



Full wwPDB EM Validation Report ⓘ

Jun 23, 2026 – 11:53 AM JST

PDB ID : 7CPJ / pdb_00007cpj
EMDB ID : EMD-30431
Title : ycbZ-stalled 70S ribosome
Authors : Yokoyama, T.; Shirouzu, M.; Ito, T.
Deposited on : 2020-08-07
Resolution : 3.30 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 : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
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

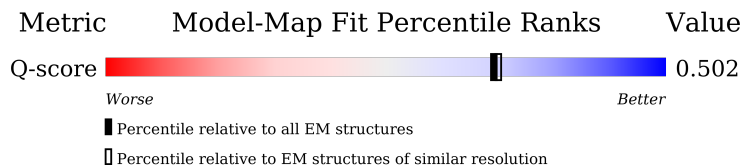
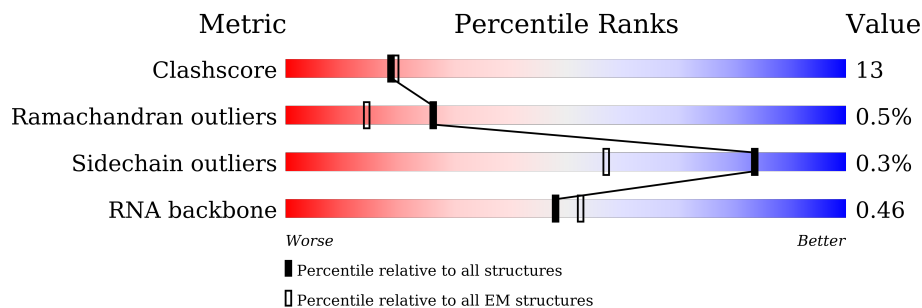
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	1539	8% 45% 44% 11%
2	b	240	88% 55% 34% 9%
3	c	233	29% 58% 31% 12%

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Mol	Chain	Length	Quality of chain
4	d	206	
5	e	167	
6	f	135	
7	g	179	
8	h	130	
9	i	130	
10	j	103	
11	k	129	
12	l	124	
13	m	118	
14	n	102	
15	o	89	
16	p	82	
17	q	84	
18	r	75	
19	s	92	
20	t	87	
21	u	71	
22	A	2903	
23	B	120	
24	C	273	
25	D	209	
26	E	201	
27	F	179	
28	G	177	

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Mol	Chain	Length	Quality of chain
29	H	149	
30	I	142	
31	J	142	
32	K	123	
33	L	144	
34	M	136	
35	N	127	
36	O	117	
37	P	115	
38	Q	118	
39	R	103	
40	S	110	
41	T	100	
42	U	104	
43	V	94	
44	W	85	
45	X	78	
46	Y	63	
47	Z	59	
48	0	57	
49	1	55	
50	2	46	
51	3	65	
52	4	38	
53	5	165	

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Mol	Chain	Length	Quality of chain
54	6	70	87% 57% 36% 6%
55	9	77	42% 48% 27% 25%
56	x	3	100%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 145941 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1539	Total	C	N	O	P	0	0
			33030	14739	6052	10700	1539		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	r	65	Total	C	N	O	0	0
			504	317	96	91		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	65	Total	C	N	O	S	0	0
			495	307	100	87	1		

- Molecule 22 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	A	2900	Total	C	N	O	P	0	0
			62276	27788	11460	20128	2900		

- Molecule 23 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	B	120	Total	C	N	O	P	0	0
			2572	1145	471	836	120		

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 26 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 28 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	H	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 30 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 31 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 32 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 33 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 34 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 35 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 36 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	O	116	Total	C	N	O		0	0
			892	552	178	162			

- Molecule 37 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 38 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Q	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 39 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 40 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 41 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 42 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	U	102	Total	C	N	O		
			779	492	146	141	0	0

- Molecule 43 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	V	94	Total	C	N	O	S	
			753	479	137	134	3	0

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	W	75	Total	C	N	O	S	
			575	356	116	102	1	0

- Molecule 45 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	X	77	Total	C	N	O	S	
			625	388	129	106	2	0

- Molecule 46 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	Y	63	Total	C	N	O	S	
			509	313	99	95	2	0

- Molecule 47 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	Z	58	Total	C	N	O	S	
			449	281	87	79	2	0

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	0	56	Total	C	N	O	S	
			444	269	94	80	1	0

- Molecule 49 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	1	50	Total	C	N	O	0	0
			409	263	75	71		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 51 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 52 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 53 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 54 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

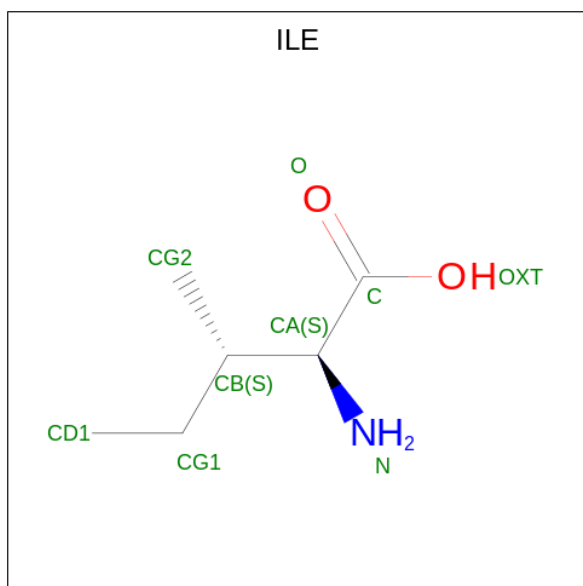
- Molecule 55 is a RNA chain called P/P tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	9	77	Total	C	N	O	P	0	0
			1646	733	295	541	77		

- Molecule 56 is a RNA chain called mRNA.

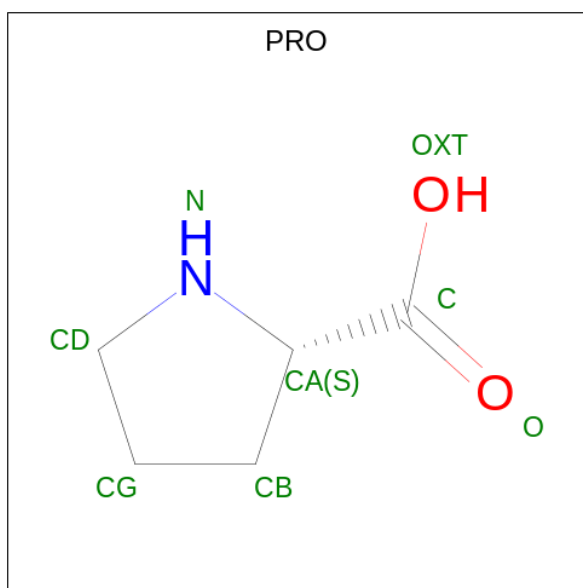
Mol	Chain	Residues	Atoms				AltConf	Trace
56	x	3	Total	C	N	O	P	
			63	28	11	21	3	
								0
								0

- Molecule 57 is ISOLEUCINE (CCD ID: ILE) (formula: $C_6H_{13}NO_2$).



Mol	Chain	Residues	Atoms				AltConf
57	A	1	Total	C	N	O	
			8	6	1	1	
							0

- Molecule 58 is PROLINE (CCD ID: PRO) (formula: $C_5H_9NO_2$).



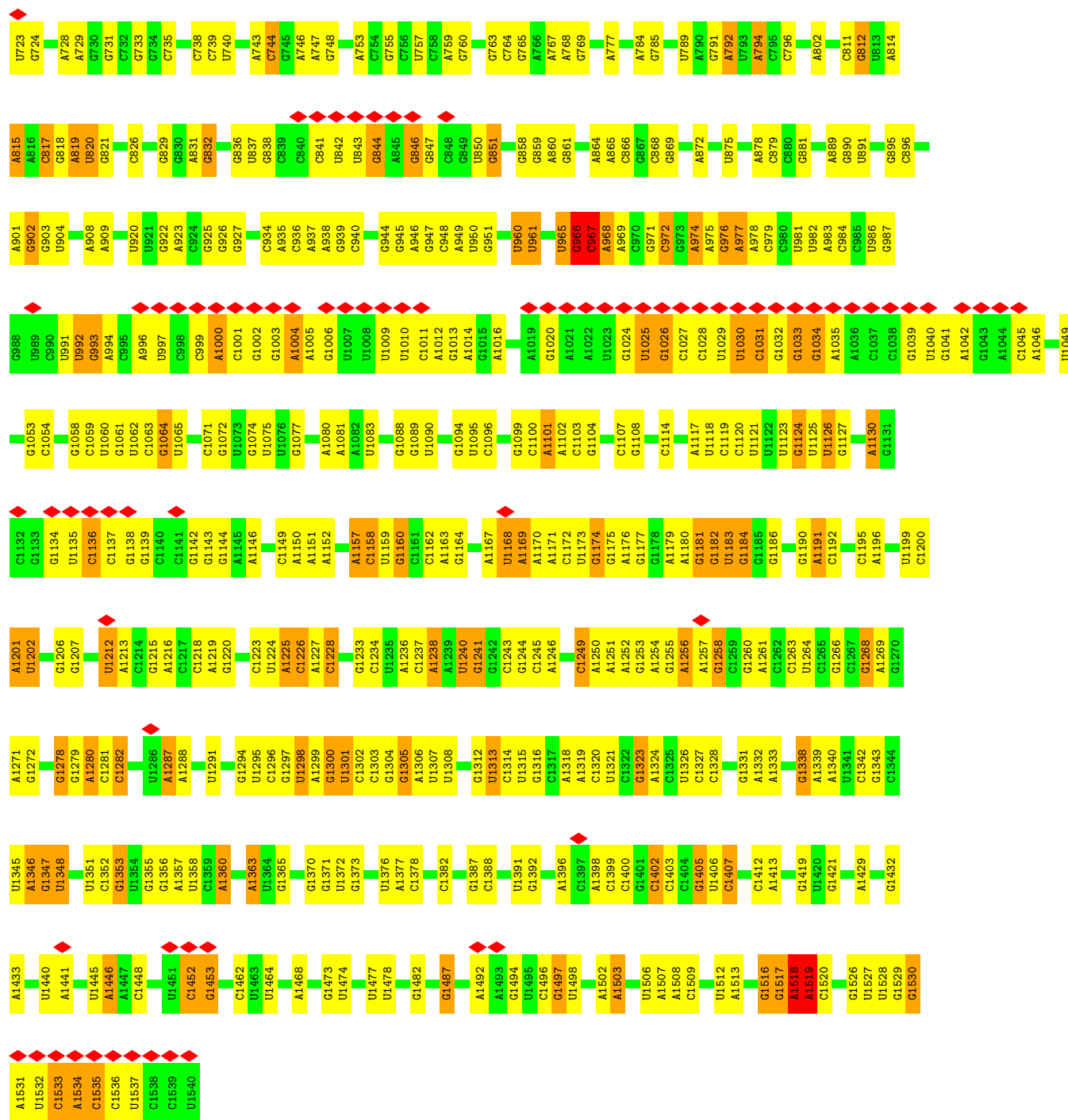
Mol	Chain	Residues	Atoms				AltConf
58	9	1	Total	C	N	O	0
			7	5	1	1	

3 Residue-property plots

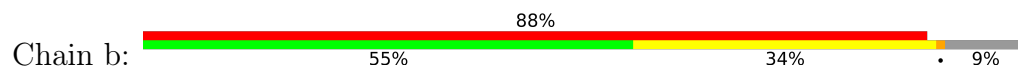
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S ribosomal RNA



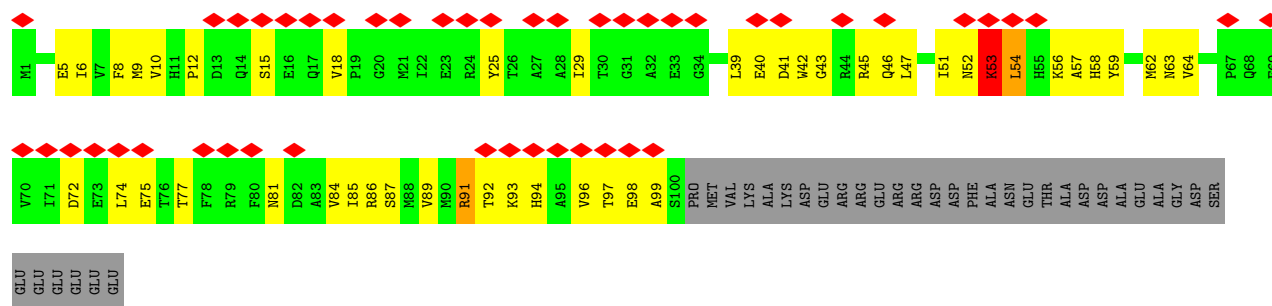


• Molecule 2: 30S ribosomal protein S2

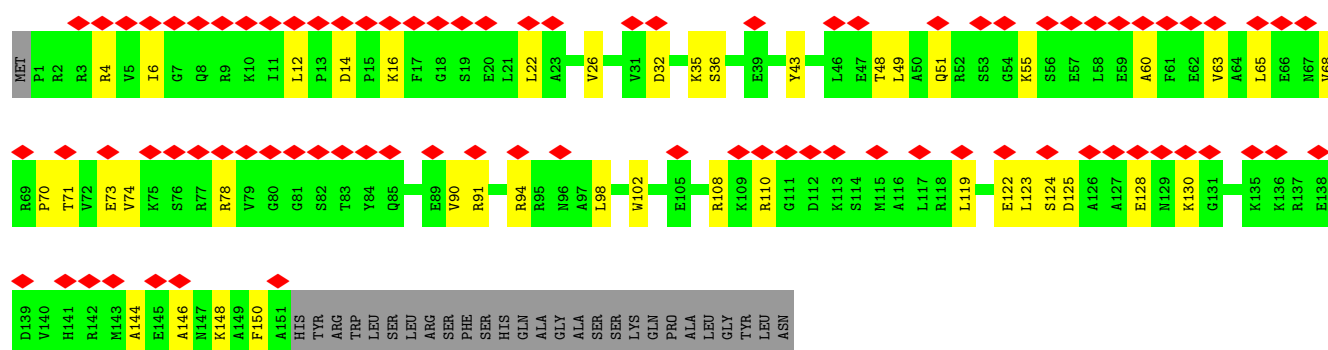




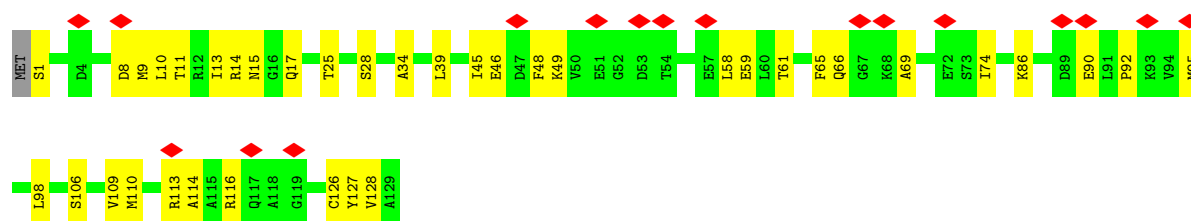
• Molecule 6: 30S ribosomal protein S6



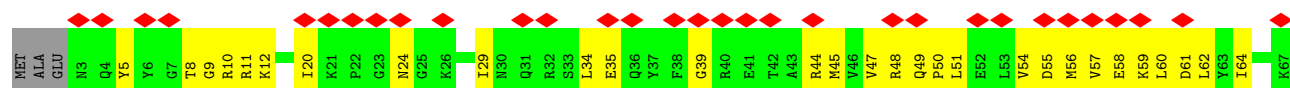
• Molecule 7: 30S ribosomal protein S7

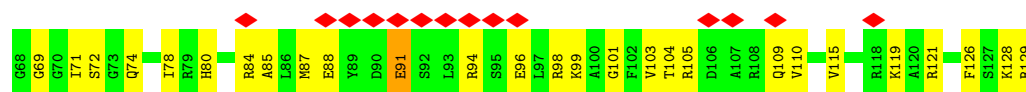


• Molecule 8: 30S ribosomal protein S8

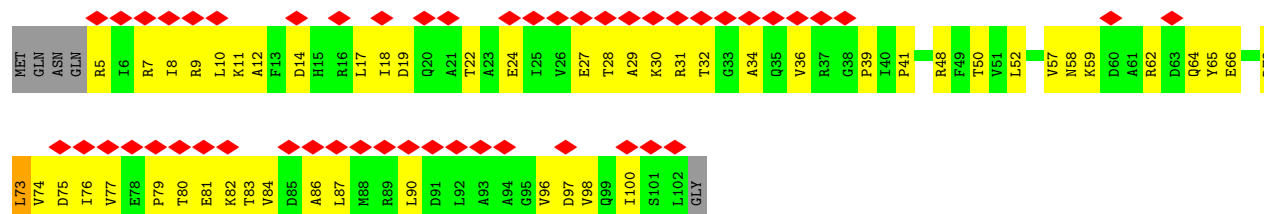


• Molecule 9: 30S ribosomal protein S9

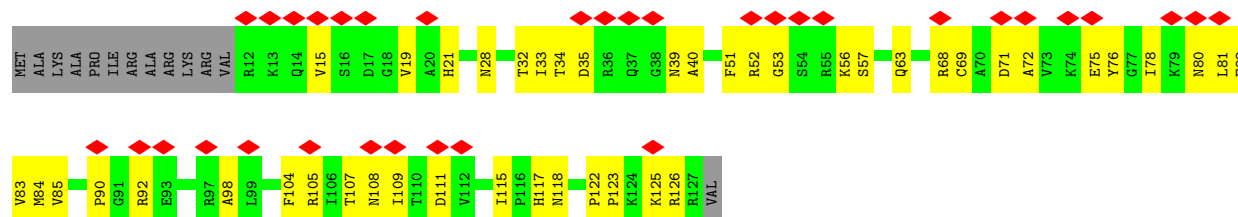




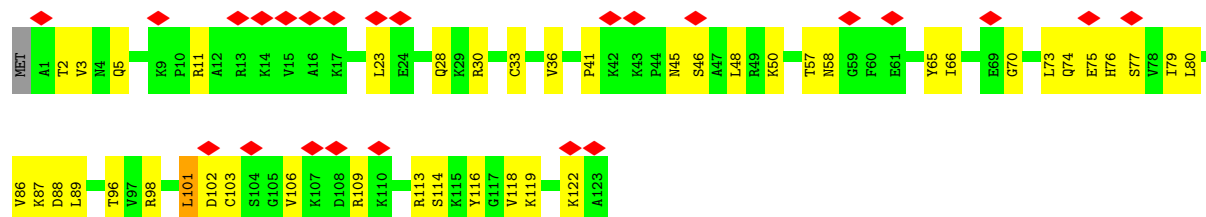
- Molecule 10: 30S ribosomal protein S10



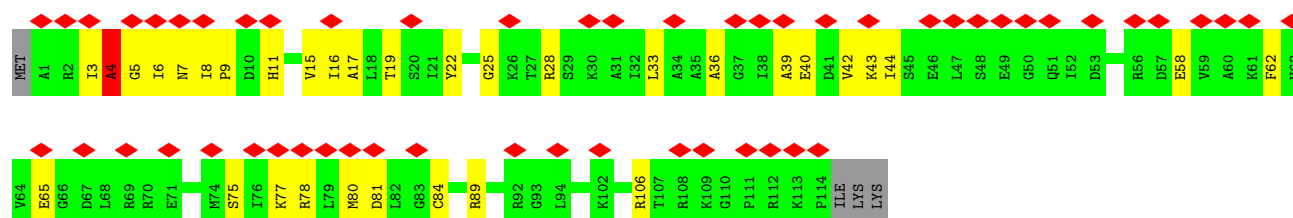
- Molecule 11: 30S ribosomal protein S11



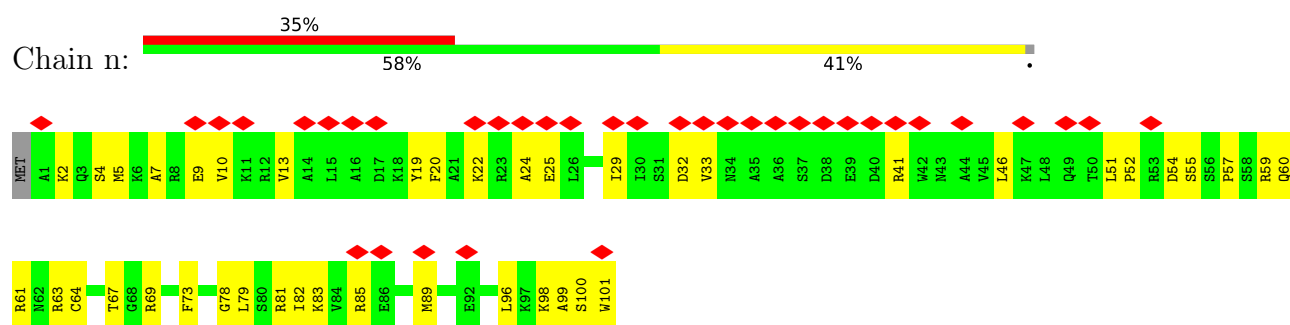
- Molecule 12: 30S ribosomal protein S12



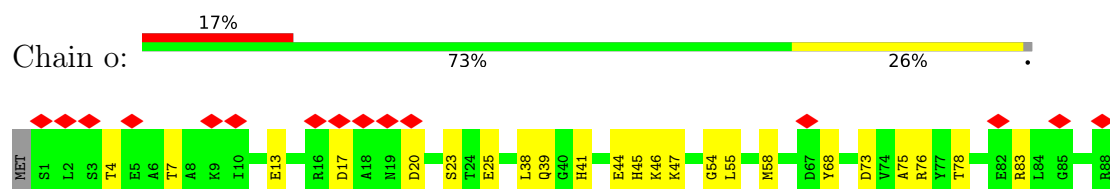
- Molecule 13: 30S ribosomal protein S13



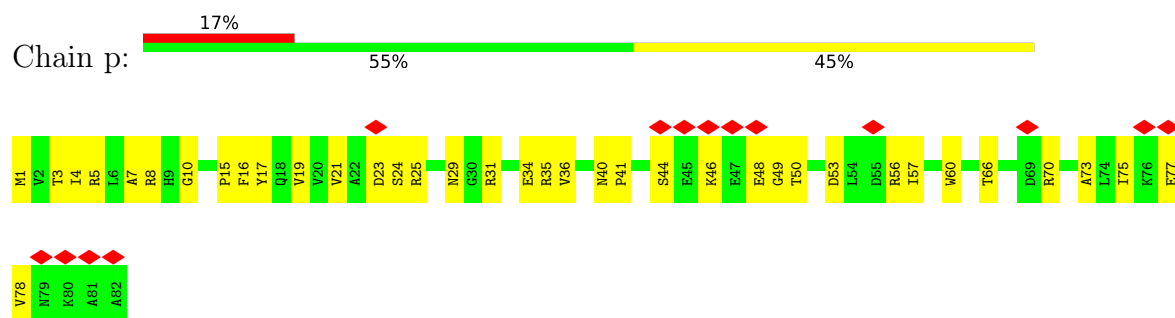
- Molecule 14: 30S ribosomal protein S14



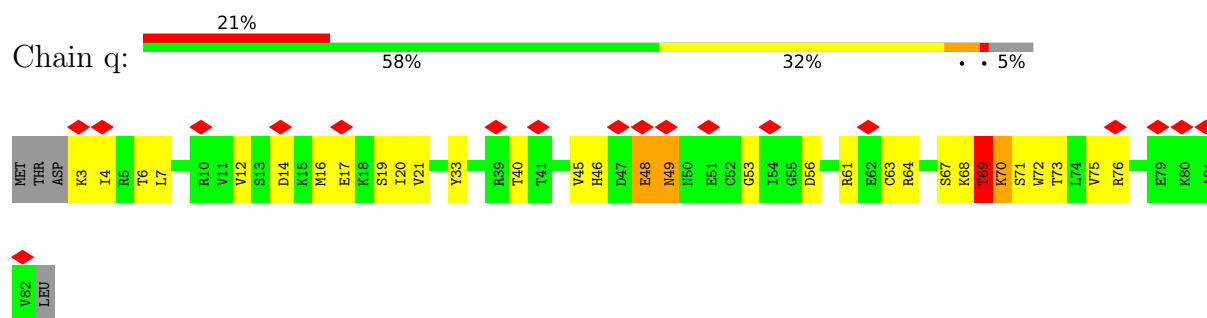
- Molecule 15: 30S ribosomal protein S15



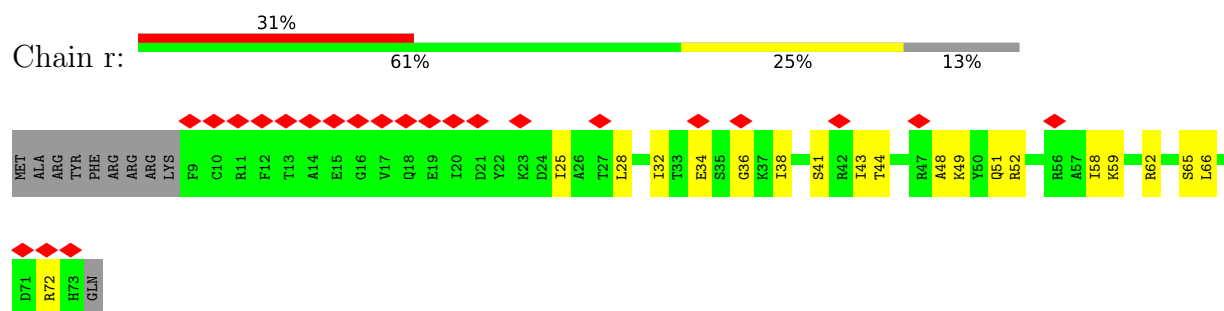
- Molecule 16: 30S ribosomal protein S16



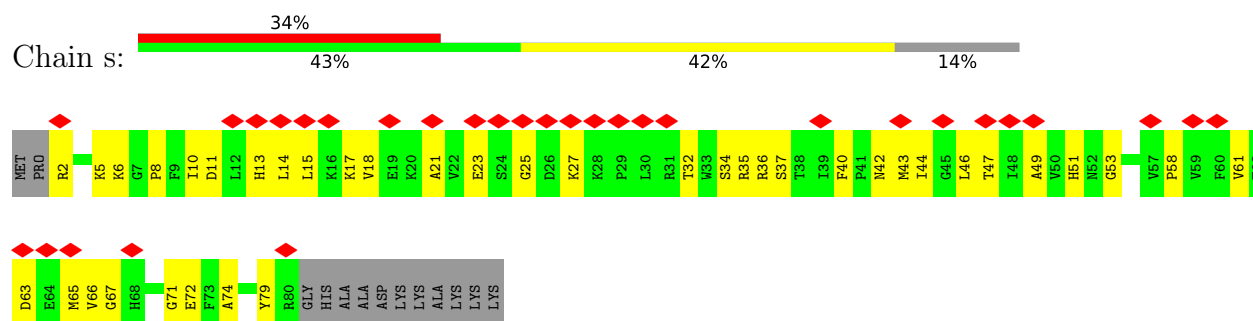
- Molecule 17: 30S ribosomal protein S17



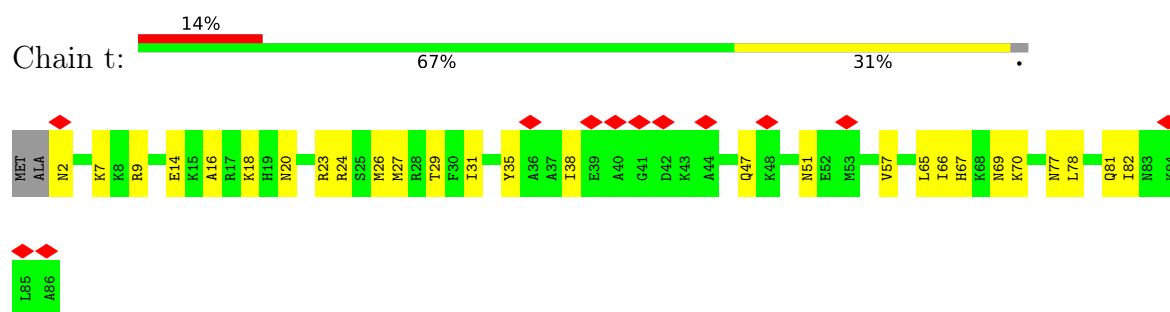
- Molecule 18: 30S ribosomal protein S18



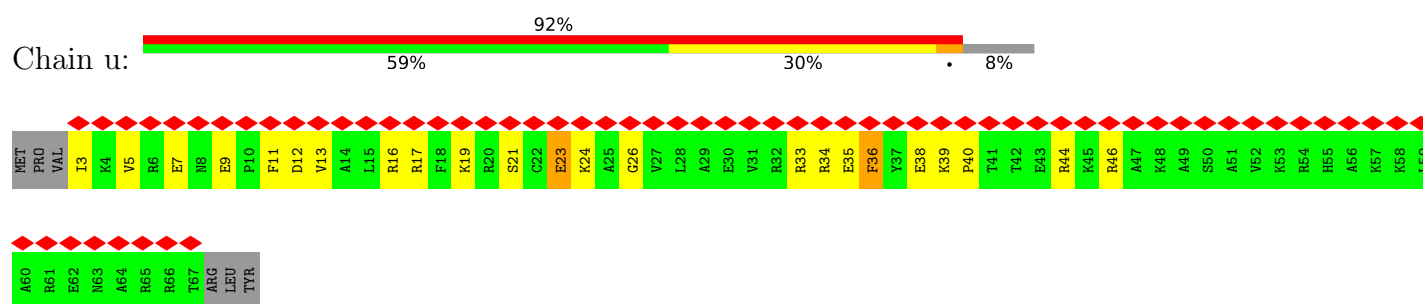
- Molecule 19: 30S ribosomal protein S19



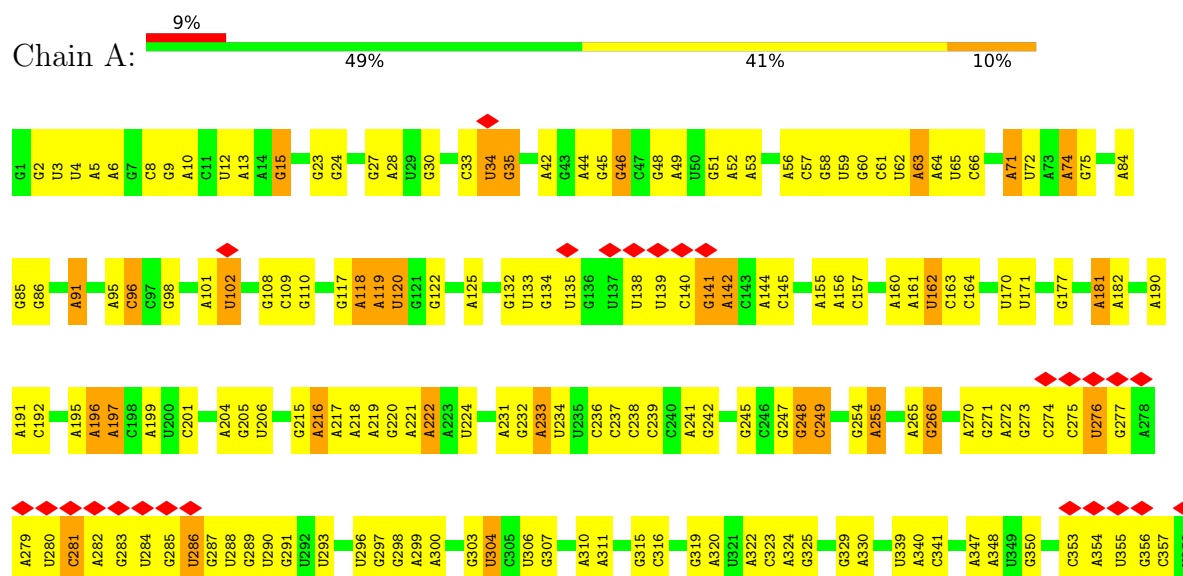
- Molecule 20: 30S ribosomal protein S20



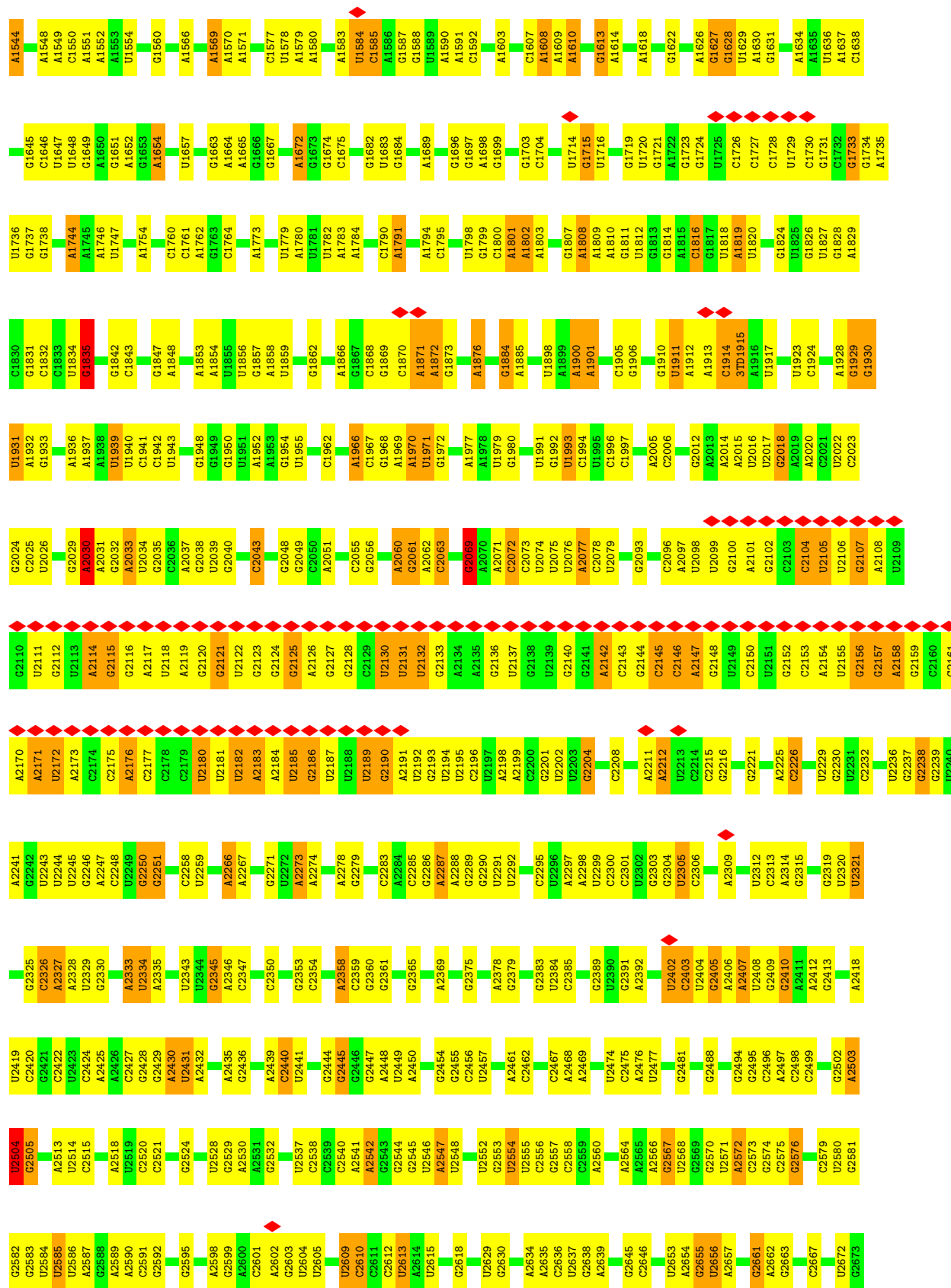
- Molecule 21: 30S ribosomal protein S21

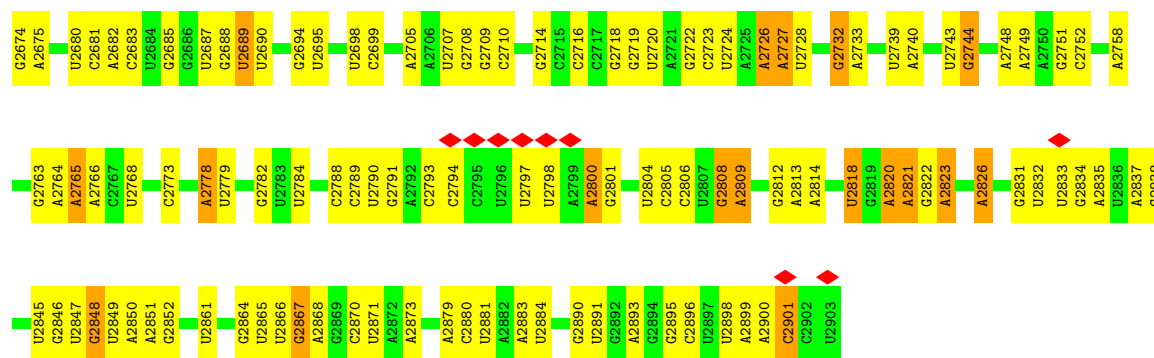


- Molecule 22: 23S ribosomal RNA

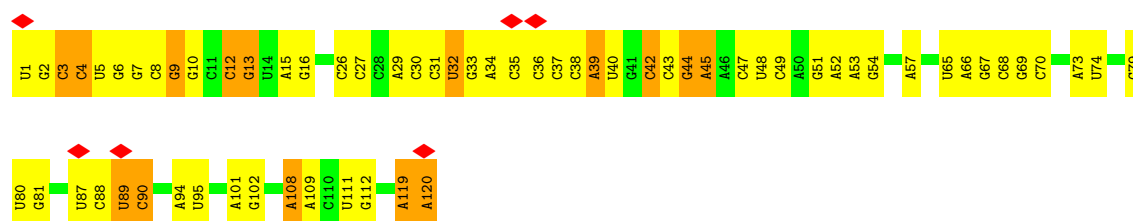




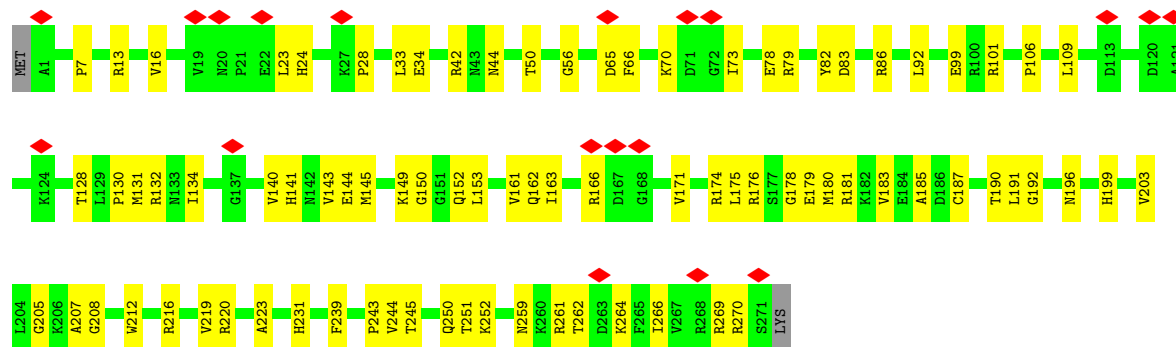




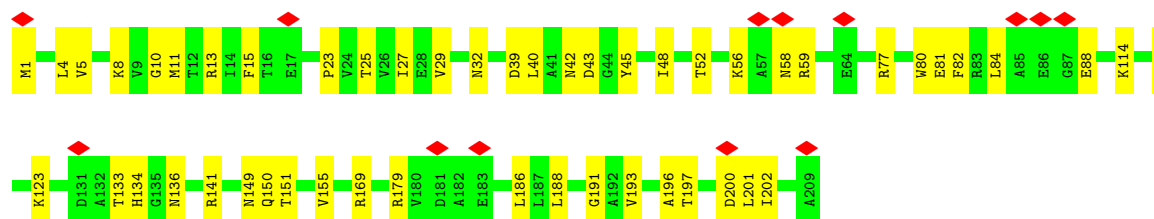
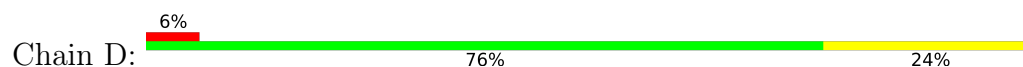
• Molecule 23: 5S ribosomal RNA



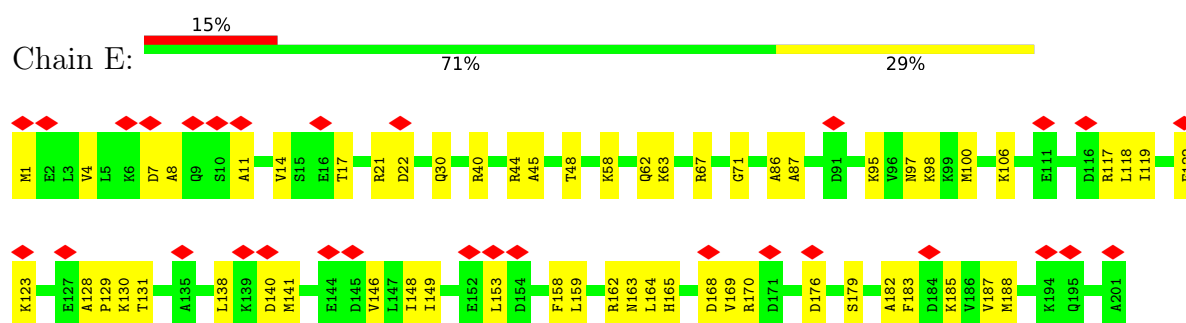
• Molecule 24: 50S ribosomal protein L2



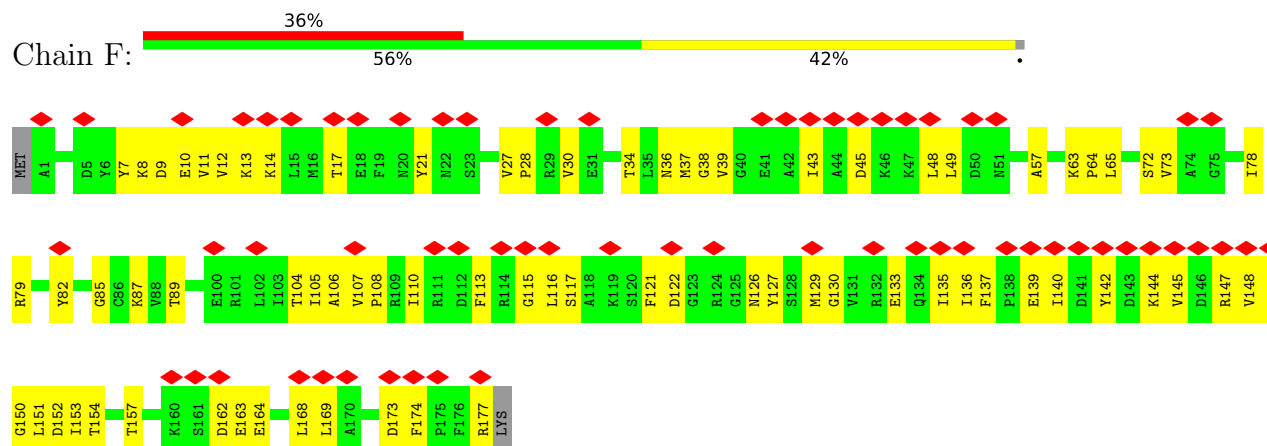
• Molecule 25: 50S ribosomal protein L3



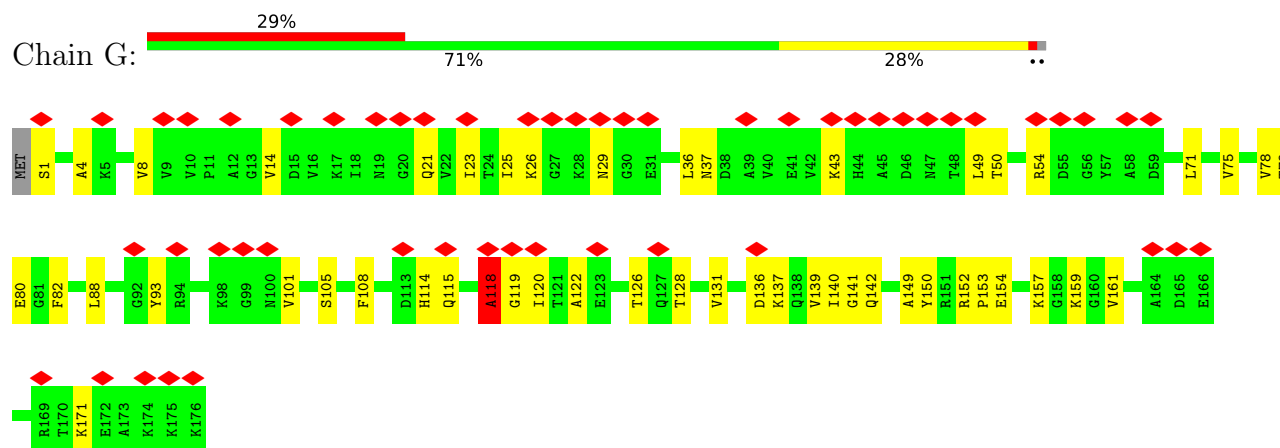
• Molecule 26: 50S ribosomal protein L4



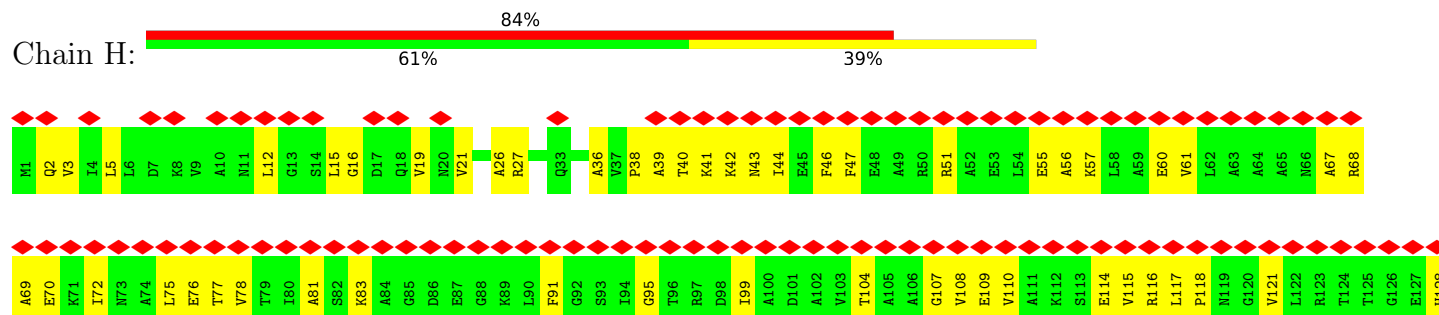
• Molecule 27: 50S ribosomal protein L5

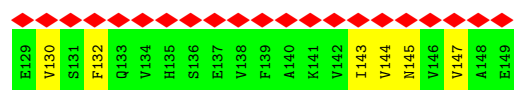


• Molecule 28: 50S ribosomal protein L6

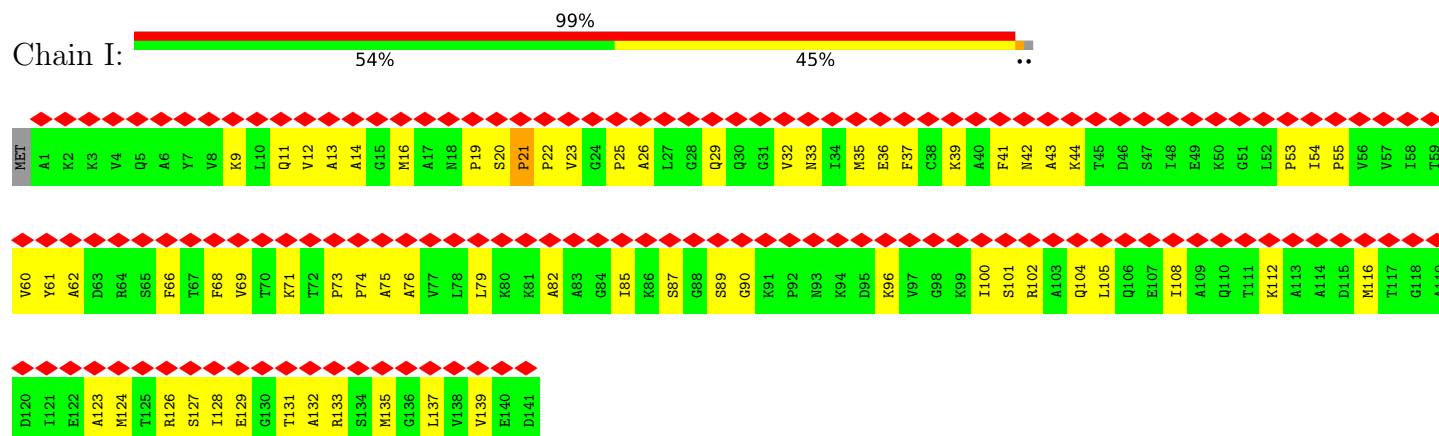


• Molecule 29: 50S ribosomal protein L9

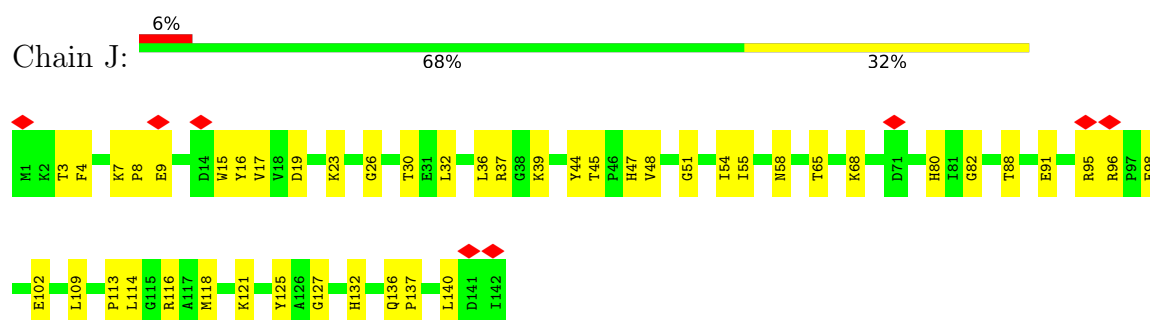




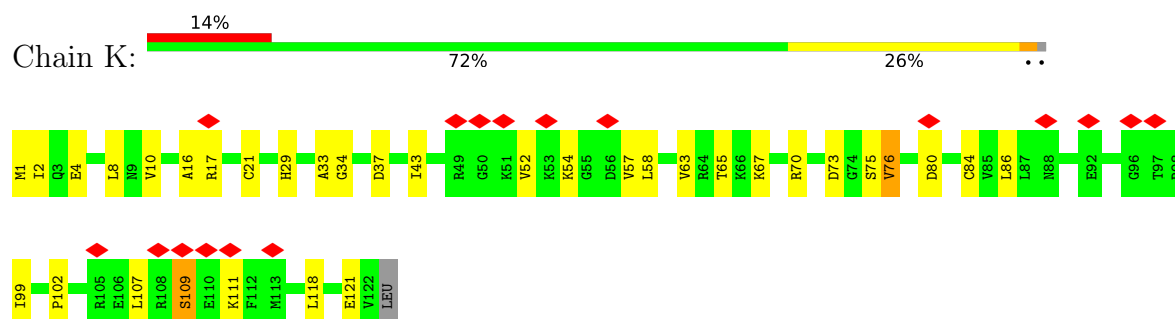
• Molecule 30: 50S ribosomal protein L11



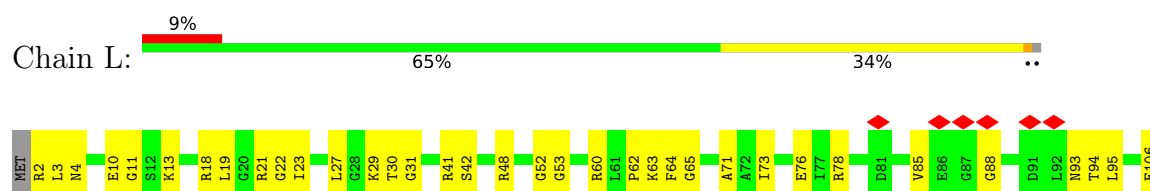
• Molecule 31: 50S ribosomal protein L13



• Molecule 32: 50S ribosomal protein L14

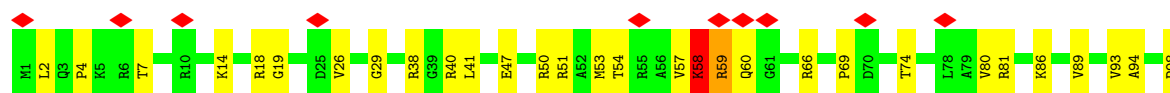
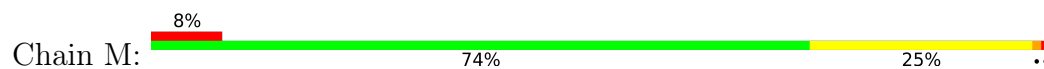


• Molecule 33: 50S ribosomal protein L15

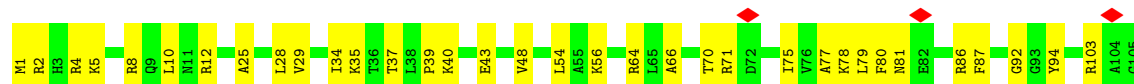




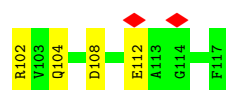
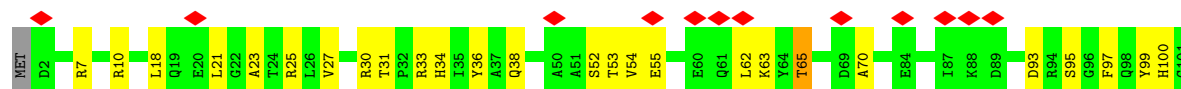
- Molecule 34: 50S ribosomal protein L16



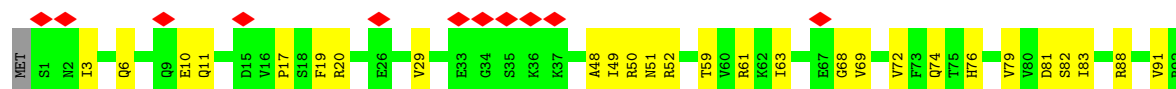
- Molecule 35: 50S ribosomal protein L17



- Molecule 36: 50S ribosomal protein L18



- Molecule 37: 50S ribosomal protein L19



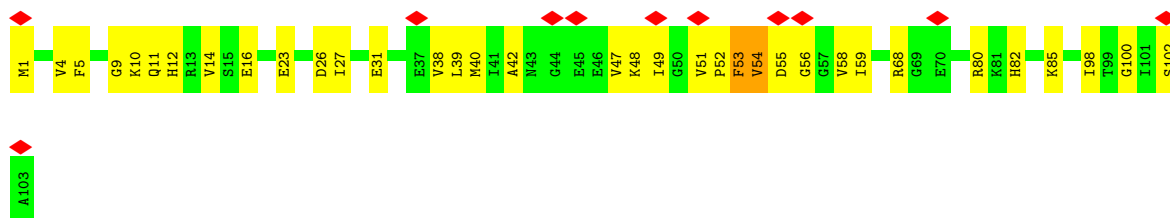
- Molecule 38: 50S ribosomal protein L20

Chain Q:  79% 20%



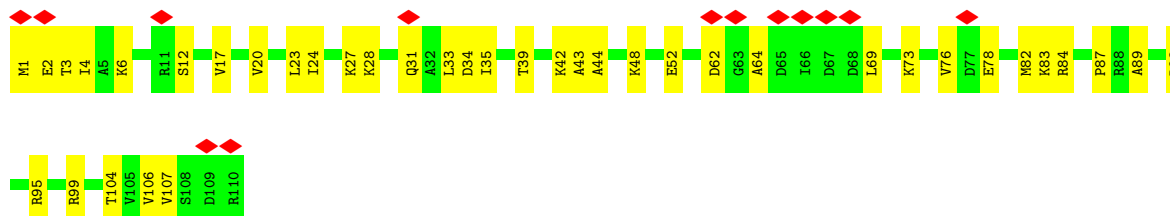
- Molecule 39: 50S ribosomal protein L21

Chain R:  11% 66% 32%



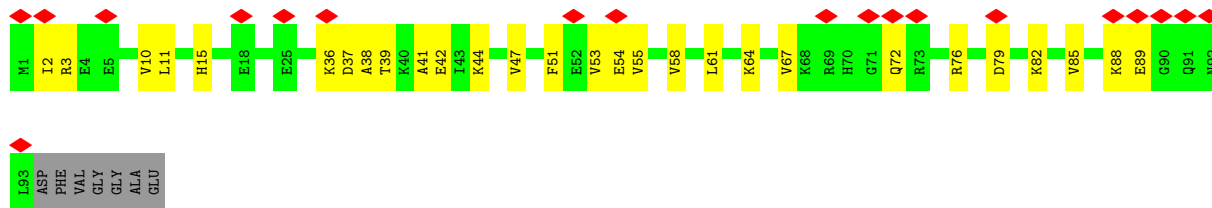
- Molecule 40: 50S ribosomal protein L22

Chain S:  12% 65% 35%



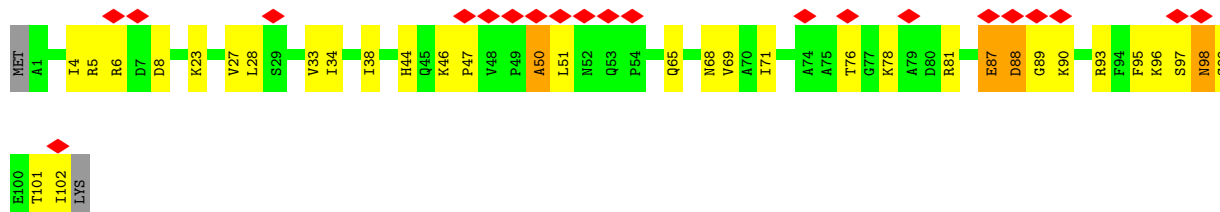
- Molecule 41: 50S ribosomal protein L23

Chain T:  19% 65% 28% 7%

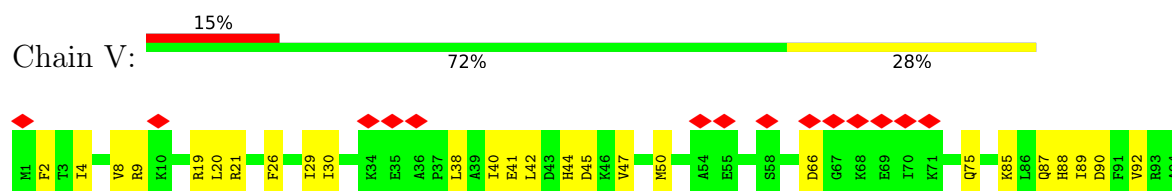


- Molecule 42: 50S ribosomal protein L24

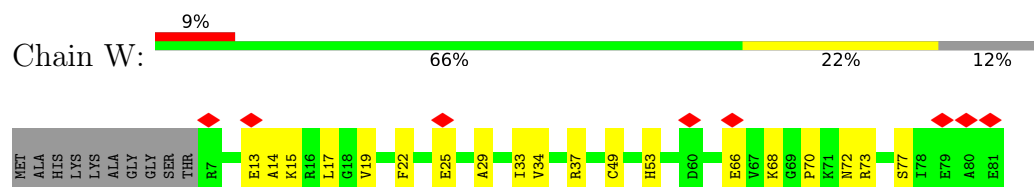
Chain U:  20% 65% 29%



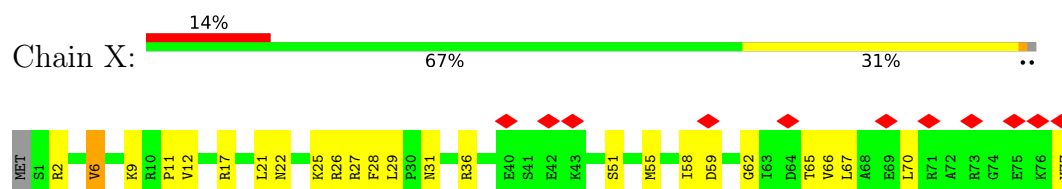
- Molecule 43: 50S ribosomal protein L25



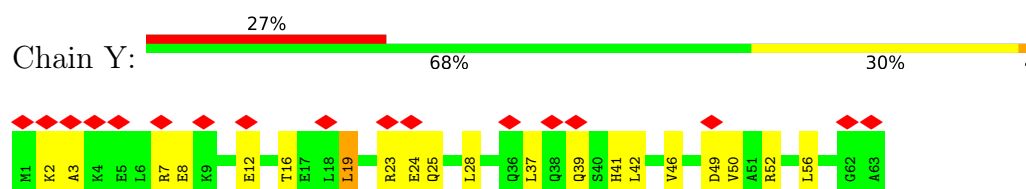
- Molecule 44: 50S ribosomal protein L27



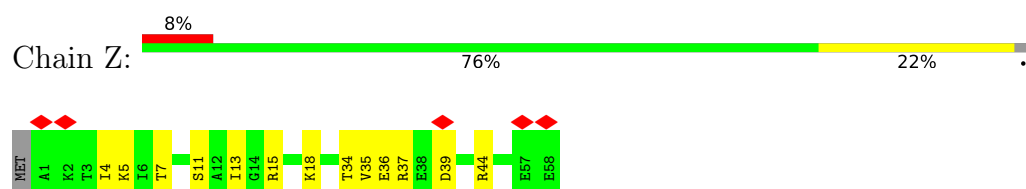
- Molecule 45: 50S ribosomal protein L28



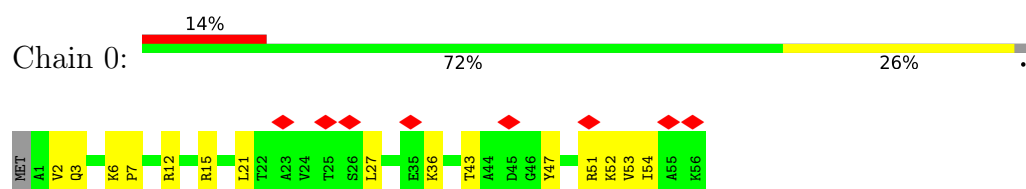
- Molecule 46: 50S ribosomal protein L29



- Molecule 47: 50S ribosomal protein L30

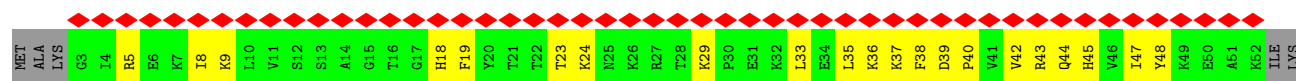


- Molecule 48: 50S ribosomal protein L32

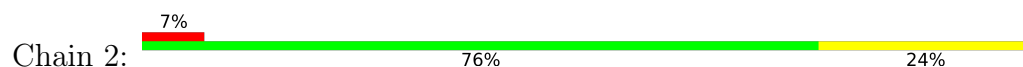


- Molecule 49: 50S ribosomal protein L33

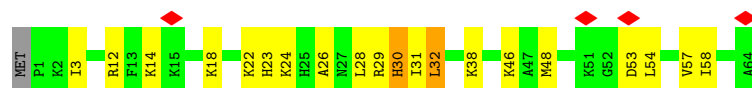




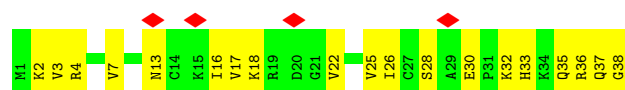
- Molecule 50: 50S ribosomal protein L34



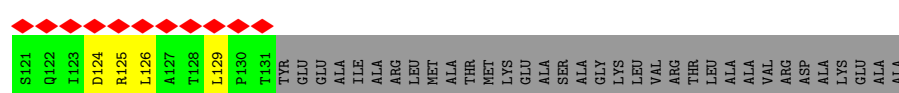
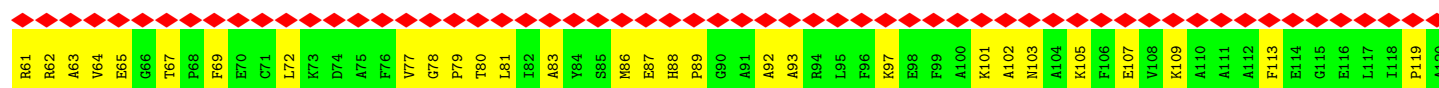
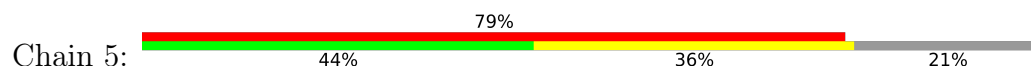
- Molecule 51: 50S ribosomal protein L35



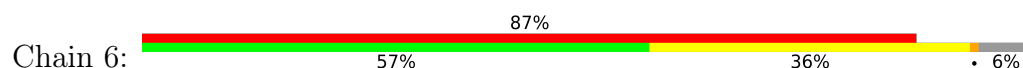
- Molecule 52: 50S ribosomal protein L36

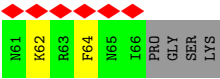


- Molecule 53: 50S ribosomal protein L10

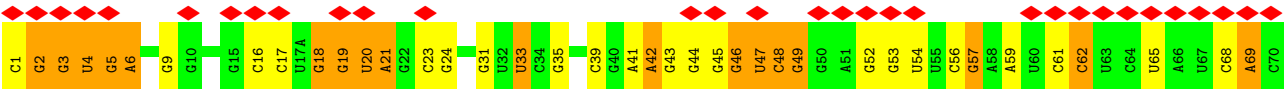


- Molecule 54: 50S ribosomal protein L31





● Molecule 55: P/P tRNA



● Molecule 56: mRNA



There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	40231	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	23500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.272	Depositor
Minimum map value	-0.164	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.046	Depositor
Map size (Å)	441.0, 441.0, 441.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.47, 1.47, 1.47	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, H2U, 5MC, 2MA, G7M, 6MZ, 1MG, UR3, PSU, MA6, 3TD, OMC, 4OC, 2MG, OMU, OMG

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	0.46	0/36675	0.42	0/57205
2	b	0.26	0/1735	0.58	0/2338
3	c	0.37	0/1651	0.51	0/2225
4	d	0.38	0/1665	0.60	0/2227
5	e	0.44	0/1154	0.61	0/1554
6	f	0.36	0/835	0.62	0/1128
7	g	0.29	0/1195	0.54	0/1602
8	h	0.44	0/989	0.51	0/1326
9	i	0.34	0/1034	0.57	0/1375
10	j	0.35	0/796	0.71	2/1077 (0.2%)
11	k	0.38	0/885	0.55	0/1195
12	l	0.45	0/969	0.62	0/1300
13	m	0.31	0/892	0.56	0/1193
14	n	0.36	0/811	0.52	0/1081
15	o	0.42	0/722	0.49	0/964
16	p	0.47	0/659	0.61	0/884
17	q	0.41	0/657	0.57	0/881
18	r	0.39	0/511	0.58	0/689
19	s	0.31	0/652	0.54	0/877
20	t	0.43	0/671	0.56	0/888
21	u	0.28	0/500	0.69	0/668
22	A	0.54	0/69174	0.43	0/107910
23	B	0.43	0/2876	0.42	0/4483
24	C	0.55	0/2121	0.57	0/2852
25	D	0.56	0/1586	0.53	0/2134
26	E	0.46	0/1571	0.48	0/2113
27	F	0.36	0/1434	0.60	0/1926
28	G	0.34	0/1343	0.51	0/1816
29	H	0.27	0/1122	0.56	0/1515
30	I	0.22	0/1046	0.59	0/1410
31	J	0.54	0/1152	0.50	0/1551
32	K	0.51	0/947	0.56	0/1268

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	L	0.51	0/1054	0.58	0/1403
34	M	0.50	0/1093	0.50	0/1460
35	N	0.54	0/973	0.65	0/1301
36	O	0.40	0/902	0.52	0/1209
37	P	0.51	0/929	0.52	0/1242
38	Q	0.61	0/960	0.56	0/1278
39	R	0.51	0/829	0.60	0/1107
40	S	0.53	0/864	0.60	0/1156
41	T	0.42	0/744	0.46	0/994
42	U	0.38	0/787	0.54	0/1051
43	V	0.44	0/766	0.49	0/1025
44	W	0.53	0/582	0.47	0/769
45	X	0.51	0/635	0.52	0/848
46	Y	0.37	0/510	0.54	0/677
47	Z	0.49	0/453	0.50	0/605
48	0	0.52	0/450	0.57	0/599
49	1	0.24	0/416	0.49	0/554
50	2	0.53	0/380	0.57	0/498
51	3	0.51	0/513	0.68	0/676
52	4	0.52	0/303	0.52	0/397
53	5	0.24	0/1001	0.60	0/1350
54	6	0.27	0/531	0.61	2/709 (0.3%)
55	9	0.32	0/1839	0.45	0/2866
56	x	0.42	0/69	0.37	0/105
All	All	0.49	0/157613	0.47	4/235534 (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
2	b	0	1
5	e	0	2
6	f	0	3
7	g	0	1
12	l	0	1
13	m	0	1
16	p	0	1
17	q	0	2
21	u	0	1
27	F	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
28	G	0	1
29	H	0	1
30	I	0	1
32	K	0	1
34	M	0	1
39	R	0	1
42	U	0	1
51	3	0	1
All	All	0	22

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	6	5	ILE	CA-C-N	-6.58	108.47	123.15
54	6	5	ILE	C-N-CA	-6.58	108.47	123.15
10	j	73	LEU	CA-C-N	-6.37	112.61	121.53
10	j	73	LEU	C-N-CA	-6.37	112.61	121.53

There are no chirality outliers.

All (22) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
51	3	30	HIS	Peptide
27	F	173	ASP	Peptide
28	G	118	ALA	Peptide
29	H	107	GLY	Peptide
30	I	21	PRO	Peptide
32	K	109	SER	Peptide
34	M	58	LYS	Peptide
39	R	53	PHE	Peptide
42	U	88	ASP	Peptide
2	b	87	ASP	Peptide
5	e	120	HIS	Peptide
5	e	121	ASN	Peptide
6	f	52	ASN	Peptide
6	f	53	LYS	Peptide
6	f	91	ARG	Peptide
7	g	63	VAL	Peptide
12	l	101	LEU	Peptide
13	m	4	ALA	Peptide

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Mol	Chain	Res	Type	Group
16	p	44	SER	Peptide
17	q	49	ASN	Peptide
17	q	69	THR	Peptide
21	u	23	GLU	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	33030	0	16647	712	0
2	b	1704	0	1732	63	0
3	c	1624	0	1699	46	0
4	d	1643	0	1710	94	0
5	e	1141	0	1170	45	0
6	f	817	0	808	38	0
7	g	1181	0	1240	28	0
8	h	979	0	1034	27	0
9	i	1022	0	1070	59	0
10	j	786	0	828	38	0
11	k	869	0	878	43	0
12	l	955	0	1019	34	0
13	m	883	0	944	24	0
14	n	799	0	841	38	0
15	o	714	0	737	17	0
16	p	649	0	666	32	0
17	q	648	0	691	24	0
18	r	504	0	502	14	0
19	s	637	0	665	34	0
20	t	665	0	714	28	0
21	u	495	0	486	27	0
22	A	62276	0	31344	1001	0
23	B	2572	0	1302	55	0
24	C	2082	0	2157	66	0
25	D	1565	0	1616	40	0
26	E	1552	0	1619	42	0
27	F	1410	0	1447	63	0
28	G	1323	0	1374	33	0
29	H	1111	0	1148	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	I	1032	0	1088	58	0
31	J	1129	0	1162	37	0
32	K	938	0	1012	24	0
33	L	1045	0	1117	49	0
34	M	1074	0	1157	29	0
35	N	960	0	1000	32	0
36	O	892	0	923	25	0
37	P	917	0	965	26	0
38	Q	947	0	1022	22	0
39	R	816	0	839	31	0
40	S	857	0	922	29	0
41	T	738	0	807	22	0
42	U	779	0	834	24	0
43	V	753	0	780	15	0
44	W	575	0	592	13	0
45	X	625	0	655	21	0
46	Y	509	0	543	16	0
47	Z	449	0	491	10	0
48	0	444	0	461	15	0
49	1	409	0	440	15	0
50	2	377	0	418	7	0
51	3	504	0	574	20	0
52	4	302	0	343	15	0
53	5	988	0	1025	49	0
54	6	522	0	524	27	0
55	9	1646	0	831	28	0
56	x	63	0	34	0	0
57	A	8	0	10	1	0
58	9	7	0	7	2	0
All	All	145941	0	98664	3063	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 (3063) 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:1405:G7M:H22	1:a:1518:MA6:H8	1.19	1.06
30:I:25:PRO:O	30:I:29:GLN:HB3	1.60	0.99
22:A:883:G:N2	22:A:893:C:O2	1.97	0.95
22:A:1093:G:H21	22:A:1098:A:H62	1.13	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:437:U:H3	1:a:495:A:H62	1.16	0.92
1:a:62:U:H4'	1:a:378:G:H21	1.37	0.89
22:A:284:U:H3	22:A:356:G:H1	1.12	0.89
1:a:406:G:N3	4:d:115:GLN:NE2	2.21	0.87
34:M:19:GLY:O	34:M:38:ARG:NH1	2.08	0.86
55:9:31:G:N1	55:9:39:C:N3	2.22	0.86
1:a:409:U:O4	1:a:433:G:O6	1.94	0.85
37:P:88:ARG:NH1	37:P:114:ASN:OD1	2.09	0.85
22:A:545:U:H3	22:A:548:G:H1	0.85	0.85
1:a:1405:G7M:N2	1:a:1518:MA6:H8	1.92	0.84
1:a:459:A:H2'	1:a:460:A:H8	1.42	0.84
19:s:40:PHE:H	19:s:43:MET:HE3	1.41	0.84
24:C:141:HIS:ND1	24:C:192:GLY:O	2.11	0.83
55:9:49:G:H1	55:9:65:U:H3	0.85	0.83
9:i:91:GLU:HA	9:i:94:ARG:HB3	1.61	0.83
22:A:284:U:O2	22:A:356:G:N2	2.12	0.83
22:A:197:A:N6	22:A:2430:A:O2'	2.12	0.82
22:A:270:A:N1	22:A:369:U:O2'	2.10	0.82
12:l:113:ARG:HB2	12:l:118:VAL:HG23	1.59	0.82
22:A:1086:A:O2'	22:A:1087:G:N7	2.12	0.82
22:A:1645:G:H5''	22:A:1646:C:H5'	1.60	0.82
55:9:31:G:N2	55:9:39:C:O2	2.11	0.82
22:A:517:C:OP1	48:0:12:ARG:NH2	2.13	0.81
1:a:9:G:OP2	5:e:125:LYS:NZ	2.13	0.81
36:O:62:LEU:HD11	36:O:70:ALA:HA	1.63	0.81
10:j:31:ARG:HG3	10:j:32:THR:HG23	1.62	0.81
11:k:111:ASP:OD2	21:u:19:LYS:NZ	2.14	0.81
1:a:437:U:O4	1:a:495:A:N7	2.13	0.80
22:A:249:C:O2'	33:L:63:LYS:NZ	2.12	0.80
22:A:1072:C:N4	22:A:1098:A:OP2	2.13	0.80
55:9:49:G:O6	55:9:65:U:O4	2.00	0.80
6:f:29:ILE:HD13	6:f:64:VAL:HG21	1.63	0.80
22:A:976:G:HO2'	22:A:1155:A:HO2'	1.27	0.80
5:e:80:LEU:HG	5:e:122:VAL:HG11	1.63	0.80
13:m:28:ARG:HH21	13:m:62:PHE:HB2	1.45	0.80
4:d:24:VAL:HA	4:d:160:LEU:HD11	1.64	0.80
25:D:123:LYS:HE2	35:N:1:MET:HE1	1.64	0.79
44:W:13:GLU:O	44:W:15:LYS:NZ	2.14	0.79
4:d:102:TYR:OH	4:d:108:ALA:O	2.00	0.79
4:d:12:ARG:NH2	4:d:36:ALA:O	2.14	0.79
7:g:14:ASP:OD1	7:g:43:TYR:OH	2.00	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:d:104:MET:HG3	4:d:170:LEU:HD13	1.65	0.78
22:A:1869:G:N2	22:A:1872:A:OP2	2.17	0.78
29:H:41:LYS:HA	29:H:44:ILE:HB	1.63	0.78
30:I:85:ILE:HG22	30:I:87:SER:H	1.46	0.78
4:d:149:LYS:NZ	4:d:177:MET:SD	2.56	0.78
1:a:451:A:H5'	16:p:70:ARG:HH22	1.48	0.78
1:a:1218:C:H2'	1:a:1219:A:C8	2.17	0.78
15:o:45:HIS:O	15:o:47:LYS:N	2.16	0.78
1:a:938:A:N3	1:a:1376:U:O2'	2.17	0.78
22:A:2682:A:H61	22:A:2728:U:H1'	1.49	0.78
23:B:31:C:O2'	23:B:53:A:N6	2.17	0.78
1:a:436:C:O2'	4:d:151:GLN:O	2.01	0.77
22:A:956:G:O6	34:M:14:LYS:NZ	2.17	0.77
14:n:32:ASP:O	14:n:41:ARG:NH1	2.17	0.77
6:f:96:VAL:HG12	6:f:97:THR:H	1.48	0.77
22:A:155:A:H2'	22:A:156:A:C8	2.19	0.77
6:f:15:SER:HA	6:f:18:VAL:HG23	1.66	0.77
19:s:14:LEU:HD12	19:s:32:THR:HG21	1.65	0.77
22:A:2547:A:H4'	32:K:29:HIS:HE1	1.50	0.77
41:T:47:VAL:HG11	41:T:85:VAL:HG11	1.67	0.77
22:A:1801:A:OP2	24:C:149:LYS:NZ	2.18	0.77
9:i:35:GLU:HA	9:i:39:GLY:HA3	1.66	0.77
38:Q:49:ARG:O	38:Q:53:LYS:NZ	2.17	0.77
22:A:500:G:N1	22:A:503:A:OP2	2.17	0.77
24:C:28:PRO:HG2	24:C:33:LEU:HD11	1.66	0.77
1:a:1009:U:H3	1:a:1020:G:H1	1.31	0.76
22:A:141:G:H5''	22:A:142:A:C8	2.20	0.76
22:A:2305:U:H5''	27:F:130:GLY:HA3	1.66	0.76
22:A:2743:U:O2'	28:G:152:ARG:NH1	2.17	0.76
1:a:413:G:H2'	1:a:428:G:H22	1.50	0.76
39:R:40:MET:SD	39:R:48:LYS:NZ	2.58	0.76
8:h:46:GLU:O	8:h:61:THR:OG1	2.03	0.76
9:i:129:ARG:NH1	55:9:33:U:OP2	2.17	0.76
20:t:67:HIS:ND1	20:t:67:HIS:O	2.19	0.76
22:A:2107:G:N2	22:A:2182:U:O2	2.18	0.76
28:G:136:ASP:HB3	28:G:139:VAL:HG12	1.69	0.75
22:A:1173:U:O2'	22:A:1177:G:N2	2.19	0.75
22:A:2530:A:N7	28:G:171:LYS:NZ	2.33	0.75
22:A:475:C:O2	22:A:479:A:N6	2.20	0.75
22:A:1363:C:O2'	22:A:1809:A:N3	2.18	0.75
22:A:1858:A:N6	22:A:1884:G:O2'	2.19	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:880:G:H2'	22:A:881:G:H8	1.51	0.75
1:a:675:A:OP1	18:r:72:ARG:NH2	2.20	0.74
19:s:66:VAL:HG21	54:6:57:VAL:HG22	1.68	0.74
10:j:59:LYS:HE2	10:j:62:ARG:HH22	1.52	0.74
27:F:21:TYR:OH	27:F:164:GLU:OE2	2.03	0.74
53:5:57:ASN:HB3	53:5:62:ARG:HD2	1.68	0.74
55:9:18:G:O2'	55:9:57:G:N2	2.19	0.74
1:a:1255:G:O2'	1:a:1258:G:N3	2.20	0.74
1:a:1356:G:H2'	1:a:1357:A:H8	1.51	0.74
22:A:1093:G:N2	22:A:1098:A:H62	1.85	0.74
1:a:1280:A:OP1	10:j:9:ARG:NH1	2.21	0.74
25:D:5:VAL:H	25:D:32:ASN:HD21	1.35	0.74
27:F:79:ARG:NH1	55:9:19:G:O6	2.21	0.74
1:a:366:A:O2'	1:a:394:G:N2	2.19	0.74
20:t:38:ILE:HD11	20:t:82:ILE:HG12	1.70	0.74
1:a:974:A:OP1	14:n:69:ARG:NH2	2.21	0.74
9:i:45:MET:O	9:i:49:GLN:HB2	1.88	0.74
22:A:2328:A:H2'	22:A:2329:U:C6	2.23	0.74
22:A:2541:A:O2'	22:A:2765:A:N1	2.20	0.74
1:a:1180:A:OP2	9:i:98:ARG:NH2	2.21	0.74
1:a:687:A:N6	1:a:703:G:O2'	2.21	0.73
22:A:1590:A:H2'	22:A:1591:A:H8	1.51	0.73
1:a:826:C:O2	8:h:15:ASN:ND2	2.21	0.73
22:A:1070:A:N6	22:A:1096:A:O2'	2.22	0.73
22:A:1799:G:N2	22:A:1818:U:O2'	2.21	0.73
23:B:34:A:N3	23:B:36:C:N4	2.31	0.73
27:F:73:VAL:HG22	27:F:78:ILE:HG12	1.70	0.73
35:N:2:ARG:HA	35:N:5:LYS:HD2	1.70	0.73
1:a:105:G:H21	1:a:379:C:H5'	1.53	0.73
22:A:155:A:H2'	22:A:156:A:H8	1.50	0.73
1:a:160:A:H61	1:a:347:G:N2	1.86	0.73
22:A:1012:U:OP2	38:Q:69:ARG:NH1	2.21	0.73
22:A:1936:A:H2	22:A:1943:U:H3	1.35	0.73
22:A:2532:G:O2'	22:A:2657:A:N1	2.22	0.73
22:A:2689:U:OP2	22:A:2719:G:N2	2.16	0.73
24:C:244:VAL:HG12	24:C:250:GLN:HA	1.71	0.73
4:d:10:LEU:HD13	4:d:62:ARG:HD2	1.71	0.72
25:D:42:ASN:ND2	25:D:43:ASP:OD2	2.22	0.72
1:a:673:A:H2'	1:a:674:G:C8	2.23	0.72
24:C:106:PRO:HD2	24:C:109:LEU:HD22	1.69	0.72
35:N:114:GLU:OE1	35:N:118:ARG:NH2	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:283:G:N2	22:A:357:C:O2	2.19	0.72
43:V:26:PHE:HE1	43:V:89:ILE:HG13	1.54	0.72
14:n:46:LEU:HD21	19:s:15:LEU:HD21	1.70	0.72
20:t:16:ALA:O	20:t:20:ASN:ND2	2.13	0.72
22:A:2101:A:H2'	22:A:2102:G:C8	2.24	0.72
36:O:31:THR:O	36:O:102:ARG:NH1	2.16	0.72
22:A:476:G:N1	22:A:479:A:OP2	2.23	0.72
30:I:102:ARG:NH2	30:I:129:GLU:OE2	2.22	0.72
11:k:52:ARG:HH21	11:k:56:LYS:HE2	1.54	0.72
1:a:714:G:H2'	1:a:715:A:C8	2.25	0.72
3:c:46:LEU:HB3	3:c:49:ALA:HB3	1.71	0.72
8:h:10:LEU:HD22	8:h:74:ILE:HD11	1.72	0.72
5:e:98:ALA:HB1	5:e:101:GLY:HA3	1.70	0.72
22:A:1093:G:H21	22:A:1098:A:N6	1.88	0.72
22:A:1103:A:OP2	22:A:1104:C:N4	2.23	0.71
1:a:722:G:H1	1:a:733:G:H1	1.38	0.71
1:a:1071:C:H2'	1:a:1072:G:H8	1.55	0.71
6:f:97:THR:HG22	6:f:98:GLU:H	1.55	0.71
1:a:1032:G:H5'	1:a:1033:G:H5''	1.72	0.71
1:a:1348:U:OP2	1:a:1373:G:N1	2.21	0.71
22:A:1816:C:N4	24:C:34:GLU:OE2	2.22	0.71
4:d:36:ALA:HA	4:d:41:GLY:HA3	1.72	0.71
22:A:355:U:H2'	22:A:356:G:H8	1.56	0.71
22:A:781:A:OP1	24:C:216:ARG:NH2	2.24	0.71
30:I:132:ALA:HA	30:I:135:MET:HE2	1.72	0.71
1:a:1251:A:H2'	1:a:1252:A:C8	2.26	0.71
1:a:1356:G:H2'	1:a:1357:A:C8	2.26	0.71
2:b:110:ILE:HG22	2:b:147:LEU:HD13	1.73	0.71
3:c:35:ASP:OD1	3:c:58:ARG:NH2	2.19	0.71
22:A:224:U:OP2	22:A:408:G:N2	2.23	0.71
22:A:1102:C:H2'	22:A:1103:A:H8	1.54	0.71
28:G:118:ALA:O	28:G:120:ILE:N	2.24	0.71
13:m:6:ILE:HG23	13:m:7:ASN:H	1.56	0.70
29:H:16:GLY:HA2	29:H:47:PHE:CE2	2.26	0.70
17:q:16:MET:HB3	17:q:19:SER:HB2	1.72	0.70
28:G:21:GLN:OE1	28:G:54:ARG:NH1	2.24	0.70
22:A:2469:A:N6	22:A:2481:G:O2'	2.24	0.70
31:J:125:TYR:OH	31:J:132:HIS:NE2	2.25	0.70
29:H:2:GLN:OE1	29:H:2:GLN:N	2.24	0.70
22:A:1607:C:N4	22:A:1622:G:OP2	2.23	0.70
23:B:80:U:OP1	34:M:18:ARG:NH2	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:p:16:PHE:HD1	16:p:40:ASN:HB3	1.55	0.70
26:E:118:LEU:HD11	26:E:188:MET:HE2	1.74	0.70
34:M:66:ARG:NH1	34:M:104:GLU:OE2	2.25	0.70
52:4:7:VAL:HG22	52:4:38:GLY:HA3	1.74	0.70
1:a:542:G:OP1	4:d:9:LYS:NZ	2.19	0.70
1:a:1001:C:H2'	1:a:1002:G:H8	1.56	0.70
22:A:355:U:H2'	22:A:356:G:C8	2.25	0.70
1:a:219:U:H2'	1:a:220:G:H8	1.56	0.70
42:U:27:VAL:HG22	42:U:33:VAL:HG12	1.74	0.70
53:5:5:LEU:O	53:5:9:GLN:HG2	1.92	0.70
10:j:27:GLU:HA	10:j:30:LYS:HG2	1.74	0.69
22:A:283:G:N1	22:A:357:C:N3	2.34	0.69
3:c:61:LYS:NZ	3:c:96:VAL:O	2.17	0.69
22:A:1614:A:N6	40:S:92:ARG:O	2.25	0.69
22:A:2189:U:H2'	22:A:2190:G:H8	1.55	0.69
43:V:42:LEU:HD13	43:V:47:VAL:HG21	1.73	0.69
22:A:1055:G:N2	22:A:1105:U:O2	2.25	0.69
1:a:811:C:O2'	1:a:901:A:N1	2.26	0.69
10:j:66:GLU:HB3	14:n:99:ALA:HB2	1.75	0.69
19:s:32:THR:HG22	19:s:34:SER:H	1.57	0.69
29:H:21:VAL:HG21	29:H:26:ALA:HB2	1.74	0.69
21:u:34:ARG:HB3	21:u:36:PHE:HE1	1.57	0.69
22:A:782:A:O2'	24:C:223:ALA:O	2.09	0.69
26:E:170:ARG:NH2	26:E:179:SER:OG	2.26	0.69
1:a:1096:C:O2	1:a:1170:A:O2'	2.11	0.69
8:h:39:LEU:HD21	8:h:128:VAL:HG21	1.74	0.69
4:d:54:LEU:HD12	4:d:202:LEU:HD11	1.75	0.69
10:j:8:ILE:HG22	10:j:100:ILE:HG23	1.73	0.69
22:A:2849:U:O4	37:P:20:ARG:NH2	2.21	0.69
25:D:5:VAL:HG12	25:D:202:ILE:HG12	1.75	0.69
52:4:2:LYS:NZ	52:4:32:LYS:O	2.25	0.69
1:a:126:G:OP1	1:a:605:U:O2'	2.10	0.69
1:a:409:U:H3'	1:a:410:G:C8	2.28	0.69
1:a:458:U:H3	1:a:474:G:H1	1.41	0.69
22:A:2818:U:OP1	22:A:2837:A:O2'	2.07	0.69
24:C:70:LYS:NZ	24:C:99:GLU:OE1	2.24	0.69
1:a:1083:U:O2'	1:a:1102:A:OP2	2.10	0.69
22:A:1536:C:O2'	22:A:1537:G:N2	2.25	0.68
22:A:2099:U:O2	22:A:2190:G:N2	2.27	0.68
22:A:1010:A:OP1	38:Q:65:ASN:ND2	2.25	0.68
2:b:128:LEU:HD22	2:b:132:GLU:HG2	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:c:130:ARG:NH1	3:c:165:GLU:OE1	2.25	0.68
22:A:63:A:H61	22:A:91:A:H61	1.40	0.68
22:A:1386:C:H2'	22:A:1387:A:H8	1.58	0.68
1:a:993:G:O2'	1:a:994:A:N7	2.26	0.68
25:D:77:ARG:NH2	25:D:200:ASP:OD1	2.26	0.68
1:a:459:A:H2'	1:a:460:A:C8	2.27	0.68
15:o:25:GLU:OE2	15:o:76:ARG:NE	2.23	0.68
22:A:993:G:OP1	38:Q:49:ARG:NH2	2.26	0.68
24:C:261:ARG:O	24:C:264:LYS:NZ	2.27	0.68
1:a:1126:U:O2'	1:a:1281:C:O4'	2.12	0.68
22:A:2719:G:H4'	22:A:2846:G:H4'	1.76	0.68
4:d:201:GLU:OE1	5:e:111:ARG:NH2	2.26	0.68
23:B:43:C:H5''	54:6:1:MET:HG2	1.76	0.68
1:a:475:C:H2'	1:a:476:U:C6	2.29	0.67
22:A:569:U:O2'	22:A:983:A:N1	2.25	0.67
22:A:1587:G:H2'	22:A:1588:G:H8	1.59	0.67
1:a:979:C:O2	14:n:59:ARG:NH1	2.27	0.67
22:A:880:G:H2'	22:A:881:G:C8	2.29	0.67
22:A:2199:A:OP1	45:X:36:ARG:NH2	2.28	0.67
27:F:7:TYR:HA	27:F:11:VAL:HG12	1.76	0.67
22:A:1054:A:H2'	22:A:1055:G:C8	2.29	0.67
1:a:62:U:H4'	1:a:378:G:N2	2.08	0.67
22:A:1631:G:N1	22:A:1634:A:OP2	2.24	0.67
30:I:12:VAL:HG13	30:I:23:VAL:HG23	1.75	0.67
55:9:23:C:H2'	55:9:24:G:C8	2.29	0.67
1:a:382:A:H2'	1:a:383:A:C8	2.30	0.67
1:a:451:A:OP2	16:p:70:ARG:NH2	2.28	0.67
22:A:138:U:O4	41:T:3:ARG:NH1	2.28	0.67
1:a:1009:U:O4	1:a:1020:G:O6	2.13	0.67
13:m:3:ILE:HG22	13:m:4:ALA:H	1.58	0.67
28:G:23:ILE:HD11	28:G:71:LEU:HD21	1.76	0.67
35:N:29:VAL:HG23	35:N:75:ILE:HD12	1.76	0.67
53:5:18:VAL:HG12	53:5:86:MET:HG2	1.76	0.67
1:a:159:G:N2	1:a:162:A:OP2	2.25	0.67
1:a:401:C:O2'	1:a:621:A:N3	2.22	0.67
12:l:70:GLY:O	12:l:98:ARG:NH2	2.26	0.67
26:E:149:ILE:HB	26:E:188:MET:HG2	1.77	0.67
22:A:529:A:OP2	31:J:116:ARG:NH2	2.27	0.67
22:A:1103:A:H5''	22:A:1104:C:H5	1.58	0.67
2:b:66:ILE:HG23	2:b:88:GLN:HG3	1.75	0.67
16:p:19:VAL:HG12	16:p:36:VAL:HG23	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:274:C:H2'	22:A:275:C:O4'	1.95	0.67
22:A:370:G:O2'	22:A:424:G:OP1	2.13	0.67
22:A:1131:G:OP1	31:J:82:GLY:HA2	1.95	0.67
29:H:16:GLY:HA2	29:H:47:PHE:HE2	1.60	0.67
53:5:59:LEU:HD23	53:5:61:ARG:H	1.59	0.67
5:e:162:GLU:O	8:h:113:ARG:NH1	2.28	0.67
22:A:275:C:H2'	22:A:276:U:H4'	1.75	0.66
29:H:39:ALA:HB1	29:H:44:ILE:HD11	1.76	0.66
54:6:41:HIS:CE1	54:6:43:PHE:HB3	2.30	0.66
22:A:2304:G:O2'	27:F:152:ASP:OD1	2.13	0.66
27:F:57:ALA:HB2	27:F:64:PRO:HD3	1.76	0.66
30:I:54:ILE:HD12	30:I:73:PRO:HD3	1.77	0.66
47:Z:39:ASP:OD1	47:Z:44:ARG:NH2	2.27	0.66
22:A:340:A:O2'	26:E:162:ARG:NH1	2.28	0.66
22:A:1103:A:H5''	22:A:1104:C:C5	2.30	0.66
35:N:86:ARG:NE	35:N:117:ASP:OD1	2.24	0.66
27:F:121:PHE:HB3	27:F:162:ASP:HB2	1.76	0.66
35:N:77:ALA:O	35:N:81:ASN:HB2	1.95	0.66
39:R:49:ILE:HB	39:R:52:PRO:HA	1.77	0.66
3:c:141:MET:HG3	3:c:169:GLU:HG2	1.76	0.66
22:A:1434:A:H2'	22:A:1435:G:H8	1.61	0.66
13:m:84:CYS:HB2	19:s:72:GLU:HG2	1.78	0.66
22:A:1080:A:N3	30:I:127:SER:HB2	2.10	0.66
22:A:2773:C:OP1	25:D:169:ARG:NH2	2.29	0.66
1:a:201:G:O2'	1:a:469:C:O2'	2.12	0.66
1:a:1253:G:H2'	1:a:1254:A:H8	1.59	0.66
1:a:1432:G:O2'	1:a:1468:A:N6	2.29	0.66
1:a:1530:G:N7	21:u:46:ARG:NH2	2.43	0.66
22:A:84:A:N1	22:A:98:G:O2'	2.28	0.66
1:a:718:A:H5'	11:k:118:ASN:HB2	1.78	0.66
1:a:1249:C:H4'	9:i:74:GLN:HE22	1.61	0.66
1:a:1377:A:OP1	7:g:91:ARG:NH2	2.29	0.66
22:A:1171:G:N2	22:A:1178:C:N3	2.44	0.66
40:S:1:MET:HG2	40:S:2:GLU:H	1.59	0.66
1:a:606:G:N2	1:a:633:G:N7	2.44	0.65
39:R:55:ASP:OD1	39:R:56:GLY:N	2.25	0.65
42:U:88:ASP:O	42:U:90:LYS:N	2.29	0.65
1:a:518:C:H5'	1:a:519:C:C6	2.31	0.65
1:a:561:U:O2'	1:a:562:U:OP2	2.14	0.65
2:b:17:HIS:HE2	2:b:188:THR:H	1.42	0.65
23:B:1:U:H3	23:B:120:A:H2	1.45	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1190:G:O2'	3:c:2:GLN:HB2	1.96	0.65
9:i:54:VAL:HG12	9:i:55:ASP:H	1.62	0.65
19:s:44:ILE:HD12	19:s:63:ASP:HA	1.77	0.65
1:a:1176:A:H2'	1:a:1177:G:C8	2.31	0.65
22:A:141:G:N2	22:A:141:G:OP2	2.30	0.65
22:A:1490:A:O2'	22:A:1491:G:OP1	2.14	0.65
22:A:1638:C:O2	22:A:2698:U:O2'	2.14	0.65
22:A:1715:G:HO2'	22:A:1716:U:H6	1.44	0.65
40:S:20:VAL:HG11	40:S:44:ALA:HA	1.79	0.65
40:S:73:LYS:HB2	40:S:106:VAL:HB	1.78	0.65
53:5:15:VAL:HA	53:5:18:VAL:HG22	1.79	0.65
1:a:1025:U:H5''	1:a:1026:G:H5'	1.78	0.65
1:a:1200:C:H5''	1:a:1201:A:H3'	1.77	0.65
1:a:1251:A:H2'	1:a:1252:A:H8	1.59	0.65
3:c:84:GLU:OE1	3:c:87:ARG:NH2	2.30	0.65
19:s:67:GLY:HA3	54:6:56:ARG:HH12	1.62	0.65
43:V:21:ARG:NH2	43:V:87:GLN:O	2.27	0.65
53:5:67:THR:HB	53:5:72:LEU:HA	1.77	0.65
12:l:3:VAL:HG13	17:q:33:TYR:HB3	1.77	0.65
20:t:67:HIS:O	20:t:69:ASN:N	2.28	0.65
36:O:27:VAL:HA	36:O:93:ASP:HB3	1.78	0.65
1:a:1149:C:OP2	9:i:10:ARG:NH2	2.23	0.65
3:c:139:ASN:OD1	3:c:142:ARG:NH2	2.30	0.65
13:m:15:VAL:HG23	13:m:16:ILE:HD12	1.79	0.65
20:t:35:TYR:OH	20:t:77:ASN:ND2	2.30	0.65
2:b:71:THR:HG22	2:b:72:LYS:H	1.62	0.65
2:b:156:LEU:HD22	2:b:178:LEU:HD22	1.79	0.65
22:A:1250:G:N7	33:L:18:ARG:NH2	2.44	0.65
32:K:76:VAL:HG12	37:P:72:VAL:HB	1.78	0.65
43:V:2:PHE:HB3	43:V:50:MET:HE2	1.77	0.65
53:5:56:ARG:HG2	53:5:83:ALA:HB2	1.76	0.65
1:a:379:C:H2'	1:a:380:G:C4	2.31	0.65
1:a:673:A:H4'	6:f:86:ARG:HH12	1.60	0.65
1:a:920:U:HO2'	1:a:1081:A:HO2'	1.39	0.65
1:a:1179:A:OP2	9:i:94:ARG:NH2	2.30	0.65
22:A:545:U:O2	22:A:548:G:N2	2.21	0.65
22:A:645:C:H2'	22:A:647:G:C8	2.32	0.65
22:A:1102:C:H2'	22:A:1103:A:C8	2.31	0.65
30:I:13:ALA:HA	30:I:53:PRO:HA	1.77	0.65
8:h:92:PRO:O	8:h:116:ARG:NH2	2.30	0.65
23:B:3:C:O2'	23:B:4:C:O4'	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:5:80:THR:OG1	53:5:81:LEU:N	2.30	0.65
1:a:925:G:N2	1:a:1503:A:OP1	2.30	0.64
1:a:950:U:H2'	1:a:951:G:C8	2.31	0.64
3:c:6:PRO:O	3:c:10:ARG:NH1	2.29	0.64
11:k:125:LYS:O	21:u:34:ARG:NH2	2.25	0.64
22:A:280:U:O4	22:A:361:G:N2	2.31	0.64
22:A:627:A:H2'	33:L:78:ARG:HH12	1.62	0.64
37:P:6:GLN:O	37:P:10:GLU:HG2	1.97	0.64
1:a:17:U:H2'	1:a:18:C:C6	2.31	0.64
22:A:307:G:N1	22:A:310:A:OP2	2.26	0.64
52:4:7:VAL:HG11	52:4:36:ARG:O	1.97	0.64
1:a:683:G:H21	11:k:39:ASN:HD22	1.45	0.64
22:A:63:A:N6	22:A:91:A:H61	1.93	0.64
22:A:597:G:O2'	33:L:11:GLY:O	2.14	0.64
32:K:63:VAL:HG12	32:K:107:LEU:HD21	1.76	0.64
22:A:219:A:N3	22:A:234:U:O2'	2.27	0.64
22:A:242:G:N2	22:A:255:A:OP2	2.22	0.64
22:A:2683:C:O2	32:K:70:ARG:NH1	2.19	0.64
21:u:34:ARG:HB3	21:u:36:PHE:CE1	2.32	0.64
22:A:1338:G:O2'	22:A:1393:A:N1	2.29	0.64
22:A:1417:C:O2'	22:A:1587:G:O2'	2.16	0.64
22:A:2848:G:O2'	22:A:2868:A:N6	2.31	0.64
30:I:44:LYS:HD3	30:I:68:PHE:HE2	1.62	0.64
1:a:1306:A:N6	1:a:1331:G:O2'	2.30	0.64
22:A:684:G:N2	22:A:788:A:OP2	2.22	0.64
1:a:437:U:H5'	4:d:151:GLN:HB2	1.80	0.64
16:p:16:PHE:CD1	16:p:40:ASN:HB3	2.31	0.64
40:S:4:ILE:H	40:S:4:ILE:HD12	1.63	0.64
1:a:110:C:O2'	16:p:25:ARG:O	2.14	0.64
1:a:1316:G:N1	1:a:1319:A:OP2	2.30	0.64
5:e:54:GLU:HG3	5:e:56:PRO:HD2	1.80	0.64
22:A:3:U:H2'	22:A:4:U:C6	2.32	0.64
22:A:277:G:H8	22:A:361:G:H1	1.46	0.64
22:A:2063:C:HO2'	55:9:76:A:HO2'	1.45	0.64
22:A:2718:G:O2'	22:A:2847:U:OP1	2.15	0.64
46:Y:16:THR:HA	46:Y:19:LEU:HD23	1.78	0.64
1:a:160:A:H61	1:a:347:G:H21	1.44	0.64
1:a:1001:C:H2'	1:a:1002:G:C8	2.32	0.64
3:c:57:GLU:HG3	3:c:64:ARG:HH21	1.61	0.64
22:A:1550:C:OP1	22:A:1720:U:O2'	2.09	0.64
22:A:1950:G:N1	22:A:1954:G:O2'	2.25	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:2107:G:C2	22:A:2182:U:O2	2.51	0.64
12:l:101:LEU:O	12:l:103:CYS:N	2.31	0.64
26:E:117:ARG:NH2	26:E:183:PHE:O	2.31	0.64
1:a:1249:C:O2'	9:i:74:GLN:NE2	2.31	0.63
19:s:35:ARG:NH2	19:s:74:ALA:O	2.31	0.63
22:A:2125:G:H22	22:A:2171:A:H5'	1.62	0.63
55:9:31:G:O6	55:9:39:C:N4	2.25	0.63
1:a:147:G:H2'	1:a:148:G:C8	2.34	0.63
2:b:71:THR:OG1	2:b:168:GLU:OE2	2.11	0.63
22:A:1614:A:C6	40:S:87:PRO:HB3	2.33	0.63
24:C:70:LYS:HE2	24:C:73:ILE:HD12	1.81	0.63
24:C:132:ARG:HH21	24:C:185:ALA:HB3	1.63	0.63
29:H:57:LYS:O	29:H:60:GLU:HG3	1.98	0.63
1:a:524:G:H2'	1:a:525:C:C6	2.33	0.63
1:a:660:C:N3	1:a:746:A:N6	2.46	0.63
1:a:1152:A:H5'	10:j:72:ARG:HH22	1.63	0.63
22:A:365:U:H2'	22:A:366:C:C6	2.33	0.63
1:a:846:G:H2'	1:a:847:G:C8	2.33	0.63
22:A:1434:A:H2'	22:A:1435:G:C8	2.33	0.63
53:5:87:GLU:CD	53:5:93:ALA:H	2.06	0.63
1:a:768:A:N3	1:a:1512:U:O2'	2.31	0.63
22:A:511:U:H4'	22:A:1235:G:H4'	1.78	0.63
26:E:97:ASN:ND2	26:E:100:MET:SD	2.71	0.63
28:G:8:VAL:HB	28:G:49:LEU:HB3	1.80	0.63
29:H:15:LEU:HD21	29:H:56:ALA:HA	1.79	0.63
49:1:39:ASP:HB3	49:1:42:VAL:HG12	1.80	0.63
1:a:149:A:H1'	1:a:1446:A:H2	1.64	0.63
22:A:1094:U:N3	22:A:1097:U:OP2	2.30	0.63
2:b:41:ASN:HD22	2:b:44:LYS:HG2	1.64	0.63
22:A:1063:G:H1'	30:I:135:MET:HG3	1.80	0.63
33:L:128:THR:OG1	33:L:129:LYS:N	2.19	0.63
1:a:259:G:OP1	20:t:77:ASN:ND2	2.27	0.63
1:a:1452:C:H4'	1:a:1453:G:C2	2.34	0.63
5:e:80:LEU:HD22	5:e:146:MET:HE1	1.79	0.63
22:A:1039:A:N1	22:A:1116:G:O6	2.32	0.63
22:A:1543:G:HO2'	22:A:1544:A:H8	1.43	0.63
22:A:1992:G:N2	22:A:1996:C:O2'	2.32	0.63
22:A:1365:A:OP1	45:X:27:ARG:NH2	2.31	0.63
22:A:2258:C:O2'	22:A:2427:C:OP2	2.16	0.63
23:B:111:U:H2'	23:B:112:G:H8	1.64	0.63
27:F:36:ASN:OD1	27:F:37:MET:N	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:104:THR:HG22	27:F:105:ILE:HG13	1.80	0.63
29:H:40:THR:OG1	29:H:43:ASN:OD1	2.14	0.63
55:9:23:C:H2'	55:9:24:G:H8	1.64	0.63
22:A:819:A:OP2	22:A:1187:G:N2	2.22	0.62
22:A:1000:A:H2'	22:A:1001:A:C8	2.34	0.62
27:F:30:VAL:HG23	27:F:157:THR:HG22	1.80	0.62
31:J:4:PHE:O	38:Q:63:ARG:NH2	2.25	0.62
4:d:109:THR:OG1	4:d:112:GLU:OE1	2.12	0.62
19:s:10:ILE:HD12	19:s:37:SER:OG	1.99	0.62
22:A:620:G:O6	26:E:98:LYS:NZ	2.32	0.62
22:A:1275:A:OP2	22:A:1646:C:N4	2.32	0.62
22:A:2101:A:H2'	22:A:2102:G:H8	1.64	0.62
22:A:2102:G:N2	22:A:2187:U:O2	2.32	0.62
22:A:2326:C:O2'	22:A:2327:A:OP1	2.16	0.62
22:A:2720:U:OP1	37:P:52:ARG:NH2	2.33	0.62
47:Z:4:ILE:O	47:Z:36:GLU:HA	1.99	0.62
1:a:837:U:H2'	1:a:838:G:H8	1.64	0.62
1:a:950:U:H2'	1:a:951:G:H8	1.64	0.62
22:A:3:U:H2'	22:A:4:U:H6	1.61	0.62
22:A:247:G:OP2	22:A:249:C:N4	2.32	0.62
1:a:713:G:H2'	1:a:714:G:C8	2.35	0.62
1:a:1039:G:H2'	1:a:1040:U:H6	1.64	0.62
4:d:110:ARG:HA	4:d:113:ALA:HB3	1.80	0.62
22:A:160:A:N3	22:A:2208:C:O2'	2.32	0.62
22:A:2444:G:OP2	26:E:63:LYS:NZ	2.32	0.62
23:B:65:U:H3'	23:B:108:A:H61	1.64	0.62
1:a:1503:A:H5'	1:a:1531:A:H1'	1.80	0.62
1:a:1526:G:OP2	21:u:38:GLU:HB2	1.98	0.62
22:A:1868:C:N4	22:A:1869:G:O6	2.33	0.62
3:c:135:ARG:HH11	3:c:138:GLN:HE21	1.46	0.62
22:A:644:A:H2'	22:A:645:C:O4'	2.00	0.62
26:E:58:LYS:NZ	26:E:62:GLN:OE1	2.32	0.62
1:a:210:C:H4'	1:a:211:G:C2	2.34	0.62
1:a:1320:C:O2	19:s:35:ARG:NH1	2.33	0.62
1:a:1338:G:O2'	55:9:42:A:OP1	2.14	0.62
22:A:2848:G:C8	37:P:94:ALA:HB2	2.35	0.62
33:L:127:VAL:HG21	33:L:142:ILE:HD13	1.82	0.62
22:A:1364:G:N2	22:A:1367:A:OP2	2.30	0.62
16:p:4:ILE:HG13	16:p:21:VAL:HG22	1.82	0.62
22:A:2:G:H2'	22:A:3:U:C6	2.35	0.62
22:A:624:C:O2'	22:A:657:U:OP1	2.18	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:1386:C:H2'	22:A:1387:A:C8	2.35	0.62
1:a:411:A:C4	1:a:413:G:H1'	2.35	0.61
1:a:1142:G:H3'	1:a:1143:G:H8	1.64	0.61
1:a:1372:U:OP2	9:i:12:LYS:NZ	2.22	0.61
21:u:40:PRO:O	21:u:44:ARG:HB2	1.99	0.61
22:A:1590:A:H2'	22:A:1591:A:C8	2.33	0.61
22:A:1856:U:H2'	22:A:1857:G:O4'	2.00	0.61
55:9:5:G:O2'	55:9:6:A:O5'	2.17	0.61
22:A:190:A:OP2	45:X:25:LYS:NZ	2.33	0.61
22:A:291:G:C6	22:A:350:G:C6	2.88	0.61
22:A:1058:U:H3	30:I:116:MET:HE1	1.64	0.61
22:A:1682:G:OP2	22:A:1699:G:N2	2.30	0.61
37:P:29:VAL:HG23	37:P:79:VAL:HG12	1.82	0.61
46:Y:3:ALA:O	46:Y:7:ARG:NH1	2.33	0.61
1:a:254:G:O3'	17:q:70:LYS:NZ	2.34	0.61
1:a:442:G:H2'	1:a:443:C:H6	1.66	0.61
1:a:1026:G:H1	1:a:1035:A:H61	1.47	0.61
15:o:38:LEU:HD23	15:o:55:LEU:HD13	1.83	0.61
22:A:1212:G:O2'	22:A:1236:G:N2	2.32	0.61
34:M:69:PRO:HA	34:M:94:ALA:HB2	1.83	0.61
1:a:424:G:H2'	1:a:425:G:H8	1.66	0.61
1:a:1004:A:H2'	1:a:1005:A:C8	2.36	0.61
1:a:1291:U:OP1	7:g:36:SER:OG	2.16	0.61
22:A:1111:A:O2'	22:A:1112:G:OP1	2.13	0.61
22:A:1779:U:H5	22:A:1784:A:N7	1.98	0.61
23:B:33:G:N2	23:B:36:C:H42	1.98	0.61
32:K:1:MET:HE3	32:K:67:LYS:HG2	1.82	0.61
35:N:28:LEU:HD23	35:N:48:VAL:HG21	1.81	0.61
39:R:14:VAL:HG21	39:R:98:ILE:HG13	1.83	0.61
1:a:442:G:H2'	1:a:443:C:C6	2.35	0.61
1:a:1041:G:H2'	1:a:1042:A:C8	2.36	0.61
1:a:1223:C:H5''	1:a:1224:U:H5''	1.83	0.61
17:q:46:HIS:N	17:q:72:TRP:O	2.33	0.61
39:R:58:VAL:HG12	39:R:102:SER:HB3	1.81	0.61
1:a:86:G:H1'	1:a:87:C:H5	1.66	0.61
1:a:1060:U:C5	3:c:1:GLY:HA3	2.36	0.61
4:d:149:LYS:HA	4:d:154:VAL:HG21	1.82	0.61
30:I:33:ASN:HD21	30:I:35:MET:HB3	1.66	0.61
1:a:1162:C:H2'	1:a:1163:A:H8	1.66	0.61
7:g:4:ARG:HB3	7:g:6:ILE:HG23	1.83	0.61
22:A:980:A:N3	22:A:2037:A:O2'	2.28	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:M:58:LYS:O	34:M:60:GLN:N	2.33	0.61
42:U:4:ILE:HD13	42:U:69:VAL:HG23	1.82	0.61
22:A:1538:G:H2'	22:A:1539:U:C6	2.36	0.61
1:a:123:U:OP1	1:a:311:C:O2'	2.19	0.60
29:H:81:ALA:HA	29:H:147:VAL:HB	1.83	0.60
39:R:5:PHE:HB3	39:R:59:ILE:HD12	1.81	0.60
1:a:689:C:HO2'	1:a:705:G:HO2'	1.49	0.60
22:A:1532:A:N1	22:A:1540:G:C6	2.68	0.60
22:A:2768:U:O2'	31:J:95:ARG:NH2	2.33	0.60
27:F:63:LYS:HD2	54:6:5:ILE:HD11	1.83	0.60
30:I:36:GLU:HA	30:I:39:LYS:HZ3	1.66	0.60
55:9:21:A:N6	55:9:47:U:O2'	2.35	0.60
1:a:409:U:H3	1:a:433:G:H1	0.66	0.60
9:i:80:HIS:HE1	9:i:84:ARG:HH21	1.49	0.60
22:A:453:A:N3	22:A:457:A:O2'	2.34	0.60
22:A:1901:A:OP2	24:C:252:LYS:NZ	2.34	0.60
22:A:2540:C:O2'	22:A:2740:A:N3	2.30	0.60
30:I:131:THR:HG22	30:I:135:MET:HE1	1.82	0.60
6:f:10:VAL:HG22	6:f:84:VAL:HG12	1.83	0.60
9:i:80:HIS:CE1	9:i:84:ARG:HH21	2.20	0.60
15:o:73:ASP:OD2	15:o:76:ARG:NH1	2.31	0.60
20:t:67:HIS:C	20:t:69:ASN:H	2.08	0.60
22:A:1245:G:OP1	33:L:13:LYS:NZ	2.28	0.60
22:A:2591:C:N4	22:A:2592:G:O6	2.34	0.60
23:B:27:C:OP1	36:O:34:HIS:NE2	2.33	0.60
39:R:47:VAL:HG12	39:R:54:VAL:HG11	1.83	0.60
1:a:1071:C:H2'	1:a:1072:G:C8	2.35	0.60
5:e:90:GLY:O	5:e:129:SER:N	2.34	0.60
10:j:80:THR:HB	10:j:83:THR:HG23	1.83	0.60
16:p:46:LYS:NZ	16:p:48:GLU:O	2.34	0.60
22:A:363:G:H2'	22:A:364:C:H6	1.66	0.60
22:A:993:G:N2	39:R:23:GLU:OE2	2.34	0.60
22:A:994:C:O2	39:R:10:LYS:NZ	2.34	0.60
22:A:1009:A:N3	22:A:1153:C:O2'	2.31	0.60
22:A:1223:G:OP1	39:R:68:ARG:NH2	2.34	0.60
22:A:1629:U:O4	22:A:1630:A:N6	2.34	0.60
36:O:52:SER:OG	36:O:55:GLU:OE1	2.17	0.60
51:3:30:HIS:C	51:3:32:LEU:H	2.08	0.60
1:a:337:G:H2'	1:a:338:A:C8	2.36	0.60
1:a:1253:G:H2'	1:a:1254:A:C8	2.37	0.60
11:k:105:ARG:HD3	21:u:9:GLU:HG2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:l:23:LEU:HD13	12:l:58:ASN:HB2	1.84	0.60
12:l:75:GLU:O	12:l:76:HIS:ND1	2.35	0.60
16:p:48:GLU:OE2	16:p:50:THR:N	2.33	0.60
18:r:25:ILE:HA	18:r:28:LEU:HB2	1.83	0.60
22:A:627:A:OP1	33:L:78:ARG:NH1	2.21	0.60
22:A:2117:A:N6	22:A:2170:A:N1	2.49	0.60
39:R:4:VAL:HG12	39:R:40:MET:HB3	1.83	0.60
1:a:437:U:H4'	4:d:151:GLN:CD	2.26	0.60
6:f:47:LEU:HG	6:f:56:LYS:H	1.66	0.60
41:T:39:THR:HG22	41:T:41:ALA:H	1.65	0.60
1:a:380:G:N2	1:a:382:A:H62	1.98	0.60
1:a:1323:G:H2'	1:a:1324:A:C8	2.37	0.60
9:i:55:ASP:HB2	9:i:59:LYS:HG3	1.83	0.60
22:A:639:U:H2'	22:A:640:C:C6	2.36	0.60
22:A:1000:A:OP2	22:A:1154:G:N1	2.23	0.60
22:A:2359:C:O2'	51:3:53:ASP:OD2	2.16	0.60
22:A:2505:G:H2'	22:A:2576:G:H1	1.66	0.60
22:A:2834:G:H2'	22:A:2879:A:H61	1.66	0.60
1:a:177:G:OP1	20:t:23:ARG:NH2	2.34	0.60
22:A:651:G:H5'	51:3:18:LYS:HG2	1.84	0.60
22:A:659:G:N2	26:E:30:GLN:OE1	2.29	0.60
22:A:1081:U:H4'	30:I:123:ALA:HB1	1.83	0.60
1:a:397:A:N7	1:a:547:A:O2'	2.35	0.60
8:h:45:ILE:HG22	8:h:46:GLU:H	1.67	0.60
22:A:902:C:H2'	22:A:903:C:H6	1.66	0.60
22:A:2327:A:H2'	22:A:2328:A:C8	2.37	0.60
22:A:2579:C:O2'	25:D:136:ASN:ND2	2.34	0.60
1:a:24:U:O2'	1:a:524:G:O2'	2.18	0.59
1:a:757:U:O2'	1:a:879:C:O2	2.20	0.59
23:B:12:C:O2'	23:B:13:G:O5'	2.20	0.59
24:C:231:HIS:NE2	24:C:243:PRO:HA	2.18	0.59
19:s:15:LEU:HA	19:s:18:VAL:HG12	1.84	0.59
31:J:9:GLU:OE1	31:J:9:GLU:N	2.35	0.59
33:L:88:GLY:O	33:L:121:THR:N	2.29	0.59
1:a:28:A:O2'	1:a:296:U:OP1	2.13	0.59
22:A:191:A:H2'	22:A:192:C:C6	2.37	0.59
22:A:363:G:H2'	22:A:364:C:C6	2.37	0.59
22:A:534:U:O2'	38:Q:48:ASP:OD2	2.10	0.59
22:A:1715:G:N2	22:A:1744:A:OP2	2.31	0.59
51:3:23:HIS:ND1	51:3:24:LYS:O	2.33	0.59
1:a:9:G:H5'	5:e:107:GLY:HA3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:976:G:O5'	1:a:1358:U:O2'	2.19	0.59
1:a:977:A:OP1	14:n:61:ARG:NH2	2.32	0.59
1:a:1508:A:H2'	1:a:1509:C:H6	1.67	0.59
54:6:18:CYS:HB3	54:6:40:CYS:SG	2.42	0.59
1:a:219:U:H2'	1:a:220:G:C8	2.38	0.59
22:A:2190:G:H2'	22:A:2191:A:C8	2.37	0.59
22:A:2193:G:H2'	22:A:2194:U:C6	2.37	0.59
1:a:436:C:O2'	4:d:153:ARG:HG2	2.02	0.59
3:c:174:LEU:HD11	3:c:200:TRP:CD1	2.38	0.59
6:f:18:VAL:HG21	6:f:58:HIS:CD2	2.37	0.59
22:A:879:G:H2'	22:A:880:G:H8	1.68	0.59
22:A:1062:G:H1	22:A:1077:A:H2	1.51	0.59
1:a:618:C:N4	1:a:621:A:OP2	2.33	0.59
4:d:23:GLY:H	4:d:109:THR:HG22	1.68	0.59
10:j:30:LYS:HA	10:j:34:ALA:HA	1.85	0.59
14:n:20:PHE:CG	14:n:24:ALA:HB2	2.37	0.59
22:A:30:G:O2'	22:A:1214:A:N3	2.27	0.59
22:A:672:C:OP2	33:L:42:SER:OG	2.21	0.59
22:A:948:C:O2	22:A:984:A:O2'	2.18	0.59
22:A:1203:U:H1'	33:L:4:ASN:HB3	1.84	0.59
27:F:110:ILE:HB	27:F:113:PHE:HB2	1.82	0.59
27:F:147:ARG:HG2	27:F:148:VAL:H	1.67	0.59
38:Q:85:ALA:HB2	38:Q:115:ALA:HB2	1.83	0.59
42:U:98:ASN:ND2	42:U:98:ASN:O	2.36	0.59
1:a:1345:U:OP1	9:i:121:ARG:NH1	2.36	0.59
4:d:75:TYR:HE1	4:d:200:VAL:HG12	1.68	0.59
22:A:1082:U:H4'	53:5:38:MET:HE1	1.83	0.59
22:A:2144:G:N2	22:A:2146:C:O2'	2.35	0.59
22:A:2439:A:H4'	22:A:2440:C:H5''	1.83	0.59
26:E:1:MET:HB3	26:E:14:VAL:HG12	1.85	0.59
1:a:457:G:H2'	1:a:458:U:C6	2.38	0.59
5:e:88:HIS:CE1	5:e:137:ARG:HD3	2.37	0.59
23:B:30:C:H1'	23:B:57:A:H61	1.67	0.59
25:D:25:THR:HG21	25:D:193:VAL:HG22	1.83	0.59
34:M:4:PRO:HB2	34:M:7:THR:CG2	2.33	0.59
1:a:1315:U:O2'	1:a:1360:A:N3	2.27	0.58
5:e:98:ALA:HB3	5:e:122:VAL:HA	1.84	0.58
7:g:144:ALA:C	7:g:146:ALA:H	2.11	0.58
22:A:1068:G:N2	22:A:1095:A:O2'	2.36	0.58
22:A:2106:U:H2'	22:A:2107:G:C8	2.38	0.58
22:A:2131:U:H5'	22:A:2132:U:H5''	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:3:30:HIS:O	51:3:32:LEU:N	2.36	0.58
1:a:321:A:H2'	1:a:322:C:H6	1.68	0.58
1:a:1010:U:H2'	1:a:1011:C:H6	1.69	0.58
9:i:8:THR:HG23	9:i:9:GLY:H	1.68	0.58
22:A:548:G:H2'	22:A:549:G:O4'	2.02	0.58
22:A:831:G:N2	33:L:52:GLY:O	2.36	0.58
22:A:1047:G:H8	53:5:59:LEU:HD11	1.68	0.58
22:A:1187:G:OP1	39:R:85:LYS:NZ	2.27	0.58
22:A:1281:G:H2'	22:A:1282:U:C6	2.38	0.58
28:G:154:GLU:OE2	28:G:157:LYS:N	2.29	0.58
30:I:96:LYS:HZ2	30:I:133:ARG:HH22	1.50	0.58
30:I:100:ILE:HD11	30:I:137:LEU:HB3	1.85	0.58
55:9:1:C:H2'	55:9:2:G:C8	2.38	0.58
1:a:947:G:H2'	1:a:948:C:C6	2.39	0.58
8:h:25:THR:HG22	8:h:59:GLU:HG2	1.84	0.58
14:n:2:LYS:O	14:n:5:MET:N	2.36	0.58
23:B:13:G:O2'	23:B:15:A:H2'	2.03	0.58
4:d:201:GLU:CD	5:e:111:ARG:HH21	2.12	0.58
8:h:28:SER:OG	8:h:58:LEU:N	2.36	0.58
22:A:2823:A:OP1	25:D:118:PHE:HB2	2.03	0.58
1:a:337:G:H2'	1:a:338:A:H8	1.69	0.58
1:a:1010:U:H2'	1:a:1011:C:C6	2.39	0.58
10:j:80:THR:O	10:j:83:THR:OG1	2.16	0.58
22:A:1263:U:O2'	48:0:7:PRO:HD2	2.04	0.58
22:A:2157:G:H2'	22:A:2158:A:N3	2.18	0.58
22:A:2182:U:H3	22:A:2183:A:H62	1.49	0.58
6:f:98:GLU:HG3	6:f:99:ALA:H	1.69	0.58
22:A:1074:G:H2'	22:A:1075:C:C6	2.38	0.58
22:A:2333:A:OP2	44:W:73:ARG:NH2	2.36	0.58
25:D:25:THR:OG1	25:D:191:GLY:O	2.21	0.58
29:H:78:VAL:O	29:H:144:VAL:HA	2.03	0.58
30:I:14:ALA:O	30:I:42:ASN:ND2	2.37	0.58
5:e:56:PRO:O	5:e:60:GLN:HG2	2.04	0.58
22:A:1814:G:H4'	24:C:50:THR:HG21	1.86	0.58
33:L:29:LYS:HB3	39:R:82:HIS:CE1	2.39	0.58
1:a:36:C:H5''	12:l:119:LYS:HG2	1.86	0.58
22:A:811:U:H2'	33:L:21:ARG:HA	1.86	0.58
22:A:2163:A:C5	22:A:2164:C:H1'	2.39	0.58
22:A:2848:G:H8	37:P:94:ALA:HB2	1.68	0.58
1:a:360:G:H2'	1:a:361:G:C8	2.39	0.58
1:a:409:U:O2	1:a:433:G:N2	2.27	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:202:ASN:HD21	2:b:204:ASP:HB2	1.69	0.58
6:f:92:THR:HG23	6:f:93:LYS:H	1.69	0.58
22:A:2123:G:N2	22:A:2124:G:O6	2.36	0.58
23:B:81:G:O6	23:B:95:U:O2	2.21	0.58
46:Y:49:ASP:OD1	46:Y:52:ARG:NH2	2.37	0.58
1:a:108:G:N1	20:t:9:ARG:HG2	2.19	0.57
13:m:11:HIS:HA	13:m:43:LYS:HD3	1.84	0.57
22:A:876:C:H2'	22:A:877:A:O4'	2.03	0.57
22:A:1506:U:H2'	22:A:1507:C:C6	2.39	0.57
22:A:1726:C:H2'	22:A:1727:C:O4'	2.04	0.57
1:a:26:A:N6	1:a:558:G:H1'	2.19	0.57
1:a:380:G:N7	1:a:381:C:H3'	2.20	0.57
1:a:407:U:H5''	4:d:111:ALA:HB1	1.84	0.57
1:a:432:A:C5	1:a:433:G:C5	2.92	0.57
1:a:1005:A:OP2	1:a:1024:G:N2	2.35	0.57
22:A:320:A:N3	26:E:163:ASN:ND2	2.51	0.57
24:C:259:ASN:ND2	24:C:262:THR:OG1	2.35	0.57
27:F:39:VAL:HG23	27:F:85:GLY:HA2	1.86	0.57
44:W:33:ILE:HG22	44:W:34:VAL:HG23	1.86	0.57
49:1:39:ASP:OD1	49:1:48:TYR:OH	2.22	0.57
55:9:68:C:H2'	55:9:69:A:C8	2.38	0.57
1:a:468:A:H2'	1:a:469:C:C6	2.38	0.57
2:b:206:ILE:HA	2:b:209:VAL:HG22	1.87	0.57
22:A:1853:A:H2'	22:A:1854:A:C8	2.38	0.57
22:A:2831:G:OP2	25:D:59:ARG:NH1	2.24	0.57
41:T:58:VAL:HG22	41:T:85:VAL:HG22	1.87	0.57
53:5:56:ARG:HH11	53:5:81:LEU:HD11	1.69	0.57
54:6:36:VAL:HG13	54:6:41:HIS:HB2	1.86	0.57
1:a:476:U:H2'	1:a:477:C:C6	2.40	0.57
20:t:47:GLN:O	20:t:51:ASN:ND2	2.38	0.57
22:A:1248:G:OP1	26:E:44:ARG:NH1	2.37	0.57
16:p:57:ILE:HD11	16:p:75:ILE:HD11	1.85	0.57
18:r:43:ILE:HG13	18:r:44:THR:HG23	1.85	0.57
22:A:1394:U:H4'	22:A:1603:A:H4'	1.86	0.57
22:A:2199:A:N1	22:A:2226:C:N4	2.53	0.57
23:B:48:U:OP1	36:O:30:ARG:NH2	2.37	0.57
43:V:8:VAL:HG12	43:V:38:LEU:HD11	1.86	0.57
1:a:1477:U:H2'	1:a:1478:U:C6	2.39	0.57
10:j:29:ALA:HB2	10:j:87:LEU:HD21	1.87	0.57
22:A:782:A:N7	24:C:219:VAL:HG21	2.19	0.57
22:A:2365:G:N7	51:3:38:LYS:NZ	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:K:73:ASP:OD1	32:K:75:SER:OG	2.18	0.57
2:b:160:LEU:HD13	2:b:175:ALA:HB2	1.87	0.57
6:f:25:TYR:HD2	6:f:62:MET:HE1	1.68	0.57
10:j:24:GLU:O	10:j:28:THR:OG1	2.14	0.57
11:k:15:VAL:HG12	11:k:76:TYR:HB3	1.85	0.57
15:o:4:THR:HA	15:o:7:THR:HG22	1.84	0.57
22:A:1331:G:O2'	22:A:1332:G:H5'	2.05	0.57
22:A:1380:G:O2'	22:A:1569:A:N6	2.37	0.57
22:A:1429:G:H2'	22:A:1430:G:H8	1.70	0.57
22:A:1808:A:H3'	22:A:1809:A:C8	2.39	0.57
27:F:37:MET:HE2	27:F:151:LEU:HG	1.86	0.57
41:T:64:LYS:HA	41:T:79:ASP:OD1	2.04	0.57
1:a:1090:U:HO2'	1:a:1171:A:HO2'	1.53	0.57
1:a:1167:A:N7	1:a:1169:A:N6	2.52	0.57
22:A:695:G:O6	22:A:767:U:O2	2.23	0.57
22:A:1682:G:H2'	22:A:1683:U:C6	2.40	0.57
30:I:37:PHE:HA	30:I:41:PHE:HB2	1.87	0.57
40:S:23:LEU:HD21	48:0:21:LEU:HB2	1.85	0.57
52:4:16:ILE:HG12	52:4:25:VAL:HG22	1.87	0.57
1:a:1268:G:H2'	1:a:1269:A:C8	2.40	0.57
27:F:107:VAL:HG12	27:F:108:PRO:HD3	1.87	0.57
1:a:1347:G:O6	9:i:11:ARG:NH2	2.38	0.57
1:a:1405:G7M:O5'	1:a:1405:G7M:H8	2.05	0.57
9:i:29:ILE:HG22	9:i:64:ILE:HB	1.87	0.57
22:A:630:G:N2	22:A:633:A:OP2	2.38	0.57
41:T:37:ASP:N	41:T:37:ASP:OD1	2.37	0.57
1:a:850:U:H2'	1:a:851:G:H5''	1.87	0.56
7:g:22:LEU:O	7:g:26:VAL:HG23	2.05	0.56
22:A:238:C:O2'	22:A:608:A:N3	2.38	0.56
22:A:1198:U:H2'	22:A:1199:U:C6	2.40	0.56
36:O:30:ARG:H	36:O:97:PHE:HE2	1.52	0.56
50:2:10:LEU:HD11	50:2:14:ARG:HE	1.69	0.56
1:a:1266:G:N2	1:a:1269:A:OP2	2.29	0.56
5:e:98:ALA:O	5:e:101:GLY:N	2.32	0.56
21:u:23:GLU:O	21:u:26:GLY:N	2.38	0.56
22:A:988:A:C8	47:Z:13:ILE:HD12	2.40	0.56
22:A:1847:G:O2'	22:A:1848:A:H8	1.88	0.56
22:A:2467:C:O2	34:M:123:LYS:NZ	2.31	0.56
53:5:14:GLU:O	53:5:18:VAL:HG13	2.04	0.56
1:a:109:A:C6	1:a:326:G:C6	2.94	0.56
1:a:461:A:H2'	1:a:462:G:H8	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1075:U:OP1	2:b:177:ASN:ND2	2.35	0.56
1:a:1191:A:OP2	1:a:1191:A:H8	1.88	0.56
1:a:1281:C:O2'	1:a:1282:C:OP1	2.21	0.56
1:a:1304:G:N1	1:a:1332:A:OP2	2.32	0.56
4:d:94:GLU:HA	4:d:99:ASN:ND2	2.21	0.56
5:e:156:ARG:O	5:e:158:LYS:N	2.38	0.56
9:i:101:GLY:O	9:i:103:VAL:N	2.37	0.56
12:l:2:THR:O	12:l:5:GLN:N	2.38	0.56
17:q:70:LYS:HG3	17:q:70:LYS:O	2.06	0.56
22:A:528:A:C2	22:A:2043:C:H4'	2.41	0.56
22:A:927:A:H2'	22:A:928:A:C8	2.41	0.56
22:A:1173:U:C2	22:A:1174:U:H1'	2.41	0.56
22:A:2016:U:O2	48:0:3:GLN:NE2	2.38	0.56
22:A:2100:G:H2'	22:A:2101:A:C8	2.40	0.56
22:A:2846:G:H2'	22:A:2847:U:O4'	2.05	0.56
31:J:17:VAL:HG23	31:J:137:PRO:HB2	1.86	0.56
53:5:23:LEU:HD11	53:5:119:PRO:HD3	1.86	0.56
1:a:1508:A:H2'	1:a:1509:C:C6	2.40	0.56
17:q:3:LYS:HG2	17:q:4:ILE:H	1.70	0.56
22:A:161:A:H3'	22:A:162:U:H5''	1.86	0.56
22:A:1930:G:H4'	22:A:1931:U:O5'	2.05	0.56
22:A:2271:G:OP1	44:W:14:ALA:HB1	2.05	0.56
2:b:17:HIS:ND1	2:b:40:ILE:HD11	2.20	0.56
22:A:84:A:OP1	42:U:5:ARG:NH1	2.38	0.56
22:A:2167:U:H1'	22:A:2169:A:C8	2.41	0.56
1:a:12:U:H4'	1:a:526:C:H4'	1.87	0.56
1:a:674:G:H2'	1:a:675:A:H8	1.70	0.56
4:d:93:LEU:HD12	4:d:96:ARG:HD3	1.86	0.56
14:n:13:VAL:HA	14:n:60:GLN:HE21	1.69	0.56
22:A:306:U:H2'	22:A:307:G:O4'	2.05	0.56
22:A:1842:G:H1	22:A:1898:U:H3	1.53	0.56
24:C:175:LEU:HD11	24:C:181:ARG:HD3	1.88	0.56
38:Q:48:ASP:HA	38:Q:51:GLN:HB2	1.88	0.56
1:a:321:A:H2'	1:a:322:C:C6	2.40	0.56
1:a:413:G:C2'	1:a:428:G:H22	2.18	0.56
1:a:708:C:H2'	1:a:709:U:H6	1.71	0.56
20:t:31:ILE:HD11	20:t:57:VAL:HG11	1.87	0.56
22:A:1469:A:H2'	22:A:1470:A:H8	1.71	0.56
22:A:2570:G:H2'	22:A:2571:U:O4'	2.06	0.56
27:F:117:SER:O	27:F:127:TYR:OH	2.16	0.56
36:O:7:ARG:NH1	36:O:95:SER:OG	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:P:91:VAL:HG21	37:P:96:LEU:HD21	1.87	0.56
53:5:103:ASN:HA	53:5:107:GLU:HB3	1.88	0.56
3:c:189:HIS:HD2	3:c:194:VAL:HG22	1.71	0.56
22:A:1117:C:H2'	22:A:1118:C:C6	2.41	0.56
22:A:1469:A:H2'	22:A:1470:A:C8	2.41	0.56
24:C:56:GLY:HA2	24:C:212:TRP:HA	1.87	0.56
33:L:29:LYS:O	33:L:30:THR:OG1	2.18	0.56
39:R:49:ILE:HG22	39:R:54:VAL:HA	1.88	0.56
40:S:28:LYS:H	40:S:31:GLN:NE2	2.03	0.56
1:a:1176:A:H2'	1:a:1177:G:H8	1.70	0.56
11:k:82:GLU:HG3	11:k:108:ASN:OD1	2.06	0.56
22:A:592:A:H2	51:3:3:ILE:HD11	1.71	0.56
22:A:1062:G:H8	22:A:1062:G:OP2	1.88	0.56
22:A:1332:G:N7	22:A:1609:A:O2'	2.39	0.56
22:A:1438:U:H2'	22:A:1439:A:H8	1.71	0.56
22:A:2584:U:H3'	22:A:2585:U:H5''	1.87	0.56
24:C:83:ASP:OD2	24:C:86:ARG:NE	2.31	0.56
54:6:41:HIS:ND1	54:6:43:PHE:HB3	2.21	0.56
9:i:115:VAL:HG11	10:j:62:ARG:HB2	1.88	0.56
35:N:29:VAL:HG21	35:N:75:ILE:HG23	1.88	0.56
44:W:19:VAL:HG22	44:W:34:VAL:HG22	1.88	0.56
49:1:5:ARG:HG2	49:1:23:THR:HB	1.88	0.56
1:a:26:A:H61	1:a:558:G:H1'	1.70	0.55
1:a:261:U:OP2	20:t:70:LYS:NZ	2.38	0.55
9:i:44:ARG:H	9:i:44:ARG:HD3	1.71	0.55
18:r:34:GLU:OE2	21:u:3:ILE:N	2.39	0.55
22:A:1176:U:H2'	22:A:1177:G:C8	2.41	0.55
22:A:2246:G:H2'	22:A:2247:A:C8	2.41	0.55
23:B:42:C:C6	27:F:65:LEU:HB2	2.41	0.55
26:E:176:ASP:OD1	26:E:176:ASP:N	2.38	0.55
30:I:100:ILE:HG21	30:I:105:LEU:HG	1.88	0.55
34:M:40:ARG:HB3	34:M:93:VAL:HB	1.89	0.55
40:S:35:ILE:O	40:S:39:THR:OG1	2.20	0.55
1:a:522:C:OP2	12:l:65:TYR:OH	2.22	0.55
1:a:1046:A:H61	1:a:1213:A:H2	1.54	0.55
15:o:54:GLY:O	15:o:58:MET:HG3	2.06	0.55
27:F:139:GLU:OE1	27:F:139:GLU:N	2.39	0.55
34:M:41:LEU:HD11	34:M:102:LEU:HD13	1.87	0.55
41:T:61:LEU:HD11	41:T:82:LYS:HE2	1.87	0.55
1:a:945:G:C2	1:a:946:A:C8	2.94	0.55
1:a:1006:G:N7	1:a:1024:G:N2	2.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1039:G:H2'	1:a:1040:U:C6	2.41	0.55
8:h:1:SER:O	8:h:1:SER:OG	2.17	0.55
12:l:33:CYS:HB3	12:l:76:HIS:O	2.06	0.55
22:A:849:A:H2'	22:A:850:U:H6	1.72	0.55
51:3:30:HIS:O	51:3:32:LEU:HG	2.06	0.55
1:a:82:G:H2'	1:a:83:C:C6	2.42	0.55
1:a:108:G:C6	20:t:9:ARG:HG2	2.42	0.55
1:a:224:U:H2'	1:a:225:C:C6	2.41	0.55
1:a:279:A:H5''	1:a:280:C:H3'	1.89	0.55
1:a:296:U:O2'	1:a:556:C:O2	2.23	0.55
22:A:1100:C:H2'	22:A:1101:U:C6	2.42	0.55
22:A:1587:G:H2'	22:A:1588:G:C8	2.39	0.55
22:A:2557:G:H2'	22:A:2558:C:C6	2.42	0.55
22:A:2895:G:H2'	22:A:2896:C:C6	2.41	0.55
24:C:7:PRO:HB3	24:C:13:ARG:HA	1.88	0.55
31:J:45:THR:HG23	31:J:48:VAL:HB	1.89	0.55
42:U:95:PHE:O	42:U:99:SER:HA	2.06	0.55
48:0:53:VAL:HG23	48:0:54:ILE:HG12	1.87	0.55
1:a:437:U:H3	1:a:495:A:N6	1.97	0.55
1:a:842:U:N3	1:a:844:G:OP2	2.39	0.55
1:a:1240:U:O4	7:g:108:ARG:NE	2.33	0.55
14:n:20:PHE:C	14:n:22:LYS:H	2.13	0.55
22:A:1490:A:HO2'	22:A:1491:G:P	2.28	0.55
22:A:2653:U:OP2	22:A:2654:A:O2'	2.20	0.55
24:C:128:THR:HB	24:C:190:THR:HG22	1.88	0.55
25:D:186:LEU:HD21	37:P:3:ILE:HG21	1.89	0.55
32:K:2:ILE:HB	32:K:33:ALA:HB3	1.88	0.55
1:a:35:G:N3	12:l:114:SER:OG	2.38	0.55
1:a:1219:A:H2'	1:a:1220:G:H8	1.72	0.55
22:A:1613:G:O2'	50:2:3:ARG:HD2	2.05	0.55
1:a:1237:C:O2'	1:a:1300:G:N2	2.37	0.55
2:b:8:MET:HB2	2:b:46:VAL:HG21	1.87	0.55
4:d:102:TYR:HB2	4:d:114:ARG:HH12	1.72	0.55
22:A:356:G:H2'	22:A:357:C:C6	2.42	0.55
22:A:721:A:H2'	22:A:722:A:C8	2.42	0.55
22:A:2430:A:O2'	22:A:2431:U:H5'	2.07	0.55
22:A:2618:G:H21	25:D:155:VAL:HG21	1.71	0.55
22:A:2788:C:H2'	22:A:2789:C:C6	2.41	0.55
35:N:37:THR:HG22	35:N:39:PRO:HD2	1.89	0.55
53:5:3:LEU:HG	53:5:6:GLN:HB3	1.89	0.55
4:d:187:ARG:NH1	4:d:187:ARG:O	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:1096:A:C2	30:I:25:PRO:HB2	2.42	0.55
28:G:36:LEU:HD23	28:G:36:LEU:H	1.71	0.55
36:O:31:THR:HB	36:O:33:ARG:O	2.07	0.55
1:a:545:C:OP1	4:d:68:GLU:HG3	2.07	0.55
1:a:1060:U:OP1	14:n:85:ARG:NH2	2.39	0.55
1:a:1175:G:H2'	1:a:1176:A:H8	1.72	0.55
1:a:1402:4OC:H2'	1:a:1403:C:O4'	2.07	0.55
4:d:64:TYR:HE2	4:d:99:ASN:HD21	1.54	0.55
18:r:36:GLY:O	18:r:62:ARG:NH1	2.34	0.55
22:A:1779:U:O2	22:A:1783:A:N6	2.40	0.55
27:F:21:TYR:HD2	27:F:27:VAL:HG12	1.71	0.55
41:T:10:VAL:HG21	41:T:42:GLU:HB3	1.89	0.55
1:a:511:C:O2'	1:a:512:U:O5'	2.25	0.55
1:a:689:C:O2'	1:a:705:G:O2'	2.21	0.55
1:a:1040:U:H2'	1:a:1041:G:C8	2.42	0.55
4:d:57:LYS:HA	4:d:199:ILE:HD12	1.89	0.55
8:h:86:LYS:HE3	8:h:90:GLU:O	2.06	0.55
19:s:49:ALA:HA	19:s:58:PRO:HA	1.87	0.55
22:A:690:G:H21	24:C:42:ARG:HH12	1.54	0.55
22:A:1056:G:N2	22:A:1104:C:H42	2.05	0.55
22:A:1923:U:H2'	22:A:1924:C:C6	2.42	0.55
6:f:40:GLU:HG2	6:f:42:TRP:HE1	1.73	0.54
10:j:19:ASP:HA	10:j:22:THR:HG22	1.88	0.54
12:l:66:ILE:HG12	12:l:96:THR:HG21	1.89	0.54
22:A:2430:A:N3	22:A:2430:A:H2'	2.22	0.54
22:A:2726:A:O2'	22:A:2727:A:O5'	2.25	0.54
22:A:2581:G:OP2	22:A:2581:G:N2	2.41	0.54
24:C:134:ILE:O	24:C:166:ARG:NH2	2.40	0.54
29:H:40:THR:O	29:H:41:LYS:HG2	2.07	0.54
30:I:82:ALA:HB2	30:I:108:ILE:HD13	1.89	0.54
40:S:34:ASP:OD1	40:S:35:ILE:N	2.39	0.54
46:Y:16:THR:HA	46:Y:19:LEU:CD2	2.37	0.54
1:a:410:G:H2'	1:a:429:U:O4	2.07	0.54
1:a:1026:G:N2	1:a:1035:A:N1	2.53	0.54
1:a:1440:U:HO2'	1:a:1441:A:H8	1.55	0.54
2:b:12:GLY:HA2	2:b:207:ARG:HH12	1.72	0.54
7:g:73:GLU:HG2	7:g:74:VAL:H	1.71	0.54
22:A:528:A:H5''	31:J:113:PRO:HG3	1.89	0.54
22:A:1103:A:P	22:A:1104:C:H41	2.30	0.54
22:A:1141:U:H2'	31:J:65:THR:HG21	1.88	0.54
22:A:1316:U:H2'	22:A:1317:G:H8	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:1441:G:H2'	22:A:1442:U:C6	2.43	0.54
22:A:1802:A:H2'	22:A:1803:A:C8	2.43	0.54
22:A:2164:C:H41	22:A:2171:A:N6	2.06	0.54
22:A:2532:G:N2	22:A:2663:G:O2'	2.40	0.54
26:E:146:VAL:HG12	26:E:185:LYS:HB2	1.88	0.54
32:K:34:GLY:N	32:K:37:ASP:OD2	2.38	0.54
36:O:34:HIS:HA	36:O:53:THR:OG1	2.07	0.54
44:W:49:CYS:SG	44:W:53:HIS:HA	2.48	0.54
49:1:36:LYS:HG2	49:1:47:ILE:HG12	1.90	0.54
52:4:25:VAL:HG21	52:4:35:GLN:HE21	1.72	0.54
1:a:539:A:H2'	1:a:540:G:C8	2.42	0.54
1:a:738:C:H2'	1:a:739:C:C6	2.43	0.54
2:b:17:HIS:NE2	2:b:187:ASP:OD1	2.36	0.54
22:A:1149:G:H2'	22:A:1150:C:C6	2.43	0.54
22:A:2635:A:O2'	25:D:81:GLU:OE1	2.24	0.54
36:O:99:TYR:CE2	36:O:104:GLN:HG3	2.42	0.54
13:m:36:ALA:HB2	13:m:58:GLU:OE2	2.08	0.54
21:u:36:PHE:CE2	21:u:40:PRO:HD3	2.42	0.54
1:a:35:G:H2'	1:a:36:C:H6	1.72	0.54
1:a:946:A:H2'	1:a:947:G:H8	1.73	0.54
4:d:113:ALA:HB1	4:d:114:ARG:NH2	2.21	0.54
11:k:34:THR:HG22	11:k:40:ALA:HA	1.88	0.54
16:p:48:GLU:OE2	16:p:49:GLY:N	2.40	0.54
31:J:32:LEU:HD22	31:J:54:ILE:HG21	1.89	0.54
1:a:1074:G:OP1	5:e:68:ARG:NH2	2.41	0.54
1:a:1120:C:H2'	1:a:1121:U:H6	1.72	0.54
1:a:1216:A:H5''	14:n:4:SER:HB2	1.89	0.54
11:k:92:ARG:HE	21:u:24:LYS:HE3	1.73	0.54
27:F:34:THR:HB	27:F:89:THR:HG22	1.88	0.54
29:H:77:THR:HA	29:H:143:ILE:O	2.08	0.54
33:L:135:ILE:HB	33:L:142:ILE:HD11	1.88	0.54
1:a:335:C:O2'	1:a:1433:A:N3	2.34	0.54
1:a:1186:G:H21	14:n:101:TRP:C	2.16	0.54
1:a:1314:C:H2'	1:a:1315:U:C6	2.42	0.54
22:A:807:U:OP2	33:L:41:ARG:NH1	2.40	0.54
22:A:1058:U:H2'	22:A:1059:G:C8	2.43	0.54
22:A:2186:G:H2'	22:A:2187:U:C6	2.42	0.54
22:A:2405:G:O2'	22:A:2412:A:N6	2.38	0.54
34:M:74:THR:HG22	34:M:89:VAL:HG22	1.89	0.54
42:U:46:LYS:HD2	42:U:47:PRO:HD2	1.90	0.54
1:a:414:A:H62	1:a:430:A:H61	1.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1123:U:H2'	1:a:1124:G:H5'	1.90	0.54
4:d:114:ARG:NE	4:d:114:ARG:HA	2.23	0.54
7:g:48:THR:O	7:g:51:GLN:HG3	2.08	0.54
22:A:372:G:O2'	22:A:400:G:O6	2.25	0.54
22:A:1039:A:H2	22:A:1116:G:H1	1.49	0.54
22:A:2852:G:H5'	35:N:64:ARG:HH22	1.72	0.54
27:F:133:GLU:O	27:F:136:ILE:HG12	2.08	0.54
37:P:59:THR:HB	37:P:72:VAL:HG22	1.90	0.54
1:a:193:C:H2'	1:a:194:C:H6	1.73	0.54
1:a:432:A:H2'	1:a:433:G:C8	2.43	0.54
1:a:458:U:H2'	1:a:459:A:C8	2.43	0.54
9:i:9:GLY:HA2	9:i:80:HIS:ND1	2.23	0.54
17:q:63:CYS:SG	17:q:64:ARG:N	2.81	0.54
22:A:879:G:H2'	22:A:880:G:C8	2.42	0.54
22:A:1857:G:H1'	22:A:1885:A:N6	2.23	0.54
22:A:2243:U:H2'	22:A:2244:U:C6	2.43	0.54
22:A:2246:G:H2'	22:A:2247:A:H8	1.71	0.54
28:G:93:TYR:HA	28:G:105:SER:O	2.08	0.54
50:2:34:ARG:NE	50:2:42:LEU:O	2.40	0.54
1:a:429:U:H3'	4:d:8:LEU:HD12	1.89	0.53
1:a:505:G:H2'	1:a:506:G:H8	1.72	0.53
1:a:1149:C:H2'	1:a:1150:A:C8	2.43	0.53
22:A:458:G:O2'	22:A:469:G:O6	2.23	0.53
22:A:1905:C:O2'	22:A:1929:G:H1'	2.08	0.53
33:L:85:VAL:HG12	33:L:94:THR:HG22	1.90	0.53
54:6:16:CYS:SG	54:6:17:SER:N	2.81	0.53
1:a:390:U:H2'	1:a:391:G:H8	1.74	0.53
1:a:765:G:H1	1:a:812:G:HO2'	1.54	0.53
1:a:936:C:H2'	1:a:937:A:H8	1.73	0.53
1:a:1144:G:N2	1:a:1146:A:H62	2.05	0.53
8:h:126:CYS:SG	8:h:127:TYR:N	2.81	0.53
22:A:1111:A:HO2'	22:A:1112:G:P	2.31	0.53
1:a:473:U:N3	1:a:474:G:N7	2.57	0.53
22:A:296:U:H2'	22:A:297:G:H8	1.74	0.53
22:A:1062:G:H2'	22:A:1063:G:C8	2.43	0.53
22:A:1484:U:H2'	22:A:1485:U:C6	2.43	0.53
22:A:2720:U:H5''	37:P:52:ARG:NH2	2.23	0.53
1:a:860:A:H2'	1:a:861:G:O4'	2.09	0.53
5:e:79:THR:OG1	5:e:97:PRO:O	2.23	0.53
22:A:162:U:O2'	22:A:163:C:O5'	2.24	0.53
22:A:2295:C:OP1	36:O:10:ARG:NH2	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:B:1:U:H2'	23:B:2:G:H8	1.72	0.53
26:E:170:ARG:NH2	26:E:176:ASP:OD1	2.41	0.53
30:I:25:PRO:O	30:I:29:GLN:CB	2.46	0.53
39:R:16:GLU:OE2	39:R:100:GLY:HA2	2.08	0.53
40:S:28:LYS:H	40:S:31:GLN:HE21	1.56	0.53
1:a:427:U:OP2	1:a:428:G:O2'	2.21	0.53
22:A:2291:U:H2'	22:A:2292:U:C6	2.44	0.53
22:A:2638:G:O2'	22:A:2639:A:H8	1.92	0.53
22:A:2821:A:O2'	22:A:2826:A:N1	2.36	0.53
26:E:168:ASP:N	26:E:168:ASP:OD1	2.36	0.53
53:5:57:ASN:HB3	53:5:62:ARG:CD	2.38	0.53
53:5:101:LYS:O	53:5:105:LYS:HG2	2.09	0.53
1:a:379:C:C2'	1:a:380:G:C4	2.91	0.53
1:a:433:G:C6	1:a:434:U:C4	2.96	0.53
1:a:875:U:O2'	8:h:14:ARG:NH1	2.41	0.53
1:a:1107:C:C4	1:a:1108:G:C8	2.96	0.53
5:e:84:VAL:HG11	5:e:146:MET:HB2	1.89	0.53
6:f:29:ILE:HG21	6:f:64:VAL:HG21	1.90	0.53
6:f:91:ARG:HG3	6:f:92:THR:H	1.74	0.53
14:n:9:GLU:HG3	14:n:63:ARG:HD2	1.90	0.53
18:r:58:ILE:O	18:r:62:ARG:HG3	2.07	0.53
22:A:933:A:H5''	22:A:934:U:OP2	2.08	0.53
22:A:1005:C:O2'	31:J:30:THR:HG21	2.08	0.53
22:A:1096:A:H2	30:I:25:PRO:HB2	1.73	0.53
22:A:2851:A:O2'	35:N:64:ARG:NH2	2.39	0.53
27:F:63:LYS:HG2	27:F:64:PRO:HD2	1.91	0.53
31:J:80:HIS:O	31:J:82:GLY:N	2.41	0.53
33:L:62:PRO:HB2	51:3:29:ARG:HH11	1.74	0.53
42:U:76:THR:O	42:U:78:LYS:NZ	2.41	0.53
1:a:150:U:H2'	1:a:151:A:H8	1.74	0.53
1:a:1040:U:H2'	1:a:1041:G:H8	1.72	0.53
1:a:1095:U:P	1:a:1108:G:H1	2.32	0.53
22:A:315:G:H2'	22:A:316:C:C6	2.44	0.53
22:A:347:A:H2'	22:A:348:A:C8	2.44	0.53
22:A:1352:U:O2'	22:A:1570:A:N3	2.39	0.53
22:A:1952:A:N3	22:A:2560:A:O2'	2.39	0.53
30:I:126:ARG:HA	30:I:129:GLU:HG2	1.90	0.53
54:6:35:ASP:OD1	54:6:36:VAL:N	2.42	0.53
1:a:380:G:N1	1:a:382:A:N7	2.57	0.53
1:a:517:G:N2	1:a:533:A:OP2	2.38	0.53
1:a:784:A:H2'	1:a:785:G:H8	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1256:A:H1'	1:a:1258:G:C4	2.44	0.53
6:f:6:ILE:HG13	6:f:89:VAL:HG22	1.89	0.53
12:l:36:VAL:HG21	12:l:73:LEU:HB3	1.90	0.53
53:5:92:ALA:HB3	53:5:129:LEU:HD21	1.91	0.53
12:l:45:ASN:ND2	12:l:88:ASP:OD1	2.41	0.53
22:A:1414:C:H2'	22:A:1415:U:O4'	2.09	0.53
22:A:2014:A:H2'	22:A:2015:A:C8	2.44	0.53
28:G:126:THR:HG22	28:G:128:THR:H	1.74	0.53
1:a:17:U:H2'	1:a:18:C:H6	1.72	0.53
1:a:90:C:H2'	1:a:91:U:C6	2.44	0.53
1:a:321:A:N7	1:a:328:C:O2'	2.38	0.53
1:a:495:A:H4'	1:a:496:A:OP1	2.08	0.53
2:b:30:ILE:HD12	2:b:38:HIS:CE1	2.44	0.53
22:A:1052:C:N3	22:A:1053:C:N4	2.56	0.53
22:A:1433:A:H2'	22:A:1434:A:C8	2.44	0.53
36:O:18:LEU:HD12	36:O:23:ALA:HB3	1.90	0.53
1:a:613:C:H2'	1:a:614:C:C6	2.44	0.52
2:b:153:MET:HG3	2:b:155:GLY:H	1.74	0.52
6:f:9:MET:HB2	6:f:85:ILE:O	2.10	0.52
11:k:80:ASN:HB3	11:k:105:ARG:HB3	1.92	0.52
22:A:2:G:H2'	22:A:3:U:H6	1.74	0.52
22:A:1054:A:N1	22:A:1105:U:C4	2.77	0.52
22:A:1079:C:N3	30:I:131:THR:OG1	2.42	0.52
22:A:2215:C:H2'	22:A:2216:G:C8	2.44	0.52
22:A:2542:A:H5''	22:A:2766:A:O2'	2.09	0.52
22:A:2589:A:H2'	22:A:2590:A:H8	1.74	0.52
22:A:2758:A:O2'	28:G:37:ASN:ND2	2.41	0.52
1:a:409:U:N3	1:a:433:G:N1	2.16	0.52
1:a:1391:U:H2'	1:a:1392:G:C8	2.44	0.52
5:e:55:VAL:O	5:e:59:ILE:HG12	2.09	0.52
18:r:25:ILE:HG21	18:r:66:LEU:HB3	1.91	0.52
22:A:995:C:O2	31:J:3:THR:OG1	2.24	0.52
28:G:43:LYS:HB3	28:G:50:THR:OG1	2.09	0.52
54:6:14:ALA:HA	54:6:32:LEU:O	2.09	0.52
1:a:642:A:H2'	1:a:643:C:H6	1.74	0.52
1:a:1342:C:H4'	9:i:126:PHE:O	2.09	0.52
22:A:776:G:N2	22:A:2241:A:OP1	2.41	0.52
22:A:1436:G:N3	22:A:1515:A:H2	2.08	0.52
27:F:106:ALA:HB1	27:F:136:ILE:HG22	1.92	0.52
27:F:168:LEU:HD23	27:F:169:LEU:HD23	1.91	0.52
1:a:264:C:H4'	17:q:64:ARG:HD2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:436:C:H1'	4:d:153:ARG:HE	1.75	0.52
1:a:769:G:H4'	1:a:1513:A:H4'	1.92	0.52
2:b:176:ASN:ND2	2:b:194:GLY:O	2.35	0.52
22:A:706:A:H2'	22:A:707:G:O4'	2.09	0.52
22:A:1263:U:O2	48:O:3:GLN:NE2	2.41	0.52
22:A:2079:U:O2'	45:X:22:ASN:OD1	2.28	0.52
22:A:2304:G:H22	22:A:2312:U:H3	1.57	0.52
25:D:5:VAL:HG13	25:D:82:PHE:HZ	1.75	0.52
27:F:65:LEU:HD23	27:F:87:LYS:HD3	1.90	0.52
28:G:25:ILE:HG21	28:G:78:VAL:HG11	1.91	0.52
52:4:25:VAL:HB	52:4:35:GLN:HG2	1.91	0.52
1:a:270:A:H2'	1:a:271:C:C6	2.45	0.52
1:a:944:G:N1	1:a:1338:G:OP2	2.41	0.52
1:a:1151:A:H2'	1:a:1152:A:H8	1.74	0.52
4:d:146:GLU:OE1	4:d:146:GLU:N	2.43	0.52
12:l:86:VAL:HG21	12:l:89:LEU:HB2	1.90	0.52
21:u:36:PHE:CZ	21:u:39:LYS:HE3	2.44	0.52
22:A:391:A:O2'	22:A:410:G:OP1	2.22	0.52
22:A:545:U:O4	22:A:548:G:O6	2.27	0.52
22:A:1809:A:H2'	22:A:1810:A:C8	2.45	0.52
22:A:2025:C:H2'	22:A:2026:U:C6	2.45	0.52
22:A:2850:A:N7	22:A:2868:A:O2'	2.34	0.52
29:H:12:LEU:HD12	29:H:19:VAL:HG21	1.92	0.52
1:a:35:G:H2'	1:a:36:C:C6	2.45	0.52
1:a:868:C:H2'	1:a:869:G:O4'	2.09	0.52
1:a:1287:A:H2	1:a:1353:G:H1'	1.75	0.52
3:c:9:ILE:HG23	3:c:10:ARG:HG3	1.92	0.52
10:j:52:LEU:HB2	14:n:81:ARG:HD2	1.92	0.52
14:n:25:GLU:O	14:n:29:ILE:HG12	2.09	0.52
22:A:298:G:N1	22:A:339:U:OP2	2.31	0.52
22:A:299:A:N3	22:A:319:G:O2'	2.40	0.52
22:A:971:G:H2'	22:A:972:A:O4'	2.10	0.52
26:E:21:ARG:HD3	26:E:106:LYS:HB3	1.90	0.52
52:4:26:ILE:O	52:4:26:ILE:HG13	2.10	0.52
1:a:229:U:O2'	16:p:23:ASP:OD1	2.27	0.52
1:a:273:U:O2'	17:q:17:GLU:OE2	2.23	0.52
1:a:1120:C:H2'	1:a:1121:U:C6	2.45	0.52
1:a:1151:A:H2'	1:a:1152:A:C8	2.45	0.52
22:A:639:U:H2'	22:A:640:C:H6	1.75	0.52
27:F:72:SER:OG	27:F:79:ARG:HA	2.09	0.52
1:a:180:U:H2'	1:a:181:A:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:p:73:ALA:O	16:p:77:GLU:HG2	2.10	0.52
22:A:580:U:H2'	22:A:581:C:C6	2.45	0.52
22:A:782:A:C8	24:C:219:VAL:HG21	2.44	0.52
22:A:1074:G:O2'	22:A:1075:C:O5'	2.22	0.52
31:J:58:ASN:ND2	31:J:127:GLY:O	2.43	0.52
1:a:379:C:C2	1:a:380:G:C6	2.97	0.52
1:a:1279:G:O2'	1:a:1282:C:N4	2.43	0.52
2:b:129:THR:HG22	2:b:130:LYS:H	1.73	0.52
4:d:12:ARG:HG3	4:d:33:ILE:HD13	1.92	0.52
6:f:92:THR:C	6:f:94:HIS:H	2.18	0.52
22:A:1050:A:H1'	22:A:2751:G:N2	2.25	0.52
22:A:1682:G:H2'	22:A:1683:U:H6	1.74	0.52
22:A:1869:G:H1'	22:A:1872:A:N6	2.25	0.52
22:A:2646:C:OP2	22:A:2732:G:O2'	2.23	0.52
1:a:410:G:H2'	1:a:429:U:C4	2.45	0.52
1:a:946:A:H2'	1:a:947:G:C8	2.45	0.52
2:b:57:ASN:OD1	2:b:58:LYS:N	2.43	0.52
22:A:1093:G:C2	22:A:1099:G:C6	2.98	0.52
22:A:2547:A:H2'	22:A:2548:U:C6	2.45	0.52
22:A:2788:C:O2'	22:A:2809:A:N3	2.41	0.52
23:B:44:G:H1'	23:B:47:C:H42	1.75	0.52
34:M:59:ARG:H	34:M:59:ARG:HD2	1.75	0.52
53:5:24:SER:HB2	53:5:86:MET:HA	1.91	0.52
1:a:8:A:C5	4:d:205:LYS:HA	2.44	0.51
1:a:504:C:C2	1:a:542:G:N2	2.78	0.51
1:a:532:A:N6	1:a:1206:G:O2'	2.43	0.51
1:a:946:A:O2'	1:a:1333:A:N3	2.42	0.51
2:b:16:GLY:O	2:b:17:HIS:ND1	2.44	0.51
4:d:28:ASP:C	4:d:30:LYS:H	2.17	0.51
5:e:79:THR:HB	5:e:121:ASN:HD22	1.73	0.51
7:g:110:ARG:NH1	7:g:122:GLU:OE1	2.42	0.51
22:A:300:A:P	42:U:81:ARG:HH12	2.33	0.51
22:A:2140:G:C4	22:A:2152:G:O6	2.63	0.51
24:C:130:PRO:C	24:C:132:ARG:H	2.17	0.51
30:I:20:SER:HB2	30:I:21:PRO:HD3	1.91	0.51
44:W:17:LEU:HD21	44:W:37:ARG:HH21	1.74	0.51
1:a:494:G:O5'	1:a:494:G:H8	1.94	0.51
1:a:1157:A:H5'	1:a:1158:C:C6	2.45	0.51
2:b:112:ARG:NH1	2:b:116:LEU:HD12	2.26	0.51
12:l:106:VAL:CG1	12:l:116:TYR:HB3	2.41	0.51
17:q:48:GLU:O	17:q:49:ASN:C	2.53	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:C:24:HIS:CG	24:C:79:ARG:HD2	2.45	0.51
25:D:48:ILE:HG23	25:D:84:LEU:HD11	1.92	0.51
30:I:33:ASN:ND2	30:I:35:MET:HB3	2.25	0.51
48:O:43:THR:HG23	48:O:47:TYR:O	2.10	0.51
52:4:22:VAL:HG21	52:4:36:ARG:HH12	1.75	0.51
53:5:12:VAL:HA	53:5:15:VAL:HG22	1.91	0.51
1:a:792:A:H1'	1:a:794:A:N7	2.25	0.51
1:a:996:A:H2'	1:a:997:U:H6	1.74	0.51
1:a:1355:G:H2'	1:a:1356:G:H8	1.76	0.51
3:c:141:MET:HE3	3:c:148:ILE:HG22	1.91	0.51
4:d:56:GLU:OE2	4:d:195:ASN:N	2.34	0.51
22:A:1310:G:N2	22:A:1313:U:C4	2.78	0.51
26:E:4:VAL:HA	26:E:11:ALA:HA	1.91	0.51
30:I:96:LYS:HD2	30:I:133:ARG:HH22	1.75	0.51
33:L:19:LEU:HD13	33:L:31:GLY:O	2.09	0.51
35:N:28:LEU:HD12	35:N:34:ILE:HG23	1.91	0.51
1:a:409:U:C4	1:a:433:G:O6	2.62	0.51
1:a:457:G:H2'	1:a:458:U:H6	1.75	0.51
1:a:1014:A:H4'	19:s:13:HIS:CE1	2.45	0.51
22:A:289:G:H2'	22:A:290:U:C6	2.46	0.51
22:A:298:G:O2'	22:A:322:A:N1	2.40	0.51
22:A:1799:G:O2'	24:C:179:GLU:OE1	2.19	0.51
22:A:2195:U:H2'	22:A:2196:C:H6	1.76	0.51
37:P:48:ALA:HB3	37:P:59:THR:HG22	1.92	0.51
42:U:8:ASP:OD2	42:U:93:ARG:NH1	2.31	0.51
1:a:8:A:N6	4:d:201:GLU:O	2.38	0.51
6:f:8:PHE:HA	6:f:87:SER:HA	1.91	0.51
22:A:851:C:H2'	22:A:852:U:C6	2.46	0.51
22:A:1365:A:OP1	45:X:2:ARG:NH1	2.41	0.51
22:A:2107:G:N1	22:A:2182:U:C2	2.79	0.51
22:A:2247:A:H2'	22:A:2248:C:H6	1.76	0.51
22:A:2554:U:H2'	22:A:2555:U:C6	2.46	0.51
22:A:2822:G:H8	22:A:2822:G:O5'	1.94	0.51
29:H:40:THR:C	29:H:42:LYS:H	2.19	0.51
45:X:6:VAL:HA	45:X:70:LEU:HD21	1.93	0.51
1:a:706:A:H2'	1:a:707:U:H6	1.76	0.51
1:a:996:A:H2'	1:a:997:U:C6	2.45	0.51
9:i:24:ASN:O	9:i:61:ASP:HB3	2.10	0.51
22:A:1900:A:H1'	22:A:1970:A:H2'	1.93	0.51
22:A:2029:G:N1	22:A:2033:A:OP2	2.39	0.51
22:A:2468:A:HO2'	22:A:2469:A:H8	1.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:D:10:GLY:H	25:D:197:THR:HG23	1.74	0.51
29:H:128:HIS:ND1	29:H:144:VAL:O	2.43	0.51
31:J:98:GLU:O	31:J:102:GLU:HG3	2.11	0.51
42:U:28:LEU:HD11	42:U:34:ILE:HD11	1.92	0.51
45:X:11:PRO:HB3	45:X:29:LEU:HD23	1.91	0.51
53:5:33:VAL:HG12	53:5:36:ASP:CG	2.35	0.51
55:9:3:G:H4'	55:9:4:U:OP1	2.10	0.51
1:a:113:G:H2'	1:a:114:U:C6	2.46	0.51
1:a:865:A:H2'	1:a:866:C:C6	2.46	0.51
1:a:1002:G:H2'	1:a:1003:G:C8	2.46	0.51
22:A:629:G:N3	22:A:639:U:O2'	2.43	0.51
22:A:2450:A:OP1	22:A:2497:A:O2'	2.21	0.51
24:C:144:GLU:HB2	24:C:187:CYS:HB3	1.93	0.51
52:4:30:GLU:OE1	52:4:33:HIS:NE2	2.43	0.51
1:a:747:A:H2'	1:a:748:G:C8	2.46	0.51
1:a:1029:U:H1'	1:a:1033:G:N2	2.25	0.51
1:a:1382:C:O2'	7:g:78:ARG:NH1	2.43	0.51
2:b:202:ASN:OD1	2:b:204:ASP:N	2.44	0.51
6:f:5:GLU:HA	6:f:63:ASN:HA	1.91	0.51
16:p:8:ARG:HG3	16:p:17:TYR:HE1	1.76	0.51
22:A:1437:C:O2'	22:A:1516:G:O2'	2.10	0.51
32:K:99:ILE:HD13	32:K:118:LEU:HB2	1.92	0.51
22:A:1176:U:H2'	22:A:1177:G:H8	1.76	0.51
22:A:2202:U:O2'	22:A:2204:G:OP1	2.18	0.51
22:A:2554:U:H2'	22:A:2555:U:H6	1.75	0.51
41:T:44:LYS:HG3	41:T:55:VAL:HG11	1.92	0.51
1:a:67:C:O2'	1:a:171:A:N3	2.37	0.51
1:a:1320:C:H41	19:s:36:ARG:HG2	1.76	0.51
2:b:115:ASP:HA	2:b:118:THR:HG22	1.93	0.51
12:l:41:PRO:HG2	12:l:46:SER:H	1.76	0.51
17:q:20:ILE:HG22	17:q:45:VAL:HB	1.93	0.51
22:A:483:A:H5''	42:U:46:LYS:HD3	1.93	0.51
22:A:1432:G:O2'	22:A:1433:A:H5'	2.11	0.51
22:A:1820:U:H5	24:C:176:ARG:HH12	1.58	0.51
22:A:2250:G:O5'	22:A:2250:G:H8	1.94	0.51
22:A:2273:A:H2'	22:A:2274:A:C8	2.46	0.51
23:B:2:G:C6	23:B:119:A:N1	2.79	0.51
27:F:39:VAL:HG21	27:F:49:LEU:HD13	1.93	0.51
32:K:58:LEU:HD12	32:K:86:LEU:HD13	1.93	0.51
38:Q:25:GLY:O	38:Q:29:ARG:NH1	2.44	0.51
49:1:37:LYS:HB2	49:1:48:TYR:CD2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:79:G:H2'	1:a:80:A:C8	2.46	0.50
1:a:260:G:H2'	1:a:261:U:C6	2.45	0.50
3:c:181:ILE:HG12	3:c:202:PHE:HB2	1.92	0.50
5:e:110:MET:HE2	5:e:126:ALA:HB2	1.93	0.50
17:q:71:SER:O	17:q:71:SER:OG	2.24	0.50
22:A:281:C:H2'	22:A:282:A:C8	2.46	0.50
22:A:693:A:O2'	22:A:1353:A:N3	2.33	0.50
22:A:718:A:H2'	22:A:719:C:O4'	2.11	0.50
22:A:793:A:OP2	22:A:2071:A:O2'	2.29	0.50
22:A:1319:C:O2'	22:A:1320:C:H5'	2.11	0.50
22:A:1715:G:O2'	22:A:1716:U:H6	1.93	0.50
22:A:2123:G:N2	22:A:2175:C:O2	2.44	0.50
22:A:2314:A:H2'	22:A:2315:G:C8	2.46	0.50
31:J:4:PHE:CD2	38:Q:99:VAL:HG11	2.46	0.50
49:1:44:GLN:HG2	49:1:45:HIS:H	1.77	0.50
1:a:61:G:H2'	1:a:62:U:O4'	2.11	0.50
1:a:151:A:H5''	1:a:152:A:OP2	2.11	0.50
2:b:16:GLY:O	2:b:202:ASN:HB2	2.11	0.50
5:e:125:LYS:HG2	5:e:127:TYR:CE1	2.46	0.50
13:m:16:ILE:O	13:m:19:THR:HG22	2.11	0.50
22:A:102:U:O2	46:Y:2:LYS:NZ	2.34	0.50
22:A:239:C:HO2'	22:A:622:G:HO2'	1.59	0.50
22:A:286:U:H2'	22:A:287:G:C8	2.46	0.50
22:A:902:C:H2'	22:A:903:C:C6	2.44	0.50
22:A:2071:A:H2'	22:A:2072:C:C6	2.46	0.50
22:A:2636:C:O2'	25:D:45:TYR:OH	2.27	0.50
26:E:129:PRO:HB3	26:E:159:LEU:HB2	1.93	0.50
4:d:104:MET:HG2	4:d:172:VAL:HG12	1.93	0.50
22:A:13:A:O2'	22:A:15:G:N7	2.44	0.50
22:A:445:C:OP1	38:Q:1:ALA:N	2.28	0.50
22:A:579:G:H2'	22:A:580:U:C6	2.45	0.50
22:A:593:U:H2'	22:A:594:U:C6	2.46	0.50
22:A:1636:U:H2'	22:A:1637:A:C8	2.46	0.50
22:A:1754:A:C8	37:P:93:LYS:HE3	2.47	0.50
22:A:1857:G:N2	22:A:1884:G:H2'	2.26	0.50
22:A:2305:U:N3	27:F:150:GLY:O	2.44	0.50
22:A:2609:U:H5'	22:A:2610:C:OP2	2.11	0.50
24:C:266:ILE:HG21	24:C:269:ARG:HG2	1.92	0.50
35:N:8:ARG:HD2	35:N:43:GLU:HG2	1.94	0.50
47:Z:5:LYS:NZ	47:Z:36:GLU:OE1	2.44	0.50
1:a:135:C:N3	16:p:1:MET:N	2.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:210:C:H5'	1:a:211:G:C4	2.46	0.50
1:a:407:U:H2'	1:a:408:A:H8	1.76	0.50
11:k:85:VAL:HG22	11:k:111:ASP:HB3	1.93	0.50
16:p:34:GLU:OE2	16:p:56:ARG:NH2	2.35	0.50
22:A:585:G:N7	38:Q:5:ARG:NH1	2.60	0.50
22:A:1905:C:HO2'	22:A:1929:G:H1'	1.76	0.50
22:A:2545:G:H2'	22:A:2546:U:O4'	2.11	0.50
24:C:175:LEU:O	24:C:178:GLY:N	2.44	0.50
25:D:45:TYR:OH	25:D:81:GLU:OE2	2.28	0.50
27:F:21:TYR:CD2	27:F:27:VAL:HG12	2.46	0.50
55:9:5:G:C4	55:9:6:A:C8	2.99	0.50
1:a:518:C:H4'	1:a:519:C:O5'	2.10	0.50
1:a:1167:A:H4'	1:a:1168:U:H5	1.76	0.50
1:a:1190:G:H5'	3:c:175:HIS:CE1	2.47	0.50
1:a:1295:U:H2'	1:a:1296:C:C6	2.47	0.50
2:b:103:TRP:HA	2:b:106:VAL:HG22	1.92	0.50
2:b:115:ASP:O	2:b:119:GLN:HG2	2.11	0.50
10:j:12:ALA:HB2	10:j:96:VAL:HG22	1.93	0.50
12:l:23:LEU:HD22	12:l:58:ASN:HD22	1.76	0.50
22:A:1794:A:H2'	22:A:1795:C:C6	2.46	0.50
22:A:2114:A:H5'	22:A:2115:G:OP2	2.12	0.50
24:C:78:GLU:N	24:C:92:LEU:O	2.43	0.50
53:5:67:THR:C	53:5:69:PHE:H	2.19	0.50
1:a:33:A:H2'	1:a:34:C:C6	2.46	0.50
1:a:202:G:H2'	1:a:203:G:O4'	2.12	0.50
1:a:431:A:C4	1:a:432:A:C8	3.00	0.50
1:a:837:U:H2'	1:a:838:G:C8	2.44	0.50
4:d:28:ASP:O	4:d:29:THR:OG1	2.25	0.50
11:k:75:GLU:OE1	11:k:75:GLU:N	2.44	0.50
14:n:89:MET:HE1	14:n:98:LYS:HD3	1.92	0.50
17:q:14:ASP:OD2	17:q:53:GLY:HA2	2.12	0.50
22:A:975:A:H1'	22:A:990:A:C6	2.46	0.50
22:A:1445:G:H2'	22:A:1446:C:H6	1.76	0.50
22:A:2155:U:H3'	22:A:2156:G:H8	1.77	0.50
24:C:145:MET:SD	24:C:152:GLN:NE2	2.84	0.50
1:a:424:G:H2'	1:a:425:G:C8	2.47	0.50
1:a:859:G:OP2	1:a:869:G:N1	2.35	0.50
9:i:54:VAL:HG12	9:i:55:ASP:N	2.26	0.50
23:B:2:G:H2'	23:B:3:C:C6	2.46	0.50
23:B:94:A:OP1	43:V:19:ARG:HD3	2.11	0.50
28:G:1:SER:O	28:G:4:ALA:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:414:C:H2'	22:A:415:A:C8	2.47	0.50
22:A:570:G:H2'	22:A:2030:6MZ:N7	2.26	0.50
22:A:657:U:H2'	22:A:658:U:C6	2.46	0.50
36:O:95:SER:OG	36:O:95:SER:O	2.28	0.50
39:R:4:VAL:HA	39:R:12:HIS:O	2.12	0.50
40:S:1:MET:HG2	40:S:2:GLU:N	2.27	0.50
1:a:408:A:N6	1:a:435:A:C6	2.80	0.50
1:a:1162:C:H2'	1:a:1163:A:C8	2.45	0.50
14:n:7:ALA:HA	14:n:10:VAL:HG12	1.94	0.50
22:A:144:A:H2'	22:A:145:C:C6	2.47	0.50
22:A:396:G:OP2	45:X:9:LYS:NZ	2.44	0.50
22:A:1538:G:O2'	22:A:1539:U:O4'	2.23	0.50
22:A:1577:C:H2'	22:A:1578:U:O4'	2.12	0.50
22:A:1583:A:H4'	22:A:1584:U:H5	1.76	0.50
26:E:148:ILE:HB	26:E:169:VAL:HG12	1.93	0.50
26:E:153:LEU:HD11	26:E:158:PHE:HB2	1.92	0.50
29:H:83:LYS:HG2	29:H:91:PHE:HB2	1.92	0.50
1:a:719:C:O2'	18:r:38:ILE:O	2.28	0.49
1:a:986:U:H2'	1:a:987:G:C8	2.46	0.49
3:c:104:GLU:OE1	3:c:104:GLU:N	2.45	0.49
10:j:80:THR:HG22	10:j:82:LYS:H	1.77	0.49
11:k:78:ILE:HG23	11:k:104:PHE:HE1	1.77	0.49
17:q:56:ASP:N	17:q:56:ASP:OD1	2.45	0.49
22:A:2504:PSU:O5'	22:A:2504:PSU:H6	1.95	0.49
23:B:7:G:O2'	36:O:38:GLN:NE2	2.45	0.49
29:H:110:VAL:HG13	29:H:114:GLU:HB3	1.93	0.49
1:a:468:A:H2'	1:a:469:C:H6	1.77	0.49
1:a:708:C:C2	1:a:709:U:C5	3.01	0.49
1:a:978:A:C4	1:a:1319:A:C2	3.00	0.49
1:a:1347:G:H3'	9:i:109:GLN:O	2.12	0.49
2:b:118:THR:O	2:b:122:ASP:CB	2.60	0.49
3:c:18:ASN:HB3	3:c:39:ARG:HH22	1.77	0.49
6:f:51:ILE:HD11	18:r:65:SER:HB2	1.94	0.49
16:p:78:VAL:O	16:p:78:VAL:HG12	2.13	0.49
21:u:36:PHE:O	21:u:38:GLU:N	2.45	0.49
22:A:49:A:N6	22:A:177:G:C4	2.80	0.49
22:A:65:U:H2'	22:A:66:C:H6	1.76	0.49
22:A:902:C:C2	22:A:903:C:C5	3.00	0.49
22:A:1266:G:O2'	22:A:2012:G:O6	2.29	0.49
22:A:2505:G:H2'	22:A:2576:G:N1	2.27	0.49
23:B:44:G:H5'	23:B:45:A:N7	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:J:109:LEU:HD22	31:J:118:MET:HG3	1.92	0.49
3:c:141:MET:CG	3:c:169:GLU:HG2	2.42	0.49
4:d:109:THR:O	4:d:111:ALA:N	2.44	0.49
5:e:114:LEU:HB3	5:e:119:VAL:CG2	2.42	0.49
22:A:141:G:H3'	22:A:142:A:O4'	2.13	0.49
22:A:1059:G:H2'	30:I:74:PRO:HB3	1.94	0.49
23:B:74:U:O2	43:V:29:ILE:HG12	2.12	0.49
31:J:88:THR:OG1	31:J:91:GLU:OE1	2.21	0.49
40:S:17:VAL:HA	40:S:43:ALA:HB1	1.94	0.49
45:X:2:ARG:O	45:X:11:PRO:HD3	2.12	0.49
1:a:451:A:H5'	16:p:70:ARG:NH2	2.23	0.49
20:t:23:ARG:HB2	20:t:65:LEU:HD21	1.95	0.49
22:A:59:U:O2'	22:A:74:A:OP2	2.30	0.49
22:A:529:A:OP2	31:J:113:PRO:HD3	2.13	0.49
22:A:2353:G:O2'	44:W:29:ALA:O	2.28	0.49
22:A:2360:G:H1'	33:L:60:ARG:HD2	1.94	0.49
22:A:2468:A:O2'	22:A:2469:A:H8	1.95	0.49
22:A:2834:G:H2'	22:A:2879:A:N6	2.26	0.49
43:V:45:ASP:OD2	43:V:45:ASP:N	2.45	0.49
50:2:24:THR:HG23	50:2:27:GLY:H	1.77	0.49
55:9:1:C:H2'	55:9:2:G:H8	1.75	0.49
1:a:111:G:HO2'	1:a:389:A:HO2'	1.60	0.49
1:a:202:G:N2	1:a:216:U:O2	2.46	0.49
1:a:708:C:H2'	1:a:709:U:C6	2.48	0.49
1:a:819:A:H3'	1:a:820:U:H5'	1.95	0.49
1:a:1219:A:H2'	1:a:1220:G:C8	2.48	0.49
3:c:111:ASP:HB2	3:c:114:LEU:HD12	1.95	0.49
5:e:153:ALA:O	5:e:158:LYS:HA	2.11	0.49
22:A:859:G:N2	22:A:917:A:OP2	2.42	0.49
22:A:1442:U:H2'	22:A:1443:U:C6	2.47	0.49
22:A:2576:G:O2'	22:A:2579:C:OP2	2.23	0.49
43:V:30:ILE:HD11	43:V:40:ILE:HD13	1.95	0.49
1:a:280:C:N3	17:q:40:THR:OG1	2.37	0.49
1:a:546:A:O2'	1:a:548:G:O2'	2.27	0.49
1:a:981:U:H2'	1:a:982:U:C5	2.47	0.49
1:a:1327:C:H2'	1:a:1328:C:C6	2.47	0.49
22:A:565:C:P	39:R:80:ARG:H	2.35	0.49
22:A:1060:U:C2	22:A:1088:A:H8	2.31	0.49
22:A:1315:C:O2'	22:A:1392:A:N3	2.44	0.49
22:A:1579:A:H2'	22:A:1580:A:C8	2.47	0.49
22:A:1798:U:OP2	24:C:270:ARG:NH2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:2074:U:H2'	22:A:2075:U:C6	2.47	0.49
22:A:2333:A:H4'	22:A:2334:U:H5''	1.95	0.49
22:A:2514:U:H2'	22:A:2515:C:C6	2.48	0.49
22:A:2547:A:H4'	32:K:29:HIS:CE1	2.39	0.49
25:D:13:ARG:NH2	37:P:74:GLN:OE1	2.40	0.49
27:F:9:ASP:HB2	27:F:10:GLU:OE1	2.13	0.49
1:a:947:G:H2'	1:a:948:C:H6	1.78	0.49
3:c:123:LEU:HD21	3:c:195:ILE:HD13	1.94	0.49
20:t:77:ASN:O	20:t:81:GLN:HG2	2.13	0.49
22:A:156:A:H2'	22:A:157:C:O4'	2.13	0.49
22:A:536:G:H21	31:J:47:HIS:CD2	2.31	0.49
22:A:1672:A:C2	22:A:2582:G:H5'	2.47	0.49
22:A:2864:G:H2'	22:A:2865:U:C6	2.47	0.49
26:E:117:ARG:HA	26:E:185:LYS:HD3	1.95	0.49
1:a:215:C:H2'	1:a:216:U:C6	2.48	0.49
1:a:1058:G:H1	1:a:1199:U:H3	1.60	0.49
1:a:1396:A:H2	5:e:23:THR:HG21	1.77	0.49
3:c:23:ALA:HB1	3:c:27:GLU:HG2	1.94	0.49
20:t:2:ASN:O	20:t:7:LYS:HE2	2.13	0.49
22:A:414:C:H2'	22:A:415:A:H8	1.77	0.49
22:A:465:G:N2	22:A:684:G:H1'	2.28	0.49
22:A:1181:U:H2'	22:A:1182:G:C8	2.48	0.49
22:A:2152:G:H2'	22:A:2153:C:C6	2.48	0.49
30:I:16:MET:HB3	30:I:19:PRO:HD3	1.94	0.49
41:T:53:VAL:HG12	41:T:54:GLU:N	2.28	0.49
1:a:393:A:C2	1:a:394:G:C8	3.00	0.49
1:a:982:U:H4'	1:a:983:A:O5'	2.12	0.49
2:b:74:ALA:HB1	2:b:206:ILE:HG12	1.94	0.49
4:d:100:VAL:O	4:d:104:MET:HB2	2.12	0.49
10:j:39:PRO:HA	10:j:73:LEU:O	2.13	0.49
14:n:64:CYS:SG	14:n:67:THR:OG1	2.62	0.49
22:A:1029:A:N6	22:A:1125:G:O2'	2.46	0.49
22:A:1081:U:H3'	22:A:1082:U:H5	1.78	0.49
22:A:1421:G:C2	22:A:1422:G:C8	3.01	0.49
24:C:140:VAL:HG12	24:C:191:LEU:HD23	1.94	0.49
24:C:153:LEU:HD22	24:C:175:LEU:HD22	1.95	0.49
37:P:50:ARG:NH1	37:P:52:ARG:HG3	2.28	0.49
1:a:225:C:H2'	1:a:226:G:O4'	2.13	0.49
1:a:706:A:H2'	1:a:707:U:C6	2.47	0.49
1:a:1181:G:H1'	1:a:1182:G:C5	2.48	0.49
17:q:6:THR:HG22	17:q:7:LEU:H	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:u:17:ARG:O	21:u:21:SER:HB3	2.13	0.49
22:A:48:G:N1	22:A:177:G:OP2	2.37	0.49
22:A:181:A:H2'	22:A:182:A:C8	2.47	0.49
22:A:1733:G:H2'	22:A:1734:G:C8	2.48	0.49
22:A:2680:U:O2'	22:A:2681:C:H5'	2.12	0.49
1:a:901:A:O2'	1:a:1513:A:OP1	2.19	0.48
1:a:1059:C:O3'	14:n:85:ARG:NH1	2.45	0.48
5:e:61:LYS:O	5:e:65:LYS:HG2	2.12	0.48
8:h:74:ILE:HD12	8:h:128:VAL:HG22	1.94	0.48
10:j:81:GLU:HA	10:j:84:VAL:HG22	1.94	0.48
11:k:107:THR:HG23	11:k:108:ASN:ND2	2.28	0.48
22:A:222:A:N6	22:A:232:G:H1'	2.28	0.48
22:A:871:U:H2'	22:A:872:U:C6	2.48	0.48
22:A:958:U:H2'	23:B:89:U:H1'	1.94	0.48
22:A:1339:G:OP2	41:T:15:HIS:HE1	1.95	0.48
22:A:1871:A:H2'	22:A:1872:A:N3	2.28	0.48
22:A:2015:A:C6	48:0:2:VAL:HG23	2.47	0.48
22:A:2440:C:H5'	22:A:2587:A:H4'	1.94	0.48
1:a:204:G:H2'	1:a:205:A:H8	1.77	0.48
1:a:408:A:Cl'	4:d:153:ARG:HH12	2.26	0.48
1:a:961:U:OP1	1:a:1223:C:O2'	2.24	0.48
1:a:1149:C:H2'	1:a:1150:A:H8	1.78	0.48
1:a:1338:G:H2'	1:a:1339:A:C8	2.48	0.48
2:b:76:SER:OG	2:b:92:ASN:HB2	2.13	0.48
5:e:104:ILE:HA	5:e:121:ASN:O	2.14	0.48
10:j:11:LYS:HA	10:j:18:ILE:HD11	1.94	0.48
22:A:947:A:O2'	22:A:984:A:H2	1.96	0.48
22:A:1079:C:N4	22:A:1088:A:C8	2.81	0.48
22:A:1178:C:H2'	22:A:1179:G:N7	2.27	0.48
24:C:131:MET:HE1	24:C:183:VAL:HG21	1.94	0.48
27:F:110:ILE:HA	27:F:136:ILE:HD12	1.95	0.48
34:M:53:MET:O	34:M:57:VAL:HG12	2.13	0.48
1:a:406:G:C5	1:a:495:A:C5	3.02	0.48
1:a:474:G:H2'	1:a:475:C:H6	1.79	0.48
1:a:812:G:OP1	1:a:902:G:N2	2.46	0.48
1:a:1200:C:H5''	1:a:1201:A:C3'	2.43	0.48
11:k:80:ASN:HB3	11:k:105:ARG:HE	1.78	0.48
22:A:1061:U:H4'	22:A:1070:A:C4	2.48	0.48
22:A:1485:U:H2'	22:A:1486:U:H6	1.76	0.48
28:G:29:ASN:HB2	28:G:78:VAL:O	2.13	0.48
29:H:121:VAL:HG12	29:H:121:VAL:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1026:G:H1	1:a:1035:A:N6	2.10	0.48
2:b:101:THR:HG21	2:b:177:ASN:HD22	1.78	0.48
3:c:65:VAL:HG22	3:c:100:ILE:HG12	1.94	0.48
13:m:7:ASN:C	13:m:9:PRO:HD3	2.39	0.48
22:A:296:U:H2'	22:A:297:G:C8	2.47	0.48
22:A:748:G:C8	40:S:89:ALA:HB1	2.49	0.48
22:A:1183:U:H2'	22:A:1184:U:C6	2.48	0.48
22:A:1316:U:H2'	22:A:1317:G:C8	2.49	0.48
22:A:1703:G:H2'	22:A:1704:C:C6	2.48	0.48
27:F:149:ARG:H	27:F:149:ARG:HD3	1.78	0.48
38:Q:93:ILE:HG21	39:R:4:VAL:HG21	1.94	0.48
2:b:172:ILE:HG23	2:b:182:VAL:HG11	1.96	0.48
2:b:212:TYR:O	2:b:216:VAL:HG12	2.13	0.48
9:i:29:ILE:HA	9:i:64:ILE:O	2.13	0.48
11:k:19:VAL:HG23	11:k:82:GLU:O	2.13	0.48
19:s:61:VAL:HA	19:s:65:MET:SD	2.54	0.48
22:A:163:C:H2'	22:A:164:C:C6	2.49	0.48
22:A:721:A:H2'	22:A:722:A:H8	1.78	0.48
22:A:1019:U:H3	22:A:1142:A:H62	1.61	0.48
22:A:1219:U:H2'	22:A:1220:G:H8	1.78	0.48
22:A:2165:C:N4	22:A:2167:U:O4	2.47	0.48
22:A:2285:C:OP2	49:1:5:ARG:HD2	2.14	0.48
22:A:2638:G:HO2'	22:A:2639:A:H8	1.61	0.48
23:B:111:U:H2'	23:B:112:G:C8	2.46	0.48
26:E:182:ALA:HB2	33:L:3:LEU:HD22	1.94	0.48
27:F:140:ILE:HG23	27:F:144:LYS:HB2	1.94	0.48
39:R:1:MET:HA	39:R:42:ALA:O	2.14	0.48
41:T:47:VAL:HG13	41:T:55:VAL:HG21	1.94	0.48
45:X:26:ARG:NH2	45:X:27:ARG:O	2.44	0.48
53:5:124:ASP:OD1	53:5:125:ARG:N	2.47	0.48
54:6:58:ASP:O	54:6:62:LYS:HG2	2.13	0.48
1:a:63:C:H4'	1:a:380:G:N2	2.29	0.48
1:a:215:C:H1'	1:a:465:A:H62	1.79	0.48
1:a:709:U:C2	1:a:710:G:C8	3.01	0.48
1:a:1126:U:H1'	1:a:1281:C:C2	2.48	0.48
1:a:1518:MA6:H93	1:a:1519:MA6:N6	2.28	0.48
12:l:30:ARG:HG2	12:l:57:THR:HG23	1.95	0.48
22:A:63:A:H61	22:A:91:A:N6	2.11	0.48
22:A:303:G:H2'	22:A:304:U:C6	2.49	0.48
22:A:394:C:H2'	22:A:395:U:O4'	2.12	0.48
22:A:764:A:H5''	24:C:208:GLY:HA3	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:2575:C:H5'	25:D:149:ASN:HD22	1.77	0.48
26:E:119:ILE:HB	26:E:187:VAL:HG22	1.96	0.48
1:a:246:A:C2	1:a:282:A:C5	3.02	0.48
1:a:252:U:C2	1:a:253:A:N7	2.82	0.48
1:a:371:A:H2'	1:a:372:C:O4'	2.13	0.48
1:a:409:U:H5''	4:d:24:VAL:CG2	2.44	0.48
1:a:735:C:H5'	18:r:59:LYS:HD3	1.95	0.48
1:a:1030:U:H5''	1:a:1031:C:C6	2.48	0.48
9:i:57:VAL:HG23	9:i:58:GLU:H	1.78	0.48
22:A:631:A:H5'	33:L:64:PHE:HE2	1.79	0.48
22:A:2287:A:N7	22:A:2289:G:C8	2.81	0.48
23:B:119:A:H2'	23:B:120:A:C8	2.49	0.48
24:C:7:PRO:CB	24:C:13:ARG:HE	2.27	0.48
27:F:45:ASP:OD1	27:F:48:LEU:HB2	2.13	0.48
27:F:162:ASP:OD1	27:F:163:GLU:N	2.47	0.48
32:K:65:THR:HG22	32:K:67:LYS:H	1.77	0.48
4:d:176:LYS:O	4:d:176:LYS:HD3	2.13	0.48
8:h:39:LEU:HB3	8:h:45:ILE:HG12	1.96	0.48
9:i:49:GLN:C	9:i:51:LEU:H	2.22	0.48
11:k:71:ASP:OD1	11:k:72:ALA:N	2.46	0.48
22:A:592:A:C2	51:3:3:ILE:HD11	2.48	0.48
22:A:849:A:H2'	22:A:850:U:C6	2.49	0.48
22:A:1262:A:OP1	40:S:99:ARG:NH1	2.46	0.48
22:A:2320:U:O2	22:A:2333:A:N6	2.46	0.48
22:A:2661:G:H2'	22:A:2662:A:O4'	2.13	0.48
22:A:2870:C:H2'	22:A:2871:U:O4'	2.14	0.48
1:a:539:A:H2'	1:a:540:G:H8	1.79	0.48
1:a:686:U:O4	1:a:703:G:H2'	2.14	0.48
1:a:960:U:H4'	1:a:961:U:O5'	2.11	0.48
1:a:1313:U:H2'	1:a:1314:C:C6	2.49	0.48
2:b:33:ALA:HB3	2:b:37:VAL:HG12	1.96	0.48
2:b:69:VAL:HG12	2:b:91:VAL:HG22	1.96	0.48
16:p:8:ARG:HA	16:p:17:TYR:HD1	1.78	0.48
21:u:11:PHE:CG	21:u:12:ASP:N	2.82	0.48
22:A:1447:C:O2'	22:A:1544:A:N3	2.46	0.48
22:A:2186:G:H2'	22:A:2187:U:H6	1.78	0.48
22:A:2694:G:H2'	22:A:2695:U:O4'	2.14	0.48
25:D:133:THR:O	25:D:134:HIS:HB2	2.14	0.48
30:I:32:VAL:HG11	30:I:60:VAL:HG21	1.96	0.48
43:V:9:ARG:CG	43:V:41:GLU:HB3	2.44	0.48
1:a:86:G:H1'	1:a:87:C:C5	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:107:G:N7	20:t:9:ARG:NH2	2.62	0.48
1:a:328:C:H4'	1:a:329:A:H5''	1.95	0.48
1:a:384:G:H2'	1:a:385:C:C6	2.49	0.48
1:a:632:U:H3'	1:a:633:G:H5'	1.96	0.48
1:a:796:C:H4'	11:k:126:ARG:NH2	2.29	0.48
1:a:864:A:H5'	5:e:89:THR:O	2.14	0.48
1:a:1062:U:H2'	1:a:1063:C:C6	2.49	0.48
1:a:1135:U:H4'	1:a:1136:C:H5	1.78	0.48
2:b:34:ARG:C	2:b:36:LYS:H	2.22	0.48
2:b:198:VAL:HG12	2:b:200:PRO:HD3	1.95	0.48
4:d:171:GLU:HB2	4:d:182:LYS:NZ	2.29	0.48
22:A:27:G:O2'	22:A:28:A:OP2	2.31	0.48
22:A:281:C:H2'	22:A:282:A:H8	1.79	0.48
22:A:994:C:O2'	22:A:996:A:OP1	2.31	0.48
22:A:1171:G:N2	22:A:1178:C:C4	2.81	0.48
22:A:1968:G:O2'	22:A:1969:A:O4'	2.26	0.48
22:A:2164:C:H41	22:A:2171:A:H61	1.62	0.48
22:A:2837:A:H2'	22:A:2838:G:H8	1.78	0.48
32:K:107:LEU:O	32:K:109:SER:N	2.47	0.48
39:R:4:VAL:CG1	39:R:40:MET:HB3	2.44	0.48
1:a:474:G:H2'	1:a:475:C:C6	2.49	0.47
8:h:45:ILE:HG22	8:h:46:GLU:N	2.29	0.47
9:i:39:GLY:HA2	9:i:44:ARG:HG3	1.96	0.47
22:A:2455:G:H2'	22:A:2456:C:C6	2.49	0.47
22:A:2852:G:H5'	35:N:64:ARG:NH2	2.29	0.47
29:H:21:VAL:CG2	29:H:26:ALA:HB2	2.44	0.47
31:J:51:GLY:C	31:J:121:LYS:HZ2	2.22	0.47
37:P:19:PHE:HD2	37:P:49:ILE:HD11	1.79	0.47
53:5:29:ASP:OD2	53:5:32:GLY:N	2.47	0.47
53:5:78:GLY:N	53:5:79:PRO:HD2	2.29	0.47
1:a:76:G:H1	1:a:93:U:H3	1.62	0.47
1:a:501:C:H2'	1:a:502:A:C8	2.49	0.47
1:a:567:G:H2'	1:a:568:G:O4'	2.15	0.47
1:a:784:A:H2'	1:a:785:G:C8	2.48	0.47
1:a:820:U:H4'	1:a:821:G:OP2	2.14	0.47
2:b:41:ASN:HD22	2:b:44:LYS:CG	2.26	0.47
4:d:117:VAL:HG13	4:d:122:ILE:HB	1.96	0.47
9:i:129:ARG:NH2	55:9:35:G:OP2	2.37	0.47
22:A:806:C:O2	22:A:2444:G:O2'	2.32	0.47
22:A:833:A:H2'	22:A:834:G:C8	2.49	0.47
22:A:1092:C:H3'	22:A:1093:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:1106:G:C2	22:A:1107:G:C8	3.02	0.47
22:A:1440:U:H2'	22:A:1441:G:C8	2.49	0.47
22:A:2674:G:H2'	22:A:2675:A:C8	2.49	0.47
22:A:2804:U:H2'	22:A:2805:C:H6	1.79	0.47
29:H:3:VAL:HG23	29:H:38:PRO:HA	1.96	0.47
54:6:48:GLN:HA	54:6:51:VAL:HB	1.95	0.47
1:a:320:A:H2'	1:a:321:A:O4'	2.14	0.47
1:a:406:G:H5'	4:d:4:LEU:HD11	1.97	0.47
4:d:151:GLN:HG3	4:d:153:ARG:HB2	1.95	0.47
22:A:1153:C:OP1	38:Q:91:ARG:NH2	2.31	0.47
22:A:1794:A:H2'	22:A:1795:C:H6	1.80	0.47
22:A:2537:U:H2'	22:A:2538:C:C6	2.49	0.47
23:B:37:C:O2	36:O:100:HIS:NE2	2.36	0.47
27:F:28:PRO:HB2	27:F:168:LEU:HD13	1.97	0.47
28:G:136:ASP:HB3	28:G:139:VAL:CG1	2.41	0.47
33:L:122:VAL:HG12	33:L:142:ILE:HG12	1.95	0.47
1:a:132:C:O3'	20:t:67:HIS:NE2	2.48	0.47
1:a:432:A:C4	1:a:433:G:C8	3.02	0.47
1:a:458:U:C2	1:a:459:A:C8	3.02	0.47
1:a:1149:C:P	9:i:10:ARG:HH21	2.35	0.47
1:a:1294:G:H2'	1:a:1295:U:C6	2.50	0.47
1:a:1314:C:H2'	1:a:1315:U:H6	1.80	0.47
4:d:104:MET:HG2	4:d:172:VAL:CG1	2.45	0.47
9:i:96:GLU:N	9:i:96:GLU:OE1	2.47	0.47
22:A:71:A:H4'	22:A:72:U:H5''	1.95	0.47
22:A:511:U:H2'	22:A:512:G:H5'	1.95	0.47
22:A:1055:G:H2'	22:A:1056:G:C8	2.49	0.47
22:A:1107:G:H2'	22:A:1108:U:H6	1.78	0.47
22:A:1733:G:N1	22:A:1734:G:C6	2.82	0.47
22:A:2104:C:N4	22:A:2105:U:O4	2.48	0.47
40:S:12:SER:HB2	40:S:42:LYS:NZ	2.30	0.47
46:Y:46:VAL:O	46:Y:50:VAL:HG23	2.14	0.47
53:5:64:VAL:HA	53:5:67:THR:OG1	2.14	0.47
1:a:219:U:H4'	1:a:381:C:OP2	2.14	0.47
1:a:263:A:H2'	1:a:264:C:C6	2.49	0.47
1:a:390:U:H2'	1:a:391:G:C8	2.49	0.47
1:a:411:A:C6	1:a:429:U:C4	3.03	0.47
1:a:1497:G:O2'	1:a:1518:MA6:H92	2.14	0.47
20:t:14:GLU:O	20:t:18:LYS:HG3	2.15	0.47
22:A:56:A:H2'	22:A:57:C:C6	2.49	0.47
22:A:271:G:C6	22:A:367:G:N1	2.82	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:703:U:H2'	22:A:704:G:O4'	2.13	0.47
22:A:788:A:OP1	22:A:791:C:N4	2.37	0.47
22:A:1791:A:N6	22:A:1828:G:O2'	2.42	0.47
22:A:2005:A:O2'	22:A:2049:G:OP1	2.25	0.47
23:B:3:C:O2'	23:B:4:C:O5'	2.32	0.47
35:N:103:ARG:HD2	35:N:106:ASP:OD1	2.14	0.47
1:a:57:G:H2'	1:a:58:C:C6	2.48	0.47
1:a:310:G:H5''	16:p:31:ARG:HB2	1.96	0.47
1:a:433:G:C5	1:a:434:U:C5	3.02	0.47
1:a:522:C:H1'	1:a:536:C:H5''	1.97	0.47
1:a:624:C:H4'	16:p:10:GLY:HA2	1.97	0.47
13:m:77:LYS:NZ	13:m:81:ASP:OD2	2.27	0.47
22:A:364:C:H2'	22:A:365:U:C6	2.49	0.47
22:A:1746:A:H2'	22:A:1747:U:C6	2.49	0.47
22:A:2808:G:H4'	22:A:2809:A:H5'	1.96	0.47
32:K:65:THR:HG22	32:K:67:LYS:N	2.30	0.47
36:O:108:ASP:O	36:O:112:GLU:HG3	2.15	0.47
40:S:62:ASP:N	40:S:62:ASP:OD1	2.47	0.47
55:9:2:G:O2'	55:9:3:G:H8	1.96	0.47
1:a:19:A:O2'	1:a:572:A:N1	2.36	0.47
1:a:323:U:OP1	20:t:24:ARG:NH2	2.40	0.47
1:a:433:G:H2'	1:a:434:U:H6	1.79	0.47
1:a:858:G:N2	1:a:859:G:N7	2.63	0.47
1:a:1014:A:C2	1:a:1219:A:H1'	2.50	0.47
1:a:1371:G:H2'	1:a:1372:U:H6	1.79	0.47
2:b:120:SER:OG	2:b:136:ARG:HD3	2.15	0.47
4:d:102:TYR:CZ	4:d:110:ARG:HG3	2.49	0.47
7:g:94:ARG:HD3	7:g:98:LEU:HG	1.97	0.47
14:n:54:ASP:HA	14:n:59:ARG:HD3	1.95	0.47
19:s:25:GLY:O	19:s:27:LYS:HG2	2.13	0.47
19:s:51:HIS:CD2	19:s:53:GLY:H	2.33	0.47
22:A:286:U:H2'	22:A:287:G:H8	1.79	0.47
22:A:404:A:H1'	22:A:406:G:C4	2.49	0.47
22:A:1405:U:H2'	22:A:1406:U:C6	2.50	0.47
22:A:1629:U:C4	22:A:1630:A:N7	2.82	0.47
22:A:1979:U:O2'	22:A:1980:G:H5'	2.14	0.47
22:A:2024:G:C4	22:A:2040:G:N2	2.83	0.47
22:A:2900:A:H2'	22:A:2901:C:C6	2.50	0.47
24:C:131:MET:O	24:C:171:VAL:HG21	2.15	0.47
24:C:203:VAL:O	24:C:205:GLY:N	2.46	0.47
26:E:123:LYS:HE3	26:E:123:LYS:HB3	1.73	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:P:81:ASP:OD2	37:P:82:SER:OG	2.22	0.47
39:R:48:LYS:HE2	39:R:48:LYS:HB2	1.56	0.47
46:Y:24:GLU:O	46:Y:28:LEU:HD12	2.15	0.47
52:4:13:ASN:HB3	52:4:28:SER:OG	2.14	0.47
1:a:264:C:H2'	1:a:265:G:O4'	2.15	0.47
1:a:379:C:C2	1:a:380:G:N1	2.82	0.47
1:a:1218:C:H2'	1:a:1219:A:H8	1.72	0.47
2:b:12:GLY:HA2	2:b:207:ARG:NH1	2.29	0.47
4:d:27:ILE:HD12	4:d:28:ASP:H	1.80	0.47
5:e:51:LYS:HE3	5:e:51:LYS:HB2	1.70	0.47
6:f:46:GLN:HA	6:f:56:LYS:HA	1.96	0.47
9:i:8:THR:HG23	9:i:9:GLY:N	2.29	0.47
9:i:47:VAL:HG13	9:i:48:ARG:H	1.80	0.47
22:A:245:G:O2'	22:A:384:A:N1	2.37	0.47
22:A:826:U:O2'	33:L:53:GLY:HA3	2.15	0.47
22:A:1098:A:C2	22:A:1099:G:H1'	2.50	0.47
22:A:1447:C:H2'	22:A:1448:G:C8	2.50	0.47
22:A:1649:G:O2'	35:N:106:ASP:OD2	2.19	0.47
22:A:2723:C:H2'	22:A:2724:U:O4'	2.15	0.47
23:B:101:A:H2'	23:B:102:G:O4'	2.15	0.47
24:C:65:ASP:OD2	24:C:101:ARG:NH1	2.41	0.47
54:6:44:PHE:HB3	54:6:47:LYS:NZ	2.30	0.47
1:a:908:A:H2'	1:a:909:A:C8	2.49	0.47
1:a:1355:G:H2'	1:a:1356:G:C8	2.50	0.47
14:n:55:SER:O	14:n:55:SER:OG	2.33	0.47
22:A:397:U:H5''	45:X:31:ASN:HB2	1.97	0.47
22:A:1230:A:H2'	22:A:1231:U:O4'	2.15	0.47
22:A:1509:A:H2'	22:A:1510:G:C8	2.50	0.47
22:A:1858:A:C2	22:A:1859:U:H1'	2.50	0.47
22:A:2145:C:H5''	22:A:2146:C:OP2	2.15	0.47
29:H:69:ALA:O	29:H:108:VAL:HG13	2.15	0.47
54:6:41:HIS:HB3	54:6:43:PHE:CD1	2.50	0.47
1:a:113:G:H1'	1:a:354:G:H5'	1.96	0.47
1:a:458:U:O4	1:a:459:A:N6	2.48	0.47
14:n:33:VAL:HA	14:n:41:ARG:HH12	1.79	0.47
22:A:522:A:H2'	22:A:523:C:C6	2.50	0.47
22:A:1075:C:H5''	22:A:1076:C:OP2	2.15	0.47
22:A:1442:U:H2'	22:A:1443:U:H6	1.80	0.47
22:A:1445:G:H2'	22:A:1446:C:C6	2.50	0.47
22:A:2033:A:O2'	22:A:2035:G:OP2	2.25	0.47
22:A:2077:A:H2'	22:A:2078:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:2329:U:H2'	22:A:2330:G:C8	2.50	0.47
27:F:14:LYS:HA	27:F:17:THR:HG22	1.97	0.47
28:G:101:VAL:HG12	28:G:115:GLN:HA	1.97	0.47
29:H:78:VAL:HB	29:H:144:VAL:HG22	1.97	0.47
29:H:95:GLY:HA2	29:H:121:VAL:HG13	1.97	0.47
1:a:407:U:H4'	4:d:112:GLU:HB3	1.96	0.46
1:a:458:U:O4	1:a:474:G:O6	2.33	0.46
1:a:608:A:H2'	1:a:609:A:O4'	2.15	0.46
1:a:718:A:C8	11:k:117:HIS:CG	3.03	0.46
1:a:966:2MG:HM21	9:i:128:LYS:HE2	1.97	0.46
2:b:116:LEU:HD22	2:b:140:LEU:HB2	1.98	0.46
2:b:118:THR:HG23	2:b:119:GLN:OE1	2.15	0.46
6:f:72:ASP:HA	6:f:75:GLU:HG2	1.97	0.46
15:o:39:GLN:HE22	22:A:716:A:H4'	1.79	0.46
19:s:8:PRO:HD3	54:6:64:PHE:CE1	2.50	0.46
22:A:633:A:OP1	33:L:71:ALA:HB2	2.14	0.46
22:A:686:U:H2'	22:A:788:A:N1	2.30	0.46
22:A:843:G:H2'	22:A:844:A:C8	2.50	0.46
22:A:1103:A:H2'	22:A:1103:A:N3	2.30	0.46
22:A:1534:U:O2	22:A:1538:G:N1	2.47	0.46
22:A:1871:A:H2'	22:A:1872:A:C4	2.50	0.46
22:A:2006:C:O2'	22:A:2823:A:N3	2.48	0.46
22:A:2097:A:H2'	22:A:2098:U:O4'	2.15	0.46
23:B:13:G:N7	23:B:70:C:H4'	2.29	0.46
23:B:94:A:H2'	23:B:95:U:O4'	2.15	0.46
33:L:62:PRO:HD3	51:3:26:ALA:HB2	1.96	0.46
41:T:89:GLU:N	41:T:89:GLU:OE1	2.48	0.46
45:X:17:ARG:HD2	45:X:21:LEU:HD23	1.96	0.46
1:a:150:U:H2'	1:a:151:A:C8	2.51	0.46
1:a:193:C:H2'	1:a:194:C:C6	2.50	0.46
1:a:235:C:H2'	1:a:236:A:C8	2.50	0.46
1:a:464:U:H3	1:a:467:U:P	2.38	0.46
1:a:627:G:H2'	1:a:628:G:O4'	2.15	0.46
1:a:939:G:H2'	1:a:940:C:C6	2.50	0.46
22:A:834:G:H1'	22:A:2358:A:N3	2.30	0.46
22:A:1473:G:C6	22:A:1519:G:C6	3.03	0.46
22:A:1818:U:O2'	22:A:1819:A:OP2	2.34	0.46
22:A:1857:G:H22	22:A:1884:G:H2'	1.80	0.46
22:A:2528:U:O2'	22:A:2530:A:OP1	2.31	0.46
22:A:2637:U:C2	22:A:2782:G:N2	2.83	0.46
22:A:2667:C:O2	28:G:108:PHE:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:E:48:THR:HG23	26:E:86:ALA:HB3	1.96	0.46
29:H:117:LEU:HD23	29:H:130:VAL:HG23	1.96	0.46
1:a:1225:A:H2'	1:a:1225:A:N3	2.30	0.46
1:a:1342:C:H2'	1:a:1343:G:H8	1.81	0.46
1:a:1534:A:H4'	1:a:1535:C:OP1	2.16	0.46
6:f:25:TYR:HB3	6:f:74:LEU:HD11	1.96	0.46
16:p:5:ARG:NH2	16:p:24:SER:HA	2.31	0.46
22:A:248:G:O2'	22:A:2432:A:OP1	2.31	0.46
22:A:1068:G:H21	22:A:1096:A:H5'	1.80	0.46
22:A:1196:C:H2'	22:A:1197:G:O4'	2.15	0.46
22:A:1523:U:H5''	22:A:1524:G:H8	1.80	0.46
22:A:1651:G:OP1	35:N:40:LYS:HE3	2.16	0.46
22:A:1727:C:H2'	22:A:1728:C:O4'	2.14	0.46
22:A:1913:A:H4'	22:A:1914:C:O5'	2.15	0.46
22:A:2164:C:H3'	22:A:2165:C:C5	2.50	0.46
22:A:2409:G:C6	22:A:2410:G:C5	3.03	0.46
22:A:2784:U:O2'	25:D:43:ASP:OD1	2.20	0.46
23:B:12:C:C5	44:W:70:PRO:HB3	2.51	0.46
26:E:22:ASP:OD1	26:E:22:ASP:N	2.47	0.46
26:E:131:THR:HB	26:E:164:LEU:HD11	1.98	0.46
28:G:75:VAL:HA	28:G:78:VAL:HG12	1.96	0.46
33:L:110:VAL:HB	33:L:127:VAL:HG12	1.98	0.46
34:M:57:VAL:HG21	34:M:105:MET:SD	2.55	0.46
38:Q:108:LEU:HD23	39:R:48:LYS:HD3	1.96	0.46
43:V:75:GLN:HB2	43:V:92:VAL:HG23	1.97	0.46
49:1:38:PHE:HA	49:1:45:HIS:HA	1.97	0.46
1:a:517:G:H1	1:a:533:A:P	2.38	0.46
1:a:674:G:H2'	1:a:675:A:C8	2.48	0.46
1:a:676:A:H2'	1:a:677:U:C6	2.50	0.46
1:a:1029:U:H1'	1:a:1033:G:H22	1.80	0.46
1:a:1117:A:O3'	9:i:105:ARG:HG2	2.15	0.46
3:c:158:GLY:HA2	3:c:192:TYR:CD2	2.50	0.46
4:d:147:LYS:HE3	4:d:147:LYS:HB2	1.80	0.46
4:d:196:GLU:HA	4:d:199:ILE:HG12	1.97	0.46
6:f:51:ILE:HD13	6:f:86:ARG:HE	1.79	0.46
22:A:283:G:H2'	22:A:284:U:O4'	2.15	0.46
22:A:1270:C:H5''	22:A:1271:G:O5'	2.16	0.46
22:A:1366:A:H2'	22:A:1367:A:O4'	2.14	0.46
22:A:2060:A:O2'	22:A:2061:G:OP2	2.32	0.46
22:A:2328:A:H2'	22:A:2329:U:H6	1.77	0.46
24:C:16:VAL:HB	24:C:203:VAL:HG22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:M:26:VAL:HG13	34:M:104:GLU:CD	2.40	0.46
42:U:51:LEU:H	42:U:51:LEU:HD12	1.81	0.46
55:9:2:G:O2'	55:9:3:G:O5'	2.29	0.46
1:a:545:C:H2'	1:a:546:A:O4'	2.15	0.46
1:a:1114:C:H1'	14:n:100:SER:OG	2.16	0.46
1:a:1252:A:H2'	1:a:1253:G:O4'	2.15	0.46
6:f:98:GLU:CG	6:f:99:ALA:H	2.27	0.46
22:A:636:G:N1	33:L:76:GLU:OE1	2.40	0.46
22:A:1720:U:H2'	22:A:1721:G:O4'	2.16	0.46
22:A:2130:U:C2	22:A:2131:U:H5	2.32	0.46
22:A:2153:C:C4	22:A:2154:A:C6	3.03	0.46
22:A:2800:A:H3'	22:A:2801:G:H5'	1.97	0.46
22:A:2808:G:O2'	22:A:2809:A:P	2.73	0.46
23:B:30:C:H2'	23:B:31:C:H5'	1.96	0.46
28:G:140:ILE:HG13	28:G:141:GLY:N	2.31	0.46
29:H:68:ARG:O	29:H:72:ILE:HG12	2.15	0.46
34:M:4:PRO:HB2	34:M:7:THR:HG22	1.97	0.46
51:3:48:MET:HE3	51:3:48:MET:HB3	1.88	0.46
53:5:19:ALA:HB2	53:5:69:PHE:HE2	1.81	0.46
53:5:88:HIS:HB3	53:5:89:PRO:HD3	1.98	0.46
1:a:412:A:N3	1:a:414:A:H1'	2.31	0.46
1:a:991:U:O4	1:a:1212:U:O2'	2.26	0.46
1:a:1060:U:H2'	1:a:1061:G:H8	1.81	0.46
1:a:1064:G:O2'	1:a:1190:G:N2	2.49	0.46
6:f:43:GLY:HA2	6:f:58:HIS:CE1	2.50	0.46
6:f:45:ARG:HB2	6:f:59:TYR:CE1	2.51	0.46
13:m:77:LYS:HA	13:m:80:MET:HG2	1.96	0.46
22:A:242:G:O2'	22:A:254:G:O6	2.34	0.46
22:A:1754:A:N7	37:P:93:LYS:HE3	2.30	0.46
22:A:2017:U:O2	48:O:6:LYS:HB3	2.15	0.46
23:B:52:A:H62	36:O:33:ARG:HE	1.64	0.46
23:B:120:A:H8	23:B:120:A:OP2	1.97	0.46
32:K:102:PRO:HB3	32:K:121:GLU:HG3	1.97	0.46
40:S:69:LEU:HG	40:S:107:VAL:CG1	2.46	0.46
46:Y:28:LEU:HA	46:Y:28:LEU:HD23	1.63	0.46
1:a:406:G:H2'	1:a:407:U:H5'	1.97	0.46
1:a:763:G:H2'	1:a:764:C:C6	2.50	0.46
1:a:972:C:OP2	10:j:59:LYS:NZ	2.43	0.46
1:a:1011:C:H2'	1:a:1012:A:H8	1.81	0.46
1:a:1256:A:H1'	1:a:1258:G:C5	2.50	0.46
3:c:10:ARG:NH2	3:c:174:LEU:O	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:c:71:ARG:O	3:c:75:VAL:HG23	2.15	0.46
4:d:88:ASN:O	4:d:92:LEU:HG	2.15	0.46
8:h:110:MET:HB2	8:h:114:ALA:HB3	1.97	0.46
9:i:20:ILE:HG12	9:i:62:LEU:HD22	1.98	0.46
12:l:48:LEU:HD23	12:l:48:LEU:HA	1.81	0.46
12:l:48:LEU:O	12:l:50:LYS:NZ	2.48	0.46
22:A:44:A:H2'	22:A:45:G:O4'	2.16	0.46
22:A:353:C:H2'	22:A:354:A:C8	2.51	0.46
22:A:1058:U:N3	30:I:116:MET:HE1	2.31	0.46
22:A:1900:A:O2'	22:A:1901:A:OP2	2.29	0.46
22:A:1993:U:H4'	25:D:133:THR:OG1	2.16	0.46
22:A:2419:U:H2'	22:A:2420:C:C6	2.51	0.46
30:I:96:LYS:HZ2	30:I:133:ARG:NH2	2.13	0.46
30:I:100:ILE:HB	30:I:139:VAL:HG12	1.97	0.46
36:O:36:TYR:CD1	36:O:52:SER:HB2	2.50	0.46
39:R:26:ASP:N	39:R:26:ASP:OD1	2.48	0.46
45:X:51:SER:O	45:X:55:MET:HG3	2.15	0.46
53:5:23:LEU:HD13	53:5:23:LEU:HA	1.80	0.46
1:a:212:G:C4	1:a:213:G:C8	3.03	0.46
5:e:65:LYS:HA	5:e:68:ARG:HG2	1.98	0.46
10:j:7:ARG:NE	10:j:75:ASP:OD2	2.48	0.46
11:k:51:PHE:O	11:k:56:LYS:HB3	2.16	0.46
12:l:79:ILE:HG22	12:l:103:CYS:HB2	1.97	0.46
22:A:52:A:H2'	22:A:53:A:C8	2.51	0.46
22:A:1083:U:O2	22:A:1085:A:H5''	2.16	0.46
22:A:1092:C:H2'	22:A:1093:G:O4'	2.15	0.46
22:A:2687:U:H2'	22:A:2688:G:O4'	2.15	0.46
40:S:17:VAL:HG12	40:S:76:VAL:HG21	1.97	0.46
1:a:40:C:H2'	1:a:41:G:O4'	2.16	0.46
1:a:236:A:H2'	1:a:237:G:C8	2.51	0.46
1:a:392:C:H2'	1:a:393:A:O4'	2.16	0.46
1:a:426:U:H2'	1:a:427:U:C6	2.50	0.46
2:b:30:ILE:HD12	2:b:38:HIS:ND1	2.30	0.46
5:e:159:SER:O	5:e:162:GLU:N	2.49	0.46
11:k:108:ASN:HB2	21:u:5:VAL:O	2.16	0.46
17:q:14:ASP:HA	17:q:20:ILE:HD12	1.98	0.46
22:A:996:A:H1'	39:R:9:GLY:O	2.16	0.46
22:A:2467:C:H2'	22:A:2468:A:O4'	2.16	0.46
24:C:143:VAL:HG21	24:C:161:VAL:CG2	2.46	0.46
33:L:63:LYS:HA	51:3:12:ARG:HG2	1.98	0.46
41:T:10:VAL:HG12	41:T:11:LEU:HD23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:433:G:C5	1:a:434:U:C4	3.04	0.46
1:a:581:G:N1	1:a:759:A:OP2	2.31	0.46
1:a:1287:A:H2'	1:a:1288:A:C8	2.51	0.46
2:b:91:VAL:HG23	2:b:91:VAL:O	2.16	0.46
10:j:5:ARG:HG3	10:j:79:PRO:HD3	1.98	0.46
11:k:80:ASN:CB	11:k:105:ARG:HE	2.29	0.46
20:t:78:LEU:O	20:t:82:ILE:HG13	2.16	0.46
22:A:117:G:OP2	22:A:119:A:O2'	2.18	0.46
22:A:742:A:H2'	22:A:743:A:C8	2.51	0.46
22:A:1081:U:H3'	22:A:1082:U:C5	2.51	0.46
22:A:2147:A:H2'	22:A:2148:G:O4'	2.16	0.46
22:A:2749:A:H5''	28:G:1:SER:HB2	1.98	0.46
22:A:2808:G:HO2'	22:A:2809:A:P	2.38	0.46
29:H:57:LYS:O	29:H:61:VAL:HG23	2.15	0.46
1:a:979:C:C6	1:a:1318:A:N1	2.84	0.45
1:a:983:A:H5''	1:a:984:C:OP2	2.15	0.45
9:i:8:THR:HG22	9:i:84:ARG:HD2	1.98	0.45
11:k:33:ILE:HG12	11:k:69:CYS:SG	2.56	0.45
16:p:53:ASP:OD2	16:p:53:ASP:N	2.48	0.45
22:A:64:A:H2'	22:A:65:U:C6	2.51	0.45
22:A:669:G:C2	22:A:801:G:C6	3.04	0.45
22:A:704:G:O2'	22:A:726:G:N2	2.49	0.45
22:A:745:IMG:O2'	22:A:748:G:H1'	2.15	0.45
22:A:811:U:H3'	33:L:22:GLY:H	1.81	0.45
22:A:861:A:N3	23:B:79:G:O2'	2.48	0.45
22:A:2100:G:C6	22:A:2101:A:C6	3.05	0.45
22:A:2544:G:H5'	22:A:2645:G:C2	2.51	0.45
22:A:2595:G:N2	22:A:2598:A:OP2	2.38	0.45
24:C:259:ASN:C	24:C:261:ARG:H	2.24	0.45
48:0:47:TYR:HA	48:0:51:ARG:O	2.17	0.45
1:a:87:C:H2'	1:a:88:U:C6	2.52	0.45
1:a:881:G:OP2	12:l:5:GLN:NE2	2.32	0.45
5:e:98:ALA:HB2	5:e:123:LEU:HG	1.98	0.45
8:h:95:MET:HE2	8:h:98:LEU:HB2	1.97	0.45
10:j:7:ARG:HD2	10:j:73:LEU:HD21	1.98	0.45
13:m:33:LEU:HD13	13:m:39:ALA:O	2.16	0.45
22:A:1549:A:H2'	22:A:1550:C:C6	2.51	0.45
22:A:2152:G:C6	22:A:2153:C:C4	3.04	0.45
22:A:2589:A:H2'	22:A:2590:A:C8	2.50	0.45
23:B:5:U:H2'	23:B:6:G:H8	1.81	0.45
27:F:105:ILE:C	27:F:108:PRO:HD2	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:M:47:GLU:OE1	34:M:51:ARG:NE	2.49	0.45
35:N:35:LYS:HB2	35:N:112:TYR:CE1	2.52	0.45
53:5:59:LEU:HB3	53:5:62:ARG:HB2	1.98	0.45
1:a:143:A:H2	1:a:220:G:H1	1.63	0.45
1:a:437:U:C4	1:a:495:A:N7	2.85	0.45
1:a:690:G:OP2	11:k:28:ASN:ND2	2.48	0.45
1:a:791:G:O6	1:a:792:A:N6	2.45	0.45
1:a:1101:A:H4'	1:a:1102:A:O5'	2.17	0.45
4:d:128:VAL:HG21	4:d:145:ARG:HH11	1.81	0.45
15:o:75:ALA:O	15:o:78:THR:OG1	2.30	0.45
22:A:594:U:H2'	22:A:595:C:C6	2.51	0.45
22:A:742:A:H2'	22:A:743:A:H8	1.81	0.45
22:A:1117:C:H2'	22:A:1118:C:H6	1.79	0.45
22:A:1297:C:OP1	22:A:2710:C:H4'	2.15	0.45
22:A:1509:A:H2'	22:A:1510:G:H8	1.80	0.45
22:A:1932:A:H2'	22:A:1933:G:O4'	2.17	0.45
22:A:2245:U:O2'	22:A:2436:G:OP2	2.28	0.45
22:A:2251:OMG:H1'	22:A:2251:OMG:HM23	1.57	0.45
32:K:4:GLU:HA	32:K:21:CYS:O	2.16	0.45
34:M:50:ARG:O	34:M:54:THR:HG23	2.17	0.45
1:a:181:A:H2'	1:a:182:A:C8	2.52	0.45
1:a:673:A:H2'	1:a:674:G:H8	1.77	0.45
1:a:700:G:H4'	1:a:704:A:H1'	1.96	0.45
1:a:1014:A:N3	1:a:1219:A:H1'	2.31	0.45
1:a:1175:G:H2'	1:a:1176:A:C8	2.51	0.45
1:a:1307:U:H2'	1:a:1308:U:C6	2.52	0.45
4:d:18:LEU:HD22	4:d:63:ILE:HB	1.99	0.45
8:h:34:ALA:HB1	8:h:109:VAL:HG21	1.99	0.45
9:i:71:ILE:HG13	9:i:72:SER:H	1.81	0.45
9:i:101:GLY:C	9:i:103:VAL:H	2.24	0.45
10:j:36:VAL:HG12	10:j:76:ILE:HG23	1.98	0.45
22:A:396:G:H1'	45:X:28:PHE:HB3	1.99	0.45
22:A:2030:6MZ:C2	22:A:2499:C:H5''	2.47	0.45
22:A:2162:G:N3	22:A:2162:G:H2'	2.32	0.45
23:B:65:U:H3'	23:B:108:A:N6	2.31	0.45
30:I:23:VAL:CG1	30:I:26:ALA:HB3	2.47	0.45
30:I:60:VAL:HG22	30:I:61:TYR:H	1.81	0.45
46:Y:39:GLN:HB3	46:Y:41:HIS:CE1	2.51	0.45
49:1:8:ILE:HG22	49:1:9:LYS:H	1.82	0.45
1:a:56:U:H2'	1:a:57:G:C8	2.52	0.45
1:a:121:U:H5'	1:a:122:G:OP2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:160:A:N6	1:a:347:G:H21	2.12	0.45
1:a:246:A:C2	1:a:282:A:C6	3.04	0.45
1:a:410:G:P	1:a:410:G:H8	2.40	0.45
1:a:1013:G:N2	1:a:1016:A:OP2	2.45	0.45
2:b:37:VAL:HG22	2:b:38:HIS:H	1.82	0.45
3:c:113:LYS:HE2	3:c:184:ASN:OD1	2.16	0.45
3:c:137:VAL:HG13	3:c:148:ILE:HG23	1.99	0.45
7:g:55:LYS:HD3	7:g:55:LYS:HA	1.68	0.45
13:m:3:ILE:H	13:m:3:ILE:HD12	1.81	0.45
22:A:1073:A:C4	22:A:1074:G:C8	3.05	0.45
22:A:1627:G:C2'	22:A:1628:G:H5'	2.46	0.45
22:A:1652:A:OP1	35:N:8:ARG:NE	2.48	0.45
22:A:1827:U:OP2	24:C:220:ARG:HD2	2.17	0.45
27:F:116:LEU:HD11	27:F:174:PHE:CE2	2.51	0.45
40:S:6:LYS:HG2	40:S:104:THR:OG1	2.17	0.45
51:3:30:HIS:C	51:3:32:LEU:N	2.75	0.45
1:a:309:A:O2'	1:a:607:A:N1	2.45	0.45
1:a:363:A:H4'	12:l:80:LEU:HD11	1.98	0.45
1:a:415:A:H2'	1:a:416:G:C8	2.52	0.45
1:a:432:A:H2'	1:a:433:G:H8	1.80	0.45
1:a:767:A:H2'	1:a:768:A:O4'	2.16	0.45
1:a:1249:C:O2'	9:i:69:GLY:O	2.25	0.45
1:a:1319:A:C8	1:a:1323:G:C6	3.04	0.45
10:j:5:ARG:N	10:j:77:VAL:HA	2.31	0.45
19:s:8:PRO:HD3	54:6:64:PHE:HE1	1.82	0.45
22:A:636:G:C6	33:L:111:ILE:HG21	2.52	0.45
22:A:851:C:H2'	22:A:852:U:H6	1.80	0.45
22:A:881:G:C4	22:A:882:G:C8	3.05	0.45
22:A:1059:G:H1'	30:I:71:LYS:HD3	1.98	0.45
22:A:1419:A:N7	22:A:1579:A:N6	2.64	0.45
22:A:2121:G:H2'	22:A:2122:U:C6	2.52	0.45
22:A:2171:A:O2'	22:A:2172:U:H5''	2.17	0.45
22:A:2291:U:H2'	22:A:2292:U:H6	1.82	0.45
31:J:8:PRO:HG3	31:J:48:VAL:HG22	1.99	0.45
54:6:16:CYS:HA	54:6:34:LEU:HB2	1.97	0.45
1:a:564:C:OP1	12:l:11:ARG:NE	2.43	0.45
1:a:981:U:OP1	14:n:5:MET:HE1	2.16	0.45
3:c:84:GLU:O	3:c:88:LYS:HG2	2.16	0.45
4:d:149:LYS:HE3	4:d:176:LYS:HE2	1.97	0.45
7:g:70:PRO:HG3	7:g:102:TRP:CH2	2.52	0.45
13:m:3:ILE:HB	13:m:7:ASN:CG	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:p:8:ARG:CZ	16:p:15:PRO:HB3	2.46	0.45
22:A:700:G:H2'	22:A:701:G:O4'	2.16	0.45
22:A:1440:U:H2'	22:A:1441:G:H8	1.81	0.45
22:A:1467:U:H2'	22:A:1468:U:O4'	2.16	0.45
22:A:2314:A:H2'	22:A:2315:G:H8	1.82	0.45
22:A:2808:G:H2'	22:A:2890:G:O6	2.17	0.45
1:a:167:A:H2'	1:a:168:G:H8	1.82	0.45
1:a:537:G:H2'	1:a:538:G:H8	1.81	0.45
1:a:1010:U:C2	1:a:1011:C:C5	3.05	0.45
1:a:1182:G:H4'	1:a:1183:U:O5'	2.16	0.45
2:b:100:LEU:N	2:b:174:GLU:OE2	2.41	0.45
2:b:118:THR:O	2:b:122:ASP:HB3	2.17	0.45
4:d:101:VAL:HG11	4:d:122:ILE:HD13	1.98	0.45
16:p:46:LYS:HZ3	16:p:48:GLU:H	1.63	0.45
22:A:1250:G:H5''	38:Q:5:ARG:HD3	1.98	0.45
22:A:1942:C:OP2	22:A:1943:U:O2'	2.19	0.45
22:A:2063:C:H1'	58:9:101:PRO:HA	1.99	0.45
22:A:2164:C:H3'	22:A:2165:C:C6	2.52	0.45
22:A:2638:G:H1'	22:A:2778:A:N6	2.31	0.45
22:A:2682:A:C2	25:D:23:PRO:HB3	2.52	0.45
22:A:2813:A:H2'	22:A:2814:A:O4'	2.17	0.45
27:F:110:ILE:HA	27:F:136:ILE:CD1	2.46	0.45
28:G:122:ALA:HA	28:G:131:VAL:O	2.16	0.45
29:H:104:THR:OG1	29:H:110:VAL:HB	2.16	0.45
29:H:128:HIS:CE1	29:H:145:ASN:HA	2.51	0.45
33:L:48:ARG:HE	33:L:48:ARG:HB2	1.51	0.45
44:W:66:GLU:OE2	44:W:77:SER:OG	2.22	0.45
1:a:68:G:H4'	1:a:171:A:H1'	1.99	0.45
1:a:429:U:O2	1:a:430:A:C8	2.70	0.45
1:a:476:U:H2'	1:a:477:C:H6	1.80	0.45
1:a:831:A:H2'	1:a:832:G:O4'	2.16	0.45
1:a:1268:G:H1'	1:a:1326:U:O2'	2.17	0.45
22:A:216:A:C8	22:A:432:A:C6	3.05	0.45
22:A:764:A:OP2	24:C:212:TRP:HZ3	2.00	0.45
22:A:1361:G:H2'	22:A:1362:C:C6	2.52	0.45
22:A:1537:G:H1	22:A:1538:G:N2	2.15	0.45
22:A:2229:U:H2'	22:A:2230:G:H8	1.81	0.45
22:A:2572:A:H5''	22:A:2574:G:H4'	1.98	0.45
22:A:2638:G:H1'	22:A:2778:A:H61	1.82	0.45
26:E:45:ALA:HA	26:E:87:ALA:O	2.17	0.45
28:G:25:ILE:HG22	28:G:78:VAL:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:I:89:SER:OG	30:I:135:MET:HA	2.17	0.45
40:S:33:LEU:HD23	40:S:33:LEU:HA	1.62	0.45
54:6:47:LYS:HB3	54:6:47:LYS:HE2	1.79	0.45
1:a:379:C:H2'	1:a:380:G:N9	2.31	0.45
1:a:920:U:O2'	1:a:1081:A:O2'	2.16	0.45
1:a:1494:G:H4'	22:A:1913:A:C8	2.51	0.45
4:d:86:GLY:HA3	4:d:196:GLU:HG3	1.99	0.45
8:h:8:ASP:HA	8:h:11:THR:HG22	2.00	0.45
9:i:96:GLU:HA	9:i:99:LYS:HE3	1.99	0.45
22:A:195:A:H3'	22:A:196:A:H4'	1.98	0.45
22:A:538:A:N6	22:A:555:G:H1'	2.32	0.45
22:A:609:A:H2'	22:A:610:C:O4'	2.17	0.45
22:A:1061:U:H5	30:I:55:PRO:HB3	1.81	0.45
22:A:1327:A:H2'	22:A:1328:A:O4'	2.17	0.45
22:A:1450:G:N2	22:A:1452:G:O6	2.45	0.45
22:A:1827:U:H5'	22:A:1971:U:H5'	1.99	0.45
22:A:2176:A:H2'	22:A:2177:C:O4'	2.17	0.45
24:C:196:ASN:ND2	24:C:199:HIS:HB2	2.32	0.45
34:M:57:VAL:HG13	34:M:57:VAL:O	2.17	0.45
42:U:101:THR:HG22	42:U:102:ILE:N	2.32	0.45
55:9:19:G:H4'	55:9:20:U:OP2	2.17	0.45
1:a:356:A:H2	1:a:368:U:O2	2.00	0.44
1:a:1305:G:N2	1:a:1331:G:H2'	2.32	0.44
6:f:47:LEU:HD21	6:f:57:ALA:H	1.81	0.44
16:p:8:ARG:HG3	16:p:17:TYR:CE1	2.52	0.44
22:A:273:G:C6	22:A:274:C:C4	3.05	0.44
22:A:397:U:OP1	45:X:31:ASN:N	2.46	0.44
22:A:1027:A:H2	22:A:2488:G:H4'	1.82	0.44
22:A:1570:A:H2'	22:A:1571:A:C8	2.52	0.44
22:A:1726:C:N4	22:A:1727:C:N4	2.64	0.44
22:A:1761:C:H2'	22:A:1762:A:O4'	2.17	0.44
23:B:48:U:H2'	23:B:49:C:C6	2.52	0.44
31:J:114:LEU:O	31:J:118:MET:HG2	2.17	0.44
42:U:65:GLN:HB2	42:U:68:ASN:ND2	2.32	0.44
1:a:379:C:C4	1:a:380:G:O6	2.70	0.44
1:a:465:A:H2'	1:a:466:A:C8	2.52	0.44
1:a:1118:U:H1'	1:a:1179:A:C4	2.53	0.44
4:d:55:ARG:HH12	4:d:62:ARG:NH2	2.16	0.44
4:d:56:GLU:HG2	4:d:198:LEU:HB2	1.98	0.44
5:e:37:VAL:HG12	5:e:116:VAL:HG21	1.99	0.44
7:g:12:LEU:HD21	7:g:35:LYS:NZ	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:g:148:LYS:C	7:g:150:PHE:H	2.24	0.44
16:p:7:ALA:O	16:p:29:ASN:ND2	2.50	0.44
22:A:5:A:H2'	22:A:6:A:H8	1.82	0.44
22:A:71:A:N3	22:A:71:A:H5'	2.32	0.44
22:A:633:A:O2'	22:A:2404:U:OP1	2.35	0.44
22:A:864:G:O2'	22:A:865:C:H5'	2.17	0.44
22:A:1075:C:O2'	30:I:90:GLY:O	2.21	0.44
22:A:1080:A:O2'	30:I:127:SER:HB3	2.17	0.44
22:A:1083:U:H2'	22:A:1085:A:OP2	2.18	0.44
22:A:1186:G:O5'	22:A:1186:G:H8	2.00	0.44
22:A:1608:A:O2'	22:A:1610:A:OP2	2.33	0.44
22:A:2297:A:N1	22:A:2321:U:H5	2.16	0.44
25:D:27:ILE:HG12	25:D:201:LEU:HD12	1.99	0.44
27:F:122:ASP:OD2	27:F:126:ASN:ND2	2.49	0.44
30:I:43:ALA:C	30:I:44:LYS:HD2	2.42	0.44
30:I:82:ALA:HB1	30:I:104:GLN:NE2	2.31	0.44
34:M:29:GLY:N	34:M:104:GLU:OE1	2.44	0.44
1:a:80:A:H8	1:a:80:A:O5'	2.00	0.44
1:a:107:G:OP1	1:a:325:A:N6	2.50	0.44
1:a:433:G:H2'	1:a:434:U:C6	2.52	0.44
1:a:642:A:C5	8:h:106:SER:HA	2.53	0.44
1:a:1496:C:H2'	1:a:1497:G:O4'	2.18	0.44
11:k:63:GLN:HB2	11:k:98:ALA:HB2	2.00	0.44
22:A:57:C:H2'	22:A:58:G:O4'	2.17	0.44
22:A:674:G:H5''	26:E:71:GLY:N	2.33	0.44
22:A:882:G:N2	22:A:883:G:H1'	2.32	0.44
22:A:1731:G:C2	22:A:1733:G:C5	3.05	0.44
22:A:1736:U:H2'	22:A:1737:G:O4'	2.17	0.44
22:A:2180:U:H2'	22:A:2181:U:C2	2.52	0.44
23:B:90:C:H4'	34:M:38:ARG:HE	1.81	0.44
28:G:88:LEU:HG	28:G:161:VAL:HG22	1.99	0.44
30:I:100:ILE:HG22	30:I:101:SER:N	2.33	0.44
37:P:74:GLN:O	37:P:76:HIS:N	2.50	0.44
53:5:56:ARG:HG2	53:5:83:ALA:CB	2.46	0.44
1:a:437:U:O4	1:a:495:A:C8	2.70	0.44
1:a:632:U:H5'	1:a:633:G:H8	1.82	0.44
1:a:999:C:H2'	1:a:1000:A:C8	2.53	0.44
1:a:1034:G:H3'	1:a:1035:A:H8	1.83	0.44
4:d:165:GLU:OE1	4:d:165:GLU:N	2.50	0.44
7:g:12:LEU:HD23	7:g:12:LEU:H	1.82	0.44
11:k:85:VAL:CG2	11:k:111:ASP:HB3	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:395:U:H2'	22:A:396:G:N7	2.32	0.44
22:A:910:A:H2'	22:A:911:A:C8	2.53	0.44
22:A:1529:G:H2'	22:A:1530:G:H8	1.82	0.44
22:A:1689:A:H61	22:A:1697:G:H2'	1.83	0.44
22:A:1826:G:O2'	22:A:1971:U:OP2	2.36	0.44
22:A:2185:U:H2'	22:A:2186:G:C8	2.52	0.44
24:C:231:HIS:CG	24:C:239:PHE:HE1	2.35	0.44
27:F:34:THR:HG23	27:F:154:THR:HG23	1.98	0.44
28:G:14:VAL:HG23	28:G:26:LYS:O	2.18	0.44
29:H:5:LEU:HA	29:H:36:ALA:HA	1.99	0.44
32:K:10:VAL:HG21	32:K:16:ALA:HB3	1.99	0.44
35:N:4:ARG:HA	35:N:4:ARG:HD2	1.76	0.44
35:N:79:LEU:O	35:N:80:PHE:HB2	2.17	0.44
47:Z:7:THR:OG1	47:Z:34:THR:OG1	2.16	0.44
49:1:38:PHE:CZ	49:1:43:ARG:HA	2.52	0.44
1:a:560:A:H5'	1:a:566:G:N2	2.33	0.44
1:a:1088:G:H21	1:a:1167:A:N6	2.16	0.44
1:a:1215:G:C2	1:a:1216:A:C8	3.06	0.44
1:a:1421:G:OP1	32:K:54:LYS:NZ	2.46	0.44
2:b:57:ASN:OD1	2:b:57:ASN:C	2.60	0.44
3:c:182:ASP:OD2	3:c:201:ILE:HB	2.16	0.44
6:f:12:PRO:O	6:f:15:SER:HB3	2.16	0.44
14:n:64:CYS:HB3	14:n:69:ARG:H	1.83	0.44
22:A:545:U:H2'	22:A:546:U:O4'	2.18	0.44
22:A:566:U:OP1	33:L:29:LYS:HE3	2.17	0.44
22:A:631:A:H1'	33:L:65:GLY:HA2	1.99	0.44
22:A:783:A:H2'	22:A:784:G:H4'	2.00	0.44
22:A:1452:G:O2'	22:A:1453:A:OP2	2.28	0.44
22:A:1490:A:O2'	22:A:1491:G:P	2.75	0.44
22:A:1726:C:C4	22:A:1727:C:C4	3.06	0.44
22:A:2845:U:H5''	37:P:51:ASN:O	2.18	0.44
28:G:82:PHE:CE2	28:G:137:LYS:HB2	2.52	0.44
32:K:109:SER:O	32:K:111:LYS:N	2.50	0.44
33:L:23:ILE:HG12	39:R:82:HIS:CD2	2.53	0.44
46:Y:24:GLU:O	46:Y:46:VAL:HG11	2.17	0.44
53:5:19:ALA:HB2	53:5:69:PHE:CE2	2.52	0.44
1:a:149:A:H2'	1:a:150:U:C6	2.53	0.44
1:a:329:A:C8	1:a:332:G:C6	3.06	0.44
1:a:705:G:C5	1:a:706:A:C8	3.06	0.44
1:a:1157:A:C2	1:a:1181:G:C4	3.06	0.44
1:a:1171:A:H2'	1:a:1172:C:H6	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1190:G:H4'	1:a:1191:A:OP2	2.16	0.44
9:i:47:VAL:O	9:i:50:PRO:HD2	2.17	0.44
22:A:1171:G:H8	22:A:1171:G:O5'	2.00	0.44
22:A:1447:C:H2'	22:A:1448:G:H8	1.83	0.44
22:A:1584:U:H2'	22:A:1585:C:H5'	2.00	0.44
22:A:1683:U:H2'	22:A:1684:G:H8	1.83	0.44
22:A:1842:G:H2'	22:A:1843:C:C6	2.53	0.44
22:A:1910:G:H2'	22:A:1911:PSU:O4'	2.18	0.44
22:A:2163:A:H3'	22:A:2164:C:H6	1.82	0.44
23:B:39:A:H2'	23:B:40:U:C6	2.52	0.44
24:C:128:THR:HA	24:C:190:THR:HA	1.99	0.44
31:J:19:ASP:O	31:J:23:LYS:NZ	2.47	0.44
42:U:87:GLU:O	42:U:88:ASP:C	2.60	0.44
43:V:20:LEU:HD21	43:V:41:GLU:HB2	1.99	0.44
53:5:33:VAL:HG22	53:5:34:THR:H	1.83	0.44
1:a:297:G:H4'	1:a:557:G:H4'	1.98	0.44
1:a:323:U:H2'	1:a:324:G:O4'	2.18	0.44
1:a:1407:5MC:O2'	22:A:1912:A:N1	2.43	0.44
3:c:41:TYR:CZ	3:c:89:VAL:HG11	2.52	0.44
4:d:188:SER:O	4:d:188:SER:OG	2.33	0.44
11:k:21:HIS:HA	11:k:84:MET:O	2.17	0.44
15:o:45:HIS:C	15:o:47:LYS:H	2.26	0.44
20:t:67:HIS:C	20:t:69:ASN:N	2.72	0.44
22:A:35:G:H1'	22:A:454:A:C4	2.53	0.44
22:A:271:G:C2	22:A:367:G:C2	3.06	0.44
22:A:1418:G:N2	22:A:1579:A:N7	2.65	0.44
22:A:1419:A:C8	22:A:1579:A:N6	2.86	0.44
22:A:1591:A:H2'	22:A:1592:C:C6	2.53	0.44
22:A:2743:U:H2'	22:A:2744:G:O4'	2.18	0.44
40:S:48:LYS:O	40:S:52:GLU:HG3	2.17	0.44
1:a:31:G:C8	1:a:306:A:H1'	2.52	0.44
1:a:189:A:H2'	1:a:190:A:C8	2.52	0.44
1:a:414:A:H62	1:a:430:A:N6	2.16	0.44
1:a:1271:A:H2'	1:a:1272:G:H8	1.82	0.44
1:a:1473:G:H2'	1:a:1474:U:O4'	2.17	0.44
2:b:92:ASN:OD1	2:b:93:HIS:N	2.51	0.44
4:d:97:LEU:N	4:d:134:TYR:O	2.50	0.44
13:m:19:THR:OG1	13:m:25:GLY:HA2	2.18	0.44
13:m:33:LEU:HD12	13:m:40:GLU:HG2	2.00	0.44
15:o:41:HIS:O	15:o:41:HIS:CG	2.67	0.44
17:q:68:LYS:O	17:q:69:THR:C	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:644:A:C2	22:A:2369:A:H1'	2.53	0.44
22:A:659:G:O2'	26:E:95:LYS:O	2.35	0.44
22:A:714:U:H3'	22:A:715:A:H5''	2.00	0.44
22:A:1532:A:C6	22:A:1540:G:C6	3.05	0.44
22:A:1542:U:H2'	22:A:1543:G:O4'	2.18	0.44
25:D:179:ARG:HB3	25:D:188:LEU:HD12	1.99	0.44
26:E:128:ALA:O	26:E:130:LYS:N	2.50	0.44
35:N:54:LEU:HD23	35:N:66:ALA:HB2	2.00	0.44
1:a:29:U:O2'	1:a:30:U:H5'	2.18	0.44
1:a:380:G:H8	1:a:380:G:H3'	1.83	0.44
1:a:694:A:H2'	1:a:695:A:O4'	2.18	0.44
1:a:1347:G:H1'	1:a:1348:U:OP2	2.18	0.44
2:b:69:VAL:HG22	2:b:161:PHE:O	2.18	0.44
7:g:73:GLU:HG2	7:g:74:VAL:N	2.33	0.44
11:k:83:VAL:HG13	11:k:109:ILE:HA	2.00	0.44
19:s:10:ILE:HD13	19:s:40:PHE:HD2	1.82	0.44
21:u:17:ARG:O	21:u:21:SER:CB	2.66	0.44
22:A:217:A:H2'	22:A:218:A:H8	1.83	0.44
22:A:265:A:N1	22:A:427:U:O2'	2.46	0.44
22:A:271:G:O2'	22:A:272:A:OP2	2.29	0.44
22:A:417:C:H2'	22:A:418:C:C6	2.52	0.44
22:A:716:A:H2'	22:A:717:C:O4'	2.18	0.44
22:A:720:U:H2'	22:A:721:A:C8	2.53	0.44
22:A:964:C:O2'	22:A:2273:A:N3	2.40	0.44
22:A:1485:U:H2'	22:A:1486:U:C6	2.52	0.44
22:A:2567:G:H2'	22:A:2568:U:C6	2.53	0.44
42:U:95:PHE:CZ	42:U:102:ILE:HG12	2.53	0.44
1:a:72:A:H2'	1:a:73:C:H6	1.82	0.43
1:a:224:U:H2'	1:a:225:C:H6	1.82	0.43
1:a:227:G:H2'	1:a:228:A:O4'	2.18	0.43
1:a:380:G:H3'	1:a:380:G:C8	2.53	0.43
1:a:592:G:H2'	1:a:593:U:C6	2.53	0.43
1:a:646:G:C5	1:a:647:C:C5	3.06	0.43
1:a:1125:U:HO2'	1:a:1126:U:H5	1.64	0.43
1:a:1183:U:O2'	1:a:1184:G:OP1	2.34	0.43
7:g:14:ASP:OD1	7:g:16:LYS:N	2.45	0.43
22:A:288:U:C2	22:A:289:G:C8	3.06	0.43
22:A:518:G:H2'	22:A:519:U:C6	2.53	0.43
22:A:1059:G:O3'	30:I:55:PRO:HG3	2.18	0.43
22:A:1519:G:C6	22:A:1520:U:C4	3.06	0.43
22:A:1779:U:C5	22:A:1784:A:N7	2.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:E:17:THR:O	26:E:21:ARG:HD2	2.18	0.43
31:J:37:ARG:NH1	31:J:44:TYR:OH	2.50	0.43
37:P:63:ILE:HA	37:P:68:GLY:HA2	1.99	0.43
41:T:54:GLU:HG3	41:T:88:LYS:HB2	1.99	0.43
52:4:17:VAL:HG12	52:4:18:LYS:H	1.83	0.43
53:5:102:ALA:O	53:5:105:LYS:N	2.51	0.43
54:6:43:PHE:CG	54:6:44:PHE:N	2.86	0.43
1:a:967:5MC:OP2	1:a:968:A:O2'	2.33	0.43
1:a:1099:G:H2'	1:a:1100:C:O4'	2.18	0.43
1:a:1179:A:H2'	1:a:1180:A:O4'	2.18	0.43
1:a:1517:G:N7	1:a:1518:MA6:H103	2.33	0.43
2:b:186:VAL:HG22	2:b:198:VAL:HG13	2.00	0.43
3:c:79:LYS:HA	3:c:79:LYS:HD2	1.81	0.43
6:f:39:LEU:O	6:f:41:ASP:N	2.49	0.43
12:l:109:ARG:HB2	12:l:118:VAL:HG21	2.00	0.43
22:A:729:G:H5'	22:A:730:A:H5''	2.00	0.43
22:A:1667:G:N1	22:A:1992:G:OP2	2.41	0.43
22:A:1734:G:H2'	22:A:1735:A:H8	1.82	0.43
22:A:2298:A:H2'	22:A:2299:U:O4'	2.18	0.43
22:A:2898:U:O4	22:A:2899:A:N6	2.51	0.43
30:I:76:ALA:HA	30:I:135:MET:HE3	1.98	0.43
44:W:22:PHE:N	44:W:25:GLU:OE1	2.45	0.43
51:3:24:LYS:HG3	51:3:46:LYS:HE3	2.00	0.43
54:6:47:LYS:O	54:6:51:VAL:HG23	2.18	0.43
1:a:458:U:H2'	1:a:459:A:H8	1.83	0.43
1:a:948:C:H2'	1:a:949:A:H8	1.84	0.43
4:d:106:PHE:N	4:d:106:PHE:CD1	2.85	0.43
4:d:191:SER:O	4:d:193:ASP:N	2.50	0.43
11:k:123:PRO:HB2	11:k:125:LYS:HG3	2.00	0.43
22:A:24:G:N2	40:S:78:GLU:OE2	2.50	0.43
22:A:497:A:H2'	22:A:498:G:O4'	2.19	0.43
22:A:2152:G:C6	22:A:2153:C:N4	2.85	0.43
22:A:2154:A:H2'	22:A:2155:U:C6	2.54	0.43
22:A:2236:U:H2'	22:A:2237:G:O4'	2.18	0.43
24:C:106:PRO:HG2	24:C:109:LEU:HD13	1.99	0.43
25:D:8:LYS:HB2	25:D:201:LEU:HD11	1.99	0.43
27:F:43:ILE:HD11	27:F:78:ILE:HG22	1.98	0.43
33:L:123:ARG:HG3	33:L:143:GLU:HG3	1.99	0.43
35:N:25:ALA:O	35:N:29:VAL:HG22	2.18	0.43
1:a:2:A:H1'	1:a:613:C:O2'	2.18	0.43
1:a:113:G:H2'	1:a:114:U:H6	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:331:G:OP1	1:a:332:G:H8	2.00	0.43
1:a:360:G:C6	1:a:361:G:C6	3.06	0.43
1:a:392:C:C2	1:a:393:A:C8	3.05	0.43
1:a:464:U:H2'	1:a:466:A:OP2	2.18	0.43
1:a:514:C:H2'	1:a:515:G:H8	1.83	0.43
1:a:875:U:O2'	8:h:14:ARG:HD2	2.18	0.43
1:a:986:U:H2'	1:a:987:G:H8	1.82	0.43
1:a:1134:G:H2'	1:a:1134:G:N3	2.32	0.43
1:a:1201:A:H1'	1:a:1202:U:OP2	2.19	0.43
1:a:1297:G:H4'	1:a:1298:U:O5'	2.17	0.43
2:b:22:TRP:CD1	2:b:22:TRP:H	2.36	0.43
3:c:24:ASN:O	3:c:28:PHE:HB2	2.18	0.43
16:p:34:GLU:OE2	16:p:60:TRP:NE1	2.45	0.43
17:q:67:SER:C	17:q:68:LYS:O	2.61	0.43
21:u:7:GLU:OE1	21:u:13:VAL:HG23	2.18	0.43
22:A:822:G:H2'	22:A:823:C:H6	1.83	0.43
22:A:988:A:OP2	47:Z:11:SER:OG	2.33	0.43
22:A:1022:G:N7	31:J:68:LYS:HE2	2.33	0.43
22:A:1170:C:H6	22:A:1170:C:O5'	2.01	0.43
22:A:1511:G:H2'	22:A:1512:C:H6	1.82	0.43
22:A:2805:C:H2'	22:A:2806:C:C6	2.53	0.43
22:A:2820:A:OP2	35:N:2:ARG:NH1	2.51	0.43
25:D:39:ASP:OD1	25:D:39:ASP:N	2.44	0.43
27:F:8:LYS:HA	27:F:12:VAL:HG21	2.00	0.43
33:L:30:THR:O	33:L:31:GLY:C	2.60	0.43
41:T:67:VAL:HG22	41:T:76:ARG:HG3	2.01	0.43
44:W:68:LYS:HE3	44:W:68:LYS:HB2	1.75	0.43
49:1:33:LEU:HB3	49:1:35:LEU:CD2	2.48	0.43
1:a:763:G:H2'	1:a:764:C:H6	1.82	0.43
4:d:90:LEU:HA	4:d:90:LEU:HD13	1.81	0.43
7:g:144:ALA:C	7:g:146:ALA:N	2.77	0.43
8:h:9:MET:O	8:h:13:ILE:HG13	2.18	0.43
8:h:17:GLN:HB3	8:h:69:ALA:CB	2.48	0.43
11:k:19:VAL:HG13	11:k:34:THR:OG1	2.19	0.43
11:k:57:SER:O	11:k:90:PRO:HG3	2.18	0.43
15:o:13:GLU:CD	15:o:83:ARG:HH21	2.26	0.43
22:A:492:A:H2'	22:A:493:G:O4'	2.19	0.43
22:A:756:A:H2'	22:A:757:G:O4'	2.18	0.43
22:A:813:U:H2'	22:A:814:C:C6	2.53	0.43
22:A:1056:G:N2	22:A:1104:C:N4	2.66	0.43
22:A:1425:G:H2'	22:A:1426:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:1719:G:H2'	22:A:1720:U:O4'	2.19	0.43
22:A:2305:U:H2'	22:A:2306:C:C6	2.53	0.43
22:A:2418:A:N3	49:1:19:PHE:HZ	2.17	0.43
22:A:2495:G:C5	22:A:2496:C:C5	3.06	0.43
27:F:105:ILE:HG12	54:6:34:LEU:HD11	2.01	0.43
29:H:83:LYS:HG2	29:H:91:PHE:CB	2.48	0.43
30:I:66:PHE:CD2	30:I:68:PHE:HB3	2.52	0.43
40:S:82:MET:HB3	40:S:84:ARG:NH1	2.33	0.43
1:a:505:G:H2'	1:a:506:G:C8	2.52	0.43
1:a:1202:U:C2	14:n:82:ILE:HG21	2.53	0.43
1:a:1228:C:OP2	13:m:106:ARG:NH2	2.47	0.43
2:b:47:PRO:O	2:b:51:GLU:HG2	2.19	0.43
6:f:74:LEU:HD13	6:f:74:LEU:HA	1.83	0.43
22:A:205:G:O2'	22:A:206:U:OP2	2.36	0.43
22:A:1107:G:C4	22:A:1108:U:C5	3.07	0.43
24:C:163:ILE:HG23	24:C:171:VAL:HG13	2.01	0.43
29:H:27:ARG:NH1	45:X:59:ASP:OD2	2.51	0.43
33:L:121:THR:HA	33:L:141:LYS:O	2.19	0.43
34:M:14:LYS:HB3	34:M:14:LYS:HE2	1.76	0.43
34:M:38:ARG:HG2	34:M:98:PRO:HD3	1.99	0.43
38:Q:24:TYR:O	38:Q:27:ARG:HB2	2.19	0.43
38:Q:87:VAL:HG13	39:R:49:ILE:HG13	2.01	0.43
43:V:88:HIS:HE1	43:V:90:ASP:OD1	2.02	0.43
1:a:407:U:H5''	4:d:111:ALA:C	2.44	0.43
1:a:450:G:H4'	16:p:41:PRO:HB2	2.00	0.43
1:a:642:A:C4	1:a:643:C:C5	3.07	0.43
1:a:925:G:O6	1:a:1391:U:O2	2.36	0.43
1:a:1077:G:N1	1:a:1080:A:OP2	2.49	0.43
1:a:1301:U:H2'	1:a:1303:C:H5	1.84	0.43
2:b:20:ARG:HG3	2:b:21:TYR:N	2.34	0.43
6:f:39:LEU:HA	6:f:39:LEU:HD23	1.81	0.43
9:i:34:LEU:HD11	9:i:44:ARG:HB2	1.99	0.43
10:j:83:THR:O	10:j:87:LEU:HG	2.19	0.43
14:n:96:LEU:HD12	14:n:96:LEU:HA	1.77	0.43
19:s:5:LYS:NZ	19:s:6:LYS:HD3	2.34	0.43
22:A:95:A:H2'	22:A:96:C:O4'	2.19	0.43
22:A:1173:U:C4	22:A:1174:U:C2	3.06	0.43
22:A:2409:G:C5	22:A:2410:G:C8	3.06	0.43
26:E:140:ASP:OD2	26:E:141:MET:N	2.51	0.43
31:J:36:LEU:O	31:J:51:GLY:HA3	2.19	0.43
31:J:80:HIS:C	31:J:82:GLY:H	2.25	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:M:80:VAL:HG12	34:M:81:ARG:O	2.19	0.43
48:0:47:TYR:CZ	48:0:52:LYS:HD3	2.53	0.43
54:6:48:GLN:OE1	54:6:48:GLN:N	2.42	0.43
1:a:354:G:HO2'	1:a:355:C:P	2.42	0.43
1:a:626:G:OP1	16:p:35:ARG:NH2	2.52	0.43
1:a:846:G:H2'	1:a:847:G:H8	1.82	0.43
1:a:1220:G:N2	19:s:53:GLY:O	2.43	0.43
1:a:1256:A:N7	1:a:1278:G:C4	2.87	0.43
3:c:121:SER:O	3:c:125:ARG:HG3	2.18	0.43
4:d:32:LYS:HB3	4:d:35:GLN:HB3	1.99	0.43
5:e:22:LYS:HD3	5:e:29:ILE:HD11	2.00	0.43
5:e:100:GLU:OE2	5:e:102:THR:OG1	2.23	0.43
6:f:12:PRO:HA	6:f:15:SER:HB3	2.00	0.43
9:i:59:LYS:C	9:i:60:LEU:HD12	2.44	0.43
14:n:73:PHE:CZ	14:n:78:GLY:HA2	2.54	0.43
19:s:13:HIS:O	19:s:17:LYS:HG2	2.18	0.43
22:A:271:G:C4	22:A:367:G:N2	2.87	0.43
22:A:555:G:O2'	22:A:556:A:H8	2.02	0.43
22:A:563:A:C6	22:A:2018:G:C4	3.07	0.43
22:A:659:G:H21	26:E:30:GLN:CD	2.22	0.43
22:A:852:U:H2'	22:A:853:C:C6	2.53	0.43
22:A:1801:A:N6	22:A:2201:G:O2'	2.33	0.43
22:A:1831:G:H2'	22:A:1832:C:C6	2.54	0.43
22:A:2266:A:H4'	22:A:2267:A:O5'	2.18	0.43
23:B:31:C:H2'	23:B:32:U:H6	1.83	0.43
25:D:15:PHE:H	37:P:11:GLN:NE2	2.17	0.43
33:L:110:VAL:O	33:L:110:VAL:HG12	2.18	0.43
53:5:53:ARG:HB3	53:5:55:VAL:H	1.84	0.43
53:5:67:THR:C	53:5:69:PHE:N	2.75	0.43
54:6:11:GLU:HA	54:6:25:ARG:HB3	2.00	0.43
55:9:47:U:H5'	55:9:48:C:OP1	2.19	0.43
1:a:24:U:HO2'	1:a:524:G:HO2'	1.57	0.43
1:a:676:A:H2'	1:a:677:U:H6	1.84	0.43
1:a:690:G:O2'	1:a:691:G:H5'	2.19	0.43
1:a:1088:G:H21	1:a:1167:A:H61	1.66	0.43
1:a:1167:A:H4'	1:a:1168:U:C5	2.54	0.43
10:j:36:VAL:CG1	10:j:76:ILE:HG23	2.48	0.43
22:A:2612:C:H5''	22:A:2613:U:OP1	2.19	0.43
22:A:2740:A:OP2	22:A:2763:G:N1	2.24	0.43
24:C:250:GLN:NE2	24:C:251:THR:O	2.52	0.43
25:D:11:MET:HB3	25:D:11:MET:HE2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:51:ARG:O	29:H:55:GLU:HB2	2.19	0.43
29:H:116:ARG:O	29:H:118:PRO:HD3	2.18	0.43
32:K:8:LEU:HD23	32:K:84:CYS:HB3	2.00	0.43
43:V:4:ILE:HG12	43:V:50:MET:SD	2.59	0.43
46:Y:23:ARG:C	46:Y:25:GLN:H	2.27	0.43
53:5:126:LEU:HD23	53:5:129:LEU:HD11	2.00	0.43
1:a:8:A:N7	4:d:205:LYS:HA	2.34	0.43
1:a:324:G:O2'	1:a:326:G:O6	2.34	0.43
1:a:663:A:H5''	18:r:49:LYS:NZ	2.34	0.43
1:a:709:U:H2'	1:a:710:G:H8	1.84	0.43
1:a:1100:C:N4	1:a:1103:C:OP1	2.52	0.43
1:a:1238:A:H2	1:a:1241:G:N3	2.17	0.43
8:h:65:PHE:CD2	8:h:66:GLN:HG2	2.54	0.43
18:r:48:ALA:O	18:r:52:ARG:HG3	2.19	0.43
22:A:4:U:H2'	22:A:5:A:H8	1.84	0.43
22:A:118:A:C8	22:A:119:A:C8	3.07	0.43
22:A:134:G:H2'	22:A:135:U:C6	2.53	0.43
22:A:540:C:H2'	22:A:541:A:C8	2.54	0.43
22:A:969:G:H2'	22:A:970:U:C6	2.54	0.43
22:A:1146:C:N4	22:A:1147:A:H62	2.16	0.43
22:A:1657:U:OP1	25:D:141:ARG:N	2.52	0.43
22:A:1790:C:O2'	24:C:207:ALA:HB2	2.18	0.43
22:A:2114:A:N3	22:A:2166:U:H2'	2.34	0.43
22:A:2412:A:H2'	22:A:2413:G:O4'	2.19	0.43
22:A:2524:G:C2	22:A:2540:C:C2	3.07	0.43
22:A:2812:G:H2'	22:A:2813:A:C8	2.54	0.43
22:A:2848:G:H2'	22:A:2867:G:N2	2.34	0.43
57:A:3001:ILE:O	58:9:101:PRO:C	2.61	0.43
23:B:8:C:H2'	23:B:9:G:O4'	2.19	0.43
23:B:13:G:OP2	44:W:72:ASN:ND2	2.52	0.43
24:C:162:GLN:HB3	24:C:174:ARG:HG2	2.00	0.43
25:D:186:LEU:HD23	25:D:186:LEU:HA	1.76	0.43
30:I:75:ALA:HB1	30:I:79:LEU:HD12	2.00	0.43
38:Q:75:TYR:CZ	38:Q:79:ILE:HG13	2.54	0.43
52:4:17:VAL:HG12	52:4:18:LYS:N	2.33	0.43
1:a:437:U:O2	4:d:115:GLN:NE2	2.52	0.42
1:a:501:C:H2'	1:a:502:A:H8	1.84	0.42
1:a:663:A:H2'	1:a:664:G:O4'	2.19	0.42
1:a:925:G:C6	1:a:927:G:N7	2.87	0.42
1:a:1173:U:H2'	1:a:1174:G:O4'	2.19	0.42
1:a:1278:G:O5'	1:a:1279:G:H5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1352:C:H2'	1:a:1353:G:C8	2.54	0.42
1:a:1363:A:C5	1:a:1365:G:C6	3.07	0.42
6:f:40:GLU:HG2	6:f:42:TRP:NE1	2.33	0.42
6:f:77:THR:O	6:f:81:ASN:HB2	2.19	0.42
11:k:122:PRO:HB2	21:u:33:ARG:HA	2.00	0.42
13:m:89:ARG:HD2	13:m:89:ARG:HA	1.78	0.42
14:n:20:PHE:HD2	14:n:57:PRO:HD3	1.84	0.42
17:q:12:VAL:HG22	17:q:21:VAL:O	2.19	0.42
17:q:61:ARG:NH2	17:q:73:THR:OG1	2.52	0.42
19:s:46:LEU:HD12	19:s:47:THR:H	1.84	0.42
22:A:52:A:H2'	22:A:53:A:H8	1.83	0.42
22:A:181:A:H2'	22:A:182:A:H8	1.84	0.42
22:A:1060:U:O2	22:A:1071:G:H5'	2.18	0.42
22:A:1084:A:OP1	53:5:54:VAL:N	2.31	0.42
22:A:1696:G:H8	22:A:1696:G:OP2	2.02	0.42
22:A:2144:G:C2	22:A:2147:A:N6	2.87	0.42
25:D:114:LYS:HE3	25:D:196:ALA:HB2	2.01	0.42
28:G:153:PRO:HA	28:G:159:LYS:O	2.19	0.42
39:R:49:ILE:HB	39:R:51:VAL:O	2.19	0.42
40:S:28:LYS:HB2	40:S:31:GLN:HE21	1.83	0.42
53:5:39:THR:O	53:5:43:LYS:HG3	2.19	0.42
53:5:61:ARG:O	53:5:65:GLU:HB2	2.19	0.42
1:a:360:G:H2'	1:a:361:G:H8	1.84	0.42
1:a:630:A:H2'	1:a:631:C:O4'	2.19	0.42
1:a:1130:A:H61	1:a:1144:G:H1'	1.84	0.42
1:a:1226:C:H4'	19:s:79:TYR:CZ	2.54	0.42
1:a:1268:G:O2'	1:a:1269:A:O4'	2.30	0.42
1:a:1372:U:OP1	9:i:72:SER:OG	2.24	0.42
5:e:10:LEU:HB3	5:e:38:VAL:HG12	2.01	0.42
5:e:79:THR:HB	5:e:121:ASN:ND2	2.33	0.42
12:l:106:VAL:HG12	12:l:116:TYR:HB3	2.01	0.42
13:m:22:TYR:HB3	13:m:65:GLU:HG3	2.00	0.42
13:m:39:ALA:HB3	13:m:42:VAL:HG13	2.00	0.42
17:q:49:ASN:OD1	17:q:49:ASN:N	2.52	0.42
19:s:11:ASP:OD2	19:s:13:HIS:N	2.52	0.42
22:A:546:U:N3	22:A:547:A:H1'	2.33	0.42
22:A:705:A:H2'	22:A:706:A:O4'	2.19	0.42
22:A:1814:G:C4'	24:C:50:THR:HG21	2.48	0.42
22:A:1966:A:N3	22:A:2592:G:O2'	2.48	0.42
22:A:2114:A:N6	22:A:2117:A:H62	2.17	0.42
22:A:2521:C:C2	22:A:2545:G:N2	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:13:LYS:HG3	27:F:14:LYS:N	2.34	0.42
27:F:43:ILE:HD13	27:F:82:TYR:CE2	2.54	0.42
27:F:137:PHE:C	27:F:139:GLU:H	2.27	0.42
29:H:19:VAL:HG23	29:H:21:VAL:HG13	2.01	0.42
39:R:53:PHE:N	39:R:53:PHE:CD1	2.85	0.42
45:X:12:VAL:HG12	45:X:28:PHE:HB2	2.01	0.42
48:O:27:LEU:HD23	48:O:36:LYS:HB3	2.01	0.42
49:1:24:LYS:HE2	49:1:29:LYS:HE2	2.01	0.42
53:5:97:LYS:O	53:5:101:LYS:HD3	2.19	0.42
1:a:78:A:H3'	1:a:79:G:C8	2.54	0.42
1:a:426:U:H4'	4:d:39:GLN:HA	2.01	0.42
1:a:476:U:C2	1:a:477:C:C5	3.07	0.42
9:i:64:ILE:HD13	9:i:78:ILE:HG23	2.01	0.42
15:o:20:ASP:OD1	15:o:23:SER:HB2	2.19	0.42
22:A:5:A:H2'	22:A:6:A:C8	2.54	0.42
22:A:265:A:H4'	22:A:266:G:OP1	2.19	0.42
22:A:1056:G:H22	22:A:1104:C:H42	1.67	0.42
22:A:1197:G:N2	22:A:1249:U:O2'	2.52	0.42
22:A:1205:A:C6	26:E:165:HIS:CD2	3.07	0.42
25:D:56:LYS:C	25:D:58:ASN:H	2.27	0.42
30:I:61:TYR:CG	30:I:62:ALA:N	2.87	0.42
33:L:93:ASN:C	33:L:95:LEU:H	2.26	0.42
38:Q:93:ILE:HG22	38:Q:97:ILE:HD12	2.00	0.42
52:4:36:ARG:NH1	52:4:37:GLN:HB3	2.34	0.42
1:a:413:G:C6	4:d:30:LYS:HG3	2.54	0.42
1:a:517:G:N1	1:a:533:A:OP2	2.47	0.42
1:a:946:A:C2	1:a:947:G:C5	3.07	0.42
1:a:1000:A:H2'	1:a:1001:C:C6	2.55	0.42
5:e:110:MET:O	5:e:114:LEU:HG	2.18	0.42
9:i:51:LEU:HD23	9:i:51:LEU:HA	1.92	0.42
11:k:21:HIS:HB2	11:k:32:THR:CG2	2.49	0.42
22:A:45:G:H5''	22:A:46:G:H5'	2.02	0.42
22:A:359:G:H2'	22:A:360:U:O4'	2.19	0.42
22:A:1371:G:H8	22:A:1371:G:O5'	2.02	0.42
22:A:1386:C:H1'	22:A:1470:A:H1'	2.01	0.42
22:A:1790:C:H2'	22:A:1791:A:C8	2.54	0.42
22:A:2152:G:C5	22:A:2153:C:C4	3.07	0.42
22:A:2182:U:H2'	22:A:2183:A:C8	2.54	0.42
22:A:2495:G:C6	22:A:2496:C:C4	3.07	0.42
26:E:138:LEU:HD23	26:E:138:LEU:HA	1.85	0.42
29:H:47:PHE:O	29:H:47:PHE:CG	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:114:GLU:HG3	29:H:132:PHE:HD1	1.84	0.42
35:N:70:THR:O	35:N:71:ARG:C	2.61	0.42
46:Y:8:GLU:OE1	46:Y:12:GLU:HB3	2.20	0.42
1:a:51:A:H4'	1:a:52:C:H5''	2.01	0.42
1:a:743:A:H2'	1:a:744:C:O4'	2.20	0.42
1:a:1377:A:H4'	1:a:1378:C:H5	1.84	0.42
1:a:1532:U:H2'	1:a:1533:C:O4'	2.19	0.42
2:b:71:THR:HG22	2:b:72:LYS:N	2.32	0.42
10:j:50:THR:HG22	10:j:64:GLN:HG2	2.01	0.42
11:k:68:ARG:O	11:k:71:ASP:HB3	2.19	0.42
14:n:13:VAL:HA	14:n:60:GLN:NE2	2.35	0.42
21:u:35:GLU:O	21:u:36:PHE:CD2	2.73	0.42
22:A:640:C:H2'	22:A:641:U:C6	2.54	0.42
22:A:920:A:OP1	47:Z:18:LYS:HE3	2.19	0.42
22:A:1007:C:OP1	31:J:39:LYS:HD2	2.18	0.42
22:A:1106:G:N3	22:A:1106:G:H2'	2.34	0.42
22:A:1264:A:OP1	48:O:15:ARG:NH1	2.45	0.42
22:A:1399:C:O5'	22:A:1399:C:H6	2.02	0.42
22:A:2051:A:H8	22:A:2051:A:OP2	2.03	0.42
23:B:42:C:C5	27:F:65:LEU:HD22	2.53	0.42
25:D:1:MET:HG3	25:D:88:GLU:OE2	2.18	0.42
39:R:11:GLN:HG2	39:R:39:LEU:HD22	2.00	0.42
50:2:21:ARG:O	50:2:27:GLY:HA3	2.19	0.42
51:3:28:LEU:HA	51:3:32:LEU:HD21	2.01	0.42
52:4:3:VAL:HG13	52:4:36:ARG:HD3	2.01	0.42
53:5:30:SER:OG	53:5:109:LYS:HD2	2.20	0.42
1:a:130:A:H1'	1:a:263:A:O2'	2.20	0.42
1:a:203:G:C2	1:a:215:C:N3	2.88	0.42
1:a:405:U:H3'	1:a:406:G:H5'	2.02	0.42
1:a:555:U:H2'	1:a:556:C:C6	2.54	0.42
1:a:740:U:H4'	15:o:38:LEU:HD11	2.02	0.42
4:d:120:LYS:HE2	4:d:128:VAL:HG11	2.00	0.42
19:s:27:LYS:HE2	19:s:27:LYS:HA	2.01	0.42
20:t:27:MET:HE1	20:t:66:ILE:HD13	2.00	0.42
22:A:585:G:O6	22:A:1251:C:O2'	2.25	0.42
22:A:1548:A:H2'	22:A:1549:A:C8	2.54	0.42
22:A:1654:A:N1	22:A:2048:G:O2'	2.52	0.42
22:A:1834:U:H5''	22:A:1835:2MG:H5'	2.02	0.42
22:A:2306:C:N4	27:F:38:GLY:O	2.46	0.42
30:I:116:MET:HB3	30:I:124:MET:HE2	2.02	0.42
54:6:41:HIS:HB3	54:6:43:PHE:HD1	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1245:C:H2'	1:a:1246:A:H8	1.85	0.42
10:j:9:ARG:HD3	10:j:73:LEU:HD13	2.02	0.42
11:k:109:ILE:HG21	21:u:16:ARG:HD2	2.02	0.42
11:k:115:ILE:HD13	11:k:115:ILE:HA	1.82	0.42
20:t:78:LEU:HD23	20:t:78:LEU:HA	1.81	0.42
22:A:170:U:H2'	22:A:171:U:O4'	2.20	0.42
22:A:538:A:H4'	31:J:7:LYS:HG2	2.00	0.42
22:A:549:G:HO2'	22:A:550:C:P	2.43	0.42
22:A:941:A:H2'	22:A:942:G:O4'	2.19	0.42
24:C:23:LEU:HD13	24:C:82:TYR:HB2	2.01	0.42
24:C:65:ASP:OD2	24:C:101:ARG:HD3	2.19	0.42
28:G:79:THR:OG1	28:G:80:GLU:N	2.53	0.42
1:a:212:G:H2'	1:a:213:G:O4'	2.19	0.42
1:a:414:A:C4	1:a:415:A:N7	2.88	0.42
1:a:642:A:H2'	1:a:643:C:C6	2.52	0.42
1:a:1175:G:C4	1:a:1176:A:C8	3.08	0.42
1:a:1243:C:H2'	1:a:1244:G:H8	1.85	0.42
4:d:80:ARG:HH21	4:d:81:LEU:HD23	1.85	0.42
9:i:119:LYS:HE3	9:i:119:LYS:HB3	1.77	0.42
10:j:10:LEU:HB3	10:j:98:VAL:HG23	2.01	0.42
22:A:1039:A:N1	22:A:1116:G:C6	2.87	0.42
22:A:1199:U:H2'	22:A:1200:C:H6	1.85	0.42
22:A:1219:U:H2'	22:A:1220:G:C8	2.55	0.42
22:A:1496:A:H2'	22:A:1498:C:C5	2.55	0.42
22:A:1866:A:C6	22:A:1876:A:N7	2.88	0.42
22:A:1923:U:H2'	22:A:1924:C:H6	1.84	0.42
22:A:2100:G:C6	22:A:2190:G:C5	3.08	0.42
22:A:2345:G:H4'	22:A:2346:A:H5''	2.02	0.42
22:A:2513:A:H2'	22:A:2514:U:C6	2.54	0.42
22:A:2744:G:N2	28:G:142:GLN:OE1	2.41	0.42
23:B:38:C:C2'	23:B:39:A:H5'	2.50	0.42
27:F:115:GLY:C	27:F:177:ARG:HB2	2.45	0.42
29:H:43:ASN:HA	29:H:46:PHE:HB3	2.02	0.42
36:O:62:LEU:HD23	36:O:63:LYS:N	2.35	0.42
41:T:36:LYS:HD2	41:T:36:LYS:HA	1.86	0.42
41:T:47:VAL:HG23	41:T:51:PHE:CD2	2.54	0.42
1:a:157:U:H1'	1:a:165:G:N2	2.34	0.42
1:a:204:G:C4	1:a:465:A:C2	3.08	0.42
1:a:878:A:H2'	1:a:879:C:C6	2.54	0.42
1:a:908:A:H2'	1:a:909:A:H8	1.85	0.42
1:a:978:A:C5	1:a:1319:A:C2	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1001:C:C2	1:a:1002:G:N7	2.88	0.42
1:a:1095:U:OP1	1:a:1108:G:N2	2.47	0.42
5:e:14:LEU:HD13	5:e:59:ILE:HD12	2.02	0.42
5:e:132:PRO:O	5:e:136:VAL:HG13	2.20	0.42
10:j:86:ALA:O	10:j:90:LEU:HD12	2.19	0.42
14:n:54:ASP:O	14:n:55:SER:HB3	2.20	0.42
19:s:5:LYS:HD3	19:s:6:LYS:HE3	2.01	0.42
19:s:40:PHE:C	19:s:42:ASN:H	2.28	0.42
22:A:819:A:C4	22:A:1189:A:C2	3.08	0.42
22:A:1108:U:C4	22:A:1109:C:C4	3.07	0.42
22:A:1257:C:OP1	26:E:67:ARG:NH2	2.52	0.42
22:A:2076:U:OP2	22:A:2238:G:N2	2.50	0.42
23:B:73:A:H2'	23:B:73:A:N3	2.34	0.42
27:F:30:VAL:O	27:F:30:VAL:HG13	2.20	0.42
30:I:21:PRO:HD2	30:I:22:PRO:HD3	2.02	0.42
31:J:45:THR:CG2	31:J:48:VAL:HB	2.49	0.42
42:U:38:ILE:HD13	42:U:38:ILE:HA	1.91	0.42
46:Y:28:LEU:HD11	46:Y:42:LEU:HB3	2.02	0.42
51:3:54:LEU:O	51:3:58:ILE:HG22	2.20	0.42
1:a:380:G:C6	1:a:382:A:N7	2.88	0.42
1:a:1011:C:H2'	1:a:1012:A:C8	2.54	0.42
1:a:1319:A:C8	1:a:1323:G:C5	3.08	0.42
1:a:1387:G:H2'	1:a:1388:C:C6	2.55	0.42
3:c:152:VAL:HG12	3:c:156:LEU:HD21	2.02	0.42
4:d:10:LEU:O	4:d:14:GLU:HG2	2.19	0.42
11:k:92:ARG:HE	21:u:24:LYS:CE	2.33	0.42
20:t:66:ILE:HB	20:t:70:LYS:HB3	2.02	0.42
21:u:36:PHE:HE2	21:u:40:PRO:HD3	1.84	0.42
22:A:108:G:H2'	22:A:109:C:O4'	2.20	0.42
22:A:236:C:H2'	22:A:237:C:H6	1.84	0.42
22:A:479:A:N3	22:A:481:G:H5''	2.35	0.42
22:A:1429:G:H2'	22:A:1430:G:C8	2.52	0.42
22:A:1733:G:C2	22:A:1734:G:C5	3.08	0.42
22:A:2038:G:H2'	22:A:2039:U:O4'	2.19	0.42
22:A:2120:G:N2	22:A:2121:G:H1'	2.35	0.42
23:B:53:A:H2'	23:B:54:G:O4'	2.20	0.42
27:F:145:VAL:HA	27:F:149:ARG:HH12	1.85	0.42
28:G:149:ALA:HA	28:G:152:ARG:HG3	2.02	0.42
31:J:136:GLN:N	31:J:137:PRO:HD3	2.35	0.42
33:L:122:VAL:CG2	33:L:125:LEU:HB2	2.49	0.42
35:N:10:LEU:O	35:N:12:ARG:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:P:17:PRO:HG3	37:P:83:ILE:O	2.19	0.42
1:a:222:C:H2'	1:a:223:A:H8	1.84	0.41
1:a:230:G:H4'	16:p:25:ARG:HH12	1.85	0.41
1:a:789:U:O2	1:a:792:A:H8	2.03	0.41
2:b:112:ARG:CZ	2:b:116:LEU:HD12	2.50	0.41
3:c:65:VAL:CG2	3:c:100:ILE:HG12	2.50	0.41
3:c:71:ARG:HD3	3:c:74:ILE:HG13	2.01	0.41
7:g:71:THR:O	7:g:90:VAL:HG22	2.19	0.41
12:l:28:GLN:HB3	12:l:80:LEU:HD12	2.02	0.41
13:m:17:ALA:HB1	13:m:44:ILE:HD12	2.02	0.41
22:A:220:G:O2'	22:A:233:A:N3	2.39	0.41
22:A:705:A:H8	22:A:705:A:O5'	2.03	0.41
22:A:1131:G:C8	22:A:2025:C:H4'	2.55	0.41
22:A:2379:G:H4'	36:O:21:LEU:HD11	2.00	0.41
22:A:2402:U:O2'	22:A:2403:C:O5'	2.34	0.41
27:F:105:ILE:O	27:F:108:PRO:HD2	2.20	0.41
27:F:129:MET:HE3	27:F:153:ILE:HD13	2.02	0.41
32:K:57:VAL:O	32:K:58:LEU:HD23	2.19	0.41
34:M:57:VAL:CG2	34:M:108:VAL:HG11	2.49	0.41
38:Q:24:TYR:CD2	38:Q:24:TYR:C	2.98	0.41
47:Z:15:ARG:HA	47:Z:15:ARG:HD3	1.81	0.41
1:a:1151:A:H1'	10:j:41:PRO:HB3	2.02	0.41
3:c:151:GLU:OE2	3:c:164:THR:HG23	2.20	0.41
4:d:102:TYR:CE2	4:d:110:ARG:HG3	2.55	0.41
4:d:173:ASP:C	4:d:175:GLY:H	2.28	0.41
7:g:124:SER:O	7:g:128:GLU:HG2	2.20	0.41
14:n:19:TYR:CD2	14:n:51:LEU:HD22	2.55	0.41
22:A:528:A:C8	22:A:528:A:H3'	2.55	0.41
22:A:898:C:H2'	22:A:899:A:C8	2.54	0.41
22:A:1541:C:H2'	22:A:1542:U:C6	2.55	0.41
22:A:2114:A:C8	22:A:2115:G:C8	3.08	0.41
23:B:42:C:OP1	27:F:63:LYS:NZ	2.46	0.41
34:M:112:LEU:HD12	34:M:112:LEU:HA	1.80	0.41
42:U:4:ILE:HG12	42:U:71:ILE:HG23	2.02	0.41
55:9:21:A:C5	55:9:46:G:C6	3.08	0.41
1:a:221:C:C2'	1:a:222:C:H5'	2.51	0.41
1:a:377:G:C6	1:a:378:G:C6	3.09	0.41
1:a:1032:G:H3'	1:a:1032:G:N3	2.35	0.41
1:a:1039:G:C4	1:a:1040:U:C5	3.09	0.41
1:a:1118:U:H2'	1:a:1119:C:H6	1.85	0.41
1:a:1312:G:N7	19:s:2:ARG:HG2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1327:C:H2'	1:a:1328:C:H6	1.84	0.41
1:a:1346:A:H2'	1:a:1346:A:N3	2.35	0.41
1:a:1347:G:O2'	9:i:110:VAL:HG22	2.20	0.41
1:a:1396:A:C2	5:e:23:THR:HG21	2.56	0.41
1:a:1526:G:P	21:u:38:GLU:HB2	2.60	0.41
1:a:1527:U:O2'	1:a:1528:U:H5'	2.20	0.41
4:d:56:GLU:CD	4:d:195:ASN:HB2	2.45	0.41
5:e:14:LEU:HD12	5:e:35:LEU:O	2.21	0.41
5:e:156:ARG:NH1	8:h:98:LEU:O	2.53	0.41
6:f:96:VAL:CG1	6:f:97:THR:H	2.27	0.41
9:i:51:LEU:HB3	9:i:56:MET:HB3	2.01	0.41
18:r:41:SER:HB3	18:r:51:GLN:HE21	1.84	0.41
22:A:522:A:H2'	22:A:523:C:H6	1.85	0.41
22:A:813:U:H2'	22:A:814:C:H6	1.85	0.41
22:A:883:G:H21	22:A:894:U:H1'	1.85	0.41
22:A:1493:C:O2'	22:A:1494:A:OP1	2.30	0.41
22:A:2289:G:N2	22:A:2346:A:OP1	2.42	0.41
22:A:2314:A:C5'	27:F:34:THR:HG21	2.50	0.41
22:A:2722:G:H4'	35:N:4:ARG:HB2	2.02	0.41
34:M:57:VAL:HG22	34:M:108:VAL:HG11	2.01	0.41
36:O:34:HIS:CE1	36:O:65:THR:HG21	2.56	0.41
1:a:448:A:H2'	1:a:448:A:N3	2.35	0.41
1:a:1158:C:C4	1:a:1160:G:C8	3.09	0.41
1:a:1233:G:H2'	1:a:1234:C:C6	2.55	0.41
15:o:44:GLU:HG2	15:o:45:HIS:N	2.36	0.41
20:t:23:ARG:O	20:t:26:MET:HG2	2.21	0.41
20:t:27:MET:HE2	20:t:27:MET:HB3	1.79	0.41
22:A:528:A:H3'	22:A:528:A:H8	1.85	0.41
22:A:576:U:H2'	22:A:577:G:C8	2.55	0.41
22:A:1430:G:H2'	22:A:1431:A:O4'	2.20	0.41
22:A:1714:U:H6	22:A:1714:U:O5'	2.02	0.41
22:A:2170:A:H2'	22:A:2171:A:C8	2.55	0.41
22:A:2212:A:OP2	22:A:2212:A:H8	2.03	0.41
22:A:2409:G:H2'	22:A:2410:G:O4'	2.21	0.41
22:A:2514:U:H2'	22:A:2515:C:H6	1.85	0.41
22:A:2639:A:H4'	31:J:96:ARG:HH22	1.85	0.41
22:A:2674:G:H2'	22:A:2675:A:H8	1.85	0.41
30:I:44:LYS:HD2	30:I:44:LYS:N	2.35	0.41
32:K:17:ARG:HA	32:K:17:ARG:HD3	1.90	0.41
39:R:38:VAL:HG13	39:R:54:VAL:HG23	2.01	0.41
42:U:50:ALA:O	42:U:51:LEU:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:U:96:LYS:O	42:U:97:SER:OG	2.36	0.41
49:1:18:HIS:CE1	49:1:40:PRO:HG3	2.56	0.41
51:3:14:LYS:HG3	51:3:22:LYS:HE2	2.02	0.41
1:a:704:A:C4	1:a:705:G:C8	3.08	0.41
1:a:831:A:C6	1:a:832:G:C8	3.09	0.41
1:a:936:C:C4	1:a:937:A:N7	2.89	0.41
1:a:1163:A:H2'	1:a:1164:G:H8	1.86	0.41
1:a:1412:C:H2'	1:a:1413:A:C8	2.56	0.41
1:a:1445:U:O5'	1:a:1445:U:H6	2.04	0.41
1:a:1464:U:P	37:P:108:ARG:HH12	2.43	0.41
3:c:21:TRP:HB3	3:c:58:ARG:H	1.85	0.41
9:i:71:ILE:HG13	9:i:72:SER:N	2.34	0.41
19:s:21:ALA:HB1	19:s:27:LYS:HG3	2.01	0.41
22:A:1073:A:H3'	22:A:1074:G:H8	1.85	0.41
22:A:1152:C:H2'	22:A:1153:C:C6	2.55	0.41
22:A:1183:U:H2'	22:A:1184:U:H6	1.86	0.41
22:A:1315:C:H2'	22:A:1316:U:H6	1.86	0.41
22:A:1551:A:H2'	22:A:1552:A:O4'	2.21	0.41
22:A:1703:G:H2'	22:A:1704:C:H6	1.85	0.41
24:C:179:GLU:HG2	24:C:180:MET:O	2.20	0.41
26:E:7:ASP:OD1	26:E:8:ALA:N	2.49	0.41
26:E:122:GLU:O	26:E:123:LYS:C	2.64	0.41
29:H:75:LEU:HG	29:H:76:GLU:N	2.36	0.41
45:X:67:LEU:HD13	45:X:77:TYR:CE1	2.56	0.41
53:5:64:VAL:HG12	53:5:64:VAL:O	2.20	0.41
1:a:128:G:O2'	1:a:129:A:H5'	2.21	0.41
1:a:220:G:C2	1:a:221:C:C6	3.09	0.41
1:a:293:G:C5	1:a:305:G:N2	2.88	0.41
1:a:411:A:O2'	1:a:413:G:O4'	2.28	0.41
1:a:526:C:P	12:l:87:LYS:HE3	2.61	0.41
1:a:1243:C:H2'	1:a:1244:G:C8	2.56	0.41
1:a:1315:U:O2	1:a:1360:A:H2	2.04	0.41
3:c:69:THR:OG1	3:c:70:ALA:N	2.53	0.41
9:i:129:ARG:HH21	55:9:35:G:P	2.43	0.41
10:j:11:LYS:HG2	10:j:97:ASP:OD1	2.21	0.41
11:k:35:ASP:OD1	11:k:35:ASP:N	2.47	0.41
12:l:74:GLN:O	12:l:76:HIS:N	2.53	0.41
22:A:921:C:H2'	22:A:922:C:C6	2.56	0.41
22:A:996:A:OP2	38:Q:92:LYS:HD2	2.20	0.41
22:A:1022:G:C5	22:A:1140:C:C4	3.09	0.41
22:A:1068:G:O2'	22:A:1070:A:N7	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:1079:C:C4	22:A:1080:A:C6	3.08	0.41
22:A:1415:U:H3	22:A:1587:G:H1	1.69	0.41
22:A:1638:C:H1'	22:A:2698:U:O2'	2.20	0.41
22:A:2698:U:H2'	22:A:2699:C:C6	2.56	0.41
29:H:99:ILE:HB	29:H:115:VAL:HG21	2.02	0.41
53:5:24:SER:CB	53:5:86:MET:HA	2.49	0.41
1:a:511:C:H5'	4:d:43:ARG:NH1	2.35	0.41
1:a:728:A:H2'	1:a:729:A:C8	2.55	0.41
1:a:895:G:H2'	1:a:896:C:C6	2.56	0.41
1:a:1130:A:C8	1:a:1146:A:N1	2.89	0.41
2:b:65:LYS:HB2	2:b:89:PHE:HE2	1.86	0.41
3:c:38:VAL:O	3:c:42:LEU:HD23	2.20	0.41
3:c:174:LEU:HD21	3:c:200:TRP:HE1	1.85	0.41
4:d:20:LEU:HD21	4:d:62:ARG:O	2.21	0.41
4:d:109:THR:C	4:d:111:ALA:N	2.77	0.41
4:d:114:ARG:HE	4:d:117:VAL:HB	1.86	0.41
10:j:48:ARG:HD3	14:n:101:TRP:CZ3	2.55	0.41
14:n:83:LYS:HA	14:n:83:LYS:HD2	1.74	0.41
22:A:132:G:H2'	22:A:133:U:C6	2.56	0.41
22:A:612:G:O2'	22:A:616:A:N6	2.54	0.41
22:A:677:A:O2'	22:A:2071:A:H5'	2.20	0.41
22:A:858:G:N2	22:A:920:A:C2	2.89	0.41
22:A:1111:A:O2'	22:A:1112:G:H4'	2.21	0.41
22:A:1178:C:H2'	22:A:1179:G:C8	2.56	0.41
22:A:1812:U:O2'	24:C:44:ASN:N	2.53	0.41
22:A:1842:G:H2'	22:A:1843:C:H6	1.85	0.41
22:A:2849:U:H4'	22:A:2868:A:C2	2.56	0.41
23:B:8:C:O3'	36:O:25:ARG:NH1	2.54	0.41
23:B:68:C:H2'	23:B:69:G:O4'	2.21	0.41
24:C:199:HIS:O	24:C:199:HIS:CG	2.73	0.41
27:F:63:LYS:H	54:6:6:HIS:CE1	2.39	0.41
28:G:8:VAL:O	28:G:49:LEU:N	2.53	0.41
30:I:112:LYS:HZ2	30:I:128:ILE:HD12	1.86	0.41
33:L:109:LYS:HA	33:L:126:ARG:O	2.21	0.41
35:N:92:GLY:HA2	35:N:94:TYR:CZ	2.56	0.41
36:O:52:SER:OG	36:O:54:VAL:HG12	2.20	0.41
1:a:51:A:H4'	1:a:52:C:C5'	2.51	0.41
1:a:674:G:H21	11:k:117:HIS:HB2	1.85	0.41
1:a:1095:U:H2'	1:a:1096:C:C6	2.56	0.41
11:k:53:GLY:H	11:k:56:LYS:HD3	1.85	0.41
15:o:45:HIS:C	15:o:47:LYS:N	2.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:r:32:ILE:HD12	18:r:36:GLY:HA2	2.02	0.41
21:u:19:LYS:HD2	21:u:19:LYS:HA	1.80	0.41
22:A:8:C:H2'	22:A:9:G:O4'	2.21	0.41
22:A:287:G:H2'	22:A:288:U:C6	2.55	0.41
22:A:356:G:H2'	22:A:357:C:H6	1.86	0.41
22:A:771:G:OP2	50:2:11:LYS:HE3	2.21	0.41
22:A:900:A:C5	22:A:901:C:C5	3.09	0.41
22:A:1040:A:H61	22:A:1115:G:H1	1.67	0.41
22:A:1824:G:O2'	24:C:245:THR:HG22	2.21	0.41
22:A:1994:C:H6	22:A:1994:C:O5'	2.04	0.41
22:A:2032:G:N2	25:D:151:THR:OG1	2.49	0.41
22:A:2375:G:N2	22:A:2378:A:OP2	2.43	0.41
22:A:2705:A:O2'	22:A:2852:G:OP1	2.27	0.41
23:B:52:A:N6	36:O:33:ARG:HH21	2.19	0.41
24:C:153:LEU:HD22	24:C:175:LEU:CD2	2.51	0.41
39:R:27:ILE:HG22	39:R:31:GLU:HB3	2.01	0.41
53:5:61:ARG:O	53:5:61:ARG:HG2	2.21	0.41
1:a:360:G:O2'	1:a:361:G:H5'	2.20	0.41
1:a:435:A:H2	4:d:153:ARG:NH2	2.19	0.41
1:a:436:C:H1'	4:d:153:ARG:HH21	1.86	0.41
1:a:608:A:C2	1:a:609:A:H1'	2.56	0.41
1:a:746:A:H2'	1:a:747:A:C8	2.55	0.41
1:a:747:A:H2'	1:a:748:G:H8	1.86	0.41
1:a:815:A:H4'	1:a:817:C:C5	2.56	0.41
1:a:815:A:N3	1:a:1527:U:H1'	2.36	0.41
1:a:922:G:H2'	1:a:923:A:C8	2.56	0.41
1:a:991:U:O2'	1:a:992:U:O5'	2.37	0.41
1:a:1299:A:O2'	1:a:1301:U:H5'	2.21	0.41
1:a:1313:U:H2'	1:a:1314:C:H6	1.85	0.41
1:a:1316:G:N2	1:a:1318:A:H3'	2.35	0.41
1:a:1373:G:H5''	7:g:35:LYS:HB2	2.03	0.41
1:a:1413:A:H2	1:a:1487:G:H22	1.67	0.41
2:b:161:PHE:CZ	2:b:185:ILE:HD11	2.56	0.41
3:c:107:LYS:HB3	3:c:143:LEU:HD21	2.03	0.41
4:d:178:GLU:N	4:d:178:GLU:OE1	2.54	0.41
7:g:125:ASP:O	7:g:130:LYS:N	2.48	0.41
8:h:48:PHE:O	8:h:49:LYS:HD3	2.21	0.41
9:i:5:TYR:CG	9:i:88:GLU:HB3	2.55	0.41
11:k:21:HIS:HB2	11:k:32:THR:HG22	2.02	0.41
12:l:76:HIS:O	12:l:77:SER:HB2	2.21	0.41
17:q:16:MET:HE3	17:q:19:SER:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:s:35:ARG:HB3	19:s:71:GLY:HA3	2.03	0.41
22:A:13:A:O2'	22:A:15:G:O6	2.39	0.41
22:A:33:C:O2'	22:A:34:U:H5''	2.20	0.41
22:A:483:A:O4'	42:U:44:HIS:HB3	2.20	0.41
22:A:921:C:H2'	22:A:922:C:H6	1.86	0.41
22:A:1182:G:H2'	22:A:1183:U:O4'	2.21	0.41
22:A:1315:C:C2	22:A:1338:G:N2	2.89	0.41
22:A:1636:U:H2'	22:A:1637:A:H8	1.84	0.41
22:A:2204:G:C5	22:A:2221:G:C2	3.09	0.41
22:A:2407:A:C4	22:A:2408:U:C5	3.09	0.41
22:A:2454:G:C6	22:A:2499:C:N4	2.89	0.41
22:A:2672:U:O5'	22:A:2672:U:H6	2.03	0.41
23:B:9:G:C2	23:B:10:G:C8	3.09	0.41
25:D:4:LEU:HD13	25:D:29:VAL:HG11	2.02	0.41
25:D:52:THR:HG22	25:D:80:TRP:CZ3	2.56	0.41
27:F:39:VAL:HG21	27:F:49:LEU:CD1	2.51	0.41
28:G:114:HIS:HB2	28:G:150:TYR:HE2	1.86	0.41
29:H:67:ALA:HA	29:H:70:GLU:HG3	2.03	0.41
30:I:116:MET:HG2	30:I:124:MET:SD	2.61	0.41
33:L:19:LEU:HD22	33:L:27:LEU:HD22	2.03	0.41
33:L:73:ILE:HD12	33:L:106:GLU:HG3	2.03	0.41
35:N:10:LEU:HD13	35:N:40:LYS:HG2	2.02	0.41
41:T:37:ASP:O	41:T:38:ALA:C	2.64	0.41
42:U:23:LYS:HB2	42:U:23:LYS:HE2	1.75	0.41
43:V:44:HIS:NE2	43:V:85:LYS:HB2	2.36	0.41
46:Y:28:LEU:CD1	46:Y:42:LEU:HB3	2.50	0.41
46:Y:37:LEU:HD11	46:Y:42:LEU:HD12	2.02	0.41
46:Y:56:LEU:HD23	46:Y:56:LEU:HA	1.71	0.41
1:a:184:G:H5'	1:a:224:U:O2'	2.21	0.41
1:a:274:A:H1'	1:a:275:G:C8	2.55	0.41
1:a:303:A:O2'	1:a:555:U:H4'	2.21	0.41
1:a:965:U:H5''	1:a:966:2MG:OP1	2.21	0.41
1:a:1040:U:C2	1:a:1041:G:C8	3.09	0.41
1:a:1263:C:H2'	1:a:1264:U:H6	1.86	0.41
1:a:1320:C:H2'	1:a:1321:U:C6	2.56	0.41
4:d:57:LYS:HA	4:d:199:ILE:CD1	2.51	0.41
7:g:65:LEU:O	7:g:68:VAL:HG12	2.21	0.41
12:l:122:LYS:HA	12:l:122:LYS:HD2	1.88	0.41
13:m:7:ASN:O	13:m:9:PRO:HD3	2.21	0.41
16:p:3:THR:HG22	16:p:66:THR:OG1	2.20	0.41
17:q:75:VAL:HG12	17:q:76:ARG:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:197:A:H4'	22:A:2069:G7M:OP2	2.20	0.41
22:A:324:A:H2'	22:A:325:G:O4'	2.21	0.41
22:A:340:A:H2'	22:A:341:C:O4'	2.21	0.41
22:A:664:G:H2'	22:A:665:U:O4'	2.21	0.41
22:A:1591:A:H2'	22:A:1592:C:H6	1.86	0.41
22:A:1782:U:H1'	22:A:2609:U:O4'	2.20	0.41
22:A:2477:U:C2	52:4:4:ARG:NH2	2.85	0.41
24:C:66:PHE:HB3	24:C:150:GLY:O	2.21	0.41
30:I:69:VAL:O	30:I:69:VAL:HG13	2.21	0.41
35:N:56:LYS:HE2	35:N:87:PHE:O	2.21	0.41
47:Z:5:LYS:HA	47:Z:35:VAL:O	2.21	0.41
53:5:103:ASN:HD22	53:5:113:PHE:HZ	1.69	0.41
55:9:61:C:H2'	55:9:62:C:O4'	2.21	0.41
1:a:397:A:O2'	1:a:399:G:OP2	2.38	0.40
1:a:433:G:C4	1:a:434:U:C5	3.09	0.40
1:a:903:G:H2'	1:a:904:U:C6	2.56	0.40
1:a:1279:G:O2'	1:a:1281:C:OP2	2.26	0.40
1:a:1287:A:C6	1:a:1288:A:C6	3.08	0.40
3:c:187:GLU:HB2	3:c:194:VAL:HG13	2.02	0.40
4:d:203:TYR:HD1	4:d:203:TYR:HA	1.69	0.40
6:f:53:LYS:O	6:f:54:LEU:HB2	2.21	0.40
9:i:85:ALA:C	9:i:87:MET:H	2.29	0.40
10:j:14:ASP:HB3	10:j:17:LEU:CD2	2.51	0.40
10:j:65:TYR:HB3	14:n:96:LEU:HD11	2.03	0.40
15:o:17:ASP:OD1	15:o:20:ASP:N	2.44	0.40
21:u:19:LYS:HE3	21:u:19:LYS:HB3	1.86	0.40
22:A:24:G:O2'	40:S:78:GLU:O	2.37	0.40
22:A:85:G:OP1	42:U:6:ARG:N	2.54	0.40
22:A:443:A:N7	26:E:40:ARG:HG2	2.36	0.40
22:A:1125:G:C6	22:A:1126:A:N6	2.89	0.40
22:A:1140:C:H5'	31:J:26:GLY:HA3	2.02	0.40
22:A:1198:U:H2'	22:A:1199:U:H6	1.86	0.40
22:A:1283:G:H1'	22:A:1329:U:H3	1.86	0.40
22:A:1315:C:H2'	22:A:1316:U:C6	2.56	0.40
22:A:1723:G:H2'	22:A:1724:G:H5'	2.03	0.40
22:A:2461:A:H2'	22:A:2462:C:C6	2.56	0.40
22:A:2655:G:O2'	22:A:2656:U:P	2.79	0.40
25:D:149:ASN:OD1	25:D:150:GLN:N	2.37	0.40
27:F:135:ILE:HD12	27:F:135:ILE:HA	1.94	0.40
29:H:108:VAL:HG12	29:H:109:GLU:N	2.36	0.40
1:a:109:A:C6	1:a:327:A:C6	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:377:G:H8	1:a:377:G:OP2	2.04	0.40
1:a:389:A:H5''	1:a:390:U:H5	1.87	0.40
1:a:1049:U:H2'	14:n:2:LYS:HD3	2.02	0.40
1:a:1271:A:H2'	1:a:1272:G:C8	2.56	0.40
1:a:1351:U:H4'	7:g:32:ASP:OD1	2.20	0.40
4:d:64:TYR:HE2	4:d:99:ASN:ND2	2.19	0.40
6:f:47:LEU:HD13	6:f:51:ILE:HD12	2.03	0.40
13:m:8:ILE:HG21	27:F:142:TYR:CD2	2.56	0.40
14:n:51:LEU:HB3	14:n:52:PRO:HD2	2.03	0.40
22:A:397:U:H2'	22:A:398:C:C6	2.56	0.40
22:A:955:PSU:H5'	34:M:86:LYS:HD2	2.02	0.40
22:A:1021:A:H3'	22:A:1021:A:N3	2.36	0.40
22:A:1083:U:H1'	22:A:1086:A:N1	2.36	0.40
22:A:1378:A:O2'	22:A:1380:G:OP2	2.39	0.40
22:A:2286:G:H5''	49:1:29:LYS:HD2	2.03	0.40
22:A:2636:C:H2'	22:A:2637:U:C6	2.56	0.40
30:I:11:GLN:HE22	30:I:37:PHE:HE2	1.68	0.40
33:L:2:ARG:HA	33:L:2:ARG:HD2	1.63	0.40
40:S:3:THR:OG1	40:S:3:THR:O	2.39	0.40
40:S:24:ILE:HA	40:S:27:LYS:HG3	2.03	0.40
41:T:53:VAL:HG12	41:T:54:GLU:H	1.85	0.40
47:Z:37:ARG:HA	47:Z:37:ARG:HD3	1.86	0.40
50:2:22:MET:O	50:2:28:ARG:NH1	2.53	0.40
51:3:54:LEU:HA	51:3:57:VAL:HG12	2.03	0.40
53:5:72:LEU:HD23	53:5:72:LEU:H	1.87	0.40
54:6:44:PHE:HA	54:6:47:LYS:HB3	2.03	0.40
1:a:80:A:O2'	1:a:90:C:H1'	2.21	0.40
1:a:455:G:C2	1:a:478:A:C2	3.09	0.40
1:a:753:A:OP1	15:o:68:TYR:OH	2.27	0.40
1:a:1245:C:H2'	1:a:1246:A:C8	2.57	0.40
2:b:55:GLU:O	2:b:59:ILE:HG12	2.21	0.40
2:b:187:ASP:OD1	2:b:188:THR:N	2.55	0.40
5:e:43:GLY:O	5:e:73:VAL:HG12	2.22	0.40
7:g:49:LEU:CD2	7:g:60:ALA:HB1	2.51	0.40
9:i:64:ILE:HG21	9:i:78:ILE:HG12	2.03	0.40
10:j:8:ILE:HG13	10:j:74:VAL:HG12	2.03	0.40
12:l:66:ILE:HA	12:l:96:THR:CG2	2.51	0.40
20:t:26:MET:HA	20:t:29:THR:HG22	2.02	0.40
22:A:231:A:H2'	22:A:232:G:O4'	2.21	0.40
22:A:560:C:H2'	22:A:561:G:O4'	2.22	0.40
22:A:651:G:OP1	51:3:18:LYS:HB2	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:A:713:G:H2'	22:A:714:U:O4'	2.21	0.40
22:A:774:G:H8	22:A:774:G:H2'	1.73	0.40
22:A:852:U:H2'	22:A:853:C:H6	1.85	0.40
22:A:1104:C:H2'	22:A:1105:U:N1	2.36	0.40
22:A:1495:A:H1'	22:A:1579:A:H5'	2.03	0.40
22:A:2553:G:N3	22:A:2583:G:H1'	2.36	0.40
22:A:2708:G:O2'	22:A:2709:G:H5'	2.21	0.40
23:B:29:A:H2'	23:B:30:C:O4'	2.21	0.40
32:K:43:ILE:HD13	32:K:52:VAL:HB	2.03	0.40
34:M:2:LEU:HD23	34:M:2:LEU:HA	1.91	0.40
35:N:29:VAL:O	35:N:78:LYS:HG2	2.21	0.40
40:S:83:LYS:HD3	40:S:95:ARG:NE	2.36	0.40
53:5:63:ALA:HB3	53:5:77:VAL:HG11	2.03	0.40
1:a:56:U:H2'	1:a:57:G:H8	1.87	0.40
1:a:327:A:O2'	1:a:328:C:O4'	2.37	0.40
1:a:379:C:H2'	1:a:380:G:C5	2.56	0.40
1:a:501:C:H1'	1:a:549:C:O2'	2.21	0.40
1:a:1516:2MG:HM23	1:a:1518:MA6:C2	2.52	0.40
12:l:41:PRO:HG2	12:l:46:SER:N	2.37	0.40
22:A:120:U:H5''	22:A:122:G:OP2	2.21	0.40
22:A:201:C:OP1	45:X:17:ARG:NH1	2.49	0.40
22:A:866:A:N7	22:A:914:G:C6	2.89	0.40
22:A:878:A:C8	22:A:879:G:C8	3.09	0.40
22:A:962:G:H2'	22:A:963:U:C6	2.56	0.40
22:A:1341:G:OP1	22:A:1397:U:N3	2.43	0.40
31:J:15:TRP:CE3	31:J:55:ILE:HD11	2.57	0.40
31:J:16:TYR:CG	31:J:140:LEU:HD22	2.56	0.40
33:L:10:GLU:H	33:L:10:GLU:CD	2.29	0.40
33:L:29:LYS:O	33:L:29:LYS:HD3	2.21	0.40
41:T:72:GLN:OE1	41:T:72:GLN:HA	2.22	0.40
45:X:58:ILE:HG12	45:X:66:VAL:HG21	2.03	0.40
45:X:62:GLY:O	45:X:65:THR:N	2.55	0.40
48:0:27:LEU:HD23	48:0:36:LYS:HD3	2.04	0.40
1:a:49:U:O2'	1:a:50:A:H2'	2.22	0.40
1:a:500:G:H2'	1:a:501:C:C6	2.57	0.40
1:a:1225:A:H5'	1:a:1226:C:OP2	2.21	0.40
1:a:1342:C:H2'	1:a:1343:G:C8	2.56	0.40
2:b:144:GLU:O	2:b:148:GLY:HA3	2.22	0.40
2:b:213:LEU:HD23	2:b:213:LEU:HA	1.65	0.40
4:d:32:LYS:HB3	4:d:35:GLN:CB	2.51	0.40
4:d:109:THR:O	4:d:110:ARG:C	2.64	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:e:132:PRO:HA	5:e:135:VAL:HG12	2.04	0.40
7:g:119:LEU:O	7:g:123:LEU:HD23	2.22	0.40
9:i:45:MET:O	9:i:49:GLN:CB	2.64	0.40
9:i:104:THR:H	9:i:104:THR:HG23	1.65	0.40
11:k:81:LEU:HD23	11:k:81:LEU:HA	1.90	0.40
13:m:75:SER:O	13:m:78:ARG:HG2	2.22	0.40
19:s:8:PRO:HG2	19:s:40:PHE:CZ	2.57	0.40
22:A:144:A:H4'	41:T:2:ILE:HD12	2.04	0.40
22:A:379:G:O4'	22:A:2232:C:H5''	2.21	0.40
22:A:551:G:C6	22:A:552:U:C4	3.10	0.40
22:A:631:A:H5'	33:L:64:PHE:CE2	2.57	0.40
22:A:927:A:H2'	22:A:928:A:H8	1.86	0.40
22:A:1058:U:H4'	30:I:9:LYS:HZ1	1.85	0.40
22:A:1263:U:HO2'	48:O:7:PRO:HD2	1.87	0.40
22:A:1928:A:H2'	22:A:1929:G:O4'	2.21	0.40
22:A:2114:A:H8	22:A:2115:G:C8	2.39	0.40
22:A:2122:U:H2'	22:A:2123:G:O4'	2.21	0.40
22:A:2142:A:N1	22:A:2150:C:C2	2.89	0.40
22:A:2290:G:C2	22:A:2343:U:O2	2.75	0.40
22:A:2591:C:H2'	22:A:2592:G:H8	1.87	0.40
24:C:7:PRO:HB3	24:C:13:ARG:HE	1.87	0.40
29:H:51:ARG:O	29:H:55:GLU:N	2.54	0.40
32:K:80:ASP:OD1	37:P:61:ARG:NH1	2.54	0.40
35:N:94:TYR:O	35:N:116:VAL:HG22	2.22	0.40
55:9:44:G:H2'	55:9:45:G:C8	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	
2	b	216/240 (90%)	179 (83%)	37 (17%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	c	204/233 (88%)	187 (92%)	17 (8%)	0	100	100
4	d	203/206 (98%)	158 (78%)	45 (22%)	0	100	100
5	e	155/167 (93%)	126 (81%)	27 (17%)	2 (1%)	9	35
6	f	98/135 (73%)	71 (72%)	25 (26%)	2 (2%)	6	27
7	g	149/179 (83%)	132 (89%)	17 (11%)	0	100	100
8	h	127/130 (98%)	112 (88%)	15 (12%)	0	100	100
9	i	125/130 (96%)	101 (81%)	23 (18%)	1 (1%)	16	45
10	j	96/103 (93%)	76 (79%)	18 (19%)	2 (2%)	5	26
11	k	114/129 (88%)	94 (82%)	20 (18%)	0	100	100
12	l	121/124 (98%)	87 (72%)	33 (27%)	1 (1%)	16	45
13	m	112/118 (95%)	92 (82%)	18 (16%)	2 (2%)	6	29
14	n	99/102 (97%)	82 (83%)	17 (17%)	0	100	100
15	o	86/89 (97%)	78 (91%)	7 (8%)	1 (1%)	10	37
16	p	80/82 (98%)	68 (85%)	12 (15%)	0	100	100
17	q	78/84 (93%)	66 (85%)	9 (12%)	3 (4%)	2	16
18	r	63/75 (84%)	52 (82%)	11 (18%)	0	100	100
19	s	77/92 (84%)	64 (83%)	13 (17%)	0	100	100
20	t	83/87 (95%)	75 (90%)	8 (10%)	0	100	100
21	u	63/71 (89%)	44 (70%)	18 (29%)	1 (2%)	7	31
24	C	269/273 (98%)	244 (91%)	25 (9%)	0	100	100
25	D	207/209 (99%)	183 (88%)	24 (12%)	0	100	100
26	E	199/201 (99%)	181 (91%)	18 (9%)	0	100	100
27	F	175/179 (98%)	153 (87%)	22 (13%)	0	100	100
28	G	174/177 (98%)	146 (84%)	26 (15%)	2 (1%)	11	39
29	H	147/149 (99%)	119 (81%)	28 (19%)	0	100	100
30	I	139/142 (98%)	111 (80%)	28 (20%)	0	100	100
31	J	140/142 (99%)	129 (92%)	11 (8%)	0	100	100
32	K	120/123 (98%)	102 (85%)	18 (15%)	0	100	100
33	L	141/144 (98%)	115 (82%)	25 (18%)	1 (1%)	18	49
34	M	134/136 (98%)	123 (92%)	9 (7%)	2 (2%)	8	32
35	N	118/127 (93%)	104 (88%)	14 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	O	114/117 (97%)	105 (92%)	9 (8%)	0	100	100
37	P	112/115 (97%)	100 (89%)	12 (11%)	0	100	100
38	Q	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
39	R	101/103 (98%)	84 (83%)	16 (16%)	1 (1%)	12	40
40	S	108/110 (98%)	93 (86%)	14 (13%)	1 (1%)	14	43
41	T	91/100 (91%)	77 (85%)	14 (15%)	0	100	100
42	U	100/104 (96%)	81 (81%)	15 (15%)	4 (4%)	2	15
43	V	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
44	W	73/85 (86%)	67 (92%)	6 (8%)	0	100	100
45	X	75/78 (96%)	68 (91%)	7 (9%)	0	100	100
46	Y	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
47	Z	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
48	0	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
49	1	48/55 (87%)	44 (92%)	4 (8%)	0	100	100
50	2	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
51	3	62/65 (95%)	55 (89%)	5 (8%)	2 (3%)	3	19
52	4	36/38 (95%)	28 (78%)	8 (22%)	0	100	100
53	5	129/165 (78%)	104 (81%)	25 (19%)	0	100	100
54	6	64/70 (91%)	53 (83%)	11 (17%)	0	100	100
All	All	5847/6220 (94%)	5011 (86%)	808 (14%)	28 (0%)	26	55

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	o	46	LYS
17	q	70	LYS
51	3	31	ILE
51	3	32	LEU
5	e	122	VAL
12	l	102	ASP
28	G	119	GLY
34	M	59	ARG
39	R	54	VAL
42	U	89	GLY
5	e	121	ASN

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Mol	Chain	Res	Type
13	m	4	ALA
13	m	5	GLY
21	u	36	PHE
28	G	118	ALA
33	L	128	THR
34	M	58	LYS
6	f	53	LYS
10	j	57	VAL
10	j	58	ASN
17	q	48	GLU
42	U	98	ASN
9	i	91	GLU
17	q	69	THR
40	S	64	ALA
42	U	50	ALA
42	U	87	GLU
6	f	54	LEU

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	
2	b	180/198 (91%)	177 (98%)	3 (2%)	53	71
3	c	170/190 (90%)	170 (100%)	0	100	100
4	d	172/173 (99%)	172 (100%)	0	100	100
5	e	114/126 (90%)	114 (100%)	0	100	100
6	f	87/116 (75%)	87 (100%)	0	100	100
7	g	124/147 (84%)	124 (100%)	0	100	100
8	h	104/105 (99%)	104 (100%)	0	100	100
9	i	105/107 (98%)	105 (100%)	0	100	100
10	j	86/90 (96%)	86 (100%)	0	100	100
11	k	89/99 (90%)	89 (100%)	0	100	100
12	l	103/104 (99%)	103 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	m	92/96 (96%)	92 (100%)	0	100	100
14	n	79/84 (94%)	78 (99%)	1 (1%)	61	74
15	o	76/77 (99%)	76 (100%)	0	100	100
16	p	65/65 (100%)	65 (100%)	0	100	100
17	q	74/78 (95%)	74 (100%)	0	100	100
18	r	48/65 (74%)	48 (100%)	0	100	100
19	s	70/79 (89%)	69 (99%)	1 (1%)	59	73
20	t	65/66 (98%)	65 (100%)	0	100	100
21	u	44/61 (72%)	44 (100%)	0	100	100
24	C	216/218 (99%)	216 (100%)	0	100	100
25	D	164/164 (100%)	163 (99%)	1 (1%)	78	81
26	E	165/165 (100%)	165 (100%)	0	100	100
27	F	148/150 (99%)	148 (100%)	0	100	100
28	G	137/138 (99%)	137 (100%)	0	100	100
29	H	114/114 (100%)	114 (100%)	0	100	100
30	I	109/110 (99%)	109 (100%)	0	100	100
31	J	116/116 (100%)	116 (100%)	0	100	100
32	K	103/104 (99%)	102 (99%)	1 (1%)	68	76
33	L	102/103 (99%)	102 (100%)	0	100	100
34	M	109/109 (100%)	109 (100%)	0	100	100
35	N	100/103 (97%)	100 (100%)	0	100	100
36	O	86/87 (99%)	85 (99%)	1 (1%)	63	75
37	P	99/100 (99%)	98 (99%)	1 (1%)	68	76
38	Q	89/90 (99%)	89 (100%)	0	100	100
39	R	84/84 (100%)	84 (100%)	0	100	100
40	S	93/93 (100%)	93 (100%)	0	100	100
41	T	80/84 (95%)	80 (100%)	0	100	100
42	U	83/85 (98%)	83 (100%)	0	100	100
43	V	78/78 (100%)	77 (99%)	1 (1%)	61	74
44	W	57/63 (90%)	57 (100%)	0	100	100
45	X	67/68 (98%)	66 (98%)	1 (2%)	57	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	Y	55/55 (100%)	54 (98%)	1 (2%)	51	70
47	Z	48/49 (98%)	48 (100%)	0	100	100
48	0	47/48 (98%)	47 (100%)	0	100	100
49	1	45/49 (92%)	45 (100%)	0	100	100
50	2	38/38 (100%)	38 (100%)	0	100	100
51	3	51/52 (98%)	51 (100%)	0	100	100
52	4	34/34 (100%)	34 (100%)	0	100	100
53	5	100/123 (81%)	100 (100%)	0	100	100
54	6	59/62 (95%)	58 (98%)	1 (2%)	53	71
All	All	4823/5062 (95%)	4810 (100%)	13 (0%)	84	86

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	b	20	ARG
2	b	93	HIS
2	b	147	LEU
14	n	79	LEU
19	s	23	GLU
25	D	40	LEU
32	K	76	VAL
36	O	65	THR
37	P	69	VAL
43	V	66	ASP
45	X	6	VAL
46	Y	19	LEU
54	6	13	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (93) such sidechains are listed below:

Mol	Chain	Res	Type
2	b	41	ASN
3	c	7	ASN
3	c	68	HIS
3	c	101	ASN
3	c	138	GLN
3	c	189	HIS
4	d	39	GLN

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Mol	Chain	Res	Type
4	d	40	HIS
4	d	58	GLN
4	d	88	ASN
4	d	99	ASN
4	d	119	HIS
4	d	195	ASN
4	d	197	HIS
5	e	88	HIS
7	g	8	GLN
7	g	67	ASN
9	i	30	ASN
9	i	49	GLN
9	i	74	GLN
11	k	23	HIS
11	k	27	ASN
11	k	39	ASN
11	k	80	ASN
11	k	117	HIS
13	m	13	HIS
13	m	51	GLN
13	m	104	ASN
14	n	60	GLN
14	n	66	GLN
15	o	27	GLN
15	o	36	ASN
15	o	45	HIS
16	p	18	GLN
16	p	26	ASN
17	q	30	HIS
18	r	30	ASN
18	r	51	GLN
19	s	51	HIS
19	s	56	HIS
20	t	47	GLN
20	t	51	ASN
20	t	77	ASN
24	C	20	ASN
24	C	45	ASN
24	C	52	HIS
24	C	89	ASN
24	C	127	ASN
24	C	242	HIS

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Mol	Chain	Res	Type
24	C	250	GLN
25	D	32	ASN
25	D	49	GLN
25	D	136	ASN
25	D	164	GLN
26	E	41	GLN
27	F	51	ASN
28	G	44	HIS
28	G	115	GLN
28	G	127	GLN
29	H	128	HIS
29	H	145	ASN
30	I	18	ASN
30	I	106	GLN
30	I	110	GLN
31	J	58	ASN
31	J	80	HIS
32	K	9	ASN
32	K	29	HIS
35	N	107	ASN
36	O	29	HIS
36	O	38	GLN
36	O	98	GLN
37	P	6	GLN
37	P	11	GLN
37	P	65	ASN
38	Q	70	GLN
38	Q	71	ASN
39	R	82	HIS
40	S	7	HIS
40	S	31	GLN
41	T	15	HIS
42	U	65	GLN
42	U	98	ASN
43	V	75	GLN
44	W	8	ASN
44	W	72	ASN
46	Y	15	ASN
47	Z	19	HIS
48	0	5	ASN
48	0	41	HIS
50	2	26	ASN

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Mol	Chain	Res	Type
52	4	35	GLN
54	6	41	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1538/1539 (99%)	313 (20%)	0
22	A	2898/2903 (99%)	589 (20%)	31 (1%)
23	B	119/120 (99%)	22 (18%)	2 (1%)
55	9	76/77 (98%)	28 (36%)	3 (3%)
56	x	2/3 (66%)	0	0
All	All	4633/4642 (99%)	952 (20%)	36 (0%)

All (952) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	4	U
1	a	5	U
1	a	6	G
1	a	7	A
1	a	9	G
1	a	16	A
1	a	19	A
1	a	22	G
1	a	32	A
1	a	39	G
1	a	41	G
1	a	42	G
1	a	47	C
1	a	48	C
1	a	51	A
1	a	54	C
1	a	55	A
1	a	71	A
1	a	77	A
1	a	82	G
1	a	84	U
1	a	85	U
1	a	87	C
1	a	90	C
1	a	91	U

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Mol	Chain	Res	Type
1	a	92	U
1	a	94	G
1	a	95	C
1	a	96	U
1	a	98	A
1	a	116	A
1	a	121	U
1	a	122	G
1	a	130	A
1	a	144	G
1	a	145	G
1	a	151	A
1	a	160	A
1	a	163	C
1	a	164	G
1	a	168	G
1	a	172	A
1	a	177	G
1	a	183	C
1	a	184	G
1	a	192	A
1	a	197	A
1	a	204	G
1	a	208	U
1	a	209	U
1	a	210	C
1	a	212	G
1	a	222	C
1	a	226	G
1	a	240	G
1	a	245	U
1	a	247	G
1	a	251	G
1	a	266	G
1	a	267	C
1	a	280	C
1	a	281	G
1	a	289	G
1	a	299	G
1	a	306	A
1	a	321	A
1	a	326	G

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Mol	Chain	Res	Type
1	a	328	C
1	a	329	A
1	a	330	C
1	a	344	A
1	a	345	C
1	a	351	G
1	a	352	C
1	a	353	A
1	a	355	C
1	a	356	A
1	a	359	G
1	a	360	G
1	a	366	A
1	a	367	U
1	a	372	C
1	a	373	A
1	a	374	A
1	a	375	U
1	a	377	G
1	a	379	C
1	a	381	C
1	a	384	G
1	a	388	G
1	a	389	A
1	a	406	G
1	a	409	U
1	a	411	A
1	a	413	G
1	a	415	A
1	a	421	U
1	a	422	C
1	a	423	G
1	a	424	G
1	a	425	G
1	a	426	U
1	a	429	U
1	a	433	G
1	a	436	C
1	a	437	U
1	a	439	U
1	a	441	A
1	a	442	G

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Mol	Chain	Res	Type
1	a	460	A
1	a	462	G
1	a	465	A
1	a	467	U
1	a	468	A
1	a	469	C
1	a	474	G
1	a	479	U
1	a	484	G
1	a	485	U
1	a	486	U
1	a	495	A
1	a	496	A
1	a	500	G
1	a	502	A
1	a	505	G
1	a	511	C
1	a	519	C
1	a	521	G
1	a	531	U
1	a	532	A
1	a	534	U
1	a	543	U
1	a	544	G
1	a	547	A
1	a	549	C
1	a	559	A
1	a	562	U
1	a	572	A
1	a	573	A
1	a	576	C
1	a	577	G
1	a	596	A
1	a	632	U
1	a	633	G
1	a	634	C
1	a	648	A
1	a	656	G
1	a	665	A
1	a	691	G
1	a	695	A
1	a	703	G

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Mol	Chain	Res	Type
1	a	704	A
1	a	705	G
1	a	721	G
1	a	723	U
1	a	724	G
1	a	731	G
1	a	744	C
1	a	755	G
1	a	760	G
1	a	777	A
1	a	792	A
1	a	794	A
1	a	802	A
1	a	812	G
1	a	814	A
1	a	815	A
1	a	817	C
1	a	818	G
1	a	819	A
1	a	820	U
1	a	829	G
1	a	832	G
1	a	836	G
1	a	841	C
1	a	843	U
1	a	844	G
1	a	846	G
1	a	851	G
1	a	872	A
1	a	889	A
1	a	890	G
1	a	891	U
1	a	902	G
1	a	926	G
1	a	934	C
1	a	935	A
1	a	960	U
1	a	961	U
1	a	965	U
1	a	966	2MG
1	a	967	5MC
1	a	968	A

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Mol	Chain	Res	Type
1	a	969	A
1	a	971	G
1	a	972	C
1	a	974	A
1	a	975	A
1	a	976	G
1	a	977	A
1	a	992	U
1	a	993	G
1	a	1000	A
1	a	1004	A
1	a	1025	U
1	a	1026	G
1	a	1027	C
1	a	1028	C
1	a	1030	U
1	a	1031	C
1	a	1033	G
1	a	1034	G
1	a	1045	C
1	a	1053	G
1	a	1054	C
1	a	1064	G
1	a	1065	U
1	a	1089	G
1	a	1094	G
1	a	1101	A
1	a	1104	G
1	a	1124	G
1	a	1126	U
1	a	1127	G
1	a	1130	A
1	a	1136	C
1	a	1137	C
1	a	1138	G
1	a	1139	G
1	a	1157	A
1	a	1158	C
1	a	1159	U
1	a	1160	G
1	a	1168	U
1	a	1169	A

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Mol	Chain	Res	Type
1	a	1174	G
1	a	1181	G
1	a	1182	G
1	a	1183	U
1	a	1184	G
1	a	1191	A
1	a	1192	C
1	a	1195	C
1	a	1196	A
1	a	1201	A
1	a	1202	U
1	a	1212	U
1	a	1225	A
1	a	1226	C
1	a	1227	A
1	a	1228	C
1	a	1236	A
1	a	1238	A
1	a	1240	U
1	a	1241	G
1	a	1249	C
1	a	1250	A
1	a	1256	A
1	a	1257	A
1	a	1258	G
1	a	1260	G
1	a	1261	A
1	a	1268	G
1	a	1278	G
1	a	1280	A
1	a	1282	C
1	a	1287	A
1	a	1298	U
1	a	1300	G
1	a	1301	U
1	a	1302	C
1	a	1305	G
1	a	1313	U
1	a	1323	G
1	a	1338	G
1	a	1340	A
1	a	1346	A

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Mol	Chain	Res	Type
1	a	1347	G
1	a	1348	U
1	a	1353	G
1	a	1360	A
1	a	1363	A
1	a	1370	G
1	a	1398	A
1	a	1399	C
1	a	1400	C
1	a	1406	U
1	a	1419	G
1	a	1429	A
1	a	1446	A
1	a	1448	C
1	a	1452	C
1	a	1453	G
1	a	1462	C
1	a	1482	G
1	a	1487	G
1	a	1492	A
1	a	1497	G
1	a	1502	A
1	a	1503	A
1	a	1506	U
1	a	1507	A
1	a	1517	G
1	a	1518	MA6
1	a	1519	MA6
1	a	1520	C
1	a	1529	G
1	a	1530	G
1	a	1533	C
1	a	1534	A
1	a	1535	C
1	a	1536	C
1	a	1537	U
22	A	10	A
22	A	12	U
22	A	15	G
22	A	23	G
22	A	34	U
22	A	35	G

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Mol	Chain	Res	Type
22	A	42	A
22	A	46	G
22	A	51	G
22	A	60	G
22	A	61	C
22	A	62	U
22	A	63	A
22	A	71	A
22	A	74	A
22	A	75	G
22	A	91	A
22	A	96	C
22	A	101	A
22	A	102	U
22	A	110	G
22	A	118	A
22	A	119	A
22	A	120	U
22	A	125	A
22	A	139	U
22	A	140	C
22	A	141	G
22	A	142	A
22	A	162	U
22	A	181	A
22	A	196	A
22	A	197	A
22	A	199	A
22	A	204	A
22	A	215	G
22	A	216	A
22	A	221	A
22	A	222	A
22	A	233	A
22	A	241	A
22	A	248	G
22	A	249	C
22	A	255	A
22	A	266	G
22	A	276	U
22	A	279	A
22	A	281	C

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Mol	Chain	Res	Type
22	A	285	G
22	A	286	U
22	A	293	U
22	A	304	U
22	A	311	A
22	A	323	C
22	A	329	G
22	A	330	A
22	A	361	G
22	A	362	A
22	A	369	U
22	A	371	A
22	A	372	G
22	A	386	G
22	A	387	U
22	A	388	G
22	A	395	U
22	A	396	G
22	A	404	A
22	A	405	U
22	A	406	G
22	A	411	G
22	A	412	A
22	A	422	A
22	A	424	G
22	A	443	A
22	A	454	A
22	A	477	A
22	A	480	A
22	A	481	G
22	A	482	A
22	A	491	G
22	A	496	G
22	A	503	A
22	A	504	A
22	A	505	A
22	A	509	C
22	A	510	C
22	A	529	A
22	A	531	C
22	A	532	A
22	A	533	G

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Mol	Chain	Res	Type
22	A	541	A
22	A	542	C
22	A	544	C
22	A	545	U
22	A	546	U
22	A	547	A
22	A	550	C
22	A	556	A
22	A	557	C
22	A	563	A
22	A	568	U
22	A	573	U
22	A	575	A
22	A	577	G
22	A	592	A
22	A	603	A
22	A	613	A
22	A	614	A
22	A	615	U
22	A	616	A
22	A	627	A
22	A	637	A
22	A	645	C
22	A	646	U
22	A	647	G
22	A	653	U
22	A	654	A
22	A	655	A
22	A	656	G
22	A	664	G
22	A	677	A
22	A	685	A
22	A	686	U
22	A	695	G
22	A	711	G
22	A	717	C
22	A	730	A
22	A	747	5MC
22	A	757	G
22	A	765	C
22	A	774	G
22	A	775	G

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Mol	Chain	Res	Type
22	A	776	G
22	A	782	A
22	A	783	A
22	A	784	G
22	A	785	G
22	A	789	A
22	A	791	C
22	A	792	A
22	A	800	A
22	A	805	G
22	A	807	U
22	A	812	C
22	A	819	A
22	A	827	U
22	A	828	U
22	A	844	A
22	A	845	A
22	A	846	U
22	A	847	U
22	A	851	C
22	A	858	G
22	A	859	G
22	A	869	G
22	A	878	A
22	A	883	G
22	A	885	C
22	A	886	A
22	A	893	C
22	A	896	A
22	A	897	C
22	A	910	A
22	A	915	C
22	A	933	A
22	A	934	U
22	A	938	G
22	A	939	G
22	A	941	A
22	A	946	C
22	A	957	C
22	A	958	U
22	A	959	A
22	A	961	C

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Mol	Chain	Res	Type
22	A	973	A
22	A	974	G
22	A	983	A
22	A	984	A
22	A	989	G
22	A	990	A
22	A	995	C
22	A	996	A
22	A	999	U
22	A	1001	A
22	A	1003	G
22	A	1005	C
22	A	1009	A
22	A	1012	U
22	A	1013	C
22	A	1016	G
22	A	1025	G
22	A	1026	G
22	A	1033	U
22	A	1046	A
22	A	1047	G
22	A	1052	C
22	A	1053	C
22	A	1054	A
22	A	1055	G
22	A	1057	A
22	A	1060	U
22	A	1061	U
22	A	1062	G
22	A	1066	U
22	A	1067	A
22	A	1068	G
22	A	1069	A
22	A	1070	A
22	A	1071	G
22	A	1074	G
22	A	1075	C
22	A	1076	C
22	A	1081	U
22	A	1082	U
22	A	1084	A
22	A	1087	G

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Mol	Chain	Res	Type
22	A	1088	A
22	A	1097	U
22	A	1101	U
22	A	1103	A
22	A	1104	C
22	A	1106	G
22	A	1107	G
22	A	1111	A
22	A	1112	G
22	A	1119	U
22	A	1120	G
22	A	1122	G
22	A	1126	A
22	A	1130	U
22	A	1132	U
22	A	1133	A
22	A	1135	C
22	A	1136	G
22	A	1139	G
22	A	1142	A
22	A	1143	A
22	A	1151	A
22	A	1169	A
22	A	1172	C
22	A	1174	U
22	A	1175	A
22	A	1176	U
22	A	1178	C
22	A	1179	G
22	A	1180	U
22	A	1187	G
22	A	1190	G
22	A	1211	C
22	A	1212	G
22	A	1247	A
22	A	1248	G
22	A	1253	A
22	A	1255	U
22	A	1256	G
22	A	1269	A
22	A	1271	G
22	A	1272	A

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Mol	Chain	Res	Type
22	A	1273	U
22	A	1277	G
22	A	1286	A
22	A	1300	G
22	A	1301	A
22	A	1321	A
22	A	1325	U
22	A	1330	C
22	A	1341	G
22	A	1343	G
22	A	1345	C
22	A	1352	U
22	A	1359	A
22	A	1365	A
22	A	1368	G
22	A	1378	A
22	A	1379	U
22	A	1383	A
22	A	1403	A
22	A	1416	G
22	A	1419	A
22	A	1420	A
22	A	1421	G
22	A	1427	A
22	A	1428	C
22	A	1430	G
22	A	1437	C
22	A	1453	A
22	A	1459	G
22	A	1461	C
22	A	1482	G
22	A	1490	A
22	A	1491	G
22	A	1493	C
22	A	1494	A
22	A	1495	A
22	A	1497	U
22	A	1509	A
22	A	1515	A
22	A	1523	U
22	A	1524	G
22	A	1531	C

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Mol	Chain	Res	Type
22	A	1532	A
22	A	1534	U
22	A	1535	A
22	A	1536	C
22	A	1537	G
22	A	1544	A
22	A	1554	U
22	A	1560	G
22	A	1566	A
22	A	1569	A
22	A	1584	U
22	A	1585	C
22	A	1608	A
22	A	1610	A
22	A	1613	G
22	A	1627	G
22	A	1628	G
22	A	1647	U
22	A	1648	U
22	A	1654	A
22	A	1664	A
22	A	1665	A
22	A	1672	A
22	A	1674	G
22	A	1675	C
22	A	1698	A
22	A	1715	G
22	A	1729	U
22	A	1730	C
22	A	1733	G
22	A	1738	G
22	A	1744	A
22	A	1760	C
22	A	1764	C
22	A	1773	A
22	A	1780	A
22	A	1791	A
22	A	1800	C
22	A	1801	A
22	A	1802	A
22	A	1807	G
22	A	1808	A

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Mol	Chain	Res	Type
22	A	1811	G
22	A	1816	C
22	A	1819	A
22	A	1829	A
22	A	1835	2MG
22	A	1862	G
22	A	1870	C
22	A	1871	A
22	A	1872	A
22	A	1873	G
22	A	1876	A
22	A	1884	G
22	A	1900	A
22	A	1901	A
22	A	1906	G
22	A	1914	C
22	A	1915	3TD
22	A	1929	G
22	A	1930	G
22	A	1931	U
22	A	1937	A
22	A	1939	5MU
22	A	1940	U
22	A	1941	C
22	A	1948	G
22	A	1955	U
22	A	1966	A
22	A	1967	C
22	A	1970	A
22	A	1971	U
22	A	1972	G
22	A	1977	A
22	A	1991	U
22	A	1993	U
22	A	1997	C
22	A	2018	G
22	A	2020	A
22	A	2022	U
22	A	2023	C
22	A	2030	6MZ
22	A	2031	A
22	A	2033	A

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Mol	Chain	Res	Type
22	A	2034	U
22	A	2043	C
22	A	2055	C
22	A	2056	G
22	A	2060	A
22	A	2061	G
22	A	2062	A
22	A	2063	C
22	A	2069	G7M
22	A	2072	C
22	A	2073	C
22	A	2077	A
22	A	2093	G
22	A	2096	C
22	A	2104	C
22	A	2105	U
22	A	2107	G
22	A	2108	A
22	A	2111	U
22	A	2112	G
22	A	2114	A
22	A	2115	G
22	A	2116	G
22	A	2118	U
22	A	2119	A
22	A	2121	G
22	A	2125	G
22	A	2126	A
22	A	2127	G
22	A	2128	G
22	A	2130	U
22	A	2131	U
22	A	2132	U
22	A	2133	G
22	A	2136	G
22	A	2137	U
22	A	2142	A
22	A	2143	C
22	A	2145	C
22	A	2146	C
22	A	2147	A
22	A	2156	G

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Mol	Chain	Res	Type
22	A	2157	G
22	A	2158	A
22	A	2159	G
22	A	2161	C
22	A	2164	C
22	A	2167	U
22	A	2168	G
22	A	2171	A
22	A	2172	U
22	A	2173	A
22	A	2176	A
22	A	2180	U
22	A	2182	U
22	A	2183	A
22	A	2184	A
22	A	2185	U
22	A	2186	G
22	A	2189	U
22	A	2190	G
22	A	2192	U
22	A	2198	A
22	A	2204	G
22	A	2211	A
22	A	2212	A
22	A	2225	A
22	A	2226	C
22	A	2238	G
22	A	2239	G
22	A	2250	G
22	A	2259	U
22	A	2266	A
22	A	2273	A
22	A	2278	A
22	A	2279	G
22	A	2283	C
22	A	2287	A
22	A	2288	A
22	A	2300	C
22	A	2301	C
22	A	2303	G
22	A	2305	U
22	A	2309	A

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Mol	Chain	Res	Type
22	A	2313	C
22	A	2319	G
22	A	2321	U
22	A	2325	G
22	A	2327	A
22	A	2333	A
22	A	2334	U
22	A	2335	A
22	A	2345	G
22	A	2347	C
22	A	2350	C
22	A	2354	C
22	A	2358	A
22	A	2361	G
22	A	2383	G
22	A	2384	U
22	A	2385	C
22	A	2389	G
22	A	2391	G
22	A	2392	A
22	A	2402	U
22	A	2403	C
22	A	2405	G
22	A	2406	A
22	A	2407	A
22	A	2410	G
22	A	2422	C
22	A	2424	C
22	A	2425	A
22	A	2428	G
22	A	2429	G
22	A	2430	A
22	A	2431	U
22	A	2435	A
22	A	2440	C
22	A	2441	U
22	A	2445	2MG
22	A	2447	G
22	A	2448	A
22	A	2475	C
22	A	2476	A
22	A	2494	G

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Mol	Chain	Res	Type
22	A	2502	G
22	A	2503	2MA
22	A	2504	PSU
22	A	2505	G
22	A	2518	A
22	A	2520	C
22	A	2529	G
22	A	2542	A
22	A	2547	A
22	A	2554	U
22	A	2556	C
22	A	2564	A
22	A	2566	A
22	A	2567	G
22	A	2572	A
22	A	2573	C
22	A	2576	G
22	A	2585	U
22	A	2586	U
22	A	2599	G
22	A	2601	C
22	A	2602	A
22	A	2603	G
22	A	2609	U
22	A	2610	C
22	A	2613	U
22	A	2615	U
22	A	2629	U
22	A	2630	G
22	A	2634	A
22	A	2655	G
22	A	2656	U
22	A	2661	G
22	A	2685	G
22	A	2689	U
22	A	2690	U
22	A	2707	U
22	A	2714	G
22	A	2716	C
22	A	2726	A
22	A	2727	A
22	A	2732	G

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Mol	Chain	Res	Type
22	A	2733	A
22	A	2739	U
22	A	2744	G
22	A	2748	A
22	A	2752	C
22	A	2764	A
22	A	2765	A
22	A	2778	A
22	A	2779	U
22	A	2790	U
22	A	2791	G
22	A	2793	C
22	A	2794	C
22	A	2797	U
22	A	2798	U
22	A	2800	A
22	A	2809	A
22	A	2818	U
22	A	2820	A
22	A	2821	A
22	A	2823	A
22	A	2826	A
22	A	2832	U
22	A	2833	U
22	A	2835	A
22	A	2848	G
22	A	2861	U
22	A	2866	U
22	A	2867	G
22	A	2873	A
22	A	2880	C
22	A	2881	U
22	A	2883	A
22	A	2884	U
22	A	2891	U
22	A	2893	A
22	A	2901	C
23	B	3	C
23	B	4	C
23	B	9	G
23	B	13	G
23	B	16	G

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Mol	Chain	Res	Type
23	B	26	C
23	B	32	U
23	B	35	C
23	B	39	A
23	B	42	C
23	B	44	G
23	B	45	A
23	B	51	G
23	B	67	G
23	B	87	U
23	B	88	C
23	B	89	U
23	B	90	C
23	B	108	A
23	B	109	A
23	B	119	A
23	B	120	A
55	9	3	G
55	9	4	U
55	9	5	G
55	9	6	A
55	9	9	G
55	9	16	C
55	9	17	C
55	9	18	G
55	9	19	G
55	9	20	U
55	9	21	A
55	9	33	U
55	9	41	A
55	9	42	A
55	9	43	G
55	9	46	G
55	9	47	U
55	9	48	C
55	9	49	G
55	9	52	G
55	9	53	G
55	9	54	U
55	9	56	C
55	9	57	G
55	9	59	A

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Mol	Chain	Res	Type
55	9	62	C
55	9	69	A
55	9	76	A

All (36) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
22	A	86	G
22	A	421	C
22	A	481	G
22	A	546	U
22	A	549	G
22	A	555	G
22	A	784	G
22	A	1070	A
22	A	1103	A
22	A	1111	A
22	A	1182	G
22	A	1183	U
22	A	1300	G
22	A	1358	G
22	A	1399	C
22	A	1452	G
22	A	1490	A
22	A	1493	C
22	A	1626	A
22	A	1663	G
22	A	1900	A
22	A	1930	G
22	A	1940	U
22	A	2326	C
22	A	2391	G
22	A	2402	U
22	A	2474	U
22	A	2655	G
22	A	2808	G
22	A	2820	A
22	A	2832	U
23	B	12	C
23	B	66	A
55	9	2	G
55	9	3	G

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Mol	Chain	Res	Type
55	9	41	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	G7M	A	2069	22	23,26,27	3.43	10 (43%)	35,39,42	1.64	6 (17%)
22	PSU	A	2580	22	18,21,22	1.13	2 (11%)	22,30,33	1.86	5 (22%)
1	2MG	a	1516	1	23,26,27	2.77	8 (34%)	32,38,41	2.14	12 (37%)
22	5MC	A	1962	22	18,22,23	3.56	7 (38%)	26,32,35	1.26	3 (11%)
22	6MZ	A	1618	22	22,25,26	2.82	4 (18%)	30,36,39	2.43	11 (36%)
1	2MG	a	1207	1	23,26,27	2.88	8 (34%)	32,38,41	2.17	11 (34%)
22	1MG	A	745	22	22,26,27	2.57	7 (31%)	33,39,42	2.88	9 (27%)
22	5MC	A	747	22	18,22,23	3.58	7 (38%)	26,32,35	1.14	1 (3%)
1	UR3	a	1498	1	19,22,23	2.83	7 (36%)	26,32,35	1.34	2 (7%)
22	OMC	A	2498	22	19,22,23	2.96	8 (42%)	26,31,34	0.83	1 (3%)
22	PSU	A	2504	22	18,21,22	1.11	2 (11%)	22,30,33	1.95	4 (18%)
22	H2U	A	2449	22	18,21,22	1.48	3 (16%)	21,30,33	1.94	3 (14%)
22	2MG	A	1835	22	23,26,27	2.86	8 (34%)	32,38,41	2.35	11 (34%)
22	PSU	A	746	22	18,21,22	1.04	3 (16%)	22,30,33	1.56	3 (13%)
1	MA6	a	1519	1	23,26,27	1.72	5 (21%)	34,38,41	4.00	11 (32%)
22	PSU	A	1911	22	18,21,22	1.04	2 (11%)	22,30,33	1.89	4 (18%)
22	PSU	A	2604	22	18,21,22	1.10	2 (11%)	22,30,33	1.73	4 (18%)
22	2MA	A	2503	22	22,25,26	3.49	9 (40%)	33,37,40	1.99	8 (24%)
1	2MG	a	966	1	23,26,27	2.89	8 (34%)	32,38,41	2.26	9 (28%)
22	PSU	A	955	22	18,21,22	1.13	1 (5%)	22,30,33	1.87	4 (18%)
1	5MC	a	1407	1	18,22,23	3.62	7 (38%)	26,32,35	1.04	3 (11%)
22	PSU	A	2605	22	18,21,22	1.13	3 (16%)	22,30,33	1.75	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	3TD	A	1915	22	18,22,23	4.09	7 (38%)	22,32,35	1.62	3 (13%)
22	OMG	A	2251	22,55	23,26,27	2.35	7 (30%)	33,38,41	2.36	9 (27%)
22	PSU	A	2457	22	18,21,22	1.12	2 (11%)	22,30,33	2.05	5 (22%)
1	PSU	a	516	1	18,21,22	1.00	3 (16%)	22,30,33	1.69	5 (22%)
1	4OC	a	1402	1	20,23,24	2.99	8 (40%)	26,32,35	0.86	1 (3%)
22	2MG	A	2445	22	23,26,27	2.81	8 (34%)	32,38,41	2.24	9 (28%)
22	6MZ	A	2030	22	22,25,26	2.81	6 (27%)	30,36,39	2.93	12 (40%)
22	5MU	A	1939	22	19,22,23	4.69	7 (36%)	28,32,35	4.00	10 (35%)
1	G7M	a	1405	1	23,26,27	3.39	11 (47%)	35,39,42	1.82	7 (20%)
1	MA6	a	1518	1	23,26,27	1.56	4 (17%)	34,38,41	4.33	11 (32%)
22	PSU	A	1917	22	18,21,22	1.08	2 (11%)	22,30,33	1.91	5 (22%)
1	5MC	a	967	1	18,22,23	3.76	7 (38%)	26,32,35	0.98	1 (3%)
22	OMU	A	2552	22	19,22,23	2.75	7 (36%)	26,31,34	1.79	5 (19%)
1	G7M	a	527	1	23,26,27	3.59	11 (47%)	35,39,42	1.67	7 (20%)

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
22	G7M	A	2069	22	-	2/7/25/26	0/3/3/3
22	PSU	A	2580	22	-	0/7/25/26	0/2/2/2
1	2MG	a	1516	1	-	0/9/27/28	0/3/3/3
22	5MC	A	1962	22	-	0/7/25/26	0/2/2/2
22	6MZ	A	1618	22	-	0/9/27/28	0/3/3/3
1	2MG	a	1207	1	-	0/9/27/28	0/3/3/3
22	1MG	A	745	22	-	0/7/25/26	0/3/3/3
22	5MC	A	747	22	-	1/7/25/26	0/2/2/2
1	UR3	a	1498	1	-	2/7/25/26	0/2/2/2
22	OMC	A	2498	22	-	1/9/27/28	0/2/2/2
22	PSU	A	2504	22	-	2/7/25/26	0/2/2/2
22	H2U	A	2449	22	-	0/7/38/39	0/2/2/2
22	2MG	A	1835	22	-	2/9/27/28	0/3/3/3
22	PSU	A	746	22	-	1/7/25/26	0/2/2/2
1	MA6	a	1519	1	-	1/11/29/30	0/3/3/3
22	PSU	A	1911	22	-	2/7/25/26	0/2/2/2
22	PSU	A	2604	22	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	2MA	A	2503	22	-	2/7/25/26	0/3/3/3
1	2MG	a	966	1	-	2/9/27/28	0/3/3/3
22	PSU	A	955	22	-	0/7/25/26	0/2/2/2
1	5MC	a	1407	1	-	0/7/25/26	0/2/2/2
22	PSU	A	2605	22	-	0/7/25/26	0/2/2/2
22	3TD	A	1915	22	-	5/7/25/26	0/2/2/2
22	OMG	A	2251	22,55	-	1/9/27/28	0/3/3/3
22	PSU	A	2457	22	-	0/7/25/26	0/2/2/2
1	PSU	a	516	1	-	0/7/25/26	0/2/2/2
1	4OC	a	1402	1	-	2/9/29/30	0/2/2/2
22	2MG	A	2445	22	-	2/9/27/28	0/3/3/3
22	6MZ	A	2030	22	-	3/9/27/28	0/3/3/3
22	5MU	A	1939	22	-	2/7/25/26	0/2/2/2
1	G7M	a	1405	1	-	0/7/25/26	0/3/3/3
1	MA6	a	1518	1	-	7/11/29/30	0/3/3/3
22	PSU	A	1917	22	-	2/7/25/26	0/2/2/2
1	5MC	a	967	1	-	2/7/25/26	0/2/2/2
22	OMU	A	2552	22	-	4/9/27/28	0/2/2/2
1	G7M	a	527	1	-	2/7/25/26	0/3/3/3

All (211) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	A	1915	3TD	C6-C5	12.01	1.49	1.35
22	A	1618	6MZ	C6-N6	11.76	1.46	1.34
22	A	2030	6MZ	C6-N6	10.97	1.46	1.34
22	A	2503	2MA	C4-N3	10.79	1.48	1.34
1	a	527	G7M	C8-N7	10.51	1.51	1.33
22	A	2069	G7M	C8-N7	10.24	1.51	1.33
22	A	1939	5MU	C2-N1	10.15	1.54	1.38
22	A	1939	5MU	C6-N1	10.04	1.55	1.38
1	a	1405	G7M	C8-N7	9.93	1.50	1.33
1	a	967	5MC	C6-C5	9.72	1.50	1.34
22	A	1939	5MU	C4-C5	9.68	1.60	1.44
22	A	747	5MC	C6-C5	9.50	1.50	1.34
1	a	1407	5MC	C6-C5	9.22	1.49	1.34
22	A	1915	3TD	C2-N1	8.94	1.48	1.37
22	A	1962	5MC	C6-C5	8.83	1.49	1.34
22	A	1939	5MU	C4-N3	-7.93	1.24	1.38
1	a	966	2MG	C2-N3	7.67	1.46	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	a	1207	2MG	C2-N3	7.38	1.46	1.31
22	A	1835	2MG	C2-N3	7.36	1.46	1.31
1	a	1498	UR3	C2-N1	7.06	1.48	1.38
22	A	2445	2MG	C2-N3	7.00	1.45	1.31
1	a	1498	UR3	C6-C5	6.94	1.51	1.35
22	A	2503	2MA	C2-N3	6.73	1.46	1.34
1	a	1516	2MG	C2-N3	6.72	1.44	1.31
1	a	967	5MC	C4-N3	6.71	1.45	1.34
22	A	1962	5MC	C4-N3	6.70	1.45	1.34
1	a	1402	4OC	C4-N3	6.64	1.44	1.32
22	A	1835	2MG	C4-N3	6.53	1.49	1.34
1	a	1407	5MC	C4-N3	6.49	1.45	1.34
1	a	966	2MG	C4-N3	6.39	1.49	1.34
1	a	967	5MC	C2-N3	6.38	1.49	1.36
1	a	1207	2MG	C4-N3	6.38	1.49	1.34
22	A	2445	2MG	C4-N3	6.22	1.49	1.34
22	A	1962	5MC	C2-N3	6.20	1.48	1.36
22	A	2552	OMU	C2-N3	6.19	1.49	1.38
22	A	1939	5MU	C6-C5	6.19	1.44	1.34
1	a	1407	5MC	C2-N3	6.13	1.48	1.36
1	a	1402	4OC	C6-C5	6.09	1.49	1.35
1	a	1516	2MG	C4-N3	5.97	1.48	1.34
22	A	745	1MG	C2-N2	5.95	1.45	1.34
22	A	747	5MC	C2-N3	5.95	1.48	1.36
22	A	2498	OMC	C6-C5	5.90	1.48	1.35
22	A	747	5MC	C4-N3	5.89	1.44	1.34
22	A	745	1MG	C4-N3	5.88	1.48	1.34
22	A	745	1MG	C2-N3	5.86	1.45	1.34
22	A	2251	OMG	C4-N3	5.82	1.48	1.34
22	A	2552	OMU	C2-N1	5.78	1.47	1.38
22	A	1915	3TD	C6-N1	5.70	1.45	1.36
1	a	527	G7M	C4-N3	5.69	1.47	1.34
1	a	1405	G7M	C2-N3	5.64	1.46	1.33
1	a	527	G7M	C2-N3	5.64	1.46	1.33
1	a	1402	4OC	C2-N3	5.57	1.47	1.36
22	A	2503	2MA	C2-N1	5.54	1.43	1.34
22	A	2498	OMC	C4-N4	5.52	1.46	1.33
1	a	1405	G7M	C4-N3	5.43	1.47	1.34
1	a	966	2MG	C2-N1	5.43	1.45	1.36
22	A	2552	OMU	C6-C5	5.42	1.47	1.35
1	a	1207	2MG	C2-N1	5.38	1.45	1.36
1	a	1516	2MG	C2-N1	5.35	1.45	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	A	2069	G7M	C4-N3	5.34	1.46	1.34
22	A	2498	OMC	C2-N3	5.33	1.47	1.36
1	a	1207	2MG	C2-N2	5.30	1.45	1.33
1	a	527	G7M	C8-N9	5.24	1.50	1.35
22	A	2498	OMC	C4-N3	5.20	1.45	1.34
1	a	1516	2MG	C2-N2	5.18	1.44	1.33
22	A	2069	G7M	C8-N9	5.18	1.50	1.35
22	A	1835	2MG	C2-N1	5.15	1.45	1.36
22	A	2445	2MG	C2-N1	5.15	1.45	1.36
22	A	2069	G7M	C2-N3	5.13	1.45	1.33
1	a	966	2MG	C2-N2	5.11	1.44	1.33
1	a	1405	G7M	C8-N9	5.06	1.49	1.35
22	A	1835	2MG	C2-N2	5.02	1.44	1.33
1	a	967	5MC	C4-N4	4.98	1.47	1.34
1	a	1407	5MC	C4-N4	4.97	1.47	1.34
22	A	1962	5MC	C4-N4	4.93	1.46	1.34
1	a	1498	UR3	C2-N3	4.92	1.48	1.39
22	A	2251	OMG	C2-N3	4.90	1.45	1.33
22	A	747	5MC	C4-N4	4.72	1.46	1.34
22	A	2503	2MA	C5-C6	4.67	1.54	1.41
1	a	527	G7M	C2-N2	4.66	1.45	1.34
22	A	2069	G7M	C2-N2	4.58	1.45	1.34
1	a	967	5MC	C6-N1	4.57	1.45	1.38
22	A	2445	2MG	C2-N2	4.54	1.43	1.33
22	A	1915	3TD	C2-N3	4.41	1.48	1.38
22	A	747	5MC	C6-N1	4.38	1.45	1.38
1	a	1407	5MC	C6-N1	4.29	1.45	1.38
1	a	1405	G7M	C2-N2	4.28	1.44	1.34
22	A	2251	OMG	C2-N2	4.28	1.44	1.34
1	a	1402	4OC	C4-N4	4.28	1.44	1.35
22	A	2503	2MA	C6-N1	4.26	1.41	1.35
22	A	2069	G7M	O6-C6	-4.19	1.15	1.23
1	a	967	5MC	C2-N1	4.11	1.48	1.40
1	a	1519	MA6	C5-N7	-4.06	1.31	1.39
22	A	1962	5MC	C6-N1	3.99	1.44	1.38
1	a	527	G7M	C2-N1	3.87	1.47	1.37
22	A	2251	OMG	C5-N7	-3.83	1.31	1.39
22	A	2498	OMC	O2-C2	-3.82	1.16	1.23
22	A	2498	OMC	C2-N1	3.81	1.48	1.40
22	A	1962	5MC	C2-N1	3.78	1.48	1.40
1	a	1405	G7M	O6-C6	-3.72	1.16	1.23
1	a	527	G7M	O6-C6	-3.71	1.16	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	a	1407	5MC	C2-N1	3.71	1.48	1.40
1	a	1518	MA6	C5-N7	-3.69	1.32	1.39
22	A	747	5MC	C2-N1	3.68	1.48	1.40
1	a	1402	4OC	C5-C4	3.66	1.48	1.40
22	A	2069	G7M	C2-N1	3.62	1.46	1.37
1	a	527	G7M	C5-N7	3.58	1.43	1.39
1	a	1402	4OC	O2-C2	-3.58	1.17	1.23
22	A	2449	H2U	C2-N1	-3.48	1.30	1.35
22	A	745	1MG	C5-N7	-3.42	1.32	1.39
1	a	1405	G7M	C2-N1	3.41	1.46	1.37
22	A	2030	6MZ	C5-C4	-3.39	1.32	1.39
1	a	1519	MA6	C5-C4	-3.35	1.32	1.39
22	A	747	5MC	O2-C2	-3.32	1.17	1.23
1	a	1519	MA6	C6-N6	3.28	1.46	1.36
22	A	2449	H2U	C2-N3	-3.27	1.32	1.38
22	A	2445	2MG	C5-N7	-3.24	1.32	1.39
22	A	1835	2MG	C5-N7	-3.23	1.32	1.39
22	A	2552	OMU	O4-C4	-3.23	1.18	1.24
1	a	527	G7M	C5-C6	3.20	1.52	1.43
1	a	1402	4OC	C2-N1	3.19	1.46	1.40
22	A	2449	H2U	C4-N3	-3.19	1.32	1.37
1	a	527	G7M	C6-N1	3.18	1.44	1.38
1	a	1498	UR3	O4-C4	-3.18	1.16	1.23
22	A	2552	OMU	O2-C2	-3.16	1.17	1.23
22	A	2445	2MG	CM2-N2	-3.12	1.40	1.45
1	a	1405	G7M	C5-C6	3.12	1.52	1.43
1	a	1518	MA6	C4-N9	-3.10	1.30	1.37
22	A	2552	OMU	C4-N3	3.09	1.44	1.38
1	a	1407	5MC	O2-C2	-3.08	1.18	1.23
1	a	1519	MA6	C4-N9	-3.08	1.30	1.37
1	a	1518	MA6	C6-N6	3.08	1.45	1.36
22	A	2498	OMC	C6-N1	3.06	1.45	1.38
22	A	1962	5MC	O2-C2	-3.05	1.18	1.23
22	A	1618	6MZ	C5-C4	-3.04	1.33	1.39
22	A	2069	G7M	C5-N7	3.04	1.42	1.39
1	a	966	2MG	C5-N7	-3.02	1.33	1.39
22	A	2030	6MZ	C8-N9	-3.02	1.32	1.37
1	a	1405	G7M	C5-N7	2.99	1.42	1.39
1	a	1402	4OC	C6-N1	2.96	1.45	1.38
22	A	2503	2MA	C8-N7	2.87	1.37	1.31
22	A	1911	PSU	C6-C5	2.85	1.38	1.35
22	A	2030	6MZ	C5-N7	-2.84	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	A	2030	6MZ	C6-N1	-2.83	1.30	1.35
22	A	2251	OMG	O6-C6	-2.83	1.18	1.23
1	a	1516	2MG	C5-C6	2.82	1.54	1.44
1	a	1518	MA6	C5-C4	-2.80	1.33	1.39
22	A	1915	3TD	O2-C2	-2.80	1.17	1.23
1	a	967	5MC	O2-C2	-2.74	1.18	1.23
22	A	2605	PSU	C4-C5	-2.73	1.36	1.44
22	A	2503	2MA	C5-N7	-2.72	1.33	1.39
1	a	1207	2MG	C5-N7	-2.72	1.33	1.39
22	A	2069	G7M	C6-N1	2.70	1.43	1.38
22	A	1917	PSU	C6-C5	2.68	1.38	1.35
22	A	1939	5MU	O4-C4	-2.68	1.18	1.23
1	a	1519	MA6	C8-N9	-2.68	1.32	1.37
1	a	1516	2MG	C5-N7	-2.65	1.33	1.39
1	a	1207	2MG	C6-N1	2.64	1.43	1.38
1	a	1207	2MG	C5-C6	2.63	1.54	1.44
1	a	966	2MG	C5-C6	2.63	1.54	1.44
22	A	1915	3TD	C4-N3	2.63	1.46	1.40
22	A	2504	PSU	C4-C5	-2.62	1.36	1.44
22	A	1939	5MU	O2-C2	-2.62	1.18	1.23
22	A	2251	OMG	C4-N9	-2.59	1.31	1.38
22	A	2069	G7M	C5-C6	2.56	1.50	1.43
22	A	2503	2MA	C6-N6	-2.55	1.27	1.34
1	a	1207	2MG	CM2-N2	-2.52	1.41	1.45
22	A	745	1MG	C5-C6	2.50	1.51	1.45
1	a	1516	2MG	CM2-N2	-2.50	1.41	1.45
22	A	955	PSU	C4-C5	-2.50	1.37	1.44
22	A	2457	PSU	O4'-C1'	-2.48	1.40	1.43
22	A	2580	PSU	O4'-C1'	-2.48	1.40	1.43
1	a	1405	G7M	C6-N1	2.48	1.43	1.38
22	A	1618	6MZ	C5-N7	-2.48	1.34	1.39
1	a	966	2MG	C6-N1	2.48	1.43	1.38
22	A	1835	2MG	CM2-N2	-2.45	1.41	1.45
1	a	516	PSU	C6-C5	2.44	1.38	1.35
22	A	1835	2MG	C5-C6	2.44	1.53	1.44
22	A	2552	OMU	C6-N1	2.43	1.43	1.38
22	A	1835	2MG	C6-N1	2.42	1.43	1.38
22	A	2580	PSU	C4-C5	-2.38	1.37	1.44
22	A	745	1MG	C4-N9	-2.37	1.31	1.38
22	A	745	1MG	O6-C6	-2.35	1.18	1.23
22	A	1917	PSU	C4-C5	-2.34	1.37	1.44
22	A	2251	OMG	C2-N1	2.31	1.43	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	A	1618	6MZ	C6-N1	-2.30	1.31	1.35
22	A	746	PSU	C6-C5	2.29	1.38	1.35
1	a	966	2MG	CM2-N2	-2.29	1.41	1.45
1	a	1516	2MG	C6-N1	2.29	1.43	1.38
22	A	2445	2MG	C5-C6	2.28	1.52	1.44
22	A	2504	PSU	C6-C5	2.26	1.38	1.35
22	A	2605	PSU	C6-C5	2.26	1.38	1.35
22	A	2604	PSU	C6-C5	2.25	1.37	1.35
1	a	1498	UR3	O2-C2	-2.23	1.18	1.22
22	A	746	PSU	C4-C5	-2.23	1.37	1.44
22	A	2457	PSU	C4-C5	-2.17	1.38	1.44
22	A	2445	2MG	C6-N1	2.17	1.42	1.38
1	a	516	PSU	O4'-C1'	-2.13	1.40	1.43
22	A	2030	6MZ	C4-N9	-2.13	1.32	1.37
1	a	1498	UR3	C6-N1	2.12	1.43	1.38
1	a	1498	UR3	C5-C4	2.12	1.49	1.43
1	a	1405	G7M	C4-N9	2.11	1.43	1.38
22	A	746	PSU	O4'-C1'	-2.09	1.40	1.43
22	A	2503	2MA	C5-C4	-2.08	1.35	1.39
22	A	2604	PSU	C4-C5	-2.07	1.38	1.44
1	a	516	PSU	C4-C5	-2.07	1.38	1.44
1	a	527	G7M	C4-N9	2.07	1.43	1.38
22	A	2498	OMC	C5-C4	2.07	1.47	1.42
22	A	1915	3TD	O4-C4	-2.05	1.18	1.23
22	A	1911	PSU	C4-C5	-2.03	1.38	1.44
22	A	2605	PSU	O4'-C1'	-2.01	1.41	1.43

All (219) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	a	1518	MA6	N1-C6-N6	-19.55	95.71	117.08
1	a	1519	MA6	N1-C6-N6	-16.83	98.68	117.08
22	A	1939	5MU	C5-C4-N3	13.04	126.44	115.31
22	A	1939	5MU	C5-C6-N1	-11.53	111.48	123.34
1	a	1518	MA6	C5-C6-N6	11.10	144.64	125.30
22	A	745	1MG	C1'-N9-C8	-10.03	98.14	126.70
1	a	1519	MA6	C5-C6-N6	9.63	142.07	125.30
22	A	2030	6MZ	C9-N6-C6	-9.01	115.12	122.87
22	A	745	1MG	C1'-N9-C4	8.53	151.83	126.50
22	A	2449	H2U	C4-N3-C2	-7.59	119.49	125.79
22	A	1835	2MG	C2-N3-C4	6.99	120.70	112.04
22	A	2251	OMG	C1'-N9-C8	-6.97	106.86	126.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	a	966	2MG	C2-N3-C4	6.65	120.29	112.04
1	a	1207	2MG	C2-N3-C4	6.19	119.72	112.04
1	a	1516	2MG	C2-N3-C4	6.18	119.70	112.04
22	A	2445	2MG	C2-N3-C4	6.09	119.60	112.04
22	A	1939	5MU	C4-N3-C2	-5.91	119.71	127.35
1	a	1519	MA6	C5-C4-N3	-5.77	119.22	126.75
22	A	2251	OMG	C1'-N9-C4	5.69	143.41	126.50
22	A	1618	6MZ	C5-C4-N3	-5.61	119.44	126.75
1	a	966	2MG	C5-C4-N3	-5.58	119.40	128.46
22	A	1618	6MZ	C9-N6-C6	-5.49	118.14	122.87
22	A	2030	6MZ	N9-C8-N7	-5.42	106.50	113.91
22	A	1835	2MG	C5-C4-N3	-5.42	119.67	128.46
22	A	2030	6MZ	C5-C4-N3	-5.40	119.70	126.75
22	A	2552	OMU	C4-N3-C2	-5.35	119.52	126.58
22	A	2457	PSU	N1-C2-N3	5.32	121.15	115.13
22	A	2503	2MA	C5-C4-N3	-5.30	121.22	127.19
1	a	1518	MA6	N1-C2-N3	-5.30	120.31	128.60
22	A	1618	6MZ	N1-C2-N3	-5.26	120.38	128.60
22	A	2503	2MA	N9-C8-N7	-5.26	106.72	113.91
22	A	1915	3TD	N1-C2-N3	5.23	120.27	116.14
22	A	2445	2MG	C5-C4-N3	-5.16	120.08	128.46
22	A	2457	PSU	C4-N3-C2	-5.15	118.91	126.34
1	a	1519	MA6	N1-C2-N3	-5.15	120.54	128.60
22	A	2030	6MZ	N1-C2-N3	-5.14	120.56	128.60
1	a	966	2MG	C2-N1-C6	-5.13	118.58	124.48
1	a	1519	MA6	C4-C5-C6	5.12	121.61	115.88
1	a	1518	MA6	C5-C4-N3	-5.11	120.09	126.75
1	a	1498	UR3	C4-N3-C2	-5.10	119.76	124.56
22	A	1939	5MU	N3-C2-N1	5.03	121.57	114.89
22	A	2605	PSU	C4-N3-C2	-5.00	119.13	126.34
22	A	1911	PSU	C4-N3-C2	-5.00	119.14	126.34
22	A	1835	2MG	C2-N1-C6	-5.00	118.73	124.48
22	A	955	PSU	C4-N3-C2	-4.96	119.19	126.34
22	A	1917	PSU	C4-N3-C2	-4.93	119.23	126.34
22	A	745	1MG	C5-C4-N3	-4.89	120.53	128.46
22	A	2445	2MG	C2-N1-C6	-4.86	118.88	124.48
22	A	2580	PSU	N1-C2-N3	4.73	120.49	115.13
22	A	1911	PSU	N1-C2-N3	4.73	120.48	115.13
22	A	2504	PSU	N1-C2-N3	4.70	120.45	115.13
1	a	1405	G7M	C5-C4-N3	-4.68	119.17	128.15
22	A	2552	OMU	N3-C2-N1	4.68	121.10	114.89
22	A	2251	OMG	C5-C4-N3	-4.67	120.89	128.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	A	1917	PSU	N1-C2-N3	4.66	120.41	115.13
22	A	1939	5MU	O4-C4-C5	-4.65	119.51	124.90
22	A	746	PSU	C4-N3-C2	-4.64	119.65	126.34
22	A	955	PSU	N1-C2-N3	4.59	120.33	115.13
22	A	2580	PSU	C4-N3-C2	-4.57	119.75	126.34
22	A	2604	PSU	C4-N3-C2	-4.47	119.91	126.34
22	A	2604	PSU	N1-C2-N3	4.42	120.14	115.13
1	a	527	G7M	C2-N3-C4	4.42	120.17	112.30
22	A	2504	PSU	C4-N3-C2	-4.39	120.01	126.34
1	a	1405	G7M	C2-N3-C4	4.34	120.04	112.30
1	a	1516	2MG	C5-C4-N3	-4.33	121.43	128.46
1	a	1207	2MG	C5-C4-N3	-4.30	121.48	128.46
22	A	2504	PSU	O2-C2-N1	-4.23	118.13	122.79
1	a	1207	2MG	C2-N1-C6	-4.19	119.66	124.48
1	a	516	PSU	C4-N3-C2	-4.19	120.30	126.34
1	a	1519	MA6	N9-C8-N7	-4.05	108.38	113.91
1	a	527	G7M	C5-C4-N3	-4.04	120.40	128.15
22	A	2445	2MG	CM2-N2-C2	-4.01	115.00	123.86
22	A	2251	OMG	C2-N3-C4	4.01	119.44	112.30
22	A	747	5MC	C5-C6-N1	-3.99	119.23	123.34
1	a	1405	G7M	C5-C6-N1	3.98	120.11	111.79
22	A	2069	G7M	C5-C6-N1	3.98	120.09	111.79
22	A	1618	6MZ	N9-C8-N7	-3.97	108.48	113.91
1	a	527	G7M	C5-C6-N1	3.95	120.03	111.79
1	a	516	PSU	N1-C2-N3	3.91	119.56	115.13
22	A	2069	G7M	C2-N3-C4	3.91	119.26	112.30
22	A	2030	6MZ	C4-C5-C6	3.89	119.82	116.81
22	A	1915	3TD	C4-N3-C2	-3.89	120.39	124.61
22	A	1939	5MU	O2-C2-N1	-3.83	117.69	122.79
22	A	2605	PSU	N1-C2-N3	3.82	119.46	115.13
22	A	1618	6MZ	C2-N3-C4	3.80	120.72	111.75
1	a	1516	2MG	C2-N1-C6	-3.79	120.11	124.48
22	A	2030	6MZ	C5-N7-C8	3.78	108.88	103.51
22	A	745	1MG	N9-C8-N7	-3.74	106.35	113.39
1	a	1519	MA6	N3-C4-N9	3.72	133.22	127.08
1	a	1518	MA6	C4-C5-C6	3.70	120.02	115.88
22	A	1939	5MU	C5M-C5-C6	-3.68	117.94	122.85
22	A	2504	PSU	C6-N1-C2	-3.65	118.95	122.68
22	A	745	1MG	C2-N3-C4	3.61	120.09	111.98
1	a	1518	MA6	C2-N1-C6	3.54	120.12	111.75
22	A	2069	G7M	O6-C6-C5	-3.53	120.09	128.06
22	A	2503	2MA	N3-C2-N1	-3.49	119.31	125.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	A	746	PSU	N1-C2-N3	3.48	119.08	115.13
22	A	2030	6MZ	C2-N3-C4	3.48	119.97	111.75
1	a	527	G7M	O6-C6-C5	-3.45	120.27	128.06
1	a	1405	G7M	C2-N1-C6	-3.44	118.82	125.10
22	A	1835	2MG	N9-C4-N3	3.42	132.81	125.94
1	a	1518	MA6	C2-N3-C4	3.41	119.81	111.75
1	a	966	2MG	N9-C4-N3	3.41	132.78	125.94
22	A	2030	6MZ	C4-N9-C8	3.40	109.42	105.73
1	a	1519	MA6	C2-N3-C4	3.40	119.77	111.75
22	A	1618	6MZ	C4-C5-C6	3.39	119.44	116.81
22	A	1962	5MC	C5-C6-N1	-3.38	119.86	123.34
22	A	2251	OMG	N9-C8-N7	-3.34	107.09	113.39
1	a	1519	MA6	C2-N1-C6	3.33	119.61	111.75
22	A	2069	G7M	C5-C4-N3	-3.31	121.80	128.15
1	a	1207	2MG	CM2-N2-C2	-3.29	116.59	123.86
22	A	2445	2MG	N9-C8-N7	-3.29	107.19	113.39
1	a	1516	2MG	C1'-N9-C4	-3.28	116.77	126.50
22	A	745	1MG	N9-C4-N3	3.27	132.50	125.94
1	a	516	PSU	O2-C2-N1	-3.25	119.21	122.79
22	A	1939	5MU	C5M-C5-C4	3.25	122.34	118.77
1	a	1405	G7M	O6-C6-C5	-3.23	120.78	128.06
22	A	2503	2MA	C5-N7-C8	3.22	108.08	103.51
22	A	2503	2MA	C4-N9-C8	3.21	109.20	105.73
22	A	2030	6MZ	N3-C4-N9	3.18	132.33	127.08
22	A	1939	5MU	O4-C4-N3	-3.17	114.05	120.12
22	A	2251	OMG	N9-C4-N3	3.16	132.29	125.94
22	A	2580	PSU	C6-N1-C2	-3.14	119.47	122.68
22	A	2552	OMU	C5-C4-N3	3.13	119.52	114.84
22	A	1911	PSU	O2-C2-N1	-3.12	119.35	122.79
22	A	2445	2MG	N9-C4-N3	3.12	132.20	125.94
1	a	1518	MA6	N9-C8-N7	-3.10	109.67	113.91
1	a	967	5MC	C5-C6-N1	-3.09	120.16	123.34
22	A	2457	PSU	O2-C2-N1	-3.09	119.39	122.79
22	A	1835	2MG	N9-C8-N7	-3.05	107.65	113.39
22	A	2251	OMG	C2-N1-C6	-3.04	119.56	125.10
1	a	1516	2MG	C1'-N9-C8	3.04	135.34	126.70
22	A	1835	2MG	C5-C6-N1	3.03	120.88	113.19
22	A	1618	6MZ	N3-C4-N9	3.01	132.04	127.08
22	A	1835	2MG	O6-C6-C5	-2.99	118.66	126.60
1	a	1516	2MG	N9-C8-N7	-2.98	107.77	113.39
1	a	527	G7M	C2-N1-C6	-2.98	119.67	125.10
22	A	745	1MG	C5-C6-N1	2.98	120.66	114.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	a	1519	MA6	C5-N7-C8	2.97	107.73	103.51
1	a	1207	2MG	C1'-N9-C4	-2.96	117.70	126.50
1	a	1207	2MG	N9-C8-N7	-2.88	107.97	113.39
22	A	2503	2MA	N3-C4-N9	2.84	130.93	126.99
1	a	966	2MG	CM2-N2-C2	-2.82	117.62	123.86
1	a	1207	2MG	C5-C6-N1	2.81	120.32	113.19
1	a	966	2MG	N9-C8-N7	-2.80	108.11	113.39
22	A	1618	6MZ	C5-N7-C8	2.79	107.47	103.51
1	a	966	2MG	C5-C6-N1	2.79	120.27	113.19
22	A	2030	6MZ	C4-C5-N7	-2.78	107.23	110.62
1	a	1407	5MC	C5-C6-N1	-2.77	120.49	123.34
22	A	1917	PSU	O2-C2-N1	-2.77	119.74	122.79
22	A	2069	G7M	C2-N1-C6	-2.76	120.07	125.10
22	A	955	PSU	O2-C2-N1	-2.76	119.76	122.79
1	a	1207	2MG	O6-C6-C5	-2.75	119.31	126.60
22	A	2069	G7M	N9-C8-N7	-2.74	105.44	112.21
1	a	966	2MG	O6-C6-C5	-2.70	119.43	126.60
1	a	1405	G7M	C6-C5-N7	-2.70	128.99	132.25
22	A	2457	PSU	C6-N1-C2	-2.67	119.95	122.68
22	A	2251	OMG	C5-C6-N1	2.66	119.95	113.19
22	A	1618	6MZ	C5-C6-N1	2.65	121.02	118.20
22	A	2604	PSU	O2-C2-N1	-2.64	119.88	122.79
1	a	1518	MA6	N3-C4-N9	2.64	131.43	127.08
22	A	2445	2MG	C5-C6-N1	2.63	119.88	113.19
1	a	1207	2MG	C1'-N9-C8	2.63	134.18	126.70
22	A	2445	2MG	O6-C6-C5	-2.63	119.63	126.60
1	a	1407	5MC	CM5-C5-C6	-2.62	119.35	122.85
22	A	2251	OMG	O6-C6-C5	-2.59	119.73	126.60
22	A	2449	H2U	C5-C6-N1	-2.58	103.12	111.61
22	A	955	PSU	C6-N1-C2	-2.58	120.05	122.68
1	a	1207	2MG	N1-C2-N3	-2.55	120.01	123.95
22	A	2580	PSU	O2-C2-N1	-2.54	120.00	122.79
22	A	2030	6MZ	C5-C6-N1	2.54	120.91	118.20
22	A	1835	2MG	N1-C2-N3	-2.53	120.04	123.95
22	A	2457	PSU	C6-C5-C4	2.51	119.95	118.20
22	A	1962	5MC	C1'-N1-C6	-2.49	116.98	121.12
1	a	527	G7M	N9-C8-N7	-2.47	106.11	112.21
22	A	2552	OMU	O4-C4-C5	-2.45	120.85	125.16
22	A	1835	2MG	CM2-N2-C2	-2.45	118.46	123.86
22	A	2605	PSU	O4-C4-C5	-2.43	117.70	124.05
1	a	1516	2MG	N1-C2-N3	-2.39	120.25	123.95
22	A	2605	PSU	C5-C4-N3	2.38	121.96	116.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	A	1618	6MZ	C5-C4-N9	2.36	108.53	105.78
1	a	1516	2MG	C5-C6-N1	2.34	119.13	113.19
22	A	2503	2MA	CM2-C2-N1	2.34	120.80	117.15
1	a	1516	2MG	C4-C5-N7	-2.34	107.02	110.72
1	a	1518	MA6	C5-C4-N9	2.32	108.48	105.78
22	A	1917	PSU	C6-C5-C4	2.31	119.81	118.20
1	a	1405	G7M	N9-C4-N3	2.30	130.55	125.94
1	a	516	PSU	O4'-C1'-C2'	2.26	108.34	105.14
22	A	1917	PSU	C6-N1-C2	-2.23	120.40	122.68
22	A	2604	PSU	C6-N1-C2	-2.23	120.41	122.68
22	A	1911	PSU	C6-N1-C2	-2.22	120.41	122.68
1	a	1407	5MC	C5-C4-N3	-2.22	119.28	121.67
22	A	745	1MG	C8-N7-C5	2.21	108.24	104.24
1	a	1207	2MG	N9-C4-N3	2.21	130.37	125.94
22	A	2445	2MG	C8-N7-C5	2.20	108.23	104.24
22	A	2580	PSU	O4'-C1'-C2'	2.17	108.21	105.14
22	A	1962	5MC	CM5-C5-C6	-2.17	119.95	122.85
1	a	1518	MA6	C5-N7-C8	2.17	106.59	103.51
1	a	527	G7M	C5-C4-N9	2.14	110.59	105.89
1	a	1516	2MG	CM2-N2-C2	-2.13	119.16	123.86
1	a	516	PSU	C6-N1-C2	-2.11	120.53	122.68
1	a	1402	4OC	CM4-N4-C4	-2.11	118.34	122.45
22	A	1835	2MG	C1'-N9-C4	-2.10	120.26	126.50
1	a	1516	2MG	C8-N7-C5	2.09	108.03	104.24
22	A	2449	H2U	O4-C4-N3	2.09	123.60	120.28
22	A	1618	6MZ	C4-C5-N7	-2.08	108.09	110.62
22	A	746	PSU	O2-C2-N1	-2.06	120.52	122.79
22	A	2030	6MZ	C4-N9-C1'	-2.05	121.70	126.59
1	a	966	2MG	N1-C2-N3	-2.04	120.79	123.95
22	A	2498	OMC	O2-C2-N3	-2.04	119.01	122.33
1	a	1516	2MG	C5-C4-N9	2.04	109.33	105.63
1	a	1498	UR3	C3U-N3-C4	2.04	120.80	117.89
22	A	2503	2MA	C4-C5-N7	-2.03	108.15	110.62
22	A	745	1MG	C8-N9-C4	2.03	109.91	106.05
22	A	1939	5MU	C6-C5-C4	2.02	119.72	118.03
22	A	2552	OMU	O2-C2-N1	-2.02	120.10	122.79
22	A	1835	2MG	C8-N7-C5	2.02	107.90	104.24
1	a	1519	MA6	C4-N9-C8	2.02	107.92	105.73
22	A	1915	3TD	O4'-C1'-C2'	2.02	107.99	105.14

There are no chirality outliers.

All (50) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	a	967	5MC	O4'-C4'-C5'-O5'
1	a	1498	UR3	O4'-C1'-N1-C2
1	a	1518	MA6	C3'-C4'-C5'-O5'
1	a	1518	MA6	C5-C6-N6-C10
22	A	1915	3TD	O4'-C1'-C5-C4
22	A	1915	3TD	C2'-C1'-C5-C6
22	A	1915	3TD	O4'-C1'-C5-C6
22	A	1915	3TD	O4'-C4'-C5'-O5'
22	A	1939	5MU	O4'-C4'-C5'-O5'
22	A	2030	6MZ	N1-C6-N6-C9
22	A	2030	6MZ	O4'-C4'-C5'-O5'
22	A	2030	6MZ	C3'-C4'-C5'-O5'
22	A	2251	OMG	C1'-C2'-O2'-CM2
22	A	2445	2MG	O4'-C4'-C5'-O5'
22	A	2445	2MG	C3'-C4'-C5'-O5'
22	A	2503	2MA	O4'-C4'-C5'-O5'
22	A	2552	OMU	O4'-C1'-N1-C2
22	A	2552	OMU	O4'-C1'-N1-C6
1	a	1498	UR3	O4'-C1'-N1-C6
1	a	967	5MC	C3'-C4'-C5'-O5'
1	a	1402	4OC	O4'-C4'-C5'-O5'
1	a	1518	MA6	O4'-C4'-C5'-O5'
22	A	1915	3TD	C3'-C4'-C5'-O5'
22	A	1939	5MU	C3'-C4'-C5'-O5'
1	a	1518	MA6	O4'-C1'-N9-C8
1	a	1518	MA6	O4'-C1'-N9-C4
22	A	2504	PSU	O4'-C4'-C5'-O5'
1	a	1518	MA6	N1-C6-N6-C10
1	a	1402	4OC	C3'-C4'-C5'-O5'
22	A	1835	2MG	O4'-C4'-C5'-O5'
1	a	1518	MA6	C5-C6-N6-C9
1	a	966	2MG	C3'-C4'-C5'-O5'
22	A	1835	2MG	C3'-C4'-C5'-O5'
22	A	2069	G7M	O4'-C4'-C5'-O5'
1	a	1519	MA6	C4'-C5'-O5'-P
22	A	2503	2MA	C3'-C4'-C5'-O5'
22	A	747	5MC	C4'-C5'-O5'-P
22	A	2552	OMU	C3'-C4'-C5'-O5'
22	A	2552	OMU	O4'-C4'-C5'-O5'
1	a	527	G7M	C4'-C5'-O5'-P
22	A	2069	G7M	C3'-C4'-C5'-O5'
22	A	2504	PSU	C3'-C4'-C5'-O5'
22	A	1911	PSU	O4'-C1'-C5-C4

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Mol	Chain	Res	Type	Atoms
22	A	1917	PSU	O4'-C1'-C5-C4
1	a	966	2MG	O4'-C4'-C5'-O5'
22	A	746	PSU	O4'-C1'-C5-C6
22	A	1911	PSU	O4'-C1'-C5-C6
22	A	1917	PSU	O4'-C1'-C5-C6
22	A	2498	OMC	C4'-C5'-O5'-P
1	a	527	G7M	C3'-C4'-C5'-O5'

There are no ring outliers.

16 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	A	2069	G7M	1	0
1	a	1516	2MG	1	0
22	A	745	1MG	1	0
22	A	2504	PSU	1	0
22	A	1835	2MG	1	0
1	a	1519	MA6	1	0
22	A	1911	PSU	1	0
1	a	966	2MG	2	0
22	A	955	PSU	1	0
1	a	1407	5MC	1	0
22	A	2251	OMG	1	0
1	a	1402	4OC	1	0
22	A	2030	6MZ	2	0
1	a	1405	G7M	3	0
1	a	1518	MA6	6	0
1	a	967	5MC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
57	ILE	A	3001	-	6,7,8	0.51	0	5,8,10	1.69	2 (40%)
58	PRO	9	101	55	5,7,8	0.60	0	7,8,10	2.00	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	ILE	A	3001	-	-	1/7/8/10	-
58	PRO	9	101	55	-	0/0/9/11	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	9	101	PRO	O-C-CA	-4.85	112.07	124.78
57	A	3001	ILE	CB-CA-C	-2.72	108.67	112.83
57	A	3001	ILE	O-C-CA	-2.59	117.98	124.78

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	A	3001	ILE	C-CA-CB-CG1

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	A	3001	ILE	1	0
58	9	101	PRO	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

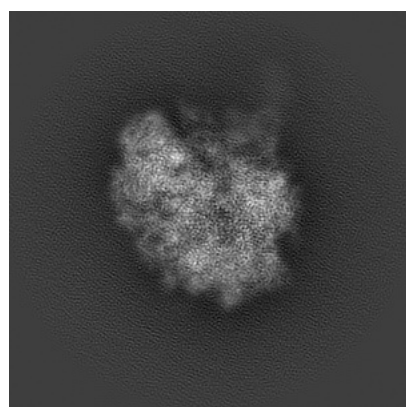
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30431. These allow visual inspection of the internal detail of the map and identification of artifacts.

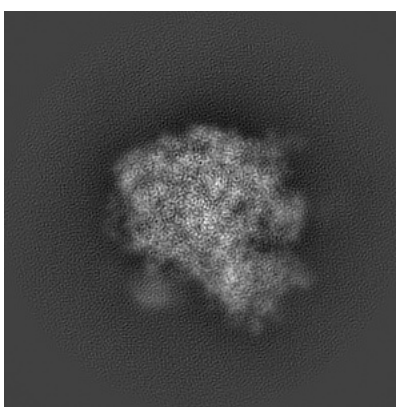
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

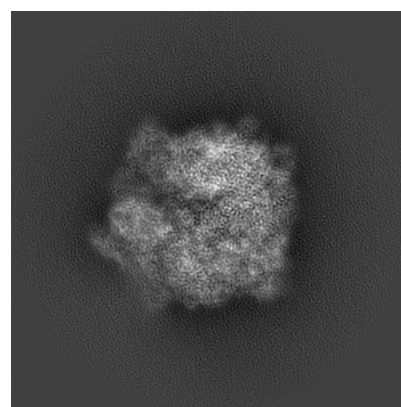
6.1.1 Primary map



X



Y

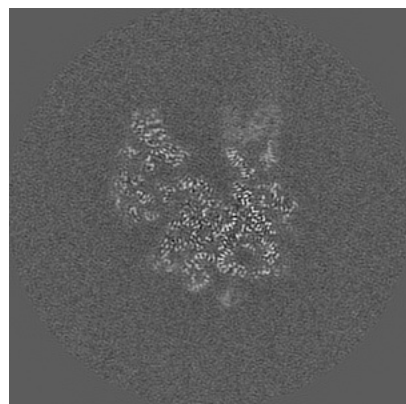


Z

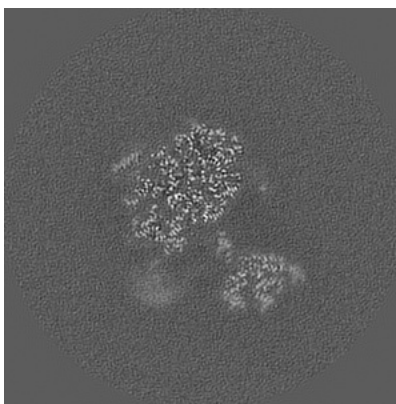
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

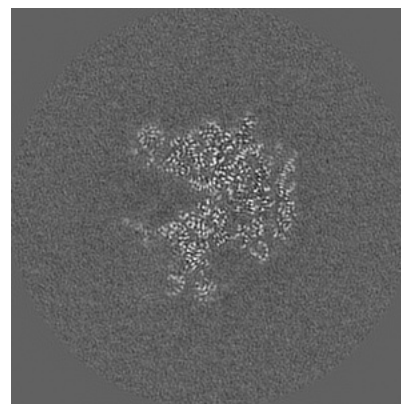
6.2.1 Primary map



X Index: 150



Y Index: 150

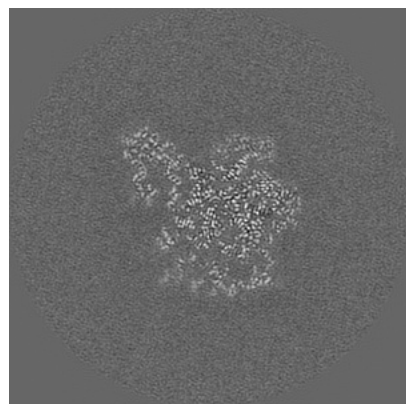


Z Index: 150

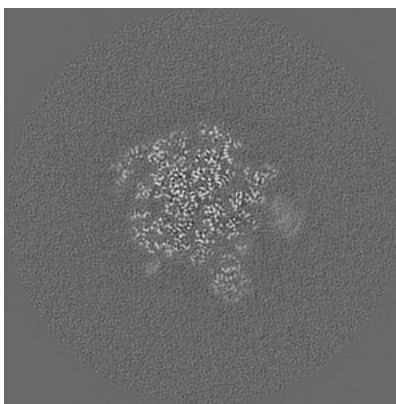
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

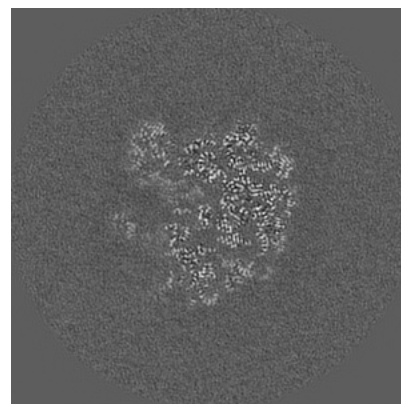
6.3.1 Primary map



X Index: 173



Y Index: 179

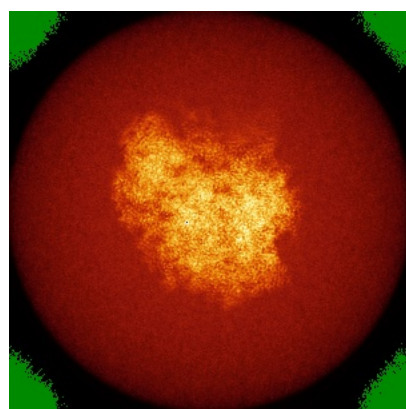


Z Index: 158

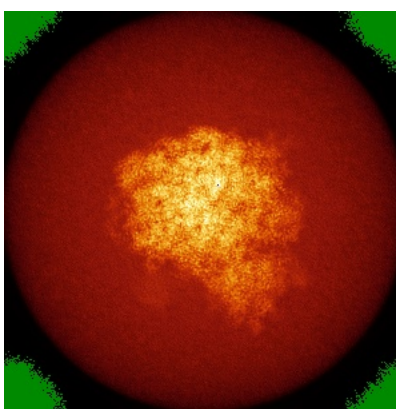
The images above show the largest variance slices of the map in three orthogonal directions.

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

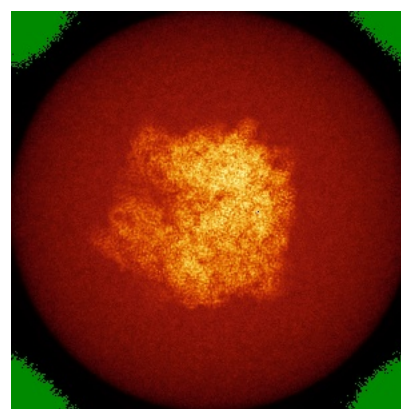
6.4.1 Primary map



X



Y

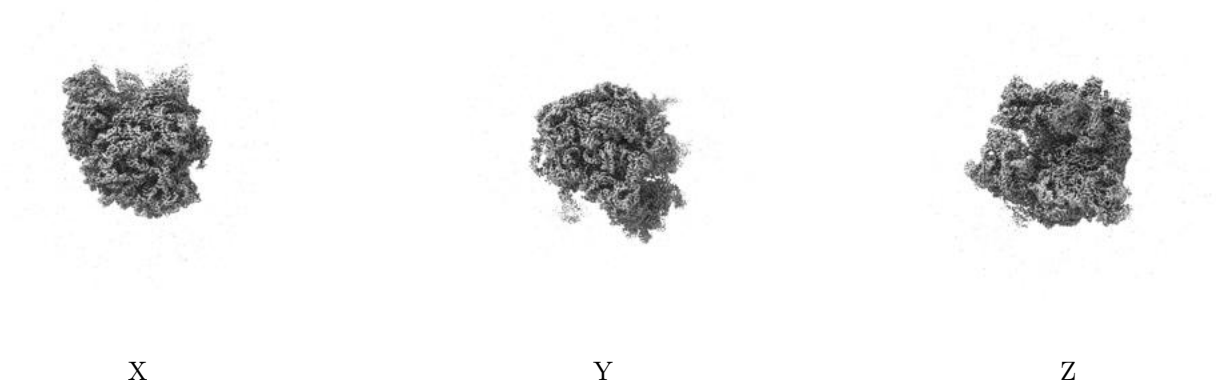


Z

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](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.046. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

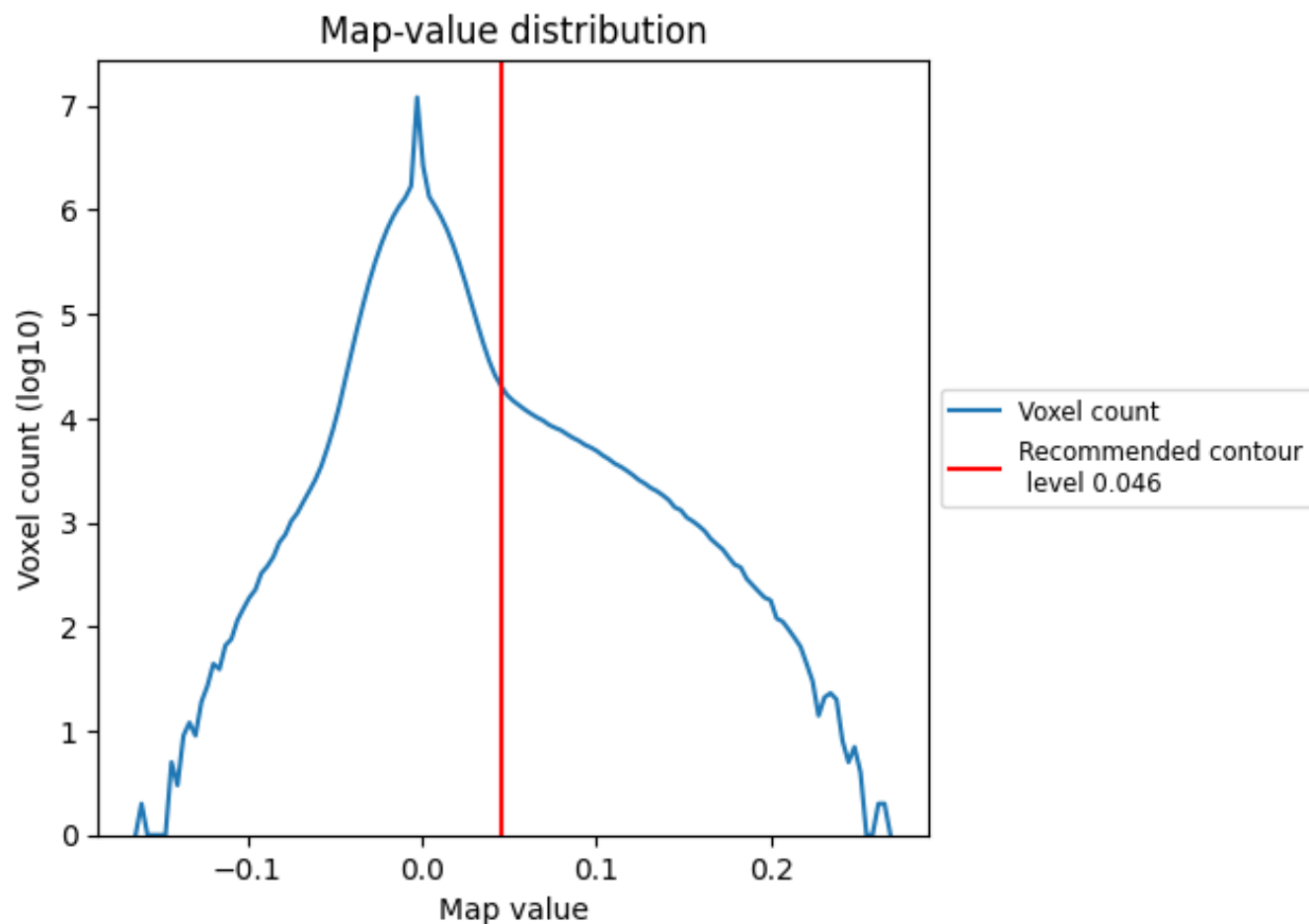
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

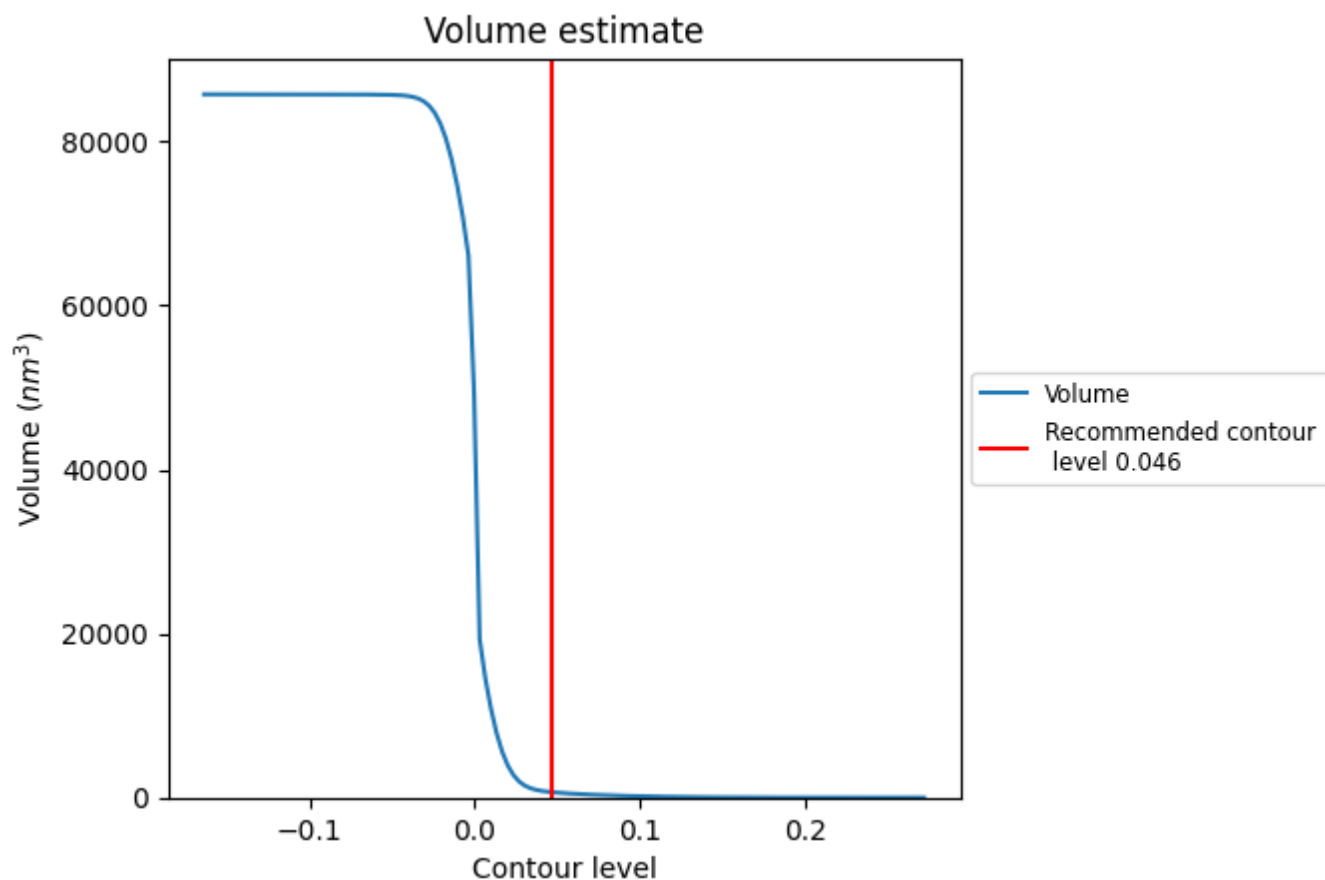
This section contains the results of statistical analysis of the map.

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.

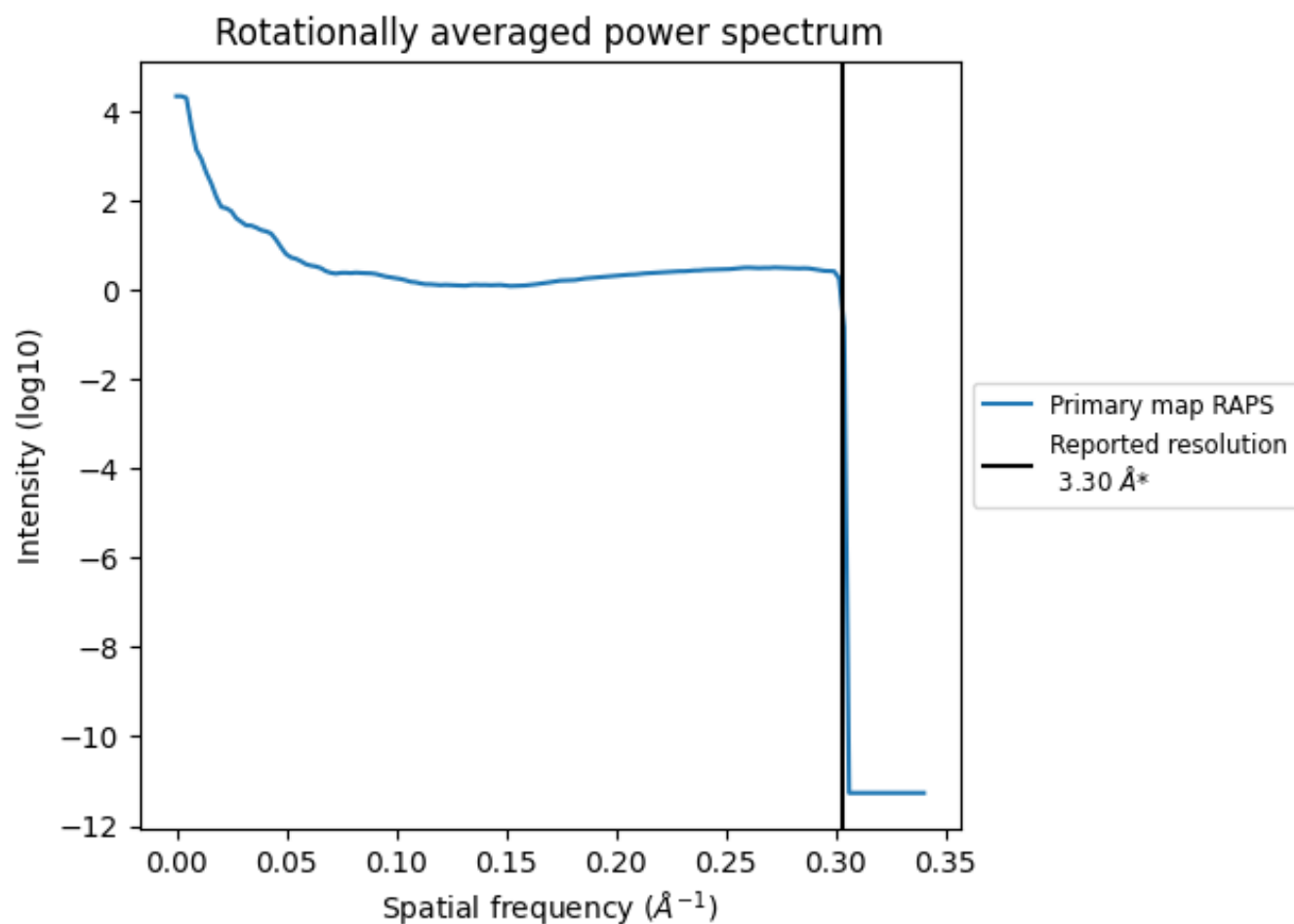
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 668 nm³; this corresponds to an approximate mass of 604 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 ⓘ

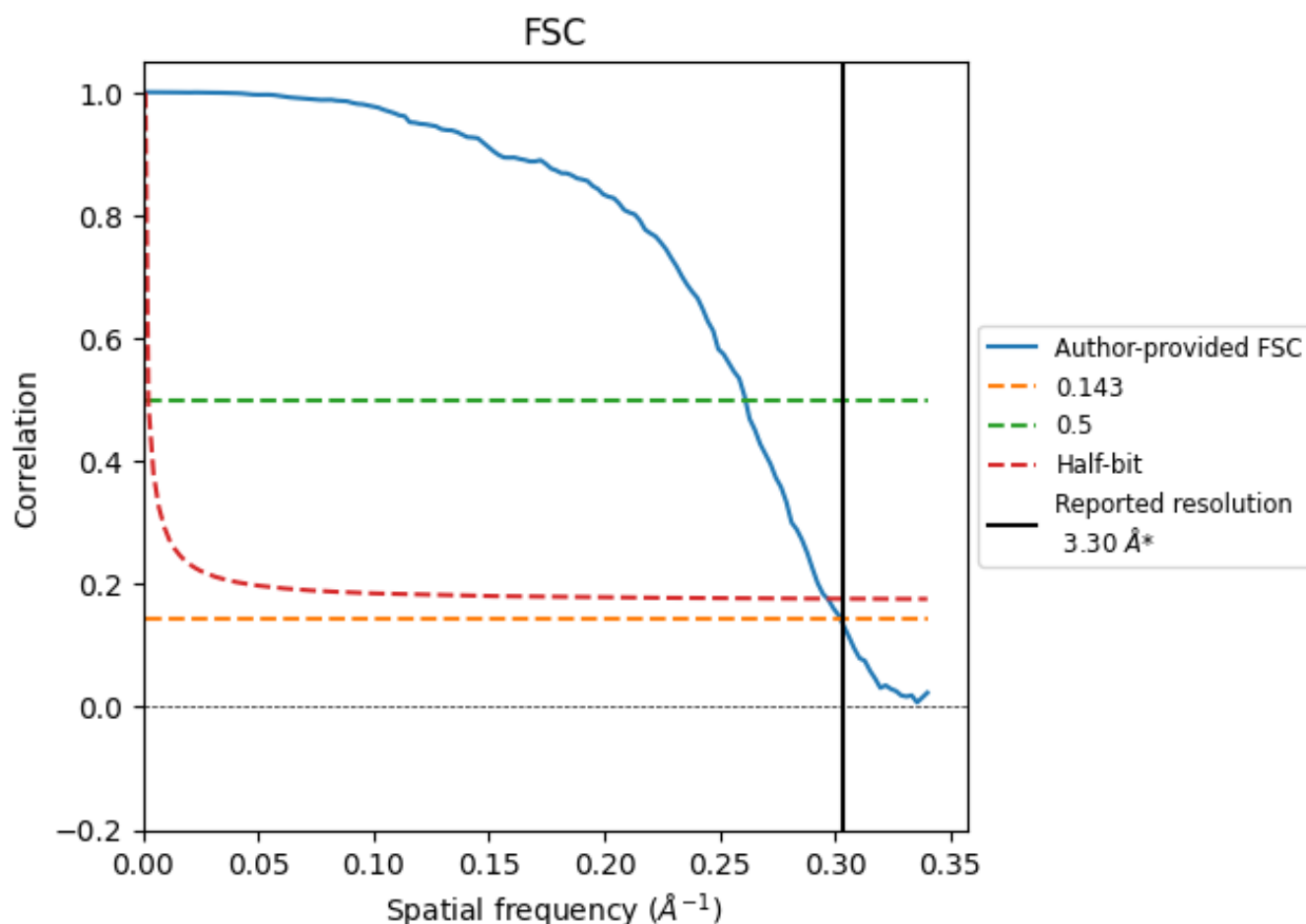


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

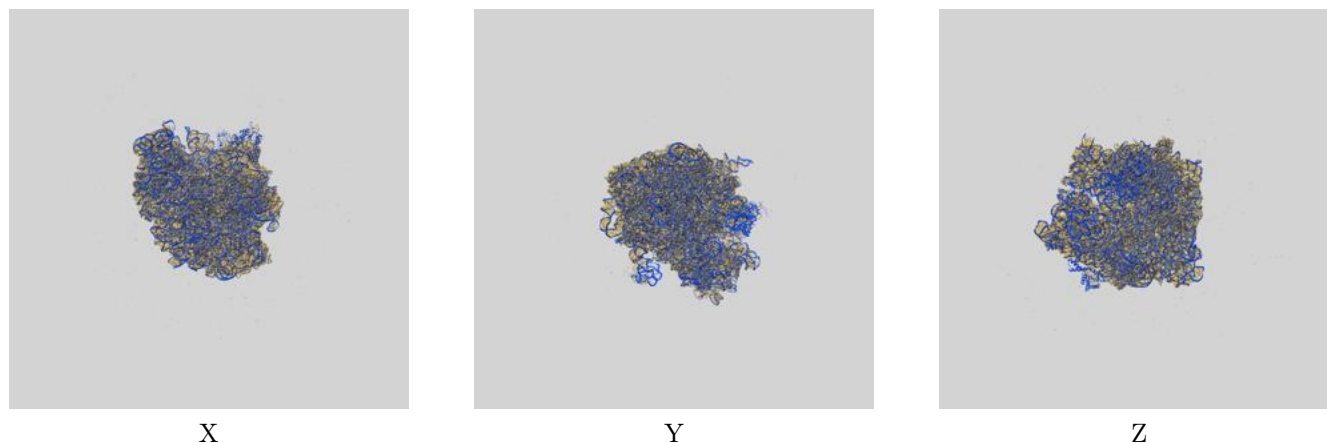
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.31	3.83	3.37
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

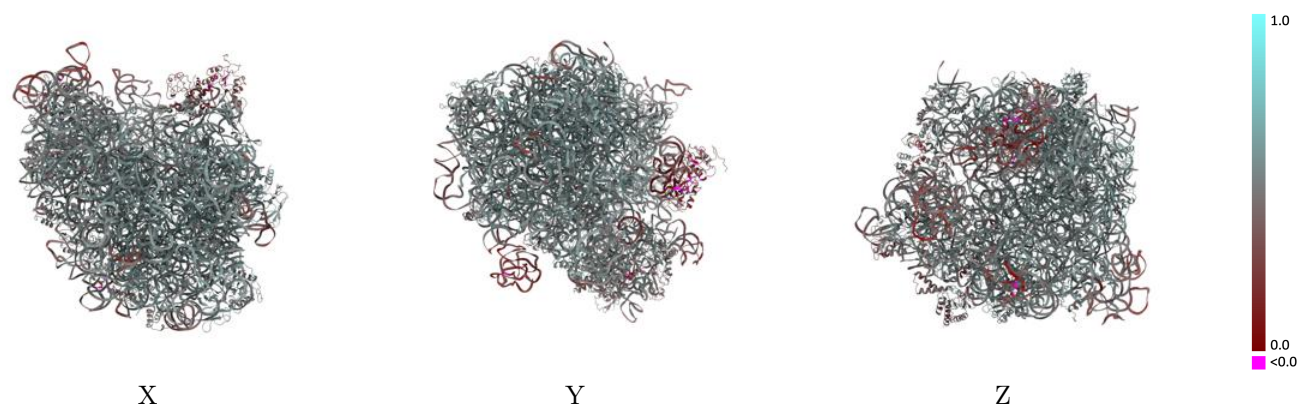
This section contains information regarding the fit between EMDB map EMD-30431 and PDB model 7CPJ. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



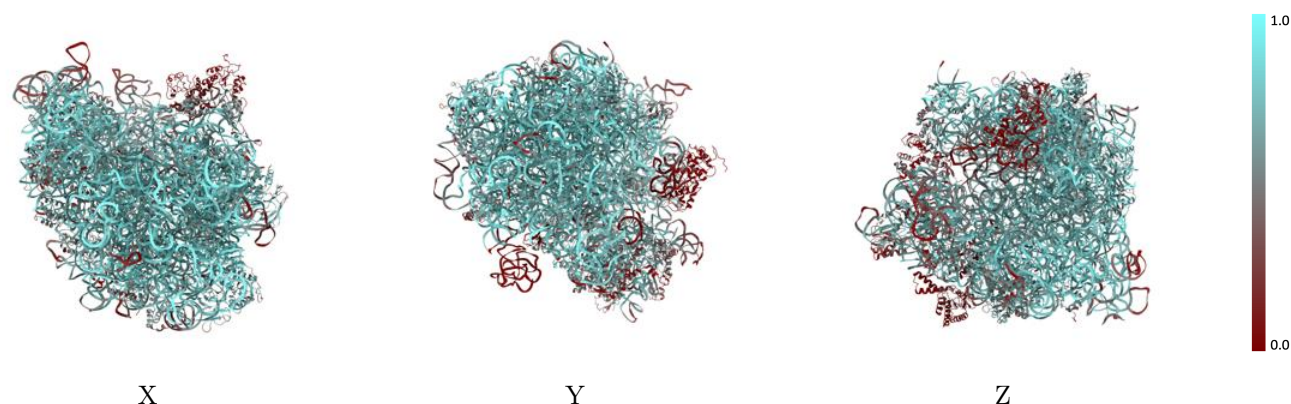
The images above show the 3D surface view of the map at the recommended contour level 0.046 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



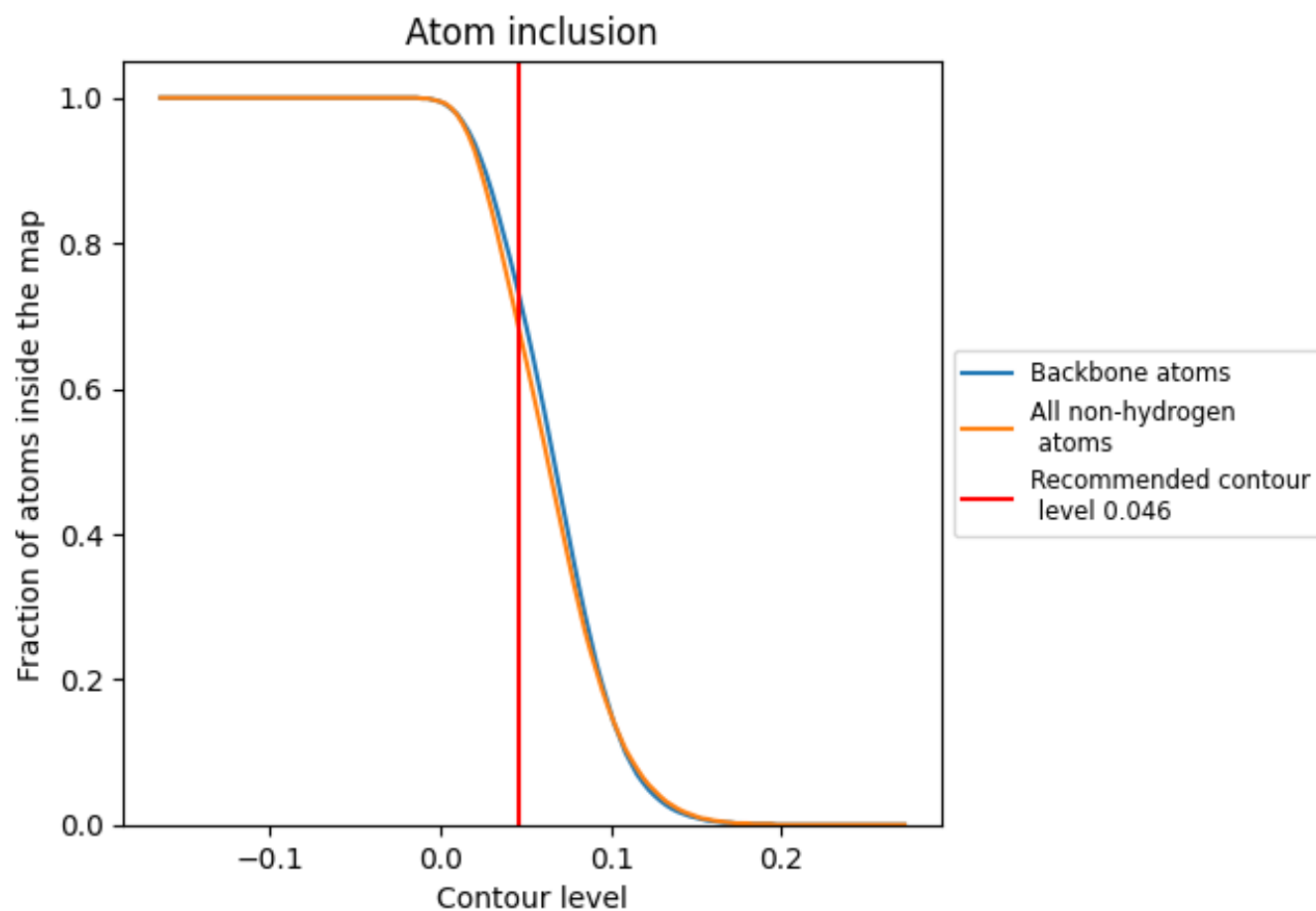
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.046).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 68% 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 (0.046) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6840	 0.5020
0	 0.6780	 0.5500
1	 0.0130	 0.3880
2	 0.7350	 0.5520
3	 0.7450	 0.5720
4	 0.6710	 0.5560
5	 0.0650	 0.2970
6	 0.1170	 0.3540
9	 0.4420	 0.4360
A	 0.7720	 0.5100
B	 0.7640	 0.5010
C	 0.6930	 0.5610
D	 0.7190	 0.5640
E	 0.6340	 0.5380
F	 0.4650	 0.4800
G	 0.4990	 0.5070
H	 0.1410	 0.3630
I	 0.0150	 0.2600
J	 0.7160	 0.5580
K	 0.6780	 0.5500
L	 0.6780	 0.5410
M	 0.6770	 0.5490
N	 0.7290	 0.5590
O	 0.6370	 0.5230
P	 0.6590	 0.5530
Q	 0.7610	 0.5640
R	 0.6830	 0.5500
S	 0.6570	 0.5470
T	 0.5890	 0.5330
U	 0.5450	 0.5180
V	 0.6410	 0.5390
W	 0.7030	 0.5720
X	 0.6570	 0.5450
Y	 0.5190	 0.4910
Z	 0.6750	 0.5490



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Chain	Atom inclusion	Q-score
a	 0.7410	 0.4930
b	 0.1030	 0.4270
c	 0.5080	 0.5040
d	 0.4910	 0.4490
e	 0.6170	 0.5220
f	 0.4520	 0.4660
g	 0.3950	 0.4650
h	 0.6140	 0.5370
i	 0.4760	 0.4770
j	 0.3840	 0.4550
k	 0.5300	 0.5020
l	 0.5960	 0.5280
m	 0.4220	 0.4830
n	 0.5080	 0.4950
o	 0.6130	 0.5160
p	 0.6300	 0.5110
q	 0.5580	 0.5200
r	 0.5150	 0.5080
s	 0.4270	 0.4760
t	 0.6230	 0.5150
u	 0.0230	 0.3580
x	 0.6980	 0.5340