G
1	A	834	U
1	A	835	G

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Mol	Chain	Res	Type
1	A	858	C
1	A	859	C
1	A	860	A
1	A	862	U
1	A	866	C
1	A	873	U
1	A	874	A
1	A	880	A
1	A	883	C
1	A	885	A
1	A	889	U
1	A	890	G
1	A	893	U
1	A	896	U
1	A	899	A
1	A	900	G
1	A	903	C
1	A	904	G
1	A	905	A
1	A	918	G
1	A	920	A
1	A	925	A
1	A	927	A
1	A	934	G
1	A	936	A
1	A	937	C
1	A	945	G
1	A	946	A
1	A	950	G
1	A	955	A
1	A	968	G
1	A	970	C
1	A	976	G
1	A	980	A
1	A	984	A
1	A	988	G
1	A	990	U
1	A	993	U
1	A	998	U
1	A	999	G
1	A	1000	C
1	A	1013	U

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Mol	Chain	Res	Type
1	A	1014	C
1	A	1015	A
1	A	1016	A
1	A	1026	G
1	A	1027	G
1	A	1028	G
1	A	1033	A
1	A	1034	A
1	A	1035	G
1	A	1036	A
1	A	1039	A
1	A	1040	A
1	A	1042	C
1	A	1043	G
1	A	1044	A
1	A	1052	A
1	A	1053	U
1	A	1056	G
1	A	1063	A
1	A	1070	A
1	A	1072	A
1	A	1073	G
1	A	1078	C
1	A	1079	U
1	A	1080	C
1	A	1081	A
1	A	1086	C
1	A	1096	G
1	A	1097	A
1	A	1099	U
1	A	1100	A
1	A	1101	A
1	A	1102	U
1	A	1106	A
1	A	1107	U
1	A	1109	U
1	A	1111	A
1	A	1113	C
1	A	1114	A
1	A	1116	G
1	A	1121	G
1	A	1122	A

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Mol	Chain	Res	Type
1	A	1123	U
1	A	1124	A
1	A	1128	A
1	A	1131	A
1	A	1132	G
1	A	1136	A
1	A	1158	G
1	A	1164	U
1	A	1168	C
1	A	1169	A
1	A	1170	A
1	A	1172	C
1	A	1174	C
1	A	1186	A
1	A	1187	A
1	A	1188	A
1	A	1191	G
1	A	1193	G
1	A	1194	A
1	A	1196	A
1	A	1197	U
1	A	1198	A
1	A	1199	A
1	A	1200	C
1	A	1202	C
1	A	1203	A
1	A	1204	A
1	A	1205	U
1	A	1206	U
1	A	1207	U
1	A	1215	A
1	A	1216	C
1	A	1217	U
1	A	1218	C
1	A	1219	A
1	A	1221	A
1	A	1222	U
1	A	1223	U
1	A	1224	A
1	A	1225	A
1	A	1226	A
1	A	1229	A

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Mol	Chain	Res	Type
1	A	1230	A
1	A	1231	A
1	A	1232	U
1	A	1233	A
1	A	1234	A
1	A	1239	A
1	A	1240	A
1	A	1245	G
1	A	1259	G
1	A	1263	A
1	A	1272	U
1	A	1273	G
1	A	1281	C
1	A	1283	C
1	A	1287	A
1	A	1288	C
1	A	1299	G
1	A	1300	G
1	A	1309	U
1	A	1310	A
1	A	1314	G
1	A	1316	U
1	A	1319	U
1	A	1320	G
1	A	1324	U
1	A	1325	C
1	A	1329	U
1	A	1330	A
1	A	1334	G
1	A	1337	G
1	A	1341	G
1	A	1344	C
1	A	1345	A
1	A	1346	U
1	A	1418	A
1	A	1420	C
1	A	1429	A
1	A	1431	A
1	A	1433	U
1	A	1435	G
1	A	1436	A
1	A	1437	U

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Mol	Chain	Res	Type
1	A	1441	G
1	A	1444	A
1	A	1445	A
1	A	1453	U
1	A	1458	A
1	A	1459	U
1	A	1460	A
1	A	1473	A
1	A	1476	A
1	A	1480	G
1	A	1481	A
1	A	1486	A
1	A	1498	U
1	A	1499	U
1	A	1503	A
1	A	1504	A
1	A	1506	C
1	A	1524	U
1	A	1529	G
1	A	1534	U
1	A	1535	G
1	A	1537	G
1	A	1538	U
1	A	1539	U
1	A	1540	G
1	A	1548	A
1	A	1549	U
1	A	1550	A
1	A	1556	G
1	A	1565	G
1	A	1567	A
1	A	1571	C
1	A	1572	U
1	A	1575	C
1	A	1577	A
1	A	1578	G
1	A	1583	G
1	A	1586	C
1	A	1592	G
1	A	1595	A
1	A	1604	U
1	A	1619	U

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Mol	Chain	Res	Type
1	A	1626	A
1	A	1630	A
1	A	1631	A
1	A	1633	U
1	A	1635	G
1	A	1636	A
1	A	1637	G
1	A	1643	U
1	A	1649	G
1	A	1651	C
1	A	1657	U
1	A	1663	A
1	A	1668	G
1	A	1672	U
1	A	1676	C
1	A	1680	C
1	A	1685	G
1	A	1688	A
1	A	1691	G
1	A	1693	U
1	A	1696	A
1	A	1703	U
1	A	1704	U
1	A	1705	A
1	A	1706	A
1	A	1707	A
1	A	1721	C
1	A	1725	U
1	A	1730	A
1	A	1732	A
1	A	1736	A
1	A	1748	A
1	A	1750	U
1	A	1751	C
1	A	1756	G
1	A	1762	A
1	A	1763	G
1	A	1766	U
1	A	1767	U
1	A	1768	A
1	A	1769	U
1	A	1770	G

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Mol	Chain	Res	Type
1	A	1771	A
1	A	1774	U
1	A	1780	G
1	A	1781	A
1	A	1782	U
1	A	1783	G
1	A	1788	C
1	A	1792	U
1	A	1794	U
1	A	1795	A
1	A	1797	A
1	A	1798	A
1	A	1800	U
1	A	1801	G
1	A	1805	U
1	A	1806	C
1	A	1807	C
1	A	1812	C
1	A	1838	U
1	A	1850	U
1	A	1852	C
1	A	1855	U
1	A	1856	U
1	A	1857	A
1	A	1871	A
1	A	1872	A
1	A	1873	U
1	A	1874	C
1	A	1881	C
1	A	1882	U
1	A	1886	A
1	A	1888	A
1	A	1892	G
1	A	1893	G
1	A	1898	U
1	A	1899	U
1	A	1900	G
1	A	1902	A
1	A	1903	C
1	A	1904	U
1	A	1905	C
1	A	1963	U

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Mol	Chain	Res	Type
1	A	1964	G
1	A	1965	U
1	A	1966	A
1	A	1967	G
1	A	1969	A
1	A	1970	A
1	A	1971	U
1	A	1976	A
1	A	1978	U
1	A	1990	A
1	A	1991	U
1	A	1996	C
1	A	1997	G
1	A	1998	A
1	A	1999	A
1	A	2000	G
1	A	2003	G
1	A	2010	C
1	A	2018	G
1	A	2019	A
1	A	2030	G
1	A	2034	G
1	A	2082	C
1	A	2084	U
1	A	2090	U
1	A	2092	G
1	A	2093	U
1	A	2094	A
1	A	2096	G
1	A	2097	A
1	A	2102	A
1	A	2106	A
1	A	2107	C
1	A	2108	A
1	A	2109	A
1	A	2113	C
1	A	2116	C
1	A	2117	A
1	A	2125	A
1	A	2133	C
1	A	2136	C
1	A	2143	U

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Mol	Chain	Res	Type
1	A	2145	A
1	A	2146	A
1	A	2147	A
1	A	2148	U
1	A	2149	A
1	A	2154	A
1	A	2160	G
1	A	2161	G
1	A	2163	A
1	A	2174	G
1	A	2186	C
1	A	2203	G
1	A	2211	C
1	A	2218	C
1	A	2219	A
1	A	2220	U
1	A	2221	U
1	A	2389	G
1	A	2393	A
1	A	2394	C
1	A	2395	U
1	A	2400	A
1	A	2403	G
1	A	2404	A
1	A	2405	A
1	A	2406	A
1	A	2408	G
1	A	2414	G
1	A	2415	G
1	A	2419	A
1	A	2424	A
1	A	2451	A
1	A	2452	A
1	A	2453	A
1	A	2477	U
1	A	2487	G
1	A	2494	G
1	A	2500	A
1	A	2501	A
1	A	2516	A
1	A	2518	U
1	A	2521	A

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Mol	Chain	Res	Type
1	A	2524	C
1	A	2537	A
1	A	2539	G
1	A	2542	G
1	A	2545	A
1	A	2548	A
1	A	2549	A
1	A	2550	C
1	A	2552	A
1	A	2554	G
1	A	2555	A
1	A	2556	C
1	A	2565	G
1	A	2566	G
1	A	2569	G
1	A	2573	A
1	A	2574	A
1	A	2575	U
1	A	2580	C
1	A	2581	G
1	A	2582	U
1	A	2584	A
1	A	2589	A
1	A	2591	U
1	A	2596	A
1	A	2598	G
1	A	2599	C
1	A	2600	G
1	A	2603	U
1	A	2606	A
1	A	2607	U
1	A	2608	G
1	A	2627	U
1	A	2628	G
1	A	2629	U
1	A	2640	U
1	A	2656	A
1	A	2659	C
1	A	2665	A
1	A	2666	A
1	A	2667	C
1	A	2668	G

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Mol	Chain	Res	Type
1	A	2671	C
1	A	2676	C
1	A	2678	A
1	A	2681	U
1	A	2684	G
1	A	2686	G
1	A	2687	G
1	A	2690	A
1	A	2694	A
1	A	2695	A
1	A	2696	G
1	A	2697	A
1	A	2704	U
1	A	2705	G
1	A	2711	U
1	A	2712	A
1	A	2715	C
1	A	2728	G
1	A	2730	G
1	A	2745	G
1	A	2809	A
1	A	2810	A
1	A	2811	A
1	A	2817	U
1	A	2819	U
1	A	2822	U
1	A	2823	U
1	A	2824	A
1	A	2831	U
1	A	2833	U
1	A	2834	A
1	A	2835	G
1	A	2837	G
1	A	2884	G
1	A	2887	U
1	A	2888	U
1	A	2928	G
1	A	2932	A
1	A	2933	C
1	A	2934	A
1	A	2945	G
1	A	2946	G

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Mol	Chain	Res	Type
1	A	2953	G
1	A	2958	G
1	A	2967	A
1	A	2968	U
1	A	2975	A
1	A	2981	A
1	A	2987	G
1	A	2991	U
1	A	2994	A
1	A	2995	A
1	A	2996	A
1	A	3005	C
1	A	3013	A
1	A	3016	G
1	A	3018	A
1	A	3020	U
1	A	3028	A
1	A	3029	G
1	A	3030	A
1	A	3033	A
1	A	3035	A
1	A	3059	U
1	A	3065	C
1	A	3067	G
1	A	3068	A
1	A	3076	G
1	A	3079	A
1	A	3081	C
1	A	3088	G
1	A	3091	U
1	A	3092	G
1	A	3093	G
1	A	3094	C
1	A	3100	G
1	A	3101	A
1	A	3108	A
1	A	3111	U
1	A	3112	U
1	A	3113	U
1	A	3116	A
1	A	3118	A
1	A	3123	C

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Mol	Chain	Res	Type
1	A	3124	G
1	A	3126	A
1	A	3127	A
1	A	3130	U
1	A	3131	A
1	A	3132	C
1	A	3135	A
1	A	3138	A
1	A	3140	U
1	A	3141	G
1	A	3146	U
1	A	3150	G
1	A	3155	G
1	A	3158	U
1	A	3159	G
1	A	3160	A
1	A	3161	A
1	A	3162	A
1	A	3164	G
1	A	3169	C
1	A	3173	G
1	A	3175	G
1	A	3176	A
1	A	3180	C
1	A	3187	G
1	A	3193	G
1	A	3201	C
1	A	3202	U
1	A	3204	C
1	A	3208	C
1	A	3212	G
1	A	3215	G
1	A	3222	G
1	A	3226	C
1	A	3230	G
1	A	3231	A
1	A	3232	U
1	A	3234	U
1	A	3245	U
1	A	3246	A
1	A	3247	U
1	A	3248	C

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Mol	Chain	Res	Type
1	A	3253	G
1	A	3257	G
1	A	3258	C
1	A	3269	A
1	A	3277	G
1	A	3282	U
1	A	3287	C
1	A	3292	A
1	A	3294	U
1	A	3295	A
1	A	3297	G
1	A	3301	C
1	A	3304	G
1	A	3305	A
1	A	3306	G
1	A	3309	G
1	A	3310	G
1	A	3313	U
1	A	3330	A
1	A	3338	U
1	A	3342	C
1	A	3343	C
1	A	3349	G
1	A	3353	A
1	A	3354	A
1	A	3356	U
1	A	3357	U
1	A	3358	U
1	A	3359	A
1	A	3361	U
1	A	3362	A
1	A	3363	U
1	A	3374	U
1	A	3375	A
1	A	3378	C
1	A	3379	A
1	A	3380	U
1	A	3381	A
1	A	3382	U
1	A	3383	A
1	A	3385	U
1	A	3389	G

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Mol	Chain	Res	Type
1	A	3391	G
1	A	3392	A
1	A	3396	U
1	A	3398	A
1	A	3415	A
1	A	3416	G
1	A	3418	A
1	A	3421	A
1	A	3425	G
1	A	3432	A
1	A	3435	A
1	A	3442	C
1	A	3443	A
1	A	3444	G
1	A	3459	A
1	A	3463	G
1	A	3464	U
1	A	3465	G
1	A	3468	G
1	A	3471	A
1	A	3472	A
1	A	3476	A
1	A	3477	A
1	A	3478	G
1	A	3483	U
1	A	3488	U
1	A	3493	G
1	A	3500	G
1	A	3506	U
1	A	3507	A
1	A	3510	C
1	A	3514	A
1	A	3515	A
1	A	3516	A
1	A	3526	U
1	A	3527	U
1	A	3528	A
1	A	3529	A
1	A	3530	A
1	A	3553	G
1	A	3568	G
1	A	3571	A

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Mol	Chain	Res	Type
1	A	3572	A
1	A	3573	U
1	A	3574	G
1	A	3576	A
1	A	3577	A
1	A	3580	G
1	A	3581	A
1	A	3582	G
1	A	3583	A
1	A	3585	A
1	A	3590	A
1	A	3591	U
1	A	3594	G
1	A	3597	C
1	A	3615	A
1	A	3616	U
1	A	3617	A
1	A	3618	A
1	A	3623	A
1	A	3624	U
1	A	3626	A
1	A	3627	C
1	A	3629	U
1	A	3659	C
1	A	3661	A
1	A	3662	U
1	A	3663	A
1	A	3664	G
1	A	3665	U
1	A	3667	C
1	A	3668	U
1	A	3669	U
1	A	3670	U
1	A	3671	A
1	A	3676	C
1	A	3677	A
1	A	3680	A
1	A	3689	C
1	A	3697	G
1	A	3698	U
1	A	3707	U
1	A	3710	U

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Mol	Chain	Res	Type
1	A	3711	U
1	A	3712	G
1	A	3716	C
1	A	3727	A
1	A	3728	A
1	A	3732	U
1	A	3733	G
1	A	3736	A
1	A	3737	G
1	A	3739	A
1	A	3740	A
1	A	3741	A
1	A	3752	C
1	A	3755	U
1	A	3761	G
1	A	3767	U
1	A	3770	C
1	A	3774	A
1	A	3775	G
1	A	3778	G
1	A	3779	U
1	A	3782	A
1	A	3783	G
2	B	7	G
2	B	13	A
2	B	16	A
2	B	18	A
2	B	22	G
2	B	25	A
2	B	26	C
2	B	33	U
2	B	38	U
2	B	48	G
2	B	51	G
2	B	53	U
2	B	54	A
2	B	63	A
2	B	64	A
2	B	69	U
2	B	71	G
2	B	74	A
2	B	76	U

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Mol	Chain	Res	Type
2	B	89	G
2	B	93	G
2	B	97	G
2	B	100	A
2	B	110	G
3	C	3	G
3	C	5	A
3	C	6	C
3	C	27	U
3	C	36	C
3	C	38	G
3	C	39	C
3	C	43	G
3	C	50	G
3	C	53	G
3	C	55	A
3	C	63	A
3	C	64	U
3	C	66	C
3	C	67	G
3	C	75	A
3	C	78	U
3	C	79	G
3	C	82	G
3	C	84	G
3	C	85	A
3	C	90	G
3	C	94	C
3	C	98	A
3	C	99	G
3	C	100	A
3	C	103	G
3	C	107	A
3	C	108	A
3	C	109	U
3	C	112	A
3	C	114	A
3	C	115	C
3	C	116	U
3	C	117	A
3	C	119	A
3	C	122	A

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Mol	Chain	Res	Type
3	C	123	A
3	C	135	G
3	C	137	A
3	C	138	U
3	C	139	A
3	C	140	G
3	C	142	G
3	C	146	C
3	C	149	C

All (190) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	11	A
1	A	21	G
1	A	25	A
1	A	40	A
1	A	65	A
1	A	71	A
1	A	132	U
1	A	155	U
1	A	162	U
1	A	215	C
1	A	250	U
1	A	270	U
1	A	289	A
1	A	290	G
1	A	337	A
1	A	344	A
1	A	383	U
1	A	416	G
1	A	500	A
1	A	501	U
1	A	504	A
1	A	505	A
1	A	579	C
1	A	580	A
1	A	581	C
1	A	583	U
1	A	594	C
1	A	607	A
1	A	608	A

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Mol	Chain	Res	Type
1	A	620	U
1	A	621	C
1	A	641	G
1	A	645	A
1	A	647	U
1	A	652	A
1	A	664	U
1	A	666	U
1	A	673	U
1	A	674	U
1	A	681	U
1	A	683	A
1	A	697	A
1	A	698	G
1	A	703	U
1	A	715	U
1	A	739	G
1	A	764	G
1	A	765	A
1	A	777	U
1	A	778	U
1	A	859	C
1	A	888	A
1	A	889	U
1	A	899	A
1	A	903	C
1	A	935	A
1	A	1025	A
1	A	1026	G
1	A	1035	G
1	A	1042	C
1	A	1080	C
1	A	1096	G
1	A	1101	A
1	A	1115	G
1	A	1197	U
1	A	1205	U
1	A	1206	U
1	A	1217	U
1	A	1221	A
1	A	1222	U
1	A	1224	A

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Mol	Chain	Res	Type
1	A	1234	A
1	A	1272	U
1	A	1336	U
1	A	1435	G
1	A	1443	U
1	A	1444	A
1	A	1457	G
1	A	1459	U
1	A	1502	G
1	A	1503	A
1	A	1537	G
1	A	1538	U
1	A	1539	U
1	A	1566	A
1	A	1574	C
1	A	1577	A
1	A	1642	G
1	A	1643	U
1	A	1705	A
1	A	1748	A
1	A	1750	U
1	A	1779	A
1	A	1794	U
1	A	1798	A
1	A	1805	U
1	A	1873	U
1	A	1881	C
1	A	1898	U
1	A	1904	U
1	A	1964	G
1	A	1989	A
1	A	1990	A
1	A	1996	C
1	A	1999	A
1	A	2002	G
1	A	2033	C
1	A	2096	G
1	A	2108	A
1	A	2116	C
1	A	2125	A
1	A	2146	A
1	A	2153	A

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Mol	Chain	Res	Type
1	A	2219	A
1	A	2394	C
1	A	2403	G
1	A	2405	A
1	A	2437	A
1	A	2452	A
1	A	2499	G
1	A	2523	U
1	A	2554	G
1	A	2575	U
1	A	2590	U
1	A	2598	G
1	A	2665	A
1	A	2678	A
1	A	2696	G
1	A	2727	U
1	A	2816	U
1	A	2822	U
1	A	2832	A
1	A	2883	U
1	A	2886	A
1	A	2932	A
1	A	3016	G
1	A	3019	A
1	A	3034	A
1	A	3067	G
1	A	3093	G
1	A	3123	C
1	A	3130	U
1	A	3137	U
1	A	3140	U
1	A	3161	A
1	A	3229	C
1	A	3245	U
1	A	3257	G
1	A	3309	G
1	A	3337	U
1	A	3342	C
1	A	3361	U
1	A	3362	A
1	A	3381	A
1	A	3382	U

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Mol	Chain	Res	Type
1	A	3391	G
1	A	3414	G
1	A	3434	A
1	A	3463	G
1	A	3476	A
1	A	3477	A
1	A	3505	U
1	A	3526	U
1	A	3529	A
1	A	3573	U
1	A	3590	A
1	A	3617	A
1	A	3623	A
1	A	3624	U
1	A	3658	G
1	A	3660	A
1	A	3661	A
1	A	3663	A
1	A	3664	G
1	A	3667	C
1	A	3711	U
1	A	3782	A
2	B	32	A
2	B	75	G
2	B	84	U
2	B	109	U
3	C	26	U
3	C	35	A
3	C	37	A
3	C	75	A
3	C	98	A
3	C	114	A
3	C	134	G
3	C	139	A
3	C	145	A

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 171 ligands modelled in this entry, 169 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
46	YMZ	A	3801	-	28,28,28	3.65	9 (32%)	41,43,43	2.72	13 (31%)
46	YMZ	K	301	-	28,28,28	2.82	5 (17%)	41,43,43	2.42	12 (29%)

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
46	YMZ	A	3801	-	-	6/20/28/28	0/3/3/3
46	YMZ	K	301	-	-	14/20/28/28	1/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	A	3801	YMZ	CAZ-CAT	-11.25	1.38	1.50
46	A	3801	YMZ	CAS-CAW	-10.43	1.38	1.52
46	K	301	YMZ	CAZ-CAT	-8.93	1.40	1.50
46	A	3801	YMZ	CAY-CAR	-8.02	1.37	1.50
46	K	301	YMZ	CAS-CAW	-7.92	1.41	1.52
46	K	301	YMZ	CAY-CAR	-6.67	1.40	1.50
46	A	3801	YMZ	CAT-CAV	-4.79	1.38	1.43
46	K	301	YMZ	CAR-NAP	3.17	1.34	1.31
46	A	3801	YMZ	FAG-CAZ	-3.01	1.21	1.32
46	A	3801	YMZ	FAF-CAZ	-2.88	1.22	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	A	3801	YMZ	FAB-CAY	-2.72	1.22	1.32
46	A	3801	YMZ	CAS-CAU	-2.62	1.38	1.43
46	K	301	YMZ	CAT-CAV	-2.55	1.40	1.43
46	A	3801	YMZ	FAC-CAY	-2.01	1.25	1.32

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	K	301	YMZ	CAK-CAR-NAP	-8.93	119.94	125.50
46	A	3801	YMZ	CAK-CAR-NAP	-8.73	120.06	125.50
46	A	3801	YMZ	CAO-CAX-CAW	-6.92	106.89	114.03
46	K	301	YMZ	CAR-NAP-CAV	5.73	122.28	116.89
46	A	3801	YMZ	FAG-CAZ-CAT	-5.52	106.59	112.32
46	A	3801	YMZ	CAR-NAP-CAV	5.51	122.07	116.89
46	K	301	YMZ	CAY-CAR-NAP	4.78	119.06	114.79
46	A	3801	YMZ	CAN-NAQ-CAX	-4.34	108.91	111.62
46	A	3801	YMZ	OAA-CAW-CAS	-4.29	104.47	111.03
46	K	301	YMZ	CAS-CAU-CAV	4.02	119.82	117.83
46	K	301	YMZ	CAZ-CAT-CAV	3.83	121.91	119.46
46	A	3801	YMZ	CAT-CAV-NAP	3.81	120.76	118.28
46	K	301	YMZ	FAE-CAZ-CAT	-3.04	109.17	112.32
46	A	3801	YMZ	CAK-CAR-CAY	3.03	123.93	120.10
46	K	301	YMZ	CAT-CAV-NAP	2.99	120.23	118.28
46	K	301	YMZ	CAN-NAQ-CAX	2.59	113.24	111.62
46	A	3801	YMZ	FAE-CAZ-CAT	-2.40	109.84	112.32
46	A	3801	YMZ	FAB-CAY-CAR	-2.38	108.40	112.47
46	A	3801	YMZ	CAZ-CAT-CAV	-2.37	117.94	119.46
46	K	301	YMZ	FAG-CAZ-CAT	-2.31	109.92	112.32
46	K	301	YMZ	CAJ-CAU-CAS	-2.31	120.71	123.40
46	K	301	YMZ	CAS-CAK-CAR	2.14	120.05	118.87
46	A	3801	YMZ	CAJ-CAH-CAI	-2.09	117.66	120.99
46	A	3801	YMZ	FAF-CAZ-CAT	2.05	114.45	112.32
46	K	301	YMZ	CAO-CAX-CAW	-2.01	111.96	114.03

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
46	K	301	YMZ	CAV-CAT-CAZ-FAE
46	K	301	YMZ	CAV-CAT-CAZ-FAF
46	K	301	YMZ	CAV-CAT-CAZ-FAG
46	K	301	YMZ	CAS-CAW-CAX-NAQ

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Mol	Chain	Res	Type	Atoms
46	K	301	YMZ	OAA-CAW-CAX-CAO
46	K	301	YMZ	OAA-CAW-CAX-NAQ
46	A	3801	YMZ	CAK-CAS-CAW-OAA
46	K	301	YMZ	CAS-CAW-CAX-CAO
46	K	301	YMZ	CAK-CAS-CAW-OAA
46	A	3801	YMZ	CAU-CAS-CAW-OAA
46	K	301	YMZ	CAU-CAS-CAW-OAA
46	A	3801	YMZ	CAS-CAW-CAX-CAO
46	A	3801	YMZ	OAA-CAW-CAX-CAO
46	A	3801	YMZ	CAS-CAW-CAX-NAQ
46	K	301	YMZ	CAU-CAS-CAW-CAX
46	K	301	YMZ	CAK-CAS-CAW-CAX
46	A	3801	YMZ	CAK-CAS-CAW-CAX
46	K	301	YMZ	CAI-CAT-CAZ-FAF
46	K	301	YMZ	CAI-CAT-CAZ-FAG
46	K	301	YMZ	CAI-CAT-CAZ-FAE

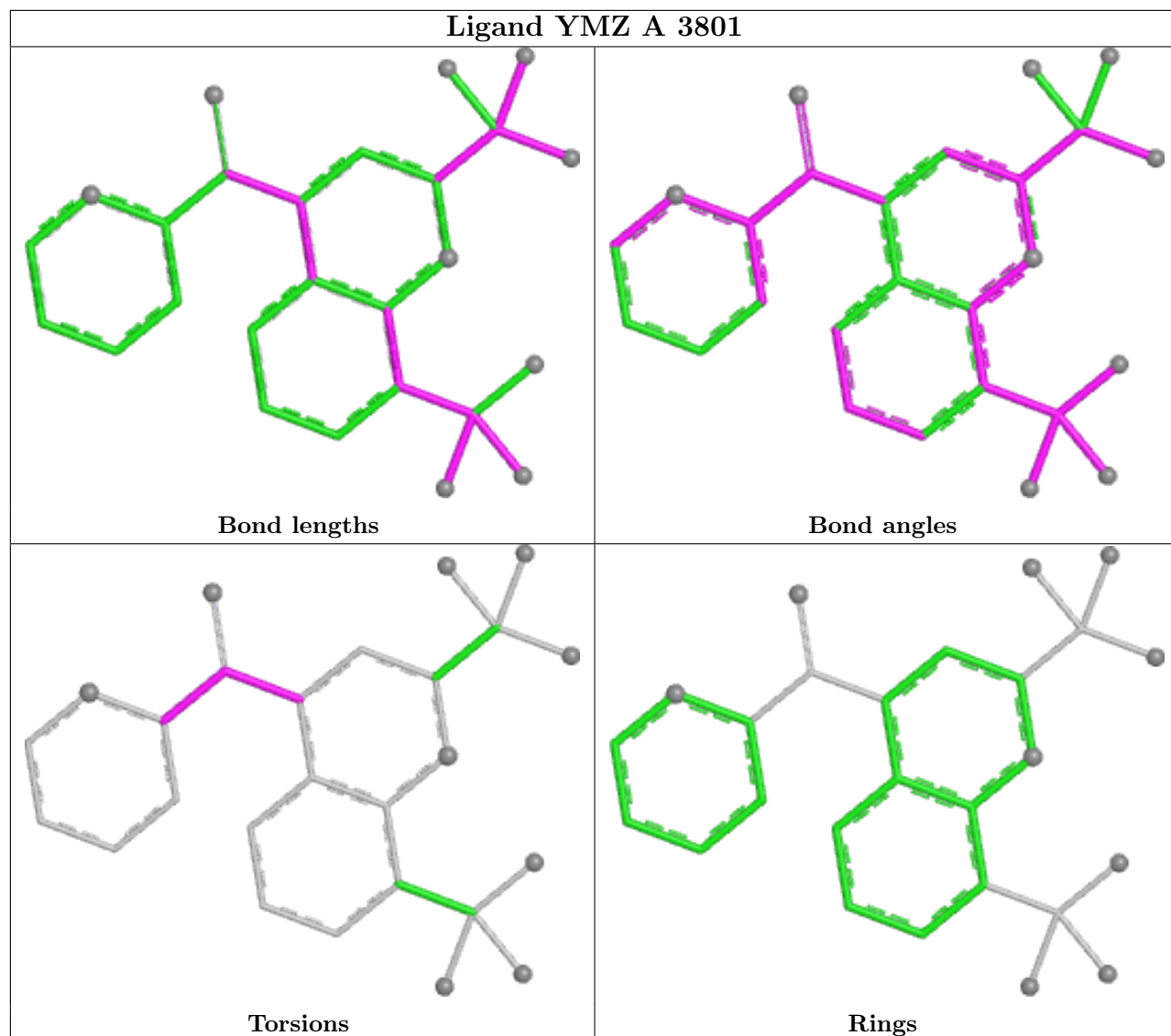
All (1) ring outliers are listed below:

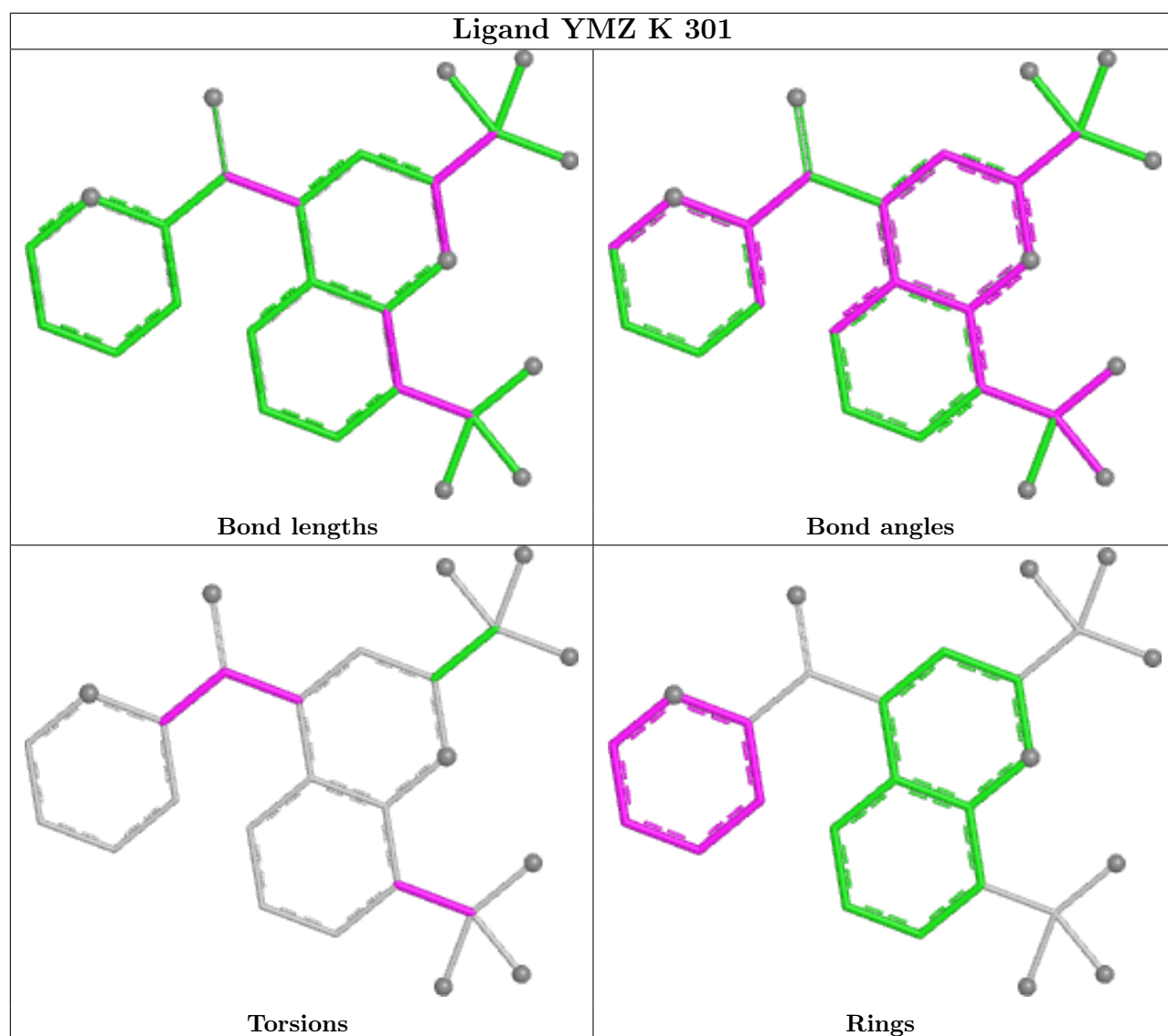
Mol	Chain	Res	Type	Atoms
46	K	301	YMZ	CAL-CAM-CAN-CAO-CAX-NAQ

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
46	A	3801	YMZ	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	9

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	3631:U	O3'	3632:U	P	5.96
1	A	3018:A	O3'	3019:A	P	4.60
1	A	1909:U	O3'	1910:C	P	4.15
1	A	3657:G	O3'	3658:G	P	3.84
1	A	181:C	O3'	182:U	P	3.44
1	A	2550:C	O3'	2551:U	P	3.40
1	A	2733:A	O3'	2734:C	P	3.38
1	A	257:U	O3'	258:U	P	3.35
1	A	2462:C	O3'	2463:U	P	3.20

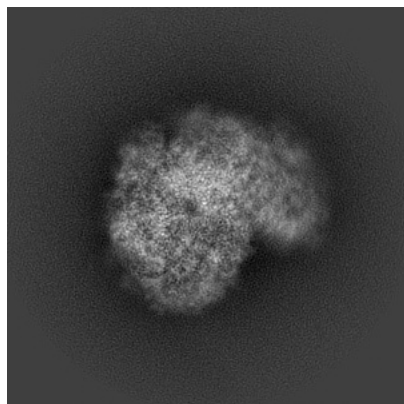
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8576. These allow visual inspection of the internal detail of the map and identification of artifacts.

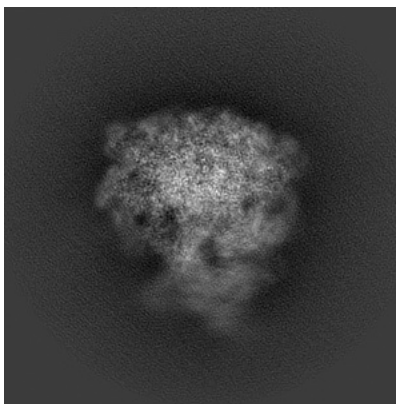
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

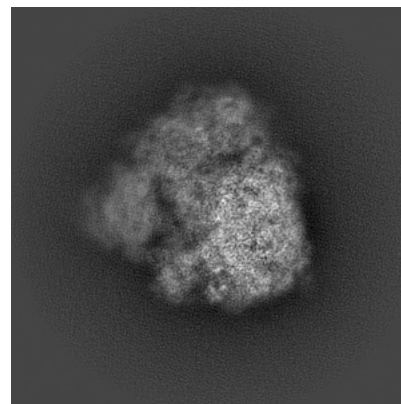
6.1.1 Primary map



X

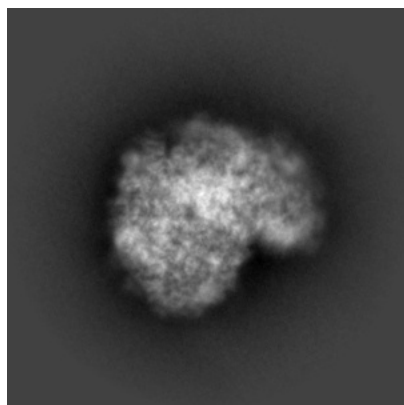


Y

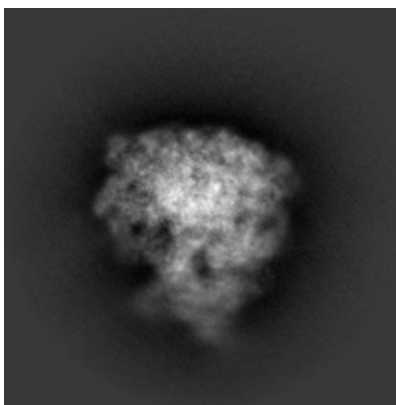


Z

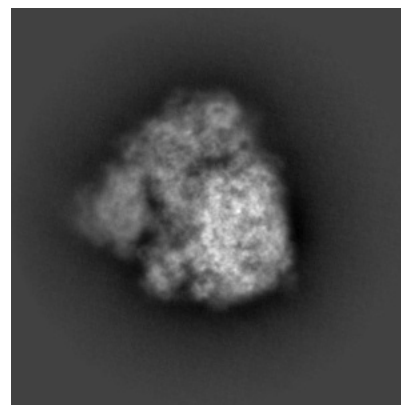
6.1.2 Raw map



X



Y

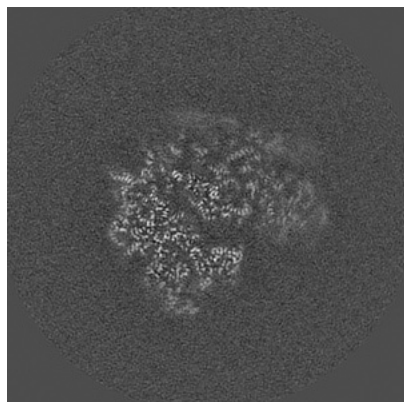


Z

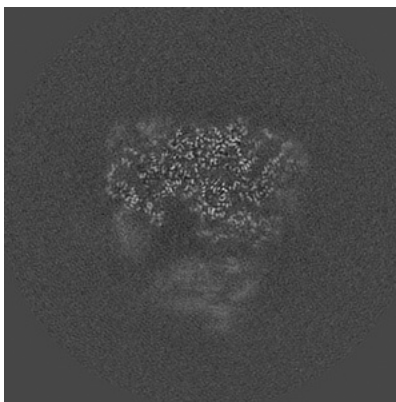
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

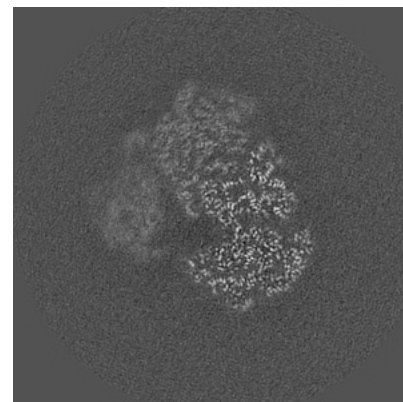
6.2.1 Primary map



X Index: 225

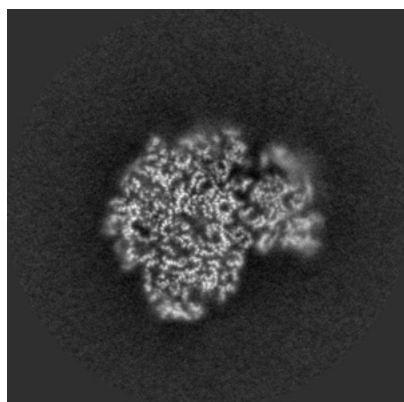


Y Index: 225

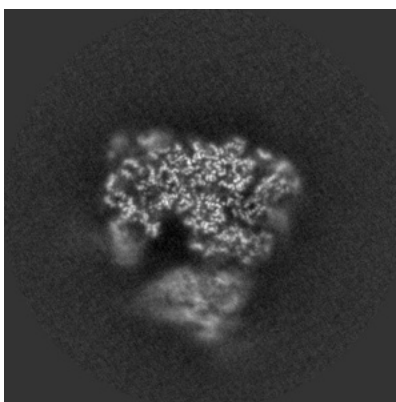


Z Index: 225

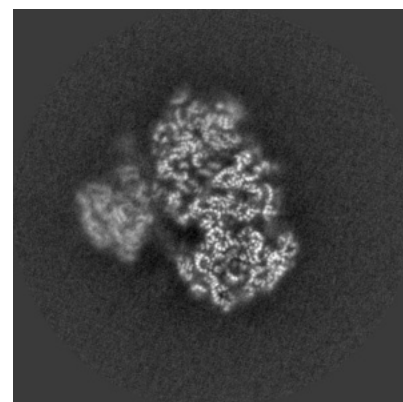
6.2.2 Raw map



X Index: 180



Y Index: 180

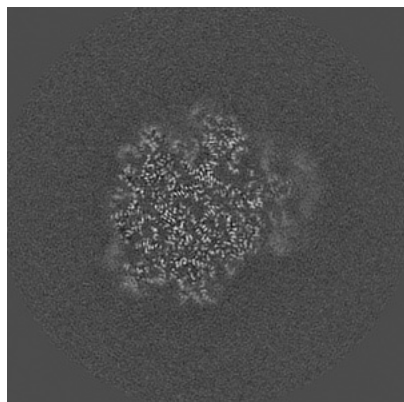


Z Index: 180

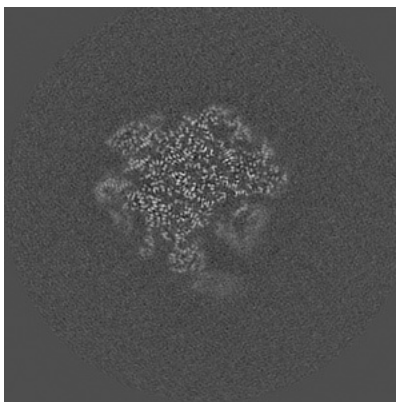
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

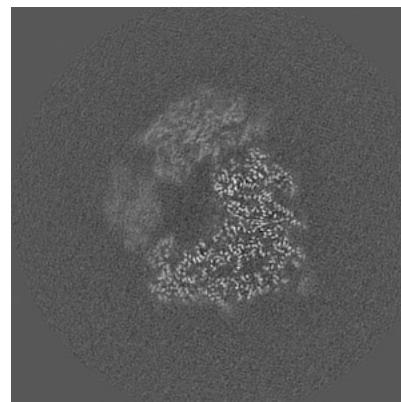
6.3.1 Primary map



X Index: 268

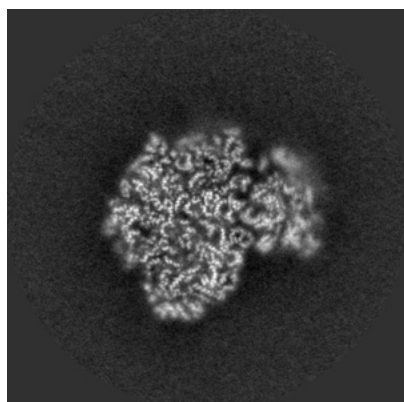


Y Index: 172

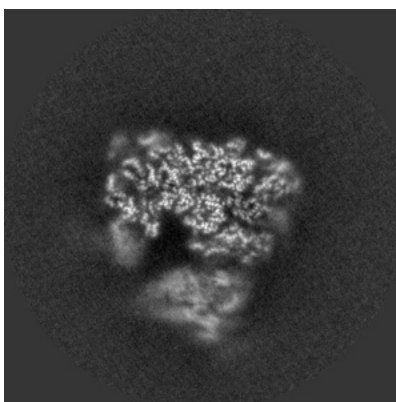


Z Index: 205

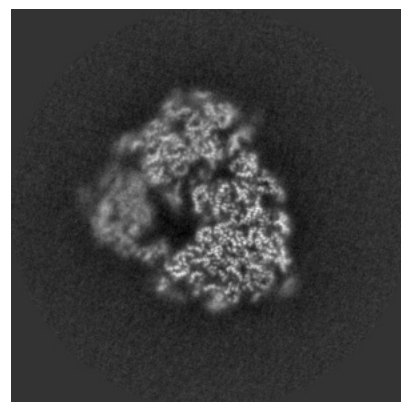
6.3.2 Raw map



X Index: 182



Y Index: 181

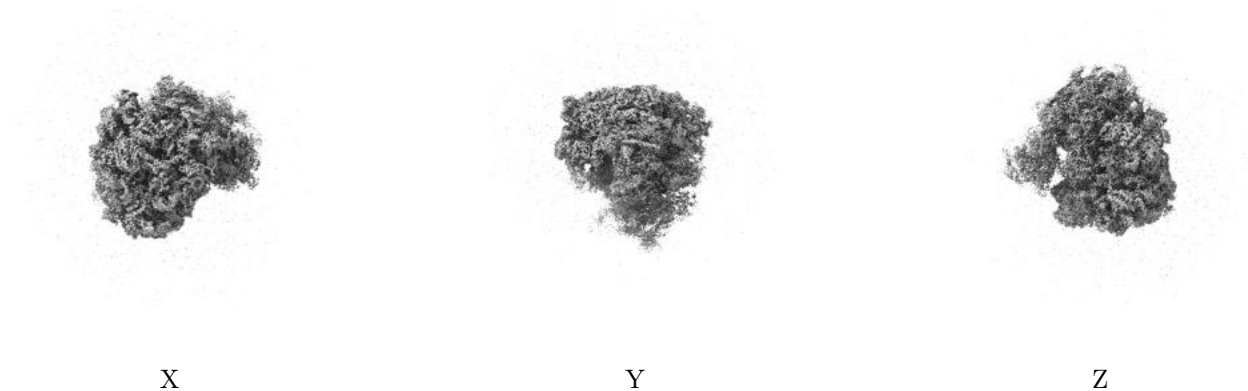


Z Index: 166

The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

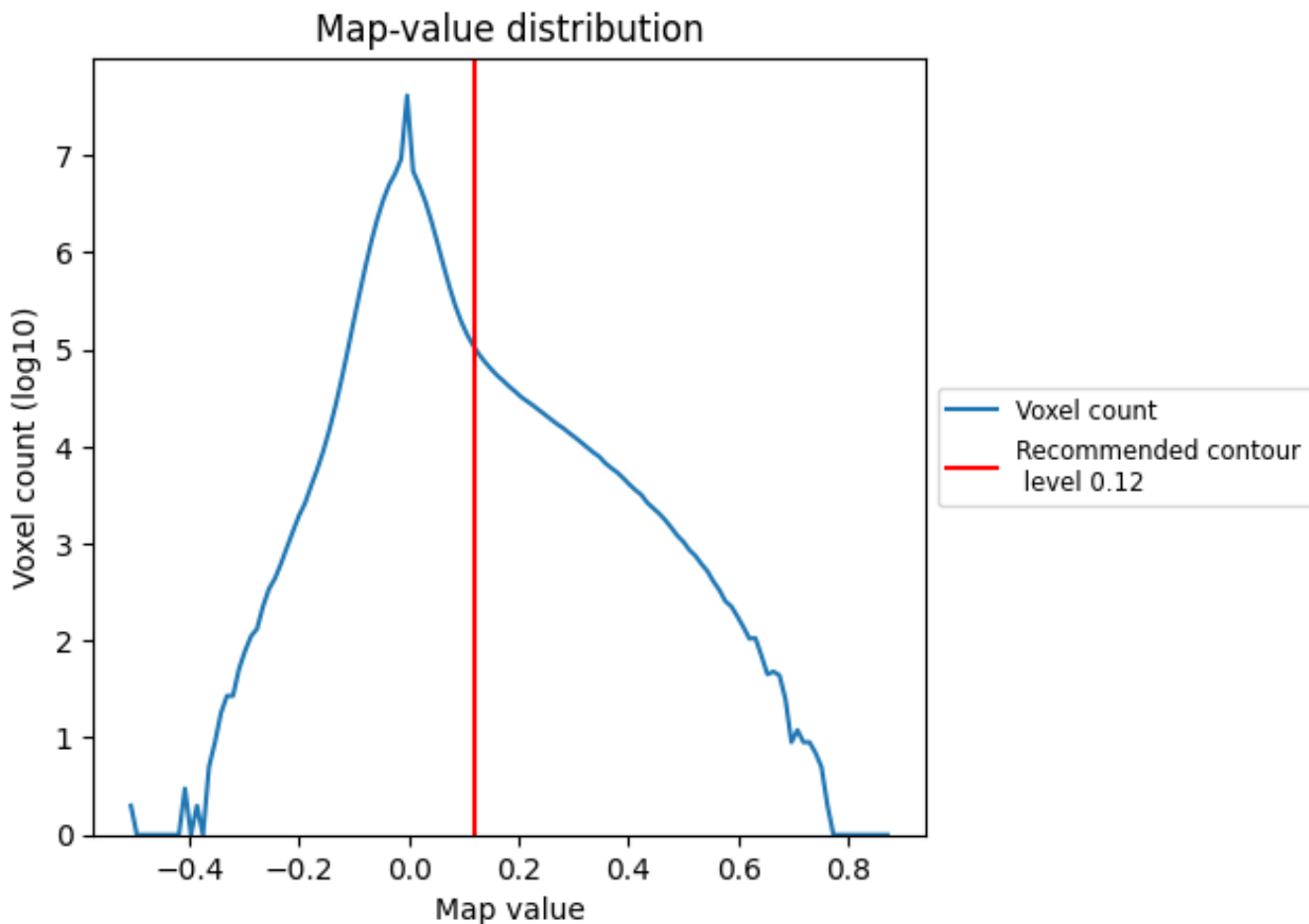
6.5 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

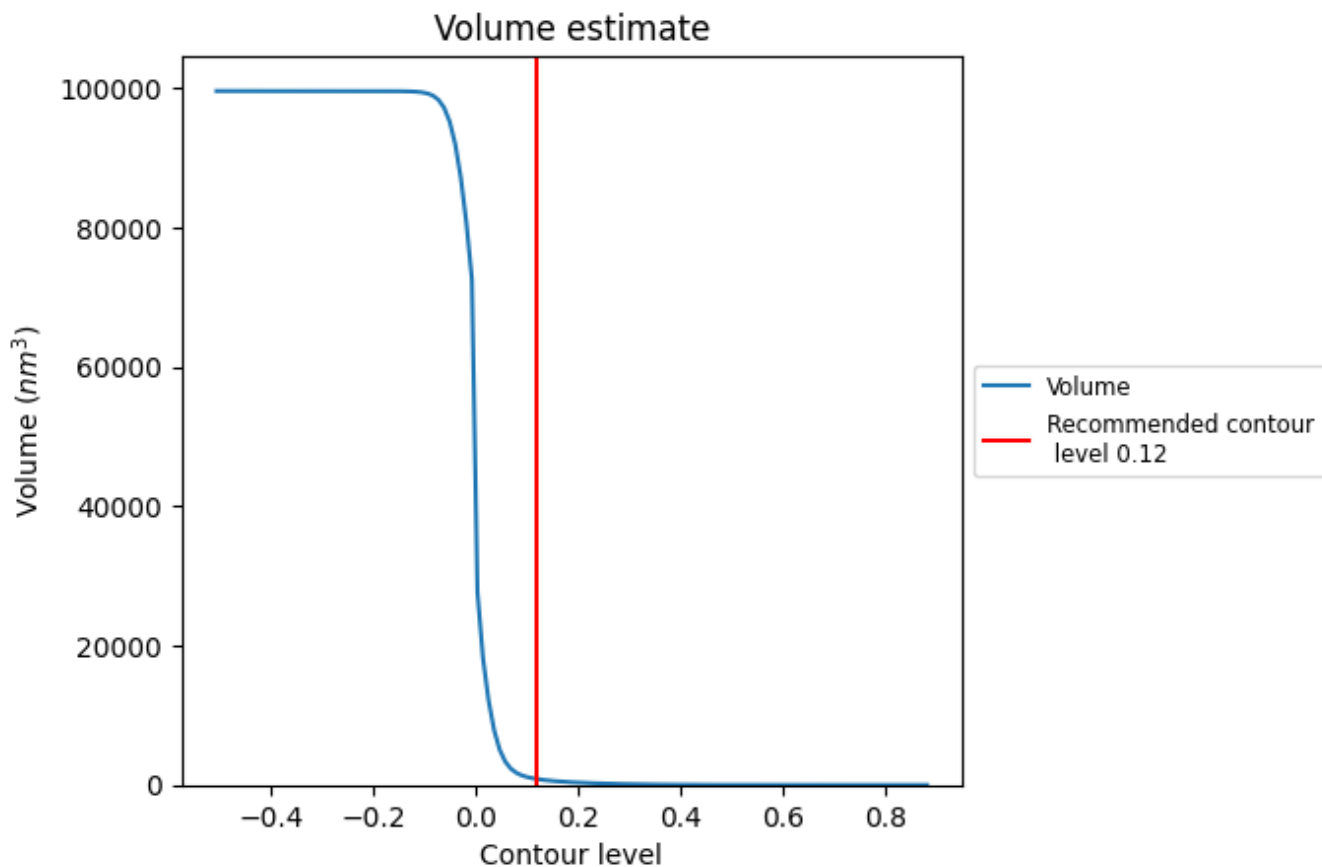
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

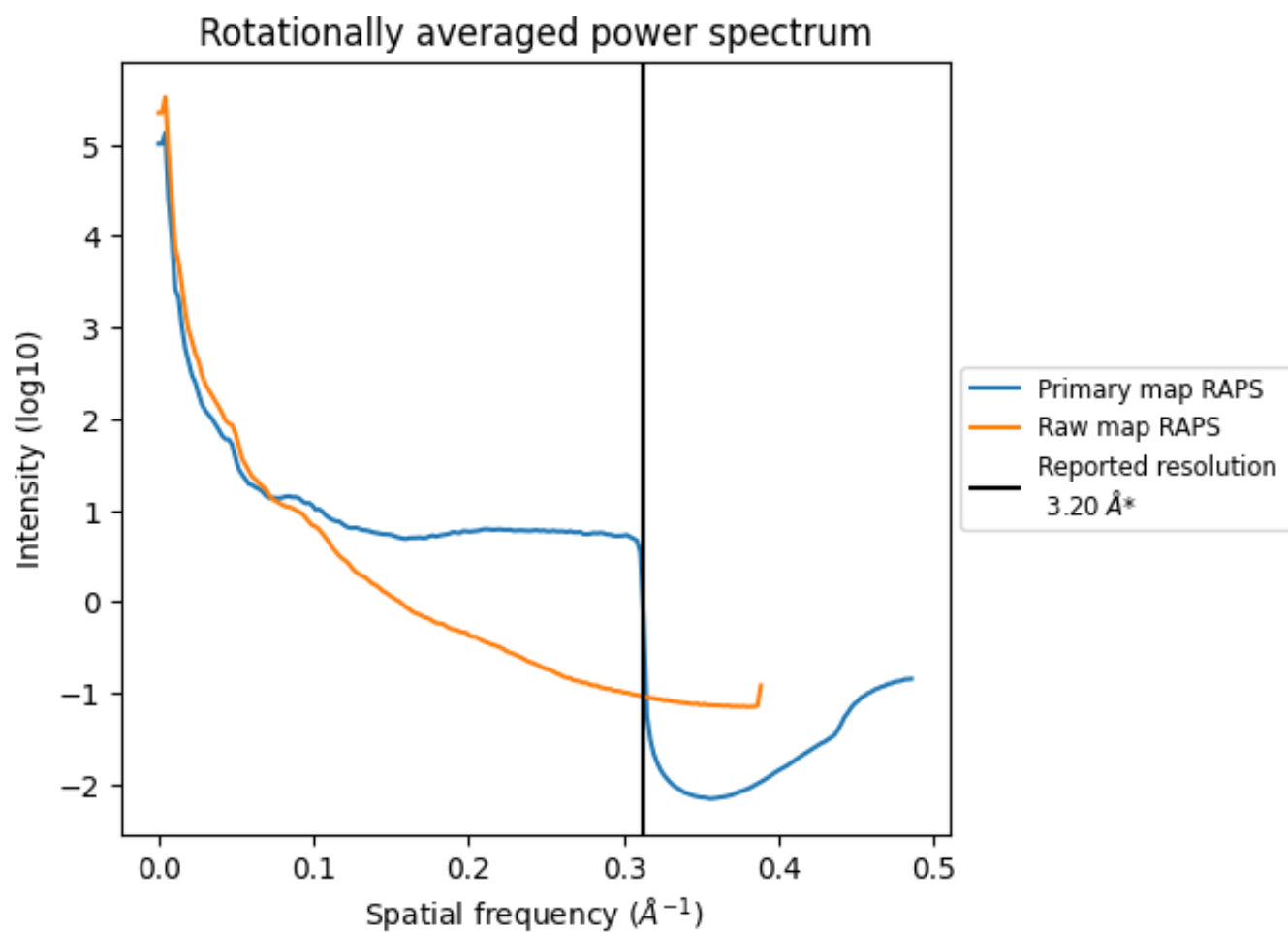
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 854 nm^3 ; this corresponds to an approximate mass of 771 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum i



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

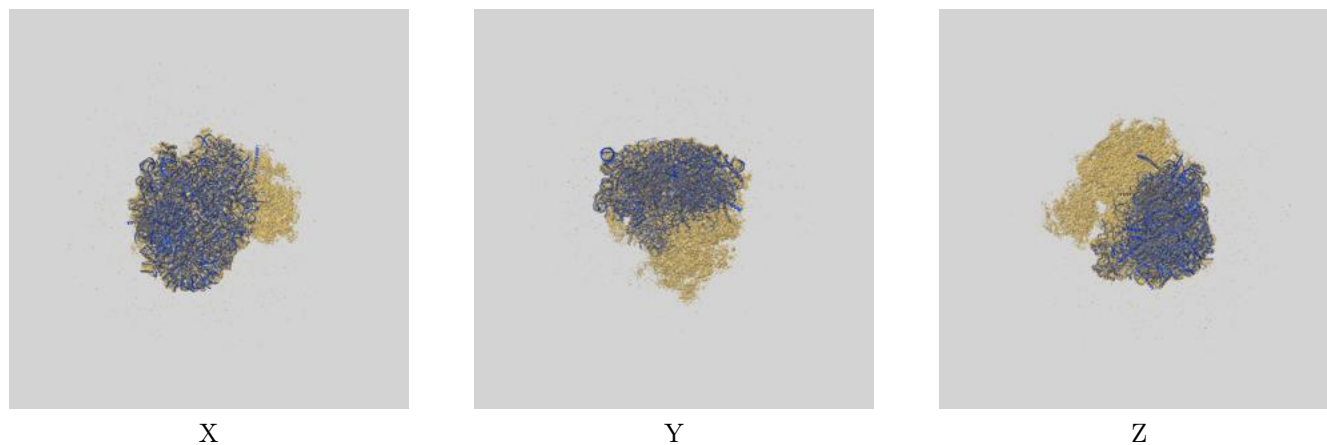
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

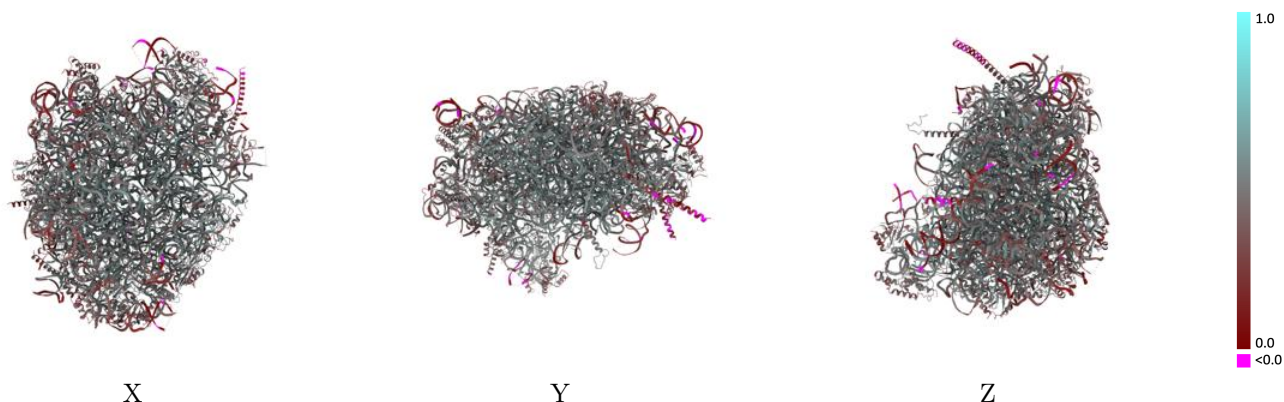
This section contains information regarding the fit between EMDB map EMD-8576 and PDB model 5UMD. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



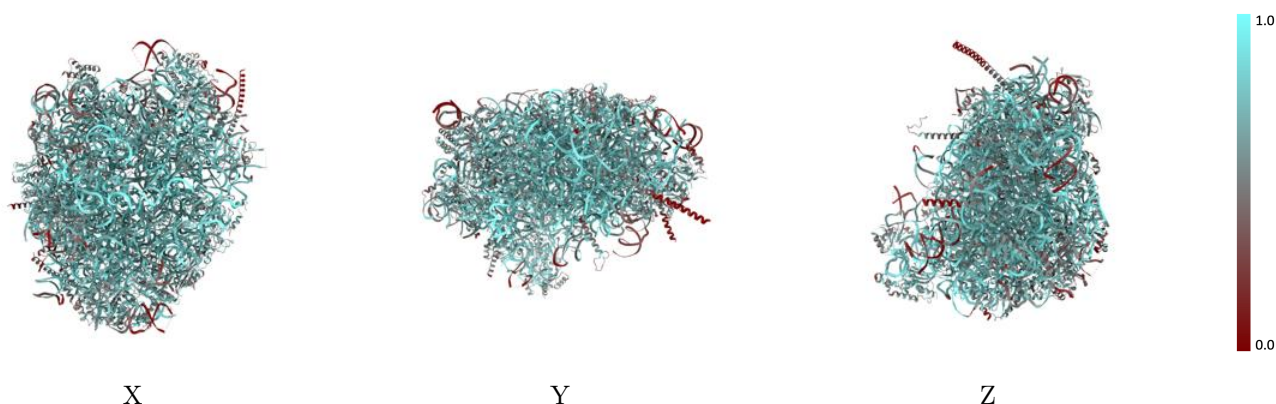
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [\(i\)](#)



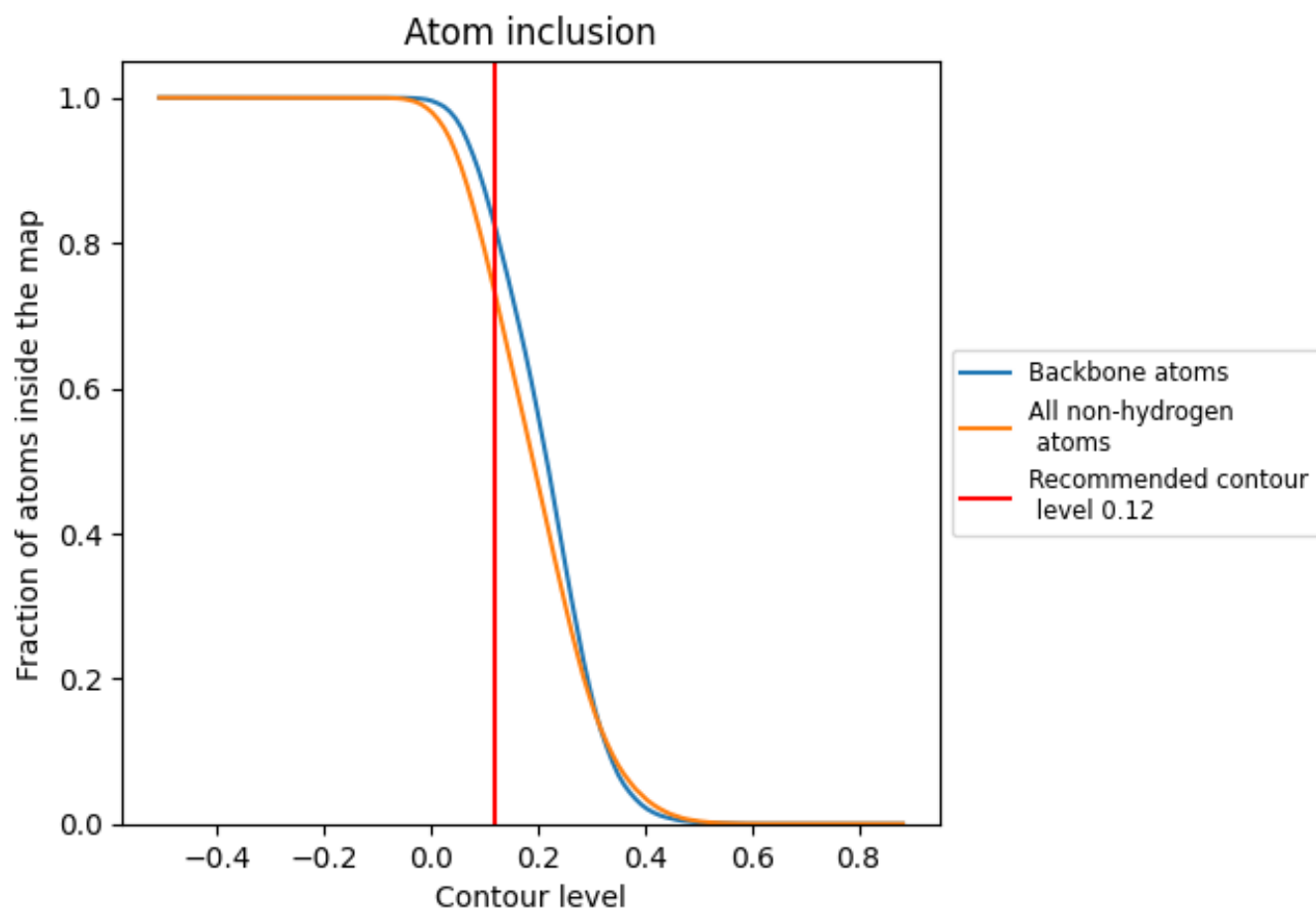
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [\(i\)](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.12).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 73% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary























The table lists the average atom inclusion at the recommended contour level (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7319	 0.4600
0	 0.6434	 0.4510
1	 0.5722	 0.3950
2	 0.6229	 0.4390
3	 0.6450	 0.4330
4	 0.5420	 0.4030
5	 0.6712	 0.4580
6	 0.5659	 0.3940
7	 0.6433	 0.4490
8	 0.6604	 0.4770
9	 0.7277	 0.4880
A	 0.7905	 0.4730
B	 0.8639	 0.4920
C	 0.8529	 0.4920
D	 0.6586	 0.4810
E	 0.6769	 0.4680
F	 0.6427	 0.4380
G	 0.6029	 0.3860
H	 0.6515	 0.4410
I	 0.6057	 0.4130
J	 0.5176	 0.3560
K	 0.6748	 0.4730
L	 0.6503	 0.4350
M	 0.6274	 0.4520
N	 0.6198	 0.4170
O	 0.7194	 0.4850
P	 0.7209	 0.4930
Q	 0.6352	 0.4410
R	 0.6335	 0.4080
S	 0.6903	 0.4810
T	 0.5347	 0.3830
U	 0.6660	 0.4610
V	 0.6262	 0.4450
W	 0.6987	 0.4830
X	 0.5235	 0.3470



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Chain	Atom inclusion	Q-score
Y	 0.5745	 0.3990
Z	 0.5990	 0.4030
a	 0.6306	 0.4770
b	 0.6049	 0.4010
c	 0.7000	 0.4720
d	 0.5537	 0.3910
e	 0.6556	 0.4630
f	 0.6925	 0.4560
g	 0.4511	 0.4040
h	 0.6375	 0.4710
i	 0.6378	 0.4660