



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 10:48 AM UTC

PDB ID : 5UMD / pdb_00005umd
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:

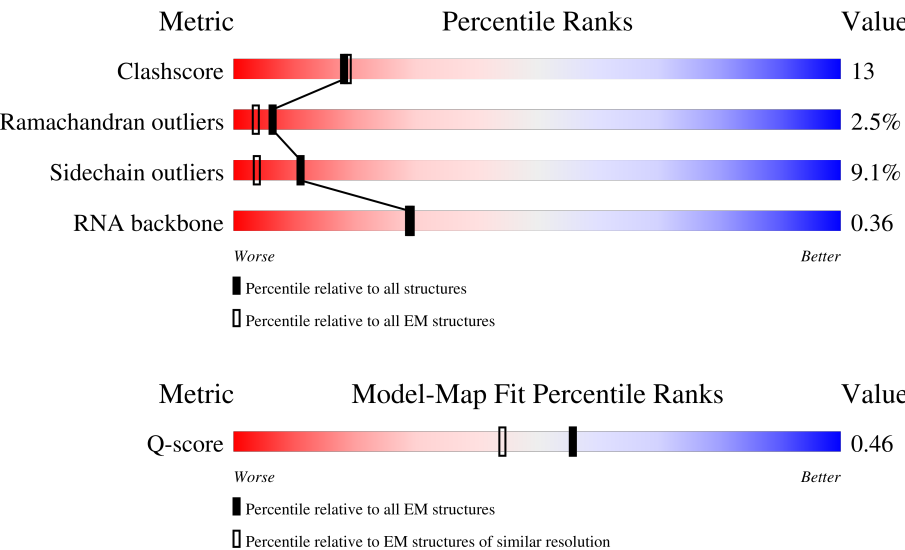
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	6% 29% 41% 13% 16%
2	B	119	45% 47% 7%
3	C	159	33% 44% 16% 5%

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Mol	Chain	Length	Quality of chain
4	D	260	
5	E	386	
6	F	411	
7	G	173	
8	H	190	
9	I	221	
10	J	283	
11	K	202	
12	L	215	
13	M	139	
14	N	165	
15	O	148	
16	P	205	
17	Q	219	
18	R	294	
19	S	187	
20	T	182	
21	U	184	
22	V	161	
23	W	203	
24	X	139	
25	Y	190	
26	Z	126	
27	0	162	
28	1	146	

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Mol	Chain	Length	Quality of chain
29	2	127	
30	3	124	
31	4	67	
32	5	257	
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	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
48	ZN	f	101	-	-	X	-

2 Entry composition

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
1	A	3191	Total	C	N	O	P	0	0
			67935	30426	12044	22274	3191		

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
2	B	118	Total	C	N	O	P	0	0
			2525	1128	461	818	118		

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
3	C	151	Total	C	N	O	P	0	0
			3224	1444	589	1040	151		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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
13	M	132	Total	C	N	O	S	0	0
			996	631	179	178	8		

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

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

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

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

- Molecule 16 is a protein called Ribosomal protein L15.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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		

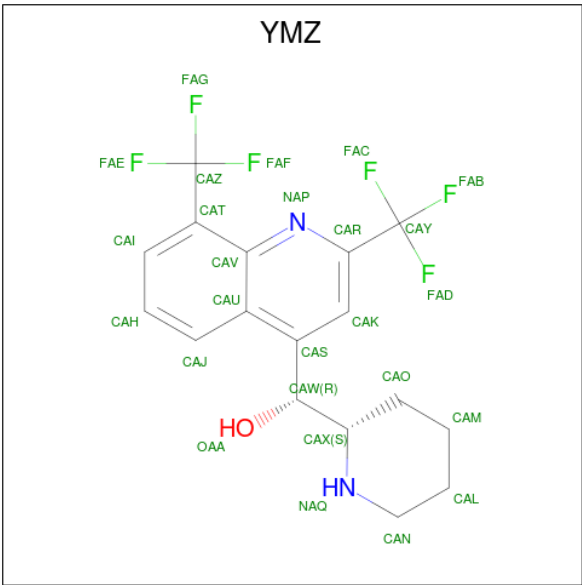
- Molecule 44 is a protein called 60S ribosomal protein L37a.

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 (11R,12S)- Mefloquine (CCD ID: 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 (CCD ID: 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 (CCD ID: 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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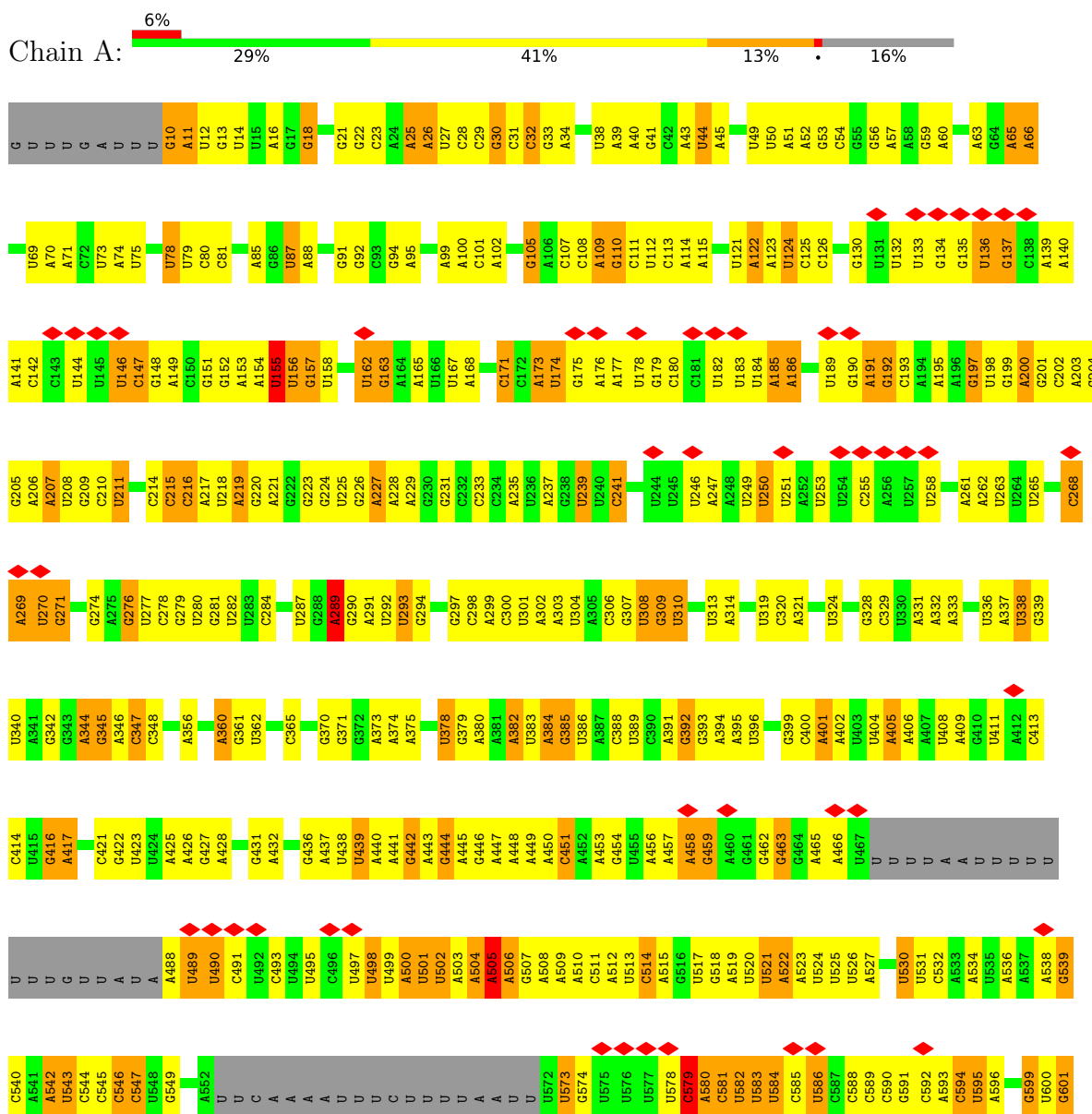
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Mol	Chain	Residues	Atoms		AltConf
48	h	1	Total 1	Zn 1	0
48	i	1	Total 1	Zn 1	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

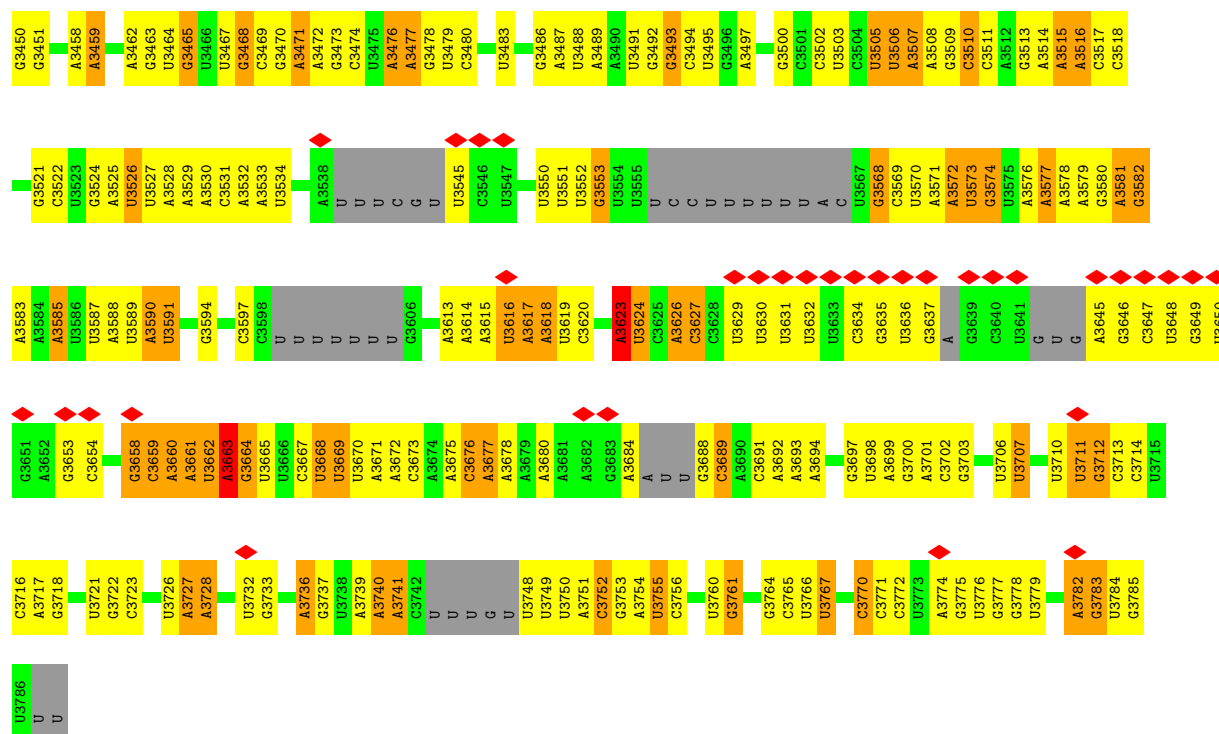
• Molecule 1: 28S ribosomal RNA





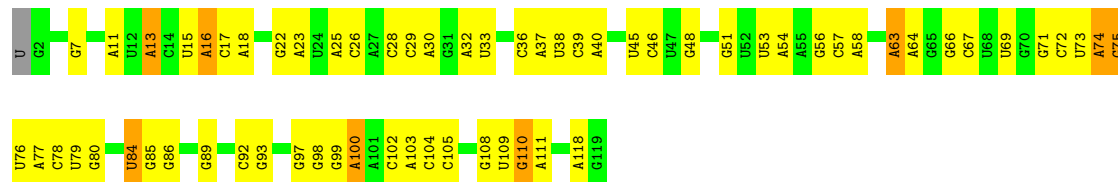






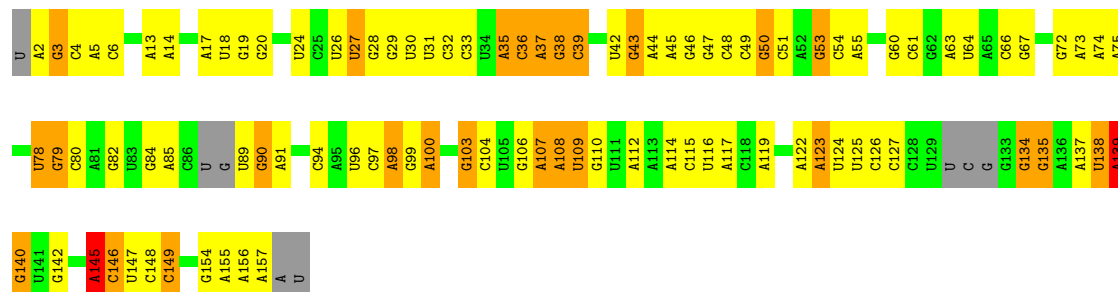
- Molecule 2: 5S ribosomal RNA

Chain B: 45% 47% 7% •



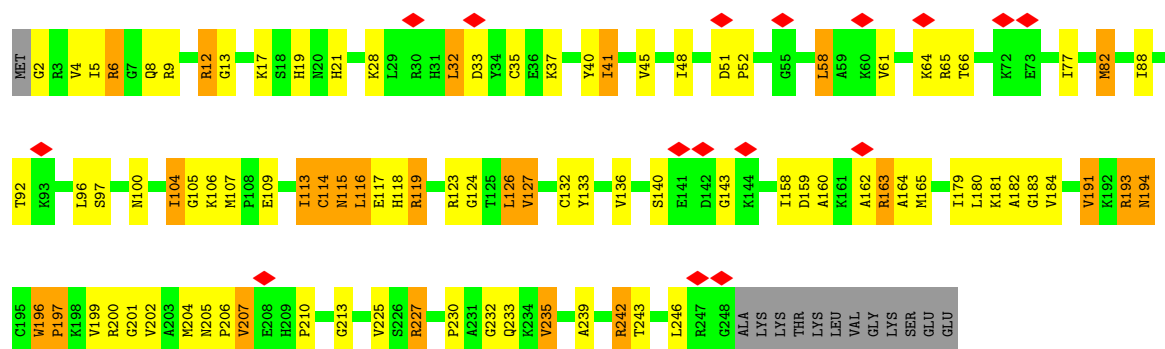
- Molecule 3: 5.8S ribosomal RNA

Chain C: 33% 44% 16% • 5%

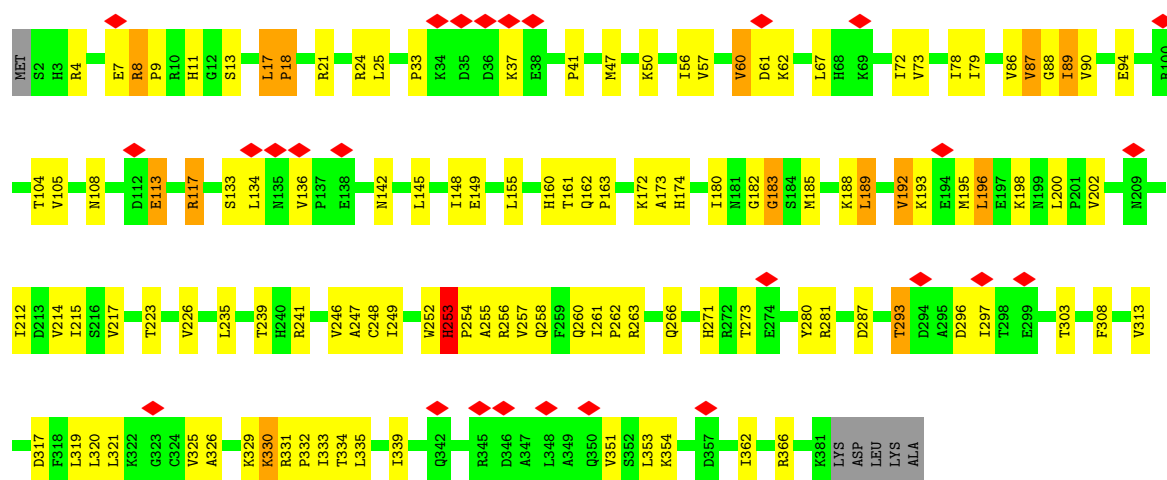


- Molecule 4: 60S ribosomal protein L2

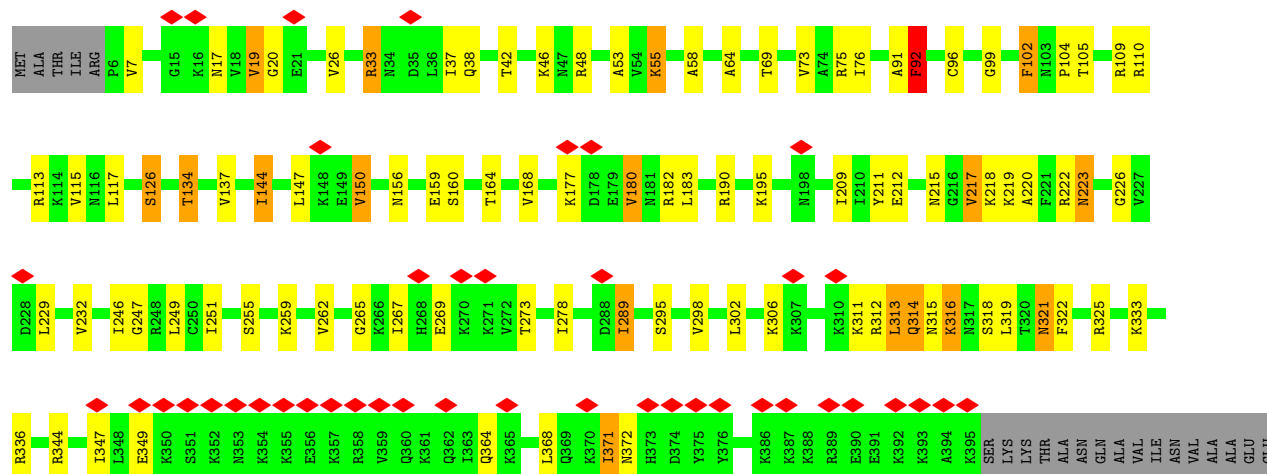
Chain D: 6% 59% 27% 9% 5%



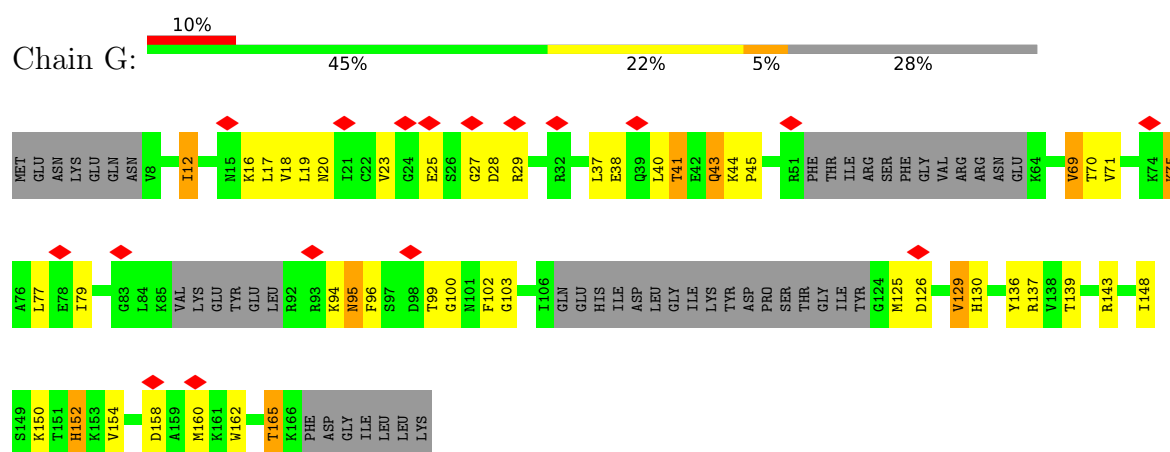
• Molecule 5: 60S ribosomal protein L3



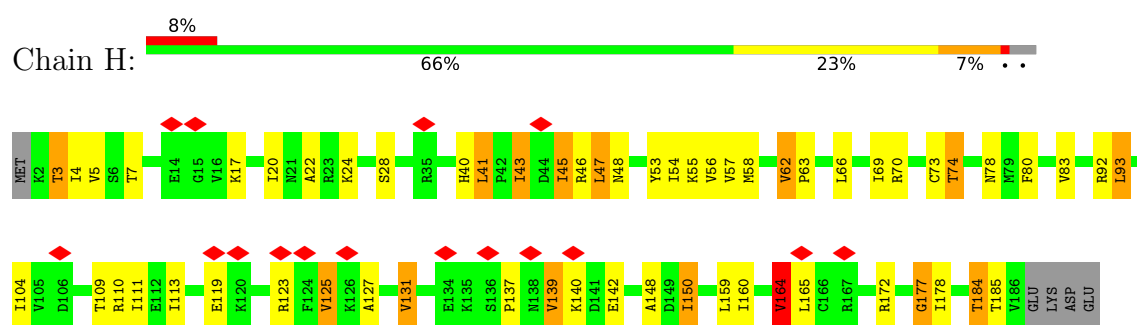
• Molecule 6: 60S ribosomal protein L4



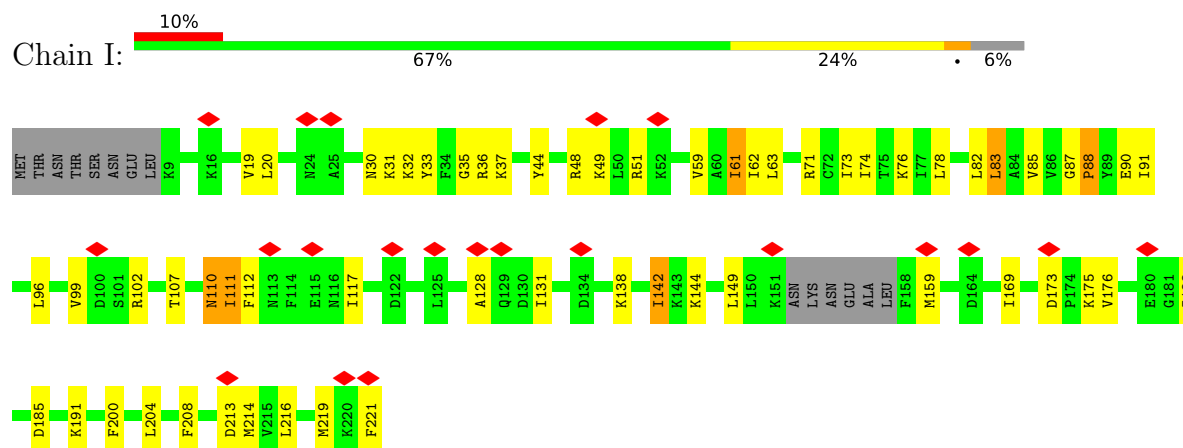
• Molecule 7: 60S ribosomal protein L11a, putative



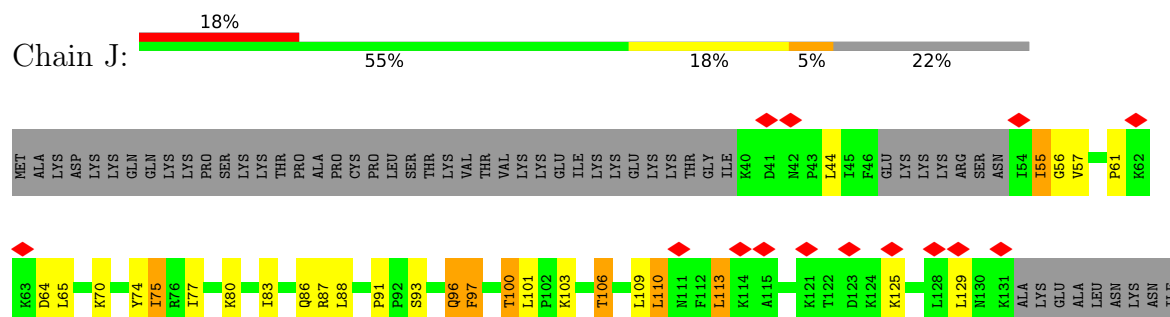
- Molecule 8: 60S ribosomal protein L6, putative

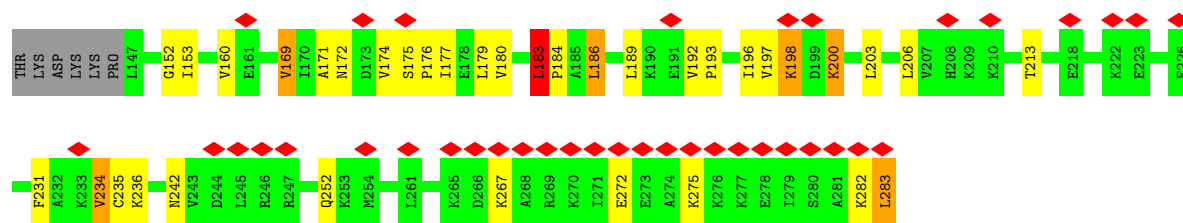


- Molecule 9: 60S ribosomal protein L6-2, putative



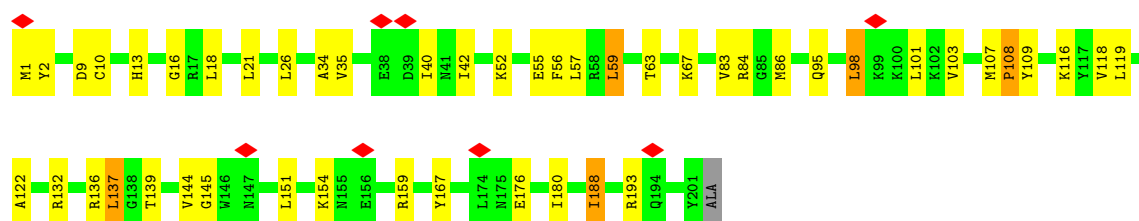
- Molecule 10: 60S ribosomal protein L7-3, putative





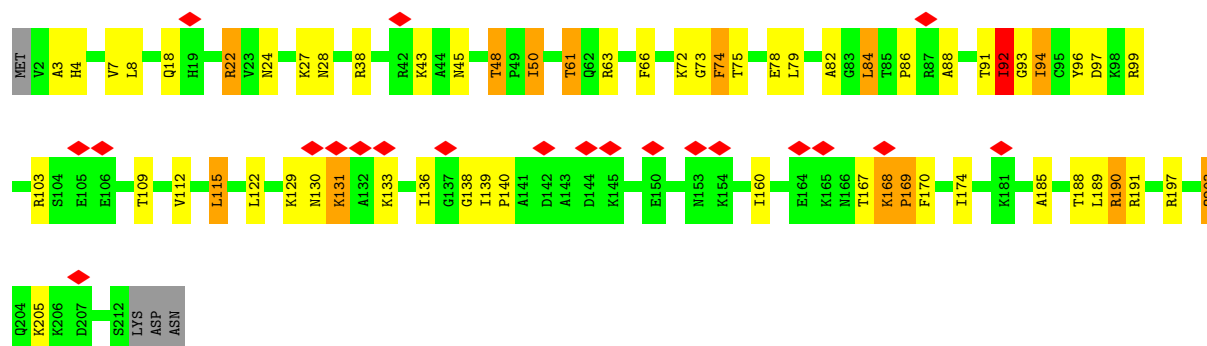
- Molecule 11: 60S ribosomal protein L13, putative

Chain K: 76% 21% .



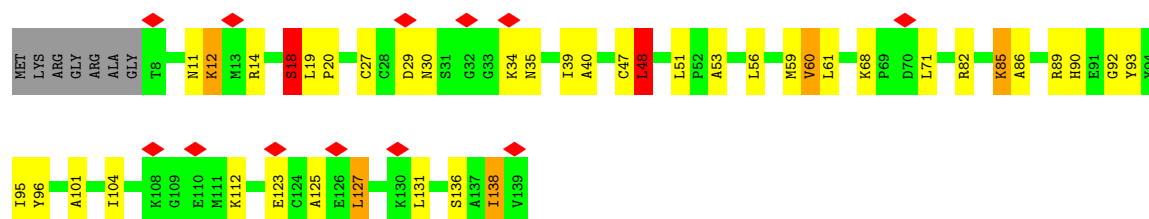
- Molecule 12: 60S ribosomal protein L13

Chain L: 10% 70% 22% 6% .



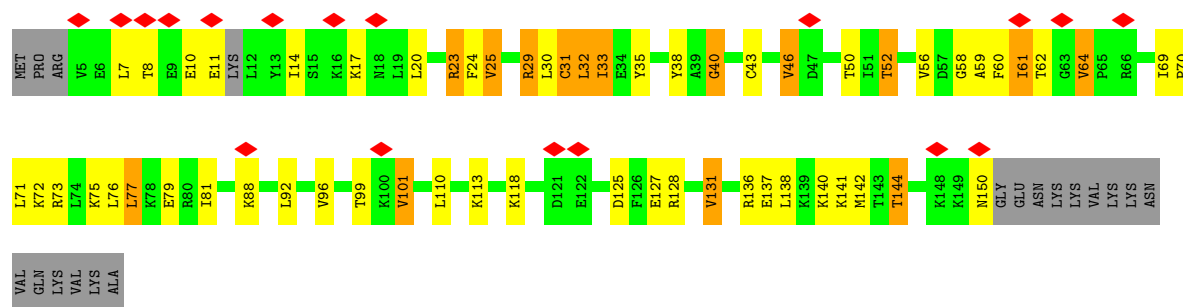
- Molecule 13: 60S ribosomal protein L23, putative

Chain M: 9% 65% 24% 5% .

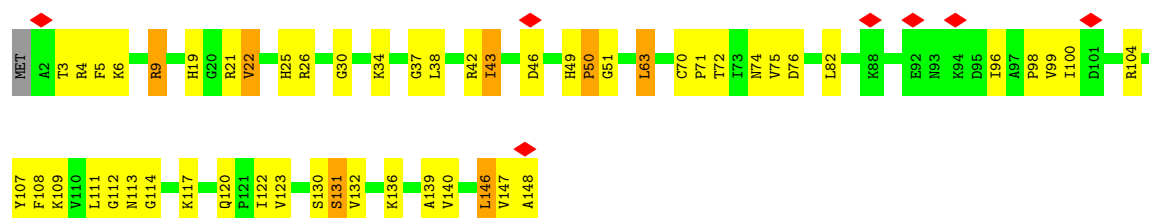


- Molecule 14: 60S ribosomal protein L14, putative

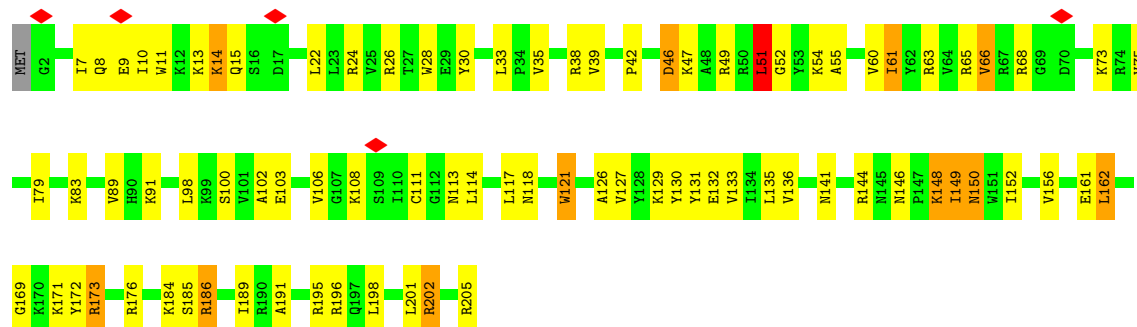
Chain N: 11% 53% 27% 9% 12% .



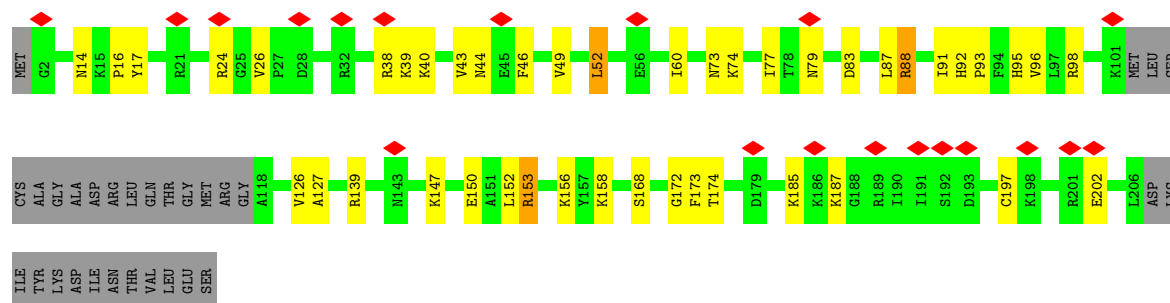
- Molecule 15: 60S ribosomal protein L27a, putative



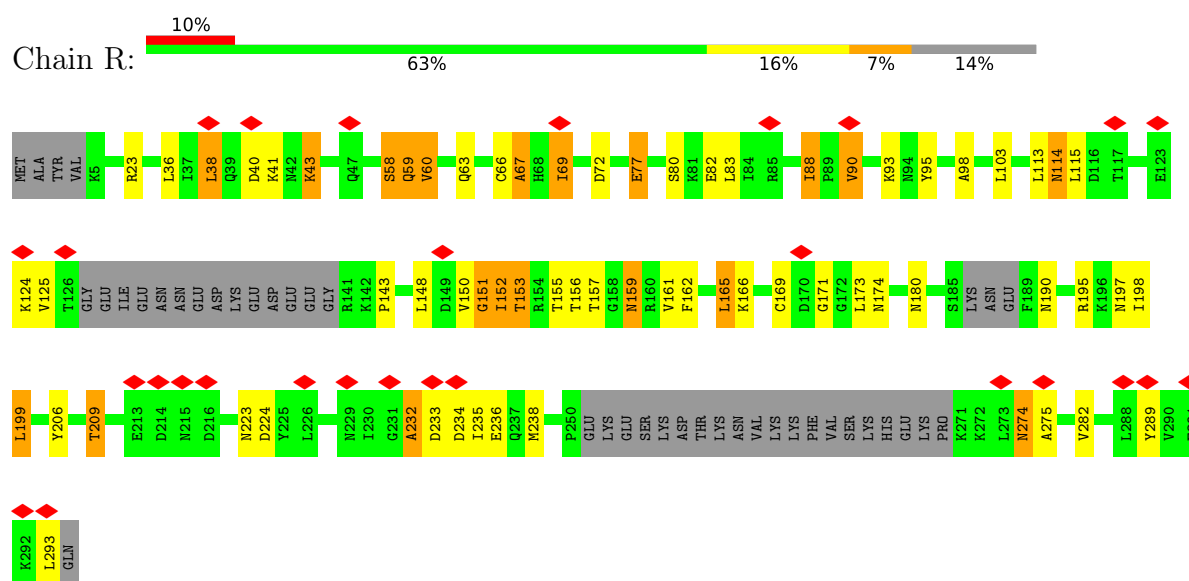
- Molecule 16: Ribosomal protein L15



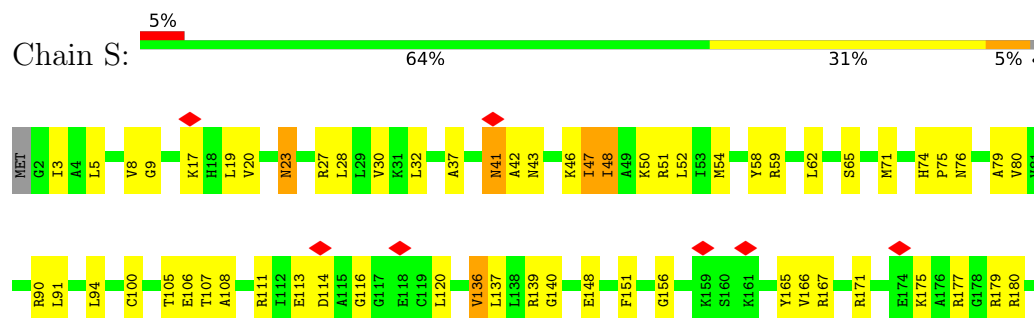
- Molecule 17: 60S ribosomal protein L10, putative



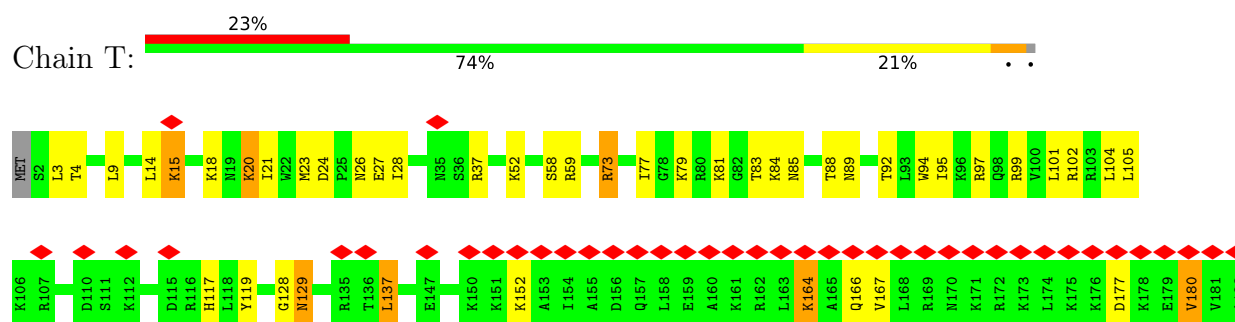
- Molecule 18: 60S ribosomal protein L5, putative



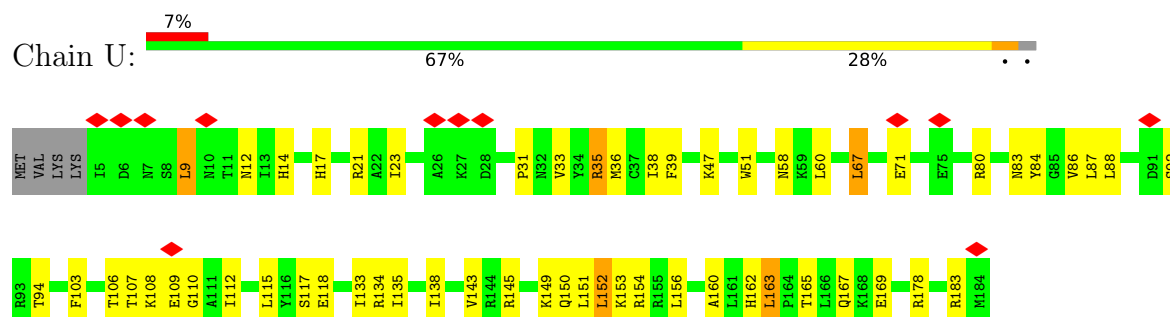
- Molecule 19: 60S ribosomal protein L18-2, putative



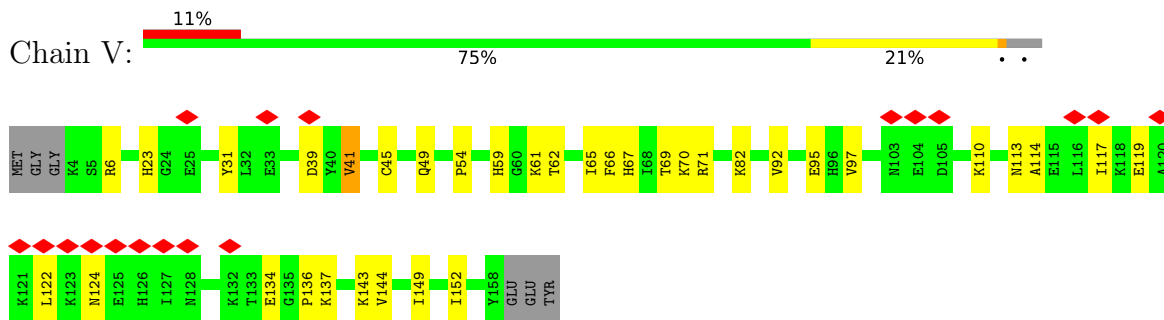
- Molecule 20: 60S ribosomal protein L19



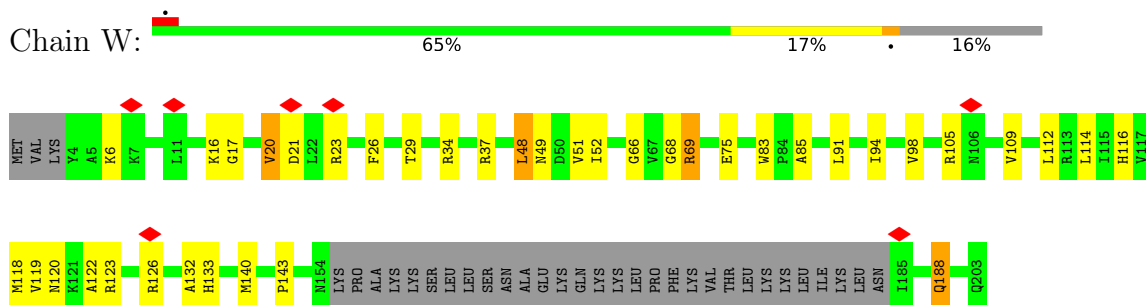
- Molecule 21: 60S ribosomal protein L18a



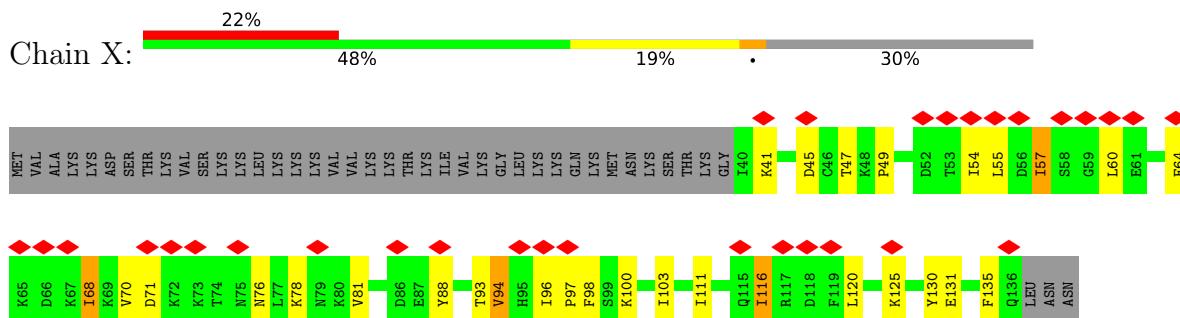
- Molecule 22: 60S ribosomal protein L21



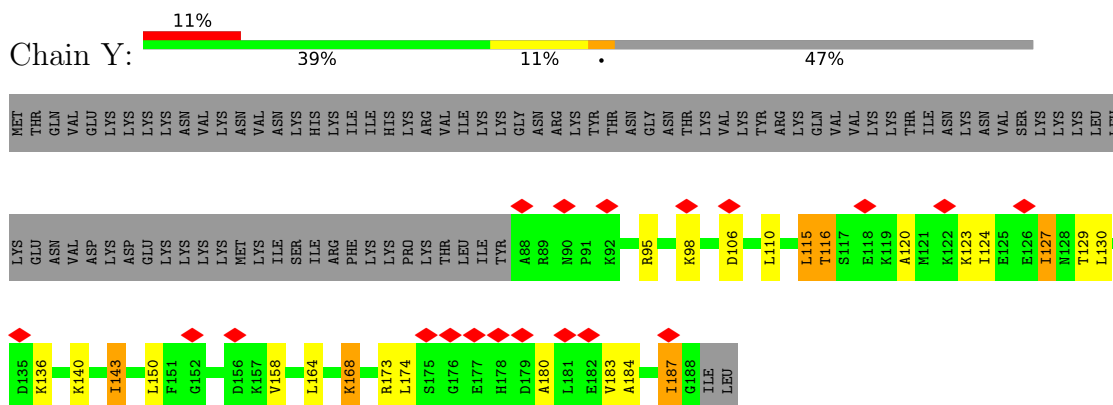
- Molecule 23: 60S ribosomal protein L17, putative



- Molecule 24: 60S ribosomal protein L22, putative

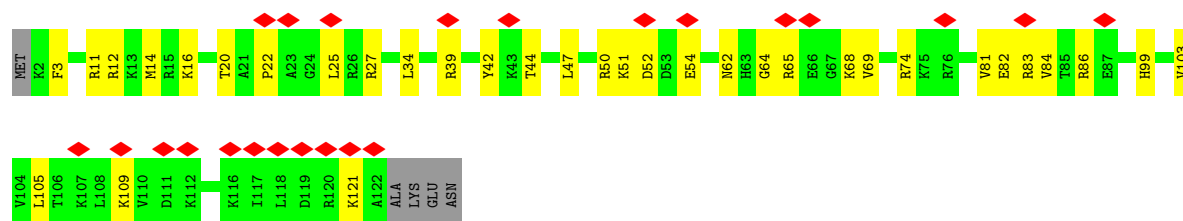


- Molecule 25: 60S ribosomal protein L23

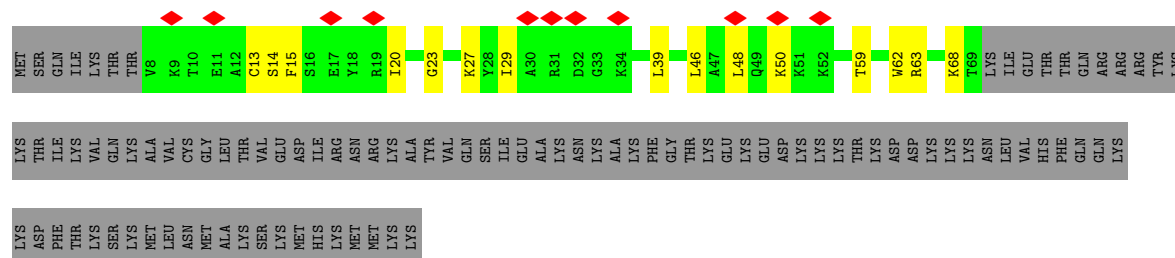


- Molecule 26: 60S ribosomal protein L26, putative

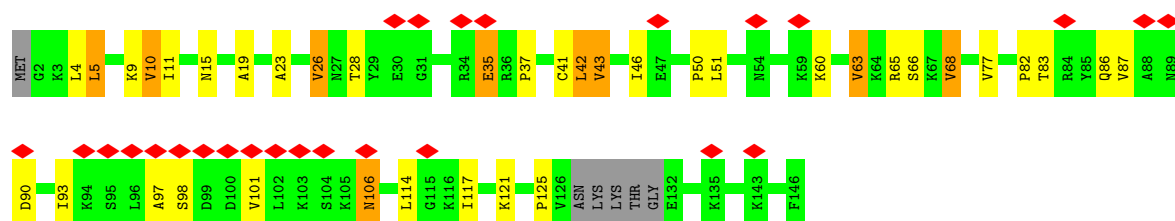




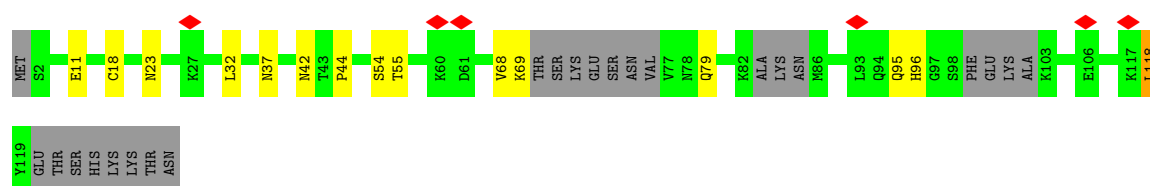
- Molecule 27: 60S ribosomal protein L24, putative



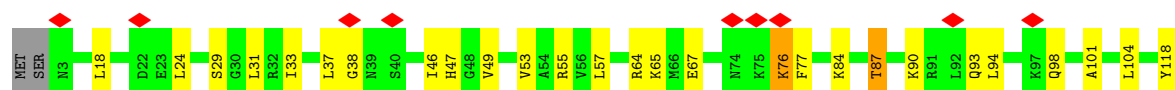
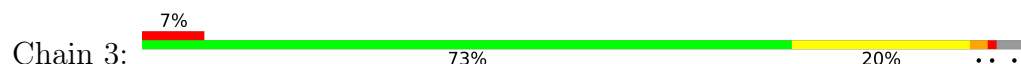
- Molecule 28: 60S ribosomal protein L27



- Molecule 29: 60S ribosomal protein L28

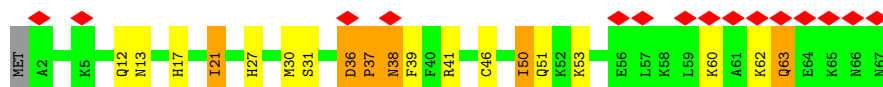


- Molecule 30: 60S ribosomal protein L35, putative

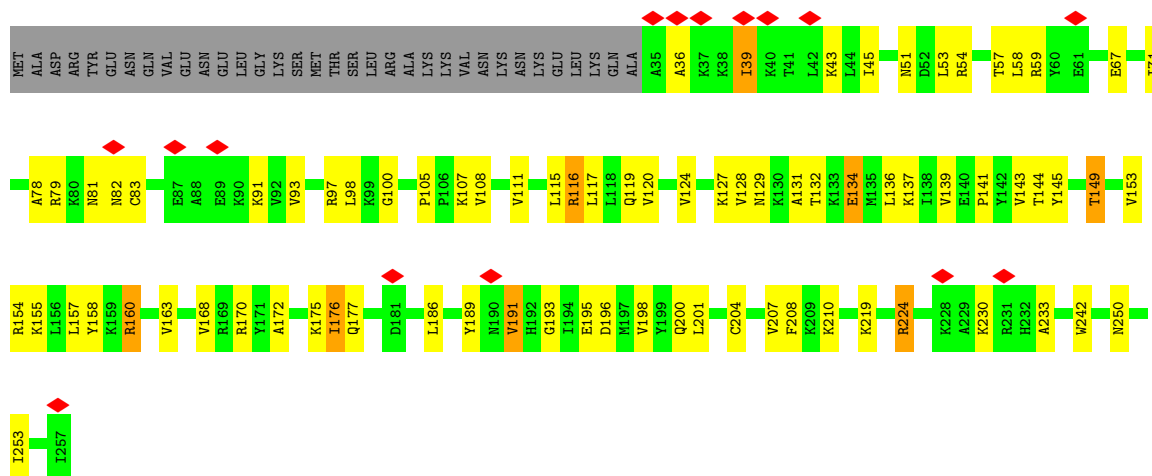




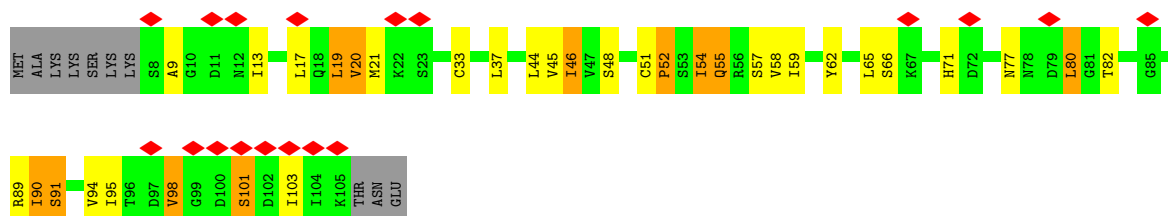
- Molecule 31: 60S ribosomal protein L29, putative



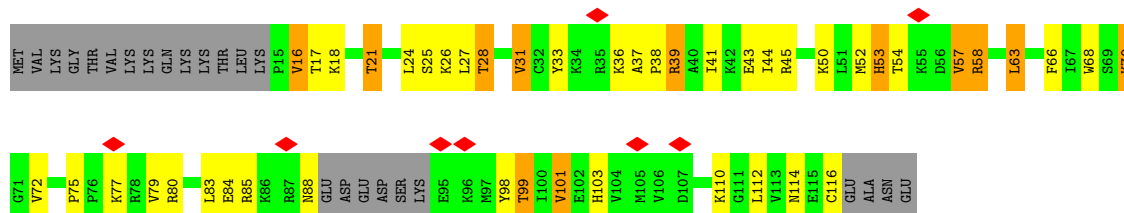
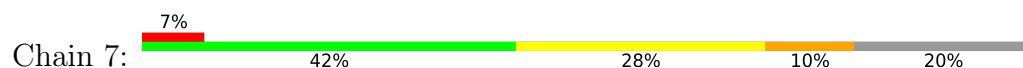
- Molecule 32: 60S ribosomal protein L7, putative



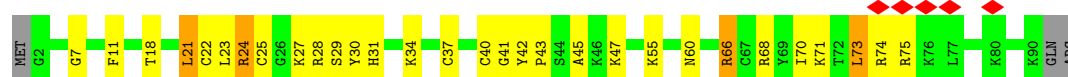
- Molecule 33: 60S ribosomal protein L30e, putative



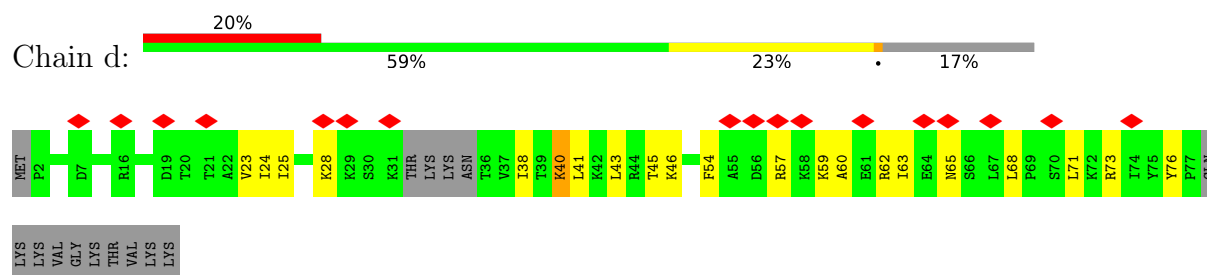
- Molecule 34: 60S ribosomal protein L31



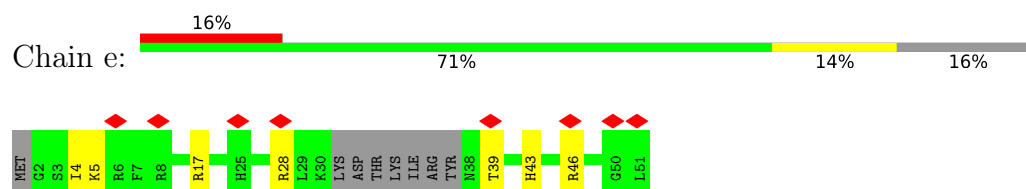
Chain 8: 6% 63% 31% 5%



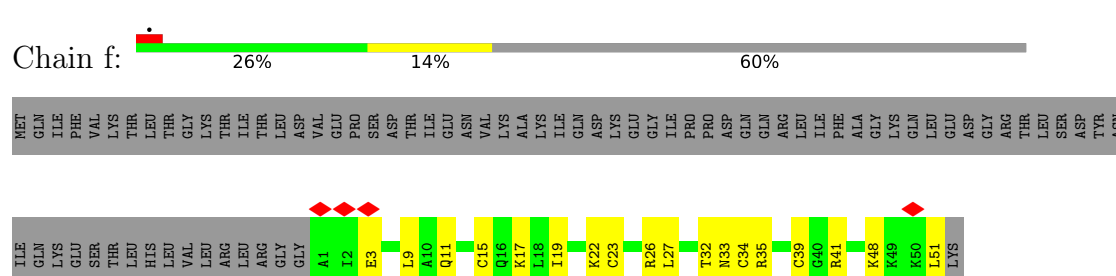
- Molecule 40: 60S ribosomal protein L38



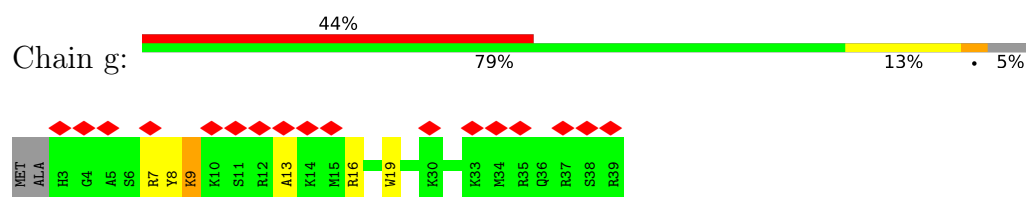
- Molecule 41: 60S ribosomal protein L39



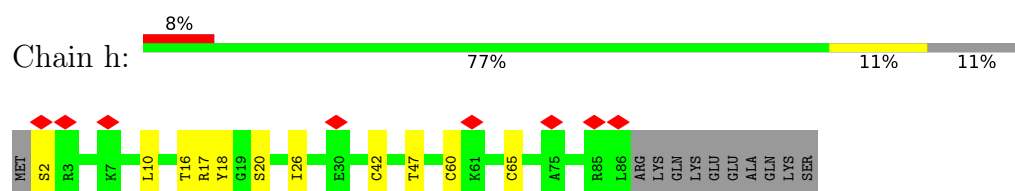
- Molecule 42: Ubiquitin-60S ribosomal protein L40



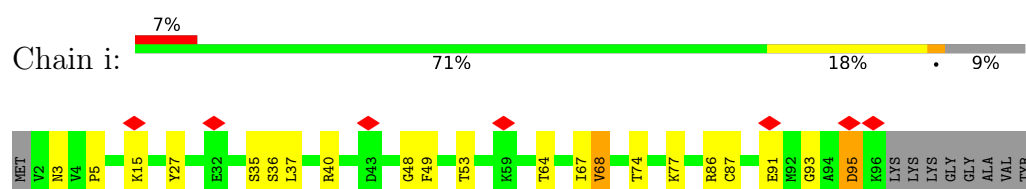
- Molecule 43: 60S ribosomal protein L41



- 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)	463.5, 463.5, 463.5	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

5.1 Standard geometry

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

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	0.36	0/75982	0.66	33/118263 (0.0%)
2	B	0.36	0/2826	0.62	0/4404
3	C	0.36	0/3608	0.68	3/5615 (0.1%)
4	D	0.54	0/1901	0.96	0/2544
5	E	0.46	0/3129	0.90	7/4195 (0.2%)
6	F	0.43	0/3144	1.01	5/4205 (0.1%)
7	G	0.42	0/1020	0.97	2/1349 (0.1%)
8	H	0.42	0/1485	0.89	2/2009 (0.1%)
9	I	0.38	0/1707	0.94	0/2274
10	J	0.44	0/1840	1.06	4/2456 (0.2%)
11	K	0.39	0/1689	1.00	0/2260
12	L	0.43	0/1788	1.00	1/2381 (0.0%)
13	M	0.49	0/1012	0.95	5/1363 (0.4%)
14	N	0.45	0/1213	1.04	3/1616 (0.2%)
15	O	0.43	0/1199	0.89	0/1597
16	P	0.45	0/1735	0.98	2/2320 (0.1%)
17	Q	0.39	0/1579	0.83	0/2113
18	R	0.40	0/2074	1.01	1/2772 (0.0%)
19	S	0.43	0/1530	0.97	2/2040 (0.1%)
20	T	0.45	0/1521	1.04	2/2012 (0.1%)
21	U	0.44	0/1526	0.85	0/2043
22	V	0.36	0/1300	0.79	0/1732
23	W	0.37	0/1338	0.92	1/1793 (0.1%)
24	X	0.46	0/841	0.95	1/1125 (0.1%)
25	Y	0.45	0/805	0.99	0/1074
26	Z	0.37	0/1012	0.84	0/1339
27	0	0.45	0/533	0.87	0/711
28	1	0.36	0/1151	0.88	1/1531 (0.1%)
29	2	0.35	0/839	0.85	0/1114
30	3	0.40	0/1004	1.04	0/1329
31	4	0.38	0/564	1.05	1/737 (0.1%)
32	5	0.43	0/1917	1.02	0/2562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
33	6	0.45	0/748	1.16	5/1001 (0.5%)
34	7	0.48	0/805	0.97	0/1073
35	8	0.50	0/1053	0.92	1/1399 (0.1%)
36	9	0.49	0/864	0.93	1/1160 (0.1%)
37	a	0.36	0/871	0.85	0/1161
38	b	0.40	0/762	1.09	1/1008 (0.1%)
39	c	0.44	0/718	0.92	1/946 (0.1%)
40	d	0.49	0/611	1.08	1/812 (0.1%)
41	e	0.45	0/396	0.90	0/521
42	f	0.53	0/418	1.02	2/556 (0.4%)
43	g	0.43	0/347	1.00	0/448
44	h	0.38	0/667	0.81	0/887
45	i	0.41	0/788	0.83	1/1032 (0.1%)
All	All	0.39	0/133860	0.77	89/196882 (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

There are no bond length outliers.

All (89) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	P	121	TRP	N-CA-C	8.20	120.00	111.14
14	N	64	VAL	N-CA-C	7.97	115.81	107.76
1	A	2219	A	C2'-C3'-O3'	7.49	120.73	109.50
33	6	51	CYS	CA-C-N	7.31	127.36	119.90
33	6	51	CYS	C-N-CA	7.31	127.36	119.90
1	A	1805	U	C2'-C3'-O3'	7.18	124.47	113.70
1	A	3663	A	C2'-C3'-O3'	7.09	120.13	109.50
10	J	198	LYS	N-CA-C	6.76	119.51	111.33
1	A	2932	A	C4'-C3'-O3'	6.57	119.25	109.40
35	8	42	VAL	N-CA-C	-6.49	104.53	110.82
1	A	620	U	C2'-C3'-O3'	6.45	119.18	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	f	3	GLU	CA-C-N	6.40	125.90	119.24
42	f	3	GLU	C-N-CA	6.40	125.90	119.24
5	E	253	HIS	CA-C-N	-6.34	111.92	119.84
5	E	253	HIS	C-N-CA	-6.34	111.92	119.84
1	A	1705	A	C2'-C3'-O3'	6.33	119.00	109.50
3	C	134	G	C2'-C3'-O3'	6.33	123.19	113.70
38	b	68	GLY	N-CA-C	6.31	122.32	114.37
31	4	17	HIS	N-CA-C	6.23	120.14	112.54
45	i	67	ILE	N-CA-C	6.20	116.37	110.42
1	A	889	U	C4'-C3'-O3'	6.14	118.61	109.40
12	L	74	PHE	N-CA-C	6.09	120.72	113.28
3	C	145	A	C2'-C3'-O3'	6.01	122.71	113.70
39	c	21	LEU	N-CA-C	6.00	118.59	111.33
1	A	155	U	C4'-C3'-O3'	5.94	118.31	109.40
1	A	683	A	C4'-C3'-O3'	5.93	118.29	109.40
5	E	354	LYS	N-CA-C	-5.87	106.66	113.88
1	A	652	A	C2'-C3'-O3'	5.84	122.46	113.70
1	A	289	A	C2'-C3'-O3'	5.79	122.38	113.70
24	X	120	LEU	N-CA-C	5.75	118.58	110.14
1	A	3130	U	C2'-C3'-O3'	5.73	118.09	109.50
6	F	289	ILE	CB-CA-C	-5.67	104.48	112.14
14	N	40	GLY	N-CA-C	-5.67	107.50	115.32
1	A	647	U	C2'-C3'-O3'	5.63	117.94	109.50
18	R	43	LYS	N-CA-C	-5.62	105.10	112.41
1	A	215	C	C2'-C3'-O3'	5.61	122.12	113.70
33	6	90	ILE	N-CA-C	5.61	117.00	111.67
6	F	344	ARG	N-CA-C	5.58	117.81	111.11
1	A	579	C	C4'-C3'-O3'	5.57	117.76	109.40
19	S	59	ARG	CA-C-N	-5.56	114.65	120.38
19	S	59	ARG	C-N-CA	-5.56	114.65	120.38
13	M	18	SER	N-CA-C	5.55	122.61	110.80
5	E	200	LEU	CA-C-N	5.54	126.76	119.84
5	E	200	LEU	C-N-CA	5.54	126.76	119.84
33	6	20	VAL	N-CA-CB	5.53	117.02	110.55
1	A	1476	A	C3'-C2'-O2'	-5.50	106.36	114.60
10	J	91	PRO	CA-C-N	5.47	124.92	119.24
10	J	91	PRO	C-N-CA	5.47	124.92	119.24
1	A	1435	G	C2'-C3'-O3'	5.46	117.69	109.50
3	C	139	A	C4'-C3'-O3'	5.45	117.58	109.40
23	W	85	ALA	N-CA-C	5.44	117.66	111.02
6	F	150	VAL	CA-C-N	-5.44	113.04	119.84
6	F	150	VAL	C-N-CA	-5.44	113.04	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	703	U	C2'-C3'-O3'	5.42	121.84	113.70
13	M	51	LEU	CA-C-N	-5.42	114.17	119.76
13	M	51	LEU	C-N-CA	-5.42	114.17	119.76
1	A	10	G	C4'-C3'-O3'	-5.34	105.00	113.00
1	A	1873	U	C2'-C3'-O3'	5.34	117.50	109.50
1	A	664	U	C4'-C3'-O3'	5.33	117.40	109.40
1	A	764	G	C2'-C3'-O3'	5.28	117.42	109.50
8	H	164	VAL	N-CA-C	5.27	115.41	110.30
1	A	2105	A	C2'-C3'-O3'	-5.26	105.81	113.70
1	A	3623	A	C2'-C3'-O3'	5.25	121.57	113.70
10	J	183	LEU	O-C-N	5.24	124.52	120.38
1	A	504	A	C2'-C3'-O3'	5.22	121.53	113.70
36	9	110	ASN	N-CA-C	5.21	121.89	110.80
28	1	93	ILE	N-CA-C	5.20	115.92	110.62
33	6	82	THR	N-CA-C	-5.18	105.81	111.82
5	E	254	PRO	N-CA-C	-5.18	101.80	112.47
1	A	3476	A	C2'-C3'-O3'	5.15	117.23	109.50
1	A	1457	G	C4'-C3'-O3'	5.15	120.72	113.00
14	N	131	VAL	N-CA-CB	5.14	116.56	110.55
13	M	19	LEU	CA-C-N	-5.14	115.28	120.31
13	M	19	LEU	C-N-CA	-5.14	115.28	120.31
20	T	24	ASP	CA-C-N	5.12	124.78	119.56
20	T	24	ASP	C-N-CA	5.12	124.78	119.56
7	G	152	HIS	N-CA-C	-5.10	108.32	114.75
1	A	1538	U	C2'-C3'-O3'	5.07	117.10	109.50
1	A	505	A	C2'-C3'-O3'	5.07	121.30	113.70
16	P	173	ARG	N-CA-C	-5.07	107.05	113.18
6	F	372	ASN	N-CA-C	-5.05	105.85	111.36
5	E	253	HIS	N-CA-C	5.05	120.97	109.81
1	A	1217	U	C2'-C3'-O3'	5.05	117.07	109.50
1	A	2523	U	C4'-C3'-O3'	5.05	116.97	109.40
1	A	2822	U	C2'-C3'-O3'	5.04	117.06	109.50
7	G	129	VAL	N-CA-C	5.04	119.45	112.35
8	H	177	GLY	N-CA-C	5.04	116.95	110.96
1	A	1574	C	C4'-C3'-O3'	5.00	116.91	109.40
40	d	73	ARG	N-CA-C	5.00	117.42	109.96

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	6	52	PRO	Peptide

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Mol	Chain	Res	Type	Group
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

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	1816	0
2	B	2525	0	1274	39	0
3	C	3224	0	1630	95	0
4	D	1866	0	1964	69	0
5	E	3061	0	3205	89	0
6	F	3094	0	3333	72	0
7	G	1010	0	1073	30	0
8	H	1460	0	1532	32	0
9	I	1684	0	1849	27	0
10	J	1813	0	1985	35	0
11	K	1659	0	1782	27	0
12	L	1756	0	1888	40	0
13	M	996	0	1044	20	0
14	N	1197	0	1312	48	0
15	O	1172	0	1230	39	0
16	P	1697	0	1802	57	0
17	Q	1544	0	1582	24	0
18	R	2045	0	2134	38	0
19	S	1502	0	1636	53	0
20	T	1505	0	1671	30	0
21	U	1496	0	1556	46	0
22	V	1275	0	1355	21	0
23	W	1318	0	1319	23	0
24	X	824	0	882	15	0
25	Y	796	0	850	20	0
26	Z	1000	0	1099	22	0
27	0	521	0	539	8	0
28	1	1134	0	1245	19	0
29	2	830	0	887	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	19	0
34	7	793	0	869	32	0
35	8	1036	0	1139	25	0
36	9	844	0	886	40	0
37	a	858	0	911	17	0
38	b	756	0	842	13	0
39	c	705	0	755	25	0
40	d	603	0	686	11	0
41	e	388	0	421	4	0
42	f	413	0	450	12	0
43	g	342	0	388	2	0
44	h	658	0	725	8	0
45	i	778	0	858	8	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	2	0
48	h	1	0	0	0	0
48	i	1	0	0	0	0
All	All	124502	0	91274	2837	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 (2837) 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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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	0.99	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
42:f:34:CYS:SG	48:f:101:ZN:ZN	1.64	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:422:G:H21	23:W:118:MET:HE1	1.48	0.76
16:P:121:TRP:O	16:P:130:TYR:O	2.04	0.76
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
39:c:24:ARG:HH11	39:c:40:CYS:HB3	1.51	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:3508:A:HO2'	8:H:40:HIS:HD1	1.35	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
42:f:23:CYS:HB3	42:f:39:CYS:SG	2.30	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:936:A:H8	39:c:18:THR:HG23	1.54	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
7:G:27:GLY:C	7:G:29:ARG:H	1.96	0.72
1:A:308:U:HO2'	1:A:309:G:H8	1.38	0.71
1:A:588:C:C2	1:A:604:G:N2	2.58	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:284:C:H5''	45:i:48:GLY:HA2	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
16:P:9:GLU:HB3	38:b:48:VAL:HG21	1.75	0.68
25:Y:183:VAL:O	25:Y:187:ILE:HG22	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
40:d:41:LEU:HB2	40:d:54:PHE:HE1	1.57	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
18:R:235:ILE:HG13	18:R:238:MET:HE2	1.75	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
9:I:214:MET:HB3	9:I:219:MET:HE1	1.76	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
39:c:74:ARG:O	39:c:75:ARG:HB2	1.95	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:d:41:LEU:HB2	40:d:54:PHE:CE1	2.30	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
27:0:13:CYS:O	27:0:15: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
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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
19:S:23:ASN:C	19:S:23:ASN:HD22	2.05	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:8:40:CYS:O	35:8:41:ARG:HB3	1.98	0.64
12:L:167:THR:O	12:L:168:LYS:HB2	1.96	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
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
4:D:196:TRP:C	4:D:197:PRO:O	2.40	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:361:G:O6	39:c:55:LYS:HE2	1.98	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
39:c:22:CYS:HB2	39:c:30:TYR:HB2	1.79	0.62
1:A:803:A:H2'	1:A:804:A:O4'	1.99	0.62
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:1262:G:O2'	1:A:2981:A:N3	2.33	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
40:d:23:VAL:HG22	40:d:43:LEU:HD23	1.81	0.61
41:e:43:HIS:HB3	41:e:46:ARG:HG2	1.82	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
21:U:151:LEU:C	21:U:153:LYS:H	2.10	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
42:f:34:CYS:HG	48:f:101:ZN:ZN	1.15	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
40:d:60:ALA:O	40:d:63:ILE:HG22	2.02	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:1335:G:H21	42:f:41:ARG:HH22	1.51	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
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
42:f:11:GLN:HG3	42:f:15:CYS:HB2	1.84	0.59
1:A:195:A:H8	1:A:216:C:O2'	1.83	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
25:Y:164:LEU:HD23	41:e:17:ARG:HD3	1.84	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:773:A:O2'	1:A:774:A:C8	2.43	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
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:1733:G:H5''	37:a:15:THR:HG21	1.86	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
1:A:2100:G:O2'	41:e:4:ILE:HA	2.05	0.57
3:C:100:A:H5'	30:3:65:LYS:HG3	1.86	0.57
13:M:47:CYS:O	13:M:48:LEU:C	2.47	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
45:i:3:ASN:HA	45:i:91:GLU:O	2.04	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
42:f:17:LYS:HB3	42:f:27:LEU:O	2.04	0.57
1:A:78:U:H3	1:A:333:A:H61	0.68	0.57
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
21:U:36:MET:HE2	21:U:38:ILE:HD11	1.86	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:1690:A:H2'	1:A:1691:G:O4'	2.05	0.56
1:A:1758:C:H5''	37:a:64:ARG:HD3	1.87	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
23:W:48:LEU:O	23:W:51:VAL:HG12	2.05	0.56
39:c:42:TYR:HB3	39:c:43:PRO:HD3	1.88	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:1881:C:O2'	1:A:1882:U:O5'	2.24	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

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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	0.56
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
33:6:58:VAL:CG2	37:a:94:LEU:HD21	2.36	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:936:A:C8	39:c:18:THR:HG23	2.40	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: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
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
7:G:94:LYS:C	7:G:96:PHE:H	2.14	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:22:G:H5''	39:c:45:ALA:O	2.07	0.55
1:A:457:A:H61	1:A:458:A:N6	2.05	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
43:g:16:ARG:HB3	43:g:19:TRP:CD1	2.42	0.55
45:i:27:TYR:HB3	45:i:68:VAL:HG13	1.89	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
37:a:20:VAL:HG11	37:a:32:ILE:HG12	1.89	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
4:D:107:MET:HE1	4:D:164:ALA:HB3	1.88	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
42:f:22:LYS:HB2	42:f:39:CYS:SG	2.47	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:c:70:ILE:O	39:c:73:LEU:HG	2.08	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
16:P:91:LYS:HB2	45:i:49:PHE:HZ	1.73	0.54
19:S:114:ASP:C	19:S:116:GLY:H	2.16	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
37:a:91:ARG:O	37:a:95:PHE:HB2	2.08	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:1643:U:H2'	41:e:17:ARG:HD2	1.89	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
39:c:27:LYS:O	39:c:29:SER:N	2.41	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:1073:G:H1'	31:4:12:GLN:CD	2.32	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
33:6:57:SER:HB3	37:a:94:LEU:HD23	1.90	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
37:a:9:ARG:O	37:a:11:ASN:N	2.41	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
1:A:3492:G:H5''	42:f:26:ARG:HD3	1.91	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
36:9:92:HIS:C	36:9:94:GLY:H	2.17	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
3:C:47:G:H4'	39:c:25:CYS:O	2.09	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
35:8:81:GLU:C	35:8:84:PRO:HD2	2.35	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:23:C:H5''	39:c:47:LYS:HB2	1.91	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:1331:A:N3	1:A:3214:A:O2'	2.41	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
1:A:1881:C:O2'	1:A:1882:U:C6	2.59	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:922:C:C2	1:A:1060:G:N2	2.78	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
33:6:58:VAL:HG23	37:a:94:LEU:HD21	1.92	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
40:d:45:THR:HG22	40:d:46:LYS:H	1.74	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:1567:A:H5''	6:F:195:LYS:HZ1	1.74	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:2195:G:C8	44:h:16:THR:HA	2.45	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
4:D:48:ILE:HD13	44:h:65:CYS:HB2	1.93	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:A:H2	1:A:207:A:C2	2.29	0.51
1:A:278:C:O2	38:b:89:ARG:NH2	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
4:D:28:LYS:HD2	4:D:123:ARG:HB3	1.93	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
42:f:32:THR:HG23	42:f:33:ASN:HD22	1.76	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
39:c:23:LEU:O	39:c:24:ARG:CB	2.59	0.50
42:f:34:CYS:O	42:f:35:ARG:HB3	2.11	0.50
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:1178:A:H5''	2:B:98:G:HO2'	1.74	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:O: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
4:D:113:ILE:HG22	4:D:165:MET:C	2.37	0.50
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
7:G:27:GLY:C	7:G:29:ARG:N	2.61	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
15:O:37:GLY:O	15:O:38:LEU:CB	2.60	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
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
45:i:36:SER:O	45:i:40:ARG:HG3	2.13	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:3123:C:H5''	12:L:205:LYS:HZ1	1.78	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
43:g:7:ARG:C	43:g:9:LYS:H	2.21	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:1905:C:H2'	1:A:1906:A:C8	2.48	0.49
1:A:2008:G:OP1	37:a:38:LYS:HE3	2.13	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
25:Y:115:LEU:HD21	25:Y:133:MET:HE2	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
38:b:7:ILE:HG22	38:b:8:LYS:HG3	1.95	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
9:I:87:GLY:O	9:I:88:PRO:C	2.55	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
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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
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
21:U:167:GLN:C	21:U:169:GLU:H	2.21	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
40:d:68:LEU:HB2	40:d:71:LEU:HD23	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:92:LEU:O	14:N:96:VAL:HG12	2.13	0.48
31:4:60:LYS:O	31:4:63:GLN:HG2	2.14	0.48
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: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
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
40:d:59:LYS:HA	40:d:62:ARG:HE	1.78	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
11:K:107:MET:HE2	11:K:159:ARG:HD2	1.96	0.47
12:L:72:LYS:HG3	12:L:72:LYS:O	2.13	0.47
12:L:203:GLN:HG3	38:b:17:PHE:CE1	2.50	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
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:O	19:S:85:ILE:HG13	2.14	0.47
24:X:70:VAL:O	24:X:71:ASP:C	2.56	0.47
28:1:15:ASN:HD21	37:a:86:ARG:HE	1.62	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
38:b:15:VAL:HG22	38:b:16:GLY:H	1.78	0.47
38:b:64:LEU:HA	38:b:67:ILE:HD12	1.97	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1756:G:C2	1:A:1757:C:C2	3.02	0.47
1:A:1886:A:N6	44:h:42:CYS:HA	2.30	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
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
39:c:23:LEU:O	39:c:24:ARG:HB3	2.15	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
37:a:39:ALA:HB2	37:a:58:ARG:HG2	1.96	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:112:U:HO2'	1:A:113:C:H6	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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
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:1003:A:OP2	39:c:7:GLY:HA3	2.16	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:2193:U:H1'	44:h:20:SER:HB3	1.97	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
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
39:c:31:HIS:ND1	39:c:34:LYS:HB2	2.31	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
21:U:151:LEU:C	21:U:153:LYS:N	2.72	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
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
10:J:186:LEU:HD23	38:b:47:VAL:HG21	1.97	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:2994:A:C2	45:i:5:PRO:HG3	2.51	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
42:f:34:CYS:O	42:f:35:ARG:CB	2.64	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
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
19:S:179:ARG:HE	19:S:187:LYS:HZ1	1.64	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
30:3:118:TYR:O	30:3:119:LEU:C	2.59	0.45
32:5:157:LEU:HD21	32:5:201:LEU:CD1	2.47	0.45
39:c:21:LEU:O	39:c:22:CYS:HB3	2.16	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
7:G:19:LEU:HD22	7:G:125:MET:HE3	1.98	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:699:U:O2'	36:9:92:HIS:O	2.34	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
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
5:E:47:MET:HE1	5:E:332:PRO:HB3	1.98	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
4:D:194:ASN:CG	4:D:194:ASN:O	2.59	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
37:a:5:VAL:HG11	37:a:32:ILE:HG13	1.99	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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:44:U:H4'	45:i:53:THR:HG22	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
21:U:23:ILE:HG23	22:V:137:LYS:HZ1	1.83	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
3:C:37:A:O2'	3:C:38:G:C5'	2.65	0.44
5:E:196:LEU:C	5:E:198:LYS:H	2.24	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:2112:G:H4'	39:c:11:PHE:HD2	1.81	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
9:I:214:MET:HE3	14:N:128:ARG:HE	1.82	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
19:S:51:ARG:HA	19:S:54:MET:HE2	2.00	0.44
34:7:21:THR:HB	34:7:80:ARG:HD2	1.99	0.44
39:c:71:LYS:HA	39:c:74:ARG:HE	1.82	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: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
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
27:0:48:LEU:C	27:0:50:LYS:H	2.26	0.44
28:1:41:CYS:SG	28:1:77:VAL:HG12	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:5:97:ARG:HA	32:5:143:VAL:HG12	2.00	0.44
40:d:59:LYS:O	40:d:62:ARG:HG2	2.18	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
44:h:42:CYS:HB3	44:h:60:CYS:SG	2.58	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:971:U:C5	44:h:2:SER:HA	2.52	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
17:Q:156:LYS:C	17:Q:158:LYS:H	2.26	0.43
21:U:108:LYS:HB3	21:U:135:ILE:HD11	1.99	0.43
39:c:66:ARG:O	39:c:71:LYS:HD3	2.18	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:979:G:OP1	44:h:17:ARG:NH1	2.50	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1611:A:H2'	1:A:1612:U:C6	2.54	0.43
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
3:C:39:C:H4'	39:c:73:LEU:HD21	2.00	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
40:d:23:VAL:HG23	40:d:71:LEU:HD12	1.99	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
5:E:155:LEU:HG	5:E:185:MET:HE1	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
38:b:7:ILE:O	38:b:8:LYS:HB2	2.19	0.43
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
37:a:20:VAL:CG1	37:a:32:ILE:HG12	2.48	0.43
38:b:17:PHE:O	38:b:18:ASN:ND2	2.52	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: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
14:N:17:LYS:HG3	14:N:17:LYS:O	2.18	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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:939:A:N3	1:A:1030:C:O2'	2.45	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
19:S:41:ASN:C	19:S:43:ASN:H	2.27	0.42
36:9:36:GLN:O	36:9:37:ALA:HB3	2.19	0.42
38:b:79:TYR:O	38:b:83:LYS:HG2	2.20	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
19:S:114:ASP:C	19:S:116:GLY:N	2.74	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
37:a:86:ARG:O	37:a:90:MET:HG2	2.20	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: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
8:H:22:ALA:C	8:H:24:LYS:H	2.27	0.42
19:S:65:SER:HA	19:S:91:LEU:HD11	2.00	0.42
24:X:111:ILE:HG23	24:X:116:ILE:C	2.44	0.42
30:3:94:LEU:HB3	30:3:98:GLN:HE21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
14:N:59:ALA:C	14:N:61:ILE:N	2.75	0.42
15:O:3:THR:HA	15:O:6:LYS:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:172:GLY:C	17:Q:174:THR:H	2.27	0.42
18:R:125:VAL:CG1	18:R:195:ARG:HG3	2.50	0.42
18:R:274:ASN:C	18:R:274:ASN:HD22	2.27	0.42
22:V:66:PHE:CD2	31:4:30:MET:HE1	2.55	0.42
36:9:41:TYR:HB3	36:9:134:LEU:HD13	2.01	0.42
40:d:41:LEU:HD23	40:d:41:LEU:HA	1.90	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
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: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:167:GLN:C	21:U:169:GLU:N	2.78	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
36:9:65:ILE:O	36:9:66:LYS:C	2.63	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
4:D:179:ILE:O	4:D:180:LEU:C	2.62	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
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
42:f:19:ILE:HD12	42:f:48:LYS:HA	2.01	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:580:A:O2'	1:A:581:C:O5'	2.26	0.41
1:A:1039:A:H61	39:c:18:THR:HG21	1.85	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
14:N:59:ALA:C	14:N:61:ILE:H	2.28	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
15:O:130:SER:O	15:O:131:SER:C	2.63	0.41
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:280:U:H1'	38:b:85:GLY:HA3	2.02	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:1693:U:O2'	1:A:2461:A:N3	2.47	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
39:c:37:CYS:HB3	39:c:42:TYR:H	1.86	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
3:C:46:G:H21	39:c:24:ARG:HA	1.84	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
36:9:124:PRO:C	36:9:126:ALA:N	2.75	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:1965:U:OP1	40:d:40:LYS:NZ	2.54	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:1330:A:H2	1:A:3215:G:HO2'	1.67	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
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: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:51:ARG:HD3	19:S:54:MET:HE2	2.01	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:1897:G:H4'	37:a:38:LYS:NZ	2.36	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
38:b:13:ILE:HG22	38:b:15:VAL:H	1.86	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
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
12:L:203:GLN:HG3	38:b:17:PHE:HE1	1.86	0.40
26:Z:51:LYS:O	26:Z:69:VAL:HB	2.21	0.40
33:6:58:VAL:HG22	37:a:94:LEU:HD21	2.02	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
45:i:35:SER:O	45:i:40:ARG:NH1	2.53	0.40
1:A:441:A:H2'	1:A:442:G:O4'	2.20	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:972:G:N7	44:h:2:SER:N	2.70	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:2025:G:H5''	37:a:70:ARG:HH11	1.85	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
7:G:94:LYS:C	7:G:96:PHE:N	2.79	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
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:2822:U:O2'	1:A:2823:U:C6	2.73	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
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
15:O:49:HIS:O	15:O:50:PRO:C	2.65	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:7:28:THR:HG21	34:7:36:LYS:CG	2.51	0.40
39:c:41:GLY:O	39:c:42:TYR:C	2.65	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%)	10	42
5	E	378/386 (98%)	340 (90%)	31 (8%)	7 (2%)	6	33
6	F	388/411 (94%)	363 (94%)	16 (4%)	9 (2%)	5	29
7	G	116/173 (67%)	101 (87%)	11 (10%)	4 (3%)	3	20
8	H	183/190 (96%)	158 (86%)	20 (11%)	5 (3%)	4	25
9	I	203/221 (92%)	174 (86%)	24 (12%)	5 (2%)	4	27
10	J	216/283 (76%)	198 (92%)	14 (6%)	4 (2%)	6	33
11	K	199/202 (98%)	181 (91%)	15 (8%)	3 (2%)	8	37
12	L	209/215 (97%)	183 (88%)	18 (9%)	8 (4%)	2	18
13	M	130/139 (94%)	117 (90%)	9 (7%)	4 (3%)	3	22
14	N	144/165 (87%)	137 (95%)	3 (2%)	4 (3%)	4	25
15	O	145/148 (98%)	131 (90%)	12 (8%)	2 (1%)	9	39
16	P	202/205 (98%)	184 (91%)	11 (5%)	7 (4%)	3	20
17	Q	185/219 (84%)	155 (84%)	27 (15%)	3 (2%)	7	36
18	R	244/294 (83%)	216 (88%)	18 (7%)	10 (4%)	2	17
19	S	184/187 (98%)	164 (89%)	14 (8%)	6 (3%)	3	21
20	T	179/182 (98%)	172 (96%)	4 (2%)	3 (2%)	7	35
21	U	178/184 (97%)	166 (93%)	8 (4%)	4 (2%)	5	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	V	153/161 (95%)	139 (91%)	10 (6%)	4 (3%)	4	26
23	W	166/203 (82%)	151 (91%)	11 (7%)	4 (2%)	4	28
24	X	95/139 (68%)	82 (86%)	9 (10%)	4 (4%)	2	16
25	Y	99/190 (52%)	91 (92%)	6 (6%)	2 (2%)	6	31
26	Z	119/126 (94%)	107 (90%)	10 (8%)	2 (2%)	7	35
27	0	60/162 (37%)	55 (92%)	4 (7%)	1 (2%)	7	35
28	1	136/146 (93%)	128 (94%)	3 (2%)	5 (4%)	2	18
29	2	96/127 (76%)	84 (88%)	11 (12%)	1 (1%)	12	45
30	3	117/124 (94%)	108 (92%)	4 (3%)	5 (4%)	2	16
31	4	64/67 (96%)	56 (88%)	5 (8%)	3 (5%)	2	14
32	5	221/257 (86%)	199 (90%)	17 (8%)	5 (2%)	5	29
33	6	96/108 (89%)	89 (93%)	4 (4%)	3 (3%)	3	22
34	7	92/120 (77%)	87 (95%)	5 (5%)	0	100	100
35	8	123/131 (94%)	110 (89%)	9 (7%)	4 (3%)	3	21
36	9	101/140 (72%)	87 (86%)	8 (8%)	6 (6%)	1	10
37	a	104/150 (69%)	96 (92%)	7 (7%)	1 (1%)	12	45
38	b	91/112 (81%)	84 (92%)	5 (6%)	2 (2%)	5	29
39	c	87/92 (95%)	72 (83%)	11 (13%)	4 (5%)	2	15
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	11
44	h	83/96 (86%)	72 (87%)	10 (12%)	1 (1%)	10	42
45	i	93/104 (89%)	83 (89%)	5 (5%)	5 (5%)	1	12
All	All	6115/7124 (86%)	5524 (90%)	436 (7%)	155 (2%)	6	27

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

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Mol	Chain	Res	Type
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
9	I	159	MET
9	I	213	ASP
10	J	56	GLY
11	K	108	PRO

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Mol	Chain	Res	Type
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
23	W	188	GLN
24	X	76	ASN
24	X	78	LYS
24	X	135	PHE

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Mol	Chain	Res	Type
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
36	9	39	ARG
36	9	104	VAL
37	a	10	HIS
39	c	66	ARG

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Mol	Chain	Res	Type
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 ⓘ

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%)	160 (84%)	31 (16%)	2	12
5	E	335/340 (98%)	313 (93%)	22 (7%)	15	47
6	F	336/352 (96%)	310 (92%)	26 (8%)	12	41
7	G	110/155 (71%)	96 (87%)	14 (13%)	4	20
8	H	164/173 (95%)	140 (85%)	24 (15%)	3	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	I	189/203 (93%)	168 (89%)	21 (11%)	6	25
10	J	204/260 (78%)	180 (88%)	24 (12%)	5	23
11	K	181/182 (100%)	167 (92%)	14 (8%)	12	41
12	L	190/194 (98%)	167 (88%)	23 (12%)	5	22
13	M	106/110 (96%)	92 (87%)	14 (13%)	4	19
14	N	134/152 (88%)	117 (87%)	17 (13%)	4	20
15	O	121/122 (99%)	109 (90%)	12 (10%)	7	31
16	P	179/180 (99%)	161 (90%)	18 (10%)	7	30
17	Q	165/190 (87%)	156 (94%)	9 (6%)	19	52
18	R	214/254 (84%)	191 (89%)	23 (11%)	6	27
19	S	158/159 (99%)	143 (90%)	15 (10%)	8	32
20	T	161/163 (99%)	148 (92%)	13 (8%)	11	39
21	U	162/166 (98%)	151 (93%)	11 (7%)	14	46
22	V	140/144 (97%)	134 (96%)	6 (4%)	26	59
23	W	128/178 (72%)	121 (94%)	7 (6%)	19	52
24	X	92/131 (70%)	87 (95%)	5 (5%)	20	53
25	Y	90/177 (51%)	82 (91%)	8 (9%)	9	34
26	Z	111/115 (96%)	106 (96%)	5 (4%)	24	58
27	0	53/146 (36%)	51 (96%)	2 (4%)	29	62
28	1	127/132 (96%)	117 (92%)	10 (8%)	11	40
29	2	97/118 (82%)	93 (96%)	4 (4%)	27	60
30	3	110/115 (96%)	98 (89%)	12 (11%)	6	26
31	4	60/61 (98%)	53 (88%)	7 (12%)	5	23
32	5	201/231 (87%)	185 (92%)	16 (8%)	11	40
33	6	83/92 (90%)	72 (87%)	11 (13%)	4	19
34	7	90/112 (80%)	71 (79%)	19 (21%)	1	6
35	8	114/120 (95%)	104 (91%)	10 (9%)	9	35
36	9	90/127 (71%)	78 (87%)	12 (13%)	4	19
37	a	89/128 (70%)	81 (91%)	8 (9%)	9	34
38	b	82/97 (84%)	80 (98%)	2 (2%)	43	70
39	c	73/77 (95%)	71 (97%)	2 (3%)	39	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	d	69/83 (83%)	61 (88%)	8 (12%)	5	24
41	e	40/48 (83%)	37 (92%)	3 (8%)	12	42
42	f	45/114 (40%)	43 (96%)	2 (4%)	25	59
43	g	34/35 (97%)	33 (97%)	1 (3%)	37	67
44	h	70/80 (88%)	67 (96%)	3 (4%)	26	59
45	i	87/93 (94%)	81 (93%)	6 (7%)	14	45
All	All	5475/6311 (87%)	4975 (91%)	500 (9%)	11	34

All (500) 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	66	THR
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	126	LEU
4	D	163	ARG
4	D	181	LYS
4	D	191	VAL
4	D	193	ARG
4	D	194	ASN
4	D	207	VAL
4	D	225	VAL
4	D	227	ARG
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	8	ARG
5	E	24	ARG
5	E	56	ILE
5	E	60	VAL
5	E	87	VAL
5	E	89	ILE
5	E	113	GLU
5	E	117	ARG
5	E	189	LEU
5	E	192	VAL
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
5	E	297	ILE
5	E	320	LEU
5	E	362	ILE
6	F	7	VAL
6	F	26	VAL
6	F	33	ARG
6	F	48	ARG
6	F	55	LYS
6	F	73	VAL
6	F	75	ARG
6	F	92	PHE
6	F	115	VAL
6	F	117	LEU
6	F	126	SER
6	F	134	THR
6	F	144	ILE
6	F	180	VAL
6	F	182	ARG
6	F	217	VAL
6	F	232	VAL
6	F	311	LYS

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Mol	Chain	Res	Type
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
6	F	371	ILE
7	G	12	ILE
7	G	23	VAL
7	G	25	GLU
7	G	40	LEU
7	G	41	THR
7	G	43	GLN
7	G	44	LYS
7	G	69	VAL
7	G	75	LYS
7	G	77	LEU
7	G	99	THR
7	G	139	THR
7	G	160	MET
7	G	165	THR
8	H	3	THR
8	H	5	VAL
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	56	VAL
8	H	57	VAL
8	H	70	ARG
8	H	73	CYS
8	H	74	THR
8	H	93	LEU
8	H	104	ILE
8	H	119	GLU
8	H	125	VAL
8	H	131	VAL
8	H	150	ILE

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Mol	Chain	Res	Type
8	H	164	VAL
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	61	ILE
9	I	62	ILE
9	I	63	LEU
9	I	73	ILE
9	I	78	LEU
9	I	82	LEU
9	I	83	LEU
9	I	85	VAL
9	I	96	LEU
9	I	99	VAL
9	I	110	ASN
9	I	111	ILE
9	I	117	ILE
9	I	142	ILE
9	I	175	LYS
9	I	185	ASP
9	I	204	LEU
9	I	216	LEU
10	J	44	LEU
10	J	55	ILE
10	J	75	ILE
10	J	83	ILE
10	J	86	GLN
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

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Mol	Chain	Res	Type
10	J	200	LYS
10	J	234	VAL
10	J	235	CYS
10	J	267	LYS
10	J	272	GLU
10	J	275	LYS
10	J	283	LEU
11	K	1	MET
11	K	18	LEU
11	K	35	VAL
11	K	42	ILE
11	K	57	LEU
11	K	59	LEU
11	K	67	LYS
11	K	98	LEU
11	K	132	ARG
11	K	137	LEU
11	K	144	VAL
11	K	154	LYS
11	K	188	ILE
11	K	193	ARG
12	L	18	GLN
12	L	22	ARG
12	L	24	ASN
12	L	27	LYS
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	84	LEU
12	L	91	THR
12	L	92	ILE
12	L	94	ILE
12	L	115	LEU
12	L	122	LEU
12	L	136	ILE
12	L	160	ILE
12	L	170	PHE
12	L	174	ILE
12	L	188	THR

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Mol	Chain	Res	Type
12	L	190	ARG
12	L	203	GLN
13	M	11	ASN
13	M	30	ASN
13	M	34	LYS
13	M	35	ASN
13	M	48	LEU
13	M	56	LEU
13	M	59	MET
13	M	60	VAL
13	M	85	LYS
13	M	89	ARG
13	M	123	GLU
13	M	127	LEU
13	M	131	LEU
13	M	138	ILE
14	N	25	VAL
14	N	29	ARG
14	N	31	CYS
14	N	32	LEU
14	N	33	ILE
14	N	46	VAL
14	N	52	THR
14	N	56	VAL
14	N	61	ILE
14	N	62	THR
14	N	69	ILE
14	N	75	LYS
14	N	77	LEU
14	N	101	VAL
14	N	118	LYS
14	N	138	LEU
14	N	144	THR
15	O	4	ARG
15	O	5	PHE
15	O	9	ARG
15	O	22	VAL
15	O	43	ILE
15	O	46	ASP
15	O	63	LEU
15	O	96	ILE
15	O	104	ARG

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Mol	Chain	Res	Type
15	O	131	SER
15	O	132	VAL
15	O	146	LEU
16	P	8	GLN
16	P	10	ILE
16	P	22	LEU
16	P	33	LEU
16	P	46	ASP
16	P	49	ARG
16	P	51	LEU
16	P	61	ILE
16	P	66	VAL
16	P	75	VAL
16	P	83	LYS
16	P	113	ASN
16	P	118	ASN
16	P	127	VAL
16	P	148	LYS
16	P	156	VAL
16	P	162	LEU
16	P	184	LYS
17	Q	26	VAL
17	Q	39	LYS
17	Q	52	LEU
17	Q	87	LEU
17	Q	88	ARG
17	Q	96	VAL
17	Q	126	VAL
17	Q	153	ARG
17	Q	187	LYS
18	R	23	ARG
18	R	38	LEU
18	R	41	LYS
18	R	43	LYS
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	103	LEU

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Mol	Chain	Res	Type
18	R	114	ASN
18	R	153	THR
18	R	156	THR
18	R	159	ASN
18	R	165	LEU
18	R	166	LYS
18	R	190	ASN
18	R	199	LEU
18	R	209	THR
18	R	223	ASN
18	R	274	ASN
19	S	17	LYS
19	S	19	LEU
19	S	23	ASN
19	S	32	LEU
19	S	47	ILE
19	S	48	ILE
19	S	76	ASN
19	S	85	ILE
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	59	ARG
20	T	73	ARG
20	T	77	ILE
20	T	79	LYS
20	T	83	THR
20	T	88	THR
20	T	104	LEU
20	T	137	LEU
20	T	152	LYS
20	T	164	LYS
20	T	166	GLN
20	T	180	VAL
21	U	9	LEU
21	U	12	ASN
21	U	35	ARG

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Mol	Chain	Res	Type
21	U	58	ASN
21	U	60	LEU
21	U	67	LEU
21	U	94	THR
21	U	106	THR
21	U	138	ILE
21	U	145	ARG
21	U	163	LEU
22	V	41	VAL
22	V	61	LYS
22	V	62	THR
22	V	69	THR
22	V	92	VAL
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	114	LEU
23	W	123	ARG
24	X	57	ILE
24	X	60	LEU
24	X	94	VAL
24	X	116	ILE
24	X	125	LYS
25	Y	95	ARG
25	Y	115	LEU
25	Y	127	ILE
25	Y	143	ILE
25	Y	150	LEU
25	Y	168	LYS
25	Y	174	LEU
25	Y	187	ILE
26	Z	14	MET
26	Z	34	LEU
26	Z	62	ASN
26	Z	103	VAL
26	Z	105	LEU
27	0	29	ILE
27	0	46	LEU
28	1	5	LEU

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Mol	Chain	Res	Type
28	1	10	VAL
28	1	26	VAL
28	1	42	LEU
28	1	43	VAL
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	37	ASN
29	2	96	HIS
29	2	118	LEU
30	3	18	LEU
30	3	31	LEU
30	3	37	LEU
30	3	46	ILE
30	3	55	ARG
30	3	57	LEU
30	3	76	LYS
30	3	77	PHE
30	3	87	THR
30	3	93	GLN
30	3	104	LEU
30	3	119	LEU
31	4	13	ASN
31	4	21	ILE
31	4	50	ILE
31	4	51	GLN
31	4	53	LYS
31	4	62	LYS
31	4	63	GLN
32	5	39	ILE
32	5	45	ILE
32	5	58	LEU
32	5	59	ARG
32	5	124	VAL
32	5	128	VAL
32	5	129	ASN
32	5	132	THR
32	5	134	GLU
32	5	136	LEU

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Mol	Chain	Res	Type
32	5	149	THR
32	5	160	ARG
32	5	163	VAL
32	5	176	ILE
32	5	191	VAL
32	5	224	ARG
33	6	19	LEU
33	6	21	MET
33	6	33	CYS
33	6	46	ILE
33	6	54	ILE
33	6	55	GLN
33	6	77	ASN
33	6	80	LEU
33	6	89	ARG
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	31	VAL
34	7	33	TYR
34	7	39	ARG
34	7	50	LYS
34	7	53	HIS
34	7	54	THR
34	7	57	VAL
34	7	58	ARG
34	7	63	LEU
34	7	70	LYS
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

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Mol	Chain	Res	Type
35	8	87	MET
35	8	111	ARG
35	8	113	LYS
35	8	125	ARG
36	9	51	ARG
36	9	52	SER
36	9	56	GLN
36	9	65	ILE
36	9	67	ASN
36	9	68	VAL
36	9	69	ASN
36	9	71	LYS
36	9	113	VAL
36	9	122	ILE
36	9	125	LYS
36	9	131	VAL
37	a	4	ARG
37	a	5	VAL
37	a	15	THR
37	a	20	VAL
37	a	32	ILE
37	a	43	LYS
37	a	74	ARG
37	a	94	LEU
38	b	18	ASN
38	b	81	LYS
39	c	60	ASN
39	c	73	LEU
40	d	24	ILE
40	d	25	ILE
40	d	28	LYS
40	d	38	ILE
40	d	40	LYS
40	d	57	ARG
40	d	65	ASN
40	d	76	TYR
41	e	5	LYS
41	e	28	ARG
41	e	39	THR
42	f	9	LEU
42	f	51	LEU
43	g	9	LYS

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Mol	Chain	Res	Type
44	h	10	LEU
44	h	26	ILE
44	h	47	THR
45	i	37	LEU
45	i	64	THR
45	i	74	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 (157) such sidechains are listed below:

Mol	Chain	Res	Type
4	D	19	HIS
4	D	22	HIS
4	D	31	HIS
4	D	86	GLN
4	D	115	ASN
4	D	139	GLN
4	D	194	ASN
4	D	205	ASN
4	D	215	ASN
4	D	217	GLN
4	D	218	HIS
5	E	121	ASN
5	E	160	HIS
5	E	240	HIS
5	E	253	HIS
5	E	271	HIS
5	E	338	ASN
6	F	14	ASN
6	F	38	GLN
6	F	146	HIS
6	F	156	ASN
6	F	215	ASN
6	F	285	HIS
6	F	286	ASN
6	F	314	GLN
6	F	317	ASN
6	F	321	ASN
7	G	15	ASN
7	G	20	ASN

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Mol	Chain	Res	Type
7	G	43	GLN
7	G	152	HIS
8	H	21	ASN
8	H	101	ASN
8	H	115	ASN
8	H	161	HIS
9	I	10	HIS
9	I	24	ASN
9	I	110	ASN
9	I	217	HIS
10	J	96	GLN
10	J	105	GLN
11	K	13	HIS
11	K	95	GLN
11	K	189	ASN
12	L	10	ASN
12	L	18	GLN
12	L	19	HIS
12	L	24	ASN
12	L	65	ASN
12	L	111	ASN
12	L	153	ASN
12	L	204	GLN
13	M	30	ASN
13	M	49	ASN
13	M	77	ASN
14	N	130	GLN
15	O	8	ASN
15	O	49	HIS
15	O	60	HIS
15	O	74	ASN
15	O	113	ASN
15	O	118	HIS
16	P	15	GLN
16	P	145	ASN
16	P	157	HIS
16	P	180	HIS
17	Q	73	ASN
17	Q	95	HIS
17	Q	183	GLN
18	R	42	ASN
18	R	45	ASN

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Mol	Chain	Res	Type
18	R	68	HIS
18	R	190	ASN
18	R	202	HIS
18	R	221	HIS
18	R	223	ASN
18	R	274	ASN
19	S	7	ASN
19	S	18	HIS
19	S	23	ASN
19	S	45	ASN
19	S	76	ASN
19	S	150	HIS
20	T	129	ASN
20	T	133	ASN
21	U	12	ASN
21	U	14	HIS
21	U	15	GLN
21	U	17	HIS
21	U	32	ASN
21	U	45	ASN
21	U	72	GLN
21	U	123	HIS
21	U	131	ASN
21	U	147	HIS
21	U	150	GLN
22	V	56	ASN
22	V	59	HIS
22	V	103	ASN
23	W	77	ASN
23	W	99	GLN
23	W	106	ASN
23	W	120	ASN
23	W	147	GLN
23	W	154	ASN
25	Y	149	ASN
25	Y	185	ASN
26	Z	4	ASN
28	1	76	ASN
28	1	79	HIS
29	2	78	ASN
29	2	79	GLN
30	3	52	ASN

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Mol	Chain	Res	Type
30	3	61	ASN
30	3	93	GLN
30	3	98	GLN
31	4	6	ASN
31	4	13	ASN
31	4	17	HIS
31	4	51	GLN
32	5	51	ASN
32	5	102	ASN
32	5	119	GLN
32	5	177	GLN
32	5	192	HIS
32	5	212	ASN
32	5	213	ASN
32	5	244	ASN
32	5	250	ASN
32	5	254	ASN
33	6	50	ASN
33	6	74	HIS
33	6	77	ASN
34	7	23	ASN
34	7	29	HIS
34	7	64	ASN
34	7	88	ASN
35	8	21	GLN
35	8	78	ASN
36	9	56	GLN
36	9	73	HIS
36	9	108	HIS
37	a	6	HIS
37	a	12	HIS
37	a	98	GLN
38	b	87	HIS
38	b	98	GLN
39	c	79	ASN
41	e	19	GLN
41	e	25	HIS
41	e	38	ASN
41	e	43	HIS
42	f	8	GLN
42	f	11	GLN
42	f	33	ASN

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Mol	Chain	Res	Type
42	f	43	ASN
45	i	82	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3161/3788 (83%)	994 (31%)	177 (5%)
2	B	117/119 (98%)	26 (22%)	4 (3%)
3	C	148/159 (93%)	47 (31%)	9 (6%)
All	All	3426/4066 (84%)	1067 (31%)	190 (5%)

All (1067) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	A
1	A	12	U
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
1	A	109	A

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Mol	Chain	Res	Type
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	182	U
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	258	U
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

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Mol	Chain	Res	Type
1	A	313	U
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	345	G
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

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Mol	Chain	Res	Type
1	A	462	G
1	A	463	G
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	584	U
1	A	585	C
1	A	586	U

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Mol	Chain	Res	Type
1	A	592	C
1	A	593	A
1	A	594	C
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

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Mol	Chain	Res	Type
1	A	675	A
1	A	677	A
1	A	678	A
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	739	G
1	A	740	U
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	777	U
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

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Mol	Chain	Res	Type
1	A	813	G
1	A	825	G
1	A	831	U
1	A	833	G
1	A	834	U
1	A	835	G
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

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Mol	Chain	Res	Type
1	A	990	U
1	A	993	U
1	A	998	U
1	A	999	G
1	A	1000	C
1	A	1013	U
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

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Mol	Chain	Res	Type
1	A	1111	A
1	A	1113	C
1	A	1114	A
1	A	1115	G
1	A	1116	G
1	A	1121	G
1	A	1122	A
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

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Mol	Chain	Res	Type
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
1	A	1230	A
1	A	1231	A
1	A	1232	U
1	A	1233	A
1	A	1234	A
1	A	1235	C
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	1336	U
1	A	1337	G
1	A	1341	G
1	A	1344	C
1	A	1345	A

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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	1799	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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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	2126	A
1	A	2133	C
1	A	2136	C
1	A	2143	U
1	A	2145	A
1	A	2146	A
1	A	2147	A
1	A	2148	U
1	A	2149	A
1	A	2153	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

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Mol	Chain	Res	Type
1	A	2424	A
1	A	2451	A
1	A	2452	A
1	A	2453	A
1	A	2463	U
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
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	2551	U
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	2590	U
1	A	2591	U
1	A	2596	A
1	A	2598	G
1	A	2599	C

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Mol	Chain	Res	Type
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
1	A	2671	C
1	A	2676	C
1	A	2678	A
1	A	2679	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	2727	U
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

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Mol	Chain	Res	Type
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
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	3017	A
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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	3229	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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
1	A	3478	G
1	A	3483	U
1	A	3488	U
1	A	3493	G
1	A	3500	G
1	A	3505	U
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
2	B	84	U
2	B	85	G
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	37	A
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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 [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	K	301	-	28,28,28	2.34	3 (10%)	41,43,43	1.64	10 (24%)
46	YMZ	A	3801	-	28,28,28	3.09	9 (32%)	41,43,43	2.20	10 (24%)

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

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	A	3801	YMZ	CAS-CAW	-8.86	1.38	1.52
46	A	3801	YMZ	CAZ-CAT	-8.66	1.38	1.50
46	A	3801	YMZ	CAY-CAR	-7.27	1.37	1.50
46	K	301	YMZ	CAZ-CAT	-6.87	1.40	1.50
46	K	301	YMZ	CAS-CAW	-6.72	1.41	1.52
46	K	301	YMZ	CAY-CAR	-6.05	1.40	1.50
46	A	3801	YMZ	FAG-CAZ	-3.11	1.21	1.33
46	A	3801	YMZ	CAT-CAV	-2.98	1.38	1.43
46	A	3801	YMZ	FAF-CAZ	-2.98	1.22	1.33
46	A	3801	YMZ	FAB-CAY	-2.82	1.22	1.33
46	A	3801	YMZ	CAS-CAU	-2.63	1.38	1.43
46	A	3801	YMZ	FAC-CAY	-2.09	1.25	1.33

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	A	3801	YMZ	CAO-CAX-CAW	-6.92	106.89	114.03
46	K	301	YMZ	CAK-CAR-NAP	-5.05	119.94	125.47
46	A	3801	YMZ	CAK-CAR-NAP	-4.93	120.06	125.47
46	A	3801	YMZ	FAG-CAZ-CAT	-4.91	106.59	112.30
46	A	3801	YMZ	CAN-NAQ-CAX	-4.34	108.91	111.62
46	A	3801	YMZ	OAA-CAW-CAS	-4.12	104.47	111.08
46	K	301	YMZ	CAR-NAP-CAV	3.84	122.28	116.89
46	A	3801	YMZ	CAR-NAP-CAV	3.69	122.07	116.89
46	K	301	YMZ	CAY-CAR-NAP	2.84	119.06	114.79
46	K	301	YMZ	FAE-CAZ-CAT	-2.69	109.17	112.30
46	K	301	YMZ	CAN-NAQ-CAX	2.59	113.24	111.62
46	A	3801	YMZ	CAK-CAR-CAY	2.52	123.93	120.09
46	A	3801	YMZ	FAB-CAY-CAR	-2.29	108.40	112.43
46	K	301	YMZ	CAJ-CAU-CAS	-2.19	120.71	123.37
46	K	301	YMZ	CAZ-CAT-CAV	2.17	121.91	119.45
46	A	3801	YMZ	CAJ-CAH-CAI	-2.17	117.66	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	A	3801	YMZ	FAE-CAZ-CAT	-2.12	109.84	112.30
46	K	301	YMZ	CAS-CAU-CAV	2.11	119.82	117.86
46	K	301	YMZ	FAG-CAZ-CAT	-2.04	109.92	112.30
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
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:

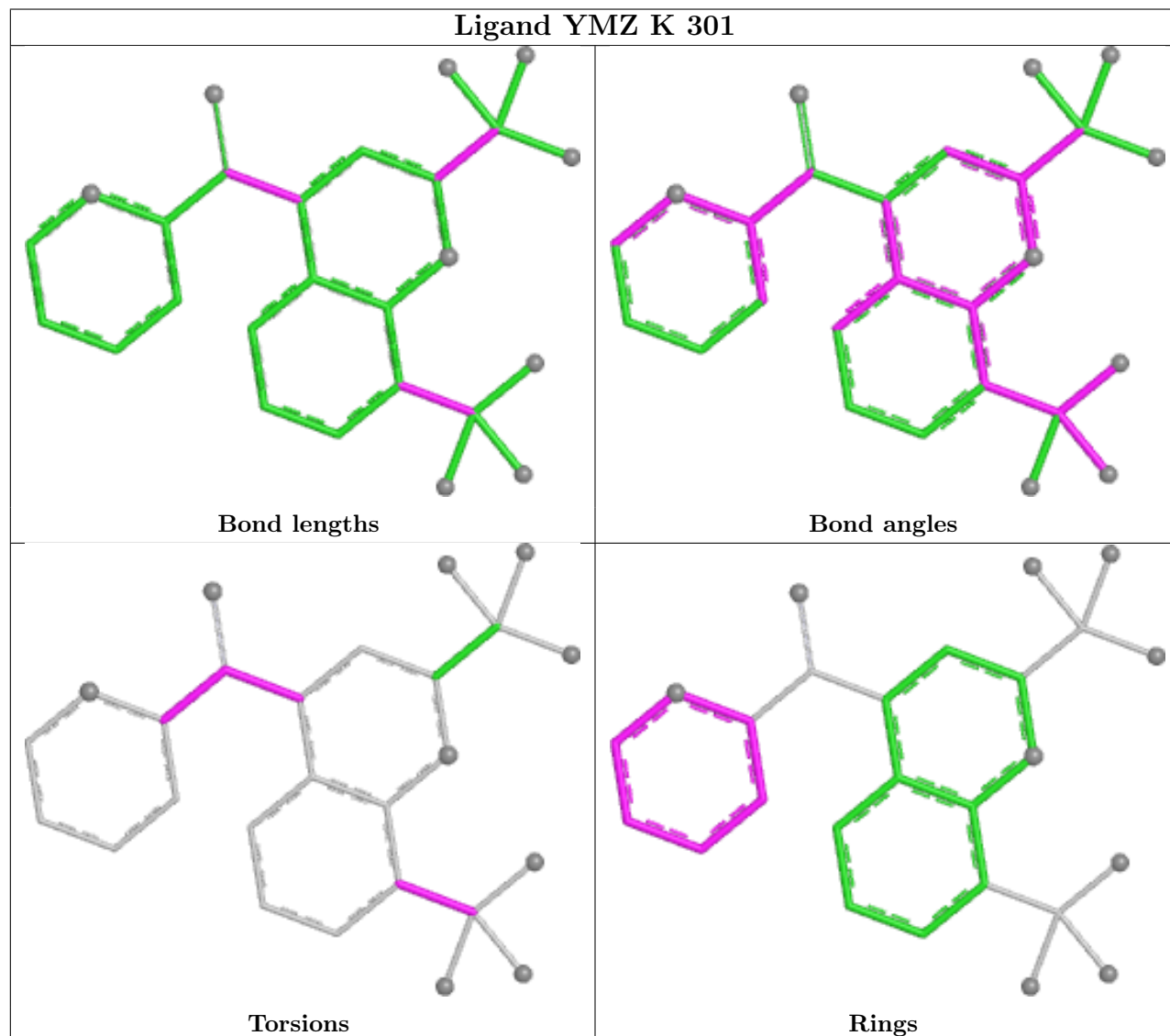
Mol	Chain	Res	Type	Atoms
46	K	301	YMZ	CAL-CAM-CAN-CAO-CAX-NAQ

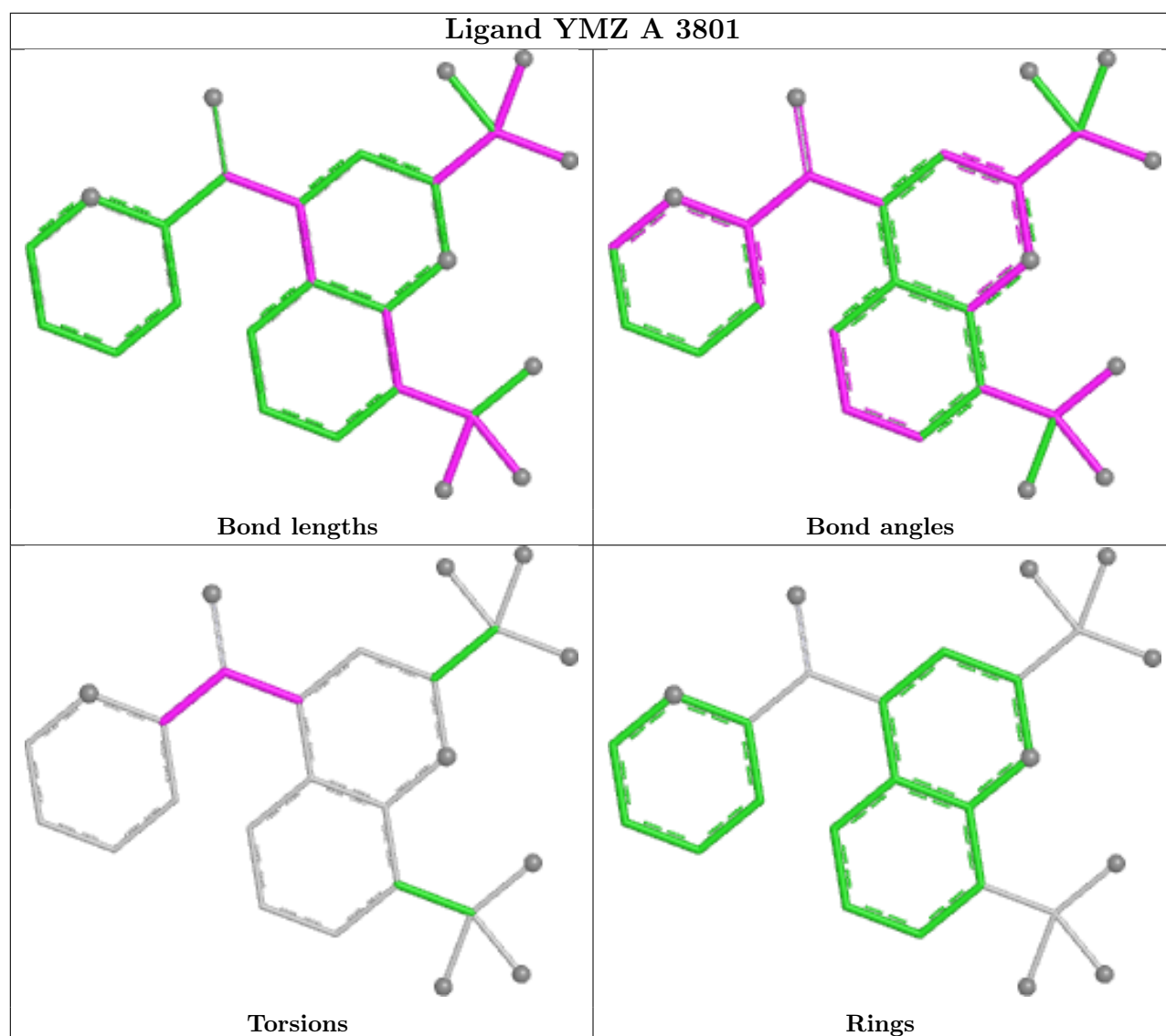
1 monomer is involved in 3 short contacts:

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

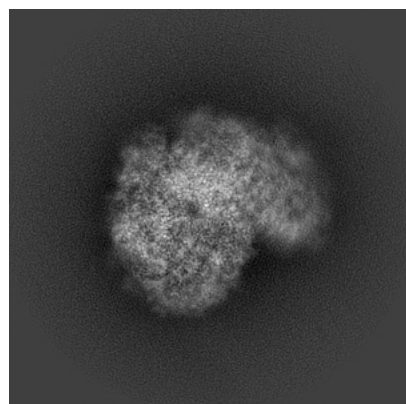
6 Map visualisation [i](#)

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.

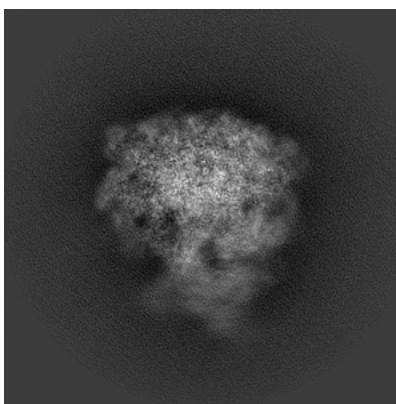
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

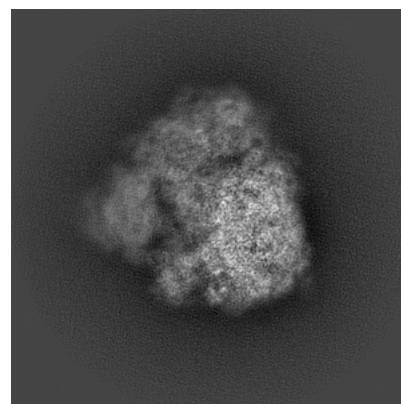
6.1.1 Primary map



X

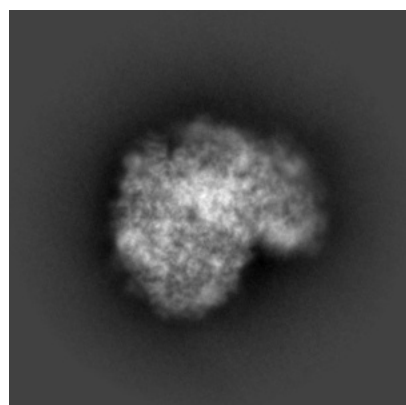


Y

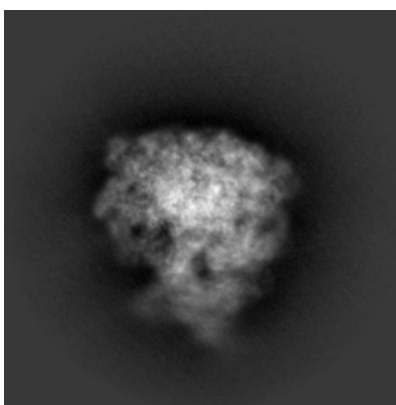


Z

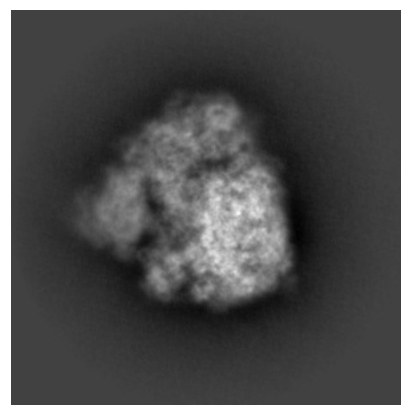
6.1.2 Raw map



X



Y

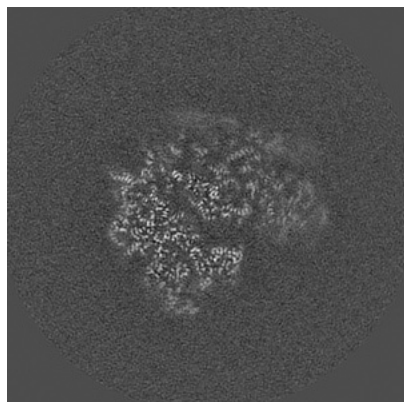


Z

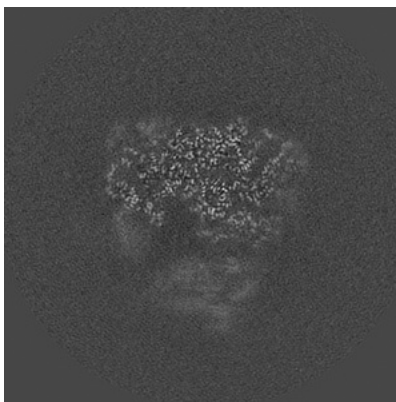
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

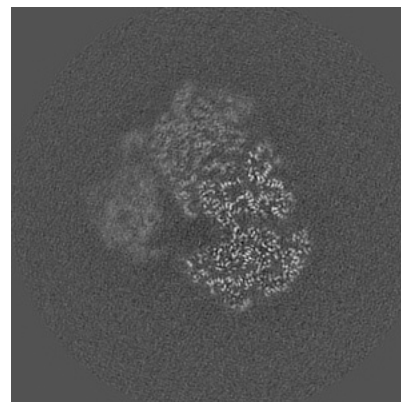
6.2.1 Primary map



X Index: 225

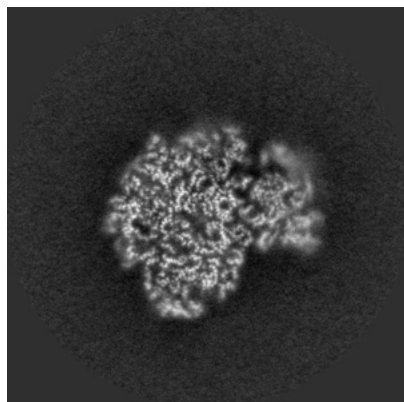


Y Index: 225

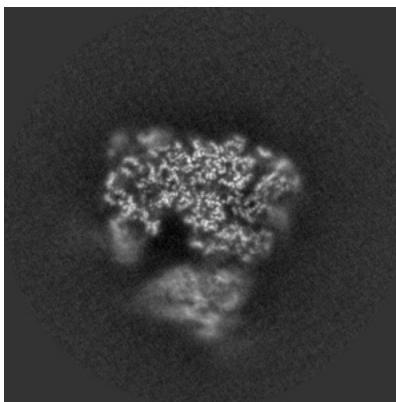


Z Index: 225

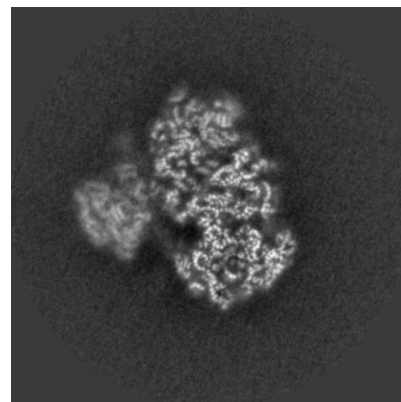
6.2.2 Raw map



X Index: 180



Y Index: 180

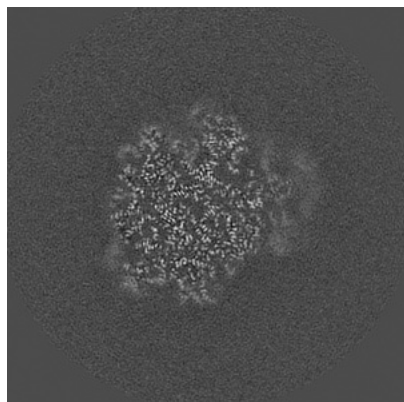


Z Index: 180

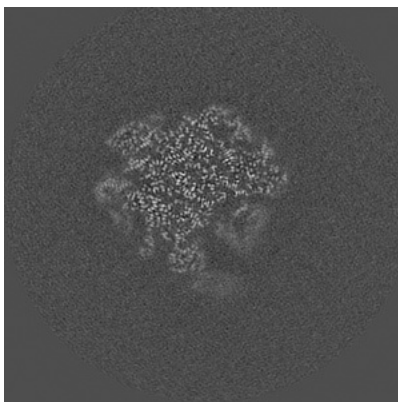
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

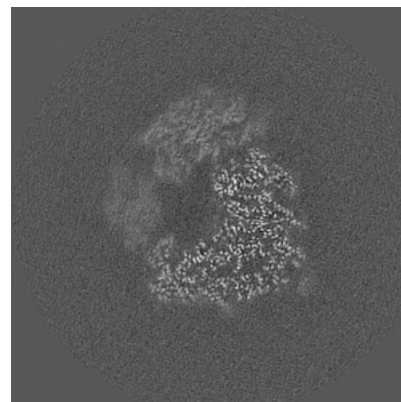
6.3.1 Primary map



X Index: 268

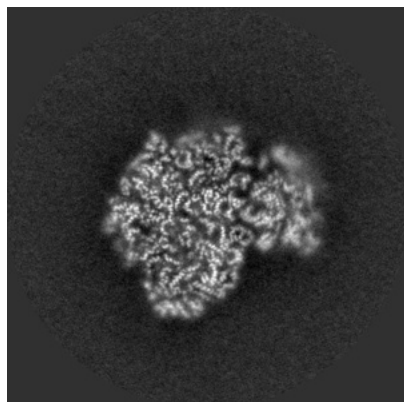


Y Index: 172

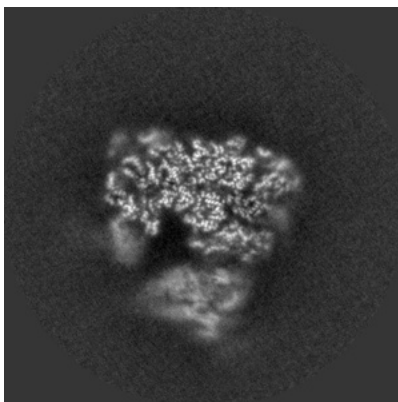


Z Index: 205

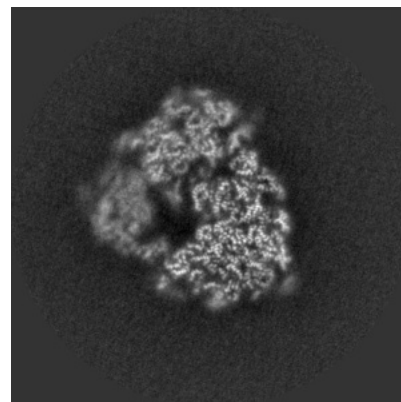
6.3.2 Raw map



X Index: 182



Y Index: 181

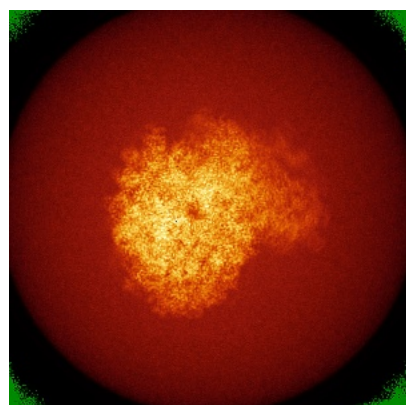


Z Index: 166

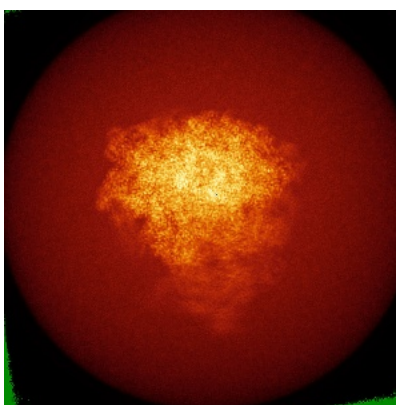
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

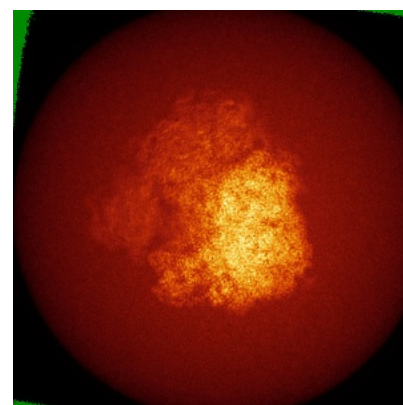
6.4.1 Primary map



X

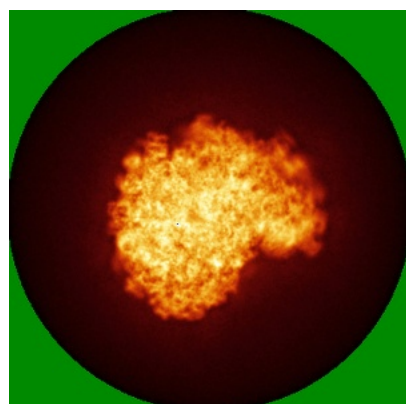


Y

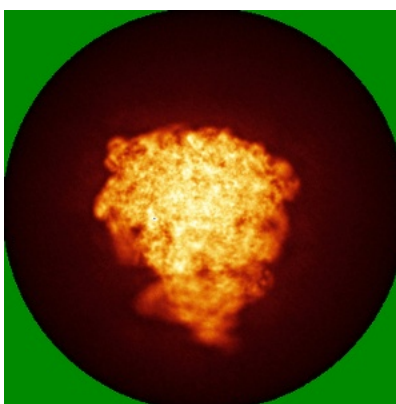


Z

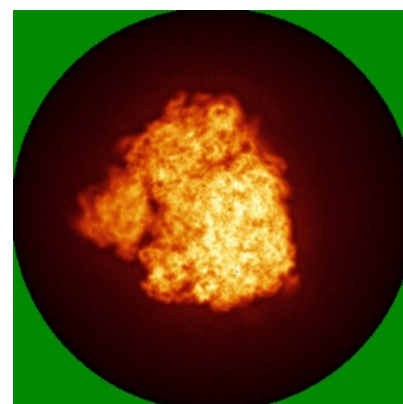
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

This section was not generated.

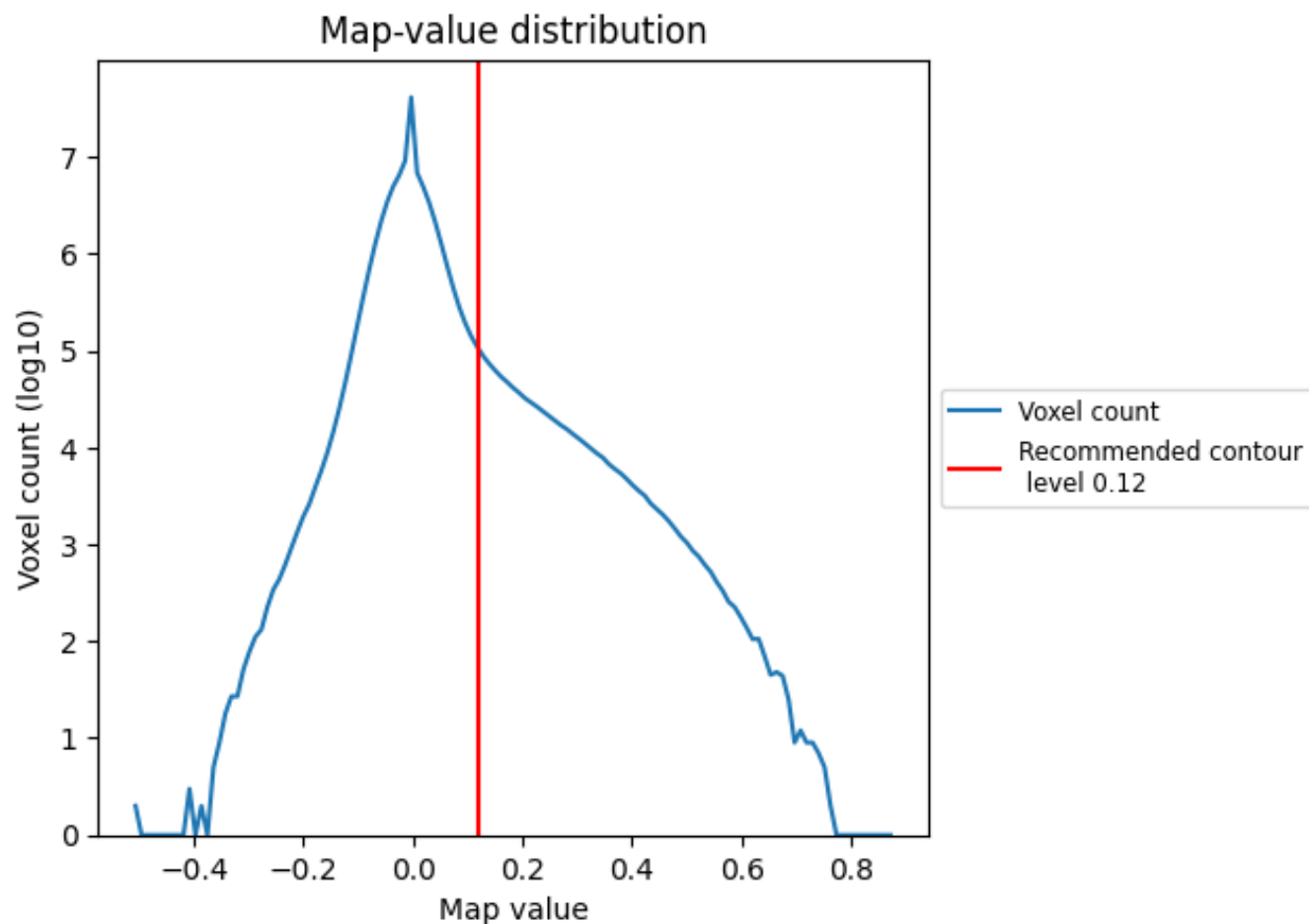
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

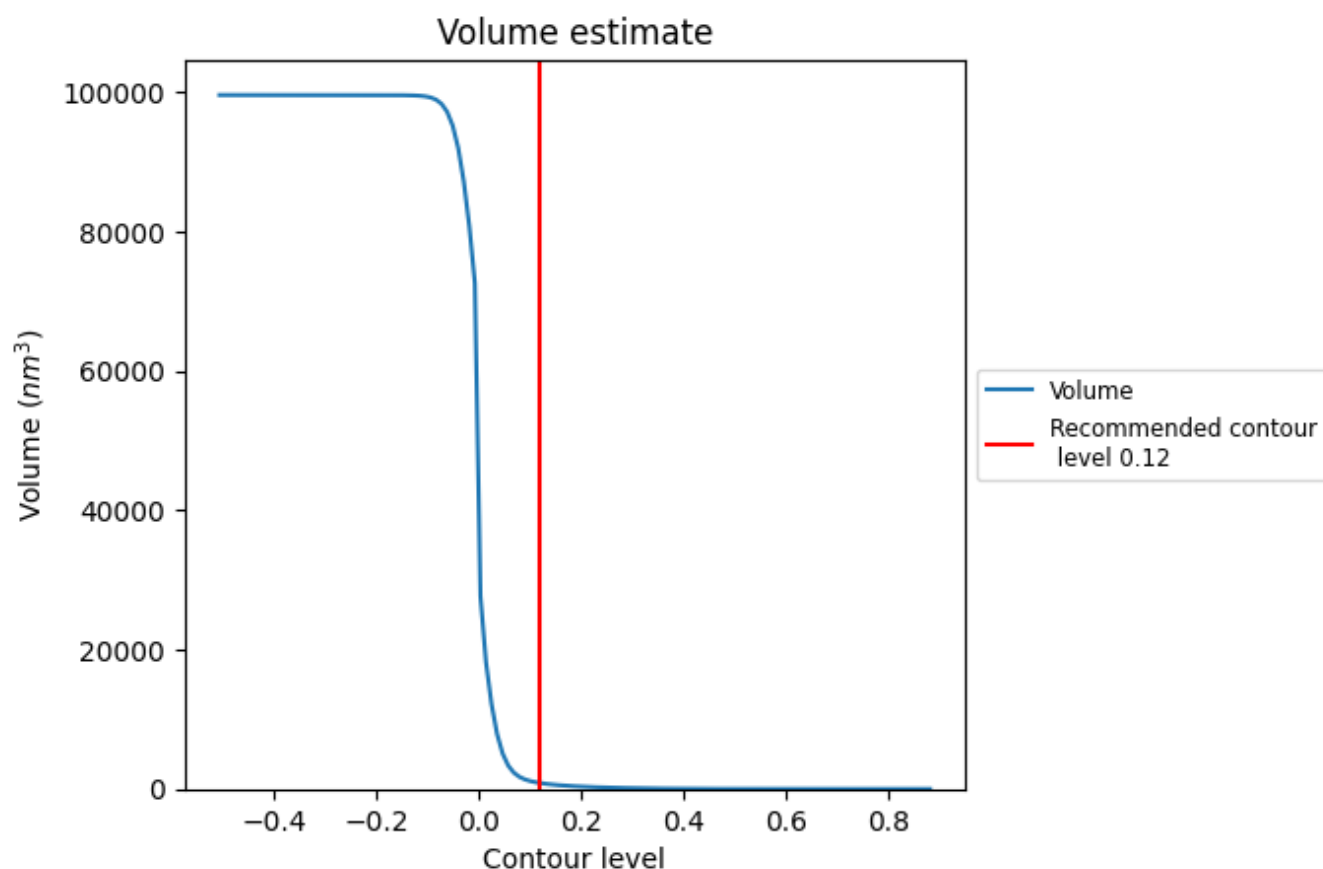
This section contains the results of statistical analysis of the map.

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.

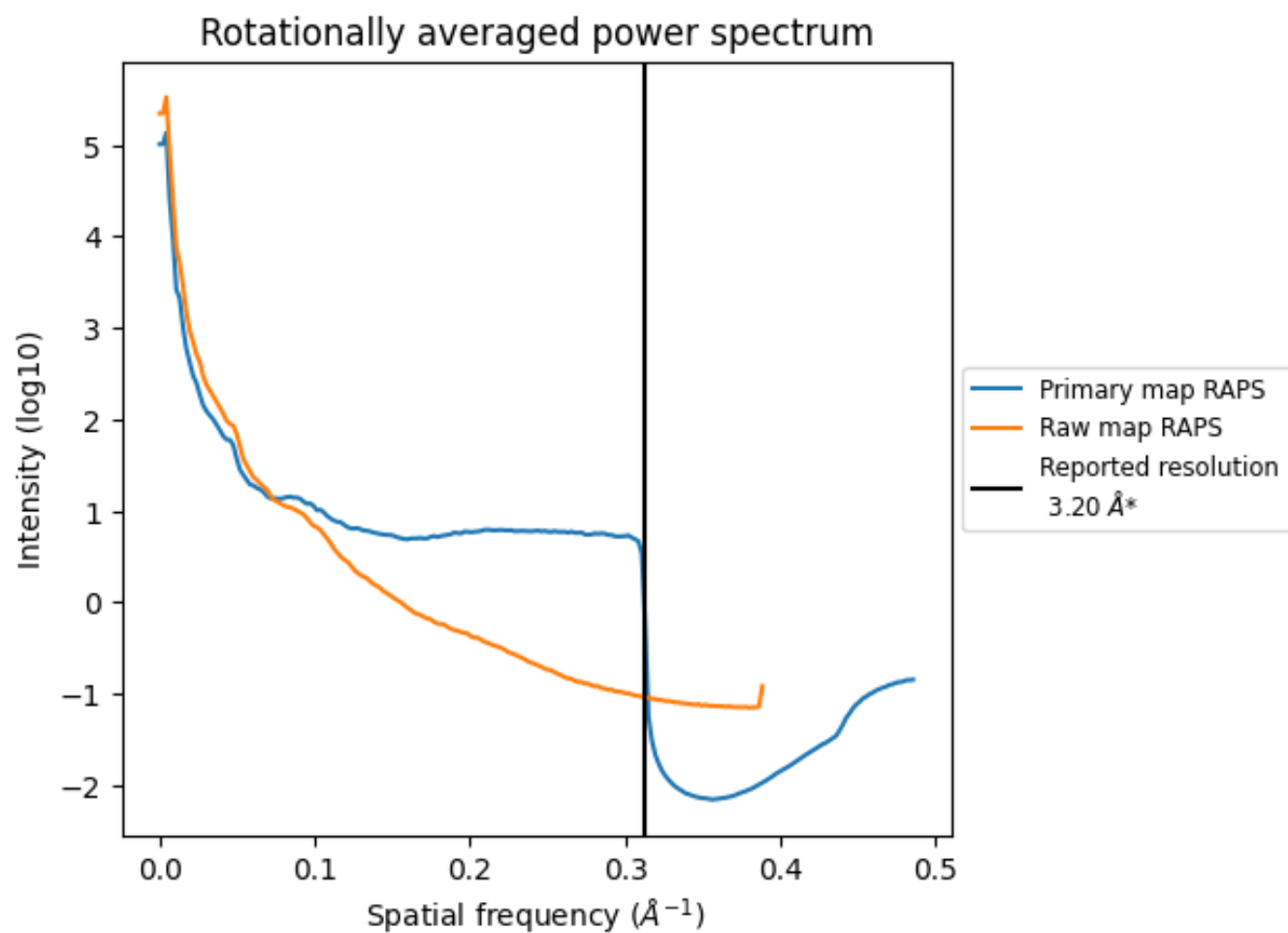
7.2 Volume estimate [i](#)



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 ⓘ



*Reported resolution corresponds to spatial frequency of $0.312 \text{ \AA}^{-1}$

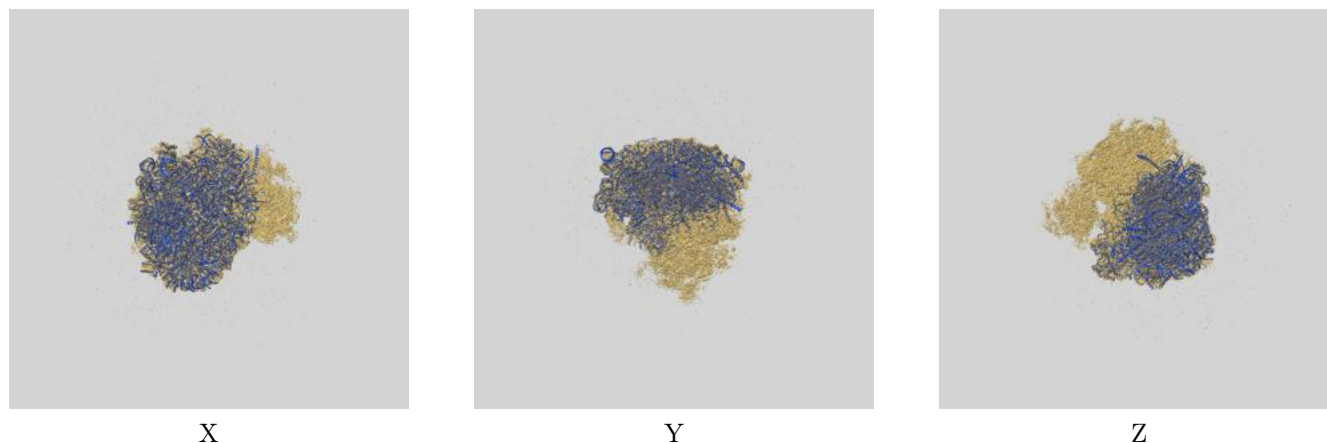
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

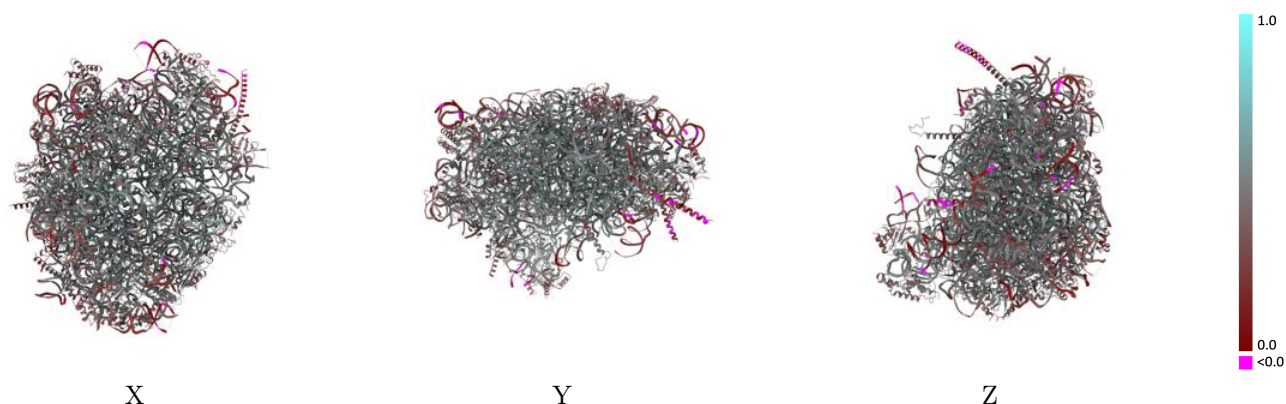
This section contains information regarding the fit between EMDB map EMD-8576 and PDB model 5UMD. Per-residue inclusion information can be found in section [3](#) on page [14](#).

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](#)

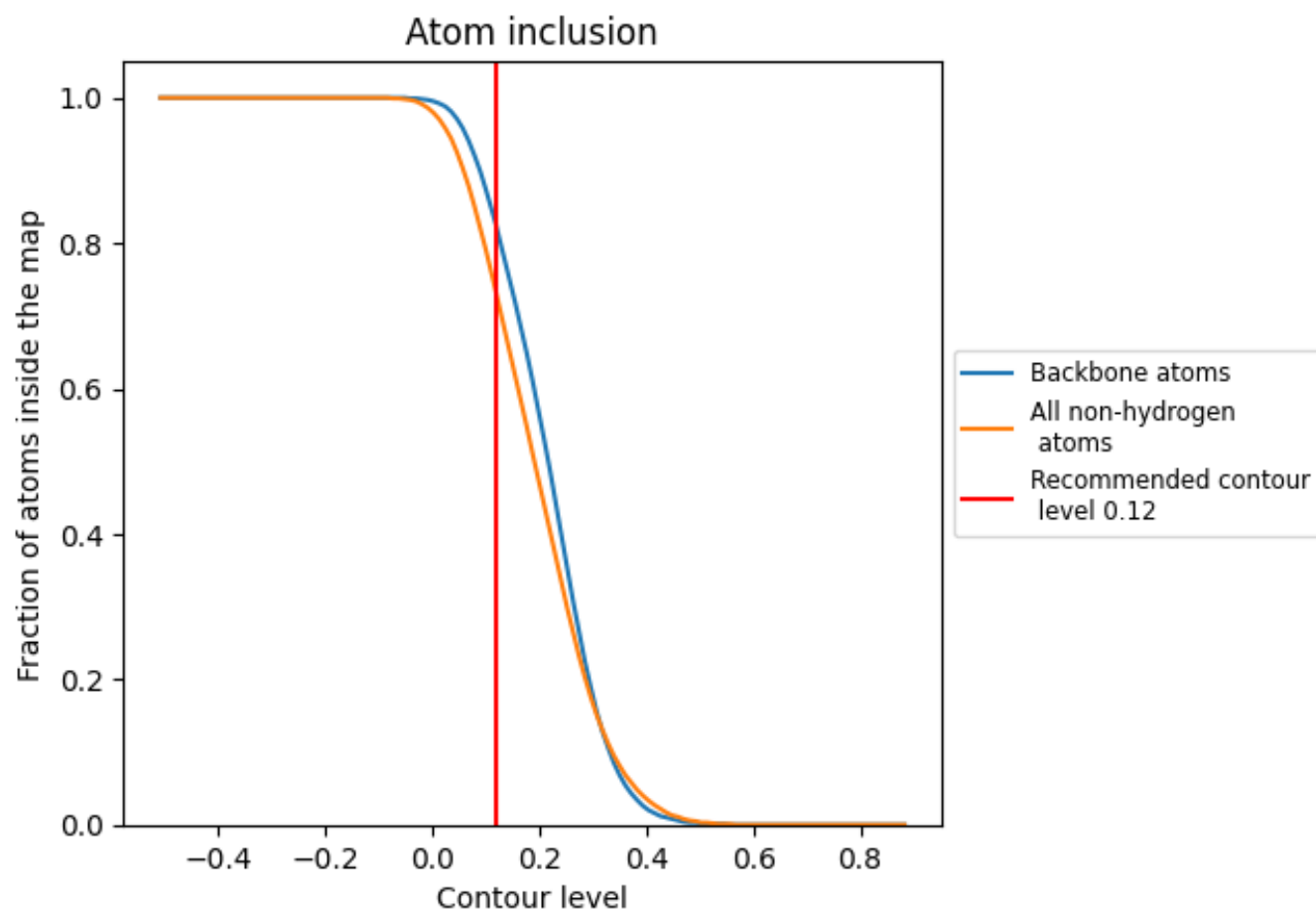


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)

This section was not generated.

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	 0.7320	 0.4600
0	 0.6430	 0.4510
1	 0.5720	 0.3950
2	 0.6230	 0.4390
3	 0.6450	 0.4330
4	 0.5420	 0.4030
5	 0.6710	 0.4580
6	 0.5660	 0.3940
7	 0.6430	 0.4490
8	 0.6600	 0.4770
9	 0.7280	 0.4880
A	 0.7900	 0.4730
B	 0.8640	 0.4920
C	 0.8530	 0.4920
D	 0.6590	 0.4810
E	 0.6770	 0.4680
F	 0.6430	 0.4380
G	 0.6030	 0.3860
H	 0.6510	 0.4410
I	 0.6060	 0.4130
J	 0.5180	 0.3560
K	 0.6750	 0.4730
L	 0.6500	 0.4350
M	 0.6270	 0.4520
N	 0.6200	 0.4170
O	 0.7190	 0.4850
P	 0.7210	 0.4930
Q	 0.6350	 0.4410
R	 0.6330	 0.4080
S	 0.6900	 0.4810
T	 0.5350	 0.3830
U	 0.6660	 0.4610
V	 0.6260	 0.4450
W	 0.6990	 0.4830
X	 0.5230	 0.3470



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Y	 0.5750	 0.3990
Z	 0.5990	 0.4030
a	 0.6310	 0.4770
b	 0.6050	 0.4010
c	 0.7000	 0.4720
d	 0.5540	 0.3910
e	 0.6560	 0.4630
f	 0.6930	 0.4560
g	 0.4510	 0.4040
h	 0.6370	 0.4710
i	 0.6380	 0.4660