



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 03:00 PM UTC

PDB ID : 8Y5Q / pdb_00008y5q
EMDB ID : EMD-38946
Title : E.coli transcription translation coupling complex in TTC-B state 4 (subclass 2) containing mRNA with 27-mer spacer, NusG, NusA, fMet-tRNA(iMet), Phe-tRNA(Phe), and GDPCP
Authors : Zhang, J.; Lu, G.; Wang, C.; Lin, J.
Deposited on : 2024-01-31
Resolution : 3.90 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

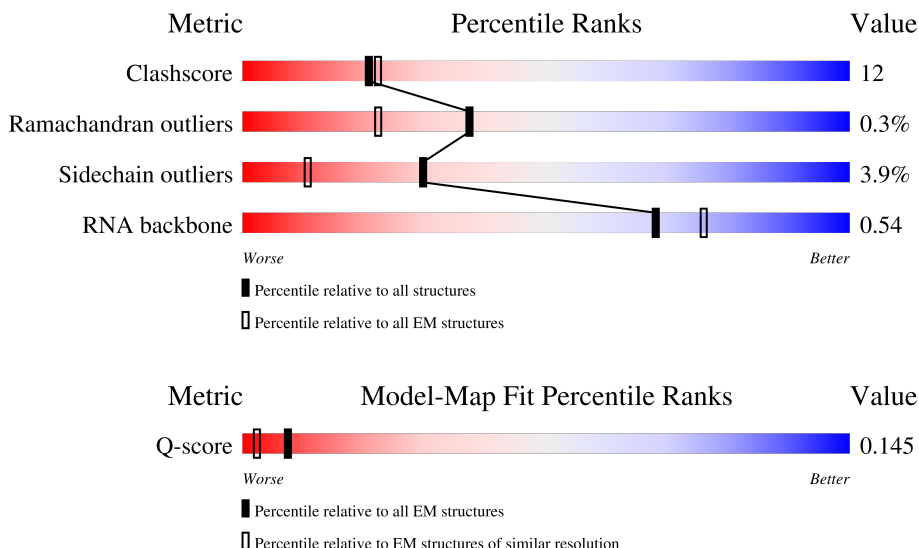
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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.



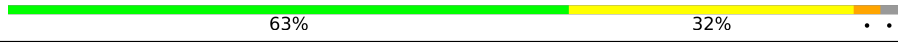
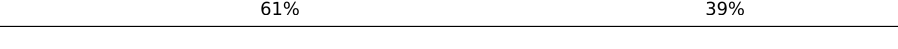
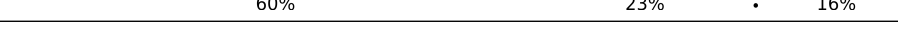
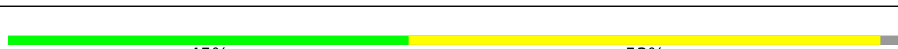
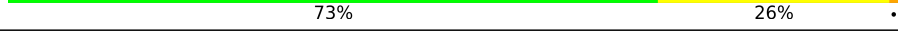
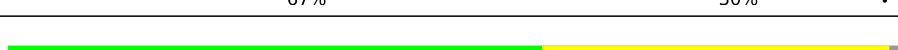
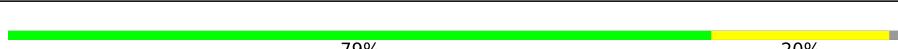
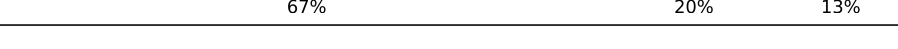
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

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	70	
2	B	57	
3	C	55	

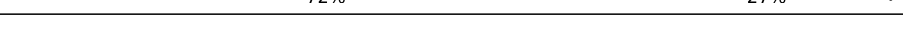
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Mol	Chain	Length	Quality of chain
4	D	46	
5	E	65	
6	F	38	
7	G	241	
8	H	233	
9	I	206	
10	J	167	
11	K	135	
12	L	179	
13	M	130	
14	N	130	
15	O	103	
16	P	129	
17	Q	124	
18	R	118	
19	S	101	
20	T	89	
21	U	82	
22	V	84	
23	W	75	
24	X	92	
25	Y	87	
26	Z	71	
27	b	273	
28	c	209	

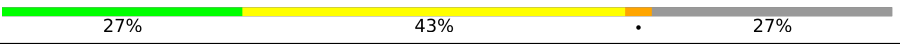
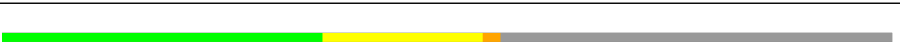
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Mol	Chain	Length	Quality of chain
29	d	201	 66% 33% .
30	e	179	 70% 28% ..
31	f	177	 77% 23% .
32	g	149	 5% 72% 25% .
33	i	142	 13% 70% 30% .
34	j	142	 77% 22% .
35	k	123	 76% 21% ..
36	l	144	 77% 20% ..
37	m	136	 69% 30% .
38	n	127	 63% 30% . 6%
39	o	117	 68% 31% .
40	p	115	 77% 22% ..
41	q	118	 78% 21% .
42	r	103	 71% 29%
43	s	110	 72% 27% .
44	t	100	 64% 28% . 7%
45	u	104	 72% 25% ..
46	v	94	 77% 23%
47	w	85	 66% 22% 12%
48	x	78	 67% 29% ..
49	y	63	 78% 22%
50	z	59	 75% 24% .
51	1	2904	 45% 48% 8%
52	2	120	 50% 40% 10%
53	3	1542	 46% 48% 6%

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Mol	Chain	Length	Quality of chain
54	4	44	
55	8	37	
56	9	37	
57	A1	329	
57	A2	329	
58	B1	1407	
59	B2	1342	
60	W0	91	
61	NA	495	
62	NG	181	
63	6	77	
64	a	234	
65	0	716	

2 Entry composition

There are 67 unique types of molecules in this entry. The entry contains 181699 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 protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	46	Total	C	N	O	S	0	0
			355	221	62	66	6		

- Molecule 2 is a protein called 50S ribosomal protein L32.

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

- Molecule 3 is a protein called 50S ribosomal protein L33.

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

- Molecule 4 is a protein called 50S ribosomal protein L34.

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

- Molecule 5 is a protein called 50S ribosomal protein L35.

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

- Molecule 6 is a protein called 50S ribosomal protein L36.

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

- Molecule 7 is a protein called 30S ribosomal protein S2.

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

- Molecule 8 is a protein called 30S ribosomal protein S3.

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

- Molecule 9 is a protein called 30S ribosomal protein S4.

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

- Molecule 10 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 11 is a protein called 30S ribosomal protein S6, fully modified isoform.

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

- Molecule 12 is a protein called 30S ribosomal protein S7.

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

- Molecule 13 is a protein called 30S ribosomal protein S8.

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

- Molecule 14 is a protein called 30S ribosomal protein S9.

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

- Molecule 15 is a protein called 30S ribosomal protein S10.

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

- Molecule 16 is a protein called 30S ribosomal protein S11.

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

- Molecule 17 is a protein called 30S ribosomal protein S12.

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

- Molecule 18 is a protein called 30S ribosomal protein S13.

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

- Molecule 19 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 20 is a protein called 30S ribosomal protein S15.

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

- Molecule 21 is a protein called 30S ribosomal protein S16.

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

- Molecule 22 is a protein called 30S ribosomal protein S17.

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

- Molecule 23 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 24 is a protein called 30S ribosomal protein S19.

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

- Molecule 25 is a protein called 30S ribosomal protein S20.

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

- Molecule 26 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 33 is a protein called 50S ribosomal protein L11.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

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

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

- Molecule 38 is a protein called 50S ribosomal protein L17.

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

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

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

- Molecule 45 is a protein called 50S ribosomal protein L24.

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

- Molecule 46 is a protein called 50S ribosomal protein L25.

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

- Molecule 47 is a protein called 50S ribosomal protein L27.

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

- Molecule 48 is a protein called 50S ribosomal protein L28.

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

- Molecule 49 is a protein called 50S ribosomal protein L29.

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

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

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

- Molecule 51 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1929590828

- Molecule 52 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	U	conflict	GB NR_103249

- Molecule 53 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	30	Total	C	N	O	P	0	0
			627	280	92	225	30		

- Molecule 55 is a DNA chain called templete DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	8	27	Total	C	N	O	P	0	0
			539	257	88	167	27		

- Molecule 56 is a DNA chain called non-templete DNA strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	9	20	Total	C	N	O	P	0	0
			417	195	84	118	20		

- Molecule 57 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	A1	301	Total	C	N	O	S	0	0
			2088	1293	380	409	6		
57	A2	288	Total	C	N	O	S	0	0
			2029	1257	366	400	6		

- Molecule 58 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	B1	1335	Total	C	N	O	S	0	0
			10353	6509	1842	1955	47		

- Molecule 59 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	B2	1340	Total	C	N	O	S	0	0
			10539	6612	1838	2046	43		

- Molecule 60 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	W0	82	Total	C	N	O	S	0	0
			650	396	122	131	1		

- Molecule 61 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	NA	492	Total	C	N	O	0	0
			2432	1448	492	492		

- Molecule 62 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	NG	154	Total	C	N	O	0	0
			758	450	154	154		

- Molecule 63 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
63	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 64 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	a	132	Total	C	N	O	S	0	0
			1013	638	183	190	2		

- Molecule 65 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	0	697	Total	C	N	O	S	0	0
			5399	3403	929	1042	25		

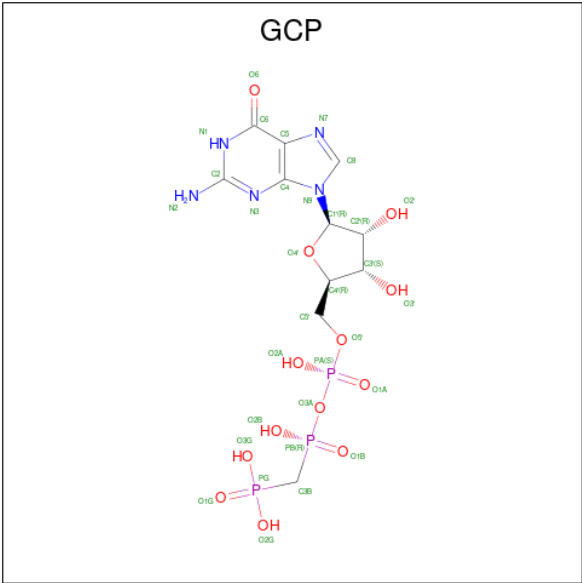
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	705	GLY	-	expression tag	UNP P0A6M8
0	706	SER	-	expression tag	UNP P0A6M8
0	707	SER	-	expression tag	UNP P0A6M8
0	708	GLY	-	expression tag	UNP P0A6M8
0	709	HIS	-	expression tag	UNP P0A6M8
0	710	HIS	-	expression tag	UNP P0A6M8
0	711	HIS	-	expression tag	UNP P0A6M8
0	712	HIS	-	expression tag	UNP P0A6M8
0	713	HIS	-	expression tag	UNP P0A6M8
0	714	HIS	-	expression tag	UNP P0A6M8
0	715	HIS	-	expression tag	UNP P0A6M8
0	716	HIS	-	expression tag	UNP P0A6M8

- Molecule 66 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
66	B1	1	Total	Mg	0
			1	1	

- Molecule 67 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).

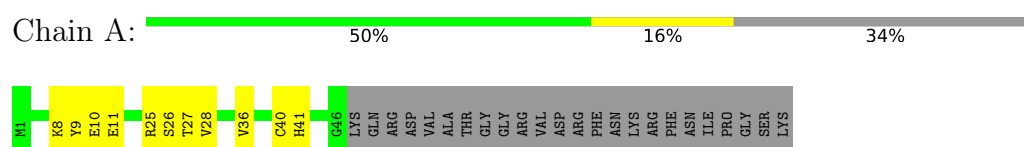


Mol	Chain	Residues	Atoms					AltConf
67	0	1	Total	C	N	O	P	0
			32	11	5	13	3	

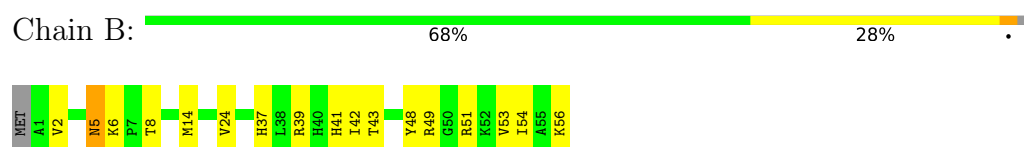
3 Residue-property plots [i](#)

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

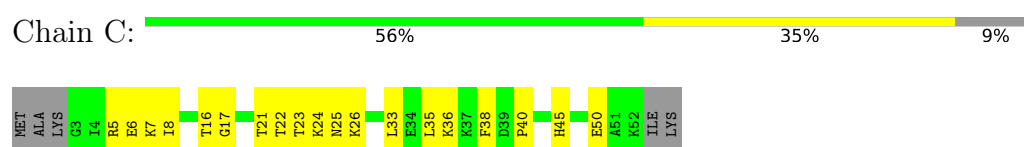
• Molecule 1: 50S ribosomal protein L31



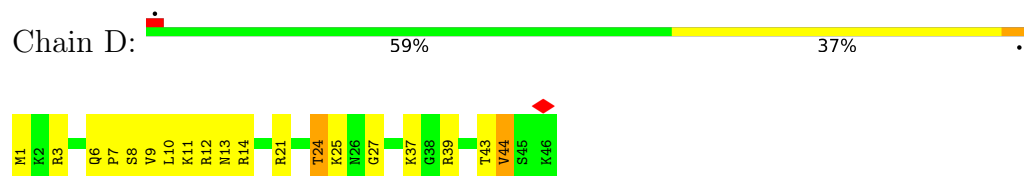
• Molecule 2: 50S ribosomal protein L32



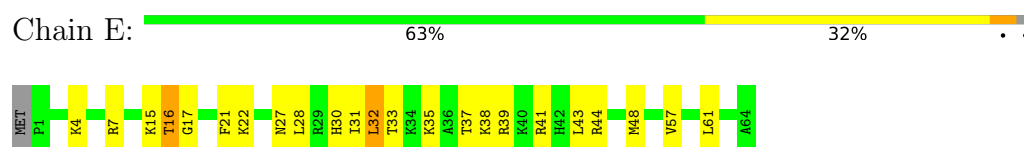
• Molecule 3: 50S ribosomal protein L33



• Molecule 4: 50S ribosomal protein L34

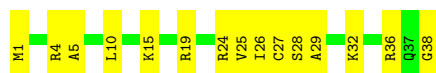


• Molecule 5: 50S ribosomal protein L35



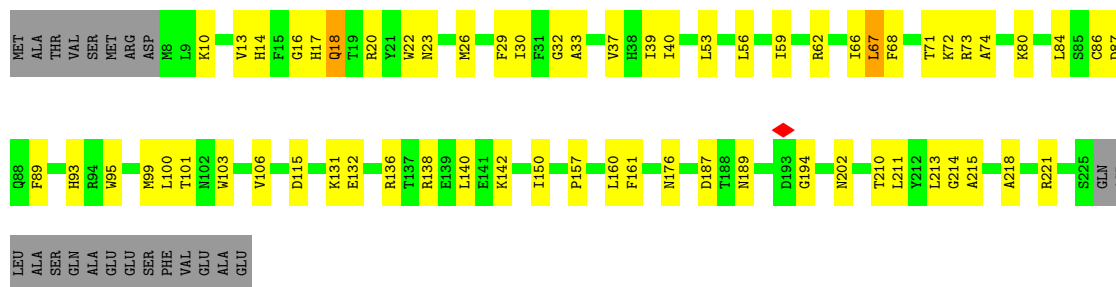
• Molecule 6: 50S ribosomal protein L36

Chain F:  61% 39%



• Molecule 7: 30S ribosomal protein S2

Chain G:  64% 25% 10%



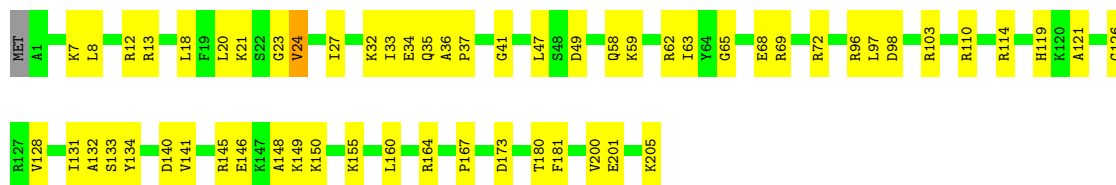
• Molecule 8: 30S ribosomal protein S3

Chain H:  61% 26% 12%



• Molecule 9: 30S ribosomal protein S4

Chain I:  71% 28%



• Molecule 10: 30S ribosomal protein S5

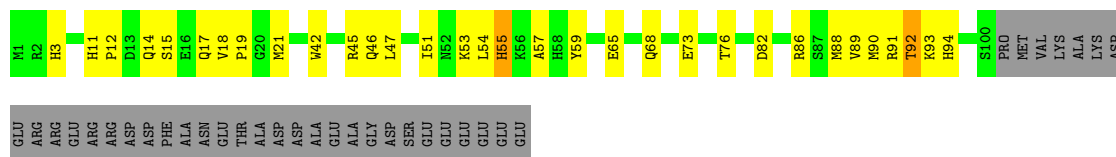
Chain J:  66% 28% 6%





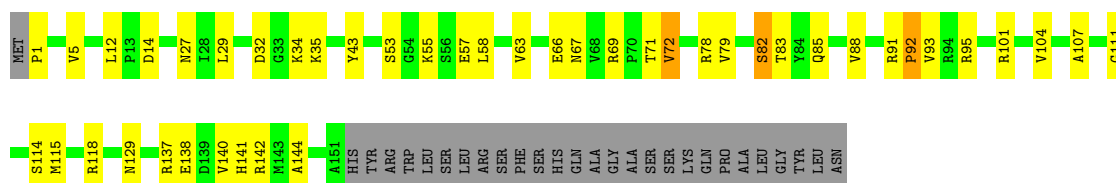
- Molecule 11: 30S ribosomal protein S6, fully modified isoform

Chain K: 50% 22% 26%



- Molecule 12: 30S ribosomal protein S7

Chain L: 60% 23% 16%



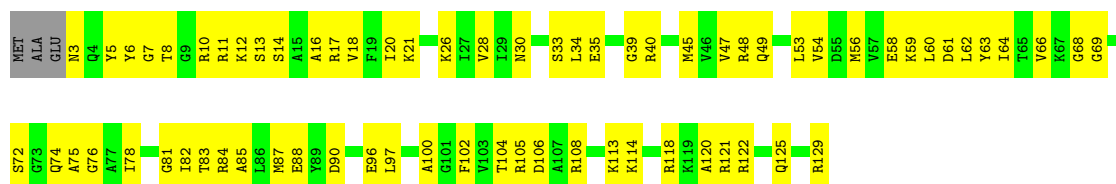
- Molecule 13: 30S ribosomal protein S8

Chain M: 66% 33%



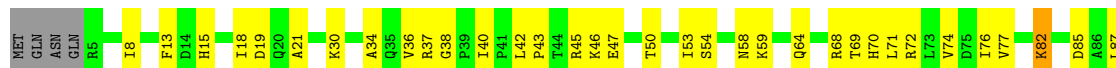
- Molecule 14: 30S ribosomal protein S9

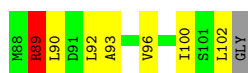
Chain N: 45% 53%



- Molecule 15: 30S ribosomal protein S10

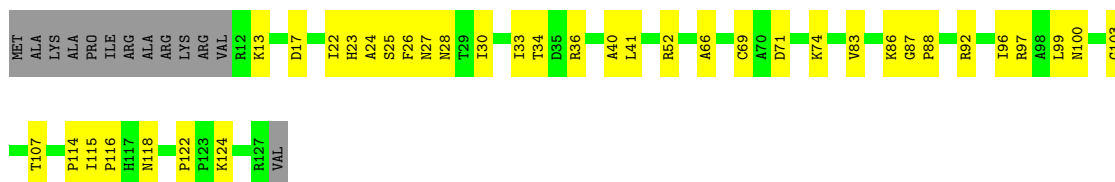
Chain O: 55% 38% 5%





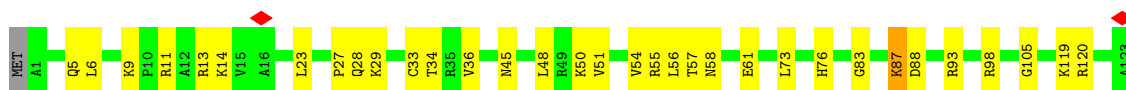
- Molecule 16: 30S ribosomal protein S11

Chain P: 61% 29% 10%



- Molecule 17: 30S ribosomal protein S12

Chain Q: 73% 26% 1%



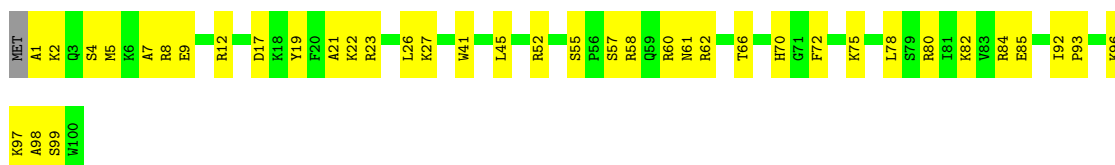
- Molecule 18: 30S ribosomal protein S13

Chain R: 67% 30% 3%



- Molecule 19: 30S ribosomal protein S14

Chain S: 60% 39% 1%



- Molecule 20: 30S ribosomal protein S15

Chain T: 79% 20% 1%



- Molecule 21: 30S ribosomal protein S16

Chain U:  72% 28%



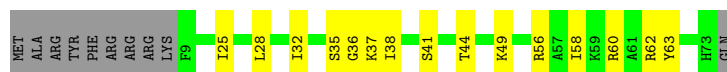
- Molecule 22: 30S ribosomal protein S17

Chain V:  65% 30% 5%



- Molecule 23: 30S ribosomal protein S18

Chain W:  67% 20% 13%



- Molecule 24: 30S ribosomal protein S19

Chain X:  64% 22% 14%



- Molecule 25: 30S ribosomal protein S20

Chain Y:  63% 34% 3%



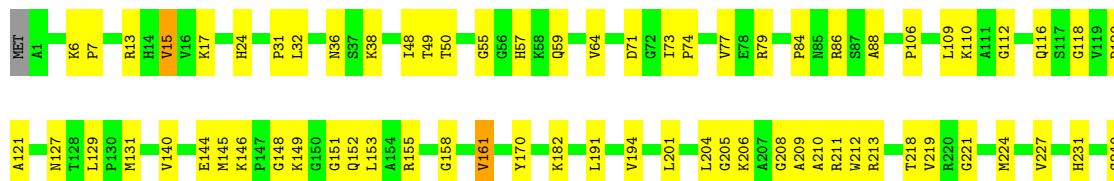
- Molecule 26: 30S ribosomal protein S21

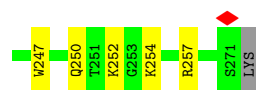
Chain Z:  61% 24% 7% 8%



- Molecule 27: 50S ribosomal protein L2

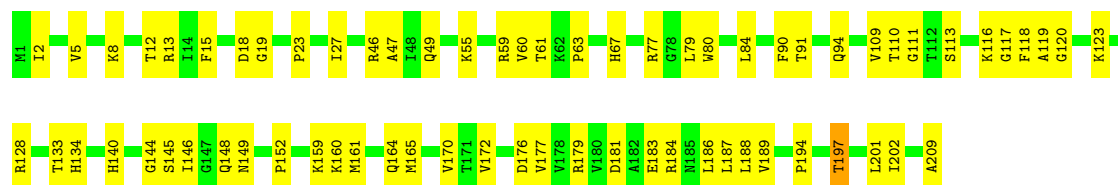
Chain b:  72% 26% 2%





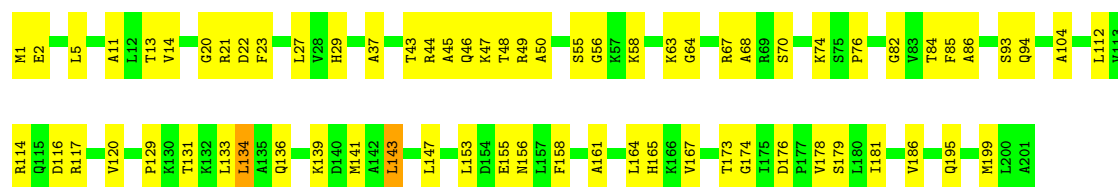
- Molecule 28: 50S ribosomal protein L3

Chain c: 67% 32%



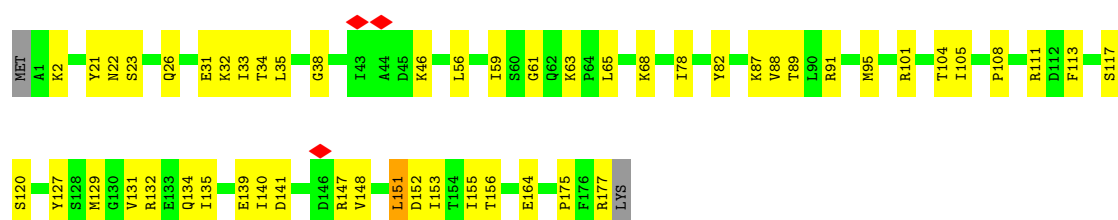
- Molecule 29: 50S ribosomal protein L4

Chain d: 66% 33%



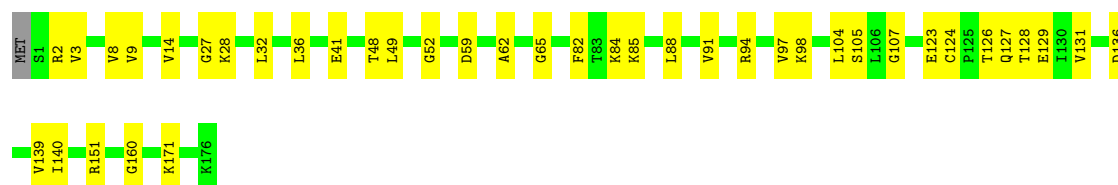
- Molecule 30: 50S ribosomal protein L5

Chain e: 70% 28%



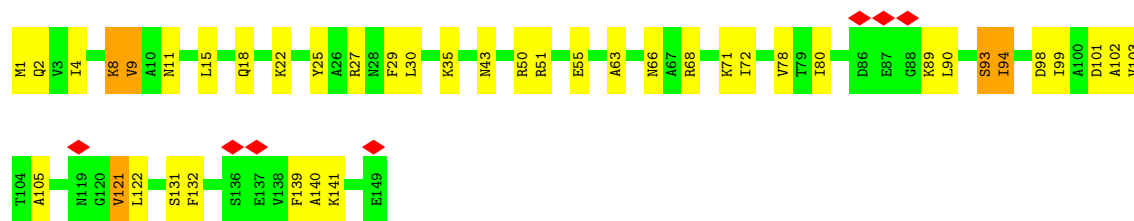
- Molecule 31: 50S ribosomal protein L6

Chain f: 77% 23%

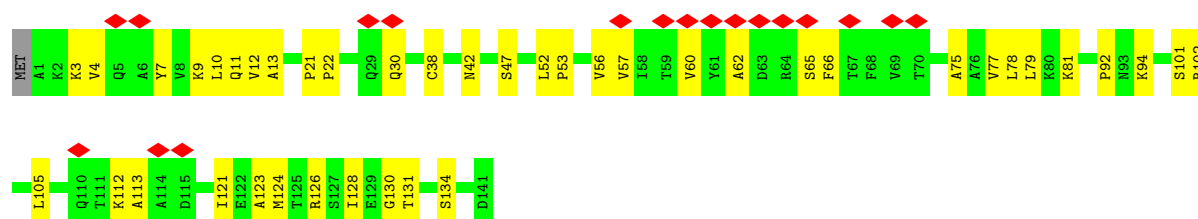


- Molecule 32: 50S ribosomal protein L9

Chain g: 5% 72% 25%



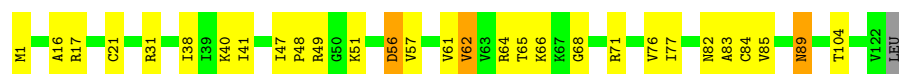
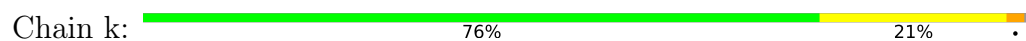
• Molecule 33: 50S ribosomal protein L11



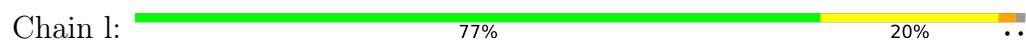
• Molecule 34: 50S ribosomal protein L13



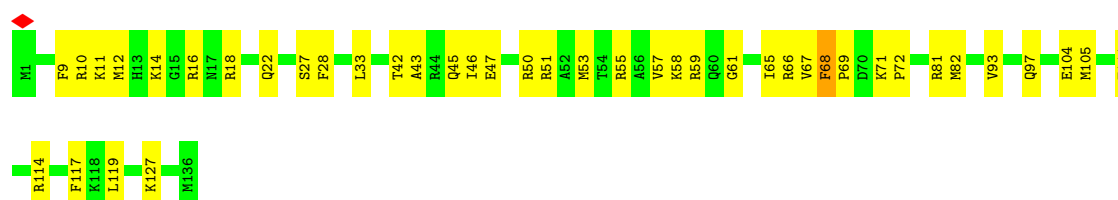
• Molecule 35: 50S ribosomal protein L14



• Molecule 36: 50S ribosomal protein L15

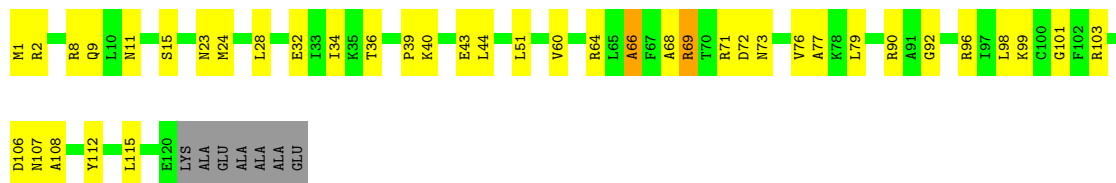


• Molecule 37: 50S ribosomal protein L16



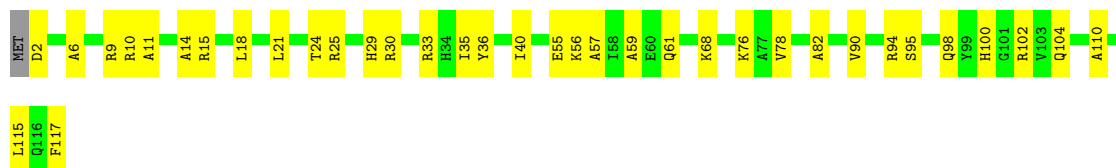
- Molecule 38: 50S ribosomal protein L17

Chain n:  63% 30% 6%



- Molecule 39: 50S ribosomal protein L18

Chain o:  68% 31% 1%



- Molecule 40: 50S ribosomal protein L19

Chain p:  77% 22% 1%



- Molecule 41: 50S ribosomal protein L20

Chain q:  78% 21% 1%



- Molecule 42: 50S ribosomal protein L21

Chain r:  71% 29% 0%



- Molecule 43: 50S ribosomal protein L22

Chain s:  72% 27% 1%



- Molecule 44: 50S ribosomal protein L23

Chain t:  64% 28% 7%



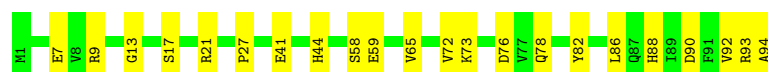
- Molecule 45: 50S ribosomal protein L24

Chain u:  72% 25% ..



- Molecule 46: 50S ribosomal protein L25

Chain v:  77% 23%



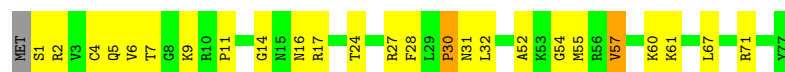
- Molecule 47: 50S ribosomal protein L27

Chain w:  66% 22% 12%



- Molecule 48: 50S ribosomal protein L28

Chain x:  67% 29% ..



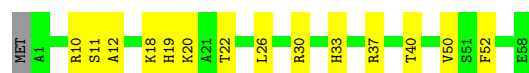
- Molecule 49: 50S ribosomal protein L29

Chain y:  78% 22%



- Molecule 50: 50S ribosomal protein L30

Chain z:  75% 24%



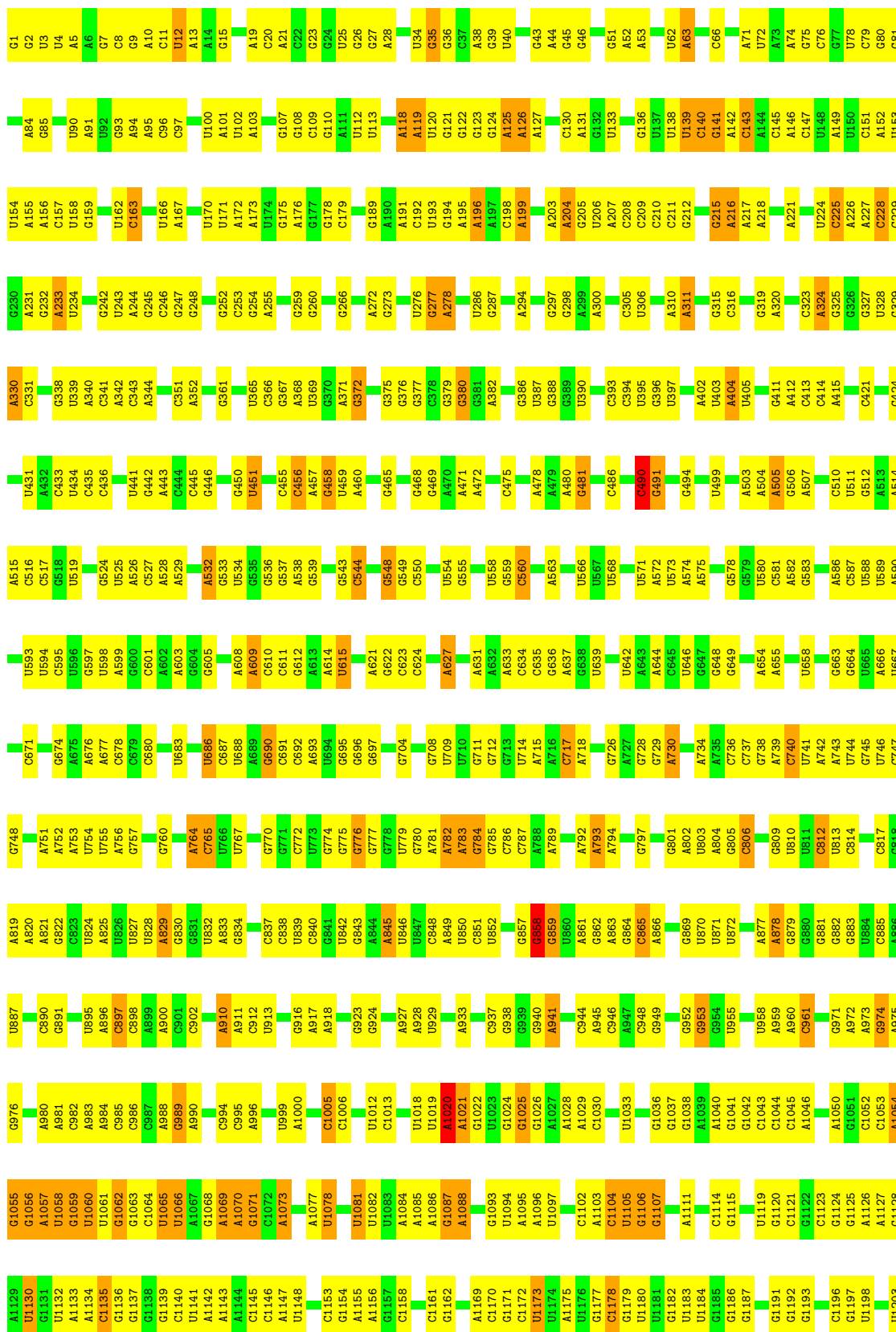
- Molecule 51: 23S rRNA

Chain 1:

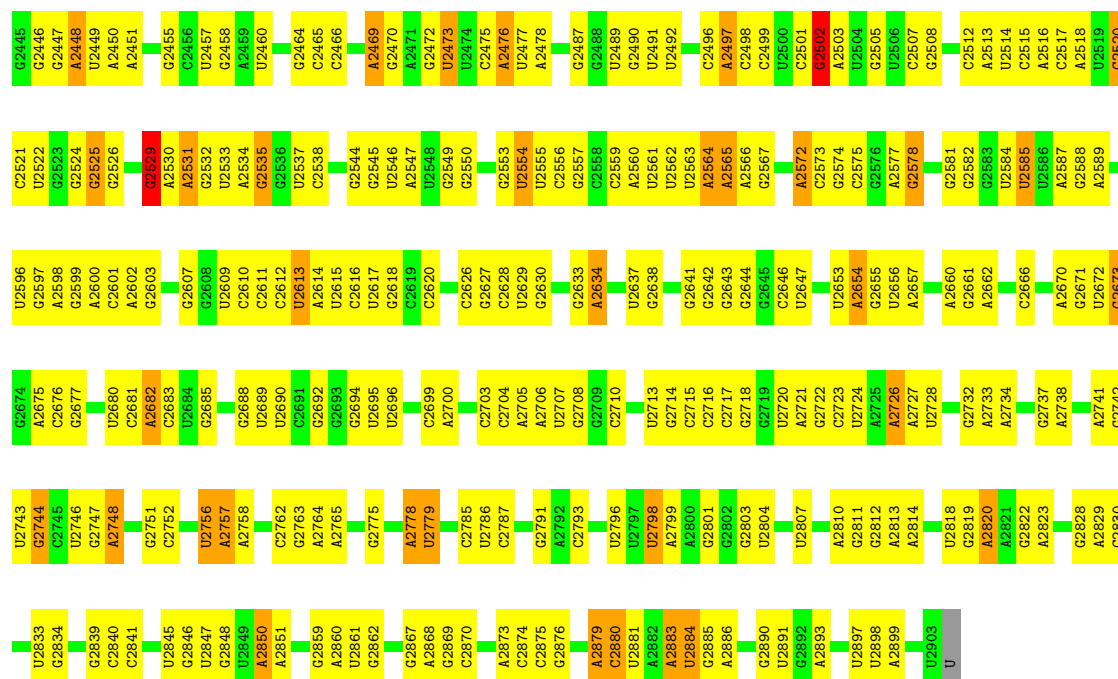
45%

48%

8%



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G2361	G2288	U2203	G2133	G2056	A1978	A1890	A1801	U1736	G1642	C1559	U1468	G1374	G1300	G1206
G2362	G2289	G2204	A2134	A2059	U1979	C1893	A1802	G1737	G1643	U1559	U1469	A1378	A1301	
G2363		A2205	G2135	A2060	G1980	C1894	C1804	G1738	G1644	C1564	A1470	U1379	A1302	U1209
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G2365	A2298	G2207	U2137	A2062	U1983	A1901	C1806	G1740	U1647	A1566	G1474	A1383	A1304	G1211
A2366	G2300	G2208	G2138	A2063	G1984	A1901	C1807	C1741	U1648	A1567	U1474	G1387	C1305	G1212
G2367	G2301	C2209	U2139	G2064	C1985	A1902	A1808	G1742	G1649	G1568	G1475	A1383	C1306	
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G2371	G2303	A2211	G2141	C2066	U1987	G1904	A1810	A1744	G1651	A1570	G1478	A1387	A1308	
G2372	G2304	U2212	A2142	C2067	C1990	C1905	G1811	A1745	G1652	A1571	G1478	G1388	A1308	U1219
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G2374	G2306	C2214	G2144	G2068	G1992	A1913	A1816	U1747	A1654	G1573	U1482	G1390	G1310	
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G2376	G2308	G2216	G2146	A2071	C1994	A1914	G1817		C1656		U1394	U1395	U1312	A1226
A2309	G2309	A2072	U2151	C2072	U1995	U1917	U1818	C1752	U1657	A1580	U1485	U1395	U1313	
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G2396	A2317	G2235	U2166	U2086	C2008	U1931	G1826	C1760	A1665	C1592	C1507	U1410	A1327	G1248
G2318	G2318	U2236	G2237	G2087	A2009	A1932	U1827	C1761	G1666	U1593	A1508	U1411	U1249	U1249
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G2326	C2326	A2094	G2168	A2094	C2021	A1938	C1832		C1676	U1599	A1515	U1415	G1334	U1254
A2327	G2327	G2248	U2172	U2099	U2022	U1939	C1833	G1770	A1677	C1600	A1515	C1417	G1337	U1255
A2328	G2328	U2249	C2173	G2100	C2023	A1940	G1836	A1772	A1678	A1603	C1518	G1418	G1338	C1257
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A2423	A2340	G2263	A2184	U2113	G2035	U1956	U1856	A1784	A1698	G1618	A1535	A1434	G1356	C1270
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G2352	G2352	G2121	G2191	G2121	C2043	G1968	G1867	A1791	G1710	A1630	A1545	G1446	G1364	C1278
A2352	G2352	U2122	U2192	U2122	G2043	A1969	C1868	G1792	A1711	A1630	A1545	C1447	A1365	G1279
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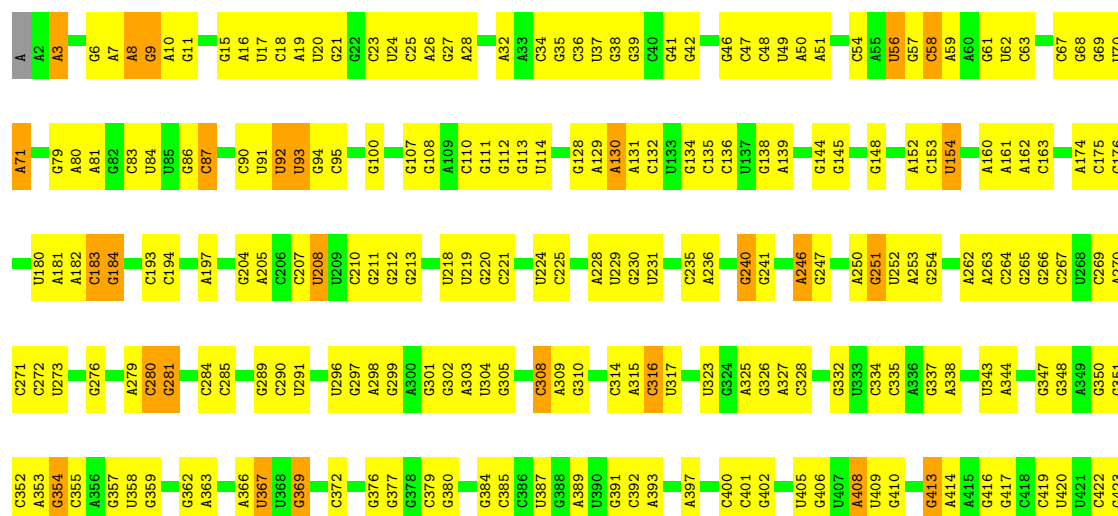
• Molecule 52: 5S rRNA

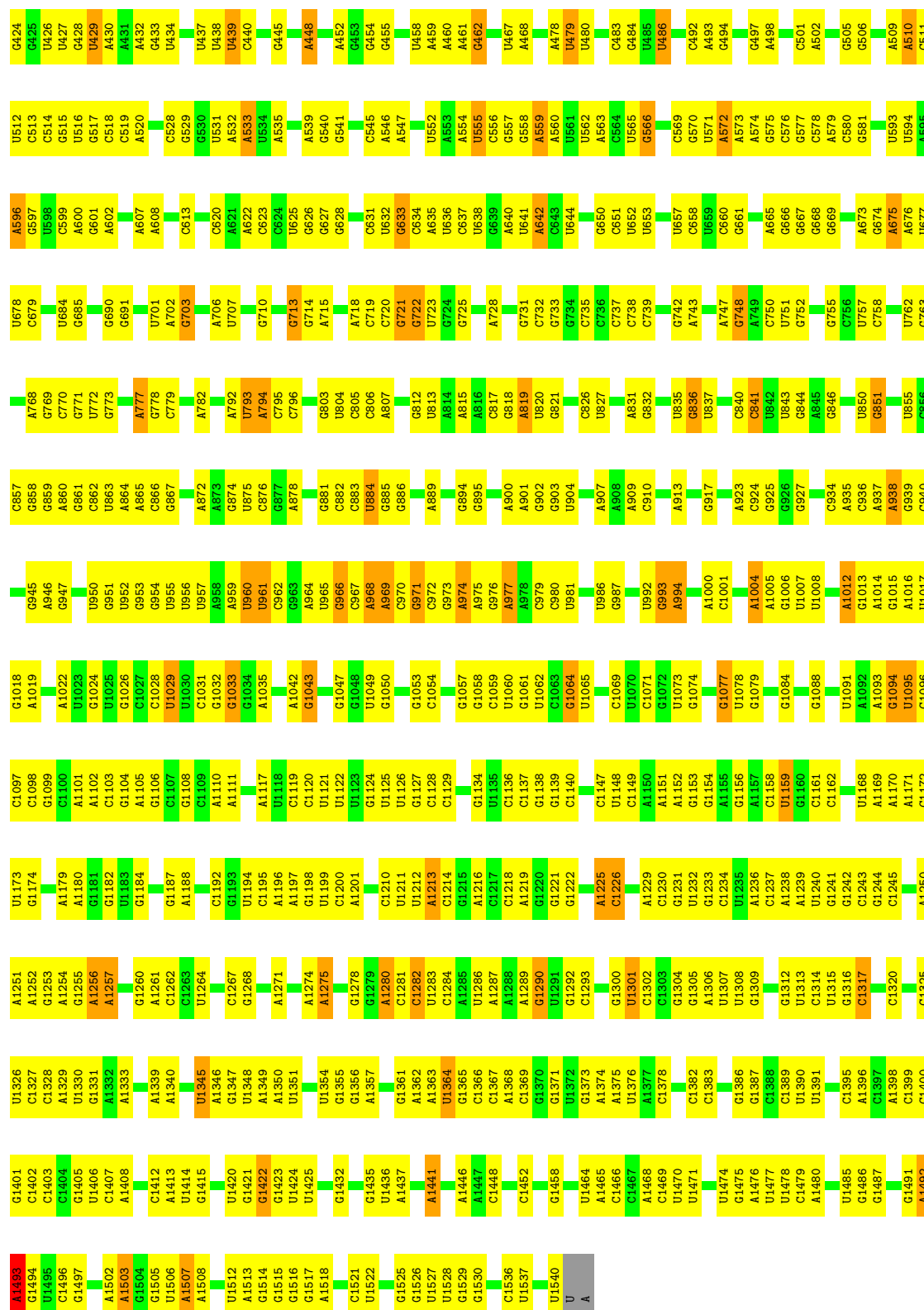
Chain 2: 50% 40% 10%



• Molecule 53: 16S rRNA

Chain 3: 46% 48% 6%





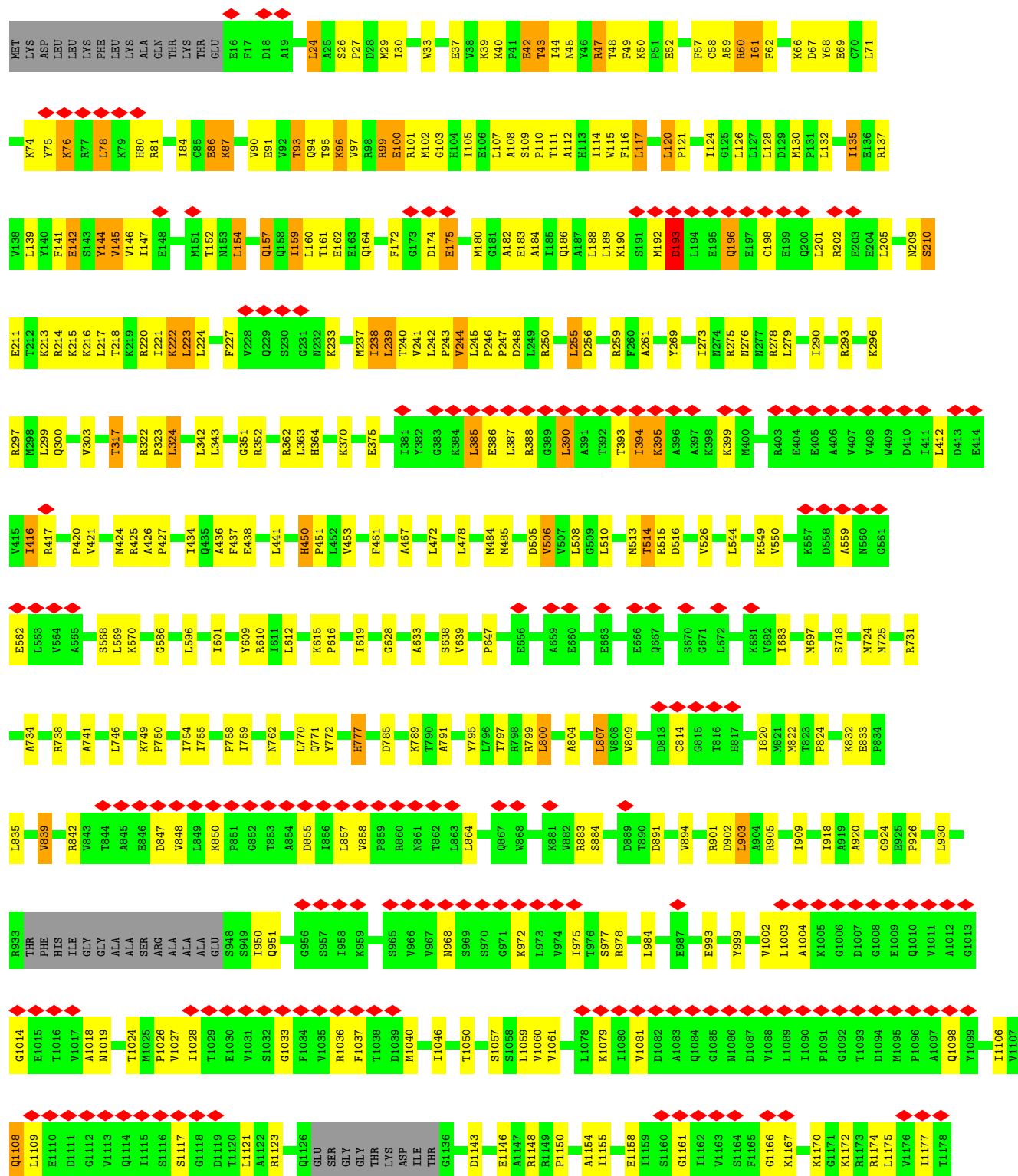
• Molecule 54: mRNA



SER
ILE
ALA
ASP
GLU

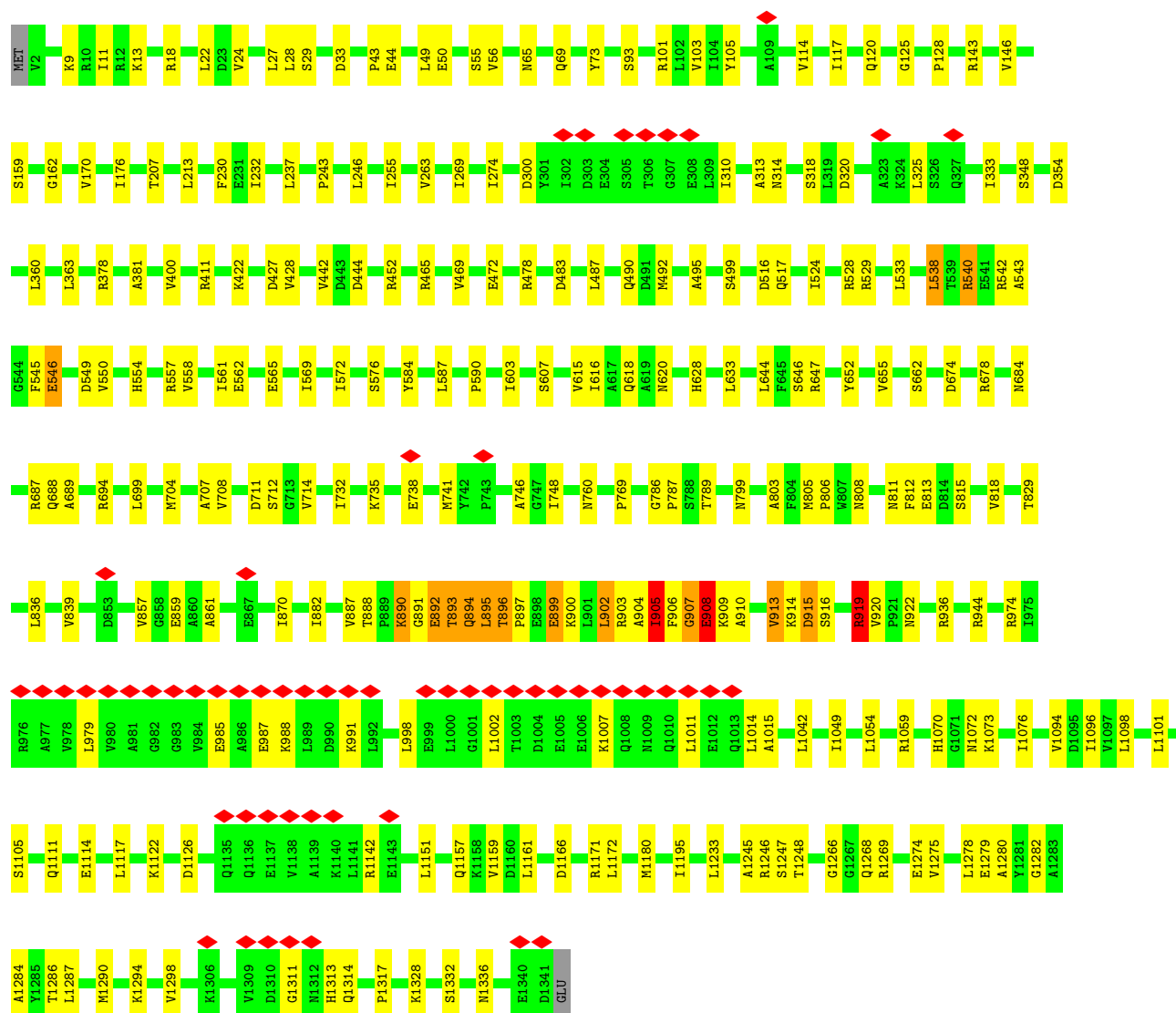
• Molecule 58: DNA-directed RNA polymerase subunit beta'

Chain B1: 16% 67% 24% 5%

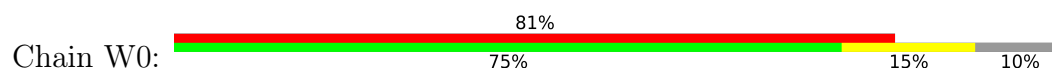


- Molecule 59: DNA-directed RNA polymerase subunit beta

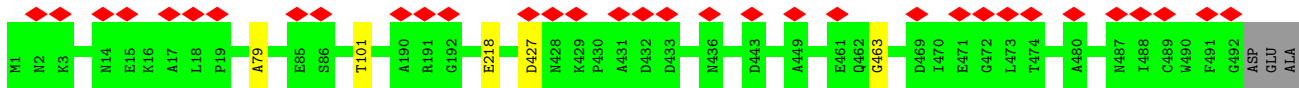
Chain B2:  81% 18%



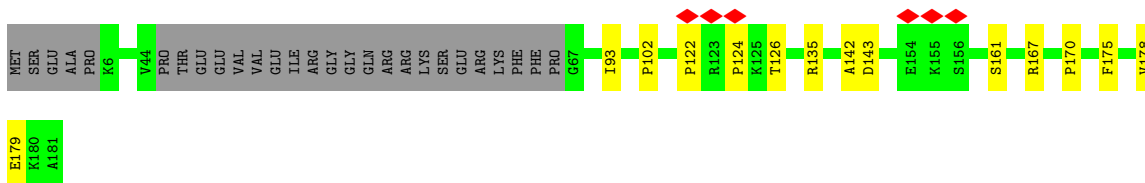
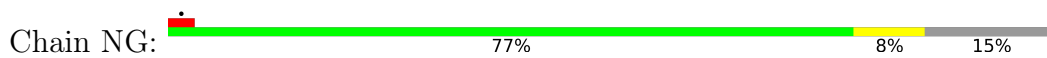
- Molecule 60: DNA-directed RNA polymerase subunit omega



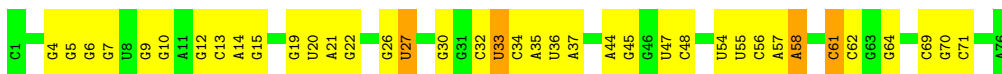
- Molecule 61: Transcription termination/antitermination protein NusA



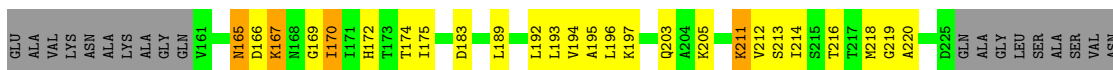
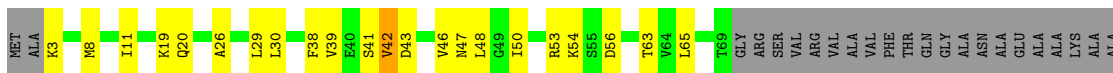
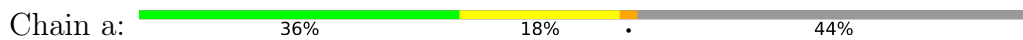
- Molecule 62: Transcription termination/antitermination protein NusG



- Molecule 63: tRNA(fMet)

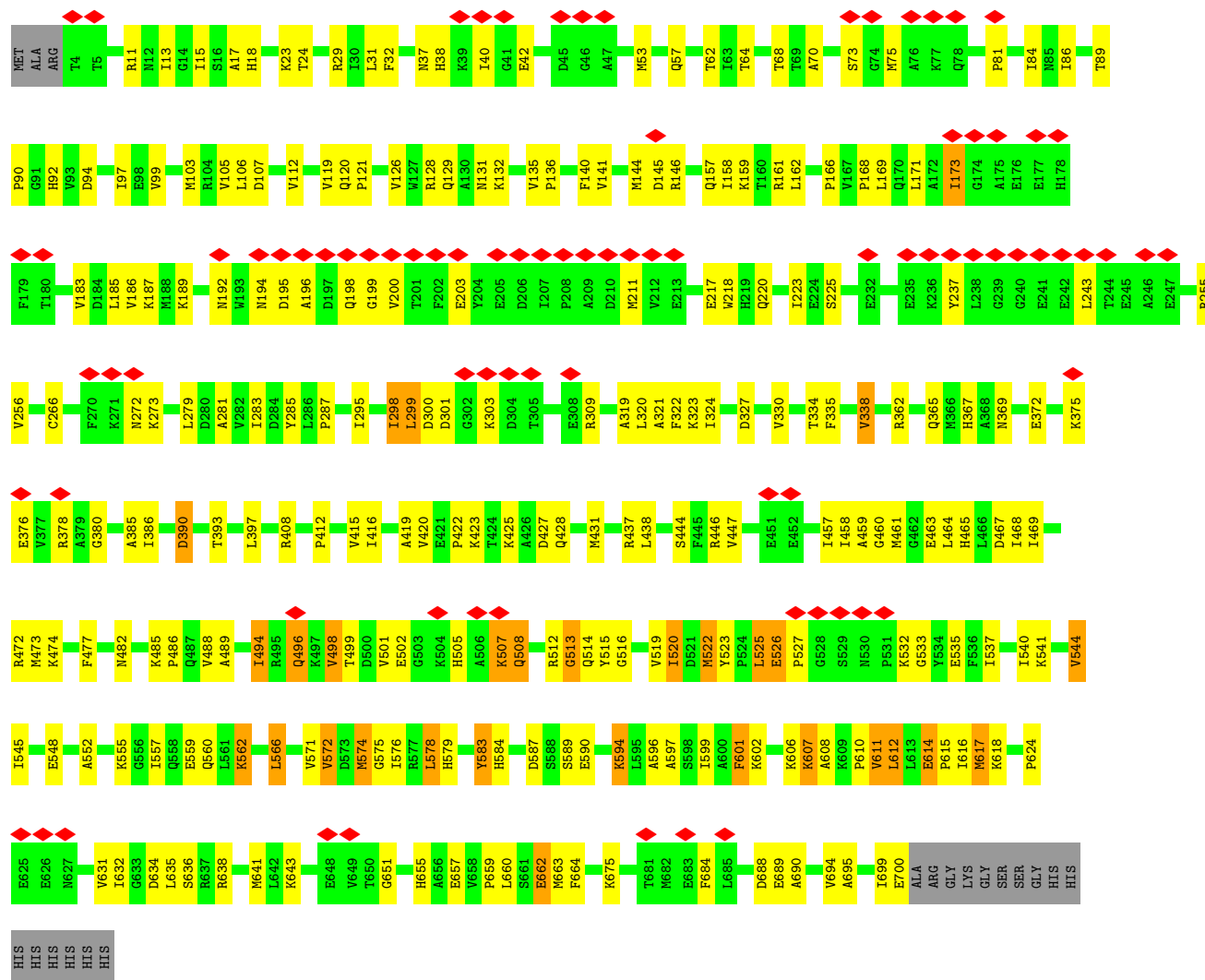


- Molecule 64: Large ribosomal subunit protein uL1



- Molecule 65: Elongation factor G





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	521880	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.087	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.005	Depositor
Map size ($\text{\AA}$)	753.60004, 753.60004, 753.60004	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.57, 1.57, 1.57	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.26	0/362	0.73	0/485
2	B	0.37	0/450	0.81	2/599 (0.3%)
3	C	0.32	0/416	0.61	0/554
4	D	0.48	0/380	0.95	0/498
5	E	0.47	0/513	0.80	0/676
6	F	0.40	0/303	0.79	0/397
7	G	0.39	0/1735	0.83	0/2338
8	H	0.42	0/1651	0.80	0/2225
9	I	0.28	0/1665	0.76	1/2227 (0.0%)
10	J	0.47	0/1169	0.81	0/1573
11	K	0.45	0/835	0.86	0/1128
12	L	0.41	0/1195	0.82	2/1602 (0.1%)
13	M	0.31	0/989	0.75	0/1326
14	N	0.29	0/1034	0.74	0/1375
15	O	0.56	0/796	0.80	0/1077
16	P	0.42	0/885	0.76	0/1195
17	Q	0.43	0/969	0.81	0/1300
18	R	0.29	0/892	0.68	0/1193
19	S	0.28	0/817	0.68	1/1088 (0.1%)
20	T	0.37	0/722	0.74	0/964
21	U	0.30	0/659	0.63	0/884
22	V	0.33	0/657	0.72	0/881
23	W	0.29	0/544	0.69	0/731
24	X	0.28	0/652	0.65	0/877
25	Y	0.26	0/671	0.64	2/888 (0.2%)
26	Z	0.56	0/550	1.09	1/728 (0.1%)
27	b	0.49	0/2121	0.82	0/2852
28	c	0.45	0/1586	0.77	0/2134
29	d	0.40	0/1571	0.80	3/2113 (0.1%)
30	e	0.30	0/1434	0.66	0/1926
31	f	0.29	0/1343	0.61	0/1816
32	g	0.34	0/1122	0.77	3/1515 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	0.40	0/1046	0.80	1/1410 (0.1%)
34	j	0.46	0/1152	0.72	0/1551
35	k	0.42	0/947	0.90	1/1268 (0.1%)
36	l	0.41	1/1054 (0.1%)	0.80	2/1403 (0.1%)
37	m	0.40	0/1093	0.81	2/1460 (0.1%)
38	n	0.54	1/973 (0.1%)	0.87	0/1301
39	o	0.32	0/902	0.68	0/1209
40	p	0.39	0/929	0.72	2/1242 (0.2%)
41	q	0.44	0/960	0.71	0/1278
42	r	0.38	0/829	0.79	1/1107 (0.1%)
43	s	0.52	0/864	0.83	0/1156
44	t	0.48	0/744	0.81	1/994 (0.1%)
45	u	0.34	0/787	0.74	2/1051 (0.2%)
46	v	0.41	1/766 (0.1%)	0.66	0/1025
47	w	0.41	0/582	0.80	2/769 (0.3%)
48	x	0.62	0/635	1.16	5/848 (0.6%)
49	y	0.28	0/510	0.71	0/677
50	z	0.36	0/453	0.76	1/605 (0.2%)
51	1	0.59	0/69796	0.60	17/108888 (0.0%)
52	2	0.60	0/2872	0.55	1/4479 (0.0%)
53	3	0.60	0/36963	0.57	6/57662 (0.0%)
54	4	0.60	0/695	0.75	0/1076
55	8	0.56	0/599	0.71	1/919 (0.1%)
56	9	0.49	0/468	0.53	0/719
57	A1	0.56	0/2106	0.81	0/2868
57	A2	0.49	0/2048	0.76	0/2786
58	B1	0.56	4/10510 (0.0%)	0.74	8/14196 (0.1%)
59	B2	0.46	0/10707	0.67	2/14451 (0.0%)
60	W0	0.30	0/652	0.61	0/879
61	NA	0.75	0/2431	1.22	1/3385 (0.0%)
62	NG	1.15	0/756	1.05	0/1048
63	6	0.60	0/1832	0.59	0/2855
64	a	0.49	0/1020	0.81	0/1370
65	0	0.55	0/5501	0.82	3/7446 (0.0%)
All	All	0.55	7/194870 (0.0%)	0.67	74/286546 (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
15	O	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
59	B2	0	1
All	All	0	2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	v	82	TYR	C-N	-6.43	1.24	1.33
38	n	66	ALA	CA-C	-6.05	1.44	1.52
58	B1	1350	ASN	CG-ND2	-5.26	1.22	1.33
58	B1	1108	GLN	CD-OE1	5.16	1.33	1.23
58	B1	424	ASN	CG-ND2	-5.08	1.22	1.33
58	B1	1268	ASN	CG-OD1	5.06	1.33	1.23
36	l	18	ARG	CA-CB	-5.01	1.44	1.52

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	92	PRO	N-CA-C	-10.53	98.41	113.47
51	1	1020	A	C2'-C3'-O3'	7.37	120.56	109.50
48	x	11	PRO	N-CA-C	-7.37	99.47	111.77
51	1	2425	A	O3'-P-O5'	-6.98	93.52	104.00
12	L	82	SER	N-CA-C	6.92	116.45	108.49
58	B1	450	HIS	CB-CG-CD2	-6.57	122.65	131.20
48	x	30	PRO	N-CA-C	6.56	125.99	112.47
59	B2	907	GLY	N-CA-C	-6.54	107.14	114.40
36	l	29	LYS	CA-C-N	6.50	133.96	121.54
36	l	29	LYS	C-N-CA	6.50	133.96	121.54
51	1	2428	G	O3'-P-O5'	-6.41	94.39	104.00
58	B1	777	HIS	CB-CG-CD2	-6.37	122.92	131.20
51	1	490	C	N1-C1'-C2'	6.35	121.52	112.00
32	g	8	LYS	CA-C-N	6.34	133.39	121.97
32	g	8	LYS	C-N-CA	6.34	133.39	121.97
58	B1	61	ILE	CA-C-N	-6.34	114.03	121.64
58	B1	61	ILE	C-N-CA	-6.34	114.03	121.64
9	I	24	VAL	N-CA-C	-6.33	107.70	113.71
45	u	45	GLN	CA-C-N	6.30	129.44	120.49
45	u	45	GLN	C-N-CA	6.30	129.44	120.49
48	x	71	ARG	N-CA-C	-6.25	105.65	113.28
53	3	1301	U	N1-C1'-C2'	6.21	121.32	112.00
48	x	67	LEU	N-CA-C	-6.10	104.55	111.14
65	0	367	HIS	CA-C-N	6.07	133.12	121.54
65	0	367	HIS	C-N-CA	6.07	133.12	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	S	21	ALA	N-CA-C	-6.06	107.72	114.62
51	1	1816	C	N1-C1'-C2'	5.84	120.75	112.00
32	g	121	VAL	N-CA-C	-5.81	106.74	111.91
48	x	54	GLY	N-CA-C	5.74	120.76	113.24
26	Z	17	ARG	N-CA-C	-5.70	104.88	113.89
2	B	5	ASN	CA-C-N	5.69	128.97	120.83
2	B	5	ASN	C-N-CA	5.69	128.97	120.83
58	B1	450	HIS	CB-CG-ND1	5.68	131.22	122.70
33	i	62	ALA	N-CA-C	5.62	117.10	110.97
51	1	1343	G	N9-C1'-C2'	5.61	120.41	112.00
53	3	1493	A	C4'-C3'-O3'	5.58	117.78	109.40
59	B2	908	GLU	N-CA-C	-5.56	105.11	112.34
37	m	57	VAL	CA-C-N	5.51	132.06	121.54
37	m	57	VAL	C-N-CA	5.51	132.06	121.54
53	3	130	A	N9-C1'-C2'	5.50	120.25	112.00
29	d	74	LYS	CA-C-N	5.49	128.68	120.83
29	d	74	LYS	C-N-CA	5.49	128.68	120.83
42	r	51	VAL	N-CA-C	-5.46	97.08	108.88
51	1	2502	G	O3'-P-O5'	5.44	112.16	104.00
51	1	1106	G	C2'-C3'-O3'	5.44	121.86	113.70
58	B1	777	HIS	CB-CG-ND1	5.40	130.80	122.70
53	3	813	U	N1-C1'-C2'	5.39	120.08	112.00
55	8	7	DC	C2'-C3'-O3'	-5.38	103.44	111.50
29	d	20	GLY	N-CA-C	-5.31	107.46	114.95
35	k	89	ASN	N-CA-C	5.27	117.45	111.02
25	Y	53	MET	CA-C-N	5.26	127.52	120.58
25	Y	53	MET	C-N-CA	5.26	127.52	120.58
51	1	2529	G	N9-C1'-C2'	5.25	119.88	112.00
58	B1	27	PRO	N-CA-C	-5.25	106.20	113.81
52	2	66	A	N9-C1'-C2'	5.23	119.85	112.00
51	1	858	G	C4'-C3'-O3'	5.19	120.79	113.00
51	1	1924	C	N1-C1'-C2'	5.17	119.76	112.00
50	z	40	THR	N-CA-C	-5.17	101.16	109.58
51	1	1211	C	N1-C1'-C2'	5.15	119.72	112.00
65	0	664	PHE	CA-CB-CG	5.14	118.94	113.80
47	w	15	LYS	CA-C-N	5.13	129.70	122.46
47	w	15	LYS	C-N-CA	5.13	129.70	122.46
58	B1	61	ILE	CA-C-O	-5.12	115.62	120.95
51	1	278	A	N9-C1'-C2'	5.12	119.68	112.00
53	3	1043	G	N9-C1'-C2'	5.12	119.67	112.00
61	NA	427	ASP	N-CA-C	-5.11	107.72	114.31
44	t	65	GLY	N-CA-C	5.10	117.33	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	1	1087	G	N9-C1'-C2'	5.08	119.61	112.00
53	3	722	G	N9-C1'-C2'	5.07	119.60	112.00
51	1	933	A	N9-C1'-C2'	5.06	119.59	112.00
51	1	1508	A	N9-C1'-C2'	5.04	119.55	112.00
51	1	2071	A	N9-C1'-C2'	5.02	119.53	112.00
40	p	15	ASP	CA-C-N	5.01	131.39	122.13
40	p	15	ASP	C-N-CA	5.01	131.39	122.13

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
59	B2	919	ARG	Sidechain
15	O	89	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	355	0	353	10	0
2	B	444	0	461	14	0
3	C	409	0	440	17	0
4	D	377	0	418	17	0
5	E	504	0	574	17	0
6	F	302	0	341	14	0
7	G	1704	0	1732	44	0
8	H	1624	0	1699	46	0
9	I	1643	0	1710	43	0
10	J	1156	0	1199	39	0
11	K	817	0	808	23	0
12	L	1181	0	1240	46	0
13	M	979	0	1034	32	0
14	N	1022	0	1070	56	0
15	O	786	0	828	37	0
16	P	869	0	878	28	0
17	Q	955	0	1019	31	0
18	R	883	0	944	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	S	805	0	847	36	0
20	T	714	0	737	16	0
21	U	649	0	666	21	0
22	V	648	0	691	18	0
23	W	535	0	552	15	0
24	X	637	0	665	17	0
25	Y	665	0	714	22	0
26	Z	544	0	579	16	0
27	b	2082	0	2157	66	0
28	c	1565	0	1616	58	0
29	d	1552	0	1619	50	0
30	e	1410	0	1447	43	0
31	f	1323	0	1374	32	0
32	g	1111	0	1148	32	0
33	i	1032	0	1088	34	0
34	j	1129	0	1162	32	0
35	k	938	0	1012	21	0
36	l	1045	0	1117	30	0
37	m	1074	0	1157	30	0
38	n	960	0	1000	34	0
39	o	892	0	923	22	0
40	p	917	0	965	23	0
41	q	947	0	1022	22	0
42	r	816	0	839	22	0
43	s	857	0	922	19	0
44	t	738	0	807	15	0
45	u	779	0	834	22	0
46	v	753	0	780	14	0
47	w	575	0	592	19	0
48	x	625	0	655	22	0
49	y	509	0	543	9	0
50	z	449	0	491	10	0
51	1	62317	0	31346	1368	0
52	2	2568	0	1303	58	0
53	3	33012	0	16618	720	0
54	4	627	0	313	6	0
55	8	539	0	305	28	0
56	9	417	0	224	1	0
57	A1	2088	0	1895	25	0
57	A2	2029	0	1864	17	0
58	B1	10353	0	10548	332	0
59	B2	10539	0	10537	173	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	W0	650	0	658	11	0
61	NA	2432	0	1171	5	0
62	NG	758	0	334	10	0
63	6	1640	0	837	27	0
64	a	1013	0	1081	41	0
65	0	5399	0	5363	143	0
66	B1	1	0	0	0	0
67	0	32	0	13	0	0
All	All	181699	0	131879	3756	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 12.

All (3756) 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)
12:L:92:PRO:HA	12:L:95:ARG:HE	1.11	1.14
53:3:112:G:H21	53:3:354:G:H5'	1.16	1.11
51:1:2061:G:H2'	51:1:2501:C:O2'	1.52	1.09
51:1:1060:U:H4'	51:1:1061:U:H5'	1.32	1.09
50:z:37:ARG:HH12	51:1:929:U:H5'	1.12	1.08
9:I:131:ILE:HG21	53:3:620:C:H1'	1.40	1.04
51:1:45:G:H5''	51:1:46:G:H5'	1.35	1.03
51:1:1104:C:H2'	51:1:1105:U:H4'	1.38	1.02
51:1:1607:C:H4'	51:1:1608:A:H5'	1.40	1.02
51:1:1796:U:H2'	51:1:1797:G:H8	1.19	1.01
58:B1:111:THR:HG23	58:B1:300:GLN:CD	1.86	1.01
51:1:2324:U:H3'	51:1:2325:G:H5''	1.45	0.99
51:1:572:A:H61	51:1:2029:G:H21	1.04	0.98
51:1:1645:G:H5''	51:1:1646:C:H5'	1.45	0.98
58:B1:750:PRO:HB3	59:B2:549:ASP:OD2	1.60	0.98
58:B1:352:ARG:HD2	59:B2:1268:GLN:NE2	1.79	0.97
51:1:1597:A:H5''	51:1:1598:A:H5'	1.45	0.96
10:J:120:HIS:ND1	10:J:121:ASN:ND2	2.14	0.96
51:1:2672:U:H2'	51:1:2673:G:H5''	1.43	0.96
51:1:413:C:H42	51:1:2410:G:H1	1.15	0.95
52:2:90:C:H2'	52:2:91:C:H5''	1.44	0.95
7:G:16:GLY:HA2	7:G:39:ILE:HA	1.49	0.95
58:B1:68:TYR:O	58:B1:75:TYR:CE2	2.20	0.95
52:2:118:C:H2'	52:2:119:A:H4'	1.46	0.94
38:n:39:PRO:HG3	51:1:1651:G:H5'	1.49	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:s:59:GLU:HA	43:s:64:ALA:HA	1.50	0.94
53:3:1156:G:H1'	53:3:1179:A:H61	1.31	0.94
42:r:79:ARG:HH22	51:1:572:A:H5'	1.33	0.93
51:1:828:U:H2'	51:1:829:A:C8	2.02	0.93
23:W:38:ILE:HD11	53:3:720:C:H1'	1.52	0.92
51:1:2068:U:H3	51:1:2430:A:H62	1.15	0.92
53:3:674:G:H2'	53:3:675:A:C8	2.05	0.91
58:B1:202:ARG:HG2	58:B1:202:ARG:HH11	1.35	0.91
53:3:674:G:H2'	53:3:675:A:H8	1.34	0.90
51:1:1558:C:H4'	51:1:1559:U:H5''	1.51	0.90
53:3:91:U:H2'	53:3:92:U:H5''	1.53	0.90
53:3:1218:C:H2'	53:3:1219:A:C8	2.06	0.90
58:B1:68:TYR:C	58:B1:75:TYR:HE2	1.80	0.90
51:1:2653:U:H3'	51:1:2654:A:H5''	1.52	0.89
53:3:409:U:H3	53:3:433:G:H1	1.12	0.89
12:L:92:PRO:HA	12:L:95:ARG:NE	1.88	0.89
29:d:68:ALA:HA	51:1:1255:U:C5	2.08	0.88
54:4:44:G:H21	58:B1:427:PRO:HD3	1.34	0.88
53:3:1422:G:H22	53:3:1478:U:H3	1.22	0.88
52:2:78:A:H62	52:2:98:G:H21	1.17	0.88
50:z:37:ARG:NH1	51:1:929:U:H5'	1.89	0.88
51:1:1796:U:H2'	51:1:1797:G:C8	2.08	0.88
51:1:1473:G:H1	51:1:1518:C:H42	1.21	0.88
58:B1:317:THR:HA	58:B1:323:PRO:HA	1.55	0.88
12:L:91:ARG:HB3	12:L:93:VAL:HG12	1.54	0.87
51:1:435:C:H2'	51:1:436:C:H5'	1.56	0.87
65:0:508:GLN:HA	65:0:513:GLY:HA2	1.57	0.87
52:2:3:C:H2'	52:2:4:C:H5''	1.55	0.87
53:3:1395:C:HO2'	53:3:1396:A:H8	0.89	0.87
7:G:131:LYS:HD2	53:3:1158:C:H4'	1.57	0.86
14:N:68:GLY:HA2	53:3:1250:A:H5'	1.55	0.86
51:1:2128:G:OP1	64:a:38:PHE:CE1	2.29	0.85
42:r:79:ARG:NH2	51:1:572:A:H5'	1.91	0.85
53:3:1218:C:H2'	53:3:1219:A:H8	1.41	0.85
51:1:2822:G:H2'	51:1:2823:A:H5''	1.58	0.85
51:1:2443:C:H2'	51:1:2444:G:H8	1.42	0.85
58:B1:633:ALA:HB2	59:B2:808:ASN:H	1.41	0.85
58:B1:68:TYR:HB3	58:B1:75:TYR:OH	1.76	0.85
51:1:1783:A:C6	51:1:2587:A:C2	2.66	0.84
19:S:70:HIS:HB2	53:3:974:A:H5'	1.59	0.84
37:m:12:MET:HA	51:1:910:A:H62	1.41	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1783:A:N1	51:1:2587:A:C4	2.46	0.84
53:3:835:U:H2'	53:3:836:G:H5''	1.60	0.84
12:L:27:ASN:HD22	53:3:1374:A:H4'	1.42	0.84
53:3:3:A:H5'	53:3:613:C:H4'	1.58	0.83
51:1:2262:U:H2'	51:1:2263:C:C6	2.13	0.83
53:3:1424:U:H3	53:3:1476:A:H61	1.26	0.83
34:j:116:ARG:NH2	51:1:528:A:H5''	1.92	0.83
65:0:40:ILE:HG23	65:0:198:GLN:OE1	1.79	0.83
51:1:554:U:H2'	51:1:555:G:O4'	1.79	0.82
23:W:37:LYS:HB3	53:3:719:C:H1'	1.60	0.82
53:3:1512:U:H2'	53:3:1513:A:C8	2.14	0.82
58:B1:68:TYR:O	58:B1:75:TYR:HE2	1.58	0.82
51:1:1937:A:O2'	51:1:1938:A:H5'	1.78	0.82
51:1:2050:C:H2'	51:1:2051:A:H5'	1.62	0.82
53:3:572:A:H5''	53:3:917:G:H4'	1.59	0.82
58:B1:141:PHE:CE2	58:B1:296:LYS:HB2	2.15	0.81
14:N:13:SER:OG	53:3:1251:A:H5'	1.80	0.81
51:1:1433:A:H2'	51:1:1434:A:O4'	1.79	0.81
51:1:1680:U:H2'	51:1:1681:G:H5'	1.60	0.81
51:1:695:G:H1	51:1:767:U:H3	1.26	0.81
58:B1:770:LEU:HD13	59:B2:618:GLN:HG3	1.61	0.81
55:8:1:DC:H5''	58:B1:210:SER:OG	1.80	0.81
27:b:55:GLY:HA2	51:1:692:C:OP1	1.81	0.81
53:3:555:U:H2'	53:3:556:C:C6	2.15	0.81
26:Z:7:GLU:HB2	26:Z:11:PHE:HB3	1.63	0.80
51:1:1064:C:H3'	51:1:1065:U:H5''	1.62	0.80
58:B1:144:TYR:HE1	58:B1:162:GLU:OE2	1.64	0.80
51:1:2128:G:OP1	64:a:38:PHE:CD1	2.35	0.80
58:B1:141:PHE:HE2	58:B1:296:LYS:HB2	1.44	0.79
51:1:2402:U:C2'	51:1:2403:C:H5''	2.11	0.79
58:B1:111:THR:HG23	58:B1:300:GLN:OE1	1.81	0.79
29:d:76:PRO:HA	29:d:82:GLY:HA3	1.62	0.79
53:3:952:U:H4'	53:3:964:A:H61	1.47	0.79
51:1:1791:A:C2'	51:1:1792:G:H5'	2.13	0.79
58:B1:37:GLU:O	58:B1:61:ILE:HD11	1.81	0.79
53:3:769:G:H4'	53:3:1513:A:H4'	1.63	0.79
51:1:2402:U:H2'	51:1:2403:C:H5''	1.64	0.78
53:3:1073:U:H3	53:3:1102:A:H61	1.29	0.78
58:B1:186:GLN:HG3	58:B1:238:ILE:HG13	1.65	0.78
51:1:2036:C:H2'	51:1:2037:A:C8	2.18	0.78
51:1:784:G:H5'	51:1:785:G:OP1	1.84	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1783:A:C6	51:1:2587:A:N3	2.51	0.78
51:1:1052:C:H42	51:1:1107:G:H1	1.30	0.78
51:1:1661:G:H2'	51:1:1662:U:H6	1.49	0.78
52:2:65:U:H3'	52:2:108:A:H61	1.49	0.78
51:1:208:C:H2'	51:1:209:C:H6	1.49	0.77
8:H:175:HIS:ND1	53:3:1108:G:H5'	2.00	0.77
51:1:2524:G:H2'	51:1:2525:G:H5''	1.66	0.77
53:3:1422:G:N2	53:3:1478:U:H3	1.80	0.77
51:1:2124:G:O2'	64:a:41:SER:HB3	1.83	0.77
51:1:2259:U:C4	51:1:2427:C:N4	2.52	0.77
53:3:153:C:H3'	53:3:154:U:H5''	1.67	0.77
51:1:52:A:H2'	51:1:53:A:C8	2.20	0.77
51:1:1853:A:H2'	51:1:1854:A:C8	2.19	0.77
51:1:20:C:H2'	51:1:21:A:C8	2.20	0.76
28:c:148:GLN:O	51:1:2052:A:H4'	1.86	0.76
22:V:68:LYS:HB3	53:3:267:C:OP1	1.85	0.76
51:1:1287:A:C2	51:1:1649:G:H4'	2.20	0.76
51:1:2443:C:H2'	51:1:2444:G:C8	2.20	0.76
55:8:13:DT:H72	58:B1:791:ALA:HB2	1.66	0.76
51:1:1126:A:H4'	51:1:1127:A:H5''	1.67	0.76
51:1:2672:U:C2'	51:1:2673:G:H5''	2.16	0.76
51:1:324:A:H62	51:1:338:G:H21	1.32	0.76
51:1:687:C:H2'	51:1:688:U:H5'	1.66	0.76
51:1:1935:G:H1'	51:1:1964:G:N2	2.00	0.76
51:1:1020:A:H1'	51:1:1021:A:OP2	1.86	0.75
53:3:1356:G:H2'	53:3:1357:A:H8	1.51	0.75
53:3:57:G:H2'	53:3:58:C:C6	2.21	0.75
58:B1:395:LYS:HZ2	58:B1:399:LYS:CD	1.99	0.75
65:0:40:ILE:CG2	65:0:198:GLN:OE1	2.33	0.75
51:1:2124:G:O2'	64:a:41:SER:CB	2.34	0.75
53:3:768:A:OP1	53:3:804:U:H4'	1.86	0.75
53:3:193:C:H2'	53:3:194:C:C6	2.21	0.75
58:B1:202:ARG:HG2	58:B1:202:ARG:NH1	1.99	0.75
53:3:850:U:H2'	53:3:851:G:H5''	1.69	0.75
33:i:10:LEU:HD11	51:1:1070:A:H2	1.51	0.75
51:1:1718:G:H2'	51:1:1719:G:H8	1.52	0.75
51:1:1783:A:C2	51:1:2587:A:C5	2.75	0.75
53:3:3:A:C5'	53:3:613:C:H4'	2.17	0.75
53:3:1330:U:H2'	53:3:1331:G:O4'	1.86	0.75
8:H:127:VAL:HG23	54:4:14:U:H4'	1.67	0.74
51:1:2375:G:H2'	51:1:2376:A:H5''	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:633:A:H2'	51:1:634:C:O4'	1.88	0.74
53:3:212:G:H2'	53:3:213:G:H8	1.53	0.74
30:e:34:THR:HG21	51:1:2314:A:H5'	1.69	0.74
53:3:354:G:H2'	53:3:355:C:C6	2.23	0.74
53:3:1412:C:H2'	53:3:1413:A:C8	2.22	0.74
55:8:15:DC:H1'	58:B1:426:ALA:HB1	1.67	0.74
51:1:208:C:H2'	51:1:209:C:C6	2.23	0.74
51:1:581:C:H2'	51:1:582:A:C8	2.23	0.74
51:1:917:A:H5''	51:1:2268:A:H61	1.53	0.74
53:3:1236:A:H4'	53:3:1304:G:H4'	1.69	0.74
51:1:2221:G:H2'	51:1:2222:C:C6	2.23	0.74
51:1:1019:U:H3	51:1:1142:A:H62	1.36	0.74
55:8:3:DC:H2'	55:8:4:DT:H72	1.69	0.74
12:L:71:THR:HG23	12:L:72:VAL:HG12	1.68	0.74
10:J:25:LYS:NZ	53:3:923:A:H5''	2.03	0.74
51:1:2743:U:H2'	51:1:2744:G:O4'	1.87	0.74
51:1:1161:C:H2'	51:1:1162:G:C8	2.23	0.73
53:3:153:C:C3'	53:3:154:U:H5''	2.19	0.73
53:3:884:U:H4'	53:3:885:G:H5''	1.70	0.73
51:1:1528:A:H2'	51:1:1529:G:H5'	1.69	0.73
58:B1:1143:ASP:OD1	58:B1:1148:ARG:NH1	2.21	0.73
47:w:28:LEU:HD22	51:1:2353:G:H4'	1.68	0.73
51:1:2859:G:H2'	51:1:2860:A:C8	2.22	0.73
53:3:279:A:H5''	53:3:281:G:H5'	1.69	0.73
51:1:1265:A:H61	51:1:2013:A:H5''	1.53	0.73
51:1:1310:G:H2'	51:1:1311:G:H5'	1.71	0.73
58:B1:210:SER:HB3	58:B1:213:LYS:HB2	1.71	0.73
15:O:45:ARG:HB3	15:O:69:THR:HB	1.71	0.73
55:8:3:DC:C2'	55:8:4:DT:H72	2.19	0.73
51:1:2030:A:N3	51:1:2499:C:H5''	2.04	0.73
53:3:175:C:H2'	53:3:176:C:C6	2.24	0.73
51:1:1940:U:H1'	51:1:1942:C:N4	2.04	0.73
58:B1:68:TYR:C	58:B1:75:TYR:CE2	2.65	0.73
30:e:65:LEU:HD22	52:2:42:C:C4	2.24	0.72
53:3:1306:A:H61	53:3:1331:G:H1'	1.54	0.72
58:B1:110:PRO:HG2	58:B1:183:GLU:HG3	1.68	0.72
9:I:23:GLY:HA3	53:3:408:A:H4'	1.71	0.72
52:2:87:U:H5''	52:2:88:C:C5	2.23	0.72
53:3:1073:U:H2'	53:3:1074:G:C8	2.24	0.72
53:3:1028:C:H3'	53:3:1029:U:H5''	1.71	0.72
53:3:840:C:H2'	53:3:841:C:H5''	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1868:C:H2'	51:1:1869:G:H5'	1.70	0.72
51:1:2061:G:H2'	51:1:2501:C:HO2'	1.53	0.72
58:B1:105:ILE:HD12	58:B1:242:LEU:HD22	1.71	0.72
46:v:9:ARG:HB3	46:v:41:GLU:HB2	1.71	0.72
53:3:1507:A:H2'	53:3:1508:A:O4'	1.89	0.72
21:U:5:ARG:HB2	53:3:376:G:H5''	1.72	0.72
51:1:96:C:H2'	51:1:97:C:H6	1.54	0.72
51:1:777:G:N7	51:1:793:A:H2	1.87	0.72
53:3:1424:U:H2'	53:3:1425:U:C6	2.24	0.72
58:B1:157:GLN:OE1	58:B1:157:GLN:HA	1.89	0.72
12:L:27:ASN:ND2	53:3:1374:A:H4'	2.05	0.72
51:1:952:G:H2'	51:1:953:G:H5''	1.71	0.72
51:1:2125:G:H5'	64:a:39:VAL:O	1.89	0.72
58:B1:142:GLU:HG3	58:B1:142:GLU:O	1.89	0.72
48:x:2:ARG:HG2	48:x:32:LEU:HD12	1.72	0.71
51:1:2733:A:H2'	51:1:2734:A:C8	2.25	0.71
36:l:79:LEU:HD12	36:l:113:ALA:H	1.52	0.71
51:1:2629:U:O2'	51:1:2630:G:H5''	1.90	0.71
51:1:2818:U:H2'	51:1:2819:G:H8	1.55	0.71
53:3:419:C:H2'	53:3:420:U:O4'	1.90	0.71
53:3:1395:C:O2'	53:3:1396:A:H8	1.71	0.71
53:3:1435:G:H2'	53:3:1436:U:C6	2.25	0.71
51:1:435:C:C2'	51:1:436:C:H5'	2.21	0.71
51:1:1064:C:H3'	51:1:1065:U:C5'	2.20	0.71
51:1:1170:C:H2'	51:1:1171:G:H8	1.54	0.71
51:1:2036:C:H2'	51:1:2037:A:H8	1.55	0.71
51:1:2562:U:H3	51:1:2566:A:H62	1.35	0.71
58:B1:211:GLU:HG2	58:B1:215:LYS:HE3	1.70	0.71
51:1:2086:U:H2'	51:1:2087:G:C8	2.25	0.71
6:F:4:ARG:HB2	51:1:2466:C:OP1	1.89	0.71
12:L:92:PRO:HA	12:L:95:ARG:HG3	1.71	0.71
53:3:1243:C:H2'	53:3:1244:G:C8	2.26	0.71
58:B1:107:LEU:HD11	58:B1:242:LEU:HB2	1.71	0.71
51:1:2491:U:H2'	51:1:2492:U:H5'	1.71	0.71
53:3:1374:A:H2'	53:3:1375:A:H8	1.56	0.71
58:B1:220:ARG:HG2	58:B1:220:ARG:HH11	1.55	0.71
51:1:52:A:H2'	51:1:53:A:H8	1.56	0.71
51:1:1791:A:H2'	51:1:1792:G:H5'	1.70	0.71
52:2:90:C:C2'	52:2:91:C:H5''	2.20	0.71
53:3:1395:C:H4'	53:3:1402:C:H4'	1.73	0.71
12:L:92:PRO:CA	12:L:95:ARG:HE	1.97	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1161:C:H2'	51:1:1162:G:H8	1.55	0.71
53:3:946:A:H2'	53:3:947:G:H8	1.56	0.71
34:j:116:ARG:HH22	51:1:528:A:H5''	1.53	0.70
53:3:939:G:H2'	53:3:940:C:C6	2.26	0.70
53:3:979:C:H2'	53:3:980:C:H5'	1.73	0.70
38:n:1:MET:HE3	51:1:2723:C:H4'	1.74	0.70
48:x:60:LYS:HD3	51:1:372:G:H5''	1.73	0.70
51:1:100:U:H4'	51:1:101:A:O4'	1.91	0.70
59:B2:65:ASN:HB3	59:B2:105:TYR:HB2	1.73	0.70
51:1:1447:C:H2'	51:1:1448:G:H8	1.56	0.70
53:3:86:G:H4'	53:3:87:C:C4	2.26	0.70
53:3:501:C:H2'	53:3:502:A:H8	1.57	0.70
53:3:1412:C:H2'	53:3:1413:A:H8	1.56	0.70
58:B1:93:THR:HB	58:B1:97:VAL:HG21	1.73	0.70
12:L:91:ARG:O	12:L:95:ARG:HG2	1.92	0.70
51:1:2514:U:H2'	51:1:2515:C:C6	2.27	0.70
36:l:17:LYS:HB2	51:1:663:G:H5''	1.74	0.70
51:1:2859:G:H2'	51:1:2860:A:H8	1.54	0.70
63:6:69:C:H2'	63:6:70:G:H8	1.55	0.70
51:1:1739:A:H2'	51:1:1740:G:O4'	1.92	0.70
51:1:2030:A:C2	51:1:2499:C:H5''	2.27	0.70
53:3:673:A:H2'	53:3:674:G:C8	2.26	0.70
51:1:677:A:H2'	51:1:678:C:H6	1.57	0.69
51:1:1270:C:H5''	51:1:1271:G:C5'	2.21	0.69
63:6:26:G:H2'	63:6:27:U:H5''	1.73	0.69
38:n:66:ALA:HA	38:n:69:ARG:HD2	1.72	0.69
51:1:2446:G:H2'	51:1:2501:C:H5	1.57	0.69
53:3:960:U:H4'	53:3:961:U:H5''	1.74	0.69
29:d:165:HIS:HB2	51:1:1205:A:C6	2.27	0.69
51:1:2818:U:H2'	51:1:2819:G:C8	2.27	0.69
58:B1:128:LEU:HD11	58:B1:189:LEU:HG	1.73	0.69
24:X:77:ARG:NH1	53:3:1225:A:H4'	2.07	0.69
51:1:958:U:H2'	52:2:89:U:H1'	1.75	0.69
58:B1:39:LYS:O	58:B1:273:ILE:CG2	2.41	0.69
65:0:29:ARG:HH21	65:0:272:ASN:HD21	1.40	0.69
65:0:610:PRO:HD2	65:0:695:ALA:HB2	1.74	0.69
27:b:6:LYS:NZ	51:1:1695:G:H5'	2.08	0.69
51:1:1077:A:H2'	51:1:1078:U:H5'	1.74	0.69
51:1:2502:G:H5''	51:1:2503:A:H5''	1.74	0.69
53:3:520:A:H62	53:3:529:G:H21	1.38	0.69
57:A1:297:LYS:CB	61:NA:79:ALA:HB1	2.22	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:243:PRO:HG2	59:B2:1332:SER:O	1.93	0.69
63:6:56:C:H2'	63:6:57:A:H8	1.58	0.69
12:L:92:PRO:O	12:L:95:ARG:HG3	1.93	0.69
51:1:1607:C:H4'	51:1:1608:A:C5'	2.19	0.69
51:1:1935:G:H1'	51:1:1964:G:C2	2.28	0.69
51:1:2628:C:H3'	51:1:2629:U:H5'	1.75	0.69
8:H:34:SER:HB3	8:H:58:ARG:HH12	1.57	0.69
14:N:17:ARG:CZ	53:3:1129:C:H4'	2.22	0.69
17:Q:23:LEU:HD12	17:Q:29:LYS:HG2	1.75	0.69
31:f:91:VAL:HG21	51:1:2657:A:O3'	1.93	0.69
53:3:1421:G:H2'	53:3:1422:G:H4'	1.74	0.69
58:B1:832:LYS:C	58:B1:1242:ARG:HH12	2.01	0.69
51:1:740:C:H6	51:1:740:C:H5'	1.58	0.68
51:1:2450:A:O2'	51:1:2451:A:H5'	1.93	0.68
53:3:70:U:H5''	53:3:71:A:OP1	1.92	0.68
14:N:121:ARG:HG3	53:3:1348:U:H4'	1.75	0.68
18:R:113:LYS:HZ3	63:6:44:A:H4'	1.57	0.68
53:3:900:A:H2'	53:3:901:A:C8	2.29	0.68
59:B2:906:PHE:HB3	61:NA:101:THR:HA	1.74	0.68
26:Z:48:LYS:HB3	53:3:723:U:H5	1.58	0.68
51:1:1481:U:H3	51:1:1510:G:H1	1.42	0.68
51:1:1697:G:H3'	51:1:1698:A:H5''	1.76	0.68
51:1:1979:U:H2'	51:1:1980:G:H5'	1.74	0.68
51:1:2553:G:H3'	51:1:2554:U:H5''	1.76	0.68
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE22	1.56	0.68
14:N:10:ARG:HH22	53:3:1148:U:H5''	1.59	0.68
53:3:478:A:H2'	53:3:479:U:H4'	1.76	0.68
58:B1:117:LEU:HD12	58:B1:117:LEU:O	1.94	0.68
58:B1:141:PHE:CD2	58:B1:293:ARG:O	2.47	0.68
62:NG:126:THR:HA	62:NG:179:GLU:HA	1.74	0.68
12:L:35:LYS:HB2	53:3:1373:G:H4'	1.76	0.68
51:1:781:A:H2'	51:1:1777:U:O2'	1.93	0.68
51:1:1024:G:H3'	51:1:1025:G:H5''	1.75	0.68
51:1:2656:U:H5''	65:0:146:ARG:CZ	2.24	0.68
53:3:1346:A:H61	53:3:1374:A:H3'	1.57	0.68
28:c:181:ASP:HB2	28:c:186:LEU:H	1.59	0.68
51:1:1219:U:H2'	51:1:1220:G:C8	2.29	0.68
51:1:2464:G:H2'	51:1:2465:C:C6	2.29	0.68
17:Q:13:ARG:HH21	53:3:303:A:H5'	1.59	0.67
53:3:501:C:H2'	53:3:502:A:C8	2.29	0.67
51:1:869:G:H2'	51:1:870:U:O4'	1.93	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1697:G:H5''	51:1:1698:A:H5''	1.76	0.67
51:1:1801:A:H5''	51:1:2203:U:H2'	1.75	0.67
55:8:3:DC:C6	55:8:4:DT:H72	2.29	0.67
58:B1:984:LEU:HB3	58:B1:993:GLU:HB2	1.77	0.67
51:1:687:C:C2'	51:1:688:U:H5'	2.23	0.67
58:B1:395:LYS:HZ2	58:B1:399:LYS:HD3	1.58	0.67
27:b:73:ILE:HG12	51:1:1490:A:C2	2.29	0.67
36:l:111:ILE:HD12	51:1:627:A:N7	2.09	0.67
51:1:84:A:H4'	51:1:85:G:O5'	1.94	0.67
29:d:27:LEU:HD22	29:d:104:ALA:HB2	1.75	0.67
58:B1:1355:ARG:NH1	58:B1:1369:ARG:HH12	1.93	0.67
15:O:89:ARG:HG2	58:B1:86:GLU:HB3	1.76	0.67
51:1:1783:A:C2	51:1:2587:A:C4	2.83	0.67
65:O:103:MET:HG3	65:O:129:GLN:HB3	1.77	0.67
18:R:102:LYS:HG2	53:3:1226:C:C5	2.29	0.67
51:1:1799:G:H4'	51:1:1800:C:O5'	1.95	0.67
53:3:1007:U:H3	53:3:1022:A:H61	1.43	0.67
63:6:69:C:H2'	63:6:70:G:C8	2.29	0.67
51:1:1139:G:O2'	51:1:1140:C:H5'	1.95	0.67
58:B1:108:ALA:CB	58:B1:279:LEU:HD22	2.25	0.67
51:1:2633:G:H2'	51:1:2634:A:H5''	1.77	0.66
58:B1:161:THR:HG22	58:B1:164:GLN:HB2	1.75	0.66
38:n:71:ARG:HH21	51:1:2708:G:H1'	1.59	0.66
51:1:621:A:H2'	51:1:622:G:O4'	1.95	0.66
53:3:747:A:H3'	53:3:748:G:H5''	1.75	0.66
58:B1:108:ALA:HB3	58:B1:279:LEU:HD22	1.77	0.66
39:o:68:LYS:HG2	52:2:50:A:OP1	1.94	0.66
58:B1:111:THR:CG2	58:B1:300:GLN:CD	2.66	0.66
38:n:96:ARG:HA	51:1:2881:U:O2'	1.95	0.66
51:1:395:U:H2'	51:1:396:G:C8	2.31	0.66
51:1:848:C:H2'	51:1:849:A:H8	1.59	0.66
51:1:849:A:H2'	51:1:850:U:C6	2.30	0.66
51:1:1755:A:H2'	51:1:1756:G:H5'	1.76	0.66
51:1:1824:G:O2'	51:1:1825:U:H5'	1.96	0.66
51:1:2177:C:O2	64:a:172:HIS:HE1	1.78	0.66
53:3:924:C:H2'	53:3:925:G:H8	1.61	0.66
53:3:1026:G:H1	53:3:1035:A:H61	1.43	0.66
53:3:1356:G:H2'	53:3:1357:A:C8	2.30	0.66
63:6:12:G:H2'	63:6:13:C:O4'	1.95	0.66
10:J:25:LYS:HE2	53:3:923:A:OP1	1.96	0.66
38:n:2:ARG:HD2	51:1:2822:G:O6	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:x:27:ARG:NH2	51:1:1365:A:OP1	2.29	0.66
51:1:1661:G:H2'	51:1:1662:U:C6	2.29	0.66
51:1:2086:U:H2'	51:1:2087:G:H8	1.59	0.66
53:3:113:G:H2'	53:3:114:U:C6	2.31	0.66
55:8:13:DT:OP2	58:B1:791:ALA:HB1	1.95	0.66
55:8:23:DC:H2''	55:8:24:DC:C5	2.30	0.66
51:1:1680:U:C2'	51:1:1681:G:H5'	2.26	0.66
53:3:955:U:H3	53:3:1225:A:H61	1.42	0.66
51:1:2415:G:H2'	51:1:2416:C:C6	2.30	0.66
4:D:8:SER:HA	51:1:1309:G:H5''	1.78	0.66
29:d:176:ASP:HB2	29:d:179:SER:HB3	1.78	0.66
51:1:1509:A:H2'	51:1:1510:G:C8	2.31	0.66
53:3:1172:C:H2'	53:3:1173:U:O4'	1.95	0.66
10:J:53:ARG:NH1	53:3:1071:C:H5'	2.12	0.65
11:K:42:TRP:HB2	11:K:59:TYR:HB2	1.77	0.65
51:1:1528:A:C2'	51:1:1529:G:H5'	2.27	0.65
52:2:3:C:C2'	52:2:4:C:H5''	2.25	0.65
35:k:76:VAL:H	40:p:72:VAL:HG12	1.61	0.65
17:Q:33:CYS:H	17:Q:54:VAL:HG13	1.60	0.65
51:1:1718:G:H2'	51:1:1719:G:C8	2.30	0.65
53:3:153:C:H2'	53:3:154:U:O4'	1.96	0.65
53:3:1125:U:H2'	53:3:1126:U:H2'	1.78	0.65
58:B1:1037:PHE:HB3	58:B1:1040:MET:HB2	1.78	0.65
51:1:1268:A:H2'	51:1:1269:A:C8	2.31	0.65
53:3:211:G:H2'	53:3:212:G:O4'	1.96	0.65
53:3:738:C:H2'	53:3:739:C:H6	1.62	0.65
53:3:835:U:C2'	53:3:836:G:H5''	2.26	0.65
58:B1:978:ARG:HG2	58:B1:1197:ASN:HD21	1.61	0.65
58:B1:141:PHE:HD2	58:B1:293:ARG:O	1.79	0.65
51:1:2029:G:O6	51:1:2032:G:H5''	1.97	0.65
4:D:7:PRO:HA	51:1:686:U:O2	1.96	0.65
22:V:60:ILE:HG22	22:V:74:LEU:HA	1.78	0.65
59:B2:314:ASN:HD21	59:B2:348:SER:HA	1.62	0.65
51:1:203:A:H3'	51:1:204:A:H5''	1.79	0.65
51:1:1170:C:H2'	51:1:1171:G:C8	2.32	0.65
51:1:2008:C:H2'	51:1:2009:A:H8	1.61	0.65
51:1:2048:G:H2'	51:1:2049:G:H5''	1.79	0.65
53:3:660:C:H2'	53:3:661:G:O4'	1.96	0.65
53:3:1173:U:H2'	53:3:1174:G:H8	1.62	0.65
55:8:3:DC:C2'	55:8:4:DT:C7	2.75	0.65
65:0:17:ALA:HB2	65:0:112:VAL:HG23	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:5:ARG:NH1	51:1:2285:C:C5	2.65	0.65
51:1:748:G:O6	51:1:751:A:H4'	1.97	0.65
52:2:13:G:H2'	52:2:14:U:H5''	1.78	0.65
53:3:1366:C:H2'	53:3:1367:C:C6	2.32	0.65
17:Q:98:ARG:HB3	17:Q:105:GLY:HA2	1.79	0.65
58:B1:975:ILE:HG22	58:B1:977:SER:H	1.62	0.65
13:M:111:THR:HG22	13:M:113:ARG:H	1.62	0.64
32:g:94:ILE:HG12	32:g:122:LEU:HB2	1.78	0.64
51:1:195:A:H3'	51:1:196:A:H4'	1.78	0.64
31:f:82:PHE:HB2	31:f:140:ILE:HG12	1.79	0.64
51:1:1474:U:H2'	51:1:1475:G:H5'	1.79	0.64
51:1:2047:C:H2'	51:1:2048:G:C8	2.32	0.64
51:1:2329:U:H2'	51:1:2330:G:C8	2.32	0.64
22:V:47:ASP:HB3	22:V:74:LEU:HB3	1.78	0.64
30:e:104:THR:HG23	30:e:105:ILE:HG13	1.80	0.64
58:B1:193:ASP:HB3	58:B1:196:GLN:HB2	1.78	0.64
10:J:25:LYS:HZ1	53:3:923:A:H5''	1.62	0.64
51:1:2704:C:H2'	51:1:2705:A:O4'	1.97	0.64
53:3:246:A:H62	53:3:281:G:N2	1.95	0.64
53:3:1156:G:H21	53:3:1179:A:H2	1.44	0.64
53:3:1436:U:H2'	53:3:1437:A:H8	1.62	0.64
58:B1:68:TYR:HB3	58:B1:75:TYR:CE2	2.32	0.64
59:B2:1282:GLY:HA3	60:W0:17:PHE:HE1	1.63	0.64
51:1:1278:C:H2'	51:1:1279:G:H8	1.62	0.64
51:1:1447:C:H2'	51:1:1448:G:C8	2.31	0.64
51:1:2215:C:H2'	51:1:2216:G:C8	2.31	0.64
23:W:41:SER:HA	23:W:44:THR:HG22	1.80	0.64
51:1:1127:A:H2'	51:1:1128:G:H5''	1.80	0.64
58:B1:461:PHE:HD2	59:B2:813:GLU:HB2	1.62	0.64
2:B:8:THR:HB	51:1:2020:A:H5'	1.80	0.64
47:w:40:LYS:NZ	51:1:2330:G:O2'	2.30	0.64
51:1:2267:A:H3'	51:1:2267:A:N3	2.13	0.64
58:B1:162:GLU:HA	58:B1:162:GLU:OE1	1.97	0.64
58:B1:245:LEU:HG	58:B1:246:PRO:HD2	1.80	0.64
17:Q:27:PRO:HB3	53:3:552:U:O2	1.98	0.64
31:f:94:ARG:H	31:f:105:SER:HB3	1.62	0.64
32:g:4:ILE:HA	32:g:18:GLN:HE22	1.63	0.64
51:1:246:C:H2'	51:1:247:G:H5'	1.80	0.64
51:1:581:C:H2'	51:1:582:A:H8	1.60	0.64
51:1:1297:C:OP1	51:1:2710:C:H4'	1.97	0.64
53:3:56:U:O2	65:0:362:ARG:NH1	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1243:C:H2'	53:3:1244:G:H8	1.63	0.64
53:3:1306:A:N6	53:3:1331:G:H1'	2.12	0.64
53:3:1474:U:H2'	53:3:1475:G:O4'	1.98	0.64
58:B1:918:ILE:HG22	59:B2:1280:ALA:HB1	1.79	0.64
65:0:624:PRO:HA	65:0:651:GLY:HA2	1.80	0.64
27:b:155:ARG:NH1	51:1:1818:U:H5	1.96	0.64
53:3:952:U:H2'	53:3:953:G:C8	2.32	0.64
53:3:1148:U:H2'	53:3:1149:C:O4'	1.98	0.64
59:B2:896:THR:N	59:B2:899:GLU:HB2	2.13	0.64
63:6:26:G:H3'	63:6:27:U:H5''	1.80	0.64
4:D:14:ARG:HG2	51:1:125:A:H5'	1.80	0.64
44:t:37:ASP:OD1	44:t:37:ASP:N	2.29	0.64
4:D:21:ARG:NH1	51:1:465:G:O3'	2.32	0.63
15:O:46:LYS:HE3	53:3:1253:G:OP1	1.98	0.63
51:1:746:U:H1'	51:1:748:G:H21	1.61	0.63
53:3:1345:U:H4'	53:3:1346:A:H5'	1.80	0.63
21:U:34:GLU:OE1	21:U:60:TRP:NE1	2.30	0.63
42:r:41:ILE:HB	42:r:47:VAL:HB	1.80	0.63
48:x:1:SER:HB2	51:1:1366:A:OP2	1.99	0.63
51:1:20:C:H2'	51:1:21:A:H8	1.60	0.63
63:6:61:C:O2'	64:a:53:ARG:HD2	1.97	0.63
33:i:112:LYS:NZ	33:i:124:MET:SD	2.69	0.63
59:B2:528:ARG:NH2	59:B2:576:SER:O	2.30	0.63
15:O:59:LYS:HE3	53:3:972:C:H5'	1.81	0.63
25:Y:54:GLN:HE22	53:3:193:C:C1'	2.11	0.63
53:3:600:A:H61	53:3:638:U:H3	1.47	0.63
58:B1:1357:ILE:HD11	59:B2:1287:LEU:HD13	1.80	0.63
6:F:1:MET:HG3	51:1:2742:G:H5'	1.79	0.63
27:b:49:THR:OG1	27:b:50:THR:N	2.31	0.63
51:1:96:C:H2'	51:1:97:C:C6	2.33	0.63
63:6:54:U:H3	63:6:58:A:H8	1.47	0.63
48:x:60:LYS:CD	51:1:372:G:H5''	2.28	0.63
51:1:1597:A:H5''	51:1:1598:A:C5'	2.24	0.63
51:1:2464:G:H2'	51:1:2465:C:H6	1.64	0.63
53:3:67:C:H2'	53:3:68:G:H8	1.63	0.63
8:H:10:ARG:HH12	8:H:181:ILE:H	1.45	0.63
51:1:158:U:H2'	51:1:159:G:O4'	1.97	0.63
53:3:492:C:H2'	53:3:493:A:C8	2.34	0.63
53:3:966:G:C2	63:6:34:C:H5'	2.33	0.63
53:3:1007:U:H2'	53:3:1008:U:C6	2.34	0.63
58:B1:201:LEU:HB2	58:B1:221:ILE:HD13	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:105:ARG:HD2	53:3:1117:A:O2'	1.99	0.63
32:g:4:ILE:HD11	32:g:43:ASN:HB3	1.80	0.63
34:j:78:THR:HB	51:1:2641:G:H5''	1.81	0.63
51:1:340:A:H2'	51:1:341:C:H5'	1.81	0.63
51:1:764:A:O2'	51:1:765:C:H5'	1.99	0.63
51:1:2066:C:O2'	51:1:2067:G:H5'	1.99	0.63
51:1:2339:C:H2'	51:1:2340:A:H8	1.64	0.63
52:2:13:G:N7	52:2:70:C:H4'	2.14	0.63
63:6:26:G:C3'	63:6:27:U:H5''	2.29	0.63
65:0:94:ASP:HB2	65:0:465:HIS:HB2	1.81	0.63
14:N:17:ARG:NH2	53:3:1129:C:H4'	2.13	0.63
15:O:89:ARG:HD3	58:B1:86:GLU:H	1.64	0.63
47:w:19:VAL:HG13	47:w:34:VAL:HG22	1.81	0.63
51:1:2656:U:H5''	65:0:146:ARG:NH1	2.14	0.63
51:1:948:C:H2'	51:1:949:G:C8	2.34	0.62
58:B1:144:TYR:CE1	58:B1:162:GLU:OE2	2.51	0.62
30:e:35:LEU:HB3	30:e:151:LEU:HD11	1.81	0.62
51:1:1063:G:H3'	51:1:1064:C:H6	1.63	0.62
51:1:1783:A:C5	51:1:2587:A:C2	2.87	0.62
51:1:2898:U:H2'	51:1:2899:A:C8	2.34	0.62
14:N:68:GLY:HA2	53:3:1250:A:C5'	2.27	0.62
19:S:75:LYS:NZ	53:3:1357:A:H5''	2.14	0.62
51:1:1395:A:H4'	51:1:1397:U:C5	2.35	0.62
51:1:1736:U:H2'	51:1:1737:G:O4'	2.00	0.62
51:1:2123:G:H8	51:1:2125:G:H21	1.44	0.62
53:3:946:A:H2'	53:3:947:G:C8	2.34	0.62
58:B1:128:LEU:HA	58:B1:192:MET:HE1	1.81	0.62
12:L:92:PRO:CA	12:L:95:ARG:HG3	2.28	0.62
51:1:315:G:H2'	51:1:316:C:C6	2.33	0.62
51:1:1173:U:H2'	51:1:1177:G:H1	1.64	0.62
53:3:34:C:H2'	53:3:35:G:C8	2.33	0.62
53:3:668:G:H1	53:3:738:C:H42	1.47	0.62
7:G:89:PHE:HB3	7:G:150:ILE:HD12	1.81	0.62
14:N:12:LYS:H	14:N:105:ARG:HH22	1.46	0.62
16:P:17:ASP:HB2	16:P:36:ARG:HH22	1.64	0.62
23:W:38:ILE:CD1	53:3:720:C:H1'	2.27	0.62
41:q:12:ARG:NH1	51:1:1251:C:H5''	2.15	0.62
51:1:481:G:H1'	51:1:506:G:N2	2.14	0.62
51:1:1675:C:H2'	51:1:1676:A:O4'	2.00	0.62
51:1:2810:A:H62	51:1:2890:G:H21	1.46	0.62
53:3:91:U:C2'	53:3:92:U:H5''	2.27	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:19:SER:OG	22:V:20:ILE:N	2.33	0.62
51:1:1867:G:H1	51:1:1874:C:H42	1.48	0.62
6:F:27:CYS:SG	6:F:28:SER:N	2.71	0.62
7:G:32:GLY:HA2	7:G:39:ILE:H	1.64	0.62
9:I:8:LEU:HD23	9:I:21:LYS:HE2	1.82	0.62
12:L:1:PRO:HD2	12:L:5:VAL:HA	1.82	0.62
45:u:87:GLU:HG2	45:u:92:VAL:HG11	1.81	0.62
51:1:948:C:H2'	51:1:949:G:H8	1.64	0.62
51:1:1901:A:H2'	51:1:1902:C:C6	2.35	0.62
55:8:1:DC:H2''	55:8:2:DC:C5	2.35	0.62
7:G:67:LEU:HD12	7:G:160:LEU:HD12	1.82	0.62
51:1:66:C:H1'	51:1:456:C:O2	2.00	0.62
51:1:1270:C:H5''	51:1:1271:G:H5''	1.79	0.62
51:1:2384:U:O2'	51:1:2385:C:H5'	1.98	0.62
53:3:1084:G:H5'	53:3:1102:A:OP2	2.00	0.62
53:3:1347:G:N2	53:3:1373:G:H2'	2.15	0.62
58:B1:111:THR:CG2	58:B1:300:GLN:NE2	2.63	0.62
58:B1:1355:ARG:NH1	58:B1:1369:ARG:NH1	2.47	0.62
43:s:25:ARG:HH22	51:1:519:U:H5''	1.64	0.62
51:1:812:C:H5''	51:1:1250:G:O2'	2.00	0.62
55:8:3:DC:H2'	55:8:4:DT:C7	2.30	0.62
8:H:21:TRP:CD1	8:H:58:ARG:H	2.18	0.62
27:b:6:LYS:HZ1	51:1:1695:G:H5'	1.65	0.62
34:j:113:PRO:HG3	51:1:528:A:H5'	1.81	0.62
51:1:848:C:H2'	51:1:849:A:C8	2.35	0.62
51:1:2512:C:H2'	51:1:2513:A:O4'	2.00	0.62
53:3:737:C:H2'	53:3:738:C:C6	2.34	0.62
53:3:939:G:H2'	53:3:940:C:H6	1.63	0.62
9:I:119:HIS:CD2	53:3:438:U:H4'	2.35	0.61
30:e:38:GLY:HA3	51:1:2312:U:O2	2.00	0.61
51:1:677:A:H2'	51:1:678:C:C6	2.34	0.61
51:1:2082:A:C2	51:1:2083:G:H1'	2.35	0.61
51:1:2286:G:H4'	51:1:2287:A:O4'	2.00	0.61
53:3:367:U:H3	53:3:393:A:H2	1.47	0.61
59:B2:120:GLN:NE2	59:B2:490:GLN:OE1	2.32	0.61
51:1:1078:U:H4'	51:1:1088:A:H2	1.65	0.61
51:1:1746:A:H2'	51:1:1747:U:C6	2.34	0.61
51:1:368:A:O2'	51:1:369:U:H5'	2.00	0.61
55:8:13:DT:C7	58:B1:791:ALA:HB2	2.29	0.61
58:B1:100:GLU:HA	59:B2:1328:LYS:HE2	1.82	0.61
59:B2:55:SER:OG	59:B2:465:ARG:NH1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:572:A:N6	51:1:2029:G:H21	1.88	0.61
51:1:1740:G:H2'	51:1:1741:C:H6	1.65	0.61
53:3:1110:A:H2'	53:3:1111:A:C8	2.35	0.61
30:e:132:ARG:O	30:e:132:ARG:NH2	2.34	0.61
42:r:63:VAL:HG12	42:r:96:VAL:HG12	1.83	0.61
51:1:2885:G:H2'	51:1:2886:A:O4'	2.00	0.61
58:B1:223:LEU:HG	58:B1:223:LEU:O	2.00	0.61
59:B2:896:THR:HG22	59:B2:899:GLU:H	1.65	0.61
13:M:28:SER:HB2	13:M:58:LEU:HB2	1.82	0.61
17:Q:55:ARG:HA	17:Q:61:GLU:HA	1.83	0.61
53:3:452:A:H61	53:3:480:U:H3	1.49	0.61
53:3:715:A:H5''	53:3:805:C:O2'	2.00	0.61
58:B1:633:ALA:HA	59:B2:806:PRO:O	2.01	0.61
19:S:23:ARG:HH11	19:S:26:LEU:HB3	1.65	0.61
51:1:729:G:H2'	51:1:1775:U:O2	2.00	0.61
51:1:1053:C:H2'	51:1:1054:A:H5'	1.83	0.61
53:3:657:U:H2'	53:3:658:C:C6	2.36	0.61
37:m:58:LYS:O	37:m:59:ARG:NH2	2.32	0.61
46:v:72:VAL:HG13	46:v:93:ARG:HA	1.82	0.61
51:1:1361:G:H2'	51:1:1362:C:C6	2.35	0.61
57:A1:38:THR:HB	57:A2:45:ARG:HD3	1.82	0.61
57:A1:211:ILE:HG12	57:A1:219:ARG:HH12	1.65	0.61
18:R:81:ASP:OD1	30:e:111:ARG:NH2	2.34	0.61
22:V:10:ARG:NH1	22:V:11:VAL:O	2.33	0.61
34:j:113:PRO:HD2	51:1:558:U:OP1	2.00	0.61
46:v:17:SER:HB3	46:v:27:PRO:HG3	1.83	0.61
48:x:4:CYS:HB3	48:x:9:LYS:H	1.65	0.61
51:1:11:C:H2'	51:1:12:U:H5''	1.83	0.61
51:1:1063:G:H5''	51:1:1064:C:H5	1.64	0.61
51:1:2699:C:H2'	51:1:2700:A:H8	1.66	0.61
53:3:358:U:H2'	53:3:359:G:H8	1.64	0.61
53:3:924:C:H2'	53:3:925:G:C8	2.34	0.61
40:p:90:ALA:HB2	40:p:112:ARG:HA	1.81	0.60
42:r:81:LYS:HD3	51:1:973:A:H5''	1.83	0.60
51:1:971:G:H2'	51:1:972:A:O4'	2.01	0.60
51:1:2327:A:H2'	51:1:2328:A:C8	2.35	0.60
52:2:30:C:H2'	52:2:31:C:O4'	2.01	0.60
58:B1:68:TYR:HB3	58:B1:75:TYR:CZ	2.35	0.60
65:0:321:ALA:HB2	65:0:397:LEU:HD21	1.82	0.60
29:d:155:GLU:HA	29:d:158:PHE:HB3	1.82	0.60
51:1:139:U:H2'	51:1:140:C:H5	1.64	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2653:U:C3'	51:1:2654:A:H5''	2.30	0.60
58:B1:395:LYS:NZ	58:B1:399:LYS:HD3	2.15	0.60
51:1:2356:U:H2'	51:1:2357:G:O4'	2.01	0.60
58:B1:770:LEU:HD13	59:B2:618:GLN:CG	2.30	0.60
37:m:14:LYS:NZ	51:1:955:U:OP2	2.35	0.60
51:1:468:G:H2'	51:1:469:G:H5'	1.83	0.60
51:1:729:G:H5''	51:1:730:A:H5''	1.83	0.60
51:1:1818:U:H4'	51:1:1821:A:H1'	1.83	0.60
51:1:2743:U:H3'	51:1:2744:G:H5''	1.83	0.60
53:3:314:C:H2'	53:3:315:A:C8	2.37	0.60
53:3:454:G:H2'	53:3:455:G:C8	2.37	0.60
53:3:979:C:C2'	53:3:980:C:H5'	2.32	0.60
36:l:79:LEU:HB2	36:l:113:ALA:HB3	1.83	0.60
51:1:611:C:H2'	51:1:612:G:O4'	2.01	0.60
51:1:1064:C:H2'	51:1:1065:U:C6	2.37	0.60
51:1:1484:U:H2'	51:1:1485:U:C6	2.36	0.60
51:1:2208:C:H2'	51:1:2209:G:C8	2.36	0.60
63:6:26:G:C2'	63:6:27:U:H5''	2.31	0.60
64:a:216:THR:H	64:a:220:ALA:HB3	1.67	0.60
10:J:96:GLN:HG2	53:3:7:A:C6	2.36	0.60
21:U:2:VAL:HB	53:3:229:U:H4'	1.83	0.60
27:b:201:LEU:HD22	53:3:773:G:H5''	1.82	0.60
51:1:1278:C:H2'	51:1:1279:G:C8	2.37	0.60
51:1:1308:A:H61	51:1:1608:A:H61	1.48	0.60
52:2:90:C:H2'	52:2:91:C:C5'	2.24	0.60
58:B1:342:LEU:HD23	58:B1:1352:ILE:HG23	1.83	0.60
58:B1:370:LYS:HG2	58:B1:441:LEU:HD23	1.84	0.60
15:O:50:THR:HG22	15:O:64:GLN:HG3	1.83	0.60
29:d:64:GLY:O	51:1:2059:A:H4'	2.01	0.60
36:l:108:ALA:HB3	36:l:125:LEU:HD11	1.83	0.60
48:x:31:ASN:ND2	48:x:52:ALA:CB	2.65	0.60
51:1:445:C:C2'	51:1:446:G:H5'	2.32	0.60
51:1:1369:G:H21	51:1:1810:A:H2	1.48	0.60
51:1:1674:G:H21	51:1:1677:A:H61	1.49	0.60
58:B1:926:PRO:HG2	58:B1:1248:ILE:HD11	1.84	0.60
51:1:589:U:H2'	51:1:590:A:C8	2.36	0.60
53:3:419:C:H5''	53:3:513:C:H1'	1.83	0.60
53:3:1374:A:H2'	53:3:1375:A:C8	2.37	0.60
58:B1:1161:GLY:HA3	58:B1:1179:PRO:HA	1.82	0.60
32:g:51:ARG:HA	32:g:55:GLU:HB2	1.84	0.60
43:s:42:LYS:HE3	51:1:2010:G:H4'	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:192:C:H2'	51:1:193:U:H5'	1.84	0.60
9:I:121:ALA:HA	9:I:145:ARG:HB2	1.83	0.59
17:Q:48:LEU:HB2	53:3:520:A:OP1	2.02	0.59
51:1:635:C:O2'	51:1:639:U:H5''	2.02	0.59
51:1:2303:G:O2'	51:1:2304:G:H5'	2.02	0.59
51:1:2324:U:C3'	51:1:2325:G:H5''	2.26	0.59
51:1:2521:C:O2'	51:1:2522:U:H5'	2.02	0.59
51:1:2898:U:H2'	51:1:2899:A:H8	1.67	0.59
53:3:747:A:C3'	53:3:748:G:H5''	2.32	0.59
58:B1:951:GLN:NE2	58:B1:1014:GLY:O	2.35	0.59
51:1:35:G:H1	51:1:445:C:H42	1.50	0.59
51:1:1889:A:H2'	51:1:1890:A:C8	2.37	0.59
51:1:2189:U:H2'	51:1:2190:G:C8	2.37	0.59
51:1:2443:C:O2'	51:1:2444:G:H5'	2.02	0.59
53:3:207:C:H3'	53:3:208:U:H5''	1.83	0.59
58:B1:161:THR:HG23	58:B1:164:GLN:H	1.68	0.59
58:B1:438:GLU:HG3	58:B1:485:MET:HE1	1.84	0.59
19:S:12:ARG:NH1	19:S:58:ARG:O	2.35	0.59
47:w:56:PHE:CE2	51:1:2365:G:H4'	2.37	0.59
51:1:911:A:H5'	51:1:912:C:H5''	1.84	0.59
51:1:1081:U:H3'	51:1:1081:U:O2	2.02	0.59
51:1:2537:U:H2'	51:1:2538:C:C6	2.37	0.59
53:3:128:G:H2'	53:3:129:A:C8	2.37	0.59
53:3:1512:U:H2'	53:3:1513:A:H8	1.67	0.59
7:G:73:ARG:HH22	7:G:93:HIS:HA	1.67	0.59
18:R:95:PRO:HG2	18:R:105:ALA:HB1	1.83	0.59
22:V:61:ARG:NH1	22:V:73:THR:OG1	2.36	0.59
27:b:48:ILE:HG22	51:1:779:U:P	2.43	0.59
51:1:729:G:H5''	51:1:730:A:C5'	2.33	0.59
51:1:881:G:N2	51:1:897:C:N3	2.50	0.59
55:8:11:DC:H2'	55:8:12:DG:C8	2.37	0.59
59:B2:1072:ASN:ND2	59:B2:1111:GLN:OE1	2.35	0.59
21:U:5:ARG:HD3	53:3:376:G:H4'	1.85	0.59
29:d:21:ARG:NH2	29:d:22:ASP:OD1	2.35	0.59
51:1:572:A:H61	51:1:2029:G:N2	1.88	0.59
51:1:1982:U:H2'	51:1:1983:G:H8	1.68	0.59
51:1:2048:G:C3'	51:1:2049:G:H5''	2.31	0.59
53:3:34:C:H2'	53:3:35:G:H8	1.68	0.59
55:8:9:DG:H4'	58:B1:120:LEU:HG	1.84	0.59
57:A1:112:ALA:HB3	57:A1:126:PRO:HA	1.83	0.59
58:B1:412:LEU:HD22	58:B1:441:LEU:HD21	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:6:55:U:H2'	63:6:56:C:H6	1.68	0.59
18:R:26:LYS:O	18:R:30:LYS:NZ	2.36	0.59
45:u:40:LEU:HD12	45:u:59:GLU:HB3	1.84	0.59
51:1:1062:G:H5'	51:1:1071:G:H5'	1.84	0.59
51:1:1638:C:H4'	51:1:2710:C:O2	2.02	0.59
53:3:579:A:H5'	53:3:728:A:H1'	1.85	0.59
58:B1:201:LEU:HD11	58:B1:220:ARG:HH11	1.67	0.59
59:B2:69:GLN:HE21	59:B2:101:ARG:HD2	1.67	0.59
41:q:12:ARG:HH12	51:1:1251:C:H5''	1.68	0.59
51:1:1802:A:H2'	51:1:1803:A:C8	2.38	0.59
53:3:253:A:H2'	53:3:254:G:O4'	2.03	0.59
53:3:1280:A:O2'	53:3:1281:C:H5'	2.02	0.59
53:3:1521:C:H2'	53:3:1522:U:C6	2.37	0.59
58:B1:154:LEU:HD21	58:B1:160:LEU:HD21	1.83	0.59
7:G:99:MET:HA	7:G:106:VAL:HG21	1.84	0.59
7:G:142:LYS:HE2	53:3:1098:C:OP1	2.03	0.59
10:J:25:LYS:HB2	53:3:923:A:OP1	2.02	0.59
29:d:55:SER:OG	29:d:56:GLY:N	2.36	0.59
40:p:1:SER:OG	51:1:2875:C:H4'	2.02	0.59
51:1:704:G:H1'	51:1:726:G:H22	1.67	0.59
51:1:2032:G:OP2	51:1:2455:G:H5'	2.03	0.59
53:3:337:G:H2'	53:3:338:A:C8	2.38	0.59
53:3:836:G:H2'	53:3:837:U:O4'	2.02	0.59
58:B1:725:MET:SD	59:B2:1101:LEU:HD23	2.42	0.59
65:0:508:GLN:CA	65:0:513:GLY:HA2	2.32	0.59
28:c:46:ARG:HG2	28:c:84:LEU:HD12	1.85	0.59
51:1:12:U:O2	51:1:12:U:H2'	2.02	0.59
51:1:1444:G:H2'	51:1:1445:G:C8	2.37	0.59
53:3:448:A:H62	53:3:486:U:H3	1.48	0.59
53:3:677:U:H3	53:3:713:G:H1	1.51	0.59
53:3:738:C:H2'	53:3:739:C:C6	2.38	0.59
55:8:7:DC:H2''	55:8:8:DT:H71	1.84	0.59
58:B1:97:VAL:HG11	58:B1:101:ARG:NH2	2.18	0.59
17:Q:13:ARG:NH1	17:Q:14:LYS:O	2.35	0.59
51:1:952:G:C2'	51:1:953:G:H5''	2.32	0.59
53:3:59:A:H5''	53:3:387:U:H5''	1.84	0.59
58:B1:99:ARG:NH1	58:B1:99:ARG:HG3	2.17	0.59
9:I:68:GLU:HB3	53:3:546:A:OP2	2.03	0.58
13:M:38:VAL:HG11	13:M:110:MET:HA	1.83	0.58
50:z:12:ALA:O	50:z:20:LYS:NZ	2.36	0.58
51:1:1063:G:H3'	51:1:1064:C:C6	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1836:C:O2'	51:1:1837:C:H5'	2.03	0.58
51:1:1924:C:H3'	51:1:1925:C:C6	2.38	0.58
53:3:570:G:O2'	53:3:819:A:H2'	2.03	0.58
53:3:1492:A:H2'	53:3:1493:A:C8	2.38	0.58
58:B1:275:ARG:NH1	58:B1:278:ARG:NH1	2.51	0.58
28:c:194:PRO:HA	51:1:2680:U:H5'	1.85	0.58
51:1:952:G:C3'	51:1:953:G:H5''	2.33	0.58
51:1:1993:U:H2'	51:1:1994:C:H6	1.67	0.58
51:1:2121:G:H1'	64:a:167:LYS:HB2	1.86	0.58
51:1:2306:C:H2'	51:1:2307:G:C8	2.38	0.58
51:1:2446:G:H2'	51:1:2501:C:C5	2.38	0.58
65:0:515:TYR:H	65:0:587:ASP:HB3	1.68	0.58
7:G:103:TRP:HA	7:G:106:VAL:HB	1.85	0.58
19:S:17:ASP:O	19:S:22:LYS:NZ	2.35	0.58
43:s:25:ARG:NH2	51:1:519:U:H5''	2.19	0.58
53:3:885:G:H2'	53:3:886:G:C8	2.39	0.58
53:3:1421:G:H3'	53:3:1422:G:C5'	2.33	0.58
63:6:6:G:O2'	63:6:7:G:H5'	2.03	0.58
3:C:7:LYS:HA	3:C:23:THR:HA	1.85	0.58
5:E:21:PHE:HE2	5:E:61:LEU:HD23	1.68	0.58
51:1:1806:C:H2'	51:1:1807:G:O4'	2.04	0.58
53:3:41:G:H2'	53:3:42:G:H8	1.69	0.58
53:3:235:C:H2'	53:3:236:A:C8	2.38	0.58
53:3:742:G:H2'	53:3:743:A:C8	2.38	0.58
53:3:850:U:C2'	53:3:851:G:H5''	2.33	0.58
5:E:4:LYS:HD3	51:1:242:G:C8	2.38	0.58
6:F:19:ARG:NE	51:1:2756:U:OP2	2.36	0.58
9:I:12:ARG:HH21	9:I:35:GLN:H	1.50	0.58
15:O:40:ILE:CD1	53:3:1124:G:H4'	2.34	0.58
28:c:118:PHE:HD2	51:1:1654:A:H2	1.52	0.58
35:k:16:ALA:O	35:k:17:ARG:NH1	2.36	0.58
40:p:11:GLN:HB2	40:p:54:LEU:HD11	1.84	0.58
51:1:166:U:H2'	51:1:167:A:C8	2.39	0.58
51:1:1000:A:H62	51:1:1154:G:H2'	1.68	0.58
51:1:1065:U:O4	51:1:1069:A:H5''	2.03	0.58
53:3:41:G:H2'	53:3:42:G:C8	2.38	0.58
53:3:180:U:H2'	53:3:181:A:O4'	2.03	0.58
53:3:1195:C:H2'	53:3:1197:A:O4'	2.04	0.58
63:6:14:A:H2'	63:6:15:G:H5'	1.85	0.58
7:G:176:ASN:ND2	7:G:194:GLY:O	2.33	0.58
9:I:8:LEU:HD21	53:3:429:U:O5'	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:116:GLN:O	27:b:127:ASN:ND2	2.35	0.58
29:d:164:LEU:HB2	29:d:167:VAL:HG22	1.84	0.58
59:B2:1142:ARG:NH1	59:B2:1161:LEU:O	2.36	0.58
51:1:1197:G:H2'	51:1:1198:U:C6	2.39	0.58
51:1:1319:C:O2'	51:1:1320:C:H5'	2.02	0.58
51:1:2333:A:H5'	51:1:2335:A:H1'	1.85	0.58
53:3:16:A:O2'	53:3:17:U:H5'	2.03	0.58
53:3:721:G:H4'	53:3:722:G:O4'	2.04	0.58
64:a:26:ALA:HA	64:a:29:LEU:HB3	1.85	0.58
51:1:414:C:H2'	51:1:415:A:C8	2.39	0.58
51:1:2123:G:O6	51:1:2174:C:N4	2.37	0.58
53:3:626:G:H2'	53:3:627:G:C8	2.39	0.58
58:B1:37:GLU:O	58:B1:61:ILE:CD1	2.52	0.58
63:6:4:G:H2'	63:6:5:G:O4'	2.03	0.58
12:L:137:ARG:NH1	12:L:138:GLU:OE2	2.37	0.58
25:Y:73:ARG:O	25:Y:77:ASN:ND2	2.36	0.58
40:p:33:GLU:OE1	40:p:38:ARG:NH1	2.37	0.58
51:1:36:G:H4'	51:1:451:U:C2	2.38	0.58
51:1:1368:G:H2'	51:1:1369:G:H8	1.68	0.58
51:1:1787:A:C2	51:1:1788:C:C6	2.91	0.58
58:B1:750:PRO:CB	59:B2:549:ASP:OD2	2.45	0.58
23:W:56:ARG:NH1	53:3:735:C:OP1	2.37	0.58
51:1:1197:G:H2'	51:1:1198:U:H6	1.67	0.58
51:1:1770:G:H4'	51:1:1938:A:OP1	2.04	0.58
53:3:308:C:H2'	53:3:309:A:H8	1.69	0.58
53:3:1005:A:H2'	53:3:1006:G:H5'	1.85	0.58
59:B2:707:ALA:O	59:B2:711:ASP:HB2	2.03	0.58
59:B2:891:GLY:O	59:B2:913:VAL:HA	2.03	0.58
65:0:223:ILE:HB	65:0:243:LEU:HD22	1.85	0.58
8:H:18:ASN:HD21	8:H:39:ARG:HH12	1.51	0.57
45:u:42:LYS:HG3	51:1:499:U:H4'	1.85	0.57
51:1:1332:G:N7	51:1:1609:A:H2'	2.18	0.57
51:1:1843:C:H2'	51:1:1844:C:C6	2.38	0.57
51:1:1941:C:H2'	51:1:1942:C:O4'	2.04	0.57
59:B2:13:LYS:HB2	59:B2:1180:MET:HE2	1.86	0.57
9:I:58:GLN:HB3	9:I:62:ARG:HH21	1.68	0.57
10:J:87:VAL:HG13	10:J:92:ARG:HG3	1.86	0.57
20:T:13:GLU:OE1	20:T:83:ARG:NH2	2.37	0.57
42:r:79:ARG:NH1	51:1:572:A:OP2	2.37	0.57
51:1:1177:G:H2'	51:1:1178:C:H5''	1.86	0.57
51:1:1270:C:H5''	51:1:1271:G:H5'	1.84	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1069:C:O2'	53:3:1192:C:H1'	2.03	0.57
8:H:105:VAL:HG22	8:H:107:LYS:H	1.69	0.57
14:N:69:GLY:N	53:3:1250:A:H4'	2.20	0.57
15:O:13:PHE:O	15:O:70:HIS:ND1	2.36	0.57
16:P:33:ILE:HG22	16:P:41:LEU:HD12	1.85	0.57
28:c:18:ASP:OD1	28:c:18:ASP:N	2.37	0.57
28:c:110:THR:OG1	28:c:111:GLY:N	2.37	0.57
28:c:128:ARG:NH2	51:1:2512:C:OP2	2.37	0.57
32:g:15:LEU:HG	32:g:51:ARG:HH22	1.69	0.57
51:1:2196:C:H2'	51:1:2197:U:C6	2.39	0.57
52:2:24:G:H4'	52:2:25:U:C5	2.38	0.57
53:3:19:A:H1'	53:3:864:A:N3	2.19	0.57
58:B1:1167:LYS:HZ2	58:B1:1170:LYS:HB2	1.70	0.57
29:d:76:PRO:CA	29:d:82:GLY:HA3	2.35	0.57
32:g:139:PHE:O	32:g:141:LYS:NZ	2.37	0.57
44:t:38:ALA:O	44:t:81:LYS:NZ	2.37	0.57
51:1:1565:C:H2'	51:1:1567:G:N7	2.19	0.57
51:1:2675:A:H2'	51:1:2676:C:C6	2.39	0.57
58:B1:615:LYS:HG2	60:W0:5:THR:HG21	1.85	0.57
27:b:221:GLY:HA2	27:b:224:MET:HE3	1.85	0.57
37:m:66:ARG:NH1	37:m:104:GLU:OE2	2.37	0.57
47:w:51:ARG:NH2	51:1:2384:U:OP2	2.37	0.57
51:1:1697:G:C5'	51:1:1698:A:H5''	2.35	0.57
57:A2:28:LEU:HB2	57:A2:201:LEU:HB3	1.86	0.57
14:N:5:TYR:HB2	14:N:20:ILE:HD11	1.85	0.57
34:j:45:THR:OG1	41:q:63:ARG:NH2	2.37	0.57
51:1:62:U:O2'	51:1:63:A:H5'	2.04	0.57
53:3:408:A:H61	53:3:434:U:H3	1.52	0.57
53:3:1004:A:H5'	53:3:1024:G:H1	1.70	0.57
58:B1:160:LEU:HD22	58:B1:164:GLN:HB3	1.86	0.57
58:B1:510:LEU:HD22	58:B1:601:ILE:HD12	1.86	0.57
2:B:49:ARG:O	2:B:51:ARG:NH2	2.37	0.57
53:3:539:A:H2'	53:3:540:G:C8	2.40	0.57
53:3:1399:C:N3	53:3:1502:A:N1	2.53	0.57
11:K:82:ASP:OD1	11:K:82:ASP:N	2.38	0.57
12:L:91:ARG:CB	12:L:93:VAL:HG12	2.32	0.57
17:Q:119:LYS:HD3	53:3:36:C:H5''	1.86	0.57
47:w:20:LYS:HD2	51:1:2355:G:H4'	1.85	0.57
51:1:601:C:O2	51:1:605:G:H4'	2.05	0.57
51:1:1791:A:H2'	51:1:1792:G:C5'	2.34	0.57
53:3:279:A:H5''	53:3:281:G:C5'	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1271:A:H5'	53:3:1314:C:C5'	2.35	0.57
58:B1:514:THR:HG21	58:B1:596:LEU:HD12	1.84	0.57
58:B1:1361:THR:HB	59:B2:1284:ALA:HB3	1.85	0.57
3:C:5:ARG:HG3	3:C:25:ASN:HA	1.86	0.57
4:D:37:LYS:NZ	51:1:468:G:OP2	2.34	0.57
8:H:60:ALA:HB3	62:NG:167:ARG:HA	1.86	0.57
20:T:60:SER:HB2	53:3:581:G:H5'	1.86	0.57
38:n:92:GLY:HA3	51:1:2839:G:H21	1.69	0.57
51:1:211:C:H2'	51:1:212:G:C8	2.40	0.57
51:1:1069:A:H2'	51:1:1073:A:N7	2.20	0.57
51:1:2554:U:H2'	51:1:2555:U:C6	2.40	0.57
51:1:2743:U:C3'	51:1:2744:G:H5''	2.35	0.57
53:3:885:G:H2'	53:3:886:G:H8	1.69	0.57
58:B1:198:CYS:HA	58:B1:221:ILE:HD11	1.86	0.57
59:B2:897:PRO:HA	59:B2:900:LYS:HE3	1.86	0.57
59:B2:1122:LYS:NZ	59:B2:1126:ASP:OD1	2.38	0.57
59:B2:1142:ARG:NH2	59:B2:1166:ASP:OD1	2.38	0.57
11:K:90:MET:SD	23:W:60:ARG:NH1	2.78	0.57
16:P:71:ASP:HA	16:P:74:LYS:HG3	1.87	0.57
27:b:140:VAL:O	27:b:161:VAL:N	2.35	0.57
46:v:21:ARG:HH22	52:2:77:U:H5'	1.70	0.57
51:1:28:A:O2'	51:1:583:G:H5'	2.05	0.57
51:1:78:U:H2'	51:1:79:C:C6	2.40	0.57
51:1:1370:C:H2'	51:1:1371:G:O4'	2.04	0.57
51:1:2475:C:N4	51:1:2529:G:H22	2.03	0.57
53:3:302:G:H2'	53:3:303:A:C8	2.40	0.57
53:3:651:C:H2'	53:3:652:U:O4'	2.04	0.57
53:3:1016:A:H4'	53:3:1218:C:H4'	1.86	0.57
58:B1:99:ARG:CG	58:B1:99:ARG:HH11	2.17	0.57
59:B2:818:VAL:HG22	59:B2:1096:ILE:HG12	1.87	0.57
65:0:168:PRO:HG2	65:0:218:TRP:HE1	1.70	0.57
2:B:5:ASN:ND2	51:1:2020:A:N7	2.52	0.56
4:D:12:ARG:HD2	4:D:44:VAL:HG11	1.88	0.56
10:J:120:HIS:CE1	10:J:121:ASN:ND2	2.73	0.56
30:e:31:GLU:OE1	30:e:32:LYS:NZ	2.37	0.56
51:1:2420:C:O2'	51:1:2421:G:H5'	2.06	0.56
58:B1:42:GLU:HB3	58:B1:52:GLU:HG3	1.86	0.56
65:0:31:LEU:HD21	65:0:68:THR:HG21	1.87	0.56
5:E:27:ASN:O	5:E:35:LYS:NZ	2.38	0.56
16:P:116:PRO:HA	53:3:675:A:H2	1.70	0.56
20:T:19:ASN:HB2	53:3:750:C:O4'	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:t:55:VAL:O	44:t:88:LYS:NZ	2.37	0.56
51:1:1310:G:C2'	51:1:1311:G:H5'	2.34	0.56
51:1:1801:A:H5''	51:1:2203:U:C2'	2.35	0.56
51:1:2524:G:C2'	51:1:2525:G:H5''	2.34	0.56
53:3:1513:A:H2'	53:3:1514:G:C8	2.40	0.56
58:B1:102:MET:HG2	58:B1:246:PRO:HG3	1.87	0.56
3:C:8:ILE:HB	3:C:24:LYS:HB2	1.88	0.56
13:M:15:ASN:HB3	53:3:827:U:H4'	1.86	0.56
18:R:87:GLY:O	18:R:91:ARG:NH2	2.39	0.56
19:S:5:MET:O	19:S:62:ARG:NH1	2.38	0.56
25:Y:13:SER:O	25:Y:17:ARG:N	2.38	0.56
27:b:17:LYS:HD3	51:1:1565:C:OP1	2.05	0.56
29:d:2:GLU:HB2	29:d:11:ALA:HB1	1.87	0.56
33:i:123:ALA:HB1	51:1:1081:U:H4'	1.87	0.56
45:u:32:LYS:HE3	51:1:478:A:H4'	1.87	0.56
51:1:27:G:N2	51:1:512:G:H1'	2.20	0.56
51:1:324:A:H62	51:1:338:G:N2	2.00	0.56
51:1:1120:G:H2'	51:1:1121:C:O4'	2.05	0.56
51:1:2050:C:C2'	51:1:2051:A:H5'	2.32	0.56
51:1:2208:C:H2'	51:1:2209:G:H8	1.70	0.56
51:1:2396:G:O2'	51:1:2397:G:H5'	2.05	0.56
51:1:2430:A:N3	51:1:2430:A:H2'	2.20	0.56
51:1:2692:G:H1'	51:1:2847:U:H1'	1.87	0.56
52:2:4:C:H2'	52:2:5:U:C6	2.41	0.56
53:3:24:U:H2'	53:3:25:C:C6	2.40	0.56
53:3:936:C:H2'	53:3:937:A:O4'	2.04	0.56
58:B1:247:PRO:HA	58:B1:250:ARG:HG3	1.87	0.56
64:a:19:LYS:NZ	64:a:20:GLN:O	2.38	0.56
65:0:446:ARG:O	65:0:459:ALA:N	2.38	0.56
7:G:138:ARG:HH21	7:G:142:LYS:HG2	1.69	0.56
14:N:47:VAL:HG23	14:N:48:ARG:HG3	1.88	0.56
18:R:113:LYS:NZ	63:6:44:A:H4'	2.20	0.56
31:f:59:ASP:OD1	31:f:59:ASP:N	2.36	0.56
34:j:60:ASP:HA	34:j:93:ILE:HD11	1.88	0.56
40:p:87:ARG:NH2	40:p:109:ILE:O	2.36	0.56
51:1:259:G:O2'	51:1:260:G:H5'	2.05	0.56
51:1:379:G:H2'	51:1:380:G:O4'	2.05	0.56
51:1:1933:G:O2'	51:1:1974:C:H4'	2.04	0.56
58:B1:130:MET:HE2	58:B1:135:ILE:HG12	1.87	0.56
65:0:438:LEU:HD22	65:0:469:ILE:HD11	1.88	0.56
13:M:27:PRO:O	13:M:32:LYS:NZ	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:2:ASN:O	25:Y:7:LYS:NZ	2.39	0.56
30:e:113:PHE:HZ	30:e:175:PRO:HB3	1.71	0.56
51:1:1114:C:H2'	51:1:1115:G:C8	2.41	0.56
51:1:1774:C:H4'	51:1:1979:U:O2	2.05	0.56
51:1:2529:G:H5'	51:1:2530:A:H5''	1.87	0.56
53:3:428:G:H4'	53:3:429:U:H4'	1.86	0.56
65:0:322:PHE:HB3	65:0:323:LYS:HD2	1.86	0.56
3:C:36:LYS:NZ	3:C:45:HIS:O	2.38	0.56
40:p:88:ARG:HD3	40:p:112:ARG:HD3	1.86	0.56
47:w:52:ASP:OD2	51:1:2364:C:H5'	2.05	0.56
51:1:959:A:H1'	51:1:2457:U:O2'	2.06	0.56
51:1:1740:G:H2'	51:1:1741:C:C6	2.41	0.56
51:1:2584:U:H2'	51:1:2585:U:H2'	1.87	0.56
53:3:416:G:H2'	53:3:417:G:H8	1.70	0.56
57:A2:294:ASN:HA	61:NA:463:GLY:HA2	1.88	0.56
58:B1:39:LYS:O	58:B1:273:ILE:HG21	2.06	0.56
58:B1:1046:ILE:HD12	58:B1:1059:LEU:HB3	1.86	0.56
7:G:30:ILE:HG22	7:G:40:ILE:HA	1.88	0.56
8:H:32:LEU:HD13	19:S:92:ILE:HD11	1.88	0.56
9:I:65:GLY:O	9:I:96:ARG:NH1	2.39	0.56
28:c:109:VAL:HG23	28:c:172:VAL:HG13	1.88	0.56
33:i:3:LYS:HD3	51:1:1055:G:O5'	2.06	0.56
51:1:36:G:H4'	51:1:451:U:N3	2.21	0.56
51:1:1827:U:C2'	51:1:1828:G:H5'	2.35	0.56
51:1:2637:U:H2'	51:1:2638:G:O4'	2.04	0.56
53:3:882:C:O2'	53:3:883:C:H5'	2.05	0.56
57:A2:82:LEU:HD11	57:A2:171:LEU:HD23	1.86	0.56
58:B1:1166:GLY:HA3	58:B1:1174:ARG:HB2	1.88	0.56
13:M:24:VAL:HG13	13:M:62:LEU:HD11	1.87	0.56
27:b:158:GLY:HA3	51:1:1820:U:C4	2.40	0.56
46:v:72:VAL:HA	46:v:94:ALA:H	1.71	0.56
47:w:33:ILE:HG22	47:w:34:VAL:HG23	1.88	0.56
51:1:687:C:H2'	51:1:688:U:C5'	2.36	0.56
51:1:1923:U:H2'	51:1:1924:C:H6	1.71	0.56
51:1:2317:A:H2'	51:1:2318:G:O4'	2.06	0.56
53:3:416:G:H2'	53:3:417:G:C8	2.41	0.56
53:3:1093:A:C2'	53:3:1094:G:H5'	2.36	0.56
53:3:1257:A:H3'	53:3:1257:A:N3	2.21	0.56
57:A1:29:GLU:HB3	57:A1:200:LYS:HG3	1.87	0.56
58:B1:241:VAL:O	58:B1:241:VAL:HG12	2.04	0.56
58:B1:804:ALA:HA	58:B1:1259:GLN:HG3	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:20:THR:HA	19:S:93:PRO:HB3	1.88	0.56
8:H:82:ASP:HA	8:H:85:LYS:HD2	1.86	0.56
17:Q:50:LYS:NZ	17:Q:51:VAL:O	2.39	0.56
28:c:63:PRO:O	28:c:67:HIS:N	2.39	0.56
52:2:4:C:H6	52:2:4:C:H5'	1.71	0.56
53:3:301:G:H2'	53:3:302:G:C8	2.41	0.56
58:B1:638:SER:OG	58:B1:639:VAL:N	2.36	0.56
64:a:26:ALA:HB1	64:a:30:LEU:HB2	1.87	0.56
4:D:8:SER:OG	4:D:9:VAL:N	2.38	0.56
8:H:49:ALA:HA	8:H:74:ILE:HD11	1.88	0.56
26:Z:48:LYS:HB3	53:3:723:U:C5	2.41	0.56
28:c:119:ALA:O	51:1:1655:A:H4'	2.05	0.56
45:u:32:LYS:HB3	45:u:63:ALA:HB1	1.87	0.56
51:1:923:G:O2'	51:1:924:G:H5'	2.06	0.56
51:1:1141:U:H4'	51:1:1142:A:O4'	2.05	0.56
52:2:105:G:H2'	52:2:106:G:H8	1.71	0.56
53:3:212:G:H2'	53:3:213:G:C8	2.38	0.56
53:3:560:A:H5'	53:3:566:G:N2	2.21	0.56
53:3:684:U:H2'	53:3:685:G:O4'	2.06	0.56
53:3:971:G:OP1	53:3:971:G:H3'	2.06	0.56
53:3:1525:G:O2'	53:3:1526:G:H5'	2.06	0.56
58:B1:741:ALA:O	58:B1:762:ASN:ND2	2.38	0.56
65:0:11:ARG:NH2	65:0:283:ILE:O	2.39	0.56
14:N:11:ARG:NH1	14:N:106:ASP:O	2.39	0.55
14:N:83:THR:HG21	14:N:102:PHE:HB3	1.88	0.55
30:e:32:LYS:HB3	30:e:91:ARG:HE	1.71	0.55
35:k:65:THR:HA	35:k:82:ASN:HA	1.88	0.55
51:1:782:A:H4'	51:1:783:A:H5'	1.87	0.55
51:1:2041:U:H2'	51:1:2042:A:C8	2.40	0.55
51:1:2207:C:O2'	51:1:2208:C:H5'	2.07	0.55
53:3:1401:G:H2'	53:3:1402:C:O4'	2.06	0.55
53:3:1513:A:H2'	53:3:1514:G:H8	1.71	0.55
5:E:43:LEU:HD11	51:1:2362:C:P	2.46	0.55
7:G:101:THR:HG22	53:3:1074:G:H4'	1.88	0.55
10:J:19:ARG:HG2	10:J:30:PHE:HB3	1.89	0.55
11:K:89:VAL:HG23	53:3:737:C:H5'	1.88	0.55
13:M:74:ILE:HG22	13:M:128:VAL:HA	1.87	0.55
29:d:112:LEU:HD22	29:d:117:ARG:HB3	1.88	0.55
50:z:10:ARG:NH2	50:z:52:PHE:O	2.39	0.55
51:1:849:A:H2'	51:1:850:U:H6	1.68	0.55
51:1:881:G:H2'	51:1:882:G:H8	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1186:G:N2	51:1:1187:G:H1'	2.20	0.55
51:1:1255:U:OP1	51:1:1256:G:H5''	2.06	0.55
51:1:1868:C:H2'	51:1:1869:G:C5'	2.35	0.55
51:1:2508:G:C6	51:1:2582:G:O6	2.59	0.55
53:3:1244:G:H2'	53:3:1245:C:C6	2.40	0.55
58:B1:1155:ILE:HG13	58:B1:1210:ILE:HB	1.89	0.55
65:0:323:LYS:HB2	65:0:335:PHE:HB2	1.89	0.55
10:J:25:LYS:HG3	53:3:923:A:H5'	1.87	0.55
13:M:14:ARG:NH1	13:M:74:ILE:O	2.39	0.55
15:O:42:LEU:HD22	15:O:71:LEU:HB2	1.88	0.55
21:U:1:MET:HB2	53:3:135:C:N3	2.21	0.55
33:i:53:PRO:HD2	33:i:77:VAL:HG21	1.87	0.55
47:w:35:ARG:HH21	51:1:2355:G:H1'	1.69	0.55
51:1:310:A:C2'	51:1:311:A:H5''	2.36	0.55
51:1:683:U:H3	51:1:794:A:H61	1.53	0.55
51:1:1827:U:H2'	51:1:1828:G:H5'	1.88	0.55
51:1:2299:U:H2'	51:1:2300:C:C6	2.42	0.55
51:1:2796:U:H3	51:1:2799:A:H61	1.53	0.55
53:3:593:U:H2'	53:3:594:U:C6	2.41	0.55
10:J:120:HIS:CE1	10:J:121:ASN:HD21	2.23	0.55
30:e:46:LYS:NZ	30:e:82:TYR:OH	2.40	0.55
40:p:15:ASP:N	40:p:15:ASP:OD1	2.39	0.55
51:1:146:A:H2'	51:1:147:C:C6	2.42	0.55
51:1:1191:G:H2'	51:1:1192:G:H8	1.71	0.55
58:B1:833:GLU:HB2	58:B1:1242:ARG:NH1	2.22	0.55
7:G:59:ILE:HG12	7:G:62:ARG:HH21	1.71	0.55
12:L:91:ARG:O	12:L:95:ARG:CG	2.55	0.55
22:V:64:ARG:HB2	53:3:130:A:H8	1.70	0.55
28:c:118:PHE:HD2	51:1:1654:A:C2	2.24	0.55
30:e:56:LEU:HG	30:e:59:ILE:HD12	1.89	0.55
41:q:68:ALA:HB1	41:q:73:ILE:HG13	1.87	0.55
51:1:1257:C:O5'	51:1:1257:C:H6	1.90	0.55
51:1:1783:A:N1	51:1:2587:A:H2'	2.21	0.55
51:1:2563:U:H2'	51:1:2564:A:H5''	1.88	0.55
53:3:596:A:H2'	53:3:597:G:O4'	2.07	0.55
59:B2:103:VAL:HB	59:B2:114:VAL:HG11	1.89	0.55
65:0:535:GLU:HB2	65:0:575:GLY:HA2	1.88	0.55
1:A:28:VAL:HG23	30:e:139:GLU:HA	1.88	0.55
3:C:21:THR:HG21	51:1:2419:U:H5''	1.89	0.55
8:H:120:THR:HG23	8:H:188:ALA:HB2	1.87	0.55
12:L:32:ASP:HA	53:3:1350:A:O2'	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:84:ILE:HD11	13:M:86:LYS:HG2	1.89	0.55
38:n:64:ARG:O	38:n:68:ALA:N	2.40	0.55
51:1:2008:C:H2'	51:1:2009:A:C8	2.41	0.55
53:3:1348:U:H2'	53:3:1349:A:H5'	1.87	0.55
58:B1:799:ARG:HG2	58:B1:1325:PHE:HZ	1.72	0.55
15:O:85:ASP:HB3	58:B1:87:LYS:HE3	1.89	0.55
21:U:5:ARG:NH2	21:U:23:ASP:O	2.40	0.55
31:f:3:VAL:HG11	31:f:65:GLY:HA2	1.89	0.55
53:3:1127:G:H2'	53:3:1128:C:C6	2.41	0.55
6:F:10:LEU:HD21	51:1:2477:U:C5	2.42	0.55
29:d:44:ARG:HH12	51:1:1248:G:P	2.30	0.55
41:q:5:ARG:NH2	51:1:1251:C:OP2	2.40	0.55
51:1:155:A:H2'	51:1:156:A:H8	1.72	0.55
51:1:1403:A:H2'	51:1:1404:C:C6	2.42	0.55
51:1:2726:A:O2'	51:1:2727:A:H5'	2.06	0.55
53:3:46:G:H2'	53:3:366:A:H62	1.72	0.55
53:3:357:G:OP1	53:3:367:U:H5''	2.07	0.55
58:B1:144:TYR:HE1	58:B1:162:GLU:CD	2.14	0.55
59:B2:839:VAL:HG12	59:B2:1049:ILE:HG12	1.87	0.55
65:0:192:ASN:HB3	65:0:203:GLU:HB2	1.87	0.55
26:Z:13:VAL:HG13	26:Z:15:LEU:HG	1.89	0.55
27:b:140:VAL:HG12	27:b:191:LEU:HA	1.89	0.55
41:q:24:TYR:OH	51:1:2020:A:O3'	2.25	0.55
51:1:286:U:H2'	51:1:287:G:H8	1.72	0.55
51:1:305:C:H2'	51:1:306:U:C6	2.42	0.55
51:1:614:A:H5'	51:1:615:U:OP1	2.06	0.55
51:1:2682:A:H61	51:1:2728:U:H1'	1.72	0.55
53:3:459:A:H2'	53:3:460:A:C8	2.42	0.55
53:3:1213:A:O2'	53:3:1214:C:H2'	2.06	0.55
58:B1:145:VAL:HG23	58:B1:159:ILE:HG22	1.89	0.55
64:a:189:LEU:HA	64:a:192:LEU:HG	1.88	0.55
65:0:225:SER:O	65:0:255:ARG:NH1	2.39	0.55
65:0:427:ASP:O	65:0:431:MET:N	2.39	0.55
12:L:111:GLY:HA2	12:L:118:ARG:HG2	1.88	0.55
15:O:43:PRO:HA	53:3:1151:A:H5'	1.89	0.55
26:Z:66:ARG:NH1	53:3:1098:C:O2'	2.38	0.55
34:j:6:ALA:HB3	34:j:48:VAL:HG11	1.89	0.55
36:l:29:LYS:HG2	51:1:566:U:OP1	2.07	0.55
39:o:2:ASP:N	52:2:59:A:HO2'	2.04	0.55
51:1:310:A:H2'	51:1:311:A:H5''	1.89	0.55
51:1:605:G:H21	51:1:658:U:H5'	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1343:G:H1'	51:1:1597:A:C4	2.42	0.55
51:1:2128:G:H5'	64:a:218:MET:HE1	1.89	0.55
53:3:539:A:H2'	53:3:540:G:H8	1.72	0.55
65:0:92:HIS:HD2	65:0:464:LEU:HD21	1.71	0.55
10:J:16:ALA:HB3	10:J:35:LEU:H	1.71	0.54
16:P:122:PRO:HG2	26:Z:34:ARG:HA	1.89	0.54
27:b:204:LEU:HD21	27:b:213:ARG:HH21	1.72	0.54
27:b:257:ARG:HD3	51:1:1799:G:OP1	2.07	0.54
33:i:38:CYS:O	33:i:42:ASN:ND2	2.40	0.54
42:r:76:LYS:NZ	42:r:85:LYS:O	2.40	0.54
51:1:171:U:H2'	51:1:172:A:C8	2.42	0.54
51:1:486:C:H42	51:1:494:G:H1	1.56	0.54
51:1:2048:G:C2'	51:1:2049:G:H5''	2.37	0.54
51:1:2496:C:C2'	51:1:2497:A:H5'	2.36	0.54
53:3:350:G:O2'	53:3:351:G:H5'	2.08	0.54
53:3:1096:C:H2'	53:3:1097:C:C6	2.41	0.54
53:3:1414:U:H2'	53:3:1415:G:C8	2.42	0.54
59:B2:29:SER:O	59:B2:33:ASP:HB2	2.08	0.54
65:0:103:MET:HB3	65:0:135:VAL:HG21	1.89	0.54
3:C:40:PRO:HG3	51:1:2348:U:H4'	1.88	0.54
13:M:9:MET:HB2	13:M:32:LYS:HE2	1.88	0.54
38:n:2:ARG:NH1	51:1:2820:A:OP2	2.40	0.54
44:t:14:PRO:HA	44:t:32:LEU:HA	1.90	0.54
51:1:490:C:H5'	51:1:491:G:OP2	2.06	0.54
51:1:1040:A:H2'	51:1:1041:G:H8	1.72	0.54
51:1:1697:G:C3'	51:1:1698:A:H5''	2.36	0.54
51:1:2813:A:H2'	51:1:2814:A:C8	2.42	0.54
53:3:1091:U:H2'	53:3:1093:A:OP2	2.07	0.54
53:3:1105:A:H2'	53:3:1106:G:C8	2.43	0.54
53:3:1347:G:H22	53:3:1373:G:H2'	1.73	0.54
59:B2:1117:LEU:HD12	59:B2:1195:ILE:HG12	1.90	0.54
8:H:21:TRP:HD1	8:H:57:GLU:HA	1.71	0.54
9:I:96:ARG:NH2	9:I:98:ASP:OD2	2.39	0.54
27:b:206:LYS:HE3	27:b:209:ALA:HB2	1.89	0.54
29:d:147:LEU:HB3	29:d:186:VAL:HG12	1.88	0.54
48:x:2:ARG:HG2	48:x:32:LEU:CD1	2.37	0.54
51:1:207:A:H2'	51:1:208:C:O4'	2.07	0.54
53:3:866:C:C4	53:3:867:G:H1'	2.41	0.54
53:3:1042:A:H2'	53:3:1043:G:C4'	2.38	0.54
59:B2:633:LEU:HD13	59:B2:644:LEU:HD23	1.89	0.54
6:F:5:ALA:HB3	51:1:2466:C:H5'	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:46:GLN:NE2	11:K:47:LEU:O	2.39	0.54
17:Q:23:LEU:HB2	17:Q:29:LYS:HD3	1.90	0.54
33:i:11:GLN:HB2	33:i:56:VAL:HG22	1.88	0.54
39:o:33:ARG:HD3	52:2:52:A:N7	2.22	0.54
51:1:130:C:H2'	51:1:131:A:O4'	2.07	0.54
51:1:1063:G:OP2	51:1:1070:A:H4'	2.07	0.54
52:2:78:A:H62	52:2:98:G:N2	1.97	0.54
19:S:9:GLU:HA	19:S:12:ARG:HB2	1.89	0.54
30:e:127:TYR:HB3	30:e:155:ILE:HG13	1.89	0.54
38:n:11:ASN:N	51:1:1653:G:O6	2.37	0.54
38:n:98:LEU:HB2	38:n:112:TYR:HB2	1.88	0.54
51:1:471:A:H2'	51:1:472:A:O4'	2.08	0.54
51:1:1024:G:H3'	51:1:1025:G:C5'	2.37	0.54
51:1:1836:C:C2'	51:1:1837:C:H5'	2.37	0.54
53:3:874:G:H2'	53:3:875:U:C6	2.42	0.54
53:3:1042:A:H2'	53:3:1043:G:O4'	2.08	0.54
59:B2:811:ASN:HA	59:B2:815:SER:HB2	1.90	0.54
8:H:26:LYS:HE3	53:3:1256:A:H3'	1.89	0.54
51:1:1192:G:O2'	51:1:1193:G:H5'	2.08	0.54
51:1:1614:A:H2'	51:1:1615:C:H5'	1.89	0.54
51:1:1791:A:O2'	51:1:1792:G:H5'	2.07	0.54
51:1:1809:A:H2'	51:1:1810:A:C8	2.42	0.54
53:3:1390:U:H2'	53:3:1391:U:C6	2.42	0.54
58:B1:39:LYS:O	58:B1:273:ILE:HG23	2.08	0.54
58:B1:508:LEU:HD22	59:B2:1101:LEU:HD21	1.88	0.54
59:B2:985:GLU:HB3	59:B2:988:LYS:HB2	1.88	0.54
65:0:416:ILE:N	65:0:460:GLY:O	2.40	0.54
9:I:141:VAL:HA	9:I:180:THR:HA	1.88	0.54
10:J:153:ALA:HB1	10:J:160:VAL:HA	1.90	0.54
21:U:16:PHE:CE2	53:3:625:U:H5''	2.42	0.54
29:d:70:SER:C	51:1:674:G:H5''	2.33	0.54
30:e:120:SER:HA	51:1:2303:G:H4'	1.89	0.54
51:1:121:G:H4'	51:1:149:A:H5'	1.90	0.54
51:1:142:A:H2'	51:1:143:C:C6	2.42	0.54
51:1:413:C:N4	51:1:2410:G:H1	1.96	0.54
51:1:1126:A:H4'	51:1:1127:A:C5'	2.38	0.54
51:1:1652:A:H2'	51:1:1653:G:O4'	2.07	0.54
58:B1:58:CYS:SG	58:B1:59:ALA:N	2.80	0.54
58:B1:1175:LEU:HD22	58:B1:1190:ILE:HD11	1.88	0.54
25:Y:14:GLU:O	25:Y:18:LYS:NZ	2.41	0.54
51:1:1659:G:H2'	51:1:1660:G:O4'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1889:A:H2'	51:1:1890:A:H8	1.73	0.54
53:3:1325:C:H2'	53:3:1326:U:C6	2.42	0.54
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE21	1.68	0.54
65:0:393:THR:OG1	65:0:408:ARG:NH1	2.40	0.54
65:0:525:LEU:HA	65:0:574:MET:HA	1.89	0.54
65:0:617:MET:HG2	65:0:684:PHE:HD1	1.72	0.54
9:I:205:LYS:HE2	53:3:8:A:C6	2.42	0.54
13:M:105:THR:HG22	13:M:107:LYS:H	1.73	0.54
16:P:99:LEU:O	16:P:103:GLY:N	2.38	0.54
23:W:49:LYS:HB2	53:3:835:U:OP1	2.08	0.54
27:b:106:PRO:HG2	27:b:109:LEU:HB2	1.90	0.54
28:c:146:ILE:O	28:c:159:LYS:NZ	2.41	0.54
45:u:65:GLN:OE1	51:1:328:U:H4'	2.07	0.54
51:1:851:C:H2'	51:1:852:U:C6	2.42	0.54
51:1:1319:C:H2'	51:1:1320:C:H6	1.73	0.54
53:3:1234:C:H1'	53:3:1364:U:O2	2.08	0.54
53:3:1420:U:H3	53:3:1480:A:H2	1.54	0.54
57:A2:29:GLU:HG3	57:A2:200:LYS:HG3	1.88	0.54
58:B1:395:LYS:HZ2	58:B1:399:LYS:CE	2.21	0.54
59:B2:684:ASN:OD1	59:B2:687:ARG:NH2	2.41	0.54
64:a:194:VAL:HA	64:a:197:LYS:HB2	1.89	0.54
14:N:104:THR:HG22	53:3:1180:A:OP1	2.08	0.54
32:g:29:PHE:HB2	51:1:2198:A:C2	2.43	0.54
33:i:9:LYS:HD2	51:1:1059:G:OP2	2.07	0.54
39:o:15:ARG:NH2	39:o:95:SER:OG	2.39	0.54
53:3:1013:G:N2	53:3:1015:G:H3'	2.23	0.54
58:B1:814:CYS:SG	58:B1:883:ARG:NH2	2.81	0.54
65:0:171:LEU:HB2	65:0:183:VAL:HB	1.88	0.54
65:0:641:MET:HB3	65:0:657:GLU:HB2	1.90	0.54
8:H:58:ARG:HA	8:H:63:ILE:HA	1.90	0.53
12:L:91:ARG:NE	12:L:91:ARG:HA	2.22	0.53
51:1:737:C:H2'	51:1:738:G:H8	1.72	0.53
51:1:1127:A:C2'	51:1:1128:G:H5''	2.37	0.53
51:1:2375:G:C2'	51:1:2376:A:H5''	2.38	0.53
53:3:401:C:H2'	53:3:402:G:H8	1.73	0.53
53:3:1271:A:C5'	53:3:1314:C:H5''	2.39	0.53
53:3:1399:C:H4'	53:3:1400:C:H3'	1.88	0.53
58:B1:78:LEU:O	58:B1:78:LEU:HD13	2.09	0.53
58:B1:759:ILE:HG23	58:B1:771:GLN:HB3	1.89	0.53
59:B2:243:PRO:HB2	59:B2:274:ILE:HG23	1.90	0.53
65:0:632:ILE:HA	65:0:635:LEU:HB3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:20:ARG:HD2	53:3:831:A:C5'	2.39	0.53
11:K:11:HIS:ND1	11:K:14:GLN:OE1	2.41	0.53
12:L:53:SER:HB2	12:L:55:LYS:HE3	1.90	0.53
27:b:208:GLY:HA2	27:b:211:ARG:HB3	1.89	0.53
29:d:141:MET:HB2	29:d:143:LEU:HD11	1.90	0.53
51:1:231:A:H2'	51:1:232:G:O4'	2.08	0.53
51:1:1905:C:H2'	51:1:1930:G:C8	2.42	0.53
51:1:2092:U:C5	51:1:2199:A:H2	2.26	0.53
51:1:2373:G:H2'	51:1:2374:C:C6	2.43	0.53
53:3:20:U:H2'	53:3:21:G:O4'	2.08	0.53
53:3:690:G:H2'	53:3:691:G:O4'	2.08	0.53
53:3:1084:G:HO2'	53:3:1103:C:H5	1.57	0.53
53:3:1093:A:C6	53:3:1095:U:H1'	2.43	0.53
58:B1:30:ILE:HG21	58:B1:241:VAL:O	2.08	0.53
58:B1:746:LEU:HG	58:B1:758:PRO:HG3	1.90	0.53
60:W0:3:ARG:NH1	60:W0:55:GLU:OE2	2.40	0.53
37:m:127:LYS:HE2	51:1:1030:C:OP2	2.08	0.53
51:1:2125:G:H5'	64:a:39:VAL:C	2.33	0.53
51:1:2155:U:OP1	51:1:2157:G:N2	2.41	0.53
53:3:36:C:H2'	53:3:37:U:H6	1.73	0.53
53:3:112:G:N2	53:3:354:G:H5'	2.02	0.53
53:3:951:G:H2'	53:3:952:U:C6	2.43	0.53
53:3:1507:A:H61	53:3:1528:U:H3	1.56	0.53
58:B1:111:THR:HG22	58:B1:300:GLN:NE2	2.23	0.53
8:H:179:ALA:HB1	8:H:202:PHE:HE1	1.73	0.53
14:N:97:LEU:O	14:N:102:PHE:N	2.39	0.53
24:X:4:LEU:HG	24:X:6:LYS:H	1.72	0.53
38:n:60:VAL:HG12	38:n:64:ARG:HH22	1.73	0.53
51:1:772:C:H5''	51:1:1356:G:H5'	1.90	0.53
51:1:1760:C:H2'	51:1:1761:C:H5'	1.91	0.53
53:3:162:A:H2'	53:3:163:C:H5'	1.88	0.53
53:3:952:U:H2'	53:3:953:G:H8	1.73	0.53
53:3:1073:U:H2'	53:3:1074:G:H8	1.69	0.53
59:B2:360:LEU:HD13	59:B2:378:ARG:HH11	1.72	0.53
64:a:11:ILE:HG13	64:a:219:GLY:HA3	1.91	0.53
10:J:36:THR:OG1	10:J:37:VAL:N	2.38	0.53
10:J:154:ALA:O	10:J:158:LYS:NZ	2.41	0.53
16:P:124:LYS:HA	26:Z:34:ARG:HE	1.73	0.53
22:V:49:ASN:ND2	22:V:51:GLU:OE2	2.42	0.53
51:1:1550:C:H2'	51:1:1551:A:H8	1.73	0.53
51:1:1783:A:C6	51:1:2587:A:C4	2.96	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2516:A:O2'	51:1:2517:C:H5'	2.08	0.53
58:B1:99:ARG:HG3	58:B1:99:ARG:HH11	1.73	0.53
58:B1:800:LEU:HB3	58:B1:920:ALA:HB1	1.89	0.53
65:0:334:THR:OG1	65:0:385:ALA:N	2.40	0.53
8:H:190:THR:HG23	8:H:192:TYR:H	1.73	0.53
17:Q:120:ARG:HG2	53:3:37:U:H5'	1.89	0.53
25:Y:14:GLU:OE2	25:Y:18:LYS:NZ	2.41	0.53
31:f:2:ARG:HG2	51:1:2751:G:C4	2.43	0.53
32:g:25:TYR:HB2	51:1:2093:G:O3'	2.07	0.53
41:q:48:ASP:HA	41:q:51:GLN:HB3	1.89	0.53
51:1:351:C:H2'	51:1:352:A:H8	1.73	0.53
51:1:534:U:H3	51:1:559:G:H1	1.55	0.53
51:1:1433:A:H2'	51:1:1434:A:C1'	2.38	0.53
51:1:1936:A:H2	51:1:1943:U:H3	1.51	0.53
51:1:2048:G:H3'	51:1:2049:G:H5''	1.91	0.53
51:1:2276:G:O2'	51:1:2277:G:H5'	2.09	0.53
51:1:2638:G:H1	51:1:2775:G:H2'	1.74	0.53
53:3:563:A:H4'	53:3:566:G:O2'	2.09	0.53
53:3:1402:C:H2'	53:3:1403:C:O4'	2.08	0.53
58:B1:209:ASN:HA	58:B1:214:ARG:HH21	1.73	0.53
65:0:327:ASP:O	65:0:437:ARG:NH2	2.42	0.53
65:0:446:ARG:HH11	65:0:447:VAL:H	1.54	0.53
5:E:48:MET:SD	5:E:48:MET:N	2.79	0.53
6:F:24:ARG:HE	6:F:36:ARG:HG3	1.73	0.53
7:G:10:LYS:HG2	7:G:211:LEU:HD21	1.89	0.53
7:G:68:PHE:HA	7:G:161:PHE:HB3	1.90	0.53
9:I:13:ARG:NH2	9:I:37:PRO:O	2.42	0.53
12:L:63:VAL:HA	12:L:66:GLU:HG2	1.91	0.53
28:c:23:PRO:HB3	51:1:2682:A:C2	2.43	0.53
34:j:49:ASP:N	34:j:49:ASP:OD1	2.38	0.53
38:n:8:ARG:NH2	38:n:43:GLU:OE1	2.42	0.53
39:o:30:ARG:HG3	39:o:102:ARG:HD2	1.89	0.53
46:v:73:LYS:O	46:v:92:VAL:N	2.41	0.53
49:y:21:LEU:HA	49:y:25:GLN:HB3	1.90	0.53
51:1:351:C:H2'	51:1:352:A:C8	2.44	0.53
51:1:937:C:H2'	51:1:938:G:C8	2.43	0.53
53:3:337:G:H2'	53:3:338:A:H8	1.74	0.53
57:A2:28:LEU:HD22	57:A2:201:LEU:HD23	1.90	0.53
57:A2:100:LEU:HD23	57:A2:115:ILE:HG21	1.89	0.53
4:D:11:LYS:HE2	51:1:770:G:OP2	2.09	0.53
7:G:210:THR:HA	7:G:213:LEU:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:46:HIS:HB2	22:V:70:LYS:HD3	1.91	0.53
28:c:144:GLY:HA2	51:1:2578:G:H1'	1.91	0.53
29:d:63:LYS:HE3	51:1:2060:A:H3'	1.91	0.53
33:i:92:PRO:HB3	33:i:134:SER:HA	1.89	0.53
40:p:19:PHE:HE2	40:p:46:VAL:HG21	1.74	0.53
51:1:838:C:H2'	51:1:839:U:C6	2.44	0.53
51:1:859:G:N2	51:1:916:G:H2'	2.23	0.53
53:3:601:G:H2'	53:3:602:A:C8	2.44	0.53
57:A1:47:LEU:HD23	57:A1:51:MET:HG3	1.89	0.53
58:B1:68:TYR:CA	58:B1:75:TYR:HE2	2.22	0.53
58:B1:832:LYS:HB3	58:B1:1242:ARG:NH1	2.24	0.53
65:0:415:VAL:H	65:0:461:MET:HA	1.73	0.53
10:J:53:ARG:CZ	53:3:1071:C:H5'	2.39	0.53
13:M:9:MET:HE1	13:M:35:ILE:HD13	1.91	0.53
13:M:32:LYS:HA	13:M:35:ILE:HD12	1.90	0.53
14:N:45:MET:HE3	14:N:49:GLN:HA	1.90	0.53
20:T:2:LEU:HD11	20:T:30:LEU:HD11	1.90	0.53
29:d:45:ALA:HB3	51:1:38:A:H4'	1.91	0.53
29:d:68:ALA:HA	51:1:1255:U:C6	2.42	0.53
37:m:27:SER:OG	37:m:66:ARG:NH1	2.42	0.53
38:n:39:PRO:CG	51:1:1651:G:H5'	2.33	0.53
51:1:1303:G:H2'	51:1:1304:A:H8	1.74	0.53
51:1:1592:C:H2'	51:1:1593:A:C8	2.44	0.53
52:2:102:G:H2'	52:2:103:U:O4'	2.08	0.53
53:3:1421:G:H3'	53:3:1422:G:H5''	1.90	0.53
58:B1:785:ASP:O	58:B1:789:LYS:HB2	2.08	0.53
4:D:13:ASN:HB3	51:1:125:A:C4'	2.39	0.53
19:S:8:ARG:HB2	19:S:62:ARG:HH12	1.74	0.53
30:e:33:ILE:HD12	30:e:155:ILE:HG22	1.90	0.53
36:l:29:LYS:HA	51:1:810:U:C5	2.44	0.53
51:1:1656:C:H2'	51:1:1657:U:C6	2.44	0.53
51:1:2124:G:N1	51:1:2175:C:O2	2.42	0.53
51:1:2699:C:H2'	51:1:2700:A:C8	2.44	0.53
53:3:36:C:H2'	53:3:37:U:C6	2.44	0.53
64:a:63:THR:HG21	64:a:195:ALA:HB1	1.90	0.53
25:Y:67:HIS:HD2	25:Y:69:ASN:HB2	1.73	0.52
32:g:2:GLN:NE2	32:g:18:GLN:O	2.40	0.52
36:l:29:LYS:HE3	51:1:566:U:H5''	1.90	0.52
38:n:103:ARG:HB3	38:n:108:ALA:H	1.74	0.52
43:s:4:ILE:HG23	43:s:106:VAL:HG22	1.91	0.52
51:1:1065:U:H3'	51:1:1066:U:H5''	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1655:A:H2'	51:1:1656:C:H5'	1.91	0.52
52:2:33:G:H2'	52:2:34:A:O4'	2.09	0.52
53:3:737:C:H2'	53:3:738:C:H6	1.74	0.52
53:3:1479:C:H2'	53:3:1480:A:O4'	2.09	0.52
65:0:136:PRO:HG2	65:0:287:PRO:HG3	1.90	0.52
7:G:67:LEU:HD11	7:G:157:PRO:HG3	1.91	0.52
14:N:64:ILE:HG21	14:N:78:ILE:HG13	1.91	0.52
17:Q:6:LEU:HD21	17:Q:11:ARG:HH21	1.73	0.52
28:c:15:PHE:HB3	40:p:78:PRO:HD3	1.89	0.52
32:g:2:GLN:HB3	32:g:18:GLN:HB3	1.91	0.52
51:1:533:G:H1	51:1:560:C:H42	1.56	0.52
51:1:2694:G:H2'	51:1:2695:U:O4'	2.09	0.52
53:3:1077:G:N2	53:3:1079:G:H3'	2.24	0.52
58:B1:201:LEU:HD12	58:B1:224:LEU:HD12	1.92	0.52
14:N:11:ARG:HH11	14:N:105:ARG:HH12	1.57	0.52
33:i:101:SER:OG	33:i:102:ARG:N	2.42	0.52
42:r:29:THR:HA	42:r:63:VAL:HG23	1.91	0.52
42:r:77:PHE:HD1	42:r:84:ARG:HB3	1.73	0.52
49:y:44:LYS:HE2	49:y:48:ARG:HG3	1.90	0.52
51:1:803:U:O2'	51:1:804:A:H5'	2.09	0.52
51:1:1229:C:H2'	51:1:1230:A:H8	1.74	0.52
51:1:1352:U:O2'	51:1:1353:A:H5'	2.08	0.52
51:1:1674:G:N2	51:1:1677:A:H61	2.06	0.52
53:3:369:G:H22	53:3:393:A:H1'	1.75	0.52
53:3:1274:A:C2'	53:3:1275:A:H5''	2.39	0.52
58:B1:205:LEU:HG	58:B1:217:LEU:HB3	1.90	0.52
58:B1:850:LYS:HB2	58:B1:857:LEU:HB2	1.91	0.52
65:0:223:ILE:HG13	65:0:237:TYR:HE1	1.73	0.52
8:H:18:ASN:HA	8:H:55:VAL:HG22	1.91	0.52
18:R:89:ARG:NH2	18:R:95:PRO:O	2.34	0.52
19:S:82:LYS:HA	19:S:85:GLU:HB2	1.92	0.52
21:U:1:MET:SD	21:U:24:SER:OG	2.64	0.52
29:d:133:LEU:O	29:d:136:GLN:NE2	2.40	0.52
36:l:85:VAL:HG22	36:l:86:GLU:HG2	1.92	0.52
51:1:133:U:H3	51:1:146:A:H61	1.57	0.52
53:3:67:C:H2'	53:3:68:G:C8	2.44	0.52
53:3:224:U:H2'	53:3:225:C:C6	2.44	0.52
53:3:722:G:H1	53:3:733:G:H1	1.56	0.52
58:B1:290:ILE:HG21	62:NG:93:ILE:O	2.09	0.52
15:O:15:HIS:CD2	53:3:1152:A:H5'	2.44	0.52
16:P:87:GLY:O	16:P:92:ARG:NH1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:11:VAL:HG23	22:V:55:GLY:H	1.74	0.52
35:k:21:CYS:HA	35:k:41:ILE:HA	1.92	0.52
35:k:64:ARG:O	35:k:83:ALA:N	2.42	0.52
38:n:32:GLU:HG2	38:n:115:LEU:HD13	1.92	0.52
39:o:29:HIS:HB3	39:o:36:TYR:HD2	1.74	0.52
51:1:958:U:H2'	52:2:89:U:C1'	2.39	0.52
51:1:1361:G:H2'	51:1:1362:C:H6	1.74	0.52
51:1:2402:U:O2'	51:1:2403:C:H5''	2.09	0.52
53:3:299:G:N2	53:3:565:U:H3	2.06	0.52
53:3:358:U:H2'	53:3:359:G:C8	2.44	0.52
53:3:1064:G:O3'	53:3:1065:U:H4'	2.09	0.52
53:3:1169:A:H2'	53:3:1170:A:O4'	2.09	0.52
59:B2:628:HIS:HB3	59:B2:647:ARG:HH21	1.74	0.52
30:e:23:SER:HB3	30:e:26:GLN:HB2	1.92	0.52
51:1:25:U:H2'	51:1:26:G:O4'	2.10	0.52
51:1:203:A:H3'	51:1:204:A:C5'	2.39	0.52
51:1:1536:C:H4'	51:1:1537:G:C2	2.44	0.52
51:1:1635:A:H2	51:1:1761:C:O2'	1.92	0.52
51:1:1903:G:C2	51:1:1904:G:C8	2.98	0.52
51:1:2061:G:H8	51:1:2501:C:H4'	1.73	0.52
51:1:2345:G:N3	51:1:2381:A:H2'	2.25	0.52
52:2:30:C:C2'	52:2:31:C:H5'	2.40	0.52
53:3:1406:U:H2'	53:3:1407:C:O4'	2.10	0.52
65:0:217:GLU:O	65:0:220:GLN:NE2	2.41	0.52
65:0:614:GLU:CD	65:0:659:PRO:HB3	2.34	0.52
12:L:12:LEU:HD13	53:3:1374:A:OP1	2.09	0.52
12:L:92:PRO:HA	12:L:95:ARG:CG	2.38	0.52
21:U:55:ASP:OD1	21:U:55:ASP:N	2.41	0.52
27:b:7:PRO:HB3	27:b:13:ARG:HA	1.92	0.52
27:b:36:ASN:HB3	27:b:38:LYS:HG2	1.91	0.52
51:1:1841:U:H2'	51:1:1842:G:H8	1.73	0.52
51:1:1864:U:H5''	51:1:2410:G:O2'	2.10	0.52
51:1:2124:G:HO2'	64:a:41:SER:CB	2.21	0.52
51:1:2507:C:H6	51:1:2507:C:O5'	1.93	0.52
53:3:90:C:H2'	53:3:91:U:C6	2.45	0.52
53:3:977:A:H2'	53:3:977:A:N3	2.25	0.52
57:A1:205:MET:HE3	57:A1:213:PRO:HB3	1.91	0.52
57:A2:43:LEU:HD13	57:A2:217:ILE:HD11	1.90	0.52
58:B1:144:TYR:CE1	58:B1:162:GLU:CD	2.88	0.52
58:B1:975:ILE:HD11	58:B1:1003:LEU:HD11	1.91	0.52
65:0:53:MET:O	65:0:57:GLN:NE2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:0:107:ASP:OD1	65:0:107:ASP:N	2.40	0.52
8:H:181:ILE:HD11	8:H:200:TRP:HB3	1.92	0.52
11:K:47:LEU:HD21	11:K:55:HIS:HA	1.92	0.52
32:g:94:ILE:HD12	32:g:99:ILE:HD13	1.91	0.52
34:j:135:GLN:HE22	51:1:7:G:H1'	1.75	0.52
43:s:40:ASN:OD1	43:s:40:ASN:N	2.40	0.52
51:1:155:A:H2'	51:1:156:A:C8	2.44	0.52
51:1:532:A:H2'	51:1:532:A:N3	2.24	0.52
51:1:1357:C:H42	51:1:1374:G:H1	1.57	0.52
53:3:153:C:H2'	53:3:154:U:C4'	2.39	0.52
64:a:50:ILE:HG12	64:a:169:GLY:HA2	1.90	0.52
14:N:122:ARG:NH1	53:3:1350:A:OP1	2.43	0.52
28:c:59:ARG:O	28:c:59:ARG:NH2	2.37	0.52
29:d:1:MET:N	29:d:14:VAL:O	2.35	0.52
36:l:9:ALA:HB3	36:l:12:SER:HB3	1.91	0.52
41:q:57:ARG:NH2	51:1:1154:G:OP2	2.43	0.52
51:1:277:G:H4'	51:1:278:A:C8	2.44	0.52
51:1:2272:U:H5''	51:1:2273:A:OP1	2.10	0.52
51:1:2577:A:H2'	51:1:2614:A:H61	1.75	0.52
53:3:884:U:OP2	53:3:884:U:H6	1.92	0.52
53:3:1366:C:H2'	53:3:1367:C:H6	1.72	0.52
58:B1:99:ARG:HA	58:B1:248:ASP:HB2	1.92	0.52
59:B2:125:GLY:HA2	59:B2:499:SER:HB2	1.92	0.52
65:0:473:MET:HA	65:0:477:PHE:HB2	1.91	0.52
14:N:114:LYS:HE3	53:3:1188:A:P	2.49	0.52
39:o:110:ALA:HB1	39:o:115:LEU:HD12	1.92	0.52
51:1:1332:G:N3	51:1:1332:G:H5'	2.25	0.52
51:1:1409:U:H2'	51:1:1410:G:C8	2.45	0.52
51:1:1954:G:H1	51:1:1986:C:H5''	1.75	0.52
51:1:2660:A:OP1	65:0:675:LYS:HD2	2.10	0.52
53:3:148:G:H1	53:3:174:A:H61	1.58	0.52
53:3:174:A:C2'	53:3:175:C:H5'	2.40	0.52
58:B1:215:LYS:HA	58:B1:218:THR:HG22	1.92	0.52
59:B2:255:ILE:HB	59:B2:263:VAL:HB	1.92	0.52
8:H:9:ILE:HG13	8:H:177:LEU:HD21	1.91	0.51
10:J:133:ILE:HD11	53:3:1079:G:H5'	1.92	0.51
14:N:35:GLU:HA	14:N:39:GLY:HA3	1.92	0.51
17:Q:28:GLN:HB2	53:3:363:A:H1'	1.93	0.51
17:Q:45:ASN:OD1	17:Q:45:ASN:N	2.44	0.51
51:1:1082:U:H3	51:1:1086:A:H2	1.56	0.51
51:1:1767:G:O5'	51:1:1767:G:H8	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2656:U:H2'	51:1:2657:A:H8	1.75	0.51
53:3:19:A:H1'	53:3:864:A:C2	2.45	0.51
53:3:218:U:H2'	53:3:219:U:O4'	2.09	0.51
53:3:437:U:H2'	53:3:438:U:H5'	1.91	0.51
53:3:1485:U:O2'	53:3:1486:G:H5'	2.10	0.51
58:B1:112:ALA:HA	58:B1:238:ILE:HA	1.91	0.51
59:B2:974:ARG:HD2	59:B2:1014:LEU:HD21	1.92	0.51
62:NG:161:SER:HA	62:NG:170:PRO:HA	1.93	0.51
27:b:231:HIS:ND1	51:1:1826:G:OP1	2.38	0.51
28:c:161:MET:HE1	51:1:2050:C:H1'	1.91	0.51
30:e:117:SER:HB3	30:e:177:ARG:HH21	1.76	0.51
51:1:44:A:H2'	51:1:45:G:H5'	1.93	0.51
51:1:1470:A:H61	51:1:1521:G:H1'	1.75	0.51
53:3:731:G:O2'	53:3:732:C:H5'	2.10	0.51
53:3:1239:A:H5''	53:3:1240:U:C5	2.44	0.51
53:3:1496:C:H2'	53:3:1497:G:O4'	2.10	0.51
57:A1:100:LEU:HD21	57:A1:121:VAL:HG11	1.90	0.51
65:0:192:ASN:ND2	65:0:203:GLU:OE1	2.43	0.51
5:E:38:LYS:HG3	5:E:41:ARG:HH22	1.75	0.51
9:I:18:LEU:HB3	9:I:20:LEU:HD22	1.91	0.51
9:I:160:LEU:HD21	9:I:164:ARG:HH21	1.75	0.51
13:M:16:GLY:O	13:M:64:TYR:OH	2.28	0.51
38:n:64:ARG:HD3	51:1:2706:A:O2'	2.10	0.51
51:1:526:A:N6	51:1:2626:C:H4'	2.25	0.51
51:1:543:G:H3'	51:1:544:C:H5''	1.92	0.51
51:1:1187:G:O5'	51:1:1187:G:H8	1.93	0.51
51:1:1268:A:H2'	51:1:1269:A:H8	1.74	0.51
51:1:2248:C:H3'	51:1:2249:U:C6	2.46	0.51
52:2:24:G:H4'	52:2:25:U:H5	1.73	0.51
53:3:265:G:H2'	53:3:267:C:H5	1.75	0.51
53:3:1225:A:H2'	53:3:1225:A:N3	2.25	0.51
58:B1:412:LEU:HD23	58:B1:416:ILE:HG13	1.92	0.51
59:B2:246:LEU:HB3	59:B2:269:ILE:HD13	1.91	0.51
59:B2:786:GLY:N	59:B2:789:THR:OG1	2.41	0.51
1:A:26:SER:OG	30:e:139:GLU:OE2	2.28	0.51
9:I:24:VAL:HG12	53:3:409:U:H5''	1.92	0.51
19:S:7:ALA:HB1	53:3:994:A:O2'	2.09	0.51
29:d:67:ARG:O	51:1:1255:U:H5	1.93	0.51
30:e:32:LYS:O	30:e:156:THR:OG1	2.27	0.51
51:1:12:U:H2'	51:1:13:A:H5'	1.91	0.51
51:1:1710:G:H2'	51:1:1711:A:H8	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2022:U:O2'	51:1:2617:U:H5'	2.10	0.51
51:1:2082:A:H2'	51:1:2083:G:O4'	2.10	0.51
53:3:49:U:O2'	53:3:50:A:H2'	2.10	0.51
53:3:955:U:H2'	53:3:956:U:H6	1.74	0.51
59:B2:524:ILE:HG21	59:B2:708:VAL:HG13	1.92	0.51
65:0:295:ILE:HG13	65:0:309:ARG:HB2	1.91	0.51
2:B:54:ILE:HG13	2:B:56:LYS:H	1.76	0.51
24:X:35:ARG:HB2	53:3:1320:C:N4	2.25	0.51
51:1:745:G:H2'	51:1:746:U:O4'	2.09	0.51
51:1:755:U:H2'	51:1:756:A:H8	1.75	0.51
51:1:1333:G:H2'	51:1:1334:G:H8	1.75	0.51
51:1:1505:A:H2'	51:1:1506:U:O4'	2.10	0.51
51:1:1889:A:H2'	51:1:1890:A:O4'	2.10	0.51
51:1:2177:C:O2	64:a:172:HIS:CE1	2.61	0.51
51:1:2372:U:H2'	51:1:2373:G:C8	2.45	0.51
51:1:2415:G:H2'	51:1:2416:C:H6	1.75	0.51
53:3:515:G:O2'	53:3:516:U:H5'	2.10	0.51
57:A2:140:ILE:HD12	57:A2:142:MET:HE3	1.92	0.51
58:B1:375:GLU:HG2	59:B2:1245:ALA:O	2.10	0.51
9:I:146:GLU:HA	9:I:149:LYS:HE2	1.91	0.51
12:L:14:ASP:OD1	12:L:43:TYR:OH	2.24	0.51
16:P:17:ASP:N	16:P:17:ASP:OD1	2.42	0.51
19:S:78:LEU:HD13	19:S:82:LYS:HB3	1.92	0.51
32:g:22:LYS:HB2	51:1:2094:A:OP1	2.11	0.51
51:1:243:U:O2'	51:1:244:A:H5'	2.11	0.51
51:1:376:G:H2'	51:1:377:G:H8	1.74	0.51
51:1:622:G:O2'	51:1:623:C:H5'	2.10	0.51
51:1:1394:U:H4'	51:1:1603:A:H4'	1.92	0.51
51:1:1951:U:C2	51:1:1953:A:OP2	2.63	0.51
51:1:2489:U:H2'	51:1:2490:G:O4'	2.11	0.51
53:3:135:C:H2'	53:3:136:C:H5'	1.92	0.51
53:3:1105:A:H2'	53:3:1106:G:H8	1.74	0.51
58:B1:633:ALA:HB2	59:B2:808:ASN:N	2.19	0.51
8:H:38:VAL:O	8:H:42:LEU:N	2.43	0.51
13:M:11:THR:OG1	53:3:876:C:H1'	2.10	0.51
15:O:59:LYS:HE3	53:3:972:C:C5'	2.41	0.51
28:c:177:VAL:HA	28:c:189:VAL:HA	1.93	0.51
41:q:23:TYR:HD1	51:1:533:G:H5'	1.75	0.51
51:1:178:G:O2'	51:1:179:C:H5'	2.10	0.51
51:1:1210:G:P	51:1:1212:G:H5'	2.51	0.51
51:1:1599:U:H2'	51:1:1600:C:H6	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2545:G:H2'	51:1:2546:U:O4'	2.11	0.51
53:3:207:C:C3'	53:3:208:U:H5''	2.40	0.51
53:3:302:G:H2'	53:3:303:A:H8	1.74	0.51
53:3:410:G:H21	53:3:432:A:H62	1.57	0.51
53:3:1251:A:H2'	53:3:1252:A:C8	2.46	0.51
58:B1:275:ARG:HH12	58:B1:278:ARG:NH1	2.09	0.51
58:B1:1179:PRO:HD2	58:B1:1184:ASP:HA	1.93	0.51
28:c:27:ILE:HD11	28:c:187:LEU:HD23	1.93	0.51
31:f:126:THR:OG1	31:f:127:GLN:N	2.44	0.51
31:f:151:ARG:HG3	31:f:160:GLY:HA2	1.92	0.51
40:p:93:LYS:HE2	51:1:1754:A:OP1	2.11	0.51
42:r:61:ALA:HB1	42:r:96:VAL:HB	1.92	0.51
51:1:3:U:H2'	51:1:4:U:C6	2.45	0.51
51:1:216:A:H2'	51:1:217:A:O4'	2.11	0.51
51:1:548:G:H2'	51:1:549:G:O4'	2.10	0.51
57:A1:16:ILE:HG23	57:A1:26:VAL:HG22	1.91	0.51
58:B1:437:PHE:HZ	58:B1:453:VAL:HG11	1.76	0.51
58:B1:972:LYS:HD2	58:B1:1004:ALA:HA	1.93	0.51
59:B2:714:VAL:HB	59:B2:787:PRO:HD2	1.92	0.51
14:N:33:SER:OG	14:N:34:LEU:N	2.43	0.51
29:d:58:LYS:HE2	51:1:676:A:OP1	2.11	0.51
32:g:131:SER:OG	32:g:140:ALA:O	2.28	0.51
51:1:216:A:O2'	51:1:217:A:H5'	2.11	0.51
51:1:1917:U:O2'	51:1:1918:A:H5'	2.11	0.51
51:1:1963:U:C2'	51:1:1964:G:H5''	2.41	0.51
51:1:2417:C:H2'	51:1:2418:A:H8	1.75	0.51
53:3:379:C:H2'	53:3:380:G:O4'	2.10	0.51
53:3:574:A:N3	53:3:883:C:H1'	2.25	0.51
53:3:1230:C:H5'	63:6:30:G:H5''	1.93	0.51
58:B1:390:LEU:N	58:B1:390:LEU:CD1	2.73	0.51
65:0:194:ASN:OD1	65:0:200:VAL:N	2.44	0.51
8:H:67:ILE:N	8:H:101:ASN:O	2.42	0.51
15:O:8:ILE:HB	15:O:74:VAL:HB	1.91	0.51
34:j:69:ARG:NH1	34:j:90:GLU:OE2	2.38	0.51
36:l:51:GLU:HG3	36:l:56:PRO:HB3	1.93	0.51
40:p:102:ARG:HH22	51:1:1755:A:P	2.34	0.51
51:1:866:A:H61	51:1:913:U:H1'	1.76	0.51
51:1:1410:G:O2'	51:1:1411:U:H5'	2.10	0.51
51:1:1977:A:H2'	51:1:1978:A:O4'	2.12	0.51
51:1:2372:U:H2'	51:1:2373:G:H8	1.76	0.51
51:1:2616:C:H2'	51:1:2617:U:H6	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:2:29:A:H2'	52:2:30:C:O4'	2.10	0.51
53:3:793:U:O2	53:3:1516:G:H4'	2.11	0.51
58:B1:749:LYS:HB3	58:B1:755:ILE:HD11	1.93	0.51
11:K:68:GLN:NE2	53:3:738:C:O3'	2.44	0.50
15:O:37:ARG:HG2	15:O:77:VAL:HB	1.93	0.50
16:P:22:ILE:HD13	16:P:83:VAL:HG13	1.93	0.50
18:R:89:ARG:HB3	18:R:96:VAL:HG22	1.93	0.50
26:Z:16:ARG:HG3	26:Z:19:LYS:HB2	1.93	0.50
33:i:113:ALA:HB2	33:i:121:ILE:HD11	1.93	0.50
39:o:100:HIS:O	39:o:104:GLN:NE2	2.44	0.50
44:t:61:LEU:HD21	44:t:82:LYS:HD2	1.92	0.50
48:x:14:GLY:HA3	48:x:28:PHE:HE1	1.76	0.50
51:1:233:A:H2'	51:1:234:U:H5'	1.92	0.50
51:1:286:U:H2'	51:1:287:G:C8	2.46	0.50
51:1:402:A:H2'	51:1:403:U:O4'	2.11	0.50
51:1:838:C:H2'	51:1:839:U:H6	1.75	0.50
51:1:871:U:H2'	51:1:872:U:C6	2.46	0.50
51:1:1597:A:H4'	51:1:1598:A:H8	1.76	0.50
51:1:2850:A:H2'	51:1:2851:A:O4'	2.10	0.50
53:3:284:C:O2'	53:3:285:C:H5'	2.11	0.50
53:3:554:A:H2'	53:3:555:U:H5'	1.93	0.50
53:3:894:G:H2'	53:3:895:G:H8	1.75	0.50
53:3:1271:A:H5'	53:3:1314:C:H5''	1.92	0.50
65:0:141:VAL:HB	65:0:266:CYS:HA	1.92	0.50
14:N:118:ARG:NH2	53:3:1366:C:OP1	2.44	0.50
32:g:8:LYS:NZ	32:g:11:ASN:O	2.44	0.50
33:i:4:VAL:HB	51:1:1055:G:OP2	2.10	0.50
51:1:1439:A:H2'	51:1:1440:U:H5'	1.94	0.50
51:1:1550:C:H2'	51:1:1551:A:C8	2.46	0.50
51:1:1794:A:H1'	51:1:1900:A:C2	2.46	0.50
51:1:2549:G:H2'	51:1:2550:G:H8	1.76	0.50
58:B1:505:ASP:OD2	59:B2:812:PHE:HA	2.11	0.50
59:B2:400:VAL:HG11	59:B2:452:ARG:HD2	1.93	0.50
59:B2:400:VAL:HG21	59:B2:452:ARG:HE	1.76	0.50
59:B2:411:ARG:NH2	59:B2:427:ASP:OD2	2.44	0.50
27:b:31:PRO:HG2	27:b:32:LEU:HD12	1.92	0.50
32:g:50:ARG:O	32:g:55:GLU:N	2.38	0.50
51:1:403:U:O3'	51:1:404:A:H4'	2.11	0.50
51:1:558:U:H2'	51:1:559:G:C8	2.47	0.50
51:1:990:A:N6	51:1:1186:G:H1'	2.27	0.50
51:1:1810:A:H2'	51:1:1811:G:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1937:A:C2'	51:1:1938:A:H5'	2.41	0.50
53:3:162:A:C2'	53:3:163:C:H5'	2.42	0.50
53:3:953:G:H2'	53:3:954:G:O4'	2.12	0.50
53:3:1271:A:H4'	53:3:1314:C:OP1	2.11	0.50
53:3:1400:C:N4	63:6:34:C:H1'	2.26	0.50
55:8:13:DT:OP2	58:B1:791:ALA:CB	2.59	0.50
58:B1:770:LEU:CD1	59:B2:618:GLN:HG3	2.36	0.50
7:G:53:LEU:HD11	7:G:215:ALA:HB1	1.93	0.50
28:c:133:THR:OG1	28:c:134:HIS:N	2.38	0.50
51:1:801:G:H3'	51:1:802:A:H5'	1.92	0.50
51:1:1040:A:H2'	51:1:1041:G:C8	2.47	0.50
51:1:1390:U:O2'	51:1:1391:U:H5'	2.11	0.50
51:1:2358:A:H2'	51:1:2359:C:O4'	2.11	0.50
51:1:2656:U:H5''	65:0:146:ARG:NH2	2.25	0.50
52:2:88:C:H4'	52:2:90:C:N3	2.27	0.50
53:3:599:C:H2'	53:3:600:A:H8	1.77	0.50
53:3:1351:U:H3	53:3:1371:G:H1	1.58	0.50
53:3:1421:G:C2'	53:3:1422:G:H4'	2.40	0.50
53:3:1516:G:H2'	53:3:1518:A:OP2	2.10	0.50
58:B1:1361:THR:OG1	59:B2:1282:GLY:O	2.28	0.50
7:G:187:ASP:OD1	7:G:187:ASP:N	2.42	0.50
12:L:92:PRO:C	12:L:95:ARG:HG3	2.36	0.50
26:Z:27:VAL:HG22	26:Z:31:VAL:HB	1.93	0.50
41:q:10:ARG:NH1	51:1:1216:G:H5''	2.25	0.50
51:1:1473:G:H1	51:1:1518:C:N4	2.00	0.50
51:1:1700:A:H2'	51:1:1701:A:H5'	1.93	0.50
51:1:1783:A:N6	51:1:2587:A:N3	2.59	0.50
51:1:1934:C:H2'	51:1:1935:G:O4'	2.12	0.50
53:3:559:A:H4'	53:3:560:A:H3'	1.94	0.50
53:3:678:U:H2'	53:3:679:C:O4'	2.11	0.50
65:0:70:ALA:HB3	65:0:84:ILE:HB	1.94	0.50
9:I:96:ARG:NE	9:I:132:ALA:O	2.44	0.50
9:I:173:ASP:OD1	9:I:173:ASP:N	2.44	0.50
14:N:62:LEU:HD12	14:N:64:ILE:HD11	1.92	0.50
19:S:75:LYS:HZ1	53:3:1357:A:H5''	1.75	0.50
25:Y:4:LYS:HB3	25:Y:6:ALA:H	1.76	0.50
35:k:71:ARG:HG3	35:k:77:ILE:HD11	1.92	0.50
51:1:375:G:C2'	51:1:376:G:H5'	2.42	0.50
51:1:598:U:H2'	51:1:599:A:H8	1.76	0.50
51:1:704:G:H1'	51:1:726:G:N2	2.27	0.50
51:1:839:U:H2'	51:1:840:C:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2259:U:C5	51:1:2427:C:N4	2.80	0.50
53:3:138:G:H2'	53:3:139:A:C8	2.46	0.50
53:3:650:G:H2'	53:3:651:C:C6	2.47	0.50
53:3:903:G:H2'	53:3:904:U:O4'	2.11	0.50
53:3:945:G:H2'	53:3:945:G:N3	2.27	0.50
58:B1:421:VAL:O	58:B1:436:ALA:HA	2.12	0.50
59:B2:9:LYS:HG2	59:B2:1171:ARG:HH12	1.77	0.50
59:B2:232:ILE:HG12	59:B2:237:LEU:HG	1.93	0.50
59:B2:907:GLY:C	59:B2:909:LYS:N	2.65	0.50
59:B2:1070:HIS:NE2	59:B2:1114:GLU:OE1	2.36	0.50
9:I:131:ILE:HD12	53:3:620:C:C2	2.47	0.50
11:K:17:GLN:O	11:K:21:MET:N	2.44	0.50
15:O:47:GLU:HG3	53:3:1254:A:OP1	2.12	0.50
17:Q:33:CYS:HA	17:Q:54:VAL:HG22	1.94	0.50
28:c:160:LYS:HD2	51:1:2513:A:OP1	2.12	0.50
29:d:195:GLN:HE22	29:d:199:MET:HE2	1.77	0.50
38:n:107:ASN:HD22	51:1:2009:A:H4'	1.74	0.50
42:r:76:LYS:HZ1	42:r:85:LYS:HE2	1.77	0.50
42:r:80:ARG:HD3	51:1:566:U:C5	2.47	0.50
48:x:57:VAL:O	48:x:61:LYS:NZ	2.44	0.50
51:1:1686:C:H2'	51:1:1687:G:O4'	2.12	0.50
51:1:1984:G:H2'	51:1:1985:C:C6	2.47	0.50
51:1:2416:C:H2'	51:1:2417:C:C6	2.47	0.50
53:3:62:U:H2'	53:3:63:C:C6	2.46	0.50
53:3:993:G:N3	53:3:993:G:H2'	2.26	0.50
53:3:1327:C:O2'	53:3:1328:C:H5'	2.12	0.50
59:B2:93:SER:HA	59:B2:128:PRO:HA	1.92	0.50
21:U:5:ARG:NH1	21:U:26:ASN:O	2.43	0.50
24:X:76:THR:HG21	53:3:1221:G:H4'	1.94	0.50
27:b:24:HIS:CD2	27:b:79:ARG:HH21	2.30	0.50
28:c:12:THR:OG1	28:c:13:ARG:N	2.45	0.50
30:e:129:MET:HG3	30:e:153:ILE:HB	1.94	0.50
43:s:16:LYS:HE3	51:1:1266:G:N7	2.27	0.50
45:u:73:ASN:HD22	45:u:76:THR:H	1.60	0.50
51:1:198:C:O2'	51:1:199:A:H5'	2.12	0.50
51:1:227:A:O2'	51:1:228:C:H4'	2.11	0.50
51:1:2549:G:H2'	51:1:2550:G:C8	2.46	0.50
53:3:269:C:H2'	53:3:270:A:H8	1.76	0.50
53:3:812:G:OP1	53:3:903:G:H1'	2.12	0.50
58:B1:683:ILE:HD12	58:B1:754:ILE:HG21	1.93	0.50
65:0:419:ALA:HA	65:0:457:ILE:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:LYS:O	1:A:27:THR:OG1	2.28	0.50
7:G:210:THR:O	7:G:214:GLY:N	2.40	0.50
14:N:26:LYS:HG2	14:N:61:ASP:HB2	1.93	0.50
15:O:19:ASP:OD1	15:O:19:ASP:N	2.45	0.50
34:j:108:MET:HB3	51:1:1006:C:O2'	2.11	0.50
41:q:62:ALA:O	41:q:66:ALA:N	2.43	0.50
43:s:42:LYS:HB2	51:1:2010:G:H5''	1.94	0.50
51:1:123:G:H2'	51:1:124:G:H8	1.77	0.50
51:1:1042:G:H2'	51:1:1043:C:C6	2.46	0.50
51:1:1867:G:H1	51:1:1874:C:N4	2.08	0.50
51:1:2297:A:N1	51:1:2321:U:H5	2.09	0.50
52:2:53:A:C2	52:2:54:G:H1'	2.47	0.50
53:3:184:G:H4'	53:3:224:U:O3'	2.12	0.50
53:3:439:U:H2'	53:3:440:C:O4'	2.12	0.50
53:3:636:U:H2'	53:3:637:C:C6	2.46	0.50
53:3:1017:U:H2'	53:3:1018:G:O4'	2.11	0.50
57:A2:294:ASN:HA	61:NA:463:GLY:CA	2.41	0.50
58:B1:202:ARG:HH11	58:B1:202:ARG:CG	2.14	0.50
58:B1:1371:ARG:HE	58:B1:1372:ARG:NH1	2.10	0.50
59:B2:899:GLU:HA	59:B2:902:LEU:HB3	1.94	0.50
64:a:46:VAL:HG11	64:a:196:LEU:HD13	1.94	0.50
65:0:631:VAL:O	65:0:635:LEU:N	2.42	0.50
65:0:659:PRO:HB2	65:0:662:GLU:HB2	1.93	0.50
4:D:13:ASN:HB3	51:1:125:A:H4'	1.93	0.49
5:E:35:LYS:HE2	5:E:39:ARG:HE	1.76	0.49
12:L:107:ALA:HB1	12:L:115:MET:HE1	1.94	0.49
22:V:4:ILE:HD11	22:V:61:ARG:HD3	1.94	0.49
31:f:171:LYS:NZ	51:1:2529:G:OP2	2.40	0.49
33:i:9:LYS:HD3	51:1:1060:U:OP2	2.12	0.49
40:p:102:ARG:NH2	51:1:1755:A:H5'	2.26	0.49
51:1:737:C:H2'	51:1:738:G:C8	2.47	0.49
53:3:803:G:H2'	53:3:804:U:C6	2.47	0.49
53:3:1049:U:H4'	53:3:1050:G:H5''	1.93	0.49
53:3:1231:G:H2'	53:3:1232:U:C6	2.47	0.49
53:3:1339:A:H2'	53:3:1340:A:O4'	2.12	0.49
53:3:1515:G:H2'	53:3:1516:G:C8	2.46	0.49
65:0:169:LEU:HD11	65:0:186:VAL:HG13	1.94	0.49
10:J:37:VAL:HG11	10:J:113:VAL:HA	1.93	0.49
35:k:1:MET:HE1	51:1:1664:A:H2	1.77	0.49
37:m:12:MET:H	37:m:72:PRO:HG2	1.77	0.49
41:q:10:ARG:HH11	51:1:1216:G:H5''	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:w:10:ARG:HD2	51:1:2258:C:OP1	2.12	0.49
51:1:1620:G:O2'	51:1:1621:U:H5'	2.13	0.49
53:3:128:G:H2'	53:3:129:A:H8	1.76	0.49
53:3:579:A:H2'	53:3:580:C:C6	2.48	0.49
53:3:1267:C:H2'	53:3:1268:G:O4'	2.11	0.49
57:A1:18:GLN:HA	57:A1:24:ALA:HA	1.94	0.49
58:B1:145:VAL:HG12	58:B1:184:ALA:HB1	1.94	0.49
58:B1:902:ASP:HB3	58:B1:905:ARG:HB2	1.93	0.49
65:0:92:HIS:CD2	65:0:464:LEU:HD21	2.46	0.49
65:0:105:VAL:HG23	65:0:106:LEU:HD12	1.93	0.49
4:D:3:ARG:O	4:D:6:GLN:NE2	2.40	0.49
31:f:2:ARG:HD3	51:1:2751:G:OP2	2.12	0.49
42:r:10:LYS:HE2	51:1:994:C:O2'	2.12	0.49
51:1:108:G:O2'	51:1:109:C:H5'	2.11	0.49
51:1:475:C:H4'	51:1:510:C:H5'	1.93	0.49
51:1:1424:G:H2'	51:1:1425:G:O4'	2.12	0.49
51:1:2040:G:H2'	51:1:2041:U:O4'	2.12	0.49
53:3:7:A:O2'	53:3:8:A:H5'	2.12	0.49
53:3:174:A:H2'	53:3:175:C:H5'	1.94	0.49
53:3:570:G:H2'	53:3:571:U:O4'	2.12	0.49
53:3:860:A:H2'	53:3:861:G:O4'	2.13	0.49
7:G:71:THR:OG1	7:G:72:LYS:N	2.45	0.49
8:H:6:PRO:O	8:H:10:ARG:NE	2.41	0.49
10:J:79:THR:OG1	10:J:80:LEU:N	2.44	0.49
14:N:3:ASN:N	14:N:88:GLU:OE1	2.45	0.49
25:Y:54:GLN:HE22	53:3:193:C:H1'	1.75	0.49
30:e:65:LEU:HD22	52:2:42:C:C5	2.47	0.49
31:f:8:VAL:O	31:f:49:LEU:N	2.43	0.49
33:i:30:GLN:HG3	33:i:60:VAL:HG11	1.93	0.49
37:m:18:ARG:O	37:m:97:GLN:NE2	2.46	0.49
40:p:28:LYS:HD3	40:p:82:SER:HB3	1.93	0.49
41:q:65:ASN:HD21	41:q:69:ARG:HH11	1.61	0.49
44:t:58:VAL:HG22	44:t:85:VAL:HG22	1.95	0.49
51:1:90:U:H1'	51:1:456:C:H42	1.77	0.49
51:1:341:C:H2'	51:1:342:A:C8	2.46	0.49
51:1:594:U:H2'	51:1:595:C:H6	1.78	0.49
51:1:664:G:O2'	51:1:940:G:H5''	2.12	0.49
51:1:1581:G:H2'	51:1:1582:C:O4'	2.12	0.49
51:1:1937:A:C3'	51:1:1938:A:H5'	2.41	0.49
53:3:162:A:C2	53:3:348:G:H4'	2.47	0.49
53:3:1012:A:H5'	53:3:1012:A:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:0:128:ARG:HA	65:0:131:ASN:HD22	1.77	0.49
9:I:59:LYS:O	9:I:63:ILE:N	2.44	0.49
14:N:96:GLU:O	14:N:100:ALA:N	2.41	0.49
19:S:9:GLU:HA	19:S:12:ARG:HE	1.77	0.49
20:T:27:GLN:HE21	20:T:31:LEU:HG	1.78	0.49
23:W:49:LYS:NZ	53:3:836:G:OP1	2.45	0.49
32:g:80:ILE:HG13	32:g:102:ALA:HB1	1.94	0.49
35:k:89:ASN:N	35:k:89:ASN:OD1	2.45	0.49
36:l:46:VAL:HG21	51:1:832:U:H4'	1.94	0.49
42:r:8:GLY:HA3	42:r:23:GLU:HG3	1.94	0.49
44:t:34:VAL:HG11	44:t:43:ILE:HD13	1.93	0.49
47:w:52:ASP:HB2	47:w:54:THR:HG23	1.94	0.49
51:1:306:U:H3	51:1:310:A:H62	1.61	0.49
51:1:376:G:H2'	51:1:377:G:C8	2.47	0.49
51:1:1326:U:H2'	51:1:1327:A:H8	1.78	0.49
51:1:1366:A:H2'	51:1:1367:A:O4'	2.11	0.49
51:1:1952:A:H2'	51:1:1953:A:O4'	2.13	0.49
52:2:49:C:H2'	52:2:50:A:C8	2.48	0.49
52:2:87:U:H5''	52:2:88:C:H5	1.74	0.49
53:3:454:G:H2'	53:3:455:G:H8	1.77	0.49
53:3:1382:C:H3'	53:3:1382:C:O2	2.13	0.49
54:4:1:A:H2'	54:4:2:U:H6	1.78	0.49
65:0:390:ASP:OD1	65:0:390:ASP:N	2.44	0.49
9:I:12:ARG:HG3	9:I:37:PRO:HG3	1.94	0.49
11:K:73:GLU:O	11:K:76:THR:OG1	2.31	0.49
12:L:34:LYS:HE2	53:3:1290:G:H4'	1.95	0.49
14:N:72:SER:O	14:N:76:GLY:N	2.45	0.49
18:R:24:VAL:HA	53:3:1329:A:H5''	1.94	0.49
35:k:65:THR:HG23	35:k:68:GLY:H	1.78	0.49
43:s:10:ALA:N	43:s:101:SER:O	2.43	0.49
48:x:2:ARG:CG	48:x:32:LEU:HD12	2.41	0.49
48:x:7:THR:HG23	48:x:9:LYS:HG3	1.95	0.49
51:1:458:G:N2	51:1:469:G:H2'	2.27	0.49
51:1:739:A:H8	51:1:739:A:O5'	1.95	0.49
51:1:864:G:O5'	51:1:864:G:H8	1.95	0.49
51:1:1130:U:H5	51:1:2026:U:P	2.35	0.49
51:1:2235:G:H2'	51:1:2236:U:O4'	2.12	0.49
53:3:25:C:H2'	53:3:26:A:H8	1.77	0.49
53:3:153:C:C2'	53:3:154:U:H5''	2.43	0.49
53:3:967:C:H2'	53:3:968:A:N7	2.26	0.49
63:6:61:C:HO2'	64:a:53:ARG:HD2	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:a:165:ASN:HD22	64:a:169:GLY:HA2	1.78	0.49
3:C:35:LEU:CD2	51:1:2286:G:H22	2.26	0.49
9:I:7:LYS:HB3	9:I:20:LEU:HG	1.94	0.49
9:I:32:LYS:HB3	53:3:429:U:OP2	2.12	0.49
33:i:10:LEU:HD11	51:1:1070:A:C2	2.41	0.49
51:1:210:C:H2'	51:1:211:C:C6	2.48	0.49
51:1:1289:C:O2'	51:1:1330:C:H4'	2.12	0.49
51:1:1963:U:H2'	51:1:1964:G:H5''	1.93	0.49
51:1:2262:U:H2'	51:1:2263:C:H6	1.71	0.49
51:1:2339:C:H2'	51:1:2340:A:C8	2.45	0.49
51:1:2638:G:H1'	51:1:2778:A:H61	1.78	0.49
53:3:23:C:H2'	53:3:24:U:C6	2.48	0.49
53:3:505:G:H2'	53:3:506:G:C8	2.47	0.49
53:3:666:G:H5'	53:3:725:G:N2	2.27	0.49
53:3:955:U:H2'	53:3:956:U:C6	2.47	0.49
6:F:1:MET:CG	51:1:2742:G:H5'	2.43	0.49
14:N:8:THR:H	14:N:84:ARG:HB2	1.78	0.49
14:N:108:ARG:HB3	53:3:1347:G:C8	2.47	0.49
15:O:54:SER:O	19:S:80:ARG:NH2	2.44	0.49
41:q:24:TYR:N	51:1:533:G:OP1	2.38	0.49
51:1:1378:A:H1'	51:1:1379:U:C5	2.48	0.49
51:1:1999:C:O2'	51:1:2000:C:H5'	2.12	0.49
51:1:2807:U:H3	51:1:2891:U:H3	1.60	0.49
53:3:1253:G:H2'	53:3:1254:A:H8	1.78	0.49
3:C:16:THR:OG1	3:C:17:GLY:N	2.44	0.49
14:N:87:MET:HA	14:N:90:ASP:HB3	1.94	0.49
20:T:88:ARG:HH22	51:1:715:A:H5''	1.76	0.49
24:X:32:THR:O	24:X:56:HIS:NE2	2.45	0.49
27:b:155:ARG:CZ	51:1:1818:U:H5	2.26	0.49
37:m:28:PHE:N	37:m:104:GLU:OE1	2.44	0.49
47:w:65:PHE:CD2	51:1:857:G:H5'	2.48	0.49
51:1:1528:A:H2'	51:1:1529:G:C5'	2.40	0.49
51:1:2314:A:H2'	51:1:2315:G:C8	2.48	0.49
51:1:2716:C:O2'	51:1:2717:C:H5'	2.13	0.49
51:1:2810:A:H62	51:1:2890:G:N2	2.11	0.49
53:3:17:U:H2'	53:3:18:C:C6	2.48	0.49
53:3:423:G:C2	53:3:424:G:H1'	2.48	0.49
57:A1:100:LEU:HB2	57:A1:144:ILE:HG23	1.94	0.49
59:B2:529:ARG:HH11	59:B2:572:ILE:HG22	1.77	0.49
59:B2:554:HIS:HD2	59:B2:558:VAL:HB	1.77	0.49
19:S:1:ALA:N	19:S:66:THR:O	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:i:9:LYS:HZ3	51:1:1059:G:H5'	1.78	0.49
36:l:65:GLY:HA2	51:1:631:A:O2'	2.12	0.49
43:s:47:VAL:O	43:s:51:LEU:N	2.39	0.49
43:s:72:THR:OG1	43:s:73:LYS:N	2.45	0.49
51:1:1893:C:H2'	51:1:1894:C:O4'	2.13	0.49
51:1:2194:U:H2'	51:1:2195:U:H6	1.77	0.49
53:3:513:C:H2'	53:3:514:C:O4'	2.13	0.49
53:3:1354:U:H2'	53:3:1355:G:H8	1.78	0.49
55:8:3:DC:H2''	55:8:4:DT:C7	2.42	0.49
58:B1:124:ILE:HG23	58:B1:128:LEU:HD12	1.94	0.49
58:B1:1027:VAL:HB	58:B1:1121:LEU:HB2	1.95	0.49
17:Q:36:VAL:HG13	17:Q:73:LEU:HD11	1.95	0.48
17:Q:76:HIS:O	65:0:425:LYS:NZ	2.45	0.48
27:b:59:GLN:NE2	51:1:1567:G:OP1	2.46	0.48
31:f:91:VAL:CG2	51:1:2657:A:H4'	2.43	0.48
38:n:68:ALA:HA	51:1:2707:U:O2'	2.13	0.48
50:z:30:ARG:HG2	50:z:33:HIS:HB2	1.94	0.48
51:1:319:G:H2'	51:1:320:A:O4'	2.13	0.48
51:1:445:C:O2	51:1:450:G:H1'	2.13	0.48
51:1:532:A:N1	51:1:2020:A:H1'	2.27	0.48
51:1:1219:U:H2'	51:1:1220:G:H8	1.78	0.48
51:1:1595:C:H2'	51:1:1596:A:C8	2.48	0.48
51:1:1657:U:H2'	51:1:1658:C:C6	2.48	0.48
51:1:1658:C:O5'	51:1:1658:C:H6	1.95	0.48
53:3:770:C:O2'	53:3:771:G:H5'	2.13	0.48
58:B1:115:TRP:O	58:B1:1333:THR:HG21	2.13	0.48
63:6:26:G:H3'	63:6:27:U:C5'	2.42	0.48
65:0:520:ILE:HG22	65:0:578:LEU:HA	1.95	0.48
1:A:36:VAL:HG13	1:A:40:CYS:HB3	1.94	0.48
29:d:2:GLU:HA	29:d:13:THR:HA	1.96	0.48
30:e:132:ARG:NH1	30:e:148:VAL:O	2.46	0.48
33:i:75:ALA:HA	33:i:78:LEU:HB2	1.95	0.48
34:j:47:HIS:CG	51:1:536:G:H21	2.31	0.48
37:m:61:GLY:HA3	37:m:105:MET:HE1	1.95	0.48
51:1:153:U:O2'	51:1:154:U:H5'	2.13	0.48
51:1:157:C:H2'	51:1:158:U:O4'	2.13	0.48
51:1:387:U:H4'	51:1:388:G:O4'	2.13	0.48
51:1:1807:G:H2'	51:1:1808:A:H5'	1.95	0.48
51:1:2247:A:H2'	51:1:2248:C:O4'	2.13	0.48
51:1:2364:C:H2'	51:1:2365:G:O4'	2.13	0.48
51:1:2803:G:H2'	51:1:2804:U:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2834:G:H2'	51:1:2879:A:N6	2.28	0.48
55:8:14:DC:H2'	55:8:15:DC:C6	2.48	0.48
58:B1:102:MET:HG2	58:B1:246:PRO:HD3	1.94	0.48
59:B2:18:ARG:HE	59:B2:620:ASN:HA	1.77	0.48
65:0:505:HIS:HB2	65:0:596:ALA:HB2	1.95	0.48
9:I:12:ARG:NH1	9:I:36:ALA:O	2.46	0.48
12:L:78:ARG:NH1	12:L:82:SER:O	2.46	0.48
42:r:4:VAL:HG22	42:r:13:ARG:HA	1.95	0.48
44:t:36:LYS:NZ	44:t:79:ASP:OD1	2.38	0.48
51:1:1005:C:H2'	51:1:1006:C:H6	1.77	0.48
51:1:1036:G:H1	51:1:1119:U:H3	1.60	0.48
51:1:1225:G:O2'	51:1:1226:A:H5'	2.13	0.48
51:1:2786:U:H2'	51:1:2787:C:C6	2.48	0.48
53:3:714:G:H2'	53:3:715:A:C8	2.48	0.48
53:3:865:A:H8	53:3:865:A:O5'	1.96	0.48
59:B2:318:SER:OG	59:B2:320:ASP:OD1	2.31	0.48
59:B2:836:LEU:HD13	59:B2:1054:LEU:HD13	1.95	0.48
59:B2:914:LYS:O	59:B2:915:ASP:C	2.56	0.48
7:G:100:LEU:HD11	7:G:160:LEU:HD13	1.95	0.48
13:M:89:ASP:OD1	13:M:89:ASP:N	2.37	0.48
19:S:19:TYR:HB3	19:S:23:ARG:HH21	1.77	0.48
27:b:48:ILE:HG22	51:1:779:U:OP2	2.14	0.48
45:u:5:ARG:HH11	51:1:84:A:H5''	1.77	0.48
51:1:93:G:O2'	51:1:94:A:H5'	2.12	0.48
51:1:175:G:H2'	51:1:176:A:C8	2.49	0.48
51:1:445:C:H2'	51:1:446:G:H5'	1.94	0.48
51:1:511:U:H2'	51:1:512:G:H5'	1.95	0.48
51:1:821:A:H5''	51:1:822:G:C8	2.49	0.48
51:1:2600:A:H2'	51:1:2601:C:C6	2.48	0.48
53:3:1349:A:H2'	53:3:1350:A:O4'	2.13	0.48
59:B2:533:LEU:HD13	59:B2:540:ARG:HH21	1.77	0.48
64:a:43:ASP:OD1	64:a:174:THR:OG1	2.32	0.48
23:W:32:ILE:HD12	23:W:36:GLY:HA2	1.95	0.48
51:1:45:G:C5'	51:1:46:G:H5'	2.25	0.48
51:1:459:U:H2'	51:1:460:A:O4'	2.13	0.48
51:1:881:G:H1	51:1:895:U:H3	1.61	0.48
51:1:1178:C:H2'	51:1:1179:G:C8	2.48	0.48
51:1:1258:U:H2'	51:1:1259:G:C8	2.48	0.48
51:1:1755:A:C2'	51:1:1756:G:H5'	2.40	0.48
53:3:83:C:O2'	53:3:84:U:H3'	2.13	0.48
53:3:1414:U:H2'	53:3:1415:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:141:PHE:CE2	58:B1:296:LYS:CB	2.94	0.48
7:G:72:LYS:HZ2	7:G:74:ALA:HB3	1.78	0.48
15:O:15:HIS:HA	15:O:18:ILE:HG22	1.96	0.48
21:U:8:ARG:NH1	53:3:391:G:H5''	2.29	0.48
24:X:76:THR:HG21	53:3:1221:G:O2'	2.13	0.48
25:Y:34:VAL:HG22	25:Y:49:ALA:HB1	1.95	0.48
28:c:8:LYS:HB2	28:c:201:LEU:HD11	1.96	0.48
35:k:48:PRO:HB3	53:3:1422:G:OP1	2.13	0.48
37:m:53:MET:HE3	37:m:119:LEU:HB3	1.94	0.48
37:m:111:GLU:HA	37:m:114:ARG:HB3	1.96	0.48
41:q:84:LYS:HB3	41:q:115:ALA:HB1	1.94	0.48
51:1:189:G:N2	51:1:206:U:C5	2.82	0.48
51:1:937:C:H2'	51:1:938:G:H8	1.78	0.48
51:1:999:U:H5''	51:1:1154:G:O6	2.13	0.48
51:1:1912:A:N7	51:1:1917:U:H5	2.11	0.48
51:1:2531:A:H2'	51:1:2532:G:H5'	1.95	0.48
51:1:2556:C:H2'	51:1:2557:G:H5'	1.96	0.48
53:3:483:C:C3'	53:3:484:G:H5'	2.44	0.48
53:3:701:U:O4'	53:3:703:G:H1'	2.14	0.48
57:A1:182:ARG:O	57:A1:205:MET:HA	2.14	0.48
58:B1:550:VAL:O	58:B1:569:LEU:HA	2.13	0.48
58:B1:833:GLU:N	58:B1:1242:ARG:HH12	2.12	0.48
59:B2:565:GLU:HA	59:B2:569:ILE:HG12	1.95	0.48
63:6:36:U:H2'	63:6:37:A:C8	2.48	0.48
1:A:26:SER:OG	1:A:27:THR:N	2.47	0.48
11:K:91:ARG:O	11:K:93:LYS:NZ	2.39	0.48
35:k:65:THR:OG1	35:k:66:LYS:N	2.44	0.48
36:l:41:ARG:HG2	51:1:806:C:H41	1.78	0.48
51:1:404:A:H2	51:1:421:C:N3	2.11	0.48
51:1:1810:A:H2'	51:1:1811:G:H5'	1.95	0.48
53:3:153:C:H2'	53:3:154:U:H5''	1.95	0.48
53:3:193:C:H2'	53:3:194:C:C5	2.48	0.48
53:3:483:C:H3'	53:3:484:G:H5'	1.94	0.48
53:3:1424:U:H3	53:3:1476:A:N6	2.05	0.48
58:B1:103:GLY:H	58:B1:244:VAL:HG22	1.79	0.48
58:B1:1347:LEU:HG	58:B1:1357:ILE:HG23	1.96	0.48
59:B2:363:LEU:HB3	59:B2:381:ALA:HB1	1.96	0.48
64:a:211:LYS:HE2	64:a:211:LYS:HB2	1.58	0.48
4:D:24:THR:HG23	4:D:27:GLY:H	1.78	0.48
11:K:92:THR:OG1	11:K:94:HIS:O	2.29	0.48
16:P:83:VAL:HG11	16:P:96:ILE:HG12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:146:LYS:HB2	27:b:149:LYS:HB2	1.94	0.48
29:d:67:ARG:NH2	51:1:1257:C:H5'	2.29	0.48
30:e:21:TYR:OH	30:e:164:GLU:OE1	2.31	0.48
34:j:60:ASP:OD1	34:j:60:ASP:N	2.42	0.48
51:1:443:A:H2	51:1:1246:A:H1'	1.78	0.48
51:1:1993:U:H2'	51:1:1994:C:O4'	2.14	0.48
51:1:2276:G:C2'	51:1:2277:G:H5'	2.44	0.48
52:2:45:A:H2'	52:2:46:A:O4'	2.13	0.48
53:3:1251:A:H2'	53:3:1252:A:H8	1.79	0.48
53:3:1308:U:H2'	53:3:1309:G:C8	2.49	0.48
58:B1:255:LEU:HD23	58:B1:261:ALA:HB2	1.95	0.48
58:B1:1146:GLU:OE2	58:B1:1310:THR:HG22	2.14	0.48
59:B2:899:GLU:HG3	59:B2:902:LEU:HD22	1.96	0.48
65:0:99:VAL:HG11	65:0:126:VAL:HG12	1.95	0.48
29:d:23:PHE:H	29:d:114:ARG:HH22	1.60	0.48
49:y:43:LEU:HD21	49:y:47:ARG:HH11	1.79	0.48
51:1:441:U:H2'	51:1:442:G:C8	2.49	0.48
51:1:1182:G:H2'	51:1:1183:U:C6	2.48	0.48
51:1:1810:A:C2'	51:1:1811:G:H5'	2.44	0.48
51:1:2654:A:H8	51:1:2654:A:OP1	1.97	0.48
53:3:27:G:H2'	53:3:28:A:C8	2.49	0.48
53:3:92:U:H2'	53:3:93:U:H5'	1.96	0.48
53:3:316:C:H2'	53:3:317:U:H6	1.79	0.48
58:B1:201:LEU:HD11	58:B1:220:ARG:HG2	1.95	0.48
58:B1:526:VAL:HG12	58:B1:549:LYS:HB2	1.96	0.48
58:B1:809:VAL:HG21	58:B1:909:ILE:HG12	1.95	0.48
58:B1:1060:VAL:HG13	58:B1:1106:ILE:HG12	1.96	0.48
65:0:157:GLN:HE22	65:0:161:ARG:HE	1.61	0.48
7:G:18:GLN:NE2	7:G:189:ASN:HB3	2.29	0.48
9:I:37:PRO:HD2	9:I:41:GLY:HA3	1.96	0.48
20:T:19:ASN:HB2	53:3:750:C:C4'	2.43	0.48
22:V:56:ASP:HB3	22:V:80:LYS:HA	1.94	0.48
28:c:134:HIS:CD2	51:1:1675:C:H42	2.32	0.48
37:m:22:GLN:HE21	51:1:864:G:P	2.36	0.48
37:m:65:ILE:HG22	37:m:67:VAL:H	1.79	0.48
47:w:45:ALA:N	47:w:77:SER:OG	2.42	0.48
51:1:1103:A:H2'	51:1:1103:A:N3	2.29	0.48
51:1:2143:C:H3'	51:1:2144:G:C8	2.49	0.48
53:3:554:A:C2'	53:3:555:U:H5'	2.43	0.48
55:8:14:DC:H2'	55:8:15:DC:H6	1.79	0.48
65:0:422:PRO:HG3	65:0:428:GLN:HB2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:0:544:VAL:HG13	65:0:583:TYR:HB3	1.95	0.48
22:V:11:VAL:HA	22:V:22:VAL:HA	1.95	0.47
27:b:15:VAL:HB	27:b:205:GLY:HA3	1.95	0.47
33:i:65:SER:OG	33:i:66:PHE:N	2.46	0.47
36:l:37:GLY:O	36:l:41:ARG:NH2	2.44	0.47
38:n:34:ILE:HA	51:1:1279:G:OP1	2.13	0.47
50:z:18:LYS:O	50:z:22:THR:OG1	2.31	0.47
51:1:80:G:H2'	51:1:81:G:C8	2.49	0.47
51:1:1265:A:N6	51:1:2013:A:H5''	2.27	0.47
51:1:1343:G:N3	51:1:1343:G:H2'	2.28	0.47
51:1:2257:U:O2'	51:1:2258:C:H5'	2.14	0.47
51:1:2298:A:H2'	51:1:2299:U:O4'	2.13	0.47
51:1:2884:U:O2	51:1:2884:U:H3'	2.14	0.47
52:2:3:C:C3'	52:2:4:C:H5''	2.42	0.47
53:3:129:A:O2'	53:3:130:A:H5''	2.13	0.47
53:3:563:A:H5'	53:3:566:G:C2	2.49	0.47
58:B1:395:LYS:NZ	58:B1:399:LYS:CE	2.78	0.47
58:B1:1036:ARG:HE	58:B1:1081:VAL:HG11	1.79	0.47
59:B2:400:VAL:HG22	59:B2:584:TYR:HB3	1.96	0.47
59:B2:1311:GLY:O	60:W0:31:GLN:NE2	2.47	0.47
59:B2:1314:GLN:HB2	60:W0:28:ARG:HH12	1.78	0.47
62:NG:161:SER:CA	62:NG:170:PRO:HA	2.43	0.47
65:0:319:ALA:HB3	65:0:397:LEU:HB2	1.96	0.47
65:0:330:VAL:HG11	65:0:386:ILE:HD11	1.96	0.47
3:C:5:ARG:NH2	3:C:23:THR:O	2.48	0.47
19:S:12:ARG:HH22	19:S:60:ARG:H	1.61	0.47
20:T:74:VAL:HA	20:T:77:TYR:HB3	1.96	0.47
29:d:178:VAL:HA	29:d:181:ILE:HG22	1.95	0.47
37:m:22:GLN:NE2	51:1:864:G:OP1	2.47	0.47
51:1:118:A:H5'	51:1:119:A:H8	1.79	0.47
51:1:145:C:H2'	51:1:146:A:C8	2.49	0.47
51:1:858:G:H5'	51:1:859:G:OP2	2.14	0.47
51:1:1333:G:H2'	51:1:1334:G:C8	2.49	0.47
51:1:1710:G:H2'	51:1:1711:A:C8	2.49	0.47
51:1:2367:G:O2'	51:1:2368:C:H5'	2.14	0.47
51:1:2588:G:C6	51:1:2607:G:C2	3.02	0.47
51:1:2813:A:H2'	51:1:2814:A:H8	1.78	0.47
51:1:2828:G:O2'	51:1:2829:A:H5'	2.13	0.47
53:3:792:A:H4'	53:3:793:U:H5''	1.96	0.47
53:3:840:C:C2'	53:3:841:C:H5''	2.41	0.47
2:B:2:VAL:O	51:1:2615:U:C4	2.67	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:87:VAL:HA	10:J:92:ARG:HA	1.96	0.47
31:f:107:GLY:O	51:1:2666:C:N4	2.47	0.47
34:j:7:LYS:HE2	51:1:539:G:H5'	1.95	0.47
48:x:4:CYS:SG	48:x:5:GLN:N	2.87	0.47
51:1:1018:U:H2'	51:1:1019:U:O4'	2.13	0.47
51:1:1414:C:H42	51:1:1588:G:H1	1.62	0.47
51:1:2475:C:H2'	51:1:2476:A:H5'	1.97	0.47
53:3:631:C:H5''	53:3:632:U:O4'	2.15	0.47
58:B1:891:ASP:OD2	58:B1:1290:ARG:NH2	2.47	0.47
64:a:183:ASP:OD1	64:a:183:ASP:N	2.43	0.47
1:A:8:LYS:NZ	1:A:10:GLU:OE1	2.45	0.47
10:J:24:VAL:HG13	10:J:26:GLY:H	1.79	0.47
46:v:13:GLY:N	52:2:76:G:OP1	2.40	0.47
51:1:166:U:H2'	51:1:167:A:H8	1.78	0.47
51:1:739:A:H1'	51:1:740:C:H5	1.79	0.47
51:1:1095:A:C8	65:0:632:ILE:HD11	2.50	0.47
51:1:2316:G:O2'	51:1:2317:A:H5'	2.13	0.47
51:1:2721:A:H2'	51:1:2722:G:O4'	2.14	0.47
53:3:1274:A:H2'	53:3:1275:A:H5''	1.96	0.47
53:3:1465:A:H2'	53:3:1466:C:C6	2.48	0.47
53:3:1478:U:H2'	53:3:1479:C:C6	2.49	0.47
58:B1:1221:LEU:HD22	58:B1:1306:LEU:HB2	1.96	0.47
7:G:33:ALA:N	7:G:37:VAL:O	2.46	0.47
10:J:83:PRO:HD3	10:J:97:PRO:HG3	1.96	0.47
11:K:86:ARG:NH2	53:3:673:A:O3'	2.48	0.47
13:M:4:ASP:OD2	13:M:76:ARG:NH2	2.47	0.47
18:R:27:THR:HG22	53:3:1328:C:H5''	1.97	0.47
24:X:39:ILE:HD11	24:X:70:LEU:HD23	1.96	0.47
27:b:158:GLY:HA3	51:1:1820:U:C5	2.50	0.47
30:e:31:GLU:HG2	30:e:32:LYS:H	1.79	0.47
47:w:56:PHE:HE2	51:1:2365:G:H5'	1.80	0.47
51:1:215:G:O3'	51:1:216:A:H4'	2.15	0.47
51:1:367:G:H2'	51:1:368:A:O4'	2.14	0.47
51:1:1463:C:H2'	51:1:1464:G:C8	2.48	0.47
51:1:2515:C:O2'	51:1:2516:A:H5'	2.14	0.47
53:3:230:G:O2'	53:3:231:U:H5'	2.14	0.47
53:3:253:A:H4'	53:3:276:G:O2'	2.15	0.47
53:3:1015:G:H2'	53:3:1016:A:O4'	2.14	0.47
53:3:1161:C:H2'	53:3:1162:C:H6	1.78	0.47
53:3:1268:G:H21	53:3:1327:C:H1'	1.80	0.47
53:3:1382:C:H2'	53:3:1383:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:29:MET:HG2	59:B2:1336:ASN:ND2	2.29	0.47
59:B2:207:THR:OG1	59:B2:354:ASP:OD2	2.32	0.47
2:B:37:HIS:HB3	2:B:43:THR:HG22	1.97	0.47
7:G:53:LEU:HA	7:G:56:LEU:HB2	1.97	0.47
10:J:23:THR:HG21	53:3:15:G:N3	2.29	0.47
18:R:23:GLY:HA2	18:R:68:LEU:HD13	1.97	0.47
23:W:37:LYS:HE2	23:W:37:LYS:HB2	1.73	0.47
27:b:240:GLY:HA2	51:1:2597:G:H5''	1.97	0.47
44:t:89:GLU:OE1	44:t:91:GLN:NE2	2.48	0.47
51:1:139:U:H2'	51:1:140:C:C5	2.48	0.47
51:1:524:G:O2'	51:1:525:U:H5'	2.14	0.47
51:1:593:U:H2'	51:1:594:U:C6	2.49	0.47
51:1:1580:A:H2'	51:1:1581:G:O4'	2.14	0.47
51:1:2521:C:H42	51:1:2544:G:H1	1.61	0.47
53:3:325:A:H2'	53:3:326:G:O4'	2.14	0.47
53:3:1465:A:H2'	53:3:1466:C:H6	1.80	0.47
58:B1:352:ARG:HB2	59:B2:1268:GLN:NE2	2.30	0.47
59:B2:103:VAL:HG12	59:B2:117:ILE:HG22	1.97	0.47
59:B2:732:ILE:HD11	59:B2:769:PRO:HB3	1.95	0.47
3:C:6:GLU:HG2	3:C:26:LYS:HD3	1.96	0.47
8:H:32:LEU:HD21	19:S:78:LEU:HD11	1.97	0.47
19:S:41:TRP:HZ2	24:X:10:ILE:HG22	1.79	0.47
25:Y:16:ALA:O	25:Y:20:ASN:N	2.45	0.47
30:e:22:ASN:ND2	30:e:26:GLN:OE1	2.48	0.47
31:f:85:LYS:HE2	31:f:129:GLU:HB3	1.97	0.47
34:j:47:HIS:CD2	51:1:536:G:H21	2.32	0.47
36:l:43:GLY:N	51:1:671:C:OP1	2.47	0.47
36:l:109:LYS:HB3	51:1:636:G:O6	2.15	0.47
37:m:43:ALA:HB2	37:m:69:PRO:HG3	1.96	0.47
46:v:21:ARG:HH12	52:2:77:U:H5''	1.80	0.47
51:1:341:C:H2'	51:1:342:A:H8	1.79	0.47
51:1:696:G:O2'	51:1:697:G:H5'	2.15	0.47
51:1:744:U:H5''	51:1:1658:C:H5''	1.96	0.47
51:1:833:A:H2'	51:1:834:G:H8	1.78	0.47
51:1:1306:C:O2'	51:1:1307:A:H5'	2.13	0.47
51:1:1414:C:H2'	51:1:1415:U:H5'	1.95	0.47
51:1:1444:G:H2'	51:1:1445:G:H8	1.76	0.47
51:1:1856:U:H2'	51:1:1857:G:O4'	2.15	0.47
51:1:1900:A:H5'	51:1:1970:A:H5'	1.96	0.47
51:1:1924:C:H3'	51:1:1925:C:C5	2.49	0.47
53:3:211:G:H3'	53:3:211:G:N3	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:343:U:O2'	53:3:344:A:H2'	2.15	0.47
53:3:751:U:C2'	53:3:752:G:H5'	2.44	0.47
53:3:1000:A:H2'	53:3:1001:C:O4'	2.15	0.47
53:3:1161:C:H2'	53:3:1162:C:C6	2.50	0.47
53:3:1170:A:H2'	53:3:1171:A:H5'	1.97	0.47
53:3:1435:G:H1	53:3:1466:C:H42	1.62	0.47
53:3:1486:G:H2'	53:3:1487:G:O4'	2.15	0.47
57:A1:59:VAL:HG22	57:A1:144:ILE:HA	1.97	0.47
58:B1:1150:PRO:HG3	58:B1:1214:PRO:HB2	1.97	0.47
59:B2:1286:THR:O	59:B2:1290:MET:HB2	2.14	0.47
62:NG:142:ALA:O	62:NG:143:ASP:CB	2.63	0.47
63:6:62:C:H5'	64:a:53:ARG:CZ	2.45	0.47
65:0:463:GLU:O	65:0:467:ASP:N	2.42	0.47
5:E:32:LEU:HD12	5:E:32:LEU:HA	1.73	0.47
7:G:66:ILE:HD11	7:G:161:PHE:HB2	1.96	0.47
8:H:147:GLY:HA2	8:H:170:GLY:HA3	1.97	0.47
9:I:140:ASP:O	9:I:181:PHE:N	2.46	0.47
12:L:91:ARG:HG2	12:L:91:ARG:HH11	1.78	0.47
14:N:113:LYS:NZ	53:3:1368:A:OP2	2.39	0.47
15:O:21:ALA:HB2	15:O:93:ALA:HB2	1.97	0.47
17:Q:87:LYS:HB3	17:Q:87:LYS:HE3	1.69	0.47
29:d:112:LEU:O	29:d:117:ARG:N	2.43	0.47
34:j:116:ARG:HH22	51:1:528:A:H8	1.61	0.47
45:u:8:ASP:O	45:u:23:LYS:NZ	2.45	0.47
51:1:1153:C:H2'	51:1:1154:G:O4'	2.15	0.47
51:1:1209:U:H2'	51:1:1210:G:H21	1.80	0.47
51:1:1943:U:OP1	51:1:1943:U:H6	1.98	0.47
51:1:2248:C:C2'	51:1:2249:U:H5'	2.44	0.47
51:1:2450:A:OP1	51:1:2497:A:O2'	2.31	0.47
53:3:344:A:OP1	65:0:38:HIS:NE2	2.48	0.47
53:3:1059:C:H2'	53:3:1060:U:C6	2.49	0.47
53:3:1441:A:N3	53:3:1441:A:H2'	2.30	0.47
58:B1:108:ALA:HB1	58:B1:279:LEU:HD22	1.96	0.47
58:B1:220:ARG:HG2	58:B1:220:ARG:NH1	2.25	0.47
58:B1:1261:LEU:HD12	58:B1:1304:ARG:HH21	1.79	0.47
65:0:420:VAL:HB	65:0:458:ILE:HD11	1.97	0.47
7:G:17:HIS:CE1	7:G:187:ASP:HB2	2.50	0.47
13:M:63:LYS:HG2	13:M:70:VAL:HG21	1.95	0.47
19:S:96:LYS:HZ3	19:S:97:LYS:H	1.63	0.47
25:Y:22:SER:HB2	53:3:1458:G:H4'	1.97	0.47
32:g:93:SER:HB3	32:g:121:VAL:HG12	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:l:42:SER:O	36:l:42:SER:OG	2.32	0.47
44:t:67:VAL:HG12	44:t:76:ARG:HA	1.96	0.47
51:1:1639:C:H2'	51:1:1640:A:H5'	1.97	0.47
52:2:30:C:H2'	52:2:31:C:H5'	1.96	0.47
52:2:51:G:N3	52:2:52:A:H1'	2.30	0.47
53:3:1093:A:H2'	53:3:1094:G:H5'	1.96	0.47
58:B1:43:THR:HG22	58:B1:57:PHE:HE1	1.80	0.47
58:B1:842:ARG:HH22	58:B1:1250:ASP:HB2	1.80	0.47
59:B2:890:LYS:HE2	59:B2:890:LYS:HB2	1.62	0.47
3:C:8:ILE:HD11	3:C:50:GLU:HB2	1.96	0.47
8:H:30:ASP:OD1	8:H:30:ASP:N	2.47	0.47
8:H:51:VAL:HA	8:H:69:THR:HA	1.97	0.47
13:M:102:VAL:HB	13:M:126:CYS:HB3	1.96	0.47
17:Q:58:ASN:OD1	17:Q:58:ASN:N	2.46	0.47
31:f:88:LEU:O	31:f:128:THR:OG1	2.32	0.47
33:i:9:LYS:HZ2	51:1:1059:G:P	2.38	0.47
36:l:30:THR:O	36:l:33:ARG:N	2.46	0.47
51:1:1085:A:H2'	51:1:1086:A:N7	2.30	0.47
51:1:1587:G:H2'	51:1:1588:G:C8	2.50	0.47
51:1:2153:C:H3'	51:1:2154:A:H8	1.78	0.47
53:3:835:U:C3'	53:3:836:G:H5''	2.45	0.47
54:4:1:A:H2'	54:4:2:U:C6	2.50	0.47
58:B1:209:ASN:HA	58:B1:214:ARG:NH2	2.30	0.47
58:B1:1357:ILE:HD13	59:B2:1279:GLU:HG2	1.97	0.47
8:H:39:ARG:HA	8:H:42:LEU:HB3	1.97	0.46
15:O:64:GLN:HB3	19:S:98:ALA:HB3	1.96	0.46
33:i:7:TYR:CE1	51:1:1058:U:H5'	2.50	0.46
33:i:79:LEU:HD22	33:i:131:THR:HG23	1.97	0.46
51:1:940:G:H2'	51:1:941:A:H5''	1.97	0.46
51:1:1388:G:H2'	51:1:1389:G:C8	2.51	0.46
51:1:1595:C:H2'	51:1:1596:A:H8	1.80	0.46
51:1:1663:G:O2'	51:1:1664:A:H8	1.99	0.46
51:1:1826:G:H2'	51:1:1827:U:C6	2.51	0.46
51:1:1868:C:C2'	51:1:1869:G:H5'	2.42	0.46
51:1:2080:A:C6	51:1:2081:U:C4	3.03	0.46
51:1:2682:A:O2'	51:1:2683:C:H5'	2.15	0.46
51:1:2845:U:H2'	51:1:2846:G:C8	2.50	0.46
51:1:2861:U:O2'	51:1:2862:G:H5'	2.15	0.46
53:3:138:G:H2'	53:3:139:A:H8	1.79	0.46
53:3:545:C:O2'	53:3:546:A:H5'	2.14	0.46
57:A1:33:ARG:HE	57:A1:33:ARG:HB3	1.56	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:198:CYS:HA	58:B1:221:ILE:CD1	2.45	0.46
58:B1:968:ASN:HA	58:B1:1117:SER:HB2	1.96	0.46
59:B2:562:GLU:OE1	59:B2:662:SER:OG	2.28	0.46
65:0:369:ASN:OD1	65:0:369:ASN:N	2.48	0.46
65:0:514:GLN:HA	65:0:587:ASP:HA	1.97	0.46
6:F:15:LYS:N	6:F:26:ILE:O	2.40	0.46
7:G:132:GLU:OE2	7:G:136:ARG:NE	2.47	0.46
8:H:8:GLY:O	19:S:96:LYS:NZ	2.42	0.46
16:P:23:HIS:HB3	16:P:30:ILE:HG23	1.96	0.46
19:S:55:SER:OG	19:S:57:SER:OG	2.30	0.46
28:c:119:ALA:C	51:1:1655:A:H4'	2.40	0.46
42:r:80:ARG:HD3	51:1:566:U:H5	1.80	0.46
43:s:82:MET:HE1	51:1:1322:A:H4'	1.97	0.46
51:1:233:A:H5'	51:1:233:A:C8	2.50	0.46
51:1:680:C:H42	51:1:797:G:H1	1.63	0.46
51:1:786:C:O2'	51:1:787:C:H5'	2.16	0.46
51:1:820:A:O2'	51:1:821:A:H5'	2.15	0.46
51:1:1136:G:H2'	51:1:1137:G:H8	1.79	0.46
51:1:1321:A:C2	51:1:1322:A:H1'	2.50	0.46
51:1:1470:A:N6	51:1:1521:G:H1'	2.30	0.46
51:1:1572:A:O2'	51:1:1573:G:H5'	2.15	0.46
51:1:2531:A:C2'	51:1:2532:G:H5'	2.45	0.46
53:3:859:G:O2'	53:3:860:A:H5'	2.15	0.46
58:B1:385:LEU:HD23	58:B1:390:LEU:HB2	1.97	0.46
58:B1:420:PRO:HA	58:B1:437:PHE:O	2.15	0.46
59:B2:28:LEU:HD21	59:B2:524:ILE:HG13	1.97	0.46
8:H:49:ALA:O	8:H:69:THR:OG1	2.34	0.46
12:L:91:ARG:HG2	12:L:91:ARG:NH1	2.30	0.46
25:Y:79:THR:HA	25:Y:82:ILE:HB	1.98	0.46
27:b:210:ALA:HA	27:b:213:ARG:HG3	1.96	0.46
28:c:55:LYS:HG3	28:c:77:ARG:HB3	1.97	0.46
29:d:173:THR:OG1	29:d:174:GLY:N	2.48	0.46
35:k:31:ARG:HH12	51:1:2676:C:P	2.39	0.46
51:1:433:C:O2'	51:1:434:U:H5'	2.15	0.46
53:3:980:C:H2'	53:3:981:U:O4'	2.15	0.46
53:3:1084:G:O2'	53:3:1103:C:H5	1.98	0.46
58:B1:1219:ASP:O	58:B1:1223:LEU:HB2	2.15	0.46
59:B2:1002:LEU:HD21	59:B2:1007:LYS:HB2	1.98	0.46
65:0:24:THR:HG21	65:0:62:THR:HG21	1.97	0.46
12:L:101:ARG:HH22	53:3:940:C:P	2.37	0.46
17:Q:11:ARG:NH1	53:3:563:A:H2	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:53:ASP:OD1	18:R:53:ASP:N	2.48	0.46
32:g:30:LEU:HA	32:g:35:LYS:HE3	1.96	0.46
51:1:1196:C:O2'	51:1:1197:G:H5'	2.16	0.46
51:1:1485:U:H2'	51:1:1486:U:C6	2.50	0.46
51:1:1569:A:H2'	51:1:1570:A:C8	2.51	0.46
51:1:2135:A:H8	51:1:2156:G:H21	1.64	0.46
52:2:116:G:O2'	52:2:117:G:H5'	2.15	0.46
53:3:994:A:H3'	53:3:994:A:OP2	2.15	0.46
58:B1:128:LEU:HD21	58:B1:188:LEU:HB3	1.97	0.46
65:0:17:ALA:H	65:0:23:LYS:HZ3	1.62	0.46
65:0:136:PRO:HB3	65:0:256:VAL:HG12	1.97	0.46
65:0:376:GLU:OE1	65:0:378:ARG:NE	2.48	0.46
5:E:7:ARG:NH2	51:1:245:G:N7	2.63	0.46
5:E:57:VAL:O	5:E:61:LEU:N	2.41	0.46
8:H:2:GLN:NE2	53:3:1062:U:O4	2.48	0.46
9:I:103:ARG:HD2	9:I:167:PRO:HG3	1.97	0.46
10:J:158:LYS:HD3	10:J:158:LYS:HA	1.73	0.46
14:N:72:SER:HA	14:N:75:ALA:HB3	1.98	0.46
17:Q:83:GLY:H	53:3:552:U:H4'	1.80	0.46
27:b:250:GLN:HB3	27:b:254:LYS:HD2	1.96	0.46
32:g:68:ARG:O	32:g:72:ILE:N	2.48	0.46
32:g:71:LYS:HD3	32:g:71:LYS:HA	1.66	0.46
46:v:7:GLU:HG3	46:v:41:GLU:HB3	1.97	0.46
51:1:175:G:H2'	51:1:176:A:H8	1.81	0.46
51:1:742:A:O2'	51:1:743:A:H5'	2.15	0.46
51:1:1858:A:N6	51:1:1884:G:O2'	2.48	0.46
51:1:1933:G:H2'	51:1:1934:C:H6	1.80	0.46
51:1:2134:A:C5	51:1:2157:G:H4'	2.51	0.46
51:1:2741:A:H61	51:1:2763:G:H1'	1.80	0.46
53:3:556:C:H2'	53:3:557:G:O4'	2.15	0.46
53:3:1448:C:O2	53:3:1448:C:H2'	2.15	0.46
65:0:488:VAL:HG13	65:0:660:LEU:HD22	1.96	0.46
1:A:9:TYR:HE1	30:e:61:GLY:H	1.63	0.46
14:N:40:ARG:NE	53:3:1292:G:H5''	2.31	0.46
14:N:56:MET:HB2	14:N:60:LEU:HB2	1.97	0.46
27:b:86:ARG:HB3	27:b:88:ALA:H	1.80	0.46
28:c:49:GLN:HE21	28:c:79:LEU:HB3	1.79	0.46
51:1:340:A:C2'	51:1:341:C:H5'	2.43	0.46
51:1:514:A:N3	51:1:581:C:O2'	2.45	0.46
51:1:704:G:N3	51:1:726:G:C2	2.84	0.46
51:1:845:A:N3	51:1:845:A:H3'	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1661:G:O2'	51:1:1662:U:H5'	2.16	0.46
51:1:1842:G:O2'	51:1:1843:C:H5'	2.15	0.46
51:1:2259:U:C6	51:1:2427:C:C5	3.04	0.46
53:3:528:C:H4'	53:3:535:A:C6	2.51	0.46
53:3:1018:G:O2'	53:3:1019:A:H5'	2.16	0.46
53:3:1260:G:H4'	53:3:1284:C:H5'	1.98	0.46
57:A2:64:VAL:HG11	57:A2:78:ILE:HG21	1.97	0.46
57:A2:102:LEU:HD12	57:A2:115:ILE:HG12	1.96	0.46
3:C:35:LEU:HD21	51:1:2286:G:H22	1.81	0.46
12:L:66:GLU:HA	12:L:69:ARG:HG3	1.96	0.46
20:T:50:HIS:ND1	53:3:667:G:H4'	2.31	0.46
25:Y:60:GLN:HA	25:Y:63:LYS:HD2	1.98	0.46
34:j:7:LYS:HG2	34:j:10:THR:HG23	1.97	0.46
49:y:10:SER:HA	49:y:13:GLU:HB3	1.98	0.46
51:1:141:G:C8	51:1:142:A:H1'	2.51	0.46
51:1:717:C:H2'	51:1:718:A:H5'	1.97	0.46
51:1:1177:G:C2'	51:1:1178:C:H5''	2.45	0.46
51:1:1695:G:H2'	51:1:1696:G:O4'	2.15	0.46
53:3:520:A:H62	53:3:529:G:N2	2.11	0.46
58:B1:211:GLU:CG	58:B1:215:LYS:HE3	2.44	0.46
58:B1:772:TYR:HE2	59:B2:561:ILE:HG21	1.81	0.46
64:a:193:LEU:O	64:a:197:LYS:N	2.42	0.46
4:D:1:MET:HE3	4:D:3:ARG:HH21	1.80	0.46
15:O:36:VAL:HG22	15:O:38:GLY:H	1.80	0.46
29:d:49:ARG:NH1	51:1:674:G:OP2	2.48	0.46
31:f:136:ASP:HB3	31:f:139:VAL:HG12	1.97	0.46
36:l:18:ARG:NE	51:1:1249:U:C5	2.79	0.46
39:o:6:ALA:HA	39:o:9:ARG:HE	1.81	0.46
48:x:16:ASN:HB2	48:x:24:THR:HB	1.97	0.46
51:1:233:A:H5'	51:1:233:A:H8	1.81	0.46
51:1:365:U:H2'	51:1:366:C:O4'	2.16	0.46
51:1:441:U:H2'	51:1:442:G:H8	1.81	0.46
51:1:824:U:H2'	51:1:825:A:O4'	2.15	0.46
51:1:912:C:O2'	51:1:913:U:H5'	2.15	0.46
51:1:1313:U:O2	51:1:1313:U:C2'	2.64	0.46
51:1:1790:C:H2'	51:1:1791:A:C5	2.51	0.46
53:3:10:A:H2'	53:3:11:G:C8	2.51	0.46
53:3:131:A:H2'	53:3:132:C:C6	2.51	0.46
53:3:271:C:H2'	53:3:272:C:C6	2.51	0.46
53:3:460:A:H2'	53:3:461:A:C8	2.51	0.46
53:3:857:C:H2'	53:3:858:G:O4'	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1104:G:H2'	53:3:1105:A:O4'	2.16	0.46
57:A1:35:PHE:HA	57:A1:38:THR:HG22	1.97	0.46
2:B:14:MET:HG2	51:1:15:G:O2'	2.16	0.46
10:J:156:ARG:NH1	13:M:98:LEU:O	2.49	0.46
15:O:36:VAL:HA	15:O:76:ILE:HA	1.97	0.46
27:b:6:LYS:HD2	27:b:7:PRO:HD2	1.98	0.46
29:d:22:ASP:OD1	29:d:22:ASP:N	2.48	0.46
43:s:82:MET:HB2	43:s:98:LYS:HB2	1.97	0.46
51:1:690:G:H2'	51:1:691:C:H5'	1.98	0.46
51:1:2491:U:C2'	51:1:2492:U:H5'	2.42	0.46
51:1:2537:U:H2'	51:1:2538:C:H6	1.78	0.46
51:1:2643:G:O2'	51:1:2644:G:H5'	2.16	0.46
51:1:2646:C:H2'	51:1:2647:U:O4'	2.16	0.46
51:1:2695:U:H2'	51:1:2696:U:C6	2.51	0.46
53:3:250:A:O4'	53:3:252:U:H1'	2.15	0.46
53:3:556:C:O2'	53:3:557:G:H5'	2.16	0.46
53:3:1121:U:H2'	53:3:1122:U:C6	2.51	0.46
58:B1:1167:LYS:NZ	58:B1:1170:LYS:HB2	2.30	0.46
59:B2:230:PHE:HB2	59:B2:333:ILE:HB	1.97	0.46
65:0:320:LEU:HD12	65:0:320:LEU:HA	1.86	0.46
65:0:419:ALA:HB2	65:0:486:PRO:HA	1.98	0.46
65:0:607:LYS:HE2	65:0:607:LYS:HB2	1.72	0.46
12:L:79:VAL:O	12:L:79:VAL:HG12	2.16	0.46
16:P:97:ARG:HA	16:P:100:ASN:HD22	1.81	0.46
27:b:71:ASP:HB3	27:b:118:GLY:HA2	1.98	0.46
29:d:47:LYS:HG2	51:1:451:U:OP2	2.15	0.46
51:1:2751:G:O2'	51:1:2752:C:H5'	2.16	0.46
53:3:323:U:H3	53:3:327:A:H62	1.64	0.46
53:3:962:C:H1'	53:3:1201:A:C6	2.51	0.46
53:3:1069:C:H4'	53:3:1192:C:O2	2.16	0.46
53:3:1436:U:H2'	53:3:1437:A:C8	2.45	0.46
58:B1:115:TRP:HB3	58:B1:1333:THR:CG2	2.46	0.46
58:B1:1227:HIS:HA	58:B1:1230:THR:HG22	1.99	0.46
59:B2:689:ALA:HB2	59:B2:1233:LEU:HD23	1.97	0.46
59:B2:735:LYS:HA	59:B2:748:ILE:HG22	1.97	0.46
16:P:115:ILE:HD12	16:P:116:PRO:HD2	1.98	0.45
17:Q:34:THR:HG22	17:Q:76:HIS:CD2	2.51	0.45
21:U:4:ILE:HD13	21:U:21:VAL:HA	1.99	0.45
25:Y:76:ALA:O	25:Y:79:THR:OG1	2.27	0.45
27:b:155:ARG:CZ	51:1:1818:U:C5	3.00	0.45
28:c:61:THR:HB	28:c:63:PRO:HD2	1.96	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:r:49:ILE:HG22	42:r:54:VAL:HG22	1.97	0.45
43:s:25:ARG:NE	43:s:74:ILE:O	2.46	0.45
51:1:107:G:H2'	51:1:108:G:C8	2.51	0.45
51:1:393:C:H2'	51:1:394:C:H6	1.81	0.45
51:1:1642:G:O2'	51:1:1643:G:H5'	2.15	0.45
51:1:1841:U:H2'	51:1:1842:G:C8	2.51	0.45
53:3:113:G:O2'	53:3:353:A:H4'	2.16	0.45
53:3:478:A:H2'	53:3:479:U:C4'	2.45	0.45
53:3:1316:G:H2'	53:3:1317:C:H5''	1.98	0.45
55:8:13:DT:C6	58:B1:791:ALA:HA	2.51	0.45
58:B1:343:LEU:HD11	58:B1:1324:SER:HB3	1.98	0.45
65:0:15:ILE:O	65:0:89:THR:OG1	2.35	0.45
65:0:526:GLU:H	65:0:575:GLY:H	1.64	0.45
10:J:161:GLU:HA	10:J:164:LEU:HD12	1.97	0.45
12:L:140:VAL:O	12:L:144:ALA:N	2.46	0.45
15:O:15:HIS:CG	53:3:1152:A:H5'	2.51	0.45
16:P:71:ASP:OD1	16:P:71:ASP:N	2.43	0.45
29:d:131:THR:HA	29:d:134:LEU:HB3	1.97	0.45
34:j:57:LEU:HD11	34:j:130:HIS:HD2	1.82	0.45
45:u:88:ASP:OD1	45:u:88:ASP:N	2.48	0.45
51:1:1086:A:H1'	51:1:1103:A:H2	1.81	0.45
53:3:37:U:H2'	53:3:38:G:H5'	1.98	0.45
53:3:280:C:H5''	53:3:281:G:OP2	2.16	0.45
53:3:973:G:H2'	53:3:974:A:C8	2.51	0.45
53:3:1173:U:H2'	53:3:1174:G:C8	2.48	0.45
53:3:1289:A:H2'	53:3:1290:G:H5'	1.98	0.45
11:K:18:VAL:HG13	11:K:19:PRO:HD3	1.97	0.45
14:N:30:ASN:N	14:N:64:ILE:O	2.48	0.45
15:O:59:LYS:HD3	53:3:972:C:O3'	2.16	0.45
20:T:38:LEU:HD23	20:T:55:LEU:HD12	1.98	0.45
31:f:91:VAL:HG21	51:1:2657:A:H4'	1.97	0.45
31:f:94:ARG:HA	31:f:127:GLN:HB2	1.99	0.45
32:g:94:ILE:HD12	32:g:99:ILE:HG21	1.98	0.45
45:u:5:ARG:NH1	51:1:84:A:H5''	2.31	0.45
51:1:642:U:H2'	51:1:644:A:OP2	2.16	0.45
51:1:777:G:N7	51:1:793:A:C2	2.78	0.45
51:1:952:G:H3'	51:1:953:G:H5''	1.98	0.45
51:1:1614:A:C2'	51:1:1615:C:H5'	2.46	0.45
51:1:1792:G:H1	51:1:1827:U:H3	1.65	0.45
51:1:2099:U:H2'	51:1:2100:G:C8	2.51	0.45
51:1:2457:U:O2'	51:1:2458:G:H5'	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2680:U:O2'	51:1:2681:C:H5'	2.16	0.45
53:3:951:G:H2'	53:3:952:U:H6	1.79	0.45
57:A2:80:GLU:HG3	59:B2:694:ARG:HH22	1.81	0.45
58:B1:515:ARG:NH2	58:B1:718:SER:O	2.48	0.45
59:B2:24:VAL:HG11	59:B2:704:MET:HE1	1.98	0.45
59:B2:557:ARG:NH2	59:B2:607:SER:O	2.50	0.45
7:G:115:ASP:OD1	7:G:115:ASP:N	2.42	0.45
8:H:10:ARG:HA	8:H:13:ILE:HD11	1.97	0.45
14:N:16:ALA:HA	14:N:66:VAL:HA	1.98	0.45
16:P:114:PRO:O	26:Z:28:LEU:HD21	2.17	0.45
22:V:21:VAL:HG22	22:V:44:HIS:HA	1.98	0.45
31:f:84:LYS:HA	31:f:84:LYS:HD2	1.78	0.45
31:f:98:LYS:HD2	31:f:98:LYS:HA	1.79	0.45
33:i:52:LEU:HD13	33:i:77:VAL:HG13	1.97	0.45
51:1:44:A:C2'	51:1:45:G:H5'	2.45	0.45
51:1:1069:A:H2'	51:1:1073:A:C5	2.51	0.45
51:1:1954:G:H21	51:1:1956:U:H3	1.65	0.45
51:1:2101:A:H2'	51:1:2102:G:C8	2.51	0.45
51:1:2190:G:H2'	51:1:2191:A:O4'	2.16	0.45
51:1:2869:G:H2'	51:1:2870:C:O4'	2.16	0.45
52:2:30:C:H2'	52:2:31:C:C5'	2.47	0.45
52:2:118:C:C2'	52:2:119:A:H4'	2.33	0.45
53:3:144:G:H2'	53:3:145:G:O4'	2.16	0.45
53:3:569:C:H4'	53:3:574:A:N7	2.31	0.45
53:3:684:U:H3	53:3:706:A:H61	1.63	0.45
53:3:1096:C:H2'	53:3:1097:C:H6	1.80	0.45
53:3:1361:G:H2'	53:3:1362:A:O4'	2.16	0.45
57:A1:231:PHE:O	57:A2:218:ARG:NH1	2.50	0.45
58:B1:213:LYS:HA	58:B1:213:LYS:HE3	1.99	0.45
58:B1:395:LYS:HZ2	58:B1:399:LYS:HE2	1.82	0.45
59:B2:546:GLU:H	59:B2:546:GLU:HG3	1.53	0.45
65:0:144:MET:HG2	65:0:266:CYS:HB2	1.99	0.45
65:0:171:LEU:HD11	65:0:218:TRP:HD1	1.82	0.45
2:B:49:ARG:NH2	51:1:2884:U:H1'	2.32	0.45
6:F:28:SER:OG	6:F:29:ALA:N	2.50	0.45
15:O:47:GLU:OE2	15:O:69:THR:OG1	2.30	0.45
33:i:94:LYS:HD3	33:i:94:LYS:HA	1.73	0.45
34:j:12:LYS:HA	34:j:12:LYS:HD2	1.78	0.45
34:j:118:MET:HE3	34:j:118:MET:HB2	1.75	0.45
51:1:817:C:O2'	51:1:839:U:H5''	2.16	0.45
51:1:864:G:H2'	51:1:865:C:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:866:A:H61	51:1:913:U:C1'	2.28	0.45
51:1:2123:G:N3	51:1:2176:A:N6	2.65	0.45
51:1:2785:C:H2'	51:1:2786:U:C6	2.51	0.45
53:3:607:A:H2'	53:3:608:A:O4'	2.17	0.45
58:B1:201:LEU:CD1	58:B1:224:LEU:HD12	2.46	0.45
58:B1:926:PRO:HB2	58:B1:1241:TYR:HE1	1.82	0.45
59:B2:674:ASP:OD2	59:B2:1070:HIS:ND1	2.50	0.45
59:B2:895:LEU:HD13	59:B2:895:LEU:HA	1.67	0.45
65:0:560:GLN:HB2	65:0:601:PHE:HD2	1.81	0.45
5:E:7:ARG:NH1	51:1:243:U:OP2	2.49	0.45
10:J:88:HIS:HB3	10:J:134:ASN:HD21	1.81	0.45
29:d:43:THR:O	51:1:38:A:H1'	2.17	0.45
31:f:88:LEU:HB3	31:f:128:THR:HA	1.98	0.45
33:i:126:ARG:O	33:i:130:GLY:N	2.50	0.45
39:o:94:ARG:NH2	39:o:98:GLN:OE1	2.50	0.45
40:p:74:GLN:NE2	51:1:2683:C:O2'	2.49	0.45
42:r:38:VAL:HG21	42:r:57:GLY:HA3	1.97	0.45
51:1:252:G:H2'	51:1:253:C:H6	1.81	0.45
51:1:468:G:C2'	51:1:469:G:H5'	2.46	0.45
51:1:2226:C:H2'	51:1:2227:A:O4'	2.17	0.45
53:3:334:C:H2'	53:3:335:C:O4'	2.16	0.45
53:3:384:G:H2'	53:3:385:C:C6	2.52	0.45
53:3:962:C:H42	53:3:973:G:H1	1.64	0.45
55:8:20:DA:H4'	59:B2:143:ARG:NH1	2.31	0.45
58:B1:67:ASP:OD1	58:B1:67:ASP:O	2.35	0.45
58:B1:109:SER:HB2	58:B1:296:LYS:HG2	1.98	0.45
58:B1:213:LYS:HE3	58:B1:213:LYS:CA	2.47	0.45
59:B2:27:LEU:O	59:B2:528:ARG:NH1	2.43	0.45
11:K:11:HIS:HB3	11:K:14:GLN:HB2	1.99	0.45
13:M:104:SER:OG	53:3:642:A:N3	2.48	0.45
18:R:107:THR:HG21	53:3:1307:U:H4'	1.99	0.45
19:S:23:ARG:HH12	19:S:27:LYS:HB3	1.82	0.45
30:e:35:LEU:HD22	30:e:151:LEU:HD21	1.99	0.45
37:m:27:SER:H	37:m:104:GLU:CD	2.24	0.45
38:n:99:LYS:HE3	38:n:99:LYS:HB3	1.72	0.45
40:p:48:ALA:N	40:p:59:THR:OG1	2.50	0.45
51:1:91:A:H8	51:1:91:A:OP1	1.99	0.45
51:1:388:G:H2'	51:1:390:U:H5	1.81	0.45
51:1:708:G:O2'	51:1:709:U:H5'	2.17	0.45
51:1:753:A:H2'	51:1:754:U:C6	2.52	0.45
51:1:927:A:H2'	51:1:928:A:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1028:A:N6	51:1:1125:G:H2'	2.31	0.45
51:1:1337:G:O2'	51:1:1338:G:H5'	2.17	0.45
51:1:1573:G:H2'	51:1:1574:C:O4'	2.17	0.45
53:3:771:G:H2'	53:3:772:U:C6	2.51	0.45
53:3:1098:C:H2'	53:3:1099:G:O4'	2.17	0.45
58:B1:68:TYR:O	58:B1:75:TYR:CD2	2.70	0.45
58:B1:75:TYR:CD2	58:B1:75:TYR:O	2.70	0.45
58:B1:375:GLU:HB3	59:B2:1245:ALA:HB3	1.97	0.45
59:B2:517:GLN:HB3	59:B2:760:ASN:H	1.80	0.45
62:NG:135:ARG:O	62:NG:178:VAL:HA	2.16	0.45
20:T:19:ASN:O	53:3:750:C:H1'	2.16	0.45
20:T:80:LEU:O	20:T:84:LEU:N	2.42	0.45
24:X:46:LEU:HD12	24:X:48:ILE:HD11	1.99	0.45
24:X:71:GLY:HA3	53:3:1320:C:C2	2.51	0.45
27:b:155:ARG:NH1	51:1:1818:U:C5	2.81	0.45
28:c:194:PRO:HA	51:1:2680:U:C5'	2.46	0.45
29:d:37:ALA:HB1	29:d:94:GLN:H	1.82	0.45
33:i:9:LYS:HA	33:i:57:VAL:HA	1.99	0.45
35:k:61:VAL:O	35:k:85:VAL:N	2.47	0.45
49:y:38:GLN:O	51:1:95:A:H4'	2.16	0.45
51:1:191:A:H2'	51:1:192:C:H6	1.81	0.45
51:1:224:U:H2'	51:1:225:C:O4'	2.17	0.45
51:1:878:A:H3'	51:1:879:G:H8	1.82	0.45
51:1:1094:U:H2'	51:1:1096:A:OP2	2.17	0.45
51:1:1300:G:N7	51:1:1626:A:H2'	2.32	0.45
51:1:1786:A:O2'	51:1:1787:A:H5'	2.17	0.45
51:1:1979:U:O5'	51:1:1979:U:H6	1.99	0.45
51:1:2127:G:H2'	51:1:2128:G:C8	2.52	0.45
53:3:433:G:H2'	53:3:434:U:C6	2.51	0.45
53:3:1255:G:H1	53:3:1282:C:H42	1.64	0.45
58:B1:33:TRP:HZ2	59:B2:1336:ASN:OD1	2.00	0.45
59:B2:909:LYS:O	59:B2:910:ALA:C	2.59	0.45
65:0:211:MET:HB3	65:0:211:MET:HE2	1.63	0.45
65:0:520:ILE:HA	65:0:579:HIS:H	1.80	0.45
8:H:63:ILE:HG23	8:H:98:ALA:HA	1.98	0.45
10:J:72:ASN:OD1	10:J:72:ASN:N	2.50	0.45
14:N:28:VAL:HG13	14:N:63:TYR:HA	1.99	0.45
19:S:61:ASN:HB3	19:S:72:PHE:CE2	2.52	0.45
32:g:98:ASP:O	32:g:102:ALA:N	2.49	0.45
35:k:56:ASP:N	35:k:56:ASP:OD1	2.49	0.45
39:o:18:LEU:HD23	39:o:21:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:65:GLN:CD	51:1:328:U:H4'	2.42	0.45
50:z:19:HIS:CD2	50:z:50:VAL:HG12	2.52	0.45
51:1:623:C:H2'	51:1:624:C:C6	2.52	0.45
51:1:1429:G:C2	51:1:1568:G:C2	3.05	0.45
53:3:347:G:H2'	53:3:348:G:O4'	2.17	0.45
53:3:437:U:C2'	53:3:438:U:H5'	2.46	0.45
53:3:768:A:C2	53:3:1512:U:H4'	2.52	0.45
53:3:962:C:H1'	53:3:1201:A:N1	2.32	0.45
53:3:1147:C:H2'	53:3:1148:U:C6	2.52	0.45
57:A1:185:TYR:HA	57:A1:202:VAL:O	2.16	0.45
58:B1:105:ILE:HD12	58:B1:242:LEU:CD2	2.44	0.45
58:B1:388:ARG:HG2	58:B1:388:ARG:NH1	2.32	0.45
59:B2:1314:GLN:HA	60:W0:28:ARG:HH22	1.80	0.45
60:W0:25:ARG:NH1	60:W0:61:ASN:OD1	2.49	0.45
65:0:173:ILE:HD13	65:0:173:ILE:HA	1.90	0.45
1:A:41:HIS:HD2	30:e:108:PRO:HA	1.82	0.45
7:G:103:TRP:CZ3	61:NA:218:GLU:O	2.70	0.45
9:I:96:ARG:HG2	9:I:133:SER:HA	1.99	0.45
16:P:25:SER:HG	16:P:28:ASN:H	1.63	0.45
27:b:73:ILE:HG12	51:1:1490:A:H2	1.79	0.45
27:b:84:PRO:HG3	51:1:1568:G:OP1	2.16	0.45
27:b:212:TRP:NE1	51:1:1566:A:O4'	2.50	0.45
29:d:153:LEU:HD11	29:d:158:PHE:HB2	1.98	0.45
30:e:35:LEU:HB2	30:e:88:VAL:HG12	1.98	0.45
30:e:91:ARG:HA	30:e:95:MET:HG2	1.99	0.45
33:i:52:LEU:HD11	33:i:81:LYS:HD3	1.99	0.45
40:p:105:LYS:HG2	53:3:1464:U:OP1	2.17	0.45
51:1:598:U:H2'	51:1:599:A:C8	2.52	0.45
51:1:776:G:C8	51:1:793:A:C2	3.05	0.45
51:1:1432:G:H2'	51:1:1433:A:C8	2.52	0.45
51:1:2066:C:H2'	51:1:2067:G:H8	1.81	0.45
53:3:925:G:H1'	53:3:1502:A:C4	2.52	0.45
53:3:1198:G:H2'	53:3:1199:U:C6	2.51	0.45
58:B1:395:LYS:NZ	58:B1:399:LYS:HE2	2.32	0.45
58:B1:1158:GLU:HA	58:B1:1223:LEU:HD21	1.99	0.45
65:0:643:LYS:HE3	65:0:655:HIS:HB3	1.99	0.45
8:H:58:ARG:HB3	8:H:63:ILE:HB	1.98	0.44
8:H:153:SER:O	8:H:196:GLY:N	2.50	0.44
12:L:57:GLU:HG3	12:L:58:LEU:HD12	1.99	0.44
17:Q:57:THR:HG21	53:3:362:G:H5''	1.99	0.44
26:Z:44:ARG:HD3	26:Z:44:ARG:HA	1.77	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:m:9:PHE:HB3	37:m:10:ARG:H	1.67	0.44
38:n:73:ASN:O	38:n:77:ALA:N	2.50	0.44
51:1:146:A:H2'	51:1:147:C:H6	1.81	0.44
51:1:740:C:H5'	51:1:740:C:C6	2.46	0.44
51:1:918:A:H4'	52:2:97:C:O2	2.16	0.44
51:1:1020:A:C1'	51:1:1021:A:OP2	2.61	0.44
51:1:1087:G:H1	51:1:1102:C:H42	1.64	0.44
51:1:1276:A:H61	51:1:1294:U:H3	1.64	0.44
51:1:1565:C:O2'	51:1:1566:A:H2'	2.16	0.44
51:1:1954:G:N2	51:1:1956:U:H3	2.15	0.44
51:1:2061:G:C2'	51:1:2501:C:HO2'	2.25	0.44
51:1:2183:A:H2'	51:1:2184:A:C8	2.52	0.44
51:1:2737:G:H2'	51:1:2738:A:C8	2.52	0.44
52:2:16:G:N2	52:2:69:G:H1'	2.31	0.44
53:3:20:U:O2'	53:3:21:G:H5'	2.17	0.44
58:B1:87:LYS:HZ3	58:B1:87:LYS:HG3	1.34	0.44
59:B2:805:MET:HE3	59:B2:805:MET:HB2	1.86	0.44
63:6:70:G:H2'	63:6:71:C:C6	2.52	0.44
65:0:11:ARG:HG3	65:0:283:ILE:HA	1.99	0.44
16:P:25:SER:HG	16:P:28:ASN:N	2.15	0.44
25:Y:4:LYS:NZ	53:3:332:G:P	2.91	0.44
25:Y:10:ALA:O	25:Y:13:SER:OG	2.27	0.44
28:c:2:ILE:HG12	28:c:90:PHE:HZ	1.82	0.44
31:f:41:GLU:N	31:f:52:GLY:O	2.49	0.44
34:j:19:ASP:OD2	34:j:21:THR:OG1	2.29	0.44
36:l:135:ILE:HG23	36:l:140:GLY:HA3	1.99	0.44
48:x:31:ASN:ND2	48:x:52:ALA:HB3	2.32	0.44
50:z:37:ARG:NH1	51:1:928:A:O2'	2.50	0.44
51:1:162:U:H6	51:1:163:C:H5	1.65	0.44
51:1:754:U:O5'	51:1:754:U:H6	2.00	0.44
51:1:885:C:H2'	51:1:891:G:H22	1.82	0.44
51:1:1541:C:H2'	51:1:1542:U:O4'	2.17	0.44
51:1:2007:U:O5'	51:1:2007:U:H6	2.01	0.44
51:1:2073:C:O5'	51:1:2073:C:H6	1.99	0.44
51:1:2125:G:C5'	64:a:39:VAL:HG22	2.47	0.44
51:1:2599:G:H2'	51:1:2600:A:H8	1.80	0.44
52:2:6:G:O2'	52:2:7:G:H5'	2.17	0.44
53:3:757:U:H2'	53:3:758:C:H5'	1.99	0.44
53:3:782:A:O3'	53:3:1515:G:H4'	2.17	0.44
53:3:792:A:H4'	53:3:793:U:C5'	2.47	0.44
55:8:1:DC:H2''	55:8:2:DC:C6	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:76:LYS:NZ	58:B1:76:LYS:HB3	2.32	0.44
58:B1:128:LEU:CD2	58:B1:188:LEU:HB3	2.47	0.44
58:B1:484:MET:CE	59:B2:1278:LEU:HD21	2.47	0.44
58:B1:1108:GLN:HG3	58:B1:1109:LEU:HD12	1.99	0.44
59:B2:176:ILE:HD11	59:B2:428:VAL:HG21	1.98	0.44
65:0:75:MET:HG3	65:0:279:LEU:HD11	1.99	0.44
65:0:97:ILE:HD13	65:0:412:PRO:HG3	2.00	0.44
65:0:594:LYS:HB3	65:0:594:LYS:HE3	1.66	0.44
3:C:45:HIS:ND1	51:1:2372:U:H4'	2.32	0.44
5:E:15:LYS:HA	5:E:21:PHE:HA	1.99	0.44
9:I:47:LEU:HD22	53:3:510:A:OP1	2.17	0.44
17:Q:11:ARG:HH11	53:3:563:A:H2	1.64	0.44
17:Q:120:ARG:HG2	53:3:37:U:C5'	2.47	0.44
22:V:64:ARG:CB	53:3:130:A:H8	2.31	0.44
34:j:134:ALA:HB1	51:1:2898:U:O2	2.17	0.44
35:k:62:VAL:HA	35:k:84:CYS:HA	2.00	0.44
51:1:1024:G:O5'	51:1:1025:G:H5''	2.16	0.44
51:1:2194:U:H2'	51:1:2195:U:C6	2.52	0.44
53:3:272:C:H2'	53:3:273:U:H6	1.83	0.44
53:3:563:A:H2'	53:3:563:A:N3	2.32	0.44
53:3:806:C:H2'	53:3:807:A:C8	2.52	0.44
53:3:946:A:H4'	53:3:1333:A:O2'	2.17	0.44
53:3:994:A:H61	53:3:1047:G:C4'	2.30	0.44
58:B1:434:ILE:HD11	59:B2:1274:GLU:HG3	1.99	0.44
58:B1:804:ALA:HB2	58:B1:1256:ILE:CD1	2.48	0.44
58:B1:978:ARG:HD3	58:B1:999:TYR:H	1.83	0.44
58:B1:1357:ILE:HG22	58:B1:1359:ALA:H	1.82	0.44
62:NG:161:SER:CB	62:NG:170:PRO:HA	2.48	0.44
65:0:13:ILE:HG22	65:0:86:ILE:HA	1.98	0.44
65:0:507:LYS:HE2	65:0:507:LYS:HB2	1.49	0.44
7:G:20:ARG:HD2	53:3:831:A:H5''	1.98	0.44
7:G:136:ARG:O	7:G:140:LEU:N	2.47	0.44
9:I:145:ARG:HB3	9:I:148:ALA:HB3	1.99	0.44
14:N:6:TYR:OH	53:3:1148:U:H5'	2.16	0.44
18:R:94:LEU:HD12	18:R:95:PRO:HD2	2.00	0.44
19:S:2:LYS:HG2	19:S:4:SER:H	1.81	0.44
40:p:25:VAL:HG21	40:p:83:ILE:HG22	1.99	0.44
51:1:960:A:H5''	51:1:961:C:OP1	2.17	0.44
51:1:1044:C:O5'	51:1:1044:C:H6	2.00	0.44
51:1:1656:C:H2'	51:1:1657:U:H6	1.82	0.44
51:1:2560:A:O2'	51:1:2561:U:H5'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2757:A:H2'	51:1:2757:A:N3	2.31	0.44
53:3:1475:G:C2	53:3:1476:A:H1'	2.52	0.44
58:B1:375:GLU:O	59:B2:1247:SER:HB3	2.16	0.44
59:B2:998:LEU:HG	59:B2:1011:LEU:HB3	1.99	0.44
65:0:494:ILE:HA	65:0:610:PRO:HA	1.99	0.44
65:0:498:VAL:HG12	65:0:522:MET:HB2	1.99	0.44
11:K:45:ARG:N	11:K:57:ALA:O	2.44	0.44
19:S:75:LYS:HZ3	53:3:1357:A:H5''	1.82	0.44
26:Z:6:ARG:HA	26:Z:6:ARG:HD2	1.61	0.44
29:d:5:LEU:HG	29:d:120:VAL:HG13	2.00	0.44
41:q:25:GLY:O	41:q:29:ARG:NH1	2.50	0.44
45:u:27:VAL:HA	45:u:33:VAL:HG13	1.98	0.44
51:1:233:A:C2'	51:1:234:U:H5'	2.48	0.44
51:1:1130:U:C5	51:1:2025:C:H5''	2.53	0.44
51:1:1368:G:H2'	51:1:1369:G:C8	2.51	0.44
51:1:2069:G:H2'	51:1:2070:A:H8	1.82	0.44
51:1:2270:A:H2'	51:1:2271:G:O4'	2.18	0.44
53:3:152:A:H2'	53:3:153:C:H5'	1.99	0.44
53:3:240:G:H2'	53:3:241:G:C8	2.53	0.44
53:3:675:A:C2	53:3:676:A:H1'	2.52	0.44
56:9:12:DC:H3'	58:B1:47:ARG:HH12	1.83	0.44
58:B1:770:LEU:HD13	59:B2:618:GLN:CD	2.42	0.44
59:B2:444:ASP:OD1	59:B2:444:ASP:N	2.51	0.44
59:B2:1246:ARG:HH11	59:B2:1266:GLY:HA2	1.82	0.44
65:0:119:VAL:HG21	65:0:162:LEU:HD11	1.99	0.44
21:U:26:ASN:HD21	21:U:31:ARG:N	2.15	0.44
27:b:17:LYS:HE3	27:b:17:LYS:HB3	1.80	0.44
27:b:57:HIS:CE1	51:1:1567:G:H4'	2.52	0.44
37:m:81:ARG:NH1	51:1:2251:G:OP1	2.51	0.44
47:w:56:PHE:HE1	47:w:58:LYS:HE2	1.83	0.44
51:1:324:A:N6	51:1:338:G:H21	2.10	0.44
51:1:514:A:O2'	51:1:515:A:H5'	2.17	0.44
51:1:974:G:O2'	51:1:989:G:N2	2.51	0.44
51:1:1093:G:H22	51:1:1097:U:H3'	1.82	0.44
51:1:1630:A:H2'	51:1:1631:G:H5'	2.00	0.44
51:1:2102:G:H1	51:1:2187:U:H3	1.65	0.44
51:1:2102:G:H2'	51:1:2103:C:O4'	2.18	0.44
51:1:2703:C:H2'	51:1:2704:C:H6	1.82	0.44
53:3:253:A:O4'	53:3:276:G:H1'	2.18	0.44
53:3:505:G:C6	53:3:535:A:C2	3.06	0.44
53:3:563:A:H5'	53:3:566:G:N2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:969:A:H2'	53:3:970:C:O4'	2.18	0.44
57:A1:68:TYR:HE1	57:A1:79:LEU:HD13	1.82	0.44
64:a:167:LYS:HE2	64:a:167:LYS:HB3	1.55	0.44
65:0:145:ASP:OD1	65:0:273:LYS:NZ	2.45	0.44
65:0:338:VAL:HG13	65:0:380:GLY:H	1.83	0.44
12:L:67:ASN:HB3	12:L:129:ASN:HD21	1.83	0.44
14:N:125:GLN:HG3	53:3:1232:U:H5''	1.99	0.44
17:Q:48:LEU:HD12	17:Q:48:LEU:HA	1.84	0.44
19:S:92:ILE:HD13	19:S:92:ILE:HA	1.84	0.44
26:Z:24:LYS:HD3	26:Z:24:LYS:HA	1.81	0.44
28:c:197:THR:HG23	51:1:2820:A:C6	2.52	0.44
31:f:62:ALA:HA	51:1:2748:A:O2'	2.18	0.44
34:j:81:ILE:HG21	51:1:2514:U:H4'	1.99	0.44
39:o:90:VAL:HG23	39:o:117:PHE:HB3	2.00	0.44
40:p:28:LYS:HB2	40:p:82:SER:H	1.81	0.44
47:w:58:LYS:HD3	51:1:2366:A:H4'	1.99	0.44
51:1:138:U:H3'	51:1:139:U:H5'	1.99	0.44
51:1:368:A:C2'	51:1:369:U:H5'	2.47	0.44
51:1:1177:G:H2'	51:1:1178:C:C5'	2.48	0.44
51:1:1913:A:H3'	51:1:1913:A:OP2	2.18	0.44
51:1:2723:C:H2'	51:1:2724:U:O4'	2.17	0.44
53:3:68:G:H2'	53:3:69:G:O4'	2.17	0.44
53:3:290:C:H2'	53:3:291:U:O4'	2.18	0.44
53:3:369:G:N2	53:3:393:A:H1'	2.33	0.44
53:3:622:A:H2'	53:3:623:C:H5'	1.99	0.44
53:3:894:G:H2'	53:3:895:G:C8	2.53	0.44
55:8:16:DT:H2'	55:8:17:DC:C6	2.52	0.44
58:B1:62:PHE:N	58:B1:62:PHE:CD1	2.85	0.44
58:B1:107:LEU:HA	58:B1:276:ASN:ND2	2.33	0.44
58:B1:111:THR:HG21	58:B1:303:VAL:HB	1.99	0.44
58:B1:375:GLU:HB3	59:B2:1245:ALA:CB	2.48	0.44
58:B1:1024:THR:HG23	58:B1:1123:ARG:HA	2.00	0.44
59:B2:746:ALA:O	59:B2:974:ARG:NH2	2.45	0.44
60:W0:58:LEU:HD12	60:W0:59:ILE:HG12	2.00	0.44
65:0:614:GLU:OE1	65:0:690:ALA:HB2	2.18	0.44
6:F:1:MET:N	51:1:2526:G:H1'	2.32	0.44
7:G:33:ALA:HB3	7:G:37:VAL:HB	1.99	0.44
10:J:50:GLY:HA3	10:J:62:ALA:HB2	1.99	0.44
15:O:70:HIS:HD2	15:O:72:ARG:HH22	1.64	0.44
38:n:40:LYS:O	38:n:44:LEU:N	2.48	0.44
39:o:10:ARG:HE	39:o:10:ARG:HB2	1.61	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:q:32:ARG:HB2	51:1:581:C:OP1	2.18	0.44
44:t:17:SER:OG	44:t:20:ALA:N	2.48	0.44
51:1:648:G:H2'	51:1:649:G:H8	1.82	0.44
51:1:861:A:H2'	51:1:862:G:O4'	2.18	0.44
51:1:1147:A:O2'	51:1:1148:U:H5'	2.17	0.44
51:1:2073:C:O2'	51:1:2074:U:H5'	2.17	0.44
51:1:2524:G:C3'	51:1:2525:G:H5''	2.48	0.44
51:1:2599:G:H2'	51:1:2600:A:C8	2.53	0.44
52:2:115:A:H2'	52:2:116:G:C8	2.53	0.44
53:3:570:G:H5'	53:3:820:U:O4'	2.18	0.44
57:A1:192:VAL:HG12	57:A1:193:GLU:H	1.82	0.44
58:B1:45:ASN:HD22	58:B1:48:THR:H	1.65	0.44
58:B1:731:ARG:HB3	59:B2:1105:SER:HB2	2.00	0.44
59:B2:557:ARG:HB3	59:B2:587:LEU:HD13	2.00	0.44
11:K:12:PRO:O	11:K:15:SER:OG	2.32	0.44
12:L:34:LYS:NZ	53:3:1289:A:C2	2.86	0.44
13:M:45:ILE:HG12	13:M:60:LEU:HD23	2.00	0.44
14:N:45:MET:HA	14:N:48:ARG:HH21	1.82	0.44
27:b:227:VAL:HG11	51:1:784:G:C2	2.52	0.44
29:d:134:LEU:HD11	29:d:161:ALA:HB2	1.99	0.44
30:e:135:ILE:HA	30:e:140:ILE:HD11	1.99	0.44
41:q:51:GLN:O	41:q:55:GLN:N	2.48	0.44
42:r:17:GLY:H	42:r:98:ILE:HB	1.83	0.44
43:s:13:SER:OG	43:s:14:ALA:N	2.50	0.44
51:1:537:G:H22	51:1:555:G:H2'	1.83	0.44
51:1:728:G:O2'	51:1:730:A:H8	2.01	0.44
51:1:1308:A:N6	51:1:1608:A:H61	2.15	0.44
51:1:1744:A:H3'	51:1:1745:A:H8	1.83	0.44
51:1:2259:U:C2	51:1:2427:C:C4	3.06	0.44
51:1:2845:U:H2'	51:1:2846:G:H8	1.83	0.44
53:3:971:G:H4'	53:3:972:C:H5''	1.99	0.44
53:3:1057:G:H2'	53:3:1058:G:O4'	2.18	0.44
53:3:1134:G:H1	53:3:1140:C:H42	1.66	0.44
53:3:1312:G:H2'	53:3:1313:U:C6	2.52	0.44
55:8:12:DG:OP1	58:B1:795:TYR:CE1	2.71	0.44
58:B1:472:LEU:CD1	59:B2:1294:LYS:HG2	2.47	0.44
64:a:203:GLN:HG2	64:a:205:LYS:H	1.82	0.44
65:0:496:GLN:HB3	65:0:608:ALA:HA	1.98	0.44
12:L:91:ARG:O	12:L:92:PRO:C	2.59	0.43
14:N:47:VAL:HG12	14:N:78:ILE:HG21	2.00	0.43
21:U:13:LYS:CD	53:3:392:C:H5'	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:58:ILE:O	23:W:62:ARG:N	2.49	0.43
27:b:106:PRO:HD2	27:b:109:LEU:HD22	1.99	0.43
28:c:5:VAL:HG22	28:c:202:ILE:HG12	2.00	0.43
31:f:28:LYS:HE3	31:f:28:LYS:HB2	1.86	0.43
39:o:55:GLU:OE2	52:2:116:G:H5''	2.17	0.43
39:o:56:LYS:HA	39:o:59:ALA:HB3	2.00	0.43
48:x:57:VAL:HG12	48:x:61:LYS:HZ1	1.82	0.43
51:1:118:A:H5'	51:1:119:A:C8	2.53	0.43
51:1:397:U:O5'	51:1:397:U:H6	2.00	0.43
51:1:984:A:P	51:1:985:C:H5	2.41	0.43
51:1:1028:A:C2	51:1:2487:G:H1'	2.52	0.43
51:1:1056:G:H1'	51:1:1103:A:N6	2.33	0.43
51:1:1086:A:H3'	51:1:1086:A:N3	2.33	0.43
51:1:1545:A:H2'	51:1:1546:G:O4'	2.17	0.43
51:1:1697:G:H3'	51:1:1698:A:C5'	2.45	0.43
51:1:1747:U:H2'	51:1:1748:C:C6	2.52	0.43
51:1:2065:C:H2'	51:1:2066:C:C6	2.53	0.43
51:1:2248:C:H3'	51:1:2249:U:H6	1.81	0.43
53:3:182:A:N1	53:3:224:U:H5'	2.33	0.43
53:3:599:C:H2'	53:3:600:A:C8	2.53	0.43
53:3:865:A:H2'	53:3:866:C:C6	2.53	0.43
58:B1:111:THR:CG2	58:B1:300:GLN:HA	2.48	0.43
58:B1:161:THR:H	58:B1:164:GLN:HB2	1.82	0.43
58:B1:1033:GLY:HA3	58:B1:1081:VAL:O	2.18	0.43
3:C:33:LEU:HD21	51:1:2286:G:C5	2.52	0.43
8:H:66:THR:HA	8:H:101:ASN:HB2	1.99	0.43
11:K:3:HIS:ND1	11:K:65:GLU:HB2	2.33	0.43
14:N:129:ARG:NH1	63:6:32:C:OP2	2.49	0.43
23:W:35:SER:OG	23:W:37:LYS:NZ	2.37	0.43
28:c:120:GLY:H	28:c:123:LYS:HB2	1.82	0.43
29:d:129:PRO:HG3	29:d:156:ASN:HA	2.00	0.43
29:d:136:GLN:HA	29:d:139:LYS:HB2	2.00	0.43
30:e:134:GLN:NE2	30:e:147:ARG:O	2.41	0.43
32:g:27:ARG:NH2	48:x:55:MET:HB3	2.32	0.43
37:m:68:PHE:CE2	51:1:871:U:H5''	2.53	0.43
40:p:59:THR:HG22	40:p:72:VAL:HG23	2.00	0.43
51:1:152:A:H2'	51:1:153:U:C6	2.53	0.43
51:1:298:G:C2	51:1:339:U:H5	2.36	0.43
51:1:330:A:H8	51:1:1210:G:C5	2.36	0.43
51:1:728:G:H3'	51:1:729:G:H5'	2.00	0.43
51:1:974:G:C6	51:1:1186:G:C6	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2762:C:H2'	51:1:2763:G:H5'	2.00	0.43
53:3:160:A:H2'	53:3:161:A:O4'	2.18	0.43
53:3:777:A:C2	53:3:778:G:H1'	2.53	0.43
53:3:964:A:H2'	53:3:965:U:H5'	2.00	0.43
65:0:73:SER:O	65:0:73:SER:OG	2.29	0.43
8:H:68:HIS:HE2	8:H:105:VAL:HB	1.82	0.43
15:O:68:ARG:HD3	15:O:68:ARG:HA	1.68	0.43
31:f:9:VAL:HA	31:f:48:THR:HA	2.00	0.43
34:j:41:LYS:HB2	34:j:41:LYS:HE3	1.86	0.43
45:u:14:THR:OG1	45:u:15:GLY:N	2.51	0.43
51:1:755:U:H2'	51:1:756:A:C8	2.52	0.43
51:1:812:C:H1'	51:1:1250:G:C2	2.53	0.43
51:1:1057:A:H5''	51:1:1058:U:O2	2.17	0.43
53:3:296:U:H2'	53:3:297:G:O4'	2.19	0.43
53:3:635:A:H2'	53:3:636:U:C6	2.53	0.43
53:3:723:U:O2	53:3:855:U:H4'	2.18	0.43
53:3:1095:U:OP1	53:3:1108:G:N2	2.51	0.43
53:3:1508:A:H61	53:3:1527:U:H3	1.66	0.43
54:4:44:G:OP1	59:B2:1073:LYS:NZ	2.35	0.43
57:A1:212:ASP:OD1	57:A1:212:ASP:N	2.48	0.43
58:B1:388:ARG:HG2	58:B1:388:ARG:HH11	1.84	0.43
58:B1:850:LYS:HB3	58:B1:855:ASP:HB2	2.00	0.43
9:I:33:ILE:HG23	9:I:34:GLU:HG2	1.99	0.43
29:d:131:THR:HG21	51:1:320:A:H2'	1.99	0.43
33:i:128:ILE:HA	33:i:131:THR:HG22	2.01	0.43
34:j:93:ILE:HD12	34:j:93:ILE:HA	1.72	0.43
35:k:40:LYS:HZ2	35:k:57:VAL:HG12	1.84	0.43
37:m:71:LYS:HD3	37:m:72:PRO:HD2	2.00	0.43
38:n:72:ASP:O	38:n:76:VAL:HG23	2.19	0.43
43:s:36:LEU:HD23	43:s:48:LYS:HB2	2.01	0.43
48:x:9:LYS:HB3	48:x:30:PRO:CB	2.48	0.43
51:1:608:A:H2'	51:1:609:A:O4'	2.18	0.43
51:1:1943:U:OP1	51:1:1943:U:C6	2.71	0.43
51:1:1984:G:H2'	51:1:1985:C:H6	1.82	0.43
52:2:4:C:H6	52:2:4:C:C5'	2.31	0.43
53:3:1242:G:H4'	53:3:1304:G:OP1	2.18	0.43
53:3:1252:A:H2'	53:3:1253:G:O4'	2.18	0.43
53:3:1382:C:H2'	53:3:1383:C:C5	2.54	0.43
53:3:1408:A:H2	53:3:1493:A:C2	2.37	0.43
58:B1:201:LEU:HD11	58:B1:220:ARG:NH1	2.31	0.43
58:B1:478:LEU:HD21	60:W0:47:THR:HG23	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:894:VAL:HG22	58:B1:1258:ARG:HH11	1.83	0.43
12:L:29:LEU:HD23	12:L:104:VAL:HG23	2.01	0.43
14:N:68:GLY:O	14:N:74:GLN:NE2	2.37	0.43
16:P:118:ASN:OD1	53:3:718:A:H5'	2.18	0.43
17:Q:5:GLN:NE2	53:3:881:G:N7	2.67	0.43
20:T:60:SER:HB2	53:3:581:G:C5'	2.48	0.43
26:Z:66:ARG:O	53:3:1088:G:O2'	2.36	0.43
38:n:36:THR:HG22	51:1:1278:C:OP1	2.18	0.43
42:r:1:MET:N	42:r:42:ALA:O	2.42	0.43
50:z:11:SER:OG	51:1:988:A:H5''	2.18	0.43
51:1:252:G:H2'	51:1:253:C:C6	2.53	0.43
51:1:578:G:H21	51:1:1252:G:N2	2.16	0.43
51:1:1123:C:O2'	51:1:1124:G:H5'	2.18	0.43
51:1:2338:C:H6	51:1:2338:C:O5'	2.01	0.43
51:1:2556:C:H2'	51:1:2557:G:C5'	2.48	0.43
51:1:2638:G:H22	51:1:2775:G:H2'	1.83	0.43
58:B1:59:ALA:HB1	58:B1:90:VAL:HG23	2.01	0.43
58:B1:84:ILE:HG23	58:B1:90:VAL:H	1.83	0.43
58:B1:394:ILE:O	58:B1:394:ILE:HG13	2.19	0.43
58:B1:506:VAL:HG23	58:B1:628:GLY:HA3	1.99	0.43
58:B1:568:SER:HB3	58:B1:570:LYS:NZ	2.34	0.43
58:B1:824:PRO:HD3	58:B1:835:LEU:HD12	2.00	0.43
58:B1:847:ASP:OD1	58:B1:847:ASP:N	2.49	0.43
59:B2:11:ILE:HG22	59:B2:1172:LEU:HD11	1.99	0.43
59:B2:538:LEU:HD13	59:B2:543:ALA:HB2	2.01	0.43
59:B2:811:ASN:ND2	59:B2:1098:LEU:O	2.51	0.43
65:0:112:VAL:HG12	65:0:140:PHE:HB3	2.00	0.43
9:I:69:ARG:HH11	9:I:72:ARG:HH22	1.67	0.43
9:I:200:VAL:HG11	10:J:103:GLY:HA2	2.00	0.43
18:R:78:ARG:HD3	24:X:64:GLU:HG2	2.01	0.43
38:n:107:ASN:HD22	51:1:2009:A:C4'	2.31	0.43
42:r:34:GLU:HB2	42:r:58:VAL:HB	1.99	0.43
43:s:84:ARG:NH1	51:1:1322:A:O2'	2.51	0.43
47:w:56:PHE:HB2	47:w:57:ALA:H	1.73	0.43
50:z:18:LYS:HE2	50:z:18:LYS:HB3	1.89	0.43
51:1:170:U:H2'	51:1:171:U:C6	2.53	0.43
51:1:666:A:H2'	51:1:667:U:C6	2.54	0.43
51:1:824:U:H1'	51:1:2358:A:N7	2.34	0.43
51:1:1037:G:O2'	51:1:1038:G:H5'	2.18	0.43
51:1:1794:A:O2'	51:1:1795:C:H5'	2.18	0.43
51:1:1823:G:C6	51:1:1824:G:C6	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2672:U:C3'	51:1:2673:G:H5''	2.48	0.43
53:3:596:A:H61	53:3:644:U:H3	1.66	0.43
53:3:1014:A:C2	53:3:1219:A:H1'	2.54	0.43
53:3:1195:C:O5'	53:3:1195:C:H6	2.01	0.43
53:3:1515:G:H2'	53:3:1516:G:H8	1.82	0.43
58:B1:58:CYS:SG	58:B1:60:ARG:HG2	2.58	0.43
58:B1:201:LEU:CB	58:B1:221:ILE:HD13	2.47	0.43
59:B2:1157:GLN:HG3	59:B2:1159:VAL:HG13	2.00	0.43
65:0:73:SER:HB2	65:0:81:PRO:HG3	2.00	0.43
65:0:423:LYS:HA	65:0:482:ASN:HD21	1.83	0.43
3:C:35:LEU:HD12	3:C:35:LEU:HA	1.91	0.43
10:J:25:LYS:HG3	53:3:923:A:C5'	2.49	0.43
10:J:123:LEU:HD22	53:3:7:A:H2'	1.99	0.43
11:K:89:VAL:HG23	53:3:737:C:C4'	2.49	0.43
14:N:7:GLY:HA3	14:N:85:ALA:HB2	2.00	0.43
16:P:25:SER:OG	16:P:28:ASN:N	2.48	0.43
17:Q:50:LYS:HA	17:Q:50:LYS:HD2	1.86	0.43
18:R:13:HIS:HB3	18:R:15:VAL:HG12	2.00	0.43
27:b:209:ALA:HA	27:b:212:TRP:CE2	2.54	0.43
34:j:80:HIS:CD2	51:1:2642:G:H5'	2.53	0.43
34:j:130:HIS:HB2	34:j:132:HIS:HD2	1.84	0.43
35:k:49:ARG:HH22	53:3:1423:G:H5'	1.84	0.43
36:l:37:GLY:H	36:l:41:ARG:HH22	1.66	0.43
37:m:46:ILE:O	37:m:50:ARG:N	2.45	0.43
39:o:57:ALA:O	39:o:61:GLN:NE2	2.52	0.43
51:1:74:A:H2'	51:1:74:A:N3	2.33	0.43
51:1:786:C:H2'	51:1:787:C:H6	1.83	0.43
51:1:793:A:OP2	51:1:793:A:H8	2.01	0.43
51:1:862:G:H2'	51:1:863:A:O4'	2.18	0.43
51:1:1064:C:H5''	51:1:1065:U:C5	2.54	0.43
51:1:1428:C:C5	51:1:1569:A:H5''	2.54	0.43
51:1:1716:U:C2'	51:1:1717:A:H5'	2.49	0.43
51:1:1815:A:O4'	51:1:1817:G:H1'	2.18	0.43
51:1:2061:G:C8	51:1:2501:C:H4'	2.53	0.43
51:1:2101:A:H2'	51:1:2102:G:H8	1.84	0.43
51:1:2267:A:H5''	51:1:2268:A:H5'	2.01	0.43
53:3:304:U:O2'	53:3:305:G:H5'	2.19	0.43
53:3:973:G:H2'	53:3:974:A:H8	1.83	0.43
53:3:1042:A:H2'	53:3:1043:G:H4'	2.00	0.43
53:3:1158:C:H2'	53:3:1159:U:H4'	2.01	0.43
53:3:1236:A:H2'	53:3:1237:C:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:8:3:DC:N1	55:8:4:DT:H72	2.34	0.43
58:B1:139:LEU:HD23	58:B1:139:LEU:HA	1.89	0.43
58:B1:1079:LYS:HD3	58:B1:1098:GLN:HB3	1.99	0.43
59:B2:829:THR:HG23	59:B2:1059:ARG:HG2	2.00	0.43
65:0:159:LYS:HG3	65:0:166:PRO:HD2	2.00	0.43
65:0:634:ASP:O	65:0:638:ARG:NH1	2.52	0.43
13:M:10:LEU:HD13	13:M:74:ILE:HG13	2.00	0.43
14:N:18:VAL:HG21	14:N:81:GLY:HA3	2.01	0.43
27:b:120:ASP:OD1	27:b:120:ASP:N	2.49	0.43
38:n:9:GLN:HB2	51:1:1653:G:C6	2.54	0.43
51:1:481:G:H2'	51:1:507:A:N1	2.34	0.43
51:1:571:U:C4	51:1:575:A:C5	3.07	0.43
51:1:742:A:H2'	51:1:743:A:O4'	2.19	0.43
51:1:878:A:H3'	51:1:879:G:C8	2.54	0.43
51:1:960:A:O3'	51:1:961:C:H3'	2.18	0.43
51:1:1771:C:H2'	51:1:1772:A:O4'	2.19	0.43
51:1:1962:C:H1'	51:1:1963:U:C5	2.53	0.43
51:1:1998:A:H4'	51:1:2724:U:O2'	2.19	0.43
51:1:2234:G:O2'	51:1:2235:G:H5'	2.19	0.43
51:1:2311:A:H3'	51:1:2312:U:C6	2.54	0.43
53:3:37:U:C2'	53:3:38:G:H5'	2.48	0.43
53:3:439:U:O2'	53:3:440:C:H5'	2.19	0.43
53:3:640:A:H2'	53:3:641:U:H5'	2.01	0.43
53:3:1210:C:H2'	53:3:1211:U:H5'	2.00	0.43
59:B2:1275:VAL:HG13	59:B2:1287:LEU:HD11	2.01	0.43
64:a:193:LEU:HG	64:a:197:LYS:HG3	2.00	0.43
5:E:44:ARG:NH2	51:1:2349:G:OP1	2.48	0.43
14:N:53:LEU:HD12	14:N:54:VAL:HG13	2.00	0.43
18:R:74:MET:HE2	18:R:74:MET:HB3	1.84	0.43
24:X:44:ILE:HD12	24:X:44:ILE:HA	1.92	0.43
25:Y:15:LYS:HE2	25:Y:15:LYS:HB3	1.92	0.43
31:f:32:LEU:HD23	31:f:32:LEU:HA	1.86	0.43
32:g:63:ALA:HA	32:g:66:ASN:HD22	1.84	0.43
36:l:29:LYS:HA	51:1:810:U:H5	1.81	0.43
45:u:25:LYS:NZ	45:u:61:GLU:OE1	2.36	0.43
51:1:784:G:N7	51:1:792:A:C5	2.87	0.43
51:1:1313:U:O2	51:1:1313:U:H2'	2.19	0.43
51:1:1412:U:H2'	51:1:1413:A:O4'	2.18	0.43
51:1:1675:C:O2'	51:1:1676:A:H5'	2.19	0.43
51:1:1803:A:C2	51:1:1823:G:H1'	2.53	0.43
51:1:2489:U:O2'	51:1:2490:G:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2564:A:C2	51:1:2647:U:H4'	2.54	0.43
53:3:633:G:H2'	53:3:634:C:C6	2.54	0.43
53:3:778:G:H2'	53:3:779:C:O4'	2.19	0.43
57:A1:78:ILE:HA	57:A1:81:ILE:HG22	2.00	0.43
58:B1:68:TYR:HB3	58:B1:75:TYR:HE2	1.81	0.43
58:B1:141:PHE:HE2	58:B1:296:LYS:CB	2.22	0.43
58:B1:1026:PRO:HB2	58:B1:1028:ILE:HG23	2.00	0.43
64:a:48:LEU:HB3	64:a:50:ILE:HG23	2.01	0.43
65:0:129:GLN:HG3	65:0:132:LYS:HE2	2.00	0.43
4:D:10:LEU:HD13	51:1:125:A:C2	2.54	0.43
7:G:22:TRP:HA	7:G:189:ASN:HA	2.01	0.43
8:H:1:GLY:HA2	53:3:1060:U:C5	2.54	0.43
12:L:138:GLU:HA	12:L:141:HIS:HB2	2.00	0.43
33:i:105:LEU:HD13	33:i:128:ILE:HG23	2.01	0.43
34:j:116:ARG:HH21	51:1:528:A:H5''	1.81	0.43
38:n:73:ASN:HB3	51:1:1453:A:C8	2.54	0.43
46:v:88:HIS:CE1	52:2:75:G:H21	2.36	0.43
51:1:974:G:C8	51:1:989:G:C2	3.07	0.43
51:1:1135:C:O2	51:1:1135:C:H2'	2.18	0.43
51:1:1931:U:H2'	51:1:1932:A:C8	2.54	0.43
51:1:2617:U:H2'	51:1:2618:G:H5'	2.01	0.43
51:1:2626:C:O2'	51:1:2627:G:H5'	2.19	0.43
53:3:865:A:H5'	53:3:1078:U:O4	2.19	0.43
53:3:1364:U:O2'	53:3:1365:G:H5'	2.19	0.43
58:B1:175:GLU:H	58:B1:175:GLU:HG3	1.66	0.43
58:B1:1046:ILE:HG22	58:B1:1061:VAL:HA	2.00	0.43
59:B2:646:SER:OG	59:B2:647:ARG:N	2.52	0.43
5:E:28:LEU:HD12	5:E:32:LEU:HD11	2.01	0.42
6:F:38:GLY:OXT	51:1:1124:G:H1'	2.19	0.42
9:I:110:ARG:O	9:I:114:ARG:N	2.52	0.42
9:I:119:HIS:HA	53:3:439:U:H5''	2.01	0.42
14:N:58:GLU:HG2	14:N:59:LYS:HG3	2.01	0.42
16:P:24:ALA:N	16:P:86:LYS:O	2.39	0.42
23:W:25:ILE:HA	23:W:28:LEU:HD12	2.01	0.42
27:b:73:ILE:HA	27:b:74:PRO:HD3	1.90	0.42
31:f:85:LYS:HE3	31:f:131:VAL:HG22	2.01	0.42
37:m:33:LEU:HD12	37:m:117:PHE:HB3	2.00	0.42
43:s:29:VAL:HG21	43:s:55:ILE:HG21	2.01	0.42
44:t:1:MET:HG3	51:1:136:G:H21	1.84	0.42
51:1:1060:U:OP2	51:1:1060:U:H3'	2.19	0.42
51:1:1794:A:H1'	51:1:1900:A:N3	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1797:G:C4	51:1:1798:U:C6	3.07	0.42
51:1:2553:G:C3'	51:1:2554:U:H5''	2.47	0.42
51:1:2581:G:N1	51:1:2610:C:O2'	2.52	0.42
51:1:2656:U:H2'	51:1:2657:A:C8	2.54	0.42
53:3:301:G:H2'	53:3:302:G:H8	1.83	0.42
53:3:1233:G:O2'	53:3:1365:G:H5''	2.18	0.42
53:3:1423:G:H1	53:3:1477:U:H3	1.65	0.42
8:H:3:LYS:HA	8:H:3:LYS:HD3	1.95	0.42
14:N:113:LYS:HA	14:N:120:ALA:HB2	2.01	0.42
20:T:27:GLN:O	20:T:27:GLN:NE2	2.51	0.42
28:c:118:PHE:O	51:1:1655:A:H5'	2.18	0.42
28:c:183:GLU:OE2	28:c:184:ARG:NE	2.52	0.42
30:e:88:VAL:HA	52:2:42:C:O2	2.19	0.42
33:i:3:LYS:HB3	51:1:1055:G:O5'	2.19	0.42
36:l:18:ARG:NE	51:1:1249:U:C4	2.88	0.42
40:p:1:SER:N	51:1:2876:G:OP1	2.45	0.42
44:t:29:THR:HG22	44:t:86:THR:HA	2.01	0.42
51:1:343:C:C2'	51:1:344:A:H5'	2.49	0.42
51:1:503:A:H4'	51:1:505:A:H5''	2.01	0.42
51:1:597:G:H2'	51:1:598:U:O4'	2.18	0.42
51:1:832:U:C5	51:1:944:C:N4	2.87	0.42
51:1:1363:C:O2'	51:1:1809:A:H1'	2.20	0.42
51:1:1404:C:O5'	51:1:1404:C:H6	2.01	0.42
51:1:2577:A:H2'	51:1:2614:A:N6	2.33	0.42
53:3:405:U:O2	53:3:498:A:H2'	2.20	0.42
53:3:1229:A:H2'	53:3:1230:C:C6	2.54	0.42
58:B1:141:PHE:CD2	58:B1:297:ARG:HB2	2.54	0.42
58:B1:222:LYS:HD2	58:B1:222:LYS:HA	1.33	0.42
58:B1:434:ILE:HD11	59:B2:1274:GLU:CG	2.49	0.42
59:B2:22:LEU:HB3	59:B2:655:VAL:HG11	2.01	0.42
59:B2:125:GLY:H	59:B2:495:ALA:HB1	1.84	0.42
59:B2:300:ASP:OD1	59:B2:313:ALA:N	2.51	0.42
59:B2:1313:HIS:CD2	60:W0:31:GLN:HE22	2.37	0.42
8:H:174:LEU:HB3	53:3:1108:G:OP1	2.19	0.42
9:I:12:ARG:NH2	9:I:36:ALA:H	2.17	0.42
14:N:13:SER:HG	53:3:1251:A:H5'	1.81	0.42
18:R:22:TYR:HD2	18:R:65:GLU:HA	1.85	0.42
24:X:38:THR:HG23	24:X:69:LYS:HD3	2.00	0.42
28:c:118:PHE:CD2	51:1:1654:A:H2	2.35	0.42
35:k:51:LYS:HD3	35:k:51:LYS:HA	1.75	0.42
41:q:47:ARG:NH2	51:1:560:C:O2'	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:441:U:O2'	51:1:442:G:H5'	2.19	0.42
51:1:516:C:H2'	51:1:517:C:H5'	2.02	0.42
51:1:690:G:C2'	51:1:691:C:H5'	2.49	0.42
51:1:1177:G:C3'	51:1:1178:C:H5''	2.49	0.42
51:1:1797:G:N2	51:1:1798:U:H1'	2.34	0.42
51:1:1983:G:C2	51:1:1984:G:C8	3.07	0.42
51:1:2133:G:H8	51:1:2158:A:C2	2.38	0.42
51:1:2598:A:N7	51:1:2599:G:H1'	2.34	0.42
53:3:250:A:H4'	53:3:251:G:O5'	2.19	0.42
53:3:1061:G:H2'	53:3:1062:U:O4'	2.19	0.42
55:8:15:DC:H5'	59:B2:1269:ARG:HD3	2.00	0.42
58:B1:24:LEU:HD21	58:B1:116:PHE:CE2	2.54	0.42
58:B1:96:LYS:NZ	59:B2:1298:VAL:HG11	2.34	0.42
11:K:47:LEU:CD2	11:K:55:HIS:HA	2.49	0.42
13:M:15:ASN:HB3	53:3:827:U:C4'	2.48	0.42
15:O:89:ARG:HD3	58:B1:86:GLU:N	2.33	0.42
15:O:89:ARG:HH11	58:B1:87:LYS:N	2.17	0.42
27:b:218:THR:HG22	51:1:1790:C:OP1	2.19	0.42
28:c:94:GLN:H	28:c:94:GLN:HG3	1.59	0.42
33:i:12:VAL:HG12	33:i:13:ALA:H	1.83	0.42
34:j:136:GLN:NE2	51:1:2899:A:H5'	2.34	0.42
36:l:90:VAL:HG22	36:l:122:VAL:HA	2.02	0.42
46:v:58:SER:OG	46:v:59:GLU:OE1	2.31	0.42
51:1:272:A:H2'	51:1:273:G:C8	2.54	0.42
51:1:395:U:H2'	51:1:396:G:H8	1.80	0.42
51:1:809:G:O4'	51:1:1254:A:H1'	2.19	0.42
51:1:820:A:H5'	51:1:837:C:O2'	2.19	0.42
51:1:1191:G:H2'	51:1:1192:G:C8	2.51	0.42
51:1:1321:A:H3'	51:1:1322:A:H8	1.84	0.42
51:1:1801:A:C8	51:1:1801:A:H5'	2.54	0.42
51:1:2350:C:H2'	51:1:2351:G:O4'	2.19	0.42
51:1:2556:C:H2'	51:1:2557:G:O4'	2.19	0.42
53:3:1199:U:H2'	53:3:1200:C:H5'	2.01	0.42
53:3:1469:C:C2'	53:3:1470:U:H5'	2.50	0.42
57:A1:76:GLU:HB3	57:A1:80:GLU:HB3	2.01	0.42
58:B1:144:TYR:CE1	58:B1:162:GLU:OE1	2.73	0.42
58:B1:242:LEU:C	58:B1:242:LEU:HD23	2.44	0.42
58:B1:362:ARG:HB2	58:B1:364:HIS:HD2	1.83	0.42
58:B1:903:LEU:HD12	58:B1:903:LEU:HA	1.81	0.42
65:0:566:LEU:HD23	65:0:566:LEU:HA	1.80	0.42
2:B:41:HIS:HD2	38:n:101:GLY:HA2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:26:MET:HG3	7:G:29:PHE:HB2	2.00	0.42
7:G:56:LEU:HD23	7:G:56:LEU:HA	1.93	0.42
9:I:155:LYS:HA	9:I:155:LYS:HD2	1.86	0.42
24:X:32:THR:OG1	24:X:33:TRP:N	2.53	0.42
27:b:204:LEU:O	27:b:206:LYS:N	2.48	0.42
32:g:1:MET:HE3	32:g:1:MET:HB3	1.90	0.42
38:n:51:LEU:HD23	38:n:79:LEU:HD11	2.02	0.42
38:n:90:ARG:NH2	51:1:2880:C:O2'	2.48	0.42
49:y:1:MET:HA	49:y:4:LYS:HE2	2.02	0.42
51:1:194:G:H2'	51:1:195:A:O4'	2.19	0.42
51:1:981:A:H1'	51:1:2037:A:H1'	2.00	0.42
51:1:1373:A:H2'	51:1:1374:G:O4'	2.20	0.42
51:1:1592:C:H2'	51:1:1593:A:H8	1.83	0.42
51:1:2521:C:C2'	51:1:2522:U:H5'	2.50	0.42
53:3:58:C:H2'	53:3:59:A:H5'	2.01	0.42
53:3:316:C:H2'	53:3:317:U:C6	2.55	0.42
53:3:540:G:H2'	53:3:541:G:O4'	2.20	0.42
58:B1:102:MET:HG2	58:B1:246:PRO:CG	2.49	0.42
58:B1:244:VAL:HA	58:B1:269:TYR:OH	2.19	0.42
58:B1:385:LEU:CD2	58:B1:390:LEU:HB2	2.50	0.42
58:B1:513:MET:HG3	58:B1:544:LEU:HD11	2.01	0.42
58:B1:839:VAL:HG12	58:B1:864:LEU:HD12	2.02	0.42
58:B1:1002:VAL:N	58:B1:1019:ASN:O	2.45	0.42
8:H:168:ARG:NH1	53:3:1106:G:O2'	2.53	0.42
12:L:114:SER:O	12:L:118:ARG:N	2.38	0.42
18:R:77:LYS:HB2	18:R:77:LYS:HE3	1.88	0.42
25:Y:4:LYS:HE2	53:3:332:G:OP1	2.20	0.42
27:b:148:GLY:O	51:1:2205:A:H5'	2.20	0.42
28:c:161:MET:CE	51:1:2050:C:H1'	2.49	0.42
30:e:32:LYS:H	30:e:32:LYS:HG2	1.68	0.42
37:m:55:ARG:HA	37:m:58:LYS:HA	2.02	0.42
51:1:76:C:H42	51:1:110:G:H1	1.68	0.42
51:1:435:C:H2'	51:1:436:C:C5'	2.37	0.42
51:1:533:G:H5''	51:1:533:G:H8	1.83	0.42
51:1:751:A:H62	51:1:789:A:H62	1.68	0.42
51:1:780:G:H21	51:1:783:A:H62	1.67	0.42
51:1:877:A:O2'	51:1:900:A:N6	2.53	0.42
51:1:1050:A:O2'	51:1:2752:C:H1'	2.19	0.42
51:1:1145:C:H2'	51:1:1146:C:C6	2.54	0.42
51:1:2472:G:H5''	51:1:2473:U:OP2	2.20	0.42
51:1:2654:A:H1'	51:1:2656:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2733:A:H2'	51:1:2734:A:H8	1.81	0.42
53:3:264:C:H2'	53:3:265:G:O4'	2.19	0.42
53:3:269:C:H2'	53:3:270:A:C8	2.55	0.42
53:3:927:G:H4'	53:3:1503:A:N7	2.33	0.42
53:3:1271:A:H5'	53:3:1314:C:H5'	2.01	0.42
58:B1:616:PRO:HA	58:B1:619:ILE:HG22	2.02	0.42
58:B1:848:VAL:HB	58:B1:858:VAL:HG22	2.02	0.42
58:B1:930:LEU:HA	58:B1:1244:GLN:HG3	2.02	0.42
59:B2:741:MET:SD	59:B2:974:ARG:NH2	2.93	0.42
65:0:365:GLN:N	65:0:372:GLU:O	2.38	0.42
10:J:126:ALA:H	53:3:9:G:P	2.43	0.42
14:N:11:ARG:O	14:N:14:SER:OG	2.32	0.42
18:R:105:ALA:HB3	18:R:109:LYS:HE3	2.02	0.42
19:S:52:ARG:HD3	53:3:1317:C:N3	2.34	0.42
21:U:5:ARG:NH2	53:3:377:G:H5''	2.35	0.42
27:b:219:VAL:HG21	51:1:782:A:N7	2.35	0.42
28:c:152:PRO:HA	51:1:1130:U:O2	2.20	0.42
29:d:93:SER:O	29:d:93:SER:OG	2.32	0.42
37:m:42:THR:N	37:m:45:GLN:OE1	2.40	0.42
51:1:8:C:H2'	51:1:9:G:O4'	2.20	0.42
51:1:39:G:H2'	51:1:40:U:C6	2.54	0.42
51:1:172:A:H2'	51:1:173:A:C8	2.54	0.42
51:1:445:C:O2'	51:1:446:G:H5'	2.20	0.42
51:1:813:U:H2'	51:1:814:C:C6	2.54	0.42
51:1:842:U:H2'	51:1:843:G:O4'	2.19	0.42
51:1:1854:A:H2'	51:1:1855:U:H5'	2.02	0.42
51:1:2469:A:H2'	51:1:2470:G:O4'	2.20	0.42
51:1:2575:C:O5'	51:1:2575:C:H6	2.03	0.42
51:1:2633:G:C2'	51:1:2634:A:H5''	2.47	0.42
51:1:2873:A:O2'	51:1:2874:C:H5'	2.20	0.42
51:1:2897:U:H2'	51:1:2898:U:C6	2.54	0.42
52:2:79:G:H2'	52:2:80:U:O4'	2.19	0.42
53:3:228:A:H2'	53:3:229:U:O4'	2.20	0.42
53:3:1119:C:O2'	53:3:1120:C:H5'	2.20	0.42
53:3:1194:U:H2'	53:3:1195:C:C6	2.54	0.42
53:3:1405:G:H21	53:3:1518:A:H8	1.67	0.42
58:B1:245:LEU:CG	58:B1:246:PRO:HD2	2.47	0.42
58:B1:395:LYS:HE3	58:B1:395:LYS:HB3	1.45	0.42
58:B1:1272:SER:OG	58:B1:1273:ASP:N	2.53	0.42
59:B2:478:ARG:HD2	59:B2:492:MET:HA	2.02	0.42
59:B2:616:ILE:HG13	59:B2:652:TYR:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:699:LEU:HG	59:B2:799:ASN:HD22	1.85	0.42
62:NG:135:ARG:O	62:NG:178:VAL:CA	2.68	0.42
15:O:40:ILE:HD11	53:3:1124:G:H4'	2.01	0.42
17:Q:9:LYS:HE2	17:Q:9:LYS:HB2	1.85	0.42
20:T:3:SER:OG	20:T:4:THR:N	2.53	0.42
21:U:38:PHE:HZ	21:U:48:GLU:HG3	1.84	0.42
28:c:140:HIS:NE2	51:1:1658:C:OP1	2.52	0.42
29:d:46:GLN:HE21	29:d:86:ALA:HA	1.84	0.42
46:v:76:ASP:H	46:v:90:ASP:HB3	1.85	0.42
49:y:9:LYS:HD3	49:y:10:SER:H	1.84	0.42
51:1:1387:A:H2'	51:1:1388:G:C8	2.55	0.42
51:1:1564:C:C4	51:1:1565:C:C4	3.08	0.42
51:1:2060:A:O2'	51:1:2061:G:OP2	2.35	0.42
51:1:2475:C:H42	51:1:2529:G:H22	1.66	0.42
51:1:2556:C:C2'	51:1:2557:G:H5'	2.48	0.42
51:1:2670:A:H2'	51:1:2671:G:C8	2.55	0.42
53:3:627:G:H2'	53:3:628:G:C8	2.54	0.42
53:3:1005:A:C2'	53:3:1006:G:H5'	2.49	0.42
54:4:43:G:H5'	59:B2:688:GLN:HE22	1.85	0.42
58:B1:586:GLY:HA3	58:B1:612:LEU:HD11	2.01	0.42
59:B2:678:ARG:HD3	59:B2:678:ARG:HA	1.84	0.42
59:B2:998:LEU:HD21	59:B2:1015:ALA:HB2	2.02	0.42
64:a:41:SER:OG	64:a:43:ASP:OD2	2.32	0.42
65:0:281:ALA:O	65:0:285:TYR:N	2.53	0.42
65:0:324:ILE:HA	65:0:334:THR:HA	2.01	0.42
5:E:22:LYS:HZ1	51:1:631:A:H5''	1.84	0.42
8:H:24:ASN:OD1	8:H:25:THR:N	2.53	0.42
17:Q:56:LEU:HD13	17:Q:56:LEU:HA	1.91	0.42
18:R:33:LEU:HD12	18:R:33:LEU:HA	1.91	0.42
29:d:29:HIS:CE1	36:l:8:PRO:HB3	2.55	0.42
51:1:382:A:C2	51:1:393:C:N3	2.88	0.42
51:1:458:G:H21	51:1:469:G:H2'	1.84	0.42
51:1:736:C:H42	51:1:760:G:H1	1.66	0.42
51:1:1183:U:O2'	51:1:1184:U:H5'	2.20	0.42
51:1:1388:G:H2'	51:1:1389:G:H8	1.84	0.42
51:1:1512:C:O5'	51:1:1512:C:H6	2.03	0.42
51:1:1741:C:C2'	51:1:1742:U:H5'	2.50	0.42
51:1:2114:A:N6	51:1:2119:A:H61	2.18	0.42
51:1:2402:U:H2'	51:1:2403:C:C5'	2.42	0.42
53:3:7:A:H5'	53:3:298:A:O4'	2.20	0.42
53:3:668:G:H2'	53:3:669:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1292:G:H2'	53:3:1293:C:C6	2.55	0.42
58:B1:137:ARG:HA	58:B1:142:GLU:HG2	2.02	0.42
58:B1:450:HIS:HA	58:B1:451:PRO:HD3	1.91	0.42
58:B1:820:ILE:HG12	58:B1:884:SER:HB2	2.01	0.42
58:B1:1350:ASN:HA	58:B1:1353:VAL:HG12	2.02	0.42
59:B2:590:PRO:HB2	59:B2:655:VAL:HG21	2.01	0.42
2:B:24:VAL:H	43:s:35:ILE:HD11	1.84	0.42
3:C:38:PHE:HD1	3:C:45:HIS:HD2	1.68	0.42
4:D:13:ASN:HB3	51:1:125:A:O4'	2.20	0.42
8:H:12:GLY:N	8:H:15:LYS:O	2.35	0.42
9:I:149:LYS:HG2	9:I:150:LYS:HG2	2.02	0.42
14:N:21:LYS:HZ1	14:N:63:TYR:H	1.67	0.42
18:R:64:VAL:H	18:R:67:ASP:HB3	1.85	0.42
21:U:71:VAL:HA	21:U:74:LEU:HB2	2.02	0.42
27:b:144:GLU:HA	27:b:151:GLY:HA2	2.01	0.42
31:f:104:LEU:HD23	31:f:104:LEU:HA	1.94	0.42
35:k:47:ILE:HD13	35:k:47:ILE:HA	1.85	0.42
38:n:106:ASP:OD2	51:1:1287:A:C5	2.72	0.42
45:u:48:VAL:HA	45:u:49:PRO:HD3	1.92	0.42
45:u:96:LYS:HE2	51:1:300:A:P	2.60	0.42
46:v:44:HIS:CE1	46:v:86:LEU:H	2.37	0.42
51:1:1:G:H2'	51:1:2:G:C8	2.55	0.42
51:1:976:G:H5'	51:1:1156:A:N6	2.35	0.42
51:1:1229:C:H2'	51:1:1230:A:C8	2.53	0.42
51:1:1716:U:O2'	51:1:1717:A:H5'	2.19	0.42
51:1:2114:A:C5	51:1:2115:G:H1'	2.55	0.42
51:1:2520:C:H1'	51:1:2565:A:O2'	2.19	0.42
51:1:2544:G:H2'	51:1:2545:G:C8	2.55	0.42
53:3:182:A:H2'	53:3:183:C:H5''	2.02	0.42
53:3:909:A:H2'	53:3:910:C:O4'	2.20	0.42
53:3:1264:U:H3	53:3:1271:A:H61	1.67	0.42
58:B1:506:VAL:H	58:B1:506:VAL:HG12	1.59	0.42
58:B1:515:ARG:HH12	58:B1:724:MET:HG2	1.84	0.42
65:0:614:GLU:OE1	65:0:659:PRO:HB3	2.19	0.42
7:G:53:LEU:HD23	7:G:56:LEU:HD12	2.01	0.41
7:G:218:ALA:HA	7:G:221:ARG:HE	1.85	0.41
12:L:35:LYS:HD3	53:3:1373:G:H5''	2.01	0.41
13:M:7:ALA:HA	13:M:10:LEU:HB2	2.02	0.41
21:U:31:ARG:HB2	53:3:310:G:H5''	2.01	0.41
21:U:50:THR:HB	21:U:78:VAL:HB	2.02	0.41
27:b:252:LYS:HD3	27:b:252:LYS:HA	1.80	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:c:117:GLY:H	28:c:164:GLN:HE22	1.68	0.41
29:d:85:PHE:CG	51:1:588:U:H1'	2.55	0.41
35:k:38:ILE:HG22	35:k:61:VAL:HG22	2.01	0.41
39:o:11:ALA:HB1	39:o:14:ALA:HB3	2.01	0.41
48:x:17:ARG:HA	48:x:17:ARG:HD3	1.72	0.41
51:1:19:A:H2'	51:1:20:C:C6	2.55	0.41
51:1:324:A:H2'	51:1:325:G:H5'	2.01	0.41
51:1:481:G:H1'	51:1:506:G:H22	1.82	0.41
51:1:1625:C:H2'	51:1:1626:A:O4'	2.20	0.41
51:1:1741:C:H2'	51:1:1742:U:H5'	2.01	0.41
51:1:2139:U:H2'	51:1:2140:G:C8	2.54	0.41
51:1:2596:U:H2'	51:1:2597:G:O4'	2.19	0.41
51:1:2676:C:O5'	51:1:2676:C:H6	2.03	0.41
53:3:426:U:H2'	53:3:427:U:C6	2.54	0.41
53:3:866:C:N3	53:3:867:G:H1'	2.35	0.41
53:3:971:G:N7	53:3:1233:G:H1'	2.34	0.41
53:3:1032:G:H21	53:3:1033:G:H4'	1.85	0.41
53:3:1386:G:O2'	53:3:1387:G:H5'	2.20	0.41
58:B1:220:ARG:NH1	58:B1:220:ARG:CG	2.82	0.41
58:B1:246:PRO:HA	58:B1:247:PRO:HD3	1.96	0.41
59:B2:741:MET:HE3	59:B2:974:ARG:HH12	1.85	0.41
64:a:42:VAL:HG13	64:a:175:ILE:HG13	2.02	0.41
65:0:612:LEU:HD12	65:0:612:LEU:HA	1.84	0.41
14:N:21:LYS:HE2	14:N:21:LYS:HB2	1.85	0.41
16:P:34:THR:HA	16:P:40:ALA:HA	2.03	0.41
18:R:100:ARG:HG2	53:3:950:U:C5	2.55	0.41
20:T:84:LEU:HD12	20:T:84:LEU:HA	1.94	0.41
28:c:91:THR:H	28:c:94:GLN:HE21	1.66	0.41
29:d:85:PHE:CE2	51:1:587:C:H5'	2.55	0.41
31:f:14:VAL:HG12	31:f:27:GLY:HA2	2.01	0.41
31:f:97:VAL:HG12	31:f:124:CYS:HB2	2.02	0.41
32:g:22:LYS:HD3	32:g:22:LYS:HA	1.86	0.41
32:g:101:ASP:O	32:g:105:ALA:N	2.45	0.41
33:i:47:SER:O	33:i:47:SER:OG	2.31	0.41
51:1:538:A:H2'	51:1:539:G:O4'	2.20	0.41
51:1:828:U:H2'	51:1:829:A:N7	2.30	0.41
51:1:958:U:C2'	52:2:89:U:H1'	2.47	0.41
51:1:1086:A:C1'	51:1:1103:A:H2	2.33	0.41
51:1:1639:C:C2'	51:1:1640:A:H5'	2.50	0.41
51:1:1972:G:H2'	51:1:1973:G:H8	1.85	0.41
51:1:1974:C:H2'	51:1:1975:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2013:A:H61	51:1:2613:U:H3	1.68	0.41
51:1:2259:U:H1'	51:1:2427:C:H2'	2.02	0.41
51:1:2498:C:O2'	51:1:2499:C:H5'	2.20	0.41
51:1:2638:G:H1'	51:1:2778:A:N6	2.34	0.41
52:2:53:A:H2'	52:2:54:G:O4'	2.20	0.41
53:3:224:U:H2'	53:3:225:C:C5	2.56	0.41
53:3:762:U:H2'	53:3:763:G:C8	2.55	0.41
53:3:957:U:H2'	53:3:959:A:OP2	2.21	0.41
53:3:1153:G:H2'	53:3:1154:G:O4'	2.20	0.41
53:3:1368:A:O2'	53:3:1369:C:H5'	2.19	0.41
55:8:14:DC:C2	55:8:15:DC:C5	3.09	0.41
58:B1:224:LEU:HD23	58:B1:224:LEU:HA	1.89	0.41
58:B1:950:ILE:HB	58:B1:1018:ALA:HB3	2.01	0.41
59:B2:861:ALA:HB1	59:B2:882:ILE:HD13	2.02	0.41
65:0:632:ILE:O	65:0:636:SER:OG	2.36	0.41
6:F:32:LYS:HD2	51:1:2478:A:OP1	2.20	0.41
7:G:23:ASN:H	7:G:189:ASN:HA	1.86	0.41
22:V:29:LYS:HE2	22:V:29:LYS:HB3	1.83	0.41
23:W:62:ARG:NH1	53:3:718:A:N6	2.69	0.41
27:b:170:TYR:HB3	27:b:182:LYS:HB3	2.02	0.41
29:d:50:ALA:HB2	51:1:801:G:C8	2.55	0.41
30:e:68:LYS:HA	30:e:68:LYS:HD3	1.86	0.41
38:n:24:MET:O	38:n:28:LEU:N	2.53	0.41
47:w:37:ARG:HA	47:w:37:ARG:HD3	1.68	0.41
51:1:4:U:H2'	51:1:5:A:O4'	2.20	0.41
51:1:43:G:O2'	51:1:44:A:H5'	2.20	0.41
51:1:52:A:C5	51:1:118:A:C2	3.08	0.41
51:1:151:C:H5''	51:1:1360:G:OP1	2.21	0.41
51:1:711:G:H2'	51:1:712:G:O4'	2.21	0.41
51:1:1310:G:C3'	51:1:1311:G:H5'	2.50	0.41
51:1:1591:A:H2'	51:1:1592:C:C6	2.55	0.41
51:1:1609:A:H5'	51:1:1609:A:C8	2.54	0.41
51:1:2139:U:H2'	51:1:2140:G:H8	1.85	0.41
51:1:2448:A:H3'	51:1:2449:U:H2'	2.02	0.41
51:1:2840:C:H2'	51:1:2841:C:C6	2.56	0.41
53:3:850:U:O5'	53:3:850:U:H6	2.03	0.41
53:3:1422:G:N2	53:3:1479:C:N4	2.69	0.41
64:a:65:LEU:HD23	64:a:65:LEU:HA	1.92	0.41
9:I:201:GLU:OE1	10:J:111:ARG:NH1	2.54	0.41
10:J:13:LYS:NZ	10:J:14:LEU:O	2.53	0.41
21:U:12:LYS:HB3	53:3:392:C:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:c:116:LYS:HB2	28:c:165:MET:HB3	2.02	0.41
37:m:16:ARG:HD3	37:m:16:ARG:HA	1.90	0.41
39:o:24:THR:HB	39:o:90:VAL:HG12	2.02	0.41
45:u:42:LYS:HE2	45:u:42:LYS:HB3	1.90	0.41
48:x:31:ASN:ND2	48:x:52:ALA:HB2	2.34	0.41
51:1:527:C:OP2	51:1:2779:U:N3	2.51	0.41
51:1:1379:U:H2'	51:1:1380:G:H5'	2.02	0.41
51:1:2524:G:H2'	51:1:2525:G:C5'	2.43	0.41
51:1:2588:G:C2'	51:1:2589:A:H5'	2.50	0.41
53:3:79:G:H2'	53:3:80:A:H5'	2.02	0.41
53:3:111:G:O2'	53:3:389:A:H1'	2.20	0.41
53:3:458:U:H2'	53:3:459:A:C8	2.55	0.41
53:3:1007:U:H2'	53:3:1008:U:C5	2.54	0.41
53:3:1315:U:H2'	53:3:1316:G:O4'	2.21	0.41
58:B1:243:PRO:HG2	59:B2:1332:SER:C	2.44	0.41
58:B1:279:LEU:HD13	58:B1:299:LEU:HD13	2.02	0.41
58:B1:472:LEU:HD11	59:B2:1294:LYS:HG2	2.02	0.41
58:B1:609:TYR:HD2	58:B1:610:ARG:NH1	2.17	0.41
58:B1:1289:ASN:O	58:B1:1293:GLU:HB2	2.20	0.41
65:0:64:THR:HG23	65:0:472:ARG:HH22	1.86	0.41
65:0:444:SER:O	65:0:444:SER:OG	2.31	0.41
65:0:474:LYS:HD3	65:0:474:LYS:HA	1.73	0.41
65:0:615:PRO:HB2	65:0:684:PHE:CE1	2.56	0.41
1:A:11:GLU:HG2	1:A:25:ARG:HG2	2.02	0.41
5:E:7:ARG:NH1	51:1:254:G:H22	2.18	0.41
7:G:95:TRP:HZ3	7:G:99:MET:HE2	1.85	0.41
13:M:4:ASP:HB3	13:M:7:ALA:HB3	2.02	0.41
15:O:30:LYS:HA	15:O:34:ALA:HA	2.02	0.41
15:O:58:ASN:HD21	53:3:1061:G:H4'	1.85	0.41
25:Y:27:MET:H	25:Y:27:MET:HG3	1.74	0.41
28:c:47:ALA:HA	28:c:84:LEU:HG	2.01	0.41
28:c:80:TRP:CD1	28:c:202:ILE:HD11	2.55	0.41
28:c:145:SER:HB3	51:1:2578:G:N7	2.35	0.41
29:d:45:ALA:CB	51:1:38:A:H4'	2.50	0.41
30:e:65:LEU:N	30:e:87:LYS:O	2.53	0.41
32:g:89:LYS:HD2	32:g:89:LYS:HA	1.83	0.41
36:l:4:ASN:OD1	51:1:1203:U:O2	2.39	0.41
36:l:29:LYS:HA	36:l:29:LYS:HD2	1.71	0.41
36:l:78:ARG:HE	36:l:111:ILE:HD11	1.86	0.41
37:m:42:THR:HA	37:m:93:VAL:HA	2.02	0.41
37:m:82:MET:HE2	37:m:82:MET:HB2	1.80	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:w:56:PHE:HE2	51:1:2365:G:C5'	2.34	0.41
51:1:191:A:N3	51:1:192:C:C6	2.88	0.41
51:1:272:A:H2'	51:1:273:G:H8	1.86	0.41
51:1:734:A:O2'	51:1:1635:A:H4'	2.21	0.41
51:1:1054:A:H2'	51:1:1055:G:C8	2.55	0.41
51:1:1158:C:O5'	51:1:1158:C:H6	2.02	0.41
51:1:2302:U:H2'	51:1:2303:G:C8	2.56	0.41
51:1:2305:U:H2'	51:1:2306:C:H5'	2.02	0.41
51:1:2553:G:H2'	51:1:2554:U:C4'	2.49	0.41
53:3:262:A:H2'	53:3:263:A:C8	2.55	0.41
53:3:461:A:H2'	53:3:462:G:C8	2.56	0.41
53:3:678:U:H2'	53:3:679:C:C6	2.55	0.41
53:3:1327:C:H2'	53:3:1328:C:H6	1.85	0.41
58:B1:242:LEU:HA	58:B1:243:PRO:HD3	1.95	0.41
58:B1:820:ILE:HD11	58:B1:822:MET:HE2	2.02	0.41
59:B2:469:VAL:HA	59:B2:472:GLU:HG2	2.01	0.41
59:B2:906:PHE:C	59:B2:908:GLU:N	2.78	0.41
65:0:334:THR:HG1	65:0:385:ALA:H	1.68	0.41
65:0:446:ARG:HB3	65:0:459:ALA:HB3	2.02	0.41
13:M:46:GLU:O	13:M:61:THR:OG1	2.28	0.41
15:O:45:ARG:NH1	15:O:47:GLU:OE1	2.53	0.41
16:P:86:LYS:HG3	16:P:114:PRO:HD3	2.02	0.41
18:R:88:LEU:HD21	18:R:92:ARG:HE	1.86	0.41
28:c:170:VAL:HG13	28:c:194:PRO:HG3	2.01	0.41
33:i:123:ALA:CB	51:1:1081:U:H4'	2.50	0.41
34:j:114:LEU:O	34:j:118:MET:N	2.54	0.41
35:k:1:MET:HE3	51:1:1665:A:H1'	2.02	0.41
41:q:30:VAL:HG11	51:1:580:U:H4'	2.02	0.41
51:1:72:U:C4	51:1:112:U:H4'	2.55	0.41
51:1:692:C:H2'	51:1:693:A:H8	1.86	0.41
51:1:1024:G:P	51:1:1025:G:H3'	2.60	0.41
51:1:1900:A:H5'	51:1:1970:A:C5'	2.50	0.41
51:1:2049:G:N2	51:1:2620:C:C2	2.89	0.41
51:1:2081:U:H2'	51:1:2082:A:H8	1.85	0.41
53:3:68:G:C2	53:3:69:G:H1'	2.55	0.41
53:3:492:C:H2'	53:3:493:A:H8	1.83	0.41
58:B1:559:ALA:HB3	58:B1:562:GLU:HB3	2.01	0.41
58:B1:797:THR:HG22	58:B1:924:GLY:HA3	2.01	0.41
59:B2:870:ILE:HB	59:B2:944:ARG:HD3	2.02	0.41
65:0:18:HIS:ND1	65:0:120:GLN:HB3	2.36	0.41
1:A:26:SER:HB2	30:e:101:ARG:HH11	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:53:VAL:HG23	2:B:54:ILE:HG23	2.03	0.41
4:D:24:THR:OG1	4:D:25:LYS:N	2.53	0.41
13:M:3:GLN:HE21	53:3:878:A:H1'	1.86	0.41
15:O:82:LYS:HD2	15:O:82:LYS:HA	1.53	0.41
26:Z:27:VAL:O	26:Z:31:VAL:N	2.54	0.41
27:b:145:MET:SD	51:1:1800:C:H5''	2.61	0.41
28:c:19:GLY:HA2	40:p:78:PRO:HD2	2.02	0.41
28:c:55:LYS:HE3	28:c:60:VAL:HG22	2.03	0.41
28:c:209:ALA:OXT	51:1:2733:A:C2	2.74	0.41
30:e:63:LYS:O	52:2:42:C:H1'	2.21	0.41
45:u:67:SER:HB2	51:1:327:G:H21	1.85	0.41
51:1:1752:C:O2'	51:1:1753:G:H5'	2.21	0.41
51:1:2534:A:C2	51:1:2535:G:H1'	2.56	0.41
51:1:2611:C:H2'	51:1:2612:C:H6	1.85	0.41
53:3:107:G:H2'	53:3:108:G:O4'	2.20	0.41
53:3:862:C:O2'	53:3:863:U:H5'	2.20	0.41
53:3:938:A:H1'	53:3:1376:U:O2'	2.21	0.41
58:B1:120:LEU:HD22	58:B1:120:LEU:HA	1.77	0.41
58:B1:647:PRO:HG3	58:B1:697:MET:HB3	2.02	0.41
58:B1:800:LEU:HD12	58:B1:800:LEU:HA	1.79	0.41
60:W0:26:ARG:HA	60:W0:26:ARG:HD2	1.92	0.41
2:B:6:LYS:NZ	51:1:1262:A:C2	2.89	0.41
8:H:113:LYS:HA	8:H:113:LYS:HD2	1.88	0.41
10:J:37:VAL:HG21	10:J:113:VAL:HG13	2.02	0.41
11:K:53:LYS:HD3	11:K:53:LYS:HA	1.69	0.41
19:S:99:SER:HG	53:3:1187:G:H21	1.69	0.41
22:V:16:MET:HE2	22:V:16:MET:HB3	1.84	0.41
27:b:121:ALA:HA	27:b:129:LEU:HD13	2.02	0.41
27:b:153:LEU:HA	51:1:1799:G:N2	2.35	0.41
28:c:59:ARG:HA	28:c:59:ARG:HD2	1.85	0.41
28:c:113:SER:HB3	28:c:194:PRO:HB3	2.03	0.41
30:e:131:VAL:N	30:e:152:ASP:OD1	2.49	0.41
44:t:7:LEU:HD23	44:t:7:LEU:HA	1.90	0.41
51:1:140:C:C6	51:1:141:G:H4'	2.55	0.41
51:1:772:C:H5''	51:1:1356:G:C5'	2.50	0.41
51:1:917:A:H5''	51:1:2268:A:N6	2.30	0.41
51:1:986:C:H6	51:1:986:C:O5'	2.04	0.41
51:1:1063:G:OP2	51:1:1070:A:C4'	2.69	0.41
51:1:1354:A:H2'	51:1:1355:G:O4'	2.20	0.41
51:1:1853:A:H2'	51:1:1854:A:H8	1.81	0.41
51:1:2073:C:O2	51:1:2437:G:C2	2.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2356:U:H3'	51:1:2357:G:H5''	2.03	0.41
53:3:153:C:H2'	53:3:154:U:C5'	2.51	0.41
53:3:1093:A:O2'	53:3:1094:G:H5'	2.20	0.41
55:8:1:DC:H5''	58:B1:210:SER:HG	1.83	0.41
58:B1:111:THR:HG23	58:B1:300:GLN:HA	2.03	0.41
59:B2:22:LEU:HD22	59:B2:603:ILE:HG21	2.02	0.41
59:B2:542:ARG:H	59:B2:542:ARG:HG2	1.70	0.41
62:NG:175:PHE:O	62:NG:178:VAL:O	2.38	0.41
64:a:54:LYS:NZ	64:a:56:ASP:OD1	2.53	0.41
2:B:39:ARG:CZ	51:1:2884:U:H3	2.34	0.41
4:D:39:ARG:CZ	51:1:469:G:O6	2.69	0.41
6:F:10:LEU:HD21	51:1:2477:U:H5	1.82	0.41
7:G:17:HIS:HB2	7:G:202:ASN:HD22	1.86	0.41
11:K:89:VAL:HG23	53:3:737:C:C5'	2.48	0.41
13:M:86:LYS:HD2	13:M:86:LYS:HA	1.73	0.41
15:O:46:LYS:HB3	53:3:1253:G:OP1	2.21	0.41
19:S:1:ALA:HB1	53:3:1049:U:C4	2.56	0.41
21:U:60:TRP:HB3	21:U:65:ALA:HB2	2.03	0.41
24:X:20:LYS:O	24:X:24:SER:OG	2.38	0.41
27:b:7:PRO:HB3	27:b:13:ARG:HG3	2.03	0.41
27:b:110:LYS:HD2	27:b:110:LYS:HA	1.89	0.41
27:b:131:MET:HE3	27:b:131:MET:HB2	1.84	0.41
27:b:145:MET:HE3	27:b:153:LEU:HD11	2.02	0.41
27:b:240:GLY:CA	51:1:2597:G:H5''	2.51	0.41
28:c:176:ASP:OD1	28:c:176:ASP:N	2.37	0.41
31:f:123:GLU:HB2	31:f:131:VAL:HB	2.03	0.41
33:i:21:PRO:HB2	33:i:22:PRO:HD3	2.03	0.41
36:l:95:LEU:HA	36:l:95:LEU:HD23	1.90	0.41
39:o:25:ARG:HG3	39:o:40:ILE:HB	2.02	0.41
41:q:94:LEU:HA	41:q:97:ILE:HG22	2.03	0.41
44:t:49:LYS:HD2	44:t:49:LYS:HA	1.75	0.41
45:u:73:ASN:ND2	45:u:76:THR:H	2.19	0.41
48:x:57:VAL:HG13	51:1:372:G:H5'	2.03	0.41
51:1:413:C:H2'	51:1:414:C:C6	2.56	0.41
51:1:549:G:H2'	51:1:550:C:C6	2.56	0.41
51:1:838:C:C2	51:1:941:A:C6	3.09	0.41
51:1:940:G:C3'	51:1:941:A:H5''	2.51	0.41
51:1:1054:A:H2	51:1:1105:U:H3	1.68	0.41
51:1:1146:C:O2'	51:1:1147:A:H5'	2.21	0.41
51:1:1303:G:H2'	51:1:1304:A:C8	2.54	0.41
51:1:1444:G:H2'	51:1:1445:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1698:A:N7	51:1:1700:A:C8	2.89	0.41
51:1:1810:A:H2'	51:1:1811:G:C5'	2.51	0.41
51:1:1823:G:C6	51:1:1824:G:C5	3.09	0.41
51:1:1863:G:H2'	51:1:1864:U:C6	2.56	0.41
51:1:2140:G:H1	51:1:2151:U:H3	1.69	0.41
51:1:2201:G:H2'	51:1:2202:U:O4'	2.21	0.41
51:1:2559:C:H2'	51:1:2560:A:H8	1.86	0.41
51:1:2688:G:N1	51:1:2720:U:OP2	2.40	0.41
51:1:2830:C:O2	51:1:2883:A:H2	2.03	0.41
52:2:78:A:H2'	52:2:79:G:O4'	2.20	0.41
53:3:26:A:H61	53:3:558:G:H1'	1.86	0.41
53:3:240:G:H2'	53:3:241:G:H8	1.86	0.41
53:3:270:A:H2'	53:3:271:C:O4'	2.20	0.41
53:3:520:A:H61	53:3:533:A:H61	1.67	0.41
53:3:562:U:H4'	53:3:563:A:O5'	2.20	0.41
53:3:794:A:O2'	53:3:795:C:H5'	2.20	0.41
53:3:1346:A:N1	53:3:1374:A:H5''	2.35	0.41
53:3:1389:C:H2'	53:3:1390:U:O4'	2.21	0.41
58:B1:26:SER:HB3	58:B1:29:MET:H	1.86	0.41
58:B1:144:TYR:N	58:B1:144:TYR:CD1	2.88	0.41
58:B1:390:LEU:N	58:B1:390:LEU:HD13	2.35	0.41
58:B1:1050:THR:HG23	58:B1:1057:SER:HB3	2.02	0.41
59:B2:213:LEU:HD13	59:B2:422:LYS:HG2	2.03	0.41
59:B2:905:ILE:HG23	59:B2:906:PHE:H	1.86	0.41
59:B2:979:LEU:HD11	59:B2:1011:LEU:HD11	2.03	0.41
59:B2:987:GLU:HG2	59:B2:991:LYS:HE3	2.03	0.41
59:B2:1278:LEU:HD23	59:B2:1278:LEU:HA	1.86	0.41
63:6:33:U:H2'	63:6:35:A:OP2	2.21	0.41
65:0:169:LEU:HD12	65:0:185:LEU:HB3	2.01	0.41
65:0:375:LYS:HE2	65:0:375:LYS:HB2	1.89	0.41
65:0:695:ALA:HA	65:0:699:ILE:HB	2.02	0.41
12:L:82:SER:HB3	12:L:83:THR:H	1.60	0.41
22:V:46:HIS:CG	22:V:66:LEU:HD22	2.56	0.41
24:X:46:LEU:HB3	24:X:48:ILE:HG12	2.03	0.41
24:X:77:ARG:HH11	53:3:1225:A:H4'	1.83	0.41
25:Y:21:ALA:HA	25:Y:24:ARG:HD3	2.02	0.41
40:p:17:PRO:HD2	40:p:83:ILE:HB	2.03	0.41
45:u:46:LYS:HE2	45:u:46:LYS:HB2	1.91	0.41
49:y:31:GLN:HB3	49:y:37:LEU:HD12	2.02	0.41
51:1:740:C:O2'	51:1:741:U:H5'	2.21	0.41
51:1:1787:A:H2'	51:1:1787:A:N3	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1801:A:H5'	51:1:1801:A:H8	1.86	0.41
51:1:1932:A:H62	51:1:1968:G:H21	1.68	0.41
51:1:2063:C:O2	51:1:2450:A:N1	2.54	0.41
51:1:2136:G:N1	51:1:2137:U:O2	2.54	0.41
51:1:2138:G:N1	51:1:2154:A:O2'	2.47	0.41
51:1:2255:G:H2'	51:1:2256:G:C8	2.56	0.41
51:1:2643:G:H2'	51:1:2644:G:O4'	2.20	0.41
53:3:130:A:N3	53:3:130:A:H2'	2.36	0.41
53:3:204:G:H2'	53:3:205:A:C8	2.56	0.41
57:A2:57:THR:HG23	57:A2:158:ARG:HH21	1.86	0.41
58:B1:777:HIS:CD2	59:B2:550:VAL:HG13	2.56	0.41
58:B1:1154:ALA:N	58:B1:1214:PRO:O	2.50	0.41
59:B2:909:LYS:O	59:B2:913:VAL:HB	2.21	0.41
65:0:533:GLY:HA3	65:0:572:VAL:HG22	2.03	0.41
11:K:88:MET:HB2	23:W:63:TYR:HE2	1.86	0.40
15:O:53:ILE:HD12	19:S:84:ARG:HD2	2.03	0.40
16:P:66:ALA:HA	16:P:69:CYS:HB3	2.03	0.40
34:j:27:ARG:NH2	51:1:1142:A:H4'	2.36	0.40
37:m:11:LYS:O	51:1:910:A:N6	2.54	0.40
51:1:121:G:H2'	51:1:122:G:H8	1.86	0.40
51:1:1831:G:C2	51:1:1975:G:C2	3.09	0.40
51:1:2356:U:C3'	51:1:2357:G:H5''	2.52	0.40
51:1:2741:A:N6	51:1:2763:G:H1'	2.37	0.40
51:1:2811:G:O2'	51:1:2812:G:H5'	2.21	0.40
53:3:795:C:C5	53:3:796:C:C5	3.09	0.40
53:3:866:C:C2	53:3:867:G:H1'	2.56	0.40
53:3:1305:G:H22	53:3:1331:G:H2'	1.86	0.40
58:B1:324:LEU:H	58:B1:324:LEU:HG	1.76	0.40
59:B2:892:GLU:HB2	59:B2:893:THR:H	1.65	0.40
59:B2:936:ARG:HB2	59:B2:1042:LEU:HD12	2.03	0.40
64:a:46:VAL:O	64:a:170:ILE:HA	2.21	0.40
65:0:468:ILE:O	65:0:472:ARG:N	2.51	0.40
65:0:489:ALA:HB3	65:0:615:PRO:HD3	2.03	0.40
12:L:138:GLU:O	12:L:142:ARG:N	2.52	0.40
14:N:6:TYR:CZ	53:3:1147:C:H4'	2.56	0.40
14:N:82:ILE:HA	14:N:85:ALA:HB3	2.03	0.40
16:P:25:SER:HA	16:P:88:PRO:HD2	2.02	0.40
16:P:26:PHE:O	16:P:27:ASN:ND2	2.54	0.40
19:S:96:LYS:HA	19:S:96:LYS:HD2	1.79	0.40
27:b:77:VAL:HB	27:b:112:GLY:H	1.85	0.40
28:c:123:LYS:HB3	28:c:123:LYS:HE3	1.94	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:c:179:ARG:HB3	28:c:188:LEU:HB2	2.04	0.40
32:g:9:VAL:HG12	32:g:11:ASN:H	1.85	0.40
37:m:47:GLU:O	37:m:51:ARG:N	2.48	0.40
39:o:76:LYS:HE3	39:o:76:LYS:HB3	1.96	0.40
42:r:78:ARG:HH22	51:1:975:A:H4'	1.86	0.40
45:u:84:PHE:HB2	51:1:297:G:O3'	2.21	0.40
48:x:1:SER:OG	51:1:1365:A:H5'	2.20	0.40
51:1:375:G:H2'	51:1:376:G:H5'	2.03	0.40
51:1:1169:A:H2'	51:1:1170:C:O4'	2.22	0.40
51:1:1679:A:H4'	51:1:1990:C:H4'	2.03	0.40
51:1:2112:G:O6	51:1:2167:U:O2'	2.37	0.40
51:1:2313:C:H2'	51:1:2314:A:C8	2.56	0.40
51:1:2746:U:H2'	51:1:2747:G:O4'	2.21	0.40
51:1:2798:U:H4'	51:1:2799:A:C6	2.56	0.40
52:2:102:G:H2'	52:2:103:U:C1'	2.51	0.40
53:3:1283:U:O2'	53:3:1284:C:H5'	2.22	0.40
58:B1:87:LYS:HD2	58:B1:87:LYS:HA	1.81	0.40
58:B1:239:LEU:HD23	58:B1:239:LEU:N	2.36	0.40
58:B1:515:ARG:HG2	58:B1:516:ASP:H	1.85	0.40
58:B1:734:ALA:O	58:B1:738:ARG:HB2	2.21	0.40
58:B1:807:LEU:HD21	58:B1:894:VAL:HG21	2.04	0.40
58:B1:1177:ILE:HD12	58:B1:1186:TYR:HE2	1.85	0.40
59:B2:159:SER:HB2	59:B2:442:VAL:HG11	2.04	0.40
59:B2:803:ALA:HB2	59:B2:1094:VAL:HG21	2.03	0.40
59:B2:894:GLN:HB3	59:B2:899:GLU:CG	2.51	0.40
65:0:187:LYS:HE2	65:0:189:LYS:HB2	2.02	0.40
5:E:16:THR:OG1	5:E:17:GLY:N	2.52	0.40
12:L:34:LYS:CE	53:3:1290:G:H4'	2.51	0.40
12:L:115:MET:HA	12:L:118:ARG:HB2	2.04	0.40
19:S:4:SER:OG	53:3:1216:A:H5''	2.21	0.40
28:c:209:ALA:OXT	51:1:2733:A:N3	2.54	0.40
30:e:78:ILE:HD11	30:e:82:TYR:HB3	2.03	0.40
32:g:90:LEU:HD11	32:g:93:SER:HA	2.02	0.40
32:g:132:PHE:HB2	32:g:140:ALA:HB3	2.03	0.40
38:n:23:ASN:HD21	51:1:1294:U:H1'	1.87	0.40
41:q:23:TYR:HD1	51:1:533:G:C5'	2.35	0.40
49:y:31:GLN:HG2	49:y:37:LEU:HB2	2.03	0.40
51:1:126:A:C6	51:1:127:A:C2	3.10	0.40
51:1:226:A:H2'	51:1:227:A:O4'	2.21	0.40
51:1:529:A:C5	51:1:2042:A:C2	3.10	0.40
51:1:677:A:C6	51:1:802:A:C6	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1177:G:H3'	51:1:1178:C:H5''	2.02	0.40
51:1:1340:U:H4'	51:1:1394:U:O2'	2.22	0.40
51:1:1700:A:C2'	51:1:1701:A:H5'	2.50	0.40
51:1:1843:C:H2'	51:1:1844:C:H6	1.82	0.40
51:1:1917:U:O2	51:1:1917:U:O5'	2.39	0.40
51:1:2533:U:H2'	51:1:2534:A:O4'	2.21	0.40
52:2:112:G:H2'	52:2:113:C:C6	2.56	0.40
53:3:408:A:N6	53:3:434:U:H3	2.18	0.40
53:3:994:A:H61	53:3:1047:G:H4'	1.85	0.40
57:A1:224:LEU:HD23	57:A2:228:LEU:HD21	2.03	0.40
57:A2:42:ALA:HB1	57:A2:224:LEU:HD11	2.03	0.40
58:B1:108:ALA:HB2	58:B1:276:ASN:OD1	2.21	0.40
59:B2:50:GLU:HG2	59:B2:73:TYR:HE1	1.85	0.40
59:B2:310:ILE:HG21	59:B2:325:LEU:HB3	2.03	0.40
59:B2:524:ILE:HD12	59:B2:712:SER:HB2	2.02	0.40
59:B2:738:GLU:HA	59:B2:741:MET:HE2	2.03	0.40
65:0:32:PHE:HA	65:0:37:ASN:HB2	2.03	0.40
8:H:148:ILE:HG23	8:H:169:GLU:HB3	2.04	0.40
10:J:35:LEU:HD23	10:J:35:LEU:HA	1.93	0.40
13:M:26:MET:HB3	13:M:58:LEU:HB3	2.04	0.40
13:M:110:MET:HE2	13:M:110:MET:HB3	1.84	0.40
16:P:52:ARG:HA	16:P:52:ARG:HD3	1.85	0.40
18:R:69:ARG:HA	18:R:69:ARG:HD2	1.96	0.40
25:Y:78:LEU:HA	25:Y:78:LEU:HD13	1.84	0.40
26:Z:36:PHE:CE1	26:Z:40:PRO:HD3	2.57	0.40
27:b:152:GLN:HG2	51:1:1818:U:C4	2.56	0.40
27:b:247:TRP:CE2	51:1:1805:A:H5''	2.57	0.40
32:g:78:VAL:HG21	32:g:103:VAL:HG23	2.04	0.40
39:o:35:ILE:HD13	39:o:35:ILE:HA	1.95	0.40
51:1:43:G:H2'	51:1:44:A:O4'	2.22	0.40
51:1:571:U:C5	51:1:575:A:C6	3.10	0.40
51:1:1028:A:H2'	51:1:1029:A:C8	2.56	0.40
51:1:1468:U:H2'	51:1:1522:A:H61	1.86	0.40
51:1:1597:A:C5'	51:1:1598:A:H5'	2.32	0.40
53:3:517:G:H4'	53:3:519:C:C2	2.56	0.40
53:3:706:A:H2'	53:3:707:U:H5'	2.04	0.40
53:3:883:C:H2'	53:3:884:U:C6	2.56	0.40
53:3:1536:C:H2'	53:3:1537:U:C6	2.56	0.40
58:B1:182:ALA:HB1	58:B1:238:ILE:CG2	2.52	0.40
58:B1:244:VAL:HA	58:B1:269:TYR:CZ	2.57	0.40
65:0:562:LYS:HA	65:0:562:LYS:HD2	1.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:42:ILE:HG22	2:B:48:TYR:HB2	2.04	0.40
9:I:49:ASP:OD1	9:I:49:ASP:N	2.55	0.40
9:I:97:LEU:HG	9:I:134:TYR:HB3	2.04	0.40
10:J:83:PRO:HB3	10:J:97:PRO:HD3	2.02	0.40
13:M:126:CYS:SG	13:M:127:TYR:N	2.94	0.40
16:P:13:LYS:HE2	16:P:13:LYS:HB2	1.95	0.40
18:R:70:ARG:NE	30:e:141:ASP:O	2.53	0.40
28:c:149:ASN:ND2	51:1:2572:A:C8	2.90	0.40
30:e:2:LYS:O	30:e:2:LYS:NZ	2.49	0.40
31:f:3:VAL:HG21	51:1:2748:A:O3'	2.21	0.40
33:i:52:LEU:HD21	33:i:81:LYS:HB2	2.03	0.40
39:o:78:VAL:O	39:o:82:ALA:N	2.55	0.40
46:v:78:GLN:HB3	46:v:88:HIS:HB3	2.03	0.40
51:1:191:A:H2'	51:1:192:C:C6	2.56	0.40
51:1:324:A:C2'	51:1:325:G:H5'	2.51	0.40
51:1:1521:G:H2'	51:1:1522:A:C8	2.56	0.40
51:1:1666:G:N7	51:1:1667:G:C6	2.89	0.40
51:1:1967:C:H2'	51:1:1968:G:O4'	2.22	0.40
51:1:2108:A:OP1	64:a:3:LYS:HB3	2.22	0.40
51:1:2140:G:H2'	51:1:2141:G:C8	2.56	0.40
51:1:2656:U:OP1	65:0:146:ARG:NH2	2.52	0.40
53:3:42:G:H1	53:3:400:C:H42	1.69	0.40
53:3:220:G:O2'	53:3:221:C:H5'	2.21	0.40
53:3:413:G:N3	53:3:413:G:H2'	2.36	0.40
53:3:578:C:O2'	53:3:728:A:N3	2.48	0.40
53:3:962:C:H1'	53:3:1201:A:N6	2.36	0.40
53:3:986:U:H2'	53:3:987:G:O4'	2.21	0.40
53:3:1221:G:O2'	53:3:1222:G:H5'	2.22	0.40
53:3:1468:A:H2'	53:3:1469:C:O4'	2.21	0.40
57:A1:48:LEU:HD12	57:A1:48:LEU:HA	1.79	0.40
57:A1:79:LEU:HD11	58:B1:526:VAL:HG21	2.04	0.40
58:B1:117:LEU:HD22	58:B1:139:LEU:CD1	2.52	0.40
58:B1:351:GLY:O	58:B1:467:ALA:HA	2.21	0.40
59:B2:162:GLY:H	59:B2:170:VAL:HG12	1.87	0.40
59:B2:1247:SER:OG	59:B2:1248:THR:N	2.55	0.40
63:6:62:C:H5'	64:a:53:ARG:NE	2.36	0.40
65:0:23:LYS:HD2	65:0:90:PRO:HA	2.03	0.40
65:0:158:ILE:HG23	65:0:162:LEU:HB2	2.03	0.40
65:0:161:ARG:HD2	65:0:162:LEU:HD23	2.02	0.40
65:0:557:ILE:HG12	65:0:597:ALA:HB1	2.04	0.40
65:0:589:SER:HB3	65:0:590:GLU:H	1.76	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	44/70 (63%)	38 (86%)	6 (14%)	0	100	100
2	B	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
3	C	48/55 (87%)	37 (77%)	11 (23%)	0	100	100
4	D	44/46 (96%)	35 (80%)	9 (20%)	0	100	100
5	E	62/65 (95%)	48 (77%)	13 (21%)	1 (2%)	7	36
6	F	36/38 (95%)	30 (83%)	6 (17%)	0	100	100
7	G	216/241 (90%)	182 (84%)	34 (16%)	0	100	100
8	H	204/233 (88%)	187 (92%)	17 (8%)	0	100	100
9	I	203/206 (98%)	171 (84%)	31 (15%)	1 (0%)	24	59
10	J	155/167 (93%)	129 (83%)	26 (17%)	0	100	100
11	K	98/135 (73%)	79 (81%)	19 (19%)	0	100	100
12	L	149/179 (83%)	130 (87%)	19 (13%)	0	100	100
13	M	127/130 (98%)	110 (87%)	17 (13%)	0	100	100
14	N	125/130 (96%)	110 (88%)	15 (12%)	0	100	100
15	O	96/103 (93%)	82 (85%)	14 (15%)	0	100	100
16	P	114/129 (88%)	104 (91%)	10 (9%)	0	100	100
17	Q	121/124 (98%)	97 (80%)	23 (19%)	1 (1%)	16	50
18	R	112/118 (95%)	99 (88%)	13 (12%)	0	100	100
19	S	98/101 (97%)	86 (88%)	12 (12%)	0	100	100
20	T	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
21	U	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
22	V	78/84 (93%)	69 (88%)	9 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	W	63/75 (84%)	59 (94%)	4 (6%)	0	100	100
24	X	77/92 (84%)	69 (90%)	8 (10%)	0	100	100
25	Y	83/87 (95%)	77 (93%)	6 (7%)	0	100	100
26	Z	63/71 (89%)	47 (75%)	16 (25%)	0	100	100
27	b	269/273 (98%)	227 (84%)	42 (16%)	0	100	100
28	c	207/209 (99%)	177 (86%)	30 (14%)	0	100	100
29	d	199/201 (99%)	182 (92%)	17 (8%)	0	100	100
30	e	175/179 (98%)	164 (94%)	11 (6%)	0	100	100
31	f	174/177 (98%)	157 (90%)	17 (10%)	0	100	100
32	g	147/149 (99%)	125 (85%)	22 (15%)	0	100	100
33	i	139/142 (98%)	124 (89%)	15 (11%)	0	100	100
34	j	140/142 (99%)	120 (86%)	20 (14%)	0	100	100
35	k	120/123 (98%)	98 (82%)	22 (18%)	0	100	100
36	l	141/144 (98%)	117 (83%)	24 (17%)	0	100	100
37	m	134/136 (98%)	116 (87%)	18 (13%)	0	100	100
38	n	118/127 (93%)	104 (88%)	14 (12%)	0	100	100
39	o	114/117 (97%)	103 (90%)	11 (10%)	0	100	100
40	p	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
41	q	115/118 (98%)	108 (94%)	7 (6%)	0	100	100
42	r	101/103 (98%)	88 (87%)	13 (13%)	0	100	100
43	s	108/110 (98%)	92 (85%)	16 (15%)	0	100	100
44	t	91/100 (91%)	77 (85%)	14 (15%)	0	100	100
45	u	100/104 (96%)	83 (83%)	17 (17%)	0	100	100
46	v	92/94 (98%)	80 (87%)	12 (13%)	0	100	100
47	w	73/85 (86%)	63 (86%)	10 (14%)	0	100	100
48	x	75/78 (96%)	66 (88%)	9 (12%)	0	100	100
49	y	61/63 (97%)	61 (100%)	0	0	100	100
50	z	56/59 (95%)	50 (89%)	6 (11%)	0	100	100
57	A1	295/329 (90%)	274 (93%)	21 (7%)	0	100	100
57	A2	282/329 (86%)	272 (96%)	10 (4%)	0	100	100
58	B1	1329/1407 (94%)	1204 (91%)	121 (9%)	4 (0%)	36	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	B2	1338/1342 (100%)	1200 (90%)	131 (10%)	7 (0%)	24	59
60	W0	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
61	NA	490/495 (99%)	475 (97%)	15 (3%)	0	100	100
62	NG	150/181 (83%)	136 (91%)	11 (7%)	3 (2%)	6	32
64	a	128/234 (55%)	106 (83%)	22 (17%)	0	100	100
65	0	695/716 (97%)	597 (86%)	88 (13%)	10 (1%)	9	38
All	All	10484/11179 (94%)	9300 (89%)	1157 (11%)	27 (0%)	37	69

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
58	B1	121	PRO
62	NG	122	PRO
62	NG	124	PRO
59	B2	43	PRO
59	B2	905	ILE
62	NG	102	PRO
65	0	199	GLY
65	0	516	GLY
65	0	611	VAL
59	B2	888	THR
65	0	298	ILE
65	0	299	LEU
17	Q	87	LYS
58	B1	43	THR
58	B1	193	ASP
59	B2	893	THR
59	B2	904	ALA
65	0	196	ALA
5	E	16	THR
58	B1	1325	PHE
65	0	552	ALA
59	B2	919	ARG
65	0	513	GLY
65	0	527	PRO
9	I	126	GLY
59	B2	1317	PRO
65	0	121	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	42/62 (68%)	42 (100%)	0	100	100
2	B	47/48 (98%)	47 (100%)	0	100	100
3	C	45/49 (92%)	44 (98%)	1 (2%)	45	64
4	D	38/38 (100%)	35 (92%)	3 (8%)	11	36
5	E	51/52 (98%)	46 (90%)	5 (10%)	7	28
6	F	34/34 (100%)	33 (97%)	1 (3%)	37	58
7	G	180/199 (90%)	172 (96%)	8 (4%)	25	49
8	H	170/190 (90%)	162 (95%)	8 (5%)	23	48
9	I	172/173 (99%)	170 (99%)	2 (1%)	63	72
10	J	119/126 (94%)	113 (95%)	6 (5%)	22	47
11	K	87/116 (75%)	83 (95%)	4 (5%)	24	48
12	L	124/147 (84%)	121 (98%)	3 (2%)	43	63
13	M	104/105 (99%)	102 (98%)	2 (2%)	50	66
14	N	105/107 (98%)	105 (100%)	0	100	100
15	O	86/90 (96%)	78 (91%)	8 (9%)	8	30
16	P	89/99 (90%)	88 (99%)	1 (1%)	65	74
17	Q	103/104 (99%)	101 (98%)	2 (2%)	50	66
18	R	92/96 (96%)	91 (99%)	1 (1%)	65	74
19	S	83/84 (99%)	82 (99%)	1 (1%)	63	72
20	T	76/77 (99%)	76 (100%)	0	100	100
21	U	65/65 (100%)	65 (100%)	0	100	100
22	V	74/78 (95%)	74 (100%)	0	100	100
23	W	56/65 (86%)	56 (100%)	0	100	100
24	X	70/79 (89%)	70 (100%)	0	100	100
25	Y	65/66 (98%)	65 (100%)	0	100	100
26	Z	55/61 (90%)	46 (84%)	9 (16%)	2	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	b	216/218 (99%)	212 (98%)	4 (2%)	50	66
28	c	164/164 (100%)	163 (99%)	1 (1%)	78	80
29	d	165/165 (100%)	160 (97%)	5 (3%)	36	57
30	e	148/150 (99%)	146 (99%)	2 (1%)	59	71
31	f	137/138 (99%)	136 (99%)	1 (1%)	76	78
32	g	114/114 (100%)	111 (97%)	3 (3%)	40	60
33	i	109/110 (99%)	109 (100%)	0	100	100
34	j	116/116 (100%)	113 (97%)	3 (3%)	40	60
35	k	103/104 (99%)	100 (97%)	3 (3%)	37	58
36	l	102/103 (99%)	100 (98%)	2 (2%)	48	65
37	m	109/109 (100%)	108 (99%)	1 (1%)	70	75
38	n	100/103 (97%)	98 (98%)	2 (2%)	48	65
39	o	86/87 (99%)	86 (100%)	0	100	100
40	p	99/100 (99%)	99 (100%)	0	100	100
41	q	89/90 (99%)	89 (100%)	0	100	100
42	r	84/84 (100%)	84 (100%)	0	100	100
43	s	93/93 (100%)	86 (92%)	7 (8%)	12	38
44	t	80/84 (95%)	77 (96%)	3 (4%)	29	52
45	u	83/85 (98%)	82 (99%)	1 (1%)	63	72
46	v	78/78 (100%)	77 (99%)	1 (1%)	61	71
47	w	57/63 (90%)	57 (100%)	0	100	100
48	x	67/68 (98%)	65 (97%)	2 (3%)	36	57
49	y	55/55 (100%)	55 (100%)	0	100	100
50	z	48/49 (98%)	47 (98%)	1 (2%)	47	65
57	A1	185/286 (65%)	174 (94%)	11 (6%)	18	44
57	A2	186/286 (65%)	185 (100%)	1 (0%)	81	82
58	B1	1110/1168 (95%)	1021 (92%)	89 (8%)	11	35
59	B2	1148/1157 (99%)	1115 (97%)	33 (3%)	37	58
60	W0	70/75 (93%)	68 (97%)	2 (3%)	37	58
64	a	109/181 (60%)	98 (90%)	11 (10%)	7	27
65	0	574/588 (98%)	512 (89%)	62 (11%)	6	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	8116/8681 (94%)	7800 (96%)	316 (4%)	30 52

All (316) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	22	THR
4	D	24	THR
4	D	43	THR
4	D	44	VAL
5	E	30	HIS
5	E	31	ILE
5	E	32	LEU
5	E	33	THR
5	E	37	THR
6	F	25	VAL
7	G	13	VAL
7	G	14	HIS
7	G	18	GLN
7	G	67	LEU
7	G	80	LYS
7	G	84	LEU
7	G	86	CYS
7	G	87	ASP
8	H	51	VAL
8	H	57	GLU
8	H	58	ARG
8	H	61	LYS
8	H	63	ILE
8	H	65	VAL
8	H	134	LYS
8	H	135	ARG
9	I	27	ILE
9	I	128	VAL
10	J	9	GLU
10	J	10	LEU
10	J	77	ASN
10	J	89	THR
10	J	116	VAL
10	J	130	THR
11	K	51	ILE
11	K	54	LEU
11	K	55	HIS

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Mol	Chain	Res	Type
11	K	92	THR
12	L	72	VAL
12	L	85	GLN
12	L	88	VAL
13	M	100	ILE
13	M	109	VAL
15	O	82	LYS
15	O	87	LEU
15	O	89	ARG
15	O	90	LEU
15	O	92	LEU
15	O	96	VAL
15	O	100	ILE
15	O	102	LEU
16	P	107	THR
17	Q	88	ASP
17	Q	93	ARG
18	R	103	THR
19	S	45	LEU
26	Z	6	ARG
26	Z	8	ASN
26	Z	23	GLU
26	Z	24	LYS
26	Z	36	PHE
26	Z	43	GLU
26	Z	44	ARG
26	Z	46	ARG
26	Z	48	LYS
27	b	15	VAL
27	b	64	VAL
27	b	161	VAL
27	b	194	VAL
28	c	197	THR
29	d	48	THR
29	d	84	THR
29	d	116	ASP
29	d	134	LEU
29	d	143	LEU
30	e	89	THR
30	e	151	LEU
31	f	36	LEU
32	g	9	VAL

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Mol	Chain	Res	Type
32	g	93	SER
32	g	94	ILE
34	j	3	THR
34	j	81	ILE
34	j	139	VAL
35	k	56	ASP
35	k	62	VAL
35	k	104	THR
36	l	19	LEU
36	l	85	VAL
37	m	68	PHE
38	n	15	SER
38	n	69	ARG
43	s	22	ASP
43	s	65	ASP
43	s	67	ASP
43	s	74	ILE
43	s	76	VAL
43	s	92	ARG
43	s	97	LEU
44	t	6	ARG
44	t	11	LEU
44	t	37	ASP
45	u	27	VAL
46	v	65	VAL
48	x	6	VAL
48	x	57	VAL
50	z	26	LEU
57	A1	9	LEU
57	A1	12	ARG
57	A1	13	LEU
57	A1	18	GLN
57	A1	19	VAL
57	A1	22	THR
57	A1	27	THR
57	A1	28	LEU
57	A1	33	ARG
57	A1	46	ILE
57	A1	48	LEU
57	A2	29	GLU
58	B1	24	LEU
58	B1	40	LYS

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Mol	Chain	Res	Type
58	B1	42	GLU
58	B1	44	ILE
58	B1	47	ARG
58	B1	49	PHE
58	B1	50	LYS
58	B1	60	ARG
58	B1	66	LYS
58	B1	69	GLU
58	B1	71	LEU
58	B1	74	LYS
58	B1	76	LYS
58	B1	78	LEU
58	B1	80	HIS
58	B1	81	ARG
58	B1	86	GLU
58	B1	87	LYS
58	B1	91	GLU
58	B1	93	THR
58	B1	94	GLN
58	B1	95	THR
58	B1	96	LYS
58	B1	99	ARG
58	B1	100	GLU
58	B1	114	ILE
58	B1	117	LEU
58	B1	120	LEU
58	B1	126	LEU
58	B1	132	LEU
58	B1	135	ILE
58	B1	142	GLU
58	B1	144	TYR
58	B1	145	VAL
58	B1	146	VAL
58	B1	147	ILE
58	B1	152	THR
58	B1	154	LEU
58	B1	157	GLN
58	B1	159	ILE
58	B1	172	PHE
58	B1	174	ASP
58	B1	175	GLU
58	B1	180	MET

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Mol	Chain	Res	Type
58	B1	190	LYS
58	B1	193	ASP
58	B1	196	GLN
58	B1	210	SER
58	B1	216	LYS
58	B1	222	LYS
58	B1	223	LEU
58	B1	227	PHE
58	B1	233	LYS
58	B1	237	MET
58	B1	238	ILE
58	B1	239	LEU
58	B1	240	THR
58	B1	244	VAL
58	B1	255	LEU
58	B1	256	ASP
58	B1	259	ARG
58	B1	317	THR
58	B1	322	ARG
58	B1	324	LEU
58	B1	363	LEU
58	B1	385	LEU
58	B1	386	GLU
58	B1	387	LEU
58	B1	390	LEU
58	B1	393	THR
58	B1	394	ILE
58	B1	395	LYS
58	B1	416	ILE
58	B1	417	ARG
58	B1	425	ARG
58	B1	506	VAL
58	B1	514	THR
58	B1	800	LEU
58	B1	807	LEU
58	B1	839	VAL
58	B1	901	ARG
58	B1	903	LEU
58	B1	1172	LYS
58	B1	1181	ASP
58	B1	1233	ILE
58	B1	1327	GLU

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Mol	Chain	Res	Type
58	B1	1328	THR
58	B1	1331	VAL
58	B1	1332	LEU
59	B2	44	GLU
59	B2	49	LEU
59	B2	56	VAL
59	B2	146	VAL
59	B2	483	ASP
59	B2	487	LEU
59	B2	516	ASP
59	B2	538	LEU
59	B2	540	ARG
59	B2	545	PHE
59	B2	546	GLU
59	B2	615	VAL
59	B2	857	VAL
59	B2	859	GLU
59	B2	887	VAL
59	B2	890	LYS
59	B2	892	GLU
59	B2	894	GLN
59	B2	895	LEU
59	B2	896	THR
59	B2	899	GLU
59	B2	902	LEU
59	B2	903	ARG
59	B2	905	ILE
59	B2	908	GLU
59	B2	913	VAL
59	B2	915	ASP
59	B2	916	SER
59	B2	919	ARG
59	B2	920	VAL
59	B2	922	ASN
59	B2	1076	ILE
59	B2	1151	LEU
60	W0	4	VAL
60	W0	63	ILE
64	a	8	MET
64	a	42	VAL
64	a	47	ASN
64	a	165	ASN

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Mol	Chain	Res	Type
64	a	166	ASP
64	a	167	LYS
64	a	170	ILE
64	a	211	LYS
64	a	212	VAL
64	a	213	SER
64	a	214	ILE
65	0	42	GLU
65	0	173	ILE
65	0	195	ASP
65	0	298	ILE
65	0	299	LEU
65	0	300	ASP
65	0	301	ASP
65	0	303	LYS
65	0	338	VAL
65	0	390	ASP
65	0	485	LYS
65	0	494	ILE
65	0	496	GLN
65	0	498	VAL
65	0	499	THR
65	0	501	VAL
65	0	502	GLU
65	0	507	LYS
65	0	508	GLN
65	0	512	ARG
65	0	519	VAL
65	0	520	ILE
65	0	522	MET
65	0	523	TYR
65	0	525	LEU
65	0	526	GLU
65	0	532	LYS
65	0	537	ILE
65	0	540	ILE
65	0	541	LYS
65	0	544	VAL
65	0	545	ILE
65	0	548	GLU
65	0	555	LYS
65	0	559	GLU

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Mol	Chain	Res	Type
65	0	562	LYS
65	0	566	LEU
65	0	571	VAL
65	0	572	VAL
65	0	574	MET
65	0	576	ILE
65	0	578	LEU
65	0	583	TYR
65	0	584	HIS
65	0	594	LYS
65	0	599	ILE
65	0	601	PHE
65	0	602	LYS
65	0	606	LYS
65	0	607	LYS
65	0	611	VAL
65	0	612	LEU
65	0	614	GLU
65	0	616	ILE
65	0	617	MET
65	0	618	LYS
65	0	662	GLU
65	0	663	MET
65	0	688	ASP
65	0	689	GLU
65	0	694	VAL
65	0	700	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (150) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
5	E	30	HIS
7	G	18	GLN
7	G	57	ASN
7	G	93	HIS
7	G	102	ASN
7	G	119	GLN
7	G	169	HIS
7	G	202	ASN
8	H	7	ASN
8	H	18	ASN

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Mol	Chain	Res	Type
8	H	139	ASN
8	H	184	ASN
9	I	35	GLN
9	I	53	GLN
9	I	58	GLN
9	I	73	ASN
9	I	125	ASN
9	I	130	ASN
9	I	135	GLN
9	I	195	ASN
9	I	197	HIS
10	J	69	ASN
10	J	121	ASN
10	J	131	ASN
10	J	147	ASN
11	K	94	HIS
12	L	8	GLN
12	L	27	ASN
12	L	96	ASN
12	L	129	ASN
13	M	3	GLN
13	M	15	ASN
13	M	20	ASN
14	N	3	ASN
16	P	27	ASN
16	P	80	ASN
17	Q	72	ASN
17	Q	76	HIS
17	Q	111	GLN
18	R	90	HIS
19	S	48	GLN
19	S	59	GLN
20	T	45	HIS
21	U	26	ASN
21	U	29	ASN
21	U	40	ASN
21	U	79	ASN
22	V	46	HIS
23	W	53	GLN
25	Y	74	HIS
25	Y	81	GLN
25	Y	83	ASN

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Mol	Chain	Res	Type
26	Z	55	HIS
27	b	24	HIS
27	b	85	ASN
27	b	250	GLN
28	c	32	ASN
28	c	49	GLN
28	c	67	HIS
28	c	136	ASN
28	c	148	GLN
28	c	164	GLN
28	c	185	ASN
29	d	62	GLN
29	d	195	GLN
30	e	22	ASN
31	f	63	GLN
31	f	110	HIS
32	g	18	GLN
32	g	66	ASN
32	g	135	HIS
33	i	18	ASN
33	i	42	ASN
34	j	80	HIS
34	j	128	ASN
34	j	130	HIS
34	j	135	GLN
35	k	9	ASN
36	l	93	ASN
37	m	22	GLN
38	n	9	GLN
38	n	23	ASN
38	n	107	ASN
39	o	38	GLN
39	o	104	GLN
39	o	116	GLN
40	p	74	GLN
41	q	65	ASN
41	q	70	GLN
43	s	31	GLN
43	s	60	HIS
44	t	59	ASN
44	t	92	ASN
45	u	45	GLN

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Mol	Chain	Res	Type
45	u	68	ASN
45	u	73	ASN
46	v	24	ASN
46	v	78	GLN
46	v	88	HIS
48	x	31	ASN
49	y	41	HIS
57	A1	37	HIS
57	A1	66	HIS
57	A1	84	ASN
57	A1	117	HIS
57	A1	128	HIS
57	A1	227	GLN
57	A2	23	HIS
57	A2	227	GLN
58	B1	45	ASN
58	B1	196	GLN
58	B1	209	ASN
58	B1	364	HIS
58	B1	424	ASN
58	B1	450	HIS
58	B1	469	HIS
58	B1	771	GLN
58	B1	805	GLN
58	B1	865	HIS
58	B1	1238	GLN
58	B1	1259	GLN
59	B2	69	GLN
59	B2	314	ASN
59	B2	330	HIS
59	B2	343	HIS
59	B2	518	ASN
59	B2	554	HIS
59	B2	580	GLN
59	B2	688	GLN
59	B2	762	ASN
59	B2	808	ASN
59	B2	894	GLN
59	B2	1237	HIS
59	B2	1268	GLN
59	B2	1313	HIS
60	W0	7	GLN

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Mol	Chain	Res	Type
60	W0	31	GLN
60	W0	62	GLN
64	a	24	ASN
64	a	172	HIS
65	0	85	ASN
65	0	157	GLN
65	0	170	GLN
65	0	259	ASN
65	0	272	ASN
65	0	276	GLN
65	0	351	ASN
65	0	560	GLN
65	0	696	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	1	2902/2904 (99%)	438 (15%)	6 (0%)
52	2	119/120 (99%)	18 (15%)	0
53	3	1538/1542 (99%)	196 (12%)	2 (0%)
54	4	28/44 (63%)	15 (53%)	3 (10%)
63	6	76/77 (98%)	14 (18%)	0
All	All	4663/4687 (99%)	681 (14%)	11 (0%)

All (681) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	1	10	A
51	1	12	U
51	1	23	G
51	1	34	U
51	1	35	G
51	1	51	G
51	1	63	A
51	1	71	A
51	1	75	G
51	1	102	U
51	1	103	A
51	1	113	U
51	1	118	A
51	1	119	A

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Mol	Chain	Res	Type
51	1	120	U
51	1	125	A
51	1	126	A
51	1	139	U
51	1	140	C
51	1	141	G
51	1	143	C
51	1	163	C
51	1	196	A
51	1	199	A
51	1	204	A
51	1	205	G
51	1	215	G
51	1	216	A
51	1	218	A
51	1	221	A
51	1	225	C
51	1	228	C
51	1	229	C
51	1	233	A
51	1	248	G
51	1	255	A
51	1	266	G
51	1	276	U
51	1	277	G
51	1	294	A
51	1	311	A
51	1	323	C
51	1	324	A
51	1	329	G
51	1	330	A
51	1	331	C
51	1	361	G
51	1	371	A
51	1	372	G
51	1	380	G
51	1	386	G
51	1	404	A
51	1	405	U
51	1	411	G
51	1	412	A
51	1	424	G

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Mol	Chain	Res	Type
51	1	431	U
51	1	451	U
51	1	455	C
51	1	456	C
51	1	457	A
51	1	458	G
51	1	480	A
51	1	481	G
51	1	490	C
51	1	491	G
51	1	504	A
51	1	505	A
51	1	532	A
51	1	544	C
51	1	548	G
51	1	560	C
51	1	563	A
51	1	568	U
51	1	573	U
51	1	574	A
51	1	586	A
51	1	603	A
51	1	609	A
51	1	610	C
51	1	615	U
51	1	627	A
51	1	637	A
51	1	646	U
51	1	654	A
51	1	655	A
51	1	686	U
51	1	690	G
51	1	714	U
51	1	717	C
51	1	730	A
51	1	740	C
51	1	747	C
51	1	752	A
51	1	757	G
51	1	764	A
51	1	765	C
51	1	774	G

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Mol	Chain	Res	Type
51	1	775	G
51	1	776	G
51	1	782	A
51	1	783	A
51	1	784	G
51	1	793	A
51	1	805	G
51	1	806	C
51	1	812	C
51	1	819	A
51	1	827	U
51	1	829	A
51	1	830	G
51	1	845	A
51	1	846	U
51	1	858	G
51	1	859	G
51	1	865	C
51	1	878	A
51	1	883	G
51	1	887	U
51	1	890	C
51	1	896	A
51	1	897	C
51	1	898	C
51	1	902	C
51	1	910	A
51	1	941	A
51	1	945	A
51	1	946	C
51	1	953	G
51	1	961	C
51	1	974	G
51	1	980	A
51	1	982	C
51	1	983	A
51	1	989	G
51	1	995	C
51	1	996	A
51	1	1005	C
51	1	1012	U
51	1	1013	C

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Mol	Chain	Res	Type
51	1	1021	A
51	1	1022	G
51	1	1025	G
51	1	1026	G
51	1	1033	U
51	1	1045	C
51	1	1046	A
51	1	1054	A
51	1	1055	G
51	1	1056	G
51	1	1057	A
51	1	1058	U
51	1	1059	G
51	1	1060	U
51	1	1062	G
51	1	1065	U
51	1	1066	U
51	1	1068	G
51	1	1069	A
51	1	1070	A
51	1	1071	G
51	1	1073	A
51	1	1078	U
51	1	1081	U
51	1	1084	A
51	1	1088	A
51	1	1104	C
51	1	1105	U
51	1	1106	G
51	1	1107	G
51	1	1111	A
51	1	1130	U
51	1	1132	U
51	1	1133	A
51	1	1134	A
51	1	1135	C
51	1	1143	A
51	1	1155	A
51	1	1172	C
51	1	1173	U
51	1	1175	A
51	1	1178	C

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Mol	Chain	Res	Type
51	1	1180	U
51	1	1206	G
51	1	1212	G
51	1	1225	G
51	1	1236	G
51	1	1248	G
51	1	1253	A
51	1	1256	G
51	1	1271	G
51	1	1272	A
51	1	1275	A
51	1	1287	A
51	1	1300	G
51	1	1301	A
51	1	1312	U
51	1	1313	U
51	1	1321	A
51	1	1325	U
51	1	1326	U
51	1	1342	A
51	1	1365	A
51	1	1378	A
51	1	1379	U
51	1	1383	A
51	1	1397	U
51	1	1416	G
51	1	1417	C
51	1	1419	A
51	1	1420	A
51	1	1428	C
51	1	1453	A
51	1	1461	C
51	1	1478	G
51	1	1482	G
51	1	1490	A
51	1	1504	A
51	1	1515	A
51	1	1524	G
51	1	1534	U
51	1	1535	A
51	1	1537	G
51	1	1548	A

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Mol	Chain	Res	Type
51	1	1555	G
51	1	1559	U
51	1	1566	A
51	1	1569	A
51	1	1608	A
51	1	1609	A
51	1	1616	A
51	1	1617	C
51	1	1618	A
51	1	1647	U
51	1	1648	U
51	1	1654	A
51	1	1674	G
51	1	1694	C
51	1	1698	A
51	1	1707	G
51	1	1715	G
51	1	1730	C
51	1	1738	G
51	1	1758	U
51	1	1764	C
51	1	1773	A
51	1	1780	A
51	1	1781	U
51	1	1784	A
51	1	1800	C
51	1	1801	A
51	1	1802	A
51	1	1808	A
51	1	1816	C
51	1	1827	U
51	1	1829	A
51	1	1833	C
51	1	1869	G
51	1	1870	C
51	1	1901	A
51	1	1902	C
51	1	1912	A
51	1	1913	A
51	1	1930	G
51	1	1936	A
51	1	1937	A

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Mol	Chain	Res	Type
51	1	1938	A
51	1	1939	U
51	1	1955	U
51	1	1963	U
51	1	1964	G
51	1	1966	A
51	1	1967	C
51	1	1970	A
51	1	1971	U
51	1	1972	G
51	1	1991	U
51	1	1992	G
51	1	1993	U
51	1	1996	C
51	1	1997	C
51	1	2022	U
51	1	2023	C
51	1	2031	A
51	1	2034	U
51	1	2043	C
51	1	2049	G
51	1	2055	C
51	1	2056	G
51	1	2060	A
51	1	2061	G
51	1	2069	G
51	1	2072	C
51	1	2092	U
51	1	2093	G
51	1	2094	A
51	1	2103	C
51	1	2106	U
51	1	2107	G
51	1	2108	A
51	1	2111	U
51	1	2112	G
51	1	2118	U
51	1	2123	G
51	1	2124	G
51	1	2126	A
51	1	2132	U
51	1	2133	G

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Mol	Chain	Res	Type
51	1	2134	A
51	1	2135	A
51	1	2138	G
51	1	2143	C
51	1	2146	C
51	1	2153	C
51	1	2156	G
51	1	2157	G
51	1	2158	A
51	1	2162	G
51	1	2165	C
51	1	2166	U
51	1	2168	G
51	1	2172	U
51	1	2173	A
51	1	2178	C
51	1	2179	C
51	1	2180	U
51	1	2182	U
51	1	2189	U
51	1	2198	A
51	1	2199	A
51	1	2203	U
51	1	2211	A
51	1	2213	U
51	1	2214	C
51	1	2225	A
51	1	2238	G
51	1	2239	G
51	1	2249	U
51	1	2250	G
51	1	2268	A
51	1	2283	C
51	1	2287	A
51	1	2289	G
51	1	2300	C
51	1	2305	U
51	1	2307	G
51	1	2309	A
51	1	2325	G
51	1	2327	A
51	1	2344	U

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Mol	Chain	Res	Type
51	1	2350	C
51	1	2357	G
51	1	2361	G
51	1	2371	G
51	1	2376	A
51	1	2383	G
51	1	2385	C
51	1	2388	A
51	1	2402	U
51	1	2403	C
51	1	2406	A
51	1	2423	U
51	1	2425	A
51	1	2426	A
51	1	2427	C
51	1	2429	G
51	1	2430	A
51	1	2435	A
51	1	2441	U
51	1	2447	G
51	1	2448	A
51	1	2460	U
51	1	2469	A
51	1	2473	U
51	1	2476	A
51	1	2497	A
51	1	2502	G
51	1	2505	G
51	1	2518	A
51	1	2520	C
51	1	2525	G
51	1	2529	G
51	1	2531	A
51	1	2535	G
51	1	2547	A
51	1	2554	U
51	1	2564	A
51	1	2565	A
51	1	2567	G
51	1	2572	A
51	1	2573	C
51	1	2574	G

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Mol	Chain	Res	Type
51	1	2578	G
51	1	2585	U
51	1	2602	A
51	1	2603	G
51	1	2609	U
51	1	2613	U
51	1	2634	A
51	1	2654	A
51	1	2655	G
51	1	2661	G
51	1	2662	A
51	1	2673	G
51	1	2677	G
51	1	2682	A
51	1	2685	G
51	1	2689	U
51	1	2690	U
51	1	2713	U
51	1	2714	G
51	1	2715	C
51	1	2718	G
51	1	2726	A
51	1	2732	G
51	1	2744	G
51	1	2748	A
51	1	2757	A
51	1	2758	A
51	1	2764	A
51	1	2765	A
51	1	2778	A
51	1	2779	U
51	1	2791	G
51	1	2793	C
51	1	2798	U
51	1	2801	G
51	1	2820	A
51	1	2833	U
51	1	2848	G
51	1	2850	A
51	1	2867	G
51	1	2868	A
51	1	2879	A

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Mol	Chain	Res	Type
51	1	2880	C
51	1	2883	A
51	1	2884	U
51	1	2893	A
52	2	4	C
52	2	9	G
52	2	13	G
52	2	35	C
52	2	36	C
52	2	42	C
52	2	44	G
52	2	53	A
52	2	66	A
52	2	67	G
52	2	88	C
52	2	89	U
52	2	90	C
52	2	91	C
52	2	98	G
52	2	108	A
52	2	109	A
52	2	119	A
53	3	3	A
53	3	6	G
53	3	8	A
53	3	9	G
53	3	32	A
53	3	39	G
53	3	47	C
53	3	48	C
53	3	51	A
53	3	54	C
53	3	56	U
53	3	58	C
53	3	61	G
53	3	71	A
53	3	81	A
53	3	87	C
53	3	92	U
53	3	93	U
53	3	94	G
53	3	95	C

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Mol	Chain	Res	Type
53	3	100	G
53	3	110	C
53	3	134	G
53	3	154	U
53	3	183	C
53	3	184	G
53	3	197	A
53	3	208	U
53	3	210	C
53	3	240	G
53	3	246	A
53	3	247	G
53	3	251	G
53	3	266	G
53	3	280	C
53	3	281	G
53	3	289	G
53	3	308	C
53	3	316	C
53	3	328	C
53	3	352	C
53	3	354	G
53	3	367	U
53	3	369	G
53	3	372	C
53	3	397	A
53	3	406	G
53	3	408	A
53	3	413	G
53	3	414	A
53	3	422	C
53	3	429	U
53	3	430	A
53	3	439	U
53	3	445	G
53	3	448	A
53	3	462	G
53	3	467	U
53	3	468	A
53	3	479	U
53	3	486	U
53	3	494	G

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Mol	Chain	Res	Type
53	3	497	G
53	3	509	A
53	3	510	A
53	3	511	C
53	3	512	U
53	3	518	C
53	3	531	U
53	3	532	A
53	3	533	A
53	3	547	A
53	3	555	U
53	3	559	A
53	3	566	G
53	3	572	A
53	3	573	A
53	3	575	G
53	3	576	C
53	3	577	G
53	3	596	A
53	3	633	G
53	3	642	A
53	3	653	U
53	3	665	A
53	3	675	A
53	3	702	A
53	3	703	G
53	3	710	G
53	3	713	G
53	3	721	G
53	3	748	G
53	3	755	G
53	3	777	A
53	3	793	U
53	3	794	A
53	3	815	A
53	3	817	C
53	3	818	G
53	3	819	A
53	3	821	G
53	3	826	C
53	3	832	G
53	3	836	G

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Mol	Chain	Res	Type
53	3	841	C
53	3	843	U
53	3	844	G
53	3	846	G
53	3	851	G
53	3	872	A
53	3	884	U
53	3	889	A
53	3	902	G
53	3	907	A
53	3	913	A
53	3	934	C
53	3	935	A
53	3	938	A
53	3	960	U
53	3	961	U
53	3	966	G
53	3	968	A
53	3	969	A
53	3	971	G
53	3	974	A
53	3	975	A
53	3	976	G
53	3	977	A
53	3	992	U
53	3	993	G
53	3	994	A
53	3	1004	A
53	3	1012	A
53	3	1029	U
53	3	1031	C
53	3	1033	G
53	3	1053	G
53	3	1054	C
53	3	1064	G
53	3	1077	G
53	3	1094	G
53	3	1095	U
53	3	1101	A
53	3	1136	C
53	3	1137	C
53	3	1138	G

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Mol	Chain	Res	Type
53	3	1139	G
53	3	1159	U
53	3	1168	U
53	3	1182	G
53	3	1184	G
53	3	1196	A
53	3	1212	U
53	3	1213	A
53	3	1225	A
53	3	1226	C
53	3	1238	A
53	3	1241	G
53	3	1256	A
53	3	1257	A
53	3	1261	A
53	3	1262	C
53	3	1275	A
53	3	1278	G
53	3	1280	A
53	3	1282	C
53	3	1286	U
53	3	1287	A
53	3	1290	G
53	3	1300	G
53	3	1301	U
53	3	1302	C
53	3	1317	C
53	3	1345	U
53	3	1363	A
53	3	1364	U
53	3	1378	C
53	3	1398	A
53	3	1422	G
53	3	1432	G
53	3	1441	A
53	3	1446	A
53	3	1452	C
53	3	1471	U
53	3	1491	G
53	3	1492	A
53	3	1493	A
53	3	1494	G

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Mol	Chain	Res	Type
53	3	1503	A
53	3	1505	G
53	3	1506	U
53	3	1507	A
53	3	1517	G
53	3	1529	G
53	3	1530	G
53	3	1540	U
54	4	4	U
54	4	6	U
54	4	7	C
54	4	8	U
54	4	9	U
54	4	10	C
54	4	11	U
54	4	12	U
54	4	14	U
54	4	15	U
54	4	16	U
54	4	17	U
54	4	18	U
54	4	19	U
54	4	20	U
63	6	9	G
63	6	10	G
63	6	19	G
63	6	20	U
63	6	21	A
63	6	22	G
63	6	27	U
63	6	33	U
63	6	45	G
63	6	47	U
63	6	48	C
63	6	58	A
63	6	61	C
63	6	64	G

All (11) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	1	858	G

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Mol	Chain	Res	Type
51	1	1020	A
51	1	1106	G
51	1	1801	A
51	1	2326	C
51	1	2756	U
53	3	413	G
53	3	1493	A
54	4	10	C
54	4	18	U
54	4	19	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
67	GCP	0	800	-	32,34,34	3.17	12 (37%)	49,54,54	1.62	9 (18%)

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
67	GCP	0	800	-	-	6/19/38/38	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	0	800	GCP	O4'-C1'	8.92	1.62	1.42
67	0	800	GCP	C2'-C1'	-6.96	1.31	1.53
67	0	800	GCP	O4'-C4'	-6.19	1.31	1.45
67	0	800	GCP	PB-O3A	6.05	1.65	1.58
67	0	800	GCP	PA-O3A	5.33	1.65	1.59
67	0	800	GCP	C2-N2	4.81	1.45	1.34
67	0	800	GCP	C6-N1	-3.36	1.32	1.38
67	0	800	GCP	O2'-C2'	2.82	1.49	1.43
67	0	800	GCP	O6-C6	-2.59	1.18	1.23
67	0	800	GCP	PB-O2B	-2.59	1.50	1.56
67	0	800	GCP	O3'-C3'	-2.54	1.36	1.43
67	0	800	GCP	C5-N7	-2.19	1.34	1.39

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	0	800	GCP	C5-C4-N3	-5.08	120.30	128.39
67	0	800	GCP	C2-N3-C4	4.42	119.91	112.30
67	0	800	GCP	N9-C8-N7	-3.10	107.64	113.40
67	0	800	GCP	N9-C4-N3	2.84	131.62	125.95
67	0	800	GCP	C2-N1-C6	-2.80	120.03	125.11
67	0	800	GCP	C5-C6-N1	2.71	120.14	113.25
67	0	800	GCP	C8-N7-C5	2.28	108.32	104.26
67	0	800	GCP	N2-C2-N3	2.27	124.09	119.67
67	0	800	GCP	O6-C6-C5	-2.07	121.07	126.53

There are no chirality outliers.

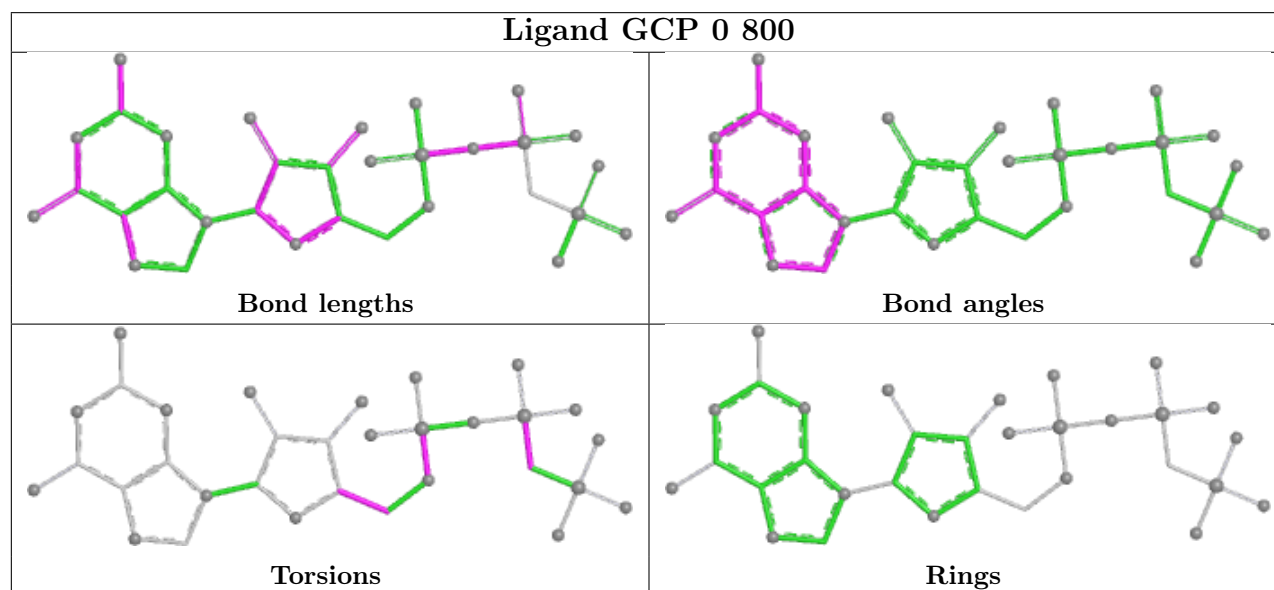
All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
67	0	800	GCP	PG-C3B-PB-O1B
67	0	800	GCP	PG-C3B-PB-O2B
67	0	800	GCP	PG-C3B-PB-O3A
67	0	800	GCP	O4'-C4'-C5'-O5'
67	0	800	GCP	C3'-C4'-C5'-O5'
67	0	800	GCP	C5'-O5'-PA-O2A

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

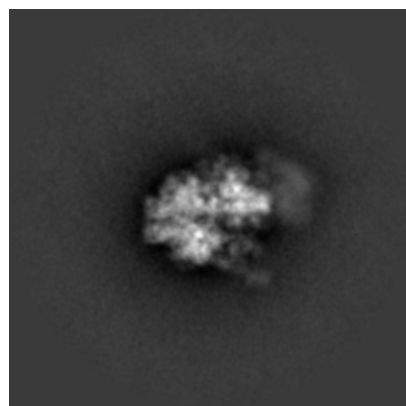
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38946. These allow visual inspection of the internal detail of the map and identification of artifacts.

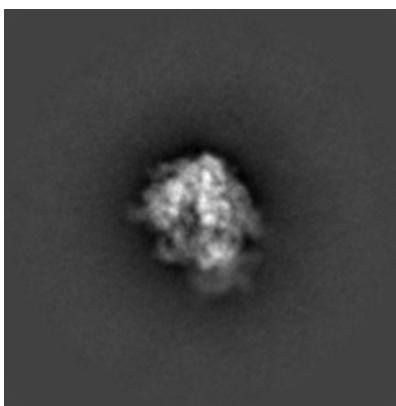
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

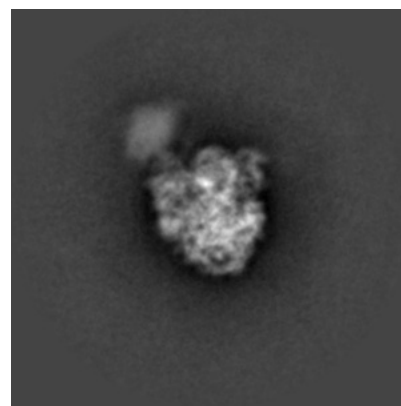
6.1.1 Primary map



X

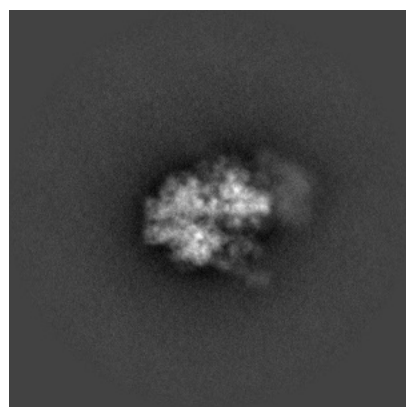


Y

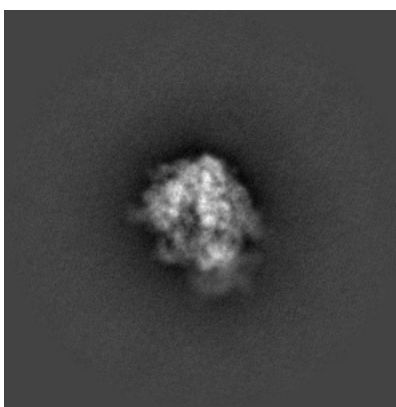


Z

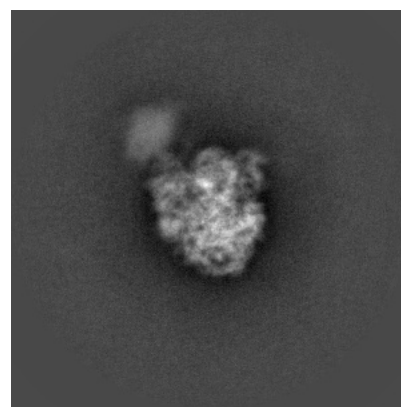
6.1.2 Raw map



X



Y

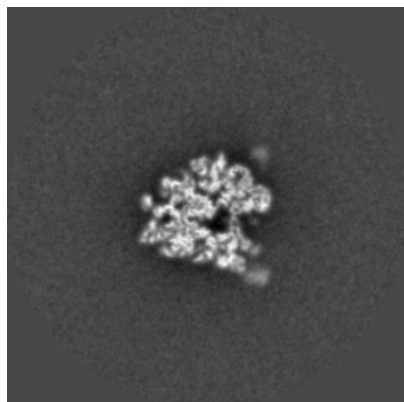


Z

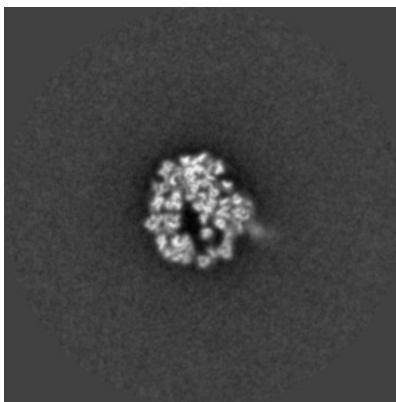
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

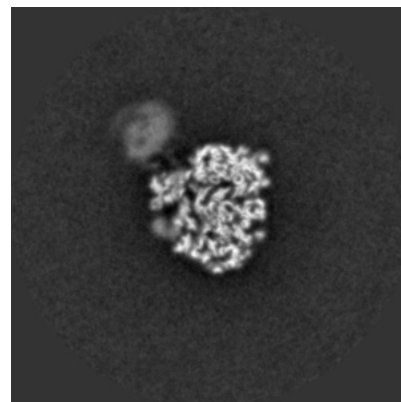
6.2.1 Primary map



X Index: 240

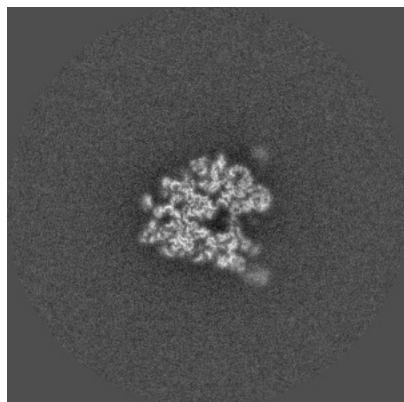


Y Index: 240

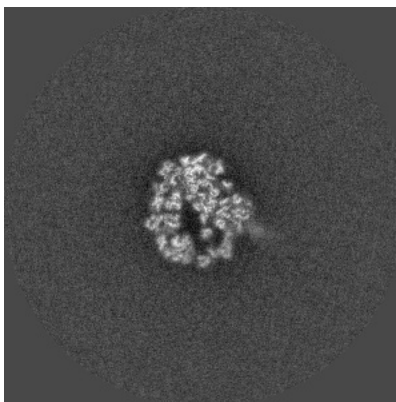


Z Index: 240

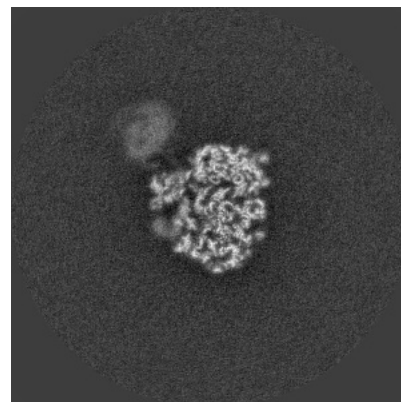
6.2.2 Raw map



X Index: 240



Y Index: 240

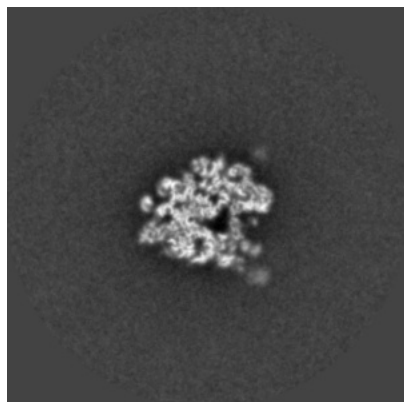


Z Index: 240

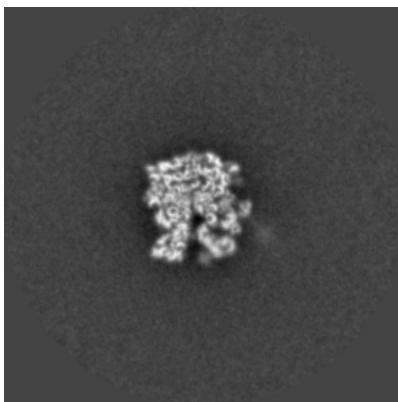
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

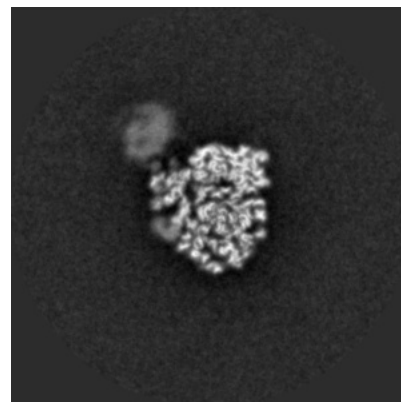
6.3.1 Primary map



X Index: 243

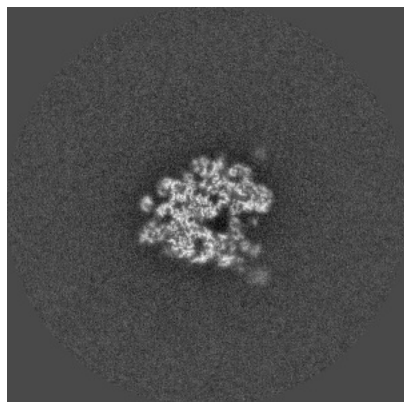


Y Index: 224

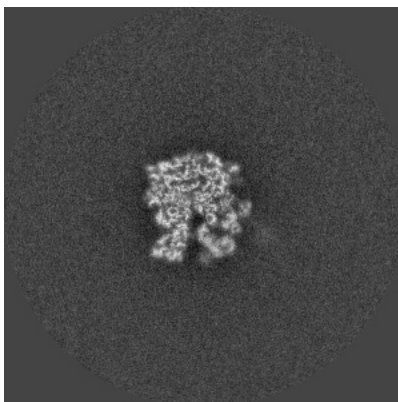


Z Index: 243

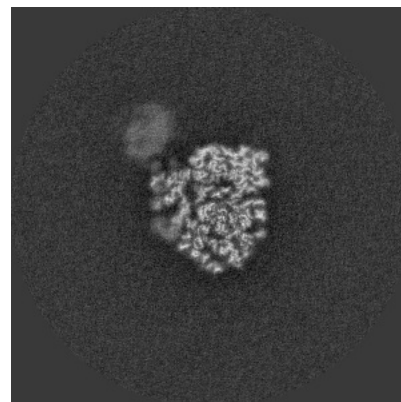
6.3.2 Raw map



X Index: 243



Y Index: 224

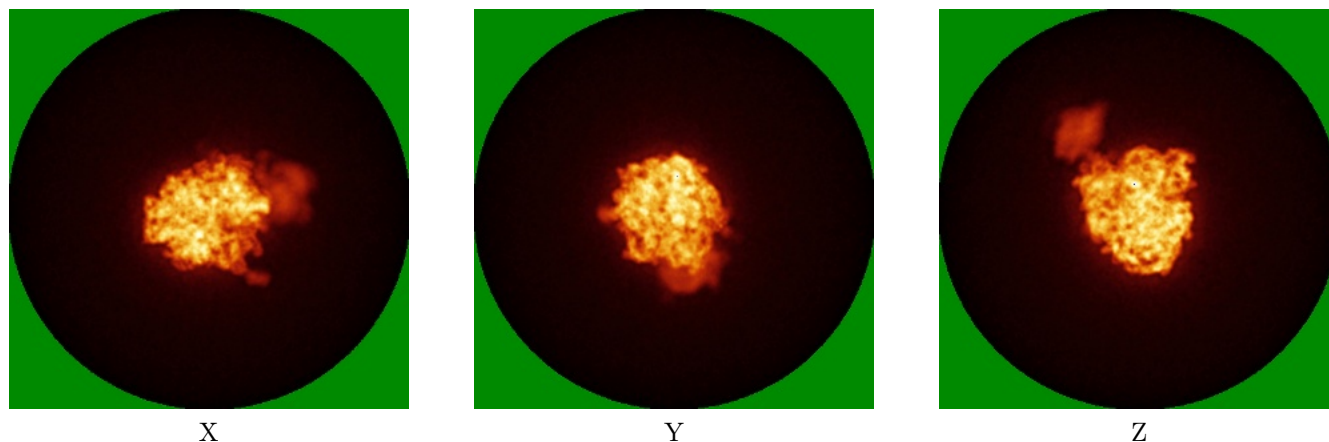


Z Index: 243

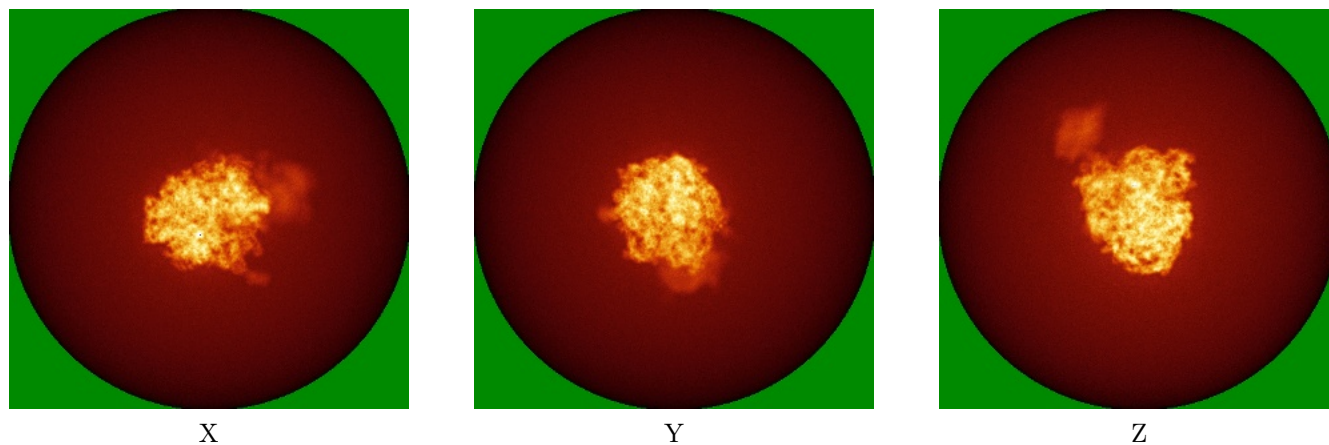
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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

6.5 Orthogonal surface views [i](#)

This section was not generated.

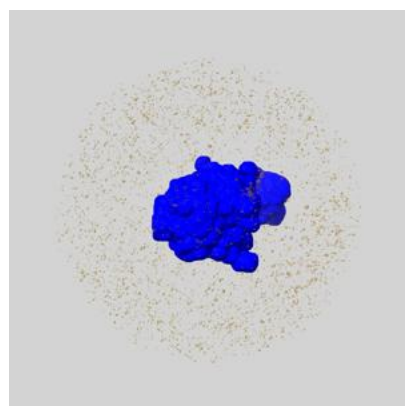
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

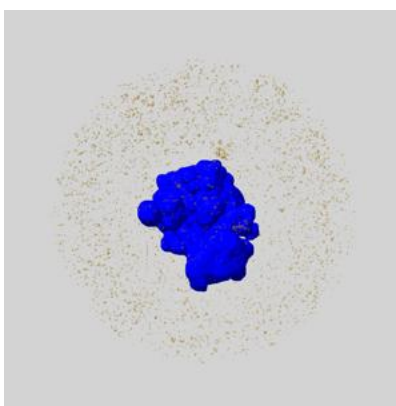
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

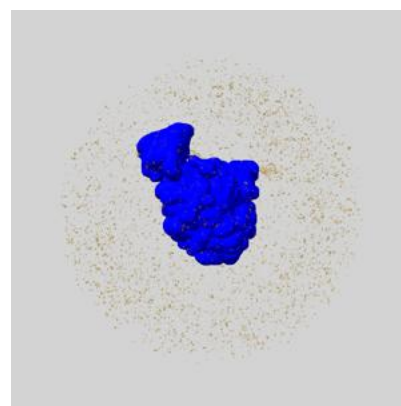
6.6.1 emd_38946_msk_1.map [i](#)



X



Y

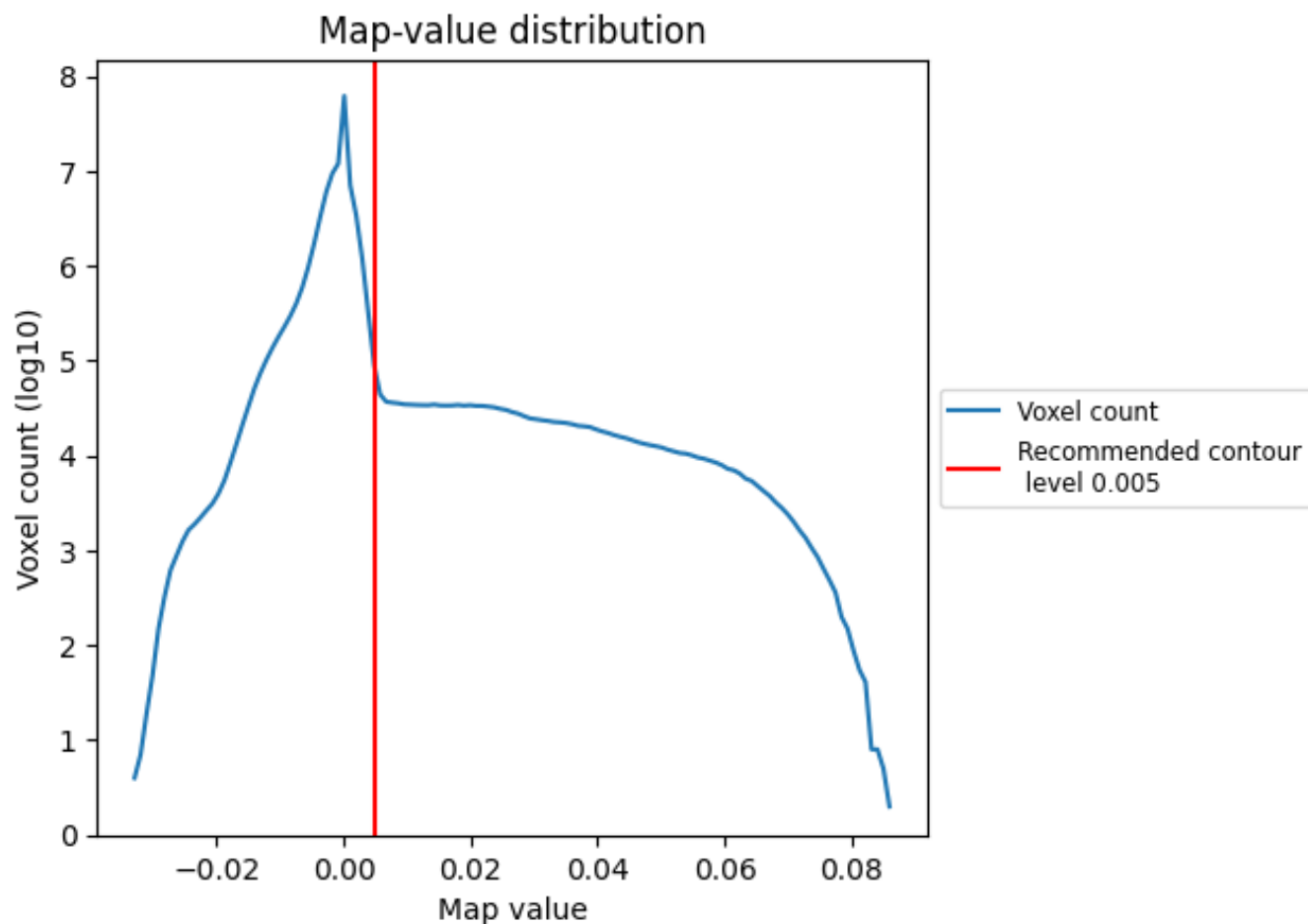


Z

7 Map analysis [i](#)

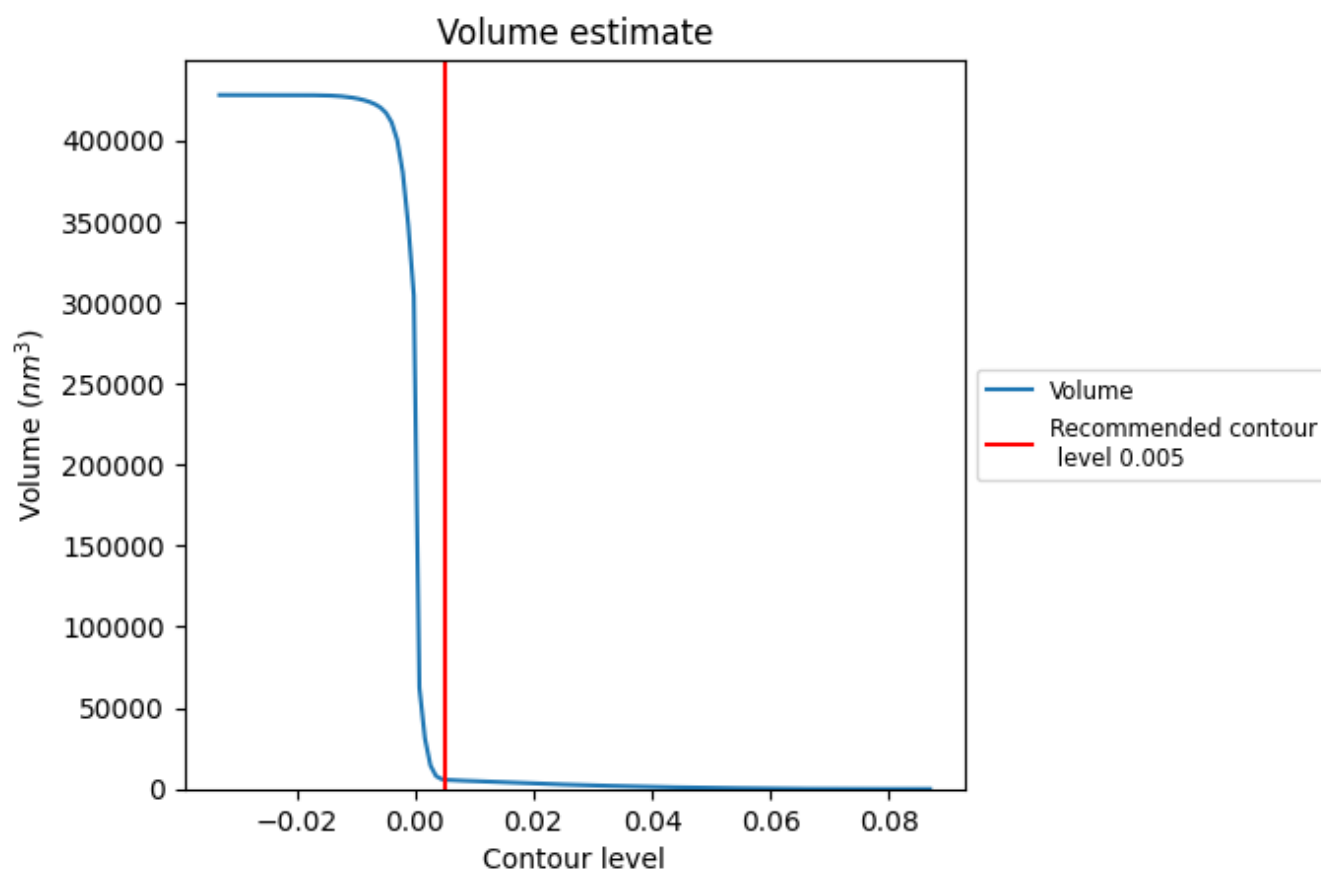
This section contains the results of statistical analysis of the map.

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.

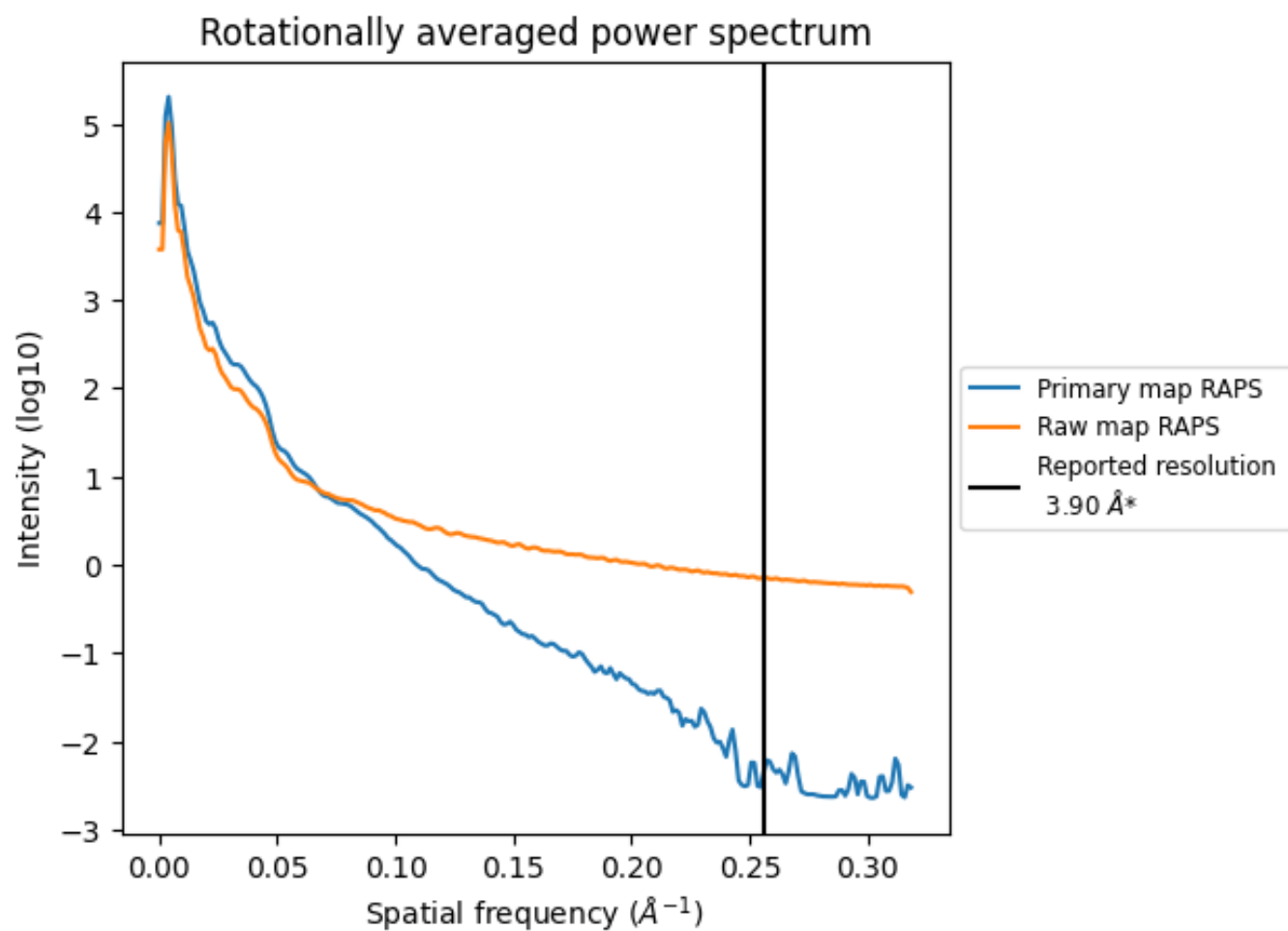
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5814 nm^3 ; this corresponds to an approximate mass of 5252 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 ⓘ

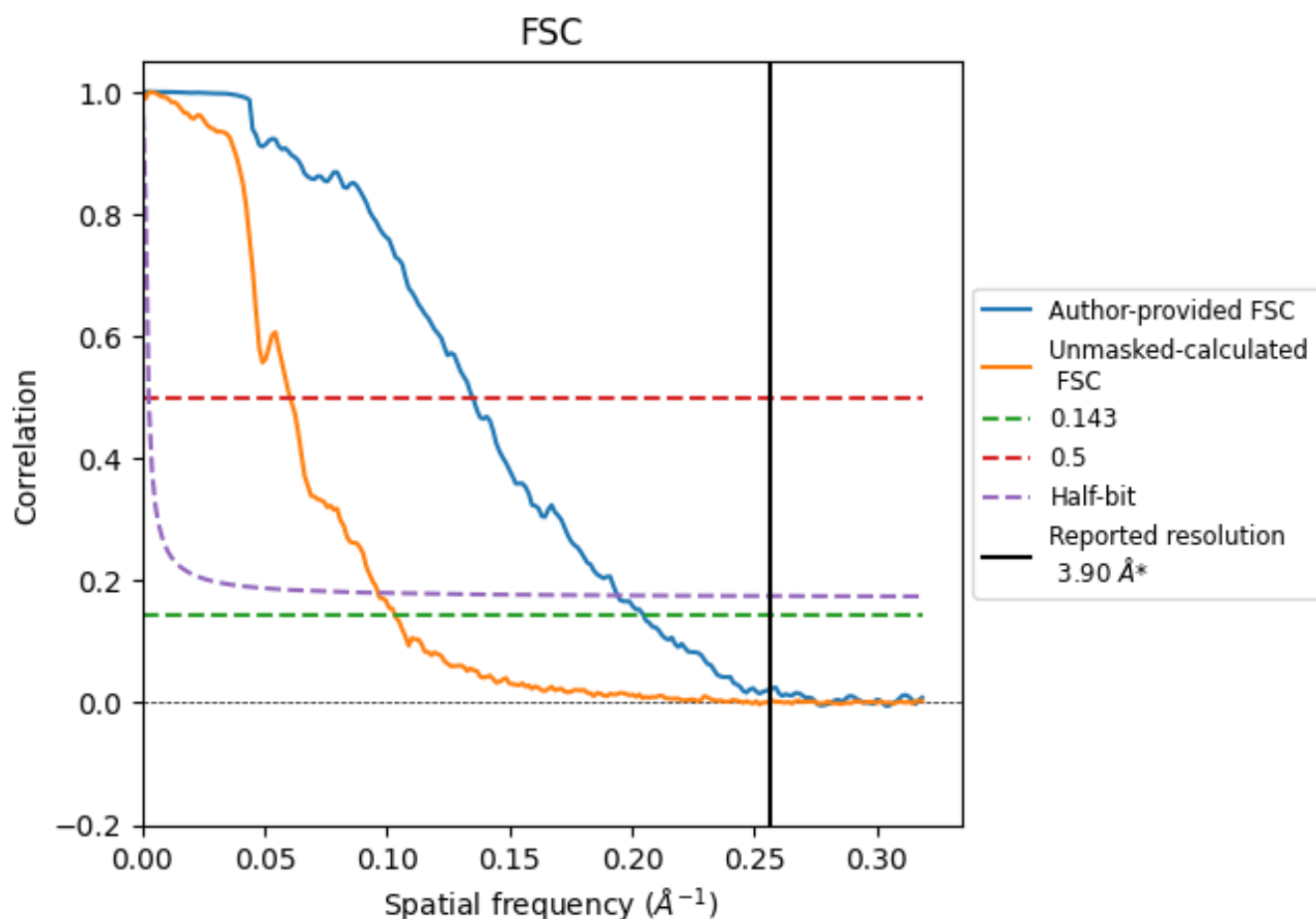


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

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 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	4.89	7.42	5.15
Unmasked-calculated*	9.69	16.56	10.38

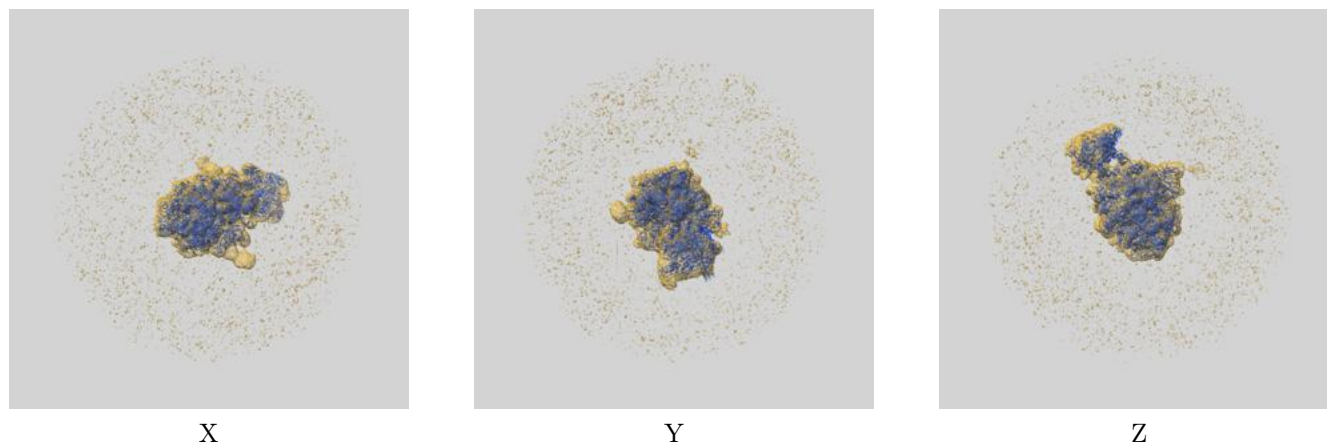
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.89 differs from the reported value 3.9 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 9.69 differs from the reported value 3.9 by more than 10 %

9 Map-model fit [i](#)

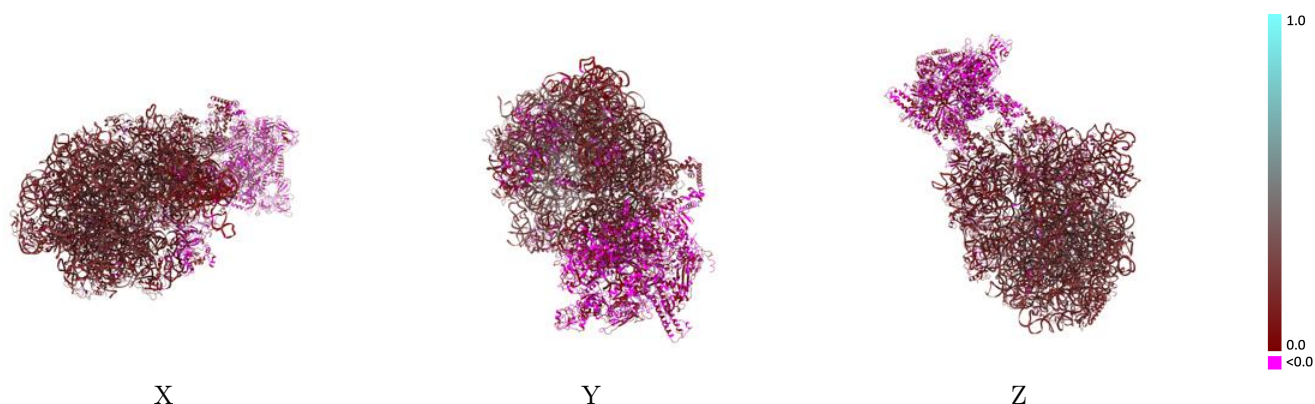
This section contains information regarding the fit between EMDB map EMD-38946 and PDB model 8Y5Q. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



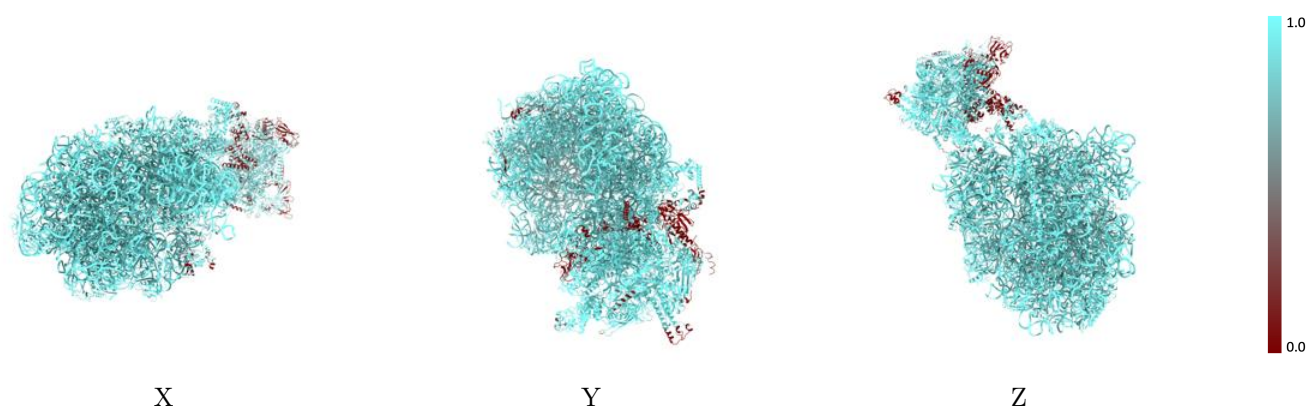
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



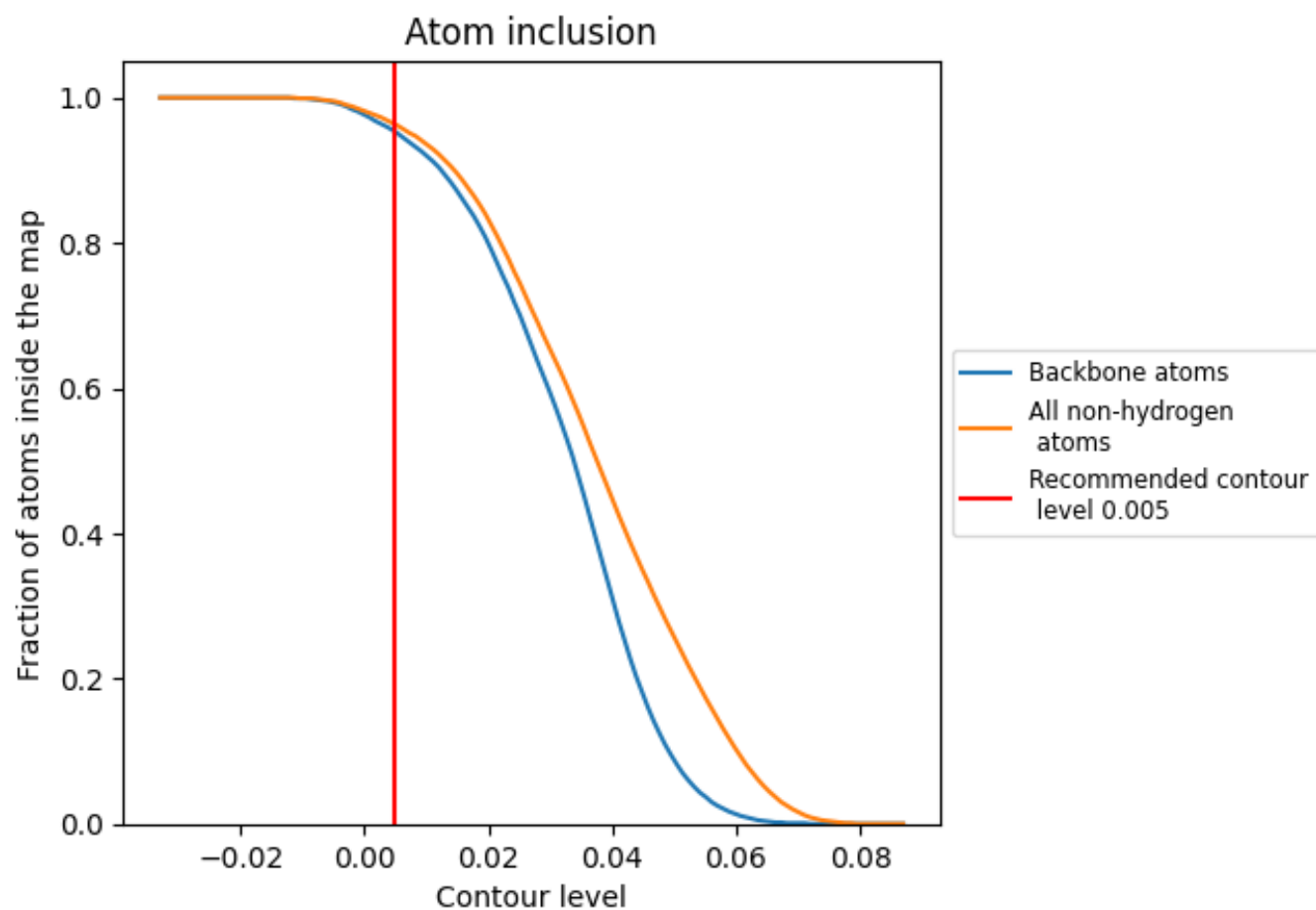
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 96% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9630	 0.1450
0	 0.8550	 0.0410
1	 0.9990	 0.2050
2	 1.0000	 0.1560
3	 0.9980	 0.1690
4	 0.9670	 0.0490
6	 0.9930	 0.1630
8	 1.0000	 0.0170
9	 1.0000	 0.0550
A	 1.0000	 0.1150
A1	 0.3920	 -0.0010
A2	 0.7070	 0.0290
B	 1.0000	 0.1570
B1	 0.8140	 0.0090
B2	 0.9460	 0.0270
C	 0.9750	 0.1460
D	 0.9800	 0.1440
E	 1.0000	 0.1240
F	 1.0000	 0.1040
G	 0.9930	 0.1540
H	 0.9940	 0.1430
I	 0.9960	 0.0940
J	 0.9970	 0.1570
K	 0.9860	 0.1460
L	 0.9950	 0.1250
M	 0.9910	 0.1420
N	 0.9850	 0.0910
NA	 0.9180	 0.1290
NG	 0.9590	 0.0140
O	 0.9960	 0.1090
P	 0.9960	 0.1570
Q	 0.9670	 0.1140
R	 0.9860	 0.1310
S	 1.0000	 0.1090
T	 0.9990	 0.1340



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Chain	Atom inclusion	Q-score
U	 1.0000	 0.0730
V	 1.0000	 0.1310
W	 1.0000	 0.1440
W0	 0.0840	 -0.0440
X	 0.9950	 0.1060
Y	 0.9880	 0.1250
Z	 0.9630	 0.1460
a	 0.9910	 0.1010
b	 0.9930	 0.1770
c	 0.9960	 0.1580
d	 0.9960	 0.1440
e	 0.9640	 0.0970
f	 0.9880	 0.1370
g	 0.9190	 0.1270
i	 0.8570	 0.0310
j	 1.0000	 0.1600
k	 0.9860	 0.1810
l	 0.9980	 0.1330
m	 0.9760	 0.1390
n	 0.9980	 0.1590
o	 1.0000	 0.0940
p	 0.9970	 0.1760
q	 1.0000	 0.1400
r	 1.0000	 0.1500
s	 0.9950	 0.1700
t	 0.9950	 0.1520
u	 0.9900	 0.1460
v	 0.9990	 0.1420
w	 0.9960	 0.1180
x	 1.0000	 0.1610
y	 0.9940	 0.1470
z	 0.9910	 0.1560