



Full wwPDB EM Validation Report ⓘ

Mar 17, 2026 – 12:45 PM UTC

PDB ID : 8Y5N / pdb_00008y5n
EMDB ID : EMD-38943
Title : E.coli transcription translation coupling complex in TTC-A state 3 containing mRNA with 21-mer spacer, NusG, NusA, fMet-tRNA(iMet), Phe-tRNA(Phe), and viomycin
Authors : Zhang, J.; Lu, G.; Wang, C.; Lin, J.
Deposited on : 2024-01-31
Resolution : 4.50 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:

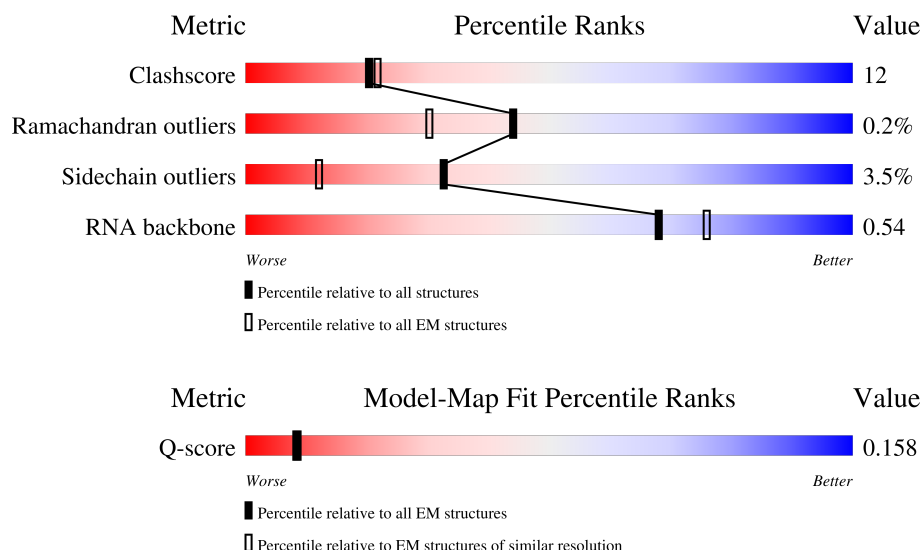
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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

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

The reported resolution of this entry is 4.50 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.



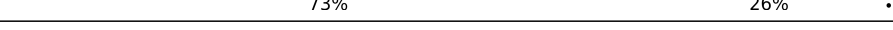
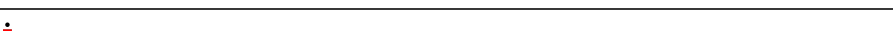
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2937 (4.00 - 5.00)

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	

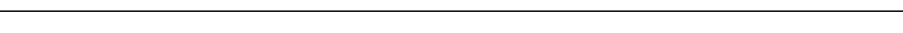
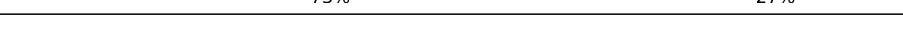
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Mol	Chain	Length	Quality of chain
4	D	46	
5	E	65	
6	F	38	
7	G	241	
8	H	233	
9	I	206	
10	J	167	
11	K	135	
12	L	179	
13	M	130	
14	N	130	
15	O	103	
16	P	129	
17	Q	124	
18	R	118	
19	S	101	
20	T	89	
21	U	82	
22	V	84	
23	W	75	
24	X	92	
25	Y	87	
26	Z	71	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

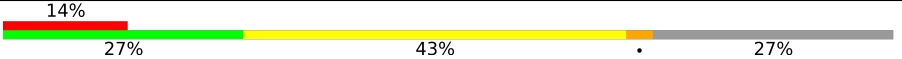
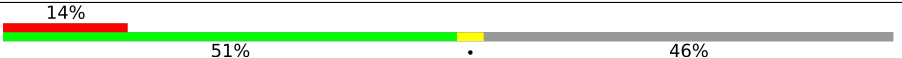
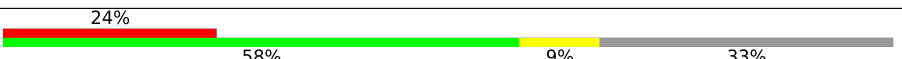
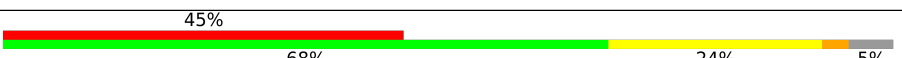
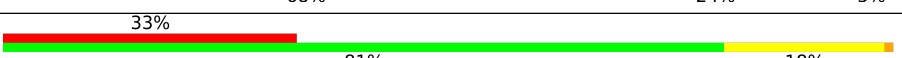
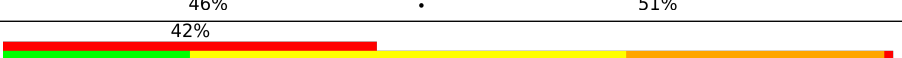
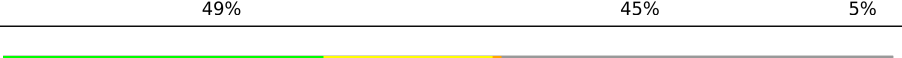
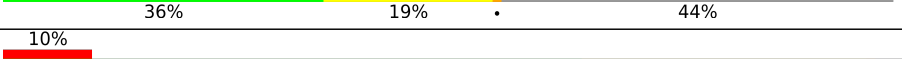
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Mol	Chain	Length	Quality of chain
29	d	201	
30	e	179	
31	f	177	
32	g	149	
33	i	142	
34	j	142	
35	k	123	
36	l	144	
37	m	136	
38	n	127	
39	o	117	
40	p	115	
41	q	118	
42	r	103	
43	s	110	
44	t	100	
45	u	104	
46	v	94	
47	w	85	
48	x	78	
49	y	63	
50	z	59	
51	1	2904	
52	2	120	
53	3	1542	

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Mol	Chain	Length	Quality of chain
54	4	38	
55	8	37	
56	9	37	
57	A1	329	
57	A2	329	
58	B1	1407	
59	B2	1342	
60	W0	91	
61	NG	181	
62	5	76	
63	6	77	
64	a	234	
65	0	716	
66	h	6	

2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 179711 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
			1637	1023	312	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	22	Total	C	N	O	P	0	0
			467	208	76	161	22		

- 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	218	Total	C	N	O	S	0	0
			1677	1048	297	326	6		
57	A2	221	Total	C	N	O	S	0	0
			1698	1060	299	333	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
			10546	6616	1839	2048	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 NusG.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	NG	88	Total	C	N	O	0	0
			433	257	88	88		

- Molecule 62 is a RNA chain called tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace
62	5	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		

- 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		

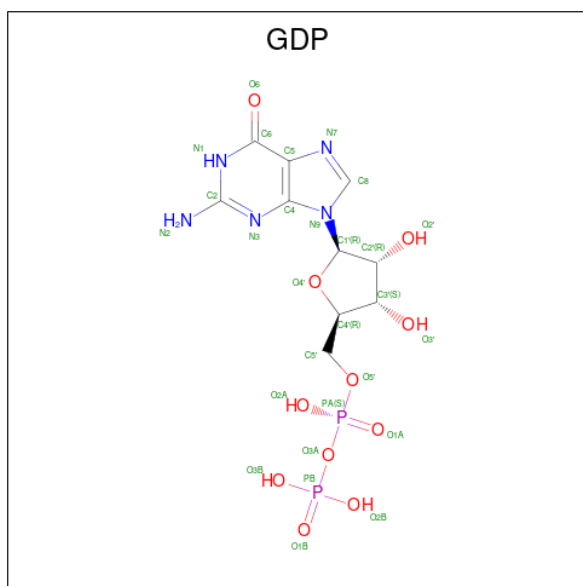
There are 12 discrepancies between the modelled and reference sequences:

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 a protein (with D amino acids) called Viomycin.

Mol	Chain	Residues	Atoms				AltConf	Trace
66	h	6	Total	C	N	O	0	0
			48	25	13	10		

- Molecule 67 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

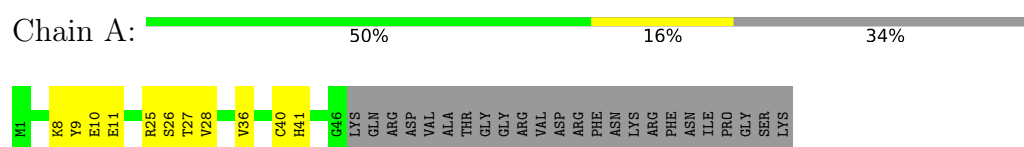


Mol	Chain	Residues	Atoms			AltConf
			Total	O	P	
68	0	1	5	4	1	0

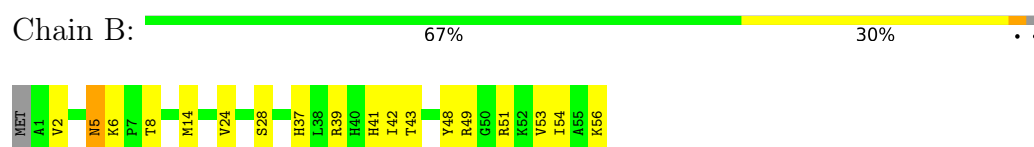
3 Residue-property plots [i](#)

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

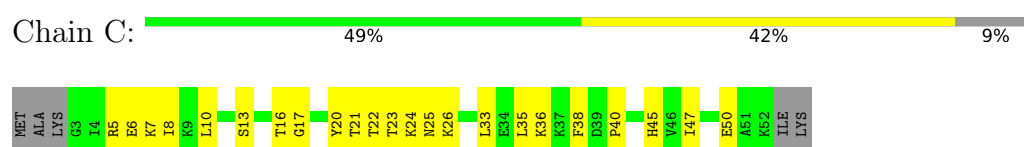
• Molecule 1: 50S ribosomal protein L31



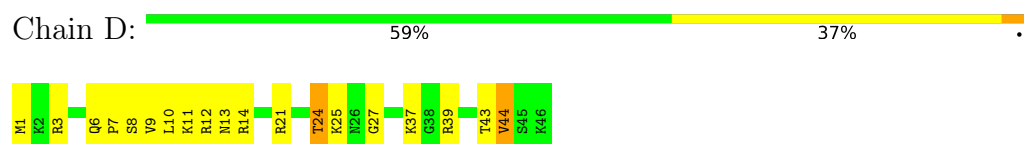
• Molecule 2: 50S ribosomal protein L32



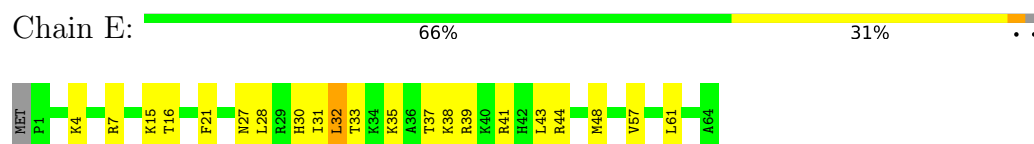
• Molecule 3: 50S ribosomal protein L33



• Molecule 4: 50S ribosomal protein L34

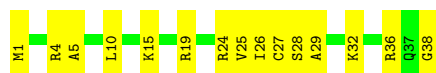


• Molecule 5: 50S ribosomal protein L35



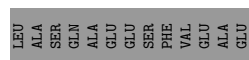
• Molecule 6: 50S ribosomal protein L36

Chain F:  61% 39%



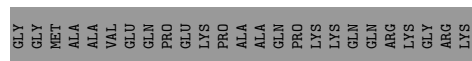
• Molecule 7: 30S ribosomal protein S2

Chain G:  64% 25% 10%



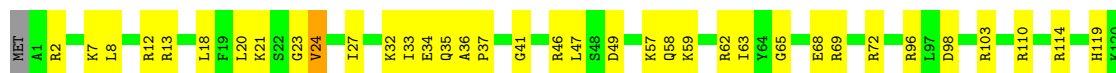
• Molecule 8: 30S ribosomal protein S3

Chain H:  58% 27% 12%



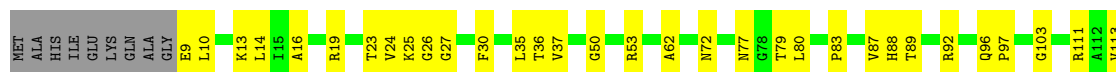
• Molecule 9: 30S ribosomal protein S4

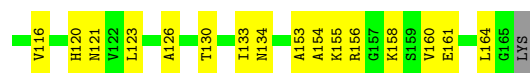
Chain I:  70% 28%



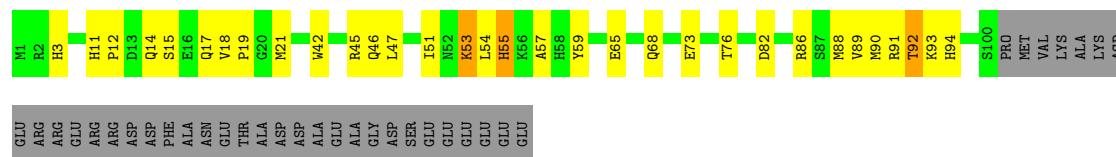
• Molecule 10: 30S ribosomal protein S5

Chain J:  65% 29% 6%

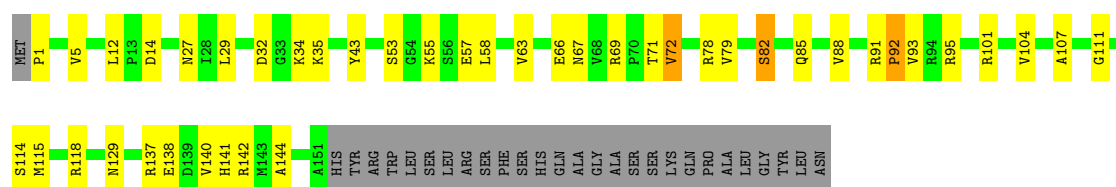




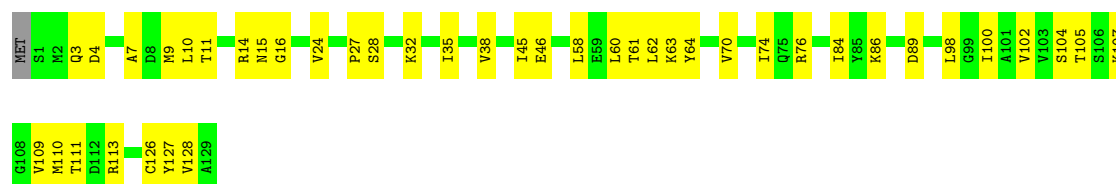
- Molecule 11: 30S ribosomal protein S6, fully modified isoform



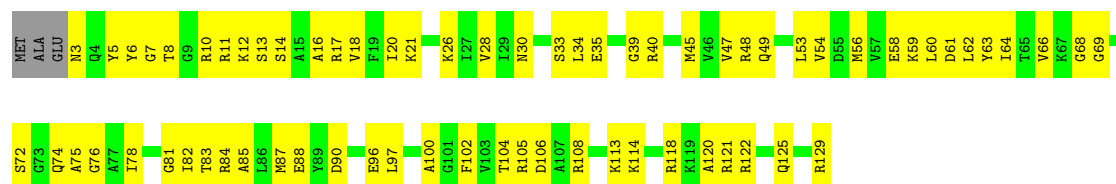
- Molecule 12: 30S ribosomal protein S7



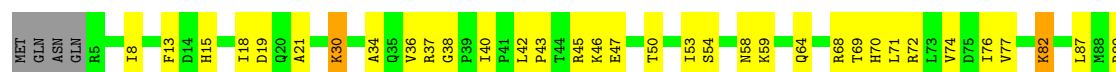
- Molecule 13: 30S ribosomal protein S8

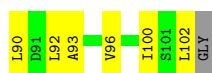


- Molecule 14: 30S ribosomal protein S9



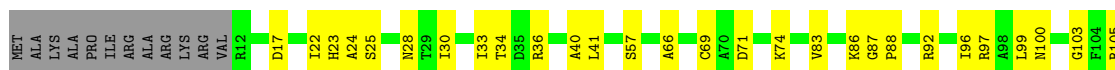
- Molecule 15: 30S ribosomal protein S10





- Molecule 16: 30S ribosomal protein S11

Chain P: 63% 27% 10%



- Molecule 17: 30S ribosomal protein S12

Chain Q: 73% 26% 1%



- Molecule 18: 30S ribosomal protein S13

Chain R: 69% 28% 3%



- Molecule 19: 30S ribosomal protein S14

Chain S: 60% 39% 1%



- Molecule 20: 30S ribosomal protein S15

Chain T: 78% 21% 1%



- Molecule 21: 30S ribosomal protein S16

Chain U: 72% 28% 0%



- Molecule 22: 30S ribosomal protein S17

Chain V: 67% 29% 5%



- Molecule 23: 30S ribosomal protein S18

Chain W: 65% 21% 13%



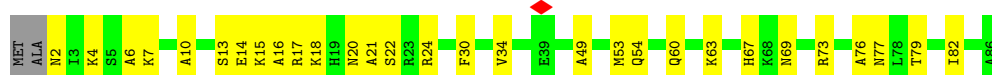
- Molecule 24: 30S ribosomal protein S19

Chain X: 64% 22% 14%



- Molecule 25: 30S ribosomal protein S20

Chain Y: 64% 33% 3%



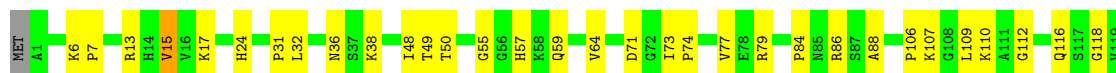
- Molecule 26: 30S ribosomal protein S21

Chain Z: 62% 24% 6% 8%



- Molecule 27: 50S ribosomal protein L2

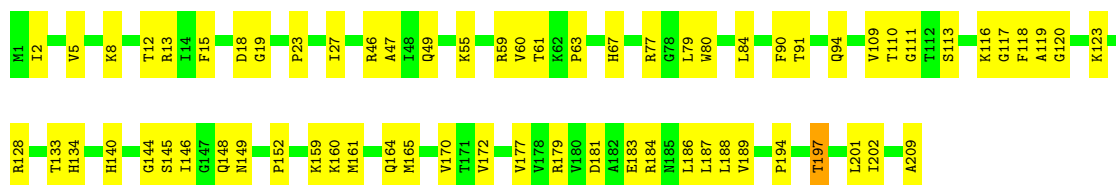
Chain b: 70% 29% 1%





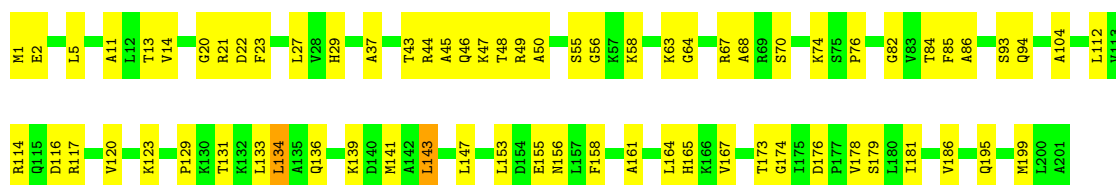
- Molecule 28: 50S ribosomal protein L3

Chain c: 68% 32%



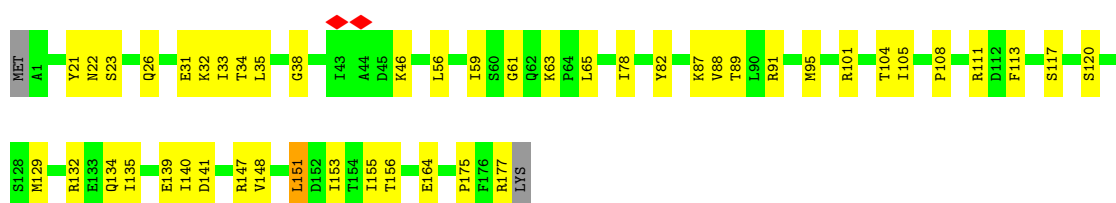
- Molecule 29: 50S ribosomal protein L4

Chain d: 65% 34%



- Molecule 30: 50S ribosomal protein L5

Chain e: 72% 26%



- Molecule 31: 50S ribosomal protein L6

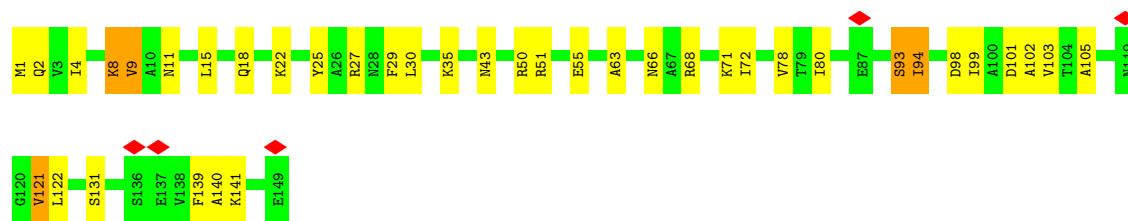
Chain f: 78% 21%



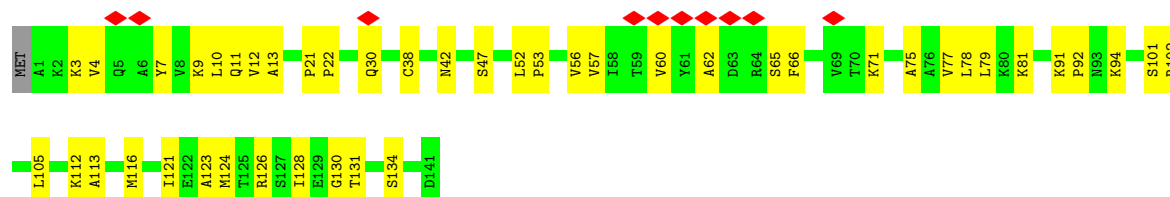
- Molecule 32: 50S ribosomal protein L9

Chain g: 74% 23%

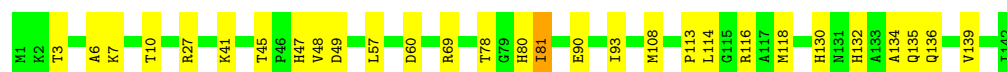
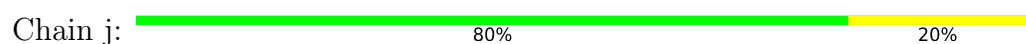




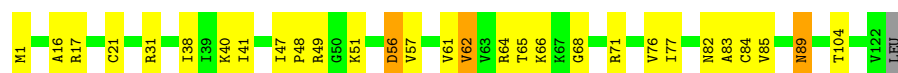
- Molecule 33: 50S ribosomal protein L11



- Molecule 34: 50S ribosomal protein L13



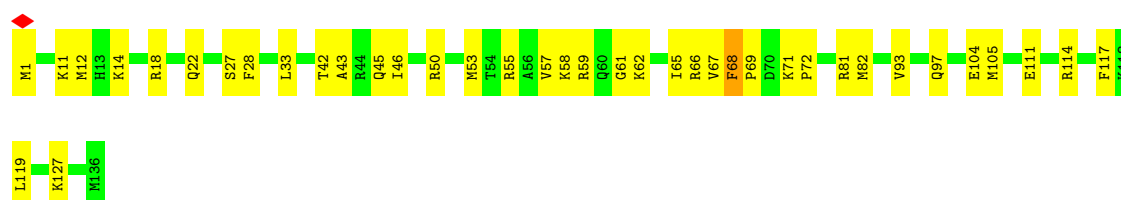
- Molecule 35: 50S ribosomal protein L14



- Molecule 36: 50S ribosomal protein L15

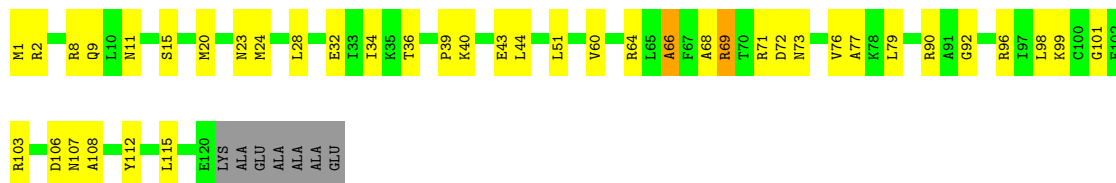


- Molecule 37: 50S ribosomal protein L16



- Molecule 38: 50S ribosomal protein L17

Chain n:  62% 31% 6%



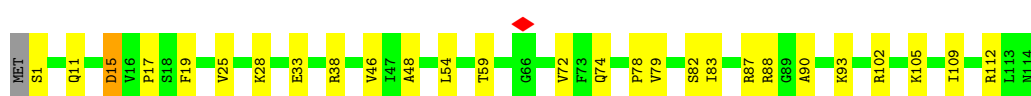
- Molecule 39: 50S ribosomal protein L18

Chain o:  71% 28%



- Molecule 40: 50S ribosomal protein L19

Chain p:  76% 23%



- Molecule 41: 50S ribosomal protein L20

Chain q:  76% 23%



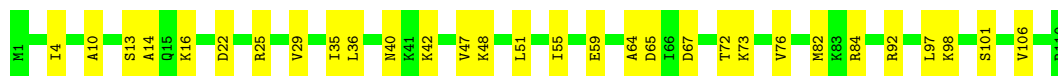
- Molecule 42: 50S ribosomal protein L21

Chain r:  71% 29%



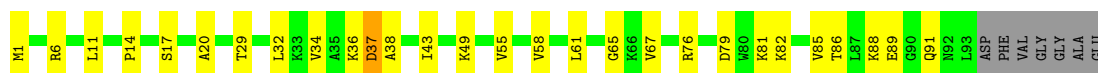
- Molecule 43: 50S ribosomal protein L22

Chain s:  73% 27%



- Molecule 44: 50S ribosomal protein L23

Chain t:  65% 27% 7%



- Molecule 45: 50S ribosomal protein L24

Chain u: 77% 20% ..



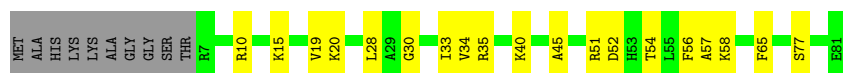
- Molecule 46: 50S ribosomal protein L25

Chain v: 78% 22%



- 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% .



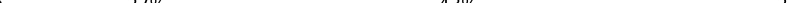
- Molecule 51: 23S rRNA

Chain 1: 44% 48% 8%

U1198	A1126	C1053	A975	A896	G818	C747	U667	A590	A513	G424	A330	G230	U154	A84	G1
A1127	A1129	A1054	G976	U887	A819	G748	C671	U593	A514	G431	C331	A231	A156	G85	G2
A1203	A1204	G1055	A980	C890	A820	A751	G674	U594	A515	U431	G338	A232	A155	U90	U3
G1206	G1207	A1056	A981	C891	A821	A752	A675	C595	A516	A432	U339	A233	C157	U158	U4
A1209	A1132	G1130	A982	U895	C823	A753	A676	U596	A517	C433	A340	U234	G159	A91	A5
G1210	A1133	U1058	A983	A896	U824	U754	A677	C597	U519	U434	C341	G242	U162	G93	G7
A1134	A1135	A1059	A984	C897	A825	U755	A678	U598	G524	U435	A342	U243	C163	A94	C8
G1211	G1136	C986	C985	C986	U827	A756	C678	A599	U525	C436	A343	A244	U166	A95	G9
G1212	G1137	A898	C987	C987	U828	G757	C680	C601	A526	U441	A344	G245	U167	C96	A10
G1216	G1138	A900	C988	A899	A829	G760	U683	A602	A527	G442	C351	G246	A167	C97	U12
U1219	G1139	C901	C989	C901	A830	A764	U686	A603	A528	G443	A352	G247	U170	U100	A13
G1220	C1140	C902	A900	C902	G831	C765	U687	G605	A532	C444	U355	G248	U171	A101	A14
G1225	A1141	A910	C994	A910	U832	C766	U688	G606	A533	G445	U356	G252	U172	A102	G15
A1226	A1142	A911	C995	A911	G833	C767	U689	A608	G533	G446	G361	G253	A173	A103	A19
C1229	A1143	C912	A996	C912	G834	U767	A689	A609	U534	G450	U365	A255	U174	G107	A21
A1236	A1144	U913	U999	U913	C837	G770	C691	C610	G536	U451	U366	G259	A175	G108	G22
A1237	C1145	G916	A1000	G916	U838	G771	C692	C611	G537	C455	U367	G260	A176	C109	G23
A1238	C1146	A917	C1005	A917	U839	C772	A693	A613	A538	C456	U368	G261	G177	G110	G24
G1236	A1147	A918	C1006	A918	G840	U773	U694	A614	G539	A457	U369	G266	C179	A111	U25
A1246	C1153	G923	G923	G923	U842	G774	G695	U615	G543	U458	G370	A272	G189	U112	G26
A1247	A1154	G924	G924	G924	G843	G775	G696	G697	G544	U459	A371	G273	A190	U113	G27
G1248	A1155	A845	A927	A927	A844	G776	G697	A621	G548	A460	G372	C273	A191	A118	A28
U1249	A1156	A846	A928	A928	U846	U779	G704	G622	G549	G465	G375	U276	A192	A119	U34
G1250	G1157	U847	U929	U929	U847	G780	G708	C624	C550	U478	G376	A277	U193	G120	G35
C1251	A1158	C848	U929	U929	U848	A781	U709	A627	U554	G468	G377	A278	U194	G121	G36
G1252	C1161	A849	A933	A933	U849	A782	U710	G637	G555	G469	G378	U286	A195	G122	C37
A1253	G1162	C851	C937	C937	U850	A783	G711	G638	U568	A470	G379	G287	A196	G123	A38
A1254	A1169	U852	G1022	G1022	G857	G785	G712	A632	U569	A471	G380	G287	A197	G124	G39
G1256	C1170	G858	G1023	G1023	G858	C786	G713	G634	C560	A472	A382	A294	A198	A125	U40
C1257	G1171	G859	G1024	G1024	G859	C787	U714	C635	A563	C475	G386	G297	A203	G130	G43
U1258	C1172	G860	G1025	G1025	U860	A788	A715	G636	U571	U478	U387	G298	A204	A44	A44
G1259	U1173	G861	A941	A941	G861	A789	C717	A637	A572	A479	G388	A299	G205	A131	G45
A1262	A1174	A862	C944	C944	A862	A792	A718	U639	U573	A480	G389	A300	U206	G132	G46
A1265	U1175	A863	A945	A945	A863	A793	G726	G638	U566	G481	U390	C305	C208	U133	A52
G1266	G1176	A864	C946	C946	A864	A794	G727	U642	U568	C486	G393	U306	C209	G136	A53
U1267	C1177	C865	A947	A947	C865	G797	A727	A643	U571	C486	C394	G315	C210	U137	U62
A1268	G1178	A866	G949	G949	A866	G798	G728	A644	A572	C490	U395	G316	C211	U138	U63
A1269	C1179	G869	G952	G952	G869	A801	G729	U645	U573	G491	G396	A311	G212	U139	A63
G1270	U1180	U870	G953	G953	U870	U803	A730	U646	A574	G494	U397	G316	C212	G140	C66
C1271	G1182	U871	G954	G954	U871	A804	A731	G647	A575	U499	A402	G319	A216	A142	A71
A1271	U1183	U872	U955	U955	U872	C805	G736	G649	G578	U499	U403	A320	A217	C143	U72
A1272	U1184	U873	U956	U956	U873	C806	C737	A654	G579	A503	U404	A321	A218	A144	A73
A1275	G1185	A877	U958	U958	A877	G809	G738	A655	U580	A504	U405	A322	A219	C145	U74
A1276	C1186	A878	A959	A959	A878	A739	A739	G656	C581	A505	G411	C323	A221	A146	A75
G1277	G1187	G879	A960	A960	G879	U810	C740	U658	A582	G506	A412	G325	U224	U148	G75
C1278	U1191	G880	C961	C961	G880	U811	U741	U658	G583	A507	C413	G326	G225	G149	G76
G1279	G1192	G881	G971	G971	G881	C812	A742	G663	A586	C510	C414	G327	A226	U150	U78
A1287	C1193	G882	A972	A972	G882	U813	A743	G664	C587	G327	C415	U328	A227	C151	G79
G1288	C1196	G883	A973	A973	G883	C814	U744	U665	U588	U511	A415	G329	C228	G80	G80
C1289	G1197	C885	G974	G974	C885	C817	U746	A666	U589	G512	C421		C229	U153	G81





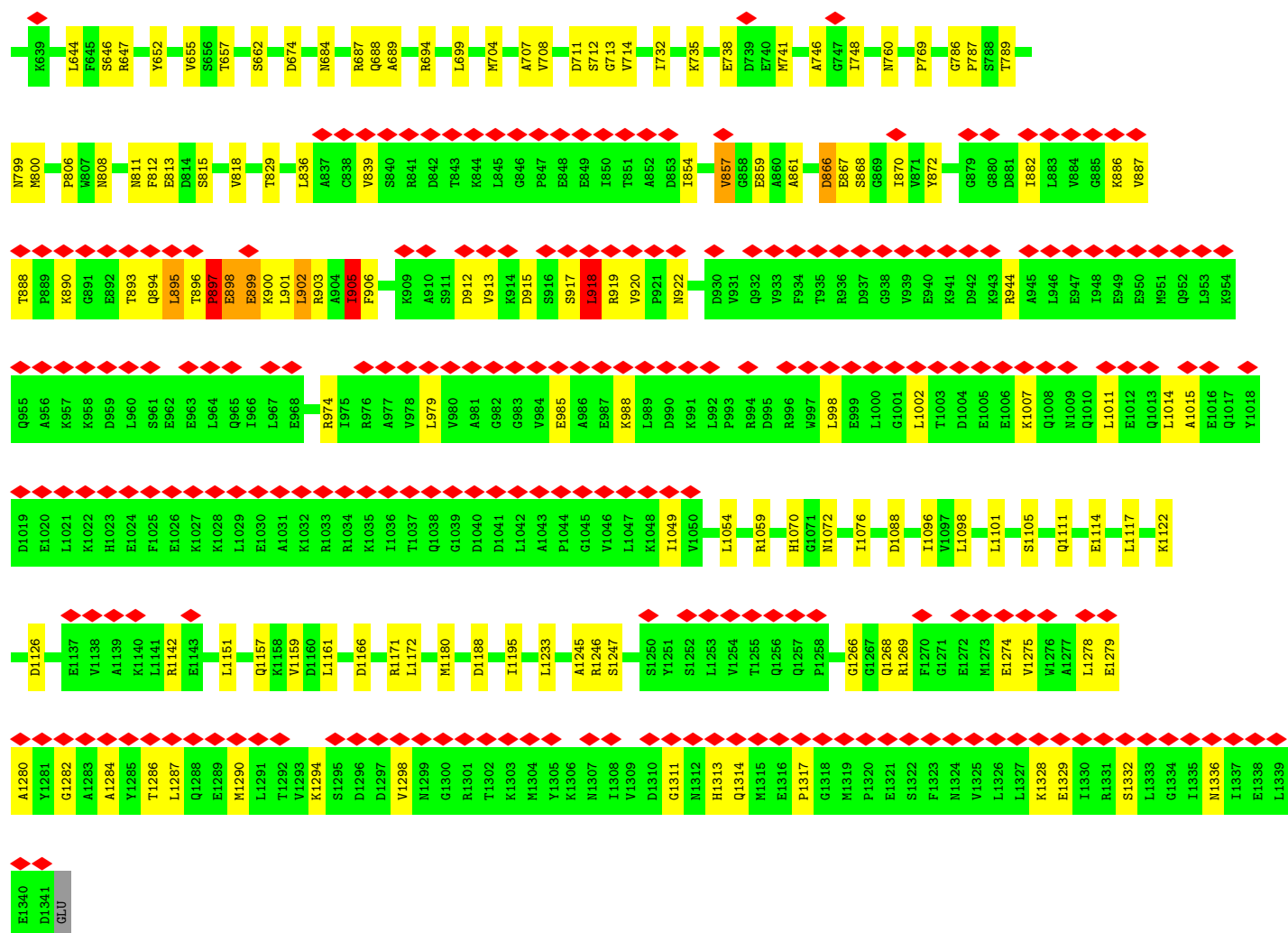
- Chain 8: 



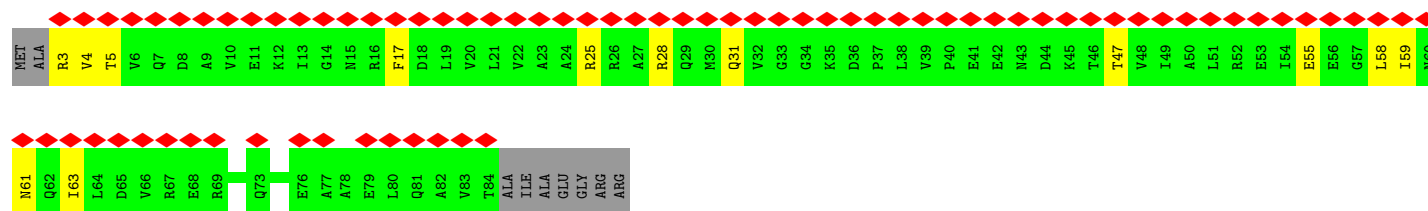
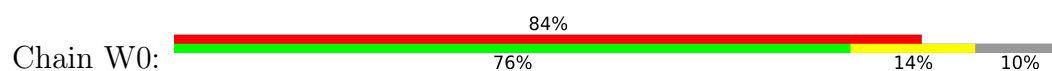
Chain B1:



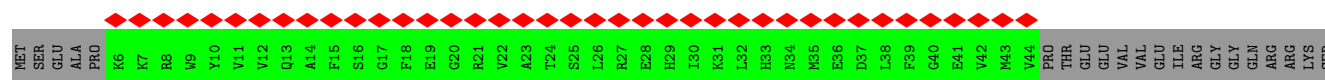


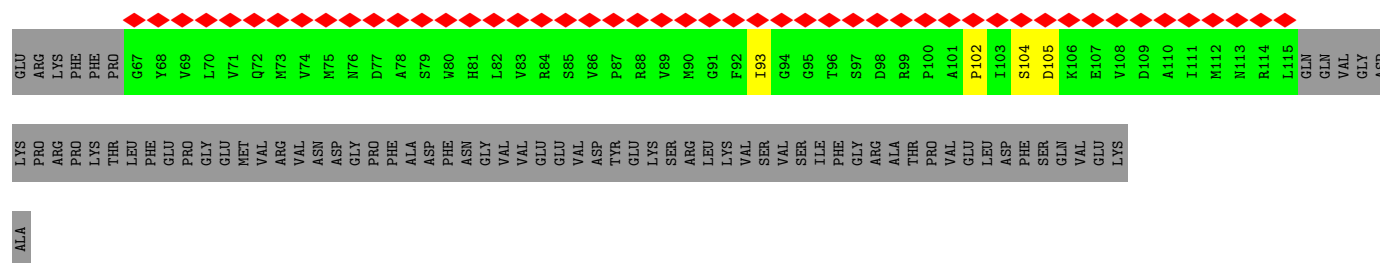


- Molecule 60: DNA-directed RNA polymerase subunit omega

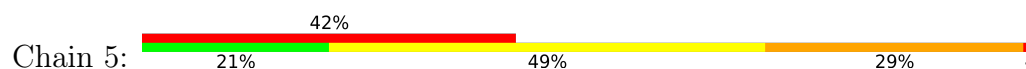


- Molecule 61: Transcription termination/antitermination protein NusG





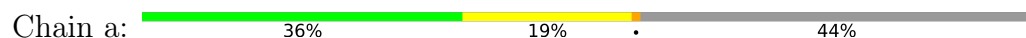
• Molecule 62: tRNA(Phe)



• Molecule 63: tRNA(fMet)

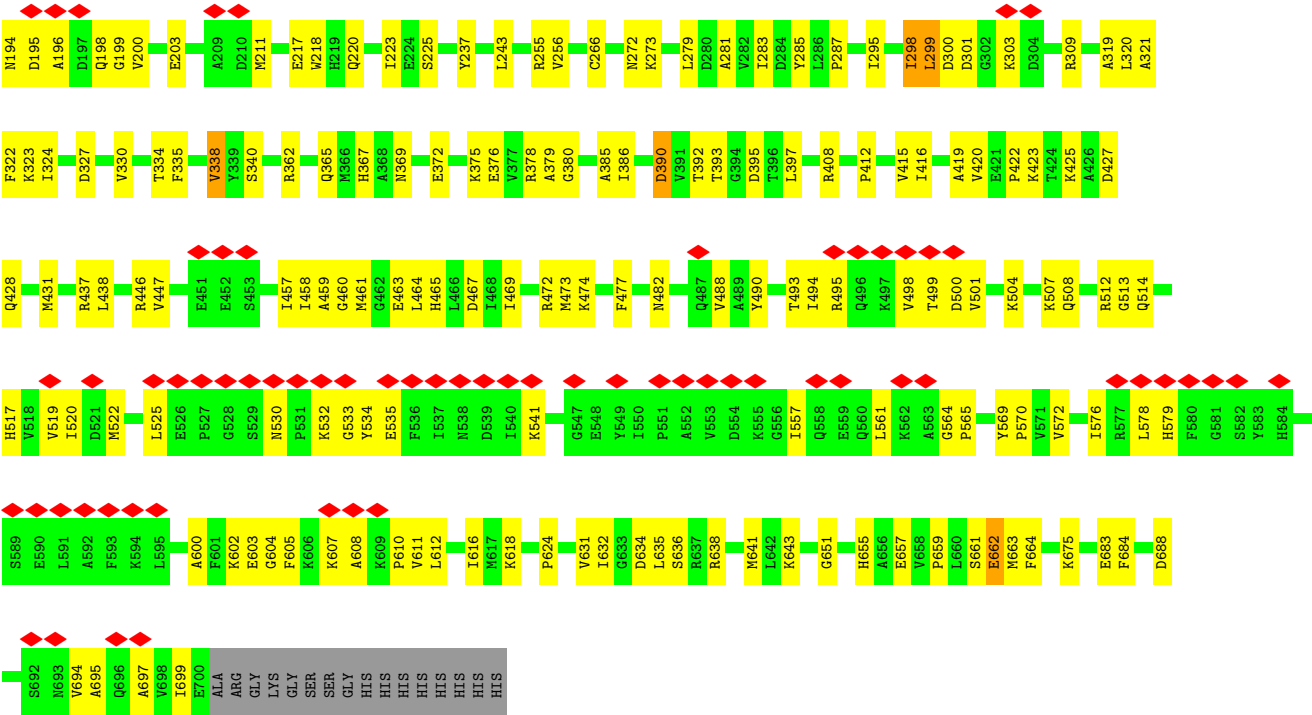


• Molecule 64: Large ribosomal subunit protein uL1

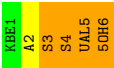


• Molecule 65: Elongation factor G





● Molecule 66: Viomycin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35002	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	0.088	Depositor
Minimum map value	-0.031	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.006	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: GDP, KBE, 5OH, PO4, DPP, UAL

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	0.25	0/362	0.72	0/485
2	B	0.37	0/450	0.80	2/599 (0.3%)
3	C	0.32	0/416	0.61	0/554
4	D	0.47	0/380	0.95	0/498
5	E	0.46	0/513	0.80	0/676
6	F	0.41	0/303	0.79	0/397
7	G	0.39	0/1735	0.83	0/2338
8	H	0.47	0/1651	0.83	0/2225
9	I	0.32	0/1659	0.77	1/2220 (0.0%)
10	J	0.47	0/1169	0.81	0/1573
11	K	0.44	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	0.59	0/796	0.86	0/1077
16	P	0.42	0/885	0.76	0/1195
17	Q	0.43	0/969	0.80	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	0.64	0/884
22	V	0.33	0/657	0.72	0/881
23	W	0.28	0/544	0.69	0/731
24	X	0.28	0/652	0.64	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	0.39	0/1046	0.80	1/1410 (0.1%)
34	j	0.46	0/1152	0.72	0/1551
35	k	0.42	0/947	0.91	1/1268 (0.1%)
36	l	0.41	0/1054	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	0.43	0/960	0.72	0/1278
42	r	0.38	0/829	0.78	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	0.33	0/787	0.74	2/1051 (0.2%)
46	v	0.35	0/766	0.66	0/1025
47	w	0.40	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	5/57662 (0.0%)
54	4	0.57	0/519	0.69	0/804
55	8	0.56	0/599	0.71	1/919 (0.1%)
56	9	0.48	0/468	0.53	0/719
57	A1	0.48	0/1696	0.69	0/2298
57	A2	0.47	0/1718	0.67	0/2328
58	B1	0.56	4/10510 (0.0%)	0.74	8/14196 (0.1%)
59	B2	0.46	0/10714	0.68	2/14459 (0.0%)
60	W0	0.30	0/652	0.61	0/879
61	NG	0.56	0/431	0.79	0/596
62	5	0.58	0/1812	0.90	3/2823 (0.1%)
63	6	0.59	0/1832	0.59	0/2855
64	a	0.49	0/1020	0.81	0/1370
65	0	0.39	0/5501	0.72	3/7446 (0.0%)
66	h	3.21	2/11 (18.2%)	0.75	0/13
All	All	0.53	7/193022 (0.0%)	0.66	75/284246 (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
8	H	0	1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	h	3	SER	CA-C	-6.76	1.38	1.52
66	h	4	SER	CA-C	-6.29	1.39	1.52
38	n	66	ALA	CA-C	-5.95	1.44	1.52
58	B1	1350	ASN	CG-ND2	-5.26	1.22	1.33
58	B1	424	ASN	CG-ND2	-5.18	1.22	1.33
58	B1	777	HIS	ND1-CE1	5.10	1.37	1.32
58	B1	1108	GLN	CD-OE1	5.03	1.33	1.23

All (75) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	92	PRO	N-CA-C	-10.49	98.47	113.47
51	1	1020	A	C2'-C3'-O3'	7.36	120.54	109.50
48	x	11	PRO	N-CA-C	-7.33	99.53	111.77
51	1	2425	A	O3'-P-O5'	-6.94	93.58	104.00
12	L	82	SER	N-CA-C	6.90	116.42	108.49
58	B1	450	HIS	CB-CG-CD2	-6.62	122.59	131.20
48	x	30	PRO	N-CA-C	6.53	125.92	112.47
36	l	29	LYS	CA-C-N	6.48	133.92	121.54
36	l	29	LYS	C-N-CA	6.48	133.92	121.54
58	B1	61	ILE	CA-C-N	-6.39	113.97	121.64
58	B1	61	ILE	C-N-CA	-6.39	113.97	121.64
51	1	2428	G	O3'-P-O5'	-6.39	94.42	104.00
58	B1	777	HIS	CB-CG-CD2	-6.38	122.91	131.20
45	u	45	GLN	CA-C-N	6.34	129.49	120.49
45	u	45	GLN	C-N-CA	6.34	129.49	120.49
51	1	490	C	N1-C1'-C2'	6.34	121.50	112.00
32	g	8	LYS	CA-C-N	6.28	133.28	121.97
32	g	8	LYS	C-N-CA	6.28	133.28	121.97
9	I	24	VAL	N-CA-C	-6.28	107.75	113.71
53	3	1301	U	N1-C1'-C2'	6.24	121.36	112.00
48	x	71	ARG	N-CA-C	-6.21	105.70	113.28
65	0	367	HIS	CA-C-N	6.07	133.14	121.54
65	0	367	HIS	C-N-CA	6.07	133.14	121.54
48	x	67	LEU	N-CA-C	-6.05	104.60	111.14
59	B2	897	PRO	N-CA-CB	-6.05	96.89	103.25
32	g	121	VAL	N-CA-C	-5.91	106.65	111.91
62	5	39	U	C3'-C2'-O2'	5.87	119.50	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	1	1816	C	N1-C1'-C2'	5.76	120.64	112.00
58	B1	450	HIS	CB-CG-ND1	5.74	131.31	122.70
2	B	5	ASN	CA-C-N	5.73	129.02	120.83
2	B	5	ASN	C-N-CA	5.73	129.02	120.83
26	Z	17	ARG	N-CA-C	-5.72	104.85	113.89
48	x	54	GLY	N-CA-C	5.72	120.73	113.24
59	B2	897	PRO	CA-N-CD	-5.57	104.21	112.00
51	1	1343	G	N9-C1'-C2'	5.55	120.33	112.00
19	S	21	ALA	N-CA-C	-5.54	107.77	114.75
33	i	62	ALA	N-CA-C	5.51	116.97	110.97
37	m	57	VAL	CA-C-N	5.47	131.99	121.54
37	m	57	VAL	C-N-CA	5.47	131.99	121.54
29	d	74	LYS	CA-C-N	5.47	128.65	120.83
29	d	74	LYS	C-N-CA	5.47	128.65	120.83
51	1	2502	G	O3'-P-O5'	5.45	112.18	104.00
53	3	130	A	N9-C1'-C2'	5.45	120.18	112.00
42	r	51	VAL	N-CA-C	-5.44	97.14	108.88
51	1	1106	G	C2'-C3'-O3'	5.43	121.85	113.70
58	B1	777	HIS	CB-CG-ND1	5.43	130.85	122.70
55	8	7	DC	C2'-C3'-O3'	-5.41	103.39	111.50
53	3	813	U	N1-C1'-C2'	5.39	120.09	112.00
29	d	20	GLY	N-CA-C	-5.31	107.46	114.95
25	Y	53	MET	CA-C-N	5.30	127.58	120.58
25	Y	53	MET	C-N-CA	5.30	127.58	120.58
58	B1	27	PRO	N-CA-C	-5.29	106.14	113.81
35	k	89	ASN	N-CA-C	5.28	117.46	111.02
62	5	39	U	C4'-C3'-O3'	5.23	120.85	113.00
65	0	664	PHE	CA-CB-CG	5.23	119.03	113.80
51	1	2529	G	N9-C1'-C2'	5.22	119.84	112.00
52	2	66	A	N9-C1'-C2'	5.22	119.84	112.00
51	1	858	G	C4'-C3'-O3'	5.22	120.83	113.00
51	1	1211	C	N1-C1'-C2'	5.21	119.81	112.00
51	1	1924	C	N1-C1'-C2'	5.18	119.77	112.00
58	B1	61	ILE	CA-C-O	-5.16	115.58	120.95
47	w	15	LYS	CA-C-N	5.16	129.73	122.46
47	w	15	LYS	C-N-CA	5.16	129.73	122.46
44	t	65	GLY	N-CA-C	5.14	117.38	111.36
62	5	74	C	C4'-C3'-O3'	-5.14	105.29	113.00
50	z	40	THR	N-CA-C	-5.12	101.24	109.58
53	3	722	G	N9-C1'-C2'	5.10	119.65	112.00
51	1	278	A	N9-C1'-C2'	5.09	119.63	112.00
53	3	1043	G	N9-C1'-C2'	5.08	119.62	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	1	1087	G	N9-C1'-C2'	5.04	119.57	112.00
51	1	2071	A	N9-C1'-C2'	5.04	119.57	112.00
40	p	15	ASP	CA-C-N	5.02	131.42	122.13
40	p	15	ASP	C-N-CA	5.02	131.42	122.13
51	1	1508	A	N9-C1'-C2'	5.02	119.53	112.00
51	1	933	A	N9-C1'-C2'	5.02	119.52	112.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	H	71	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	355	0	353	10	0
2	B	444	0	461	15	0
3	C	409	0	440	19	0
4	D	377	0	418	17	0
5	E	504	0	574	15	0
6	F	302	0	341	14	0
7	G	1704	0	1732	43	0
8	H	1624	0	1699	55	0
9	I	1637	0	1699	48	0
10	J	1156	0	1199	40	0
11	K	817	0	808	23	0
12	L	1181	0	1240	43	0
13	M	979	0	1034	32	0
14	N	1022	0	1070	56	0
15	O	786	0	828	33	0
16	P	869	0	878	27	0
17	Q	955	0	1019	32	0
18	R	883	0	944	25	0
19	S	805	0	847	34	0
20	T	714	0	737	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	U	649	0	666	21	0
22	V	648	0	691	17	0
23	W	535	0	552	16	0
24	X	637	0	665	17	0
25	Y	665	0	714	21	0
26	Z	544	0	579	15	0
27	b	2082	0	2157	72	0
28	c	1565	0	1616	55	0
29	d	1552	0	1619	51	0
30	e	1410	0	1447	40	0
31	f	1323	0	1374	31	0
32	g	1111	0	1148	28	0
33	i	1032	0	1088	35	0
34	j	1129	0	1162	30	0
35	k	938	0	1012	22	0
36	l	1045	0	1117	29	0
37	m	1074	0	1157	29	0
38	n	960	0	1000	35	0
39	o	892	0	923	21	0
40	p	917	0	965	24	0
41	q	947	0	1022	24	0
42	r	816	0	839	22	0
43	s	857	0	922	18	0
44	t	738	0	807	15	0
45	u	779	0	834	18	0
46	v	753	0	780	14	0
47	w	575	0	592	20	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	1367	0
52	2	2568	0	1303	59	0
53	3	33012	0	16618	727	0
54	4	467	0	234	5	0
55	8	539	0	305	28	0
56	9	417	0	224	1	0
57	A1	1677	0	1713	27	0
57	A2	1698	0	1718	17	0
58	B1	10353	0	10548	321	0
59	B2	10546	0	10550	173	0
60	W0	650	0	658	10	0
61	NG	433	0	193	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	5	1622	0	821	28	0
63	6	1640	0	837	28	0
64	a	1013	0	1081	38	0
65	0	5399	0	5363	151	0
66	h	48	0	40	8	0
67	0	28	0	12	1	0
68	0	5	0	0	0	0
All	All	179711	0	131022	3773	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 (3773) 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	1.12	1.12
51:1:1060:U:H4'	51:1:1061:U:H5'	1.32	1.11
53:3:112:G:H21	53:3:354:G:H5'	1.16	1.10
51:1:2061:G:H2'	51:1:2501:C:O2'	1.52	1.09
50:z:37:ARG:HH12	51:1:929:U:H5'	1.12	1.06
9:I:131:ILE:HG21	53:3:620:C:H1'	1.40	1.04
51:1:45:G:H5''	51:1:46:G:H5'	1.34	1.02
51:1:1796:U:H2'	51:1:1797:G:H8	1.18	1.02
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
58:B1:111:THR:HG23	58:B1:300:GLN:CD	1.86	1.00
58:B1:750:PRO:HB3	59:B2:549:ASP:OD2	1.60	1.00
51:1:2324:U:H3'	51:1:2325:G:H5''	1.45	0.98
51:1:572:A:H61	51:1:2029:G:H21	1.04	0.98
51:1:1645:G:H5''	51:1:1646:C:H5'	1.44	0.98
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
51:1:1597:A:H5''	51:1:1598:A:H5'	1.45	0.96
51:1:413:C:H42	51:1:2410:G:H1	1.15	0.95
58:B1:352:ARG:HD2	59:B2:1268:GLN:NE2	1.79	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	0.94
38:n:39:PRO:HG3	51:1:1651:G:H5'	1.49	0.94
52:2:118:C:H2'	52:2:119:A:H4'	1.46	0.94
53:3:1156:G:H1'	53:3:1179:A:H61	1.32	0.94
43:s:59:GLU:HA	43:s:64:ALA:HA	1.50	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:68:TYR:O	58:B1:75:TYR:CE2	2.20	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
53:3:674:G:H2'	53:3:675:A:C8	2.05	0.92
54:4:38:G:H21	58:B1:427:PRO:HD3	1.34	0.91
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
51:1:2068:U:H3	51:1:2430:A:H62	1.15	0.90
51:1:2653:U:H3'	51:1:2654:A:H5''	1.52	0.90
58:B1:68:TYR:C	58:B1:75:TYR:HE2	1.80	0.90
53:3:1218:C:H2'	53:3:1219:A:C8	2.06	0.89
53:3:674:G:H2'	53:3:675:A:H8	1.34	0.89
58:B1:202:ARG:HG2	58:B1:202:ARG:HH11	1.35	0.89
53:3:409:U:H3	53:3:433:G:H1	1.12	0.89
8:H:127:VAL:HG23	59:B2:906:PHE:HA	1.52	0.88
12:L:92:PRO:HA	12:L:95:ARG:NE	1.88	0.88
12:L:91:ARG:HB3	12:L:93:VAL:HG12	1.54	0.88
52:2:78:A:H62	52:2:98:G:H21	1.18	0.88
53:3:1422:G:H22	53:3:1478:U:H3	1.22	0.88
29:d:68:ALA:HA	51:1:1255:U:C5	2.08	0.88
50:z:37:ARG:NH1	51:1:929:U:H5'	1.89	0.88
51:1:1473:G:H1	51:1:1518:C:H42	1.21	0.88
52:2:3:C:H2'	52:2:4:C:H5''	1.55	0.88
51:1:1796:U:H2'	51:1:1797:G:C8	2.08	0.87
62:5:9:A:H2'	62:5:11:C:H41	1.38	0.87
51:1:435:C:H2'	51:1:436:C:H5'	1.56	0.86
59:B2:854:ILE:HG21	59:B2:917:SER:HB3	1.54	0.86
51:1:2128:G:OP1	64:a:38:PHE:CE1	2.29	0.86
58:B1:317:THR:HA	58:B1:323:PRO:HA	1.55	0.86
7:G:131:LYS:HD2	53:3:1158:C:H4'	1.57	0.86
58:B1:68:TYR:HB3	58:B1:75:TYR:OH	1.76	0.86
51:1:2822:G:H2'	51:1:2823:A:H5''	1.58	0.85
14:N:68:GLY:HA2	53:3:1250:A:H5'	1.55	0.85
53:3:1218:C:H2'	53:3:1219:A:H8	1.41	0.85
53:3:1395:C:HO2'	53:3:1396:A:H8	0.87	0.85
58:B1:68:TYR:O	58:B1:75:TYR:HE2	1.58	0.85
42:r:79:ARG:NH2	51:1:572:A:H5'	1.91	0.85
51:1:2443:C:H2'	51:1:2444:G:H8	1.42	0.85
37:m:12:MET:HA	51:1:910:A:H62	1.41	0.84
51:1:1783:A:C6	51:1:2587:A:C2	2.66	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:3:A:H5'	53:3:613:C:H4'	1.58	0.84
19:S:70:HIS:HB2	53:3:974:A:H5'	1.59	0.84
51:1:1783:A:N1	51:1:2587:A:C4	2.46	0.84
51:1:2262:U:H2'	51:1:2263:C:C6	2.13	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	0.83
58:B1:633:ALA:HB2	59:B2:808:ASN:H	1.41	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
58:B1:289:ASP:HB2	61:NG:104:SER:CB	2.09	0.83
53:3:1424:U:H3	53:3:1476:A:H61	1.26	0.83
51:1:1937:A:O2'	51:1:1938:A:H5'	1.78	0.82
53:3:1512:U:H2'	53:3:1513:A:C8	2.14	0.82
23:W:37:LYS:HB3	53:3:719:C:H1'	1.60	0.82
51:1:554:U:H2'	51:1:555:G:O4'	1.79	0.82
59:B2:895:LEU:HA	59:B2:899:GLU:HB3	1.60	0.82
58:B1:141:PHE:HE2	58:B1:296:LYS:HB2	1.45	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
55:8:1:DC:H5''	58:B1:210:SER:OG	1.80	0.82
51:1:695:G:H1	51:1:767:U:H3	1.26	0.82
14:N:13:SER:OG	53:3:1251:A:H5'	1.80	0.81
53:3:555:U:H2'	53:3:556:C:C6	2.15	0.81
58:B1:770:LEU:HD13	59:B2:618:GLN:HG3	1.61	0.81
58:B1:111:THR:HG23	58:B1:300:GLN:OE1	1.80	0.81
26:Z:7:GLU:HB2	26:Z:11:PHE:HB3	1.63	0.81
51:1:1433:A:H2'	51:1:1434:A:O4'	1.79	0.81
58:B1:141:PHE:CE2	58:B1:296:LYS:HB2	2.15	0.81
51:1:1680:U:H2'	51:1:1681:G:H5'	1.60	0.81
51:1:1064:C:H3'	51:1:1065:U:H5''	1.63	0.80
58:B1:144:TYR:HE1	58:B1:162:GLU:OE2	1.64	0.80
27:b:55:GLY:HA2	51:1:692:C:OP1	1.81	0.80
51:1:2128:G:OP1	64:a:38:PHE:CD1	2.34	0.80
58:B1:37:GLU:O	58:B1:61:ILE:HD11	1.81	0.80
51:1:2402:U:C2'	51:1:2403:C:H5''	2.11	0.79
53:3:952:U:H4'	53:3:964:A:H61	1.47	0.79
65:0:498:VAL:HG11	65:0:522:MET:HE3	1.65	0.79
29:d:76:PRO:HA	29:d:82:GLY:HA3	1.62	0.79
53:3:769:G:H4'	53:3:1513:A:H4'	1.63	0.79
51:1:1791:A:C2'	51:1:1792:G:H5'	2.13	0.78
51:1:2036:C:H2'	51:1:2037:A:C8	2.18	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2402:U:H2'	51:1:2403:C:H5''	1.64	0.78
51:1:1052:C:H42	51:1:1107:G:H1	1.30	0.78
58:B1:186:GLN:HG3	58:B1:238:ILE:HG13	1.65	0.78
51:1:784:G:H5'	51:1:785:G:OP1	1.84	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
51:1:1661:G:H2'	51:1:1662:U:H6	1.49	0.77
51:1:1783:A:C6	51:1:2587:A:N3	2.51	0.77
51:1:2259:U:C4	51:1:2427:C:N4	2.52	0.77
8:H:175:HIS:ND1	53:3:1108:G:H5'	2.00	0.77
53:3:1073:U:H3	53:3:1102:A:H61	1.29	0.77
55:8:13:DT:H72	58:B1:791:ALA:HB2	1.67	0.77
53:3:1422:G:N2	53:3:1478:U:H3	1.80	0.77
51:1:20:C:H2'	51:1:21:A:C8	2.19	0.77
51:1:1287:A:C2	51:1:1649:G:H4'	2.20	0.77
51:1:2124:G:O2'	64:a:41:SER:HB3	1.83	0.77
51:1:1853:A:H2'	51:1:1854:A:C8	2.19	0.77
53:3:153:C:H3'	53:3:154:U:H5''	1.66	0.77
58:B1:202:ARG:HG2	58:B1:202:ARG:NH1	1.99	0.77
51:1:52:A:H2'	51:1:53:A:C8	2.20	0.77
51:1:2524:G:H2'	51:1:2525:G:H5''	1.66	0.76
22:V:68:LYS:HB3	53:3:267:C:OP1	1.85	0.76
28:c:148:GLN:O	51:1:2052:A:H4'	1.86	0.76
51:1:687:C:H2'	51:1:688:U:H5'	1.66	0.76
65:0:40:ILE:CG2	65:0:198:GLN:OE1	2.33	0.76
51:1:2443:C:H2'	51:1:2444:G:C8	2.20	0.76
53:3:57:G:H2'	53:3:58:C:C6	2.21	0.76
51:1:2124:G:O2'	64:a:41:SER:CB	2.34	0.76
53:3:1356:G:H2'	53:3:1357:A:H8	1.51	0.76
51:1:2672:U:C2'	51:1:2673:G:H5''	2.16	0.76
53:3:768:A:OP1	53:3:804:U:H4'	1.86	0.76
51:1:324:A:H62	51:1:338:G:H21	1.32	0.75
53:3:193:C:H2'	53:3:194:C:C6	2.21	0.75
51:1:1935:G:H1'	51:1:1964:G:N2	2.00	0.75
55:8:15:DC:H1'	58:B1:426:ALA:HB1	1.67	0.75
51:1:1020:A:H1'	51:1:1021:A:OP2	1.86	0.75
65:0:490:TYR:HA	65:0:612:LEU:HD13	1.69	0.75
51:1:1126:A:H4'	51:1:1127:A:H5''	1.67	0.75
51:1:1783:A:C2	51:1:2587:A:C5	2.75	0.75
51:1:1718:G:H2'	51:1:1719:G:H8	1.52	0.75
51:1:2375:G:H2'	51:1:2376:A:H5''	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:850:U:H2'	53:3:851:G:H5''	1.69	0.75
8:H:108:PRO:HG3	59:B2:859:GLU:HB2	1.69	0.74
51:1:633:A:H2'	51:1:634:C:O4'	1.87	0.74
53:3:1236:A:H4'	53:3:1304:G:H4'	1.69	0.74
53:3:3:A:C5'	53:3:613:C:H4'	2.17	0.74
53:3:354:G:H2'	53:3:355:C:C6	2.23	0.74
51:1:1019:U:H3	51:1:1142:A:H62	1.36	0.74
53:3:212:G:H2'	53:3:213:G:H8	1.53	0.74
53:3:1330:U:H2'	53:3:1331:G:O4'	1.86	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
30:e:34:THR:HG21	51:1:2314:A:H5'	1.69	0.74
51:1:2221:G:H2'	51:1:2222:C:C6	2.23	0.74
10:J:25:LYS:NZ	53:3:923:A:H5''	2.03	0.74
12:L:71:THR:HG23	12:L:72:VAL:HG12	1.68	0.74
33:i:10:LEU:HD11	51:1:1070:A:H2	1.51	0.74
51:1:917:A:H5''	51:1:2268:A:H61	1.53	0.74
53:3:1412:C:H2'	53:3:1413:A:C8	2.22	0.73
51:1:2743:U:H2'	51:1:2744:G:O4'	1.87	0.73
51:1:2859:G:H2'	51:1:2860:A:C8	2.22	0.73
53:3:175:C:H2'	53:3:176:C:C6	2.24	0.73
51:1:1161:C:H2'	51:1:1162:G:C8	2.23	0.73
51:1:1265:A:H61	51:1:2013:A:H5''	1.53	0.73
58:B1:68:TYR:C	58:B1:75:TYR:CE2	2.65	0.73
15:O:45:ARG:HB3	15:O:69:THR:HB	1.71	0.73
47:w:28:LEU:HD22	51:1:2353:G:H4'	1.68	0.73
51:1:1528:A:H2'	51:1:1529:G:H5'	1.69	0.73
51:1:1940:U:H1'	51:1:1942:C:N4	2.04	0.73
53:3:279:A:H5''	53:3:281:G:H5'	1.69	0.73
51:1:1310:G:H2'	51:1:1311:G:H5'	1.71	0.73
53:3:884:U:H4'	53:3:885:G:H5''	1.70	0.73
53:3:1073:U:H2'	53:3:1074:G:C8	2.24	0.73
58:B1:157:GLN:OE1	58:B1:157:GLN:HA	1.88	0.73
51:1:2030:A:N3	51:1:2499:C:H5''	2.04	0.73
53:3:840:C:H2'	53:3:841:C:H5''	1.70	0.73
58:B1:110:PRO:HG2	58:B1:183:GLU:HG3	1.68	0.73
58:B1:211:GLU:HG2	58:B1:215:LYS:HE3	1.70	0.73
65:0:499:THR:HG23	65:0:500:ASP:H	1.53	0.73
53:3:1028:C:H3'	53:3:1029:U:H5''	1.71	0.72
30:e:65:LEU:HD22	52:2:42:C:C4	2.23	0.72
46:v:9:ARG:HB3	46:v:41:GLU:HB2	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:8:3:DC:H2'	55:8:4:DT:H72	1.69	0.72
53:3:1306:A:H61	53:3:1331:G:H1'	1.54	0.72
9:I:23:GLY:HA3	53:3:408:A:H4'	1.71	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
53:3:153:C:C3'	53:3:154:U:H5''	2.18	0.72
53:3:1507:A:H2'	53:3:1508:A:O4'	1.90	0.72
58:B1:142:GLU:HG3	58:B1:142:GLU:O	1.89	0.72
51:1:952:G:H2'	51:1:953:G:H5''	1.71	0.72
53:3:1424:U:H2'	53:3:1425:U:C6	2.24	0.72
55:8:3:DC:C2'	55:8:4:DT:H72	2.19	0.72
58:B1:107:LEU:HD11	58:B1:242:LEU:HB2	1.70	0.72
12:L:92:PRO:HA	12:L:95:ARG:HG3	1.71	0.72
51:1:1170:C:H2'	51:1:1171:G:H8	1.54	0.72
52:2:87:U:H5''	52:2:88:C:C5	2.23	0.72
58:B1:220:ARG:HG2	58:B1:220:ARG:HH11	1.55	0.72
51:1:2061:G:H2'	51:1:2501:C:HO2'	1.54	0.72
51:1:2562:U:H3	51:1:2566:A:H62	1.35	0.72
51:1:2818:U:H2'	51:1:2819:G:H8	1.55	0.72
58:B1:105:ILE:HD12	58:B1:242:LEU:HD22	1.71	0.72
12:L:27:ASN:ND2	53:3:1374:A:H4'	2.05	0.72
21:U:5:ARG:HB2	53:3:376:G:H5''	1.72	0.72
36:l:79:LEU:HD12	36:l:113:ALA:H	1.52	0.72
51:1:2629:U:O2'	51:1:2630:G:H5''	1.90	0.71
51:1:2733:A:H2'	51:1:2734:A:C8	2.25	0.71
6:F:4:ARG:HB2	51:1:2466:C:OP1	1.89	0.71
48:x:2:ARG:HG2	48:x:32:LEU:HD12	1.73	0.71
51:1:1868:C:H2'	51:1:1869:G:H5'	1.70	0.71
51:1:2125:G:H5'	64:a:39:VAL:O	1.89	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'	2.21	0.71
52:2:90:C:C2'	52:2:91:C:H5''	2.20	0.71
53:3:946:A:H2'	53:3:947:G:H8	1.56	0.71
53:3:1435:G:H2'	53:3:1436:U:C6	2.25	0.71
58:B1:210:SER:HB3	58:B1:213:LYS:HB2	1.71	0.71
58:B1:1143:ASP:OD1	58:B1:1148:ARG:NH1	2.21	0.71
51:1:2036:C:H2'	51:1:2037:A:H8	1.55	0.71
53:3:419:C:H2'	53:3:420:U:O4'	1.90	0.71
53:3:1243:C:H2'	53:3:1244:G:C8	2.26	0.71
34:j:116:ARG:HH22	51:1:528:A:H5''	1.53	0.71
53:3:1395:C:H4'	53:3:1402:C:H4'	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2491:U:H2'	51:1:2492:U:H5'	1.71	0.71
51:1:52:A:H2'	51:1:53:A:H8	1.56	0.71
53:3:1374:A:H2'	53:3:1375:A:H8	1.56	0.71
51:1:2086:U:H2'	51:1:2087:G:C8	2.25	0.71
53:3:86:G:H4'	53:3:87:C:C4	2.26	0.71
63:6:69:C:H2'	63:6:70:G:H8	1.55	0.71
48:x:60:LYS:HD3	51:1:372:G:H5''	1.73	0.70
51:1:1447:C:H2'	51:1:1448:G:H8	1.56	0.70
51:1:1161:C:H2'	51:1:1162:G:H8	1.55	0.70
51:1:1791:A:H2'	51:1:1792:G:H5'	1.70	0.70
51:1:2514:U:H2'	51:1:2515:C:C6	2.27	0.70
53:3:979:C:H2'	53:3:980:C:H5'	1.73	0.70
58:B1:93:THR:HB	58:B1:97:VAL:HG21	1.73	0.70
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE22	1.56	0.70
8:H:135:ARG:HH22	59:B2:905:ILE:HG22	1.55	0.70
18:R:113:LYS:HZ3	63:6:44:A:H4'	1.56	0.70
51:1:1270:C:H5''	51:1:1271:G:C5'	2.21	0.70
53:3:501:C:H2'	53:3:502:A:H8	1.57	0.70
38:n:1:MET:HE3	51:1:2723:C:H4'	1.74	0.70
8:H:131:ARG:HH12	59:B2:902:LEU:HA	1.56	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
51:1:100:U:H4'	51:1:101:A:O4'	1.91	0.70
53:3:939:G:H2'	53:3:940:C:C6	2.26	0.70
36:l:17:LYS:HB2	51:1:663:G:H5''	1.74	0.70
51:1:677:A:H2'	51:1:678:C:H6	1.57	0.70
65:0:695:ALA:HA	65:0:699:ILE:HB	1.74	0.70
59:B2:65:ASN:HB3	59:B2:105:TYR:HB2	1.74	0.70
24:X:77:ARG:NH1	53:3:1225:A:H4'	2.07	0.69
51:1:1607:C:H4'	51:1:1608:A:C5'	2.19	0.69
51:1:2446:G:H2'	51:1:2501:C:H5	1.57	0.69
12:L:91:ARG:O	12:L:95:ARG:HG2	1.91	0.69
12:L:92:PRO:CA	12:L:95:ARG:HE	1.97	0.69
53:3:520:A:H62	53:3:529:G:H21	1.38	0.69
29:d:165:HIS:HB2	51:1:1205:A:C6	2.27	0.69
51:1:1739:A:H2'	51:1:1740:G:O4'	1.92	0.69
51:1:2502:G:H5''	51:1:2503:A:H5''	1.74	0.69
51:1:2859:G:H2'	51:1:2860:A:H8	1.54	0.69
38:n:66:ALA:HA	38:n:69:ARG:HD2	1.72	0.69
53:3:1421:G:H2'	53:3:1422:G:H4'	1.73	0.69
62:5:47:U:H4'	62:5:48:C:H5'	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:6:26:G:H2'	63:6:27:U:H5''	1.73	0.69
65:0:29:ARG:HH21	65:0:272:ASN:HD21	1.40	0.69
14:N:17:ARG:CZ	53:3:1129:C:H4'	2.22	0.69
51:1:2818:U:H2'	51:1:2819:G:C8	2.27	0.69
27:b:6:LYS:NZ	51:1:1695:G:H5'	2.08	0.69
51:1:958:U:H2'	52:2:89:U:H1'	1.75	0.69
53:3:960:U:H4'	53:3:961:U:H5''	1.74	0.69
53:3:1412:C:H2'	53:3:1413:A:H8	1.56	0.69
63:6:56:C:H2'	63:6:57:A:H8	1.58	0.69
66:h:6:5OH:N	66:h:6:5OH:HS	2.07	0.69
17:Q:23:LEU:HD12	17:Q:29:LYS:HG2	1.75	0.69
26:Z:48:LYS:HB3	53:3:723:U:H5	1.58	0.69
51:1:2628:C:H3'	51:1:2629:U:H5'	1.75	0.69
58:B1:243:PRO:HG2	59:B2:1332:SER:O	1.93	0.69
58:B1:289:ASP:CB	61:NG:104:SER:CB	2.71	0.69
31:f:91:VAL:HG21	51:1:2657:A:O3'	1.93	0.69
51:1:2450:A:O2'	51:1:2451:A:H5'	1.93	0.69
51:1:1481:U:H3	51:1:1510:G:H1	1.42	0.68
58:B1:128:LEU:HD11	58:B1:189:LEU:HG	1.73	0.68
51:1:740:C:H6	51:1:740:C:H5'	1.58	0.68
53:3:1346:A:H61	53:3:1374:A:H3'	1.57	0.68
8:H:34:SER:HB3	8:H:58:ARG:HH12	1.57	0.68
14:N:121:ARG:HG3	53:3:1348:U:H4'	1.75	0.68
51:1:1935:G:H1'	51:1:1964:G:C2	2.28	0.68
55:8:3:DC:C6	55:8:4:DT:H72	2.29	0.68
58:B1:141:PHE:CD2	58:B1:293:ARG:O	2.47	0.68
58:B1:832:LYS:C	58:B1:1242:ARG:HH12	2.01	0.68
51:1:2464:G:H2'	51:1:2465:C:C6	2.29	0.68
51:1:2553:G:H3'	51:1:2554:U:H5''	1.75	0.68
12:L:92:PRO:O	12:L:95:ARG:HG3	1.93	0.68
51:1:1024:G:H3'	51:1:1025:G:H5''	1.75	0.68
53:3:900:A:H2'	53:3:901:A:C8	2.29	0.68
28:c:181:ASP:HB2	28:c:186:LEU:H	1.59	0.68
51:1:1697:G:H3'	51:1:1698:A:H5''	1.76	0.68
53:3:70:U:H5''	53:3:71:A:OP1	1.92	0.68
58:B1:161:THR:HG22	58:B1:164:GLN:HB2	1.75	0.68
51:1:1077:A:H2'	51:1:1078:U:H5'	1.74	0.68
12:L:35:LYS:HB2	53:3:1373:G:H4'	1.76	0.68
51:1:2656:U:H5''	65:0:146:ARG:CZ	2.24	0.68
51:1:781:A:H2'	51:1:1777:U:O2'	1.93	0.68
51:1:687:C:C2'	51:1:688:U:H5'	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:478:A:H2'	53:3:479:U:H4'	1.76	0.68
51:1:869:G:H2'	51:1:870:U:O4'	1.93	0.67
53:3:501:C:H2'	53:3:502:A:C8	2.29	0.67
58:B1:117:LEU:HD12	58:B1:117:LEU:O	1.94	0.67
58:B1:395:LYS:HZ2	58:B1:399:LYS:CD	2.07	0.67
66:h:4:SER:O	66:h:5:UAL:N1	2.26	0.67
14:N:10:ARG:HH22	53:3:1148:U:H5''	1.59	0.67
17:Q:13:ARG:HH21	53:3:303:A:H5'	1.59	0.67
27:b:73:ILE:HG12	51:1:1490:A:C2	2.29	0.67
51:1:1979:U:H2'	51:1:1980:G:H5'	1.75	0.67
51:1:1697:G:H5''	51:1:1698:A:H5''	1.77	0.67
36:l:111:ILE:HD12	51:1:627:A:N7	2.09	0.67
51:1:1219:U:H2'	51:1:1220:G:C8	2.29	0.67
53:3:747:A:H3'	53:3:748:G:H5''	1.75	0.67
58:B1:39:LYS:O	58:B1:273:ILE:CG2	2.41	0.67
51:1:84:A:H4'	51:1:85:G:O5'	1.94	0.67
55:8:23:DC:H2''	55:8:24:DC:C5	2.30	0.67
58:B1:1355:ARG:NH1	58:B1:1369:ARG:HH12	1.93	0.67
51:1:1801:A:H5''	51:1:2203:U:H2'	1.75	0.67
51:1:2633:G:H2'	51:1:2634:A:H5''	1.77	0.67
51:1:1799:G:H4'	51:1:1800:C:O5'	1.95	0.67
29:d:27:LEU:HD22	29:d:104:ALA:HB2	1.75	0.67
51:1:1783:A:C2	51:1:2587:A:C4	2.83	0.67
53:3:1007:U:H3	53:3:1022:A:H61	1.43	0.67
51:1:848:C:H2'	51:1:849:A:H8	1.59	0.67
51:1:1139:G:O2'	51:1:1140:C:H5'	1.95	0.67
63:6:69:C:H2'	63:6:70:G:C8	2.29	0.67
65:0:103:MET:HG3	65:0:129:GLN:HB3	1.77	0.67
8:H:76:ILE:HB	8:H:80:GLY:HA2	1.76	0.66
18:R:102:LYS:HG2	53:3:1226:C:C5	2.29	0.66
38:n:96:ARG:HA	51:1:2881:U:O2'	1.95	0.66
39:o:68:LYS:HG2	52:2:50:A:OP1	1.94	0.66
51:1:849:A:H2'	51:1:850:U:C6	2.30	0.66
51:1:2086:U:H2'	51:1:2087:G:H8	1.59	0.66
53:3:1026:G:H1	53:3:1035:A:H61	1.43	0.66
51:1:621:A:H2'	51:1:622:G:O4'	1.96	0.66
51:1:2415:G:H2'	51:1:2416:C:C6	2.29	0.66
53:3:924:C:H2'	53:3:925:G:H8	1.60	0.66
51:1:1661:G:H2'	51:1:1662:U:C6	2.29	0.66
51:1:2177:C:O2	64:a:172:HIS:HE1	1.78	0.66
53:3:955:U:H3	53:3:1225:A:H61	1.42	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:108:ALA:CB	58:B1:279:LEU:HD22	2.25	0.66
58:B1:984:LEU:HB3	58:B1:993:GLU:HB2	1.77	0.66
51:1:395:U:H2'	51:1:396:G:C8	2.31	0.66
53:3:1356:G:H2'	53:3:1357:A:C8	2.30	0.66
58:B1:108:ALA:HB3	58:B1:279:LEU:HD22	1.77	0.66
58:B1:978:ARG:HG2	58:B1:1197:ASN:HD21	1.61	0.66
63:6:12:G:H2'	63:6:13:C:O4'	1.95	0.66
51:1:1718:G:H2'	51:1:1719:G:C8	2.30	0.66
53:3:113:G:H2'	53:3:114:U:C6	2.31	0.66
38:n:71:ARG:HH21	51:1:2708:G:H1'	1.59	0.66
51:1:1680:U:C2'	51:1:1681:G:H5'	2.26	0.66
10:J:25:LYS:HE2	53:3:923:A:OP1	1.96	0.66
11:K:42:TRP:HB2	11:K:59:TYR:HB2	1.77	0.66
17:Q:33:CYS:H	17:Q:54:VAL:HG13	1.60	0.66
51:1:1824:G:O2'	51:1:1825:U:H5'	1.96	0.66
52:2:3:C:C2'	52:2:4:C:H5''	2.25	0.66
55:8:13:DT:OP2	58:B1:791:ALA:HB1	1.95	0.66
29:d:176:ASP:HB2	29:d:179:SER:HB3	1.78	0.66
51:1:1755:A:H2'	51:1:1756:G:H5'	1.76	0.66
53:3:660:C:H2'	53:3:661:G:O4'	1.96	0.66
58:B1:1037:PHE:HB3	58:B1:1040:MET:HB2	1.78	0.66
4:D:8:SER:HA	51:1:1309:G:H5''	1.78	0.66
48:x:27:ARG:NH2	51:1:1365:A:OP1	2.29	0.66
51:1:1528:A:C2'	51:1:1529:G:H5'	2.26	0.66
53:3:211:G:H2'	53:3:212:G:O4'	1.96	0.66
38:n:2:ARG:HD2	51:1:2822:G:O6	1.95	0.65
22:V:60:ILE:HG22	22:V:74:LEU:HA	1.78	0.65
53:3:153:C:H2'	53:3:154:U:O4'	1.96	0.65
53:3:835:U:C2'	53:3:836:G:H5''	2.26	0.65
53:3:1172:C:H2'	53:3:1173:U:O4'	1.95	0.65
10:J:53:ARG:NH1	53:3:1071:C:H5'	2.12	0.65
51:1:1509:A:H2'	51:1:1510:G:C8	2.31	0.65
53:3:738:C:H2'	53:3:739:C:H6	1.62	0.65
53:3:1125:U:H2'	53:3:1126:U:H2'	1.78	0.65
4:D:7:PRO:HA	51:1:686:U:O2	1.96	0.65
17:Q:98:ARG:HB3	17:Q:105:GLY:HA2	1.79	0.65
51:1:2048:G:H2'	51:1:2049:G:H5''	1.79	0.65
35:k:76:VAL:H	40:p:72:VAL:HG12	1.61	0.65
3:C:5:ARG:NH1	51:1:2285:C:C5	2.65	0.65
51:1:203:A:H3'	51:1:204:A:H5''	1.79	0.65
51:1:2029:G:O6	51:1:2032:G:H5''	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:975:ILE:HG22	58:B1:977:SER:H	1.62	0.65
65:0:17:ALA:HB2	65:0:112:VAL:HG23	1.79	0.65
22:V:47:ASP:HB3	22:V:74:LEU:HB3	1.78	0.65
51:1:748:G:O6	51:1:751:A:H4'	1.97	0.65
51:1:2008:C:H2'	51:1:2009:A:H8	1.61	0.65
53:3:1156:G:H21	53:3:1179:A:H2	1.44	0.65
53:3:1173:U:H2'	53:3:1174:G:H8	1.61	0.65
58:B1:193:ASP:HB3	58:B1:196:GLN:HB2	1.78	0.65
13:M:111:THR:HG22	13:M:113:ARG:H	1.62	0.65
51:1:581:C:H2'	51:1:582:A:H8	1.60	0.65
51:1:1268:A:H2'	51:1:1269:A:C8	2.31	0.65
51:1:2329:U:H2'	51:1:2330:G:C8	2.32	0.65
53:3:1366:C:H2'	53:3:1367:C:C6	2.32	0.65
55:8:3:DC:C2'	55:8:4:DT:C7	2.75	0.65
58:B1:141:PHE:HD2	58:B1:293:ARG:O	1.79	0.65
30:e:104:THR:HG23	30:e:105:ILE:HG13	1.80	0.64
51:1:20:C:H2'	51:1:21:A:H8	1.60	0.64
52:2:13:G:H2'	52:2:14:U:H5''	1.78	0.64
65:0:501:VAL:HG11	65:0:604:GLY:HA2	1.78	0.64
31:f:82:PHE:HB2	31:f:140:ILE:HG12	1.79	0.64
32:g:94:ILE:HG12	32:g:122:LEU:HB2	1.78	0.64
47:w:40:LYS:NZ	51:1:2330:G:O2'	2.30	0.64
51:1:195:A:H3'	51:1:196:A:H4'	1.78	0.64
51:1:1170:C:H2'	51:1:1171:G:C8	2.32	0.64
51:1:1278:C:H2'	51:1:1279:G:H8	1.62	0.64
51:1:1127:A:H2'	51:1:1128:G:H5''	1.80	0.64
51:1:2047:C:H2'	51:1:2048:G:C8	2.32	0.64
15:O:30:LYS:HA	15:O:34:ALA:HA	1.79	0.64
51:1:246:C:H2'	51:1:247:G:H5'	1.80	0.64
53:3:1306:A:N6	53:3:1331:G:H1'	2.12	0.64
58:B1:162:GLU:HA	58:B1:162:GLU:OE1	1.97	0.64
58:B1:461:PHE:HD2	59:B2:813:GLU:HB2	1.61	0.64
23:W:41:SER:HA	23:W:44:THR:HG22	1.80	0.64
51:1:2704:C:H2'	51:1:2705:A:O4'	1.97	0.64
2:B:8:THR:HB	51:1:2020:A:H5'	1.79	0.64
51:1:746:U:H1'	51:1:748:G:H21	1.61	0.64
51:1:1447:C:H2'	51:1:1448:G:C8	2.31	0.64
51:1:1474:U:H2'	51:1:1475:G:H5'	1.79	0.64
53:3:1436:U:H2'	53:3:1437:A:H8	1.62	0.64
27:b:155:ARG:NH1	51:1:1818:U:H5	1.96	0.64
58:B1:245:LEU:HG	58:B1:246:PRO:HD2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:6:26:G:H3'	63:6:27:U:H5''	1.80	0.64
51:1:2215:C:H2'	51:1:2216:G:C8	2.31	0.64
53:3:56:U:O2	65:0:362:ARG:NH1	2.30	0.64
53:3:1345:U:H4'	53:3:1346:A:H5'	1.80	0.64
58:B1:68:TYR:HB3	58:B1:75:TYR:CE2	2.32	0.64
58:B1:289:ASP:CG	61:NG:104:SER:CB	2.70	0.64
51:1:1297:C:OP1	51:1:2710:C:H4'	1.97	0.64
51:1:2267:A:H3'	51:1:2267:A:N3	2.13	0.64
53:3:246:A:H62	53:3:281:G:N2	1.95	0.64
53:3:1148:U:H2'	53:3:1149:C:O4'	1.98	0.64
53:3:1474:U:H2'	53:3:1475:G:O4'	1.98	0.64
4:D:14:ARG:HG2	51:1:125:A:H5'	1.80	0.64
15:O:46:LYS:HE3	53:3:1253:G:OP1	1.98	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	1.61	0.64
51:1:158:U:H2'	51:1:159:G:O4'	1.97	0.64
51:1:2123:G:H8	51:1:2125:G:H21	1.44	0.64
53:3:1243:C:H2'	53:3:1244:G:H8	1.63	0.64
59:B2:1282:GLY:HA3	60:W0:17:PHE:HE1	1.63	0.64
48:x:1:SER:HB2	51:1:1366:A:OP2	1.99	0.63
65:0:624:PRO:HA	65:0:651:GLY:HA2	1.80	0.63
4:D:21:ARG:NH1	51:1:465:G:O3'	2.32	0.63
10:J:25:LYS:HZ1	53:3:923:A:H5''	1.63	0.63
25:Y:54:GLN:HE22	53:3:193:C:C1'	2.11	0.63
58:B1:111:THR:CG2	58:B1:300:GLN:CD	2.66	0.63
58:B1:289:ASP:OD2	61:NG:104:SER:CB	2.46	0.63
63:6:61:C:O2'	64:a:53:ARG:HD2	1.97	0.63
32:g:4:ILE:HA	32:g:18:GLN:HE22	1.63	0.63
51:1:764:A:O2'	51:1:765:C:H5'	1.98	0.63
6:F:1:MET:HG3	51:1:2742:G:H5'	1.79	0.63
44:t:37:ASP:OD1	44:t:37:ASP:N	2.29	0.63
59:B2:314:ASN:HD21	59:B2:348:SER:HA	1.62	0.63
21:U:34:GLU:OE1	21:U:60:TRP:NE1	2.30	0.63
33:i:112:LYS:NZ	33:i:124:MET:SD	2.69	0.63
53:3:952:U:H2'	53:3:953:G:C8	2.32	0.63
53:3:966:G:C2	63:6:34:C:H5'	2.33	0.63
59:B2:120:GLN:NE2	59:B2:490:GLN:OE1	2.32	0.63
63:6:54:U:H3	63:6:58:A:H8	1.47	0.63
12:L:92:PRO:CA	12:L:95:ARG:HG3	2.28	0.63
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:918:ILE:HG22	59:B2:1280:ALA:HB1	1.79	0.63
14:N:68:GLY:HA2	53:3:1250:A:C5'	2.27	0.63
51:1:340:A:H2'	51:1:341:C:H5'	1.81	0.63
57:A2:100:LEU:HD11	57:A2:121:VAL:HG11	1.80	0.63
58:B1:201:LEU:HB2	58:B1:221:ILE:HD13	1.80	0.63
9:I:46:ARG:HH22	54:4:12:U:H2'	1.62	0.63
15:O:59:LYS:HE3	53:3:972:C:H5'	1.81	0.63
42:r:41:ILE:HB	42:r:47:VAL:HB	1.80	0.63
51:1:2464:G:H2'	51:1:2465:C:H6	1.63	0.63
51:1:2656:U:H5''	65:0:146:ARG:NH1	2.14	0.63
52:2:13:G:N7	52:2:70:C:H4'	2.14	0.63
53:3:91:U:C2'	53:3:92:U:H5''	2.27	0.63
53:3:492:C:H2'	53:3:493:A:C8	2.34	0.63
53:3:1007:U:H2'	53:3:1008:U:C6	2.34	0.63
8:H:10:ARG:HH12	8:H:181:ILE:H	1.45	0.63
51:1:96:C:H2'	51:1:97:C:C6	2.33	0.63
51:1:948:C:H2'	51:1:949:G:C8	2.34	0.63
51:1:1063:G:H3'	51:1:1064:C:H6	1.63	0.63
51:1:1270:C:H5''	51:1:1271:G:H5''	1.79	0.63
51:1:2339:C:H2'	51:1:2340:A:H8	1.64	0.63
51:1:2810:A:H62	51:1:2890:G:H21	1.46	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	0.62
23:W:38:ILE:CD1	53:3:720:C:H1'	2.27	0.62
30:e:35:LEU:HB3	30:e:151:LEU:HD11	1.81	0.62
45:u:87:GLU:HG2	45:u:92:VAL:HG11	1.81	0.62
51:1:481:G:H1'	51:1:506:G:N2	2.14	0.62
51:1:1736:U:H2'	51:1:1737:G:O4'	1.99	0.62
51:1:2066:C:O2'	51:1:2067:G:H5'	1.99	0.62
53:3:600:A:H61	53:3:638:U:H3	1.47	0.62
65:0:490:TYR:HA	65:0:612:LEU:CD1	2.29	0.62
6:F:27:CYS:SG	6:F:28:SER:N	2.71	0.62
51:1:948:C:H2'	51:1:949:G:H8	1.64	0.62
53:3:67:C:H2'	53:3:68:G:H8	1.64	0.62
7:G:32:GLY:HA2	7:G:39:ILE:H	1.64	0.62
7:G:89:PHE:HB3	7:G:150:ILE:HD12	1.81	0.62
48:x:60:LYS:CD	51:1:372:G:H5''	2.28	0.62
51:1:1901:A:H2'	51:1:1902:C:C6	2.35	0.62
34:j:78:THR:HB	51:1:2641:G:H5''	1.81	0.62
51:1:315:G:H2'	51:1:316:C:C6	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1395:A:H4'	51:1:1397:U:C5	2.35	0.62
51:1:1675:C:H2'	51:1:1676:A:O4'	2.00	0.62
51:1:1783:A:C5	51:1:2587:A:C2	2.87	0.62
53:3:668:G:H1	53:3:738:C:H42	1.48	0.62
58:B1:111:THR:CG2	58:B1:300:GLN:NE2	2.63	0.62
14:N:12:LYS:H	14:N:105:ARG:HH22	1.46	0.62
34:j:113:PRO:HG3	51:1:528:A:H5'	1.81	0.62
51:1:66:C:H1'	51:1:456:C:O2	1.99	0.62
51:1:572:A:N6	51:1:2029:G:H21	1.88	0.62
51:1:1597:A:H5''	51:1:1598:A:C5'	2.24	0.62
53:3:946:A:H2'	53:3:947:G:C8	2.34	0.62
7:G:67:LEU:HD12	7:G:160:LEU:HD12	1.82	0.62
41:q:12:ARG:NH1	51:1:1251:C:H5''	2.15	0.62
47:w:19:VAL:HG13	47:w:34:VAL:HG22	1.80	0.62
51:1:1173:U:H2'	51:1:1177:G:H1	1.64	0.62
51:1:2898:U:H2'	51:1:2899:A:C8	2.34	0.62
53:3:367:U:H3	53:3:393:A:H2	1.47	0.62
8:H:21:TRP:CD1	8:H:58:ARG:H	2.18	0.62
9:I:8:LEU:HD23	9:I:21:LYS:HE2	1.82	0.62
51:1:1867:G:H1	51:1:1874:C:H42	1.48	0.62
53:3:34:C:H2'	53:3:35:G:C8	2.33	0.62
51:1:2384:U:O2'	51:1:2385:C:H5'	1.98	0.62
58:B1:1355:ARG:NH1	58:B1:1369:ARG:NH1	2.47	0.62
12:L:1:PRO:HD2	12:L:5:VAL:HA	1.82	0.62
19:S:75:LYS:NZ	53:3:1357:A:H5''	2.14	0.62
53:3:939:G:H2'	53:3:940:C:H6	1.63	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:B1:223:LEU:HG	58:B1:223:LEU:O	2.00	0.62
27:b:6:LYS:HZ1	51:1:1695:G:H5'	1.65	0.62
51:1:812:C:H5''	51:1:1250:G:O2'	2.00	0.62
51:1:2121:G:H1'	64:a:167:LYS:HB2	1.82	0.62
53:3:737:C:H2'	53:3:738:C:C6	2.34	0.62
58:B1:395:LYS:NZ	58:B1:399:LYS:HD3	2.15	0.62
16:P:17:ASP:HB2	16:P:36:ARG:HH22	1.65	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
51:1:848:C:H2'	51:1:849:A:C8	2.35	0.61
51:1:1078:U:H4'	51:1:1088:A:H2	1.65	0.61
51:1:2082:A:C2	51:1:2083:G:H1'	2.35	0.61
55:8:13:DT:C7	58:B1:791:ALA:HB2	2.29	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:288:PRO:HB3	61:NG:105:ASP:CB	2.30	0.61
58:B1:395:LYS:HZ2	58:B1:399:LYS:HD3	1.64	0.61
51:1:368:A:O2'	51:1:369:U:H5'	2.00	0.61
51:1:1746:A:H2'	51:1:1747:U:C6	2.34	0.61
51:1:2286:G:H4'	51:1:2287:A:O4'	2.00	0.61
58:B1:128:LEU:HA	58:B1:192:MET:HE1	1.81	0.61
58:B1:144:TYR:CE1	58:B1:162:GLU:OE2	2.51	0.61
9:I:119:HIS:CD2	53:3:438:U:H4'	2.35	0.61
58:B1:770:LEU:HD13	59:B2:618:GLN:CG	2.30	0.61
55:8:1:DC:H2''	55:8:2:DC:C5	2.35	0.61
42:r:63:VAL:HG12	42:r:96:VAL:HG12	1.83	0.61
46:v:17:SER:HB3	46:v:27:PRO:HG3	1.83	0.61
51:1:729:G:H2'	51:1:1775:U:O2	2.00	0.61
51:1:2885:G:H2'	51:1:2886:A:O4'	2.00	0.61
53:3:657:U:H2'	53:3:658:C:C6	2.36	0.61
53:3:924:C:H2'	53:3:925:G:C8	2.34	0.61
55:8:3:DC:H2'	55:8:4:DT:C7	2.29	0.61
58:B1:100:GLU:HA	59:B2:1328:LYS:HE2	1.82	0.61
58:B1:1357:ILE:HD11	59:B2:1287:LEU:HD13	1.81	0.61
8:H:82:ASP:HA	8:H:85:LYS:HD2	1.82	0.61
17:Q:55:ARG:HA	17:Q:61:GLU:HA	1.83	0.61
43:s:25:ARG:HH22	51:1:519:U:H5''	1.64	0.61
51:1:2653:U:C3'	51:1:2654:A:H5''	2.30	0.61
53:3:715:A:H5''	53:3:805:C:O2'	2.00	0.61
58:B1:68:TYR:HB3	58:B1:75:TYR:CZ	2.35	0.61
13:M:28:SER:HB2	13:M:58:LEU:HB2	1.82	0.61
40:p:90:ALA:HB2	40:p:112:ARG:HA	1.81	0.61
51:1:2512:C:H2'	51:1:2513:A:O4'	2.00	0.61
53:3:452:A:H61	53:3:480:U:H3	1.49	0.61
53:3:1110:A:H2'	53:3:1111:A:C8	2.35	0.61
59:B2:55:SER:OG	59:B2:465:ARG:NH1	2.33	0.61
27:b:49:THR:OG1	27:b:50:THR:N	2.31	0.61
30:e:132:ARG:O	30:e:132:ARG:NH2	2.34	0.61
42:r:81:LYS:HD3	51:1:973:A:H5''	1.83	0.61
46:v:72:VAL:HG13	46:v:93:ARG:HA	1.82	0.61
51:1:11:C:H2'	51:1:12:U:H5''	1.83	0.61
51:1:468:G:H2'	51:1:469:G:H5'	1.83	0.61
22:V:10:ARG:NH1	22:V:11:VAL:O	2.33	0.61
51:1:1740:G:H2'	51:1:1741:C:H6	1.66	0.61
57:A1:112:ALA:HB3	57:A1:126:PRO:HA	1.83	0.61
51:1:139:U:H2'	51:1:140:C:H5	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1361:G:H2'	51:1:1362:C:C6	2.35	0.61
53:3:358:U:H2'	53:3:359:G:H8	1.64	0.61
51:1:1053:C:H2'	51:1:1054:A:H5'	1.83	0.60
51:1:1063:G:H5''	51:1:1064:C:H5	1.64	0.60
19:S:23:ARG:HH11	19:S:26:LEU:HB3	1.65	0.60
29:d:155:GLU:HA	29:d:158:PHE:HB3	1.82	0.60
48:x:4:CYS:HB3	48:x:9:LYS:H	1.65	0.60
51:1:1484:U:H2'	51:1:1485:U:C6	2.36	0.60
51:1:2699:C:H2'	51:1:2700:A:H8	1.67	0.60
52:2:30:C:H2'	52:2:31:C:O4'	2.01	0.60
8:H:78:LYS:HD2	8:H:79:LYS:HD3	1.82	0.60
18:R:81:ASP:OD1	30:e:111:ARG:NH2	2.34	0.60
36:l:79:LEU:HB2	36:l:113:ALA:HB3	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
62:5:39:U:H2'	62:5:40:C:C6	2.36	0.60
34:j:113:PRO:HD2	51:1:558:U:OP1	2.00	0.60
51:1:572:A:H61	51:1:2029:G:N2	1.88	0.60
51:1:589:U:H2'	51:1:590:A:C8	2.37	0.60
53:3:979:C:C2'	53:3:980:C:H5'	2.32	0.60
57:A1:211:ILE:HG12	57:A1:219:ARG:HH12	1.65	0.60
65:0:321:ALA:HB2	65:0:397:LEU:HD21	1.82	0.60
55:8:11:DC:H2'	55:8:12:DG:C8	2.37	0.60
58:B1:951:GLN:NE2	58:B1:1014:GLY:O	2.35	0.60
37:m:14:LYS:NZ	51:1:955:U:OP2	2.35	0.60
51:1:2208:C:H2'	51:1:2209:G:C8	2.37	0.60
53:3:314:C:H2'	53:3:315:A:C8	2.37	0.60
58:B1:154:LEU:HD21	58:B1:160:LEU:HD21	1.83	0.60
17:Q:48:LEU:HB2	53:3:520:A:OP1	2.02	0.60
51:1:1369:G:H21	51:1:1810:A:H2	1.48	0.60
51:1:1818:U:H4'	51:1:1821:A:H1'	1.83	0.60
51:1:2356:U:H2'	51:1:2357:G:O4'	2.01	0.60
53:3:747:A:C3'	53:3:748:G:H5''	2.32	0.60
19:S:12:ARG:NH1	19:S:58:ARG:O	2.35	0.60
27:b:201:LEU:HD22	53:3:773:G:H5''	1.82	0.60
32:g:51:ARG:HA	32:g:55:GLU:HB2	1.84	0.60
36:l:108:ALA:HB3	36:l:125:LEU:HD11	1.83	0.60
37:m:58:LYS:O	37:m:59:ARG:NH2	2.32	0.60
48:x:31:ASN:ND2	48:x:52:ALA:CB	2.65	0.60
51:1:192:C:H2'	51:1:193:U:H5'	1.84	0.60
51:1:445:C:C2'	51:1:446:G:H5'	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:635:C:O2'	51:1:639:U:H5''	2.02	0.60
51:1:729:G:H5''	51:1:730:A:H5''	1.83	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	1.49	0.60
53:3:454:G:H2'	53:3:455:G:C8	2.37	0.60
53:3:1512:U:H2'	53:3:1513:A:H8	1.67	0.60
58:B1:1161:GLY:HA3	58:B1:1179:PRO:HA	1.82	0.60
59:B2:528:ARG:NH2	59:B2:576:SER:O	2.30	0.60
43:s:42:LYS:HE3	51:1:2010:G:H4'	1.84	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
51:1:2303:G:O2'	51:1:2304:G:H5'	2.02	0.60
51:1:2537:U:H2'	51:1:2538:C:C6	2.37	0.60
51:1:2743:U:H3'	51:1:2744:G:H5''	1.83	0.60
51:1:2898:U:H2'	51:1:2899:A:H8	1.67	0.60
53:3:419:C:H5''	53:3:513:C:H1'	1.83	0.60
58:B1:201:LEU:HD11	58:B1:220:ARG:HH11	1.67	0.60
59:B2:918:LEU:O	59:B2:918:LEU:HD23	2.02	0.60
64:a:216:THR:H	64:a:220:ALA:HB3	1.66	0.60
21:U:2:VAL:HB	53:3:229:U:H4'	1.83	0.60
29:d:64:GLY:O	51:1:2059:A:H4'	2.01	0.60
51:1:12:U:O2	51:1:12:U:H2'	2.02	0.60
51:1:2048:G:C3'	51:1:2049:G:H5''	2.31	0.60
51:1:2189:U:H2'	51:1:2190:G:C8	2.37	0.60
51:1:2443:C:O2'	51:1:2444:G:H5'	2.02	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
59:B2:69:GLN:HE21	59:B2:101:ARG:HD2	1.67	0.60
15:O:50:THR:HG22	15:O:64:GLN:HG3	1.83	0.59
47:w:56:PHE:CE2	51:1:2365:G:H4'	2.37	0.59
58:B1:412:LEU:HD22	58:B1:441:LEU:HD21	1.84	0.59
59:B2:1072:ASN:ND2	59:B2:1111:GLN:OE1	2.34	0.59
63:6:26:G:C2'	63:6:27:U:H5''	2.31	0.59
9:I:121:ALA:HA	9:I:145:ARG:HB2	1.83	0.59
51:1:911:A:H5'	51:1:912:C:H5''	1.84	0.59
51:1:1674:G:H21	51:1:1677:A:H61	1.49	0.59
51:1:2521:C:O2'	51:1:2522:U:H5'	2.02	0.59
22:V:61:ARG:NH1	22:V:73:THR:OG1	2.36	0.59
29:d:21:ARG:NH2	29:d:22:ASP:OD1	2.35	0.59
51:1:729:G:H5''	51:1:730:A:C5'	2.33	0.59
51:1:1889:A:H2'	51:1:1890:A:C8	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1374:A:H2'	53:3:1375:A:C8	2.37	0.59
53:3:1521:C:H2'	53:3:1522:U:C6	2.37	0.59
10:J:96:GLN:HG2	53:3:7:A:C6	2.36	0.59
53:3:128:G:H2'	53:3:129:A:C8	2.37	0.59
53:3:836:G:H2'	53:3:837:U:O4'	2.02	0.59
57:A1:38:THR:HB	57:A2:45:ARG:HD3	1.82	0.59
18:R:95:PRO:HG2	18:R:105:ALA:HB1	1.83	0.59
51:1:1444:G:H2'	51:1:1445:G:C8	2.37	0.59
51:1:1982:U:H2'	51:1:1983:G:H8	1.68	0.59
55:8:7:DC:H2''	55:8:8:DT:H71	1.84	0.59
7:G:142:LYS:HE2	53:3:1098:C:OP1	2.03	0.59
18:R:26:LYS:O	18:R:30:LYS:NZ	2.36	0.59
21:U:5:ARG:HD3	53:3:376:G:H4'	1.85	0.59
27:b:48:ILE:HG22	51:1:779:U:P	2.43	0.59
51:1:35:G:H1	51:1:445:C:H42	1.50	0.59
51:1:1081:U:H3'	51:1:1081:U:O2	2.02	0.59
51:1:1802:A:H2'	51:1:1803:A:C8	2.38	0.59
51:1:1924:C:H3'	51:1:1925:C:C6	2.38	0.59
53:3:579:A:H5'	53:3:728:A:H1'	1.85	0.59
58:B1:97:VAL:HG11	58:B1:101:ARG:NH2	2.18	0.59
58:B1:633:ALA:HA	59:B2:806:PRO:O	2.01	0.59
58:B1:725:MET:SD	59:B2:1101:LEU:HD23	2.42	0.59
62:5:29:G:H5'	65:0:513:GLY:HA3	1.85	0.59
29:d:55:SER:OG	29:d:56:GLY:N	2.36	0.59
51:1:704:G:H1'	51:1:726:G:H22	1.67	0.59
51:1:1638:C:H4'	51:1:2710:C:O2	2.02	0.59
51:1:2032:G:OP2	51:1:2455:G:H5'	2.03	0.59
53:3:34:C:H2'	53:3:35:G:H8	1.68	0.59
53:3:738:C:H2'	53:3:739:C:C6	2.38	0.59
45:u:40:LEU:HD12	45:u:59:GLU:HB3	1.84	0.59
51:1:881:G:N2	51:1:897:C:N3	2.50	0.59
53:3:337:G:H2'	53:3:338:A:C8	2.38	0.59
55:8:9:DG:H4'	58:B1:120:LEU:HG	1.84	0.59
58:B1:161:THR:HG23	58:B1:164:GLN:H	1.68	0.59
58:B1:514:THR:HG21	58:B1:596:LEU:HD12	1.84	0.59
7:G:73:ARG:HH22	7:G:93:HIS:HA	1.67	0.59
27:b:116:GLN:O	27:b:127:ASN:ND2	2.35	0.59
28:c:194:PRO:HA	51:1:2680:U:H5'	1.85	0.59
40:p:1:SER:OG	51:1:2875:C:H4'	2.03	0.59
41:q:12:ARG:HH12	51:1:1251:C:H5''	1.68	0.59
51:1:1063:G:H3'	51:1:1064:C:C6	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:207:C:H3'	53:3:208:U:H5''	1.84	0.59
58:B1:275:ARG:NH1	58:B1:278:ARG:NH1	2.51	0.59
7:G:176:ASN:ND2	7:G:194:GLY:O	2.33	0.59
10:J:25:LYS:HB2	53:3:923:A:OP1	2.02	0.59
51:1:952:G:C2'	51:1:953:G:H5''	2.32	0.59
51:1:2324:U:C3'	51:1:2325:G:H5''	2.26	0.59
53:3:677:U:H3	53:3:713:G:H1	1.51	0.59
53:3:742:G:H2'	53:3:743:A:C8	2.38	0.59
58:B1:370:LYS:HG2	58:B1:441:LEU:HD23	1.84	0.59
59:B2:707:ALA:O	59:B2:711:ASP:HB2	2.03	0.59
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
51:1:2333:A:H5'	51:1:2335:A:H1'	1.85	0.58
53:3:885:G:H2'	53:3:886:G:C8	2.39	0.58
58:B1:638:SER:OG	58:B1:639:VAL:N	2.36	0.58
5:E:4:LYS:HD3	51:1:242:G:C8	2.38	0.58
9:I:68:GLU:HB3	53:3:546:A:OP2	2.04	0.58
17:Q:13:ARG:NH1	17:Q:14:LYS:O	2.35	0.58
29:d:164:LEU:HB2	29:d:167:VAL:HG22	1.84	0.58
50:z:12:ALA:O	50:z:20:LYS:NZ	2.36	0.58
51:1:1000:A:H62	51:1:1154:G:H2'	1.68	0.58
51:1:1368:G:H2'	51:1:1369:G:H8	1.68	0.58
51:1:2446:G:H2'	51:1:2501:C:C5	2.38	0.58
53:3:253:A:H2'	53:3:254:G:O4'	2.03	0.58
58:B1:926:PRO:HG2	58:B1:1248:ILE:HD11	1.84	0.58
7:G:99:MET:HA	7:G:106:VAL:HG21	1.84	0.58
9:I:12:ARG:HH21	9:I:35:GLN:H	1.50	0.58
28:c:46:ARG:HG2	28:c:84:LEU:HD12	1.85	0.58
43:s:25:ARG:NH2	51:1:519:U:H5''	2.19	0.58
53:3:448:A:H62	53:3:486:U:H3	1.48	0.58
53:3:721:G:H4'	53:3:722:G:O4'	2.03	0.58
59:B2:1142:ARG:NH1	59:B2:1161:LEU:O	2.36	0.58
63:6:6:G:O2'	63:6:7:G:H5'	2.04	0.58
63:6:55:U:H2'	63:6:56:C:H6	1.68	0.58
3:C:7:LYS:HA	3:C:23:THR:HA	1.85	0.58
15:O:40:ILE:CD1	53:3:1124:G:H4'	2.34	0.58
51:1:166:U:H2'	51:1:167:A:C8	2.38	0.58
51:1:1062:G:H5'	51:1:1071:G:H5'	1.85	0.58
51:1:1065:U:O4	51:1:1069:A:H5''	2.03	0.58
51:1:1319:C:O2'	51:1:1320:C:H5'	2.02	0.58
51:1:1836:C:O2'	51:1:1837:C:H5'	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:16:A:O2'	53:3:17:U:H5'	2.03	0.58
53:3:59:A:H5''	53:3:387:U:H5''	1.84	0.58
53:3:1195:C:H2'	53:3:1197:A:O4'	2.04	0.58
53:3:1280:A:O2'	53:3:1281:C:H5'	2.02	0.58
64:a:26:ALA:HA	64:a:29:LEU:HB3	1.84	0.58
7:G:103:TRP:HA	7:G:106:VAL:HB	1.85	0.58
13:M:38:VAL:HG11	13:M:110:MET:HA	1.83	0.58
51:1:1332:G:N7	51:1:1609:A:H2'	2.18	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:C8	2.38	0.58
53:3:41:G:H2'	53:3:42:G:H8	1.69	0.58
53:3:180:U:H2'	53:3:181:A:O4'	2.03	0.58
53:3:1421:G:H3'	53:3:1422:G:C5'	2.33	0.58
63:6:4:G:H2'	63:6:5:G:O4'	2.03	0.58
63:6:14:A:H2'	63:6:15:G:H5'	1.85	0.58
9:I:58:GLN:HB3	9:I:62:ARG:HH21	1.68	0.58
19:S:17:ASP:O	19:S:22:LYS:NZ	2.35	0.58
51:1:2306:C:H2'	51:1:2307:G:C8	2.38	0.58
53:3:235:C:H2'	53:3:236:A:C8	2.38	0.58
53:3:570:G:O2'	53:3:819:A:H2'	2.03	0.58
58:B1:438:GLU:HG3	58:B1:485:MET:HE1	1.85	0.58
28:c:118:PHE:HD2	51:1:1654:A:H2	1.52	0.58
51:1:1941:C:H2'	51:1:1942:C:O4'	2.04	0.58
53:3:626:G:H2'	53:3:627:G:C8	2.39	0.58
53:3:1069:C:O2'	53:3:1192:C:H1'	2.03	0.58
4:D:37:LYS:NZ	51:1:468:G:OP2	2.34	0.58
5:E:21:PHE:HE2	5:E:61:LEU:HD23	1.68	0.58
8:H:18:ASN:HD21	8:H:39:ARG:HH12	1.51	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
51:1:1197:G:H2'	51:1:1198:U:H6	1.67	0.58
51:1:1197:G:H2'	51:1:1198:U:C6	2.39	0.58
53:3:850:U:C2'	53:3:851:G:H5''	2.33	0.58
58:B1:1361:THR:HB	59:B2:1284:ALA:HB3	1.86	0.58
9:I:8:LEU:HD21	53:3:429:U:O5'	2.03	0.58
51:1:1270:C:H5''	51:1:1271:G:H5'	1.84	0.58
51:1:1787:A:C2	51:1:1788:C:C6	2.91	0.58
51:1:1993:U:H2'	51:1:1994:C:H6	1.68	0.58
51:1:2123:G:O6	51:1:2174:C:N4	2.37	0.58
6:F:19:ARG:NE	51:1:2756:U:OP2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:33:ILE:HG22	16:P:41:LEU:HD12	1.86	0.58
23:W:56:ARG:NH1	53:3:735:C:OP1	2.37	0.58
38:n:11:ASN:N	51:1:1653:G:O6	2.37	0.58
51:1:1843:C:H2'	51:1:1844:C:C6	2.38	0.58
51:1:2675:A:H2'	51:1:2676:C:C6	2.39	0.58
53:3:1005:A:H2'	53:3:1006:G:H5'	1.85	0.58
58:B1:1167:LYS:HZ2	58:B1:1170:LYS:HB2	1.69	0.58
8:H:105:VAL:HG22	8:H:107:LYS:H	1.69	0.57
9:I:165:GLU:HB3	58:B1:86:GLU:HB3	1.85	0.57
10:J:87:VAL:HG13	10:J:92:ARG:HG3	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
42:r:79:ARG:NH1	51:1:572:A:OP2	2.37	0.57
51:1:414:C:H2'	51:1:415:A:C8	2.39	0.57
51:1:952:G:C3'	51:1:953:G:H5''	2.34	0.57
51:1:1177:G:H2'	51:1:1178:C:H5''	1.86	0.57
53:3:1493:A:N7	66:h:6:5OH:NQ	2.51	0.57
58:B1:99:ARG:NH1	58:B1:99:ARG:HG3	2.18	0.57
12:L:137:ARG:NH1	12:L:138:GLU:OE2	2.36	0.57
51:1:2196:C:H2'	51:1:2197:U:C6	2.39	0.57
53:3:308:C:H2'	53:3:309:A:H8	1.69	0.57
57:A2:28:LEU:HB2	57:A2:201:LEU:HB3	1.86	0.57
14:N:69:GLY:N	53:3:1250:A:H4'	2.20	0.57
51:1:1770:G:H4'	51:1:1938:A:OP1	2.03	0.57
53:3:19:A:H1'	53:3:864:A:N3	2.19	0.57
2:B:49:ARG:O	2:B:51:ARG:NH2	2.37	0.57
15:O:13:PHE:O	15:O:70:HIS:ND1	2.36	0.57
20:T:13:GLU:OE1	20:T:83:ARG:NH2	2.36	0.57
32:g:15:LEU:HG	32:g:51:ARG:HH22	1.69	0.57
51:1:1565:C:H2'	51:1:1567:G:N7	2.18	0.57
51:1:1697:G:C5'	51:1:1698:A:H5''	2.35	0.57
58:B1:615:LYS:HG2	60:W0:5:THR:HG21	1.85	0.57
12:L:91:ARG:CB	12:L:93:VAL:HG12	2.33	0.57
20:T:19:ASN:HB2	53:3:750:C:O4'	2.04	0.57
28:c:110:THR:OG1	28:c:111:GLY:N	2.38	0.57
37:m:66:ARG:NH1	37:m:104:GLU:OE2	2.37	0.57
44:t:38:ALA:O	44:t:81:LYS:NZ	2.37	0.57
51:1:62:U:O2'	51:1:63:A:H5'	2.04	0.57
51:1:324:A:H62	51:1:338:G:N2	2.00	0.57
20:T:60:SER:HB2	53:3:581:G:H5'	1.86	0.57
28:c:18:ASP:OD1	28:c:18:ASP:N	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:c:128:ARG:NH2	51:1:2512:C:OP2	2.37	0.57
29:d:76:PRO:CA	29:d:82:GLY:HA3	2.35	0.57
45:u:42:LYS:HG3	51:1:499:U:H4'	1.85	0.57
53:3:885:G:H2'	53:3:886:G:H8	1.69	0.57
58:B1:510:LEU:HD22	58:B1:601:ILE:HD12	1.86	0.57
2:B:5:ASN:ND2	51:1:2020:A:N7	2.52	0.57
11:K:82:ASP:OD1	11:K:82:ASP:N	2.38	0.57
11:K:90:MET:SD	23:W:60:ARG:NH1	2.78	0.57
27:b:221:GLY:HA2	27:b:224:MET:HE3	1.85	0.57
51:1:1310:G:C2'	51:1:1311:G:H5'	2.34	0.57
51:1:1791:A:H2'	51:1:1792:G:C5'	2.34	0.57
51:1:2524:G:C2'	51:1:2525:G:H5''	2.34	0.57
52:2:24:G:H4'	52:2:25:U:C5	2.38	0.57
53:3:1271:A:H5'	53:3:1314:C:C5'	2.35	0.57
57:A2:82:LEU:HD11	57:A2:171:LEU:HD23	1.86	0.57
65:0:168:PRO:HG2	65:0:218:TRP:HE1	1.70	0.57
17:Q:119:LYS:HD3	53:3:36:C:H5''	1.86	0.57
46:v:21:ARG:HH22	52:2:77:U:H5'	1.70	0.57
51:1:78:U:H2'	51:1:79:C:C6	2.40	0.57
53:3:279:A:H5''	53:3:281:G:C5'	2.34	0.57
58:B1:160:LEU:HD22	58:B1:164:GLN:HB3	1.86	0.57
58:B1:241:VAL:O	58:B1:241:VAL:HG12	2.04	0.57
13:M:15:ASN:HB3	53:3:827:U:H4'	1.86	0.57
51:1:601:C:O2	51:1:605:G:H4'	2.05	0.57
51:1:1370:C:H2'	51:1:1371:G:O4'	2.04	0.57
51:1:2050:C:C2'	51:1:2051:A:H5'	2.32	0.57
51:1:2420:C:O2'	51:1:2421:G:H5'	2.05	0.57
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE21	1.68	0.57
32:g:139:PHE:O	32:g:141:LYS:NZ	2.37	0.57
33:i:123:ALA:HB1	51:1:1081:U:H4'	1.87	0.57
38:n:92:GLY:HA3	51:1:2839:G:H21	1.69	0.57
51:1:27:G:N2	51:1:512:G:H1'	2.20	0.57
51:1:211:C:H2'	51:1:212:G:C8	2.40	0.57
51:1:2554:U:H2'	51:1:2555:U:C6	2.40	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
53:3:1513:A:H2'	53:3:1514:G:C8	2.40	0.57
58:B1:741:ALA:O	58:B1:762:ASN:ND2	2.38	0.57
58:B1:1046:ILE:HD12	58:B1:1059:LEU:HB3	1.86	0.57
65:0:223:ILE:HB	65:0:243:LEU:HD22	1.85	0.57
65:0:322:PHE:HB3	65:0:323:LYS:HD2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:17:LYS:HD3	51:1:1565:C:OP1	2.05	0.56
47:w:20:LYS:HD2	51:1:2355:G:H4'	1.85	0.56
47:w:51:ARG:NH2	51:1:2384:U:OP2	2.37	0.56
51:1:28:A:O2'	51:1:583:G:H5'	2.05	0.56
51:1:1069:A:H2'	51:1:1073:A:N7	2.20	0.56
51:1:1801:A:H5''	51:1:2203:U:C2'	2.35	0.56
51:1:2475:C:N4	51:1:2529:G:H22	2.03	0.56
51:1:2529:G:H5'	51:1:2530:A:H5''	1.87	0.56
51:1:2743:U:C3'	51:1:2744:G:H5''	2.35	0.56
53:3:651:C:H2'	53:3:652:U:O4'	2.04	0.56
58:B1:99:ARG:CG	58:B1:99:ARG:HH11	2.18	0.56
16:P:71:ASP:HA	16:P:74:LYS:HG3	1.87	0.56
25:Y:2:ASN:O	25:Y:7:LYS:NZ	2.39	0.56
29:d:2:GLU:HB2	29:d:11:ALA:HB1	1.87	0.56
40:p:87:ARG:NH2	40:p:109:ILE:O	2.36	0.56
52:2:4:C:H2'	52:2:5:U:C6	2.41	0.56
53:3:302:G:H2'	53:3:303:A:C8	2.41	0.56
53:3:408:A:H61	53:3:434:U:H3	1.52	0.56
53:3:936:C:H2'	53:3:937:A:O4'	2.04	0.56
53:3:1004:A:H5'	53:3:1024:G:H1	1.70	0.56
3:C:5:ARG:HG3	3:C:25:ASN:HA	1.86	0.56
4:D:12:ARG:HD2	4:D:44:VAL:HG11	1.88	0.56
7:G:138:ARG:HH21	7:G:142:LYS:HG2	1.69	0.56
10:J:25:LYS:HG3	53:3:923:A:H5'	1.87	0.56
10:J:120:HIS:CE1	10:J:121:ASN:HD21	2.23	0.56
10:J:120:HIS:CE1	10:J:121:ASN:ND2	2.73	0.56
13:M:27:PRO:O	13:M:32:LYS:NZ	2.38	0.56
18:R:87:GLY:O	18:R:91:ARG:NH2	2.39	0.56
18:R:113:LYS:NZ	63:6:44:A:H4'	2.20	0.56
19:S:5:MET:O	19:S:62:ARG:NH1	2.38	0.56
30:e:31:GLU:OE1	30:e:32:LYS:NZ	2.37	0.56
31:f:59:ASP:OD1	31:f:59:ASP:N	2.36	0.56
45:u:32:LYS:HE3	51:1:478:A:H4'	1.87	0.56
47:w:52:ASP:OD2	51:1:2364:C:H5'	2.05	0.56
51:1:379:G:H2'	51:1:380:G:O4'	2.05	0.56
51:1:1923:U:H2'	51:1:1924:C:H6	1.70	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
51:1:2637:U:H2'	51:1:2638:G:O4'	2.04	0.56
51:1:2692:G:H1'	51:1:2847:U:H1'	1.87	0.56
53:3:212:G:H2'	53:3:213:G:C8	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:416:G:H2'	53:3:417:G:H8	1.70	0.56
53:3:1016:A:H4'	53:3:1218:C:H4'	1.86	0.56
64:a:19:LYS:NZ	64:a:20:GLN:O	2.38	0.56
65:0:31:LEU:HD21	65:0:68:THR:HG21	1.87	0.56
65:0:438:LEU:HD22	65:0:469:ILE:HD11	1.88	0.56
65:0:616:ILE:HG13	65:0:688:ASP:HB2	1.87	0.56
3:C:8:ILE:HB	3:C:24:LYS:HB2	1.88	0.56
3:C:36:LYS:NZ	3:C:45:HIS:O	2.38	0.56
51:1:259:G:O2'	51:1:260:G:H5'	2.06	0.56
51:1:683:U:H3	51:1:794:A:H61	1.53	0.56
53:3:882:C:O2'	53:3:883:C:H5'	2.05	0.56
53:3:1257:A:H3'	53:3:1257:A:N3	2.21	0.56
58:B1:42:GLU:HB3	58:B1:52:GLU:HG3	1.86	0.56
58:B1:130:MET:HE2	58:B1:135:ILE:HG12	1.87	0.56
62:5:38:A:C8	62:5:39:U:H1'	2.40	0.56
14:N:47:VAL:HG23	14:N:48:ARG:HG3	1.88	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
51:1:1141:U:H4'	51:1:1142:A:O4'	2.05	0.56
51:1:2430:A:N3	51:1:2430:A:H2'	2.20	0.56
53:3:428:G:H4'	53:3:429:U:H4'	1.86	0.56
53:3:1513:A:H2'	53:3:1514:G:H8	1.70	0.56
58:B1:1166:GLY:HA3	58:B1:1174:ARG:HB2	1.88	0.56
65:0:446:ARG:O	65:0:459:ALA:N	2.38	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
16:P:116:PRO:HA	53:3:675:A:H2	1.70	0.56
30:e:113:PHE:HZ	30:e:175:PRO:HB3	1.71	0.56
47:w:35:ARG:HH21	51:1:2355:G:H1'	1.69	0.56
51:1:36:G:H4'	51:1:451:U:N3	2.21	0.56
51:1:959:A:H1'	51:1:2457:U:O2'	2.06	0.56
51:1:1114:C:H2'	51:1:1115:G:C8	2.41	0.56
51:1:2041:U:H2'	51:1:2042:A:C8	2.40	0.56
51:1:2796:U:H3	51:1:2799:A:H61	1.53	0.56
59:B2:839:VAL:HG12	59:B2:1049:ILE:HG12	1.87	0.56
59:B2:1122:LYS:NZ	59:B2:1126:ASP:OD1	2.38	0.56
5:E:27:ASN:O	5:E:35:LYS:NZ	2.38	0.56
25:Y:13:SER:O	25:Y:17:ARG:N	2.38	0.56
34:j:60:ASP:HA	34:j:93:ILE:HD11	1.88	0.56
51:1:687:C:H2'	51:1:688:U:C5'	2.36	0.56
51:1:1740:G:H2'	51:1:1741:C:C6	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1774:C:H4'	51:1:1979:U:O2	2.05	0.56
51:1:1933:G:O2'	51:1:1974:C:H4'	2.04	0.56
53:3:416:G:H2'	53:3:417:G:C8	2.41	0.56
53:3:1401:G:H2'	53:3:1402:C:O4'	2.06	0.56
58:B1:102:MET:HG2	58:B1:246:PRO:HG3	1.87	0.56
29:d:112:LEU:HD22	29:d:117:ARG:HB3	1.88	0.56
40:p:88:ARG:HD3	40:p:112:ARG:HD3	1.86	0.56
45:u:32:LYS:HB3	45:u:63:ALA:HB1	1.87	0.56
51:1:1120:G:H2'	51:1:1121:C:O4'	2.05	0.56
52:2:105:G:H2'	52:2:106:G:H8	1.71	0.56
58:B1:508:LEU:HD22	59:B2:1101:LEU:HD21	1.88	0.56
59:B2:1142:ARG:NH2	59:B2:1166:ASP:OD1	2.38	0.56
7:G:30:ILE:HG22	7:G:40:ILE:HA	1.88	0.56
14:N:83:THR:HG21	14:N:102:PHE:HB3	1.88	0.56
17:Q:50:LYS:NZ	17:Q:51:VAL:O	2.39	0.56
27:b:158:GLY:HA3	51:1:1820:U:C4	2.40	0.56
28:c:63:PRO:O	28:c:67:HIS:N	2.39	0.56
51:1:1827:U:C2'	51:1:1828:G:H5'	2.35	0.56
51:1:2317:A:H2'	51:1:2318:G:O4'	2.06	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
65:0:493:THR:O	65:0:610:PRO:HA	2.06	0.56
26:Z:48:LYS:HB3	53:3:723:U:C5	2.41	0.56
27:b:140:VAL:O	27:b:161:VAL:N	2.35	0.56
41:q:68:ALA:HB1	41:q:73:ILE:HG13	1.87	0.56
51:1:1186:G:N2	51:1:1187:G:H1'	2.20	0.56
51:1:1827:U:H2'	51:1:1828:G:H5'	1.88	0.56
65:0:564:GLY:HA3	65:0:569:TYR:H	1.71	0.56
1:A:28:VAL:HG23	30:e:139:GLU:HA	1.88	0.55
8:H:120:THR:HG23	8:H:188:ALA:HB2	1.87	0.55
11:K:89:VAL:HG23	53:3:737:C:H5'	1.89	0.55
22:V:19:SER:OG	22:V:20:ILE:N	2.33	0.55
30:e:32:LYS:HB3	30:e:91:ARG:HE	1.71	0.55
46:v:72:VAL:HA	46:v:94:ALA:H	1.71	0.55
51:1:146:A:H2'	51:1:147:C:C6	2.42	0.55
51:1:881:G:H2'	51:1:882:G:H8	1.71	0.55
51:1:1255:U:OP1	51:1:1256:G:H5''	2.06	0.55
51:1:2584:U:H2'	51:1:2585:U:H2'	1.87	0.55
53:3:24:U:H2'	53:3:25:C:C6	2.40	0.55
53:3:684:U:H2'	53:3:685:G:O4'	2.06	0.55
53:3:1525:G:O2'	53:3:1526:G:H5'	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:198:CYS:HA	58:B1:221:ILE:HD11	1.86	0.55
58:B1:833:GLU:HB2	58:B1:1242:ARG:NH1	2.22	0.55
13:M:14:ARG:NH1	13:M:74:ILE:O	2.39	0.55
13:M:24:VAL:HG13	13:M:62:LEU:HD11	1.87	0.55
28:c:119:ALA:O	51:1:1655:A:H4'	2.06	0.55
30:e:46:LYS:NZ	30:e:82:TYR:OH	2.40	0.55
35:k:65:THR:HA	35:k:82:ASN:HA	1.88	0.55
40:p:15:ASP:N	40:p:15:ASP:OD1	2.39	0.55
47:w:33:ILE:HG22	47:w:34:VAL:HG23	1.88	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
59:B2:985:GLU:HB3	59:B2:988:LYS:HB2	1.88	0.55
7:G:101:THR:HG22	53:3:1074:G:H4'	1.88	0.55
8:H:20:THR:HA	19:S:93:PRO:HB3	1.88	0.55
38:n:64:ARG:O	38:n:68:ALA:N	2.40	0.55
51:1:155:A:H2'	51:1:156:A:H8	1.71	0.55
51:1:1191:G:H2'	51:1:1192:G:H8	1.71	0.55
51:1:2563:U:H2'	51:1:2564:A:H5''	1.88	0.55
53:3:560:A:H5'	53:3:566:G:N2	2.21	0.55
53:3:1093:A:C2'	53:3:1094:G:H5'	2.36	0.55
65:0:11:ARG:NH2	65:0:283:ILE:O	2.39	0.55
65:0:192:ASN:HB3	65:0:203:GLU:HB2	1.87	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
13:M:74:ILE:HG22	13:M:128:VAL:HA	1.87	0.55
28:c:118:PHE:HD2	51:1:1654:A:C2	2.24	0.55
51:1:2207:C:O2'	51:1:2208:C:H5'	2.07	0.55
53:3:971:G:OP1	53:3:971:G:H3'	2.07	0.55
59:B2:818:VAL:HG22	59:B2:1096:ILE:HG12	1.87	0.55
5:E:43:LEU:HD11	51:1:2362:C:P	2.46	0.55
10:J:16:ALA:HB3	10:J:35:LEU:H	1.71	0.55
12:L:91:ARG:O	12:L:95:ARG:CG	2.55	0.55
51:1:923:G:O2'	51:1:924:G:H5'	2.06	0.55
51:1:1403:A:H2'	51:1:1404:C:C6	2.42	0.55
51:1:2299:U:H2'	51:1:2300:C:C6	2.42	0.55
53:3:1127:G:H2'	53:3:1128:C:C6	2.41	0.55
58:B1:804:ALA:HA	58:B1:1259:GLN:HG3	1.88	0.55
58:B1:1175:LEU:HD22	58:B1:1190:ILE:HD11	1.88	0.55
59:B2:13:LYS:HB2	59:B2:1180:MET:HE2	1.87	0.55
59:B2:917:SER:O	59:B2:919:ARG:HG3	2.07	0.55
4:D:8:SER:OG	4:D:9:VAL:N	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:59:ILE:HG12	7:G:62:ARG:HH21	1.71	0.55
10:J:19:ARG:HG2	10:J:30:PHE:HB3	1.89	0.55
14:N:11:ARG:NH1	14:N:106:ASP:O	2.39	0.55
27:b:257:ARG:HD3	51:1:1799:G:OP1	2.07	0.55
50:z:10:ARG:NH2	50:z:52:PHE:O	2.39	0.55
51:1:1783:A:N1	51:1:2587:A:H2'	2.21	0.55
51:1:2008:C:H2'	51:1:2009:A:C8	2.41	0.55
51:1:2682:A:H61	51:1:2728:U:H1'	1.72	0.55
53:3:593:U:H2'	53:3:594:U:C6	2.41	0.55
58:B1:247:PRO:HA	58:B1:250:ARG:HG3	1.87	0.55
65:0:323:LYS:HB2	65:0:335:PHE:HB2	1.89	0.55
65:0:488:VAL:HG11	65:0:661:SER:HA	1.87	0.55
12:L:32:ASP:HA	53:3:1350:A:O2'	2.06	0.55
12:L:111:GLY:HA2	12:L:118:ARG:HG2	1.88	0.55
13:M:84:ILE:HD11	13:M:86:LYS:HG2	1.89	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
30:e:56:LEU:HG	30:e:59:ILE:HD12	1.89	0.55
33:i:53:PRO:HD2	33:i:77:VAL:HG21	1.87	0.55
51:1:310:A:C2'	51:1:311:A:H5''	2.37	0.55
51:1:1343:G:H1'	51:1:1597:A:C4	2.41	0.55
53:3:539:A:H2'	53:3:540:G:H8	1.72	0.55
53:3:596:A:H2'	53:3:597:G:O4'	2.07	0.55
53:3:1096:C:H2'	53:3:1097:C:C6	2.41	0.55
58:B1:759:ILE:HG23	58:B1:771:GLN:HB3	1.89	0.55
64:a:26:ALA:HB1	64:a:30:LEU:HB2	1.87	0.55
65:0:694:VAL:HA	65:0:697:ALA:HB3	1.87	0.55
3:C:21:THR:HG21	51:1:2419:U:H5''	1.89	0.55
6:F:5:ALA:HB3	51:1:2466:C:H5'	1.88	0.55
21:U:5:ARG:NH2	21:U:23:ASP:O	2.40	0.55
22:V:64:ARG:HB2	53:3:130:A:H8	1.70	0.55
27:b:204:LEU:HD21	27:b:213:ARG:HH21	1.72	0.55
39:o:33:ARG:HD3	52:2:52:A:N7	2.22	0.55
51:1:1063:G:OP2	51:1:1070:A:H4'	2.07	0.55
51:1:2048:G:C2'	51:1:2049:G:H5''	2.37	0.55
53:3:46:G:H2'	53:3:366:A:H62	1.72	0.55
62:5:40:C:H2'	62:5:41:C:C6	2.41	0.55
64:a:189:LEU:HA	64:a:192:LEU:HG	1.88	0.55
13:M:9:MET:HB2	13:M:32:LYS:HE2	1.87	0.55
29:d:44:ARG:HH12	51:1:1248:G:P	2.30	0.55
51:1:305:C:H2'	51:1:306:U:C6	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:614:A:H5'	51:1:615:U:OP1	2.06	0.55
51:1:782:A:H4'	51:1:783:A:H5'	1.88	0.55
51:1:1868:C:H2'	51:1:1869:G:C5'	2.35	0.55
53:3:357:G:OP1	53:3:367:U:H5''	2.06	0.55
53:3:1348:U:H2'	53:3:1349:A:H5'	1.87	0.55
59:B2:633:LEU:HD13	59:B2:644:LEU:HD23	1.89	0.55
3:C:40:PRO:HG3	51:1:2348:U:H4'	1.88	0.55
28:c:59:ARG:O	28:c:59:ARG:NH2	2.37	0.55
29:d:147:LEU:HB3	29:d:186:VAL:HG12	1.88	0.55
36:l:29:LYS:HG2	51:1:566:U:OP1	2.07	0.55
51:1:286:U:H2'	51:1:287:G:H8	1.72	0.55
51:1:1257:C:O5'	51:1:1257:C:H6	1.90	0.55
53:3:1042:A:H2'	53:3:1043:G:C4'	2.38	0.55
53:3:1073:U:H2'	53:3:1074:G:H8	1.69	0.55
57:A1:29:GLU:HB3	57:A1:200:LYS:HG3	1.88	0.55
58:B1:58:CYS:SG	58:B1:59:ALA:N	2.80	0.55
58:B1:800:LEU:HB3	58:B1:920:ALA:HB1	1.89	0.55
65:0:92:HIS:HD2	65:0:464:LEU:HD21	1.72	0.55
9:I:141:VAL:HA	9:I:180:THR:HA	1.88	0.54
27:b:140:VAL:HG12	27:b:191:LEU:HA	1.89	0.54
31:f:3:VAL:HG11	31:f:65:GLY:HA2	1.89	0.54
33:i:11:GLN:HB2	33:i:56:VAL:HG22	1.88	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
51:1:605:G:H21	51:1:658:U:H5'	1.72	0.54
51:1:1652:A:H2'	51:1:1653:G:O4'	2.07	0.54
51:1:2128:G:H5'	64:a:218:MET:HE1	1.89	0.54
53:3:1213:A:O2'	53:3:1214:C:H2'	2.06	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:HG21	2.06	0.54
59:B2:360:LEU:HD13	59:B2:378:ARG:HH11	1.72	0.54
65:0:103:MET:HB3	65:0:135:VAL:HG21	1.89	0.54
65:0:171:LEU:HB2	65:0:183:VAL:HB	1.88	0.54
6:F:10:LEU:HD21	51:1:2477:U:C5	2.42	0.54
34:j:6:ALA:HB3	34:j:48:VAL:HG11	1.89	0.54
41:q:5:ARG:NH2	51:1:1251:C:OP2	2.40	0.54
51:1:310:A:H2'	51:1:311:A:H5''	1.90	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
51:1:2726:A:O2'	51:1:2727:A:H5'	2.06	0.54
53:3:459:A:H2'	53:3:460:A:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:874:G:H2'	53:3:875:U:C6	2.42	0.54
53:3:1347:G:H22	53:3:1373:G:H2'	1.72	0.54
53:3:1414:U:H2'	53:3:1415:G:C8	2.43	0.54
58:B1:144:TYR:HE1	58:B1:162:GLU:CD	2.14	0.54
65:0:416:ILE:N	65:0:460:GLY:O	2.40	0.54
9:I:96:ARG:NH2	9:I:98:ASP:OD2	2.39	0.54
10:J:153:ALA:HB1	10:J:160:VAL:HA	1.90	0.54
26:Z:13:VAL:HG13	26:Z:15:LEU:HG	1.90	0.54
30:e:127:TYR:HB3	30:e:155:ILE:HG13	1.89	0.54
33:i:38:CYS:O	33:i:42:ASN:ND2	2.40	0.54
37:m:1:MET:HE1	62:5:63:G:H21	1.72	0.54
51:1:142:A:H2'	51:1:143:C:C6	2.42	0.54
51:1:486:C:H42	51:1:494:G:H1	1.56	0.54
51:1:490:C:H5'	51:1:491:G:OP2	2.06	0.54
51:1:849:A:H2'	51:1:850:U:H6	1.68	0.54
58:B1:37:GLU:O	58:B1:61:ILE:CD1	2.52	0.54
8:H:21:TRP:HD1	8:H:57:GLU:HA	1.71	0.54
12:L:91:ARG:NE	12:L:91:ARG:HA	2.22	0.54
15:O:43:PRO:HA	53:3:1151:A:H5'	1.89	0.54
44:t:14:PRO:HA	44:t:32:LEU:HA	1.90	0.54
51:1:1040:A:H2'	51:1:1041:G:H8	1.72	0.54
51:1:2496:C:C2'	51:1:2497:A:H5'	2.36	0.54
53:3:1105:A:H2'	53:3:1106:G:C8	2.42	0.54
65:0:446:ARG:HH11	65:0:447:VAL:H	1.54	0.54
65:0:501:VAL:CG1	65:0:607:LYS:HZ1	2.19	0.54
8:H:26:LYS:HE3	53:3:1256:A:H3'	1.89	0.54
16:P:99:LEU:O	16:P:103:GLY:N	2.38	0.54
39:o:15:ARG:NH2	39:o:95:SER:OG	2.39	0.54
48:x:2:ARG:HG2	48:x:32:LEU:CD1	2.37	0.54
51:1:121:G:H4'	51:1:149:A:H5'	1.89	0.54
51:1:1697:G:C3'	51:1:1698:A:H5''	2.36	0.54
51:1:1889:A:H2'	51:1:1890:A:H8	1.73	0.54
53:3:350:G:O2'	53:3:351:G:H5'	2.08	0.54
53:3:866:C:C4	53:3:867:G:H1'	2.42	0.54
53:3:1399:C:H4'	53:3:1400:C:H3'	1.88	0.54
58:B1:30:ILE:HG21	58:B1:241:VAL:O	2.08	0.54
59:B2:29:SER:O	59:B2:33:ASP:HB2	2.07	0.54
59:B2:811:ASN:HA	59:B2:815:SER:HB2	1.90	0.54
14:N:104:THR:HG22	53:3:1180:A:OP1	2.08	0.54
38:n:2:ARG:NH1	51:1:2820:A:OP2	2.40	0.54
38:n:98:LEU:HB2	38:n:112:TYR:HB2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:130:C:H2'	51:1:131:A:O4'	2.07	0.54
51:1:1809:A:H2'	51:1:1810:A:C8	2.42	0.54
51:1:1836:C:C2'	51:1:1837:C:H5'	2.37	0.54
53:3:1042:A:H2'	53:3:1043:G:O4'	2.08	0.54
53:3:1091:U:H2'	53:3:1093:A:OP2	2.07	0.54
58:B1:1155:ILE:HG13	58:B1:1210:ILE:HB	1.89	0.54
27:b:106:PRO:HG2	27:b:109:LEU:HB2	1.90	0.54
51:1:534:U:H3	51:1:559:G:H1	1.55	0.54
51:1:851:C:H2'	51:1:852:U:C6	2.43	0.54
51:1:2373:G:H2'	51:1:2374:C:C6	2.43	0.54
51:1:2813:A:H2'	51:1:2814:A:C8	2.43	0.54
57:A2:29:GLU:HG3	57:A2:200:LYS:HG3	1.88	0.54
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
26:Z:66:ARG:NH1	53:3:1098:C:O2'	2.38	0.54
28:c:146:ILE:O	28:c:159:LYS:NZ	2.41	0.54
29:d:141:MET:HB2	29:d:143:LEU:HD11	1.90	0.54
33:i:9:LYS:HD2	51:1:1059:G:OP2	2.07	0.54
53:3:162:A:H2'	53:3:163:C:H5'	1.88	0.54
53:3:1013:G:N2	53:3:1015:G:H3'	2.23	0.54
58:B1:746:LEU:HG	58:B1:758:PRO:HG3	1.90	0.54
9:I:205:LYS:HE2	53:3:8:A:C6	2.42	0.54
19:S:9:GLU:HA	19:S:12:ARG:HB2	1.89	0.54
21:U:16:PHE:CE2	53:3:625:U:H5''	2.42	0.54
23:W:49:LYS:HB2	53:3:835:U:OP1	2.08	0.54
32:g:29:PHE:HB2	51:1:2198:A:C2	2.43	0.54
45:u:65:GLN:OE1	51:1:328:U:H4'	2.07	0.54
51:1:207:A:H2'	51:1:208:C:O4'	2.07	0.54
51:1:1126:A:H4'	51:1:1127:A:C5'	2.38	0.54
51:1:1659:G:H2'	51:1:1660:G:O4'	2.08	0.54
51:1:1936:A:H2	51:1:1943:U:H3	1.51	0.54
57:A1:47:LEU:HD23	57:A1:51:MET:HG3	1.89	0.54
59:B2:103:VAL:HB	59:B2:114:VAL:HG11	1.89	0.54
65:0:334:THR:OG1	65:0:385:ALA:N	2.40	0.54
65:0:641:MET:HB3	65:0:657:GLU:HB2	1.90	0.54
11:K:11:HIS:ND1	11:K:14:GLN:OE1	2.41	0.54
16:P:122:PRO:HG2	26:Z:34:ARG:HA	1.89	0.54
25:Y:14:GLU:O	25:Y:18:LYS:NZ	2.41	0.54
27:b:206:LYS:HE3	27:b:209:ALA:HB2	1.89	0.54
27:b:208:GLY:HA2	27:b:211:ARG:HB3	1.89	0.54
29:d:70:SER:C	51:1:674:G:H5''	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:n:60:VAL:HG12	38:n:64:ARG:HH22	1.73	0.54
51:1:1192:G:O2'	51:1:1193:G:H5'	2.08	0.54
51:1:1791:A:O2'	51:1:1792:G:H5'	2.06	0.54
51:1:1905:C:H2'	51:1:1930:G:C8	2.42	0.54
51:1:2155:U:OP1	51:1:2157:G:N2	2.41	0.54
52:2:78:A:H62	52:2:98:G:N2	1.97	0.54
53:3:20:U:H2'	53:3:21:G:O4'	2.08	0.54
53:3:951:G:H2'	53:3:952:U:C6	2.43	0.54
53:3:1093:A:C6	53:3:1095:U:H1'	2.43	0.54
53:3:1325:C:H2'	53:3:1326:U:C6	2.42	0.54
65:0:632:ILE:HA	65:0:635:LEU:HB3	1.89	0.54
7:G:10:LYS:HG2	7:G:211:LEU:HD21	1.89	0.53
29:d:133:LEU:O	29:d:136:GLN:NE2	2.40	0.53
37:m:127:LYS:HE2	51:1:1030:C:OP2	2.08	0.53
51:1:1614:A:H2'	51:1:1615:C:H5'	1.89	0.53
53:3:401:C:H2'	53:3:402:G:H8	1.73	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	1.56	0.53
53:3:1271:A:C5'	53:3:1314:C:H5''	2.39	0.53
58:B1:785:ASP:O	58:B1:789:LYS:HB2	2.08	0.53
58:B1:814:CYS:SG	58:B1:883:ARG:NH2	2.81	0.53
8:H:190:THR:HG23	8:H:192:TYR:H	1.73	0.53
13:M:105:THR:HG22	13:M:107:LYS:H	1.73	0.53
25:Y:14:GLU:OE2	25:Y:18:LYS:NZ	2.41	0.53
30:e:120:SER:HA	51:1:2303:G:H4'	1.89	0.53
39:o:2:ASP:N	52:2:59:A:HO2'	2.05	0.53
51:1:1127:A:C2'	51:1:1128:G:H5''	2.37	0.53
51:1:1783:A:C6	51:1:2587:A:C4	2.96	0.53
53:3:1421:G:H3'	53:3:1422:G:H5''	1.90	0.53
58:B1:799:ARG:HG2	58:B1:1325:PHE:HZ	1.72	0.53
59:B2:243:PRO:HB2	59:B2:274:ILE:HG23	1.90	0.53
65:0:393:THR:OG1	65:0:408:ARG:NH1	2.40	0.53
8:H:58:ARG:HA	8:H:63:ILE:HA	1.90	0.53
12:L:53:SER:HB2	12:L:55:LYS:HE3	1.91	0.53
51:1:937:C:H2'	51:1:938:G:C8	2.43	0.53
51:1:1319:C:H2'	51:1:1320:C:H6	1.73	0.53
51:1:2516:A:O2'	51:1:2517:C:H5'	2.08	0.53
53:3:1234:C:H1'	53:3:1364:U:O2	2.08	0.53
53:3:1507:A:H61	53:3:1528:U:H3	1.56	0.53
58:B1:78:LEU:O	58:B1:78:LEU:HD13	2.09	0.53
58:B1:145:VAL:HG23	58:B1:159:ILE:HG22	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
22:V:49:ASN:ND2	22:V:51:GLU:OE2	2.42	0.53
32:g:2:GLN:NE2	32:g:18:GLN:O	2.40	0.53
51:1:1550:C:H2'	51:1:1551:A:H8	1.73	0.53
57:A1:16:ILE:HG23	57:A1:26:VAL:HG22	1.91	0.53
64:a:11:ILE:HG13	64:a:219:GLY:HA3	1.91	0.53
65:0:327:ASP:O	65:0:437:ARG:NH2	2.42	0.53
65:0:603:GLU:O	65:0:607:LYS:NZ	2.41	0.53
4:D:11:LYS:HE2	51:1:770:G:OP2	2.09	0.53
24:X:4:LEU:HG	24:X:6:LYS:H	1.72	0.53
29:d:68:ALA:HA	51:1:1255:U:C6	2.42	0.53
46:v:73:LYS:O	46:v:92:VAL:N	2.41	0.53
51:1:1760:C:H2'	51:1:1761:C:H5'	1.91	0.53
53:3:337:G:H2'	53:3:338:A:H8	1.74	0.53
53:3:952:U:H2'	53:3:953:G:H8	1.74	0.53
53:3:1402:C:H2'	53:3:1403:C:O4'	2.08	0.53
53:3:1420:U:H3	53:3:1480:A:H2	1.54	0.53
6:F:24:ARG:HE	6:F:36:ARG:HG3	1.73	0.53
9:I:103:ARG:NH1	9:I:165:GLU:HG3	2.23	0.53
13:M:32:LYS:HA	13:M:35:ILE:HD12	1.90	0.53
32:g:25:TYR:HB2	51:1:2093:G:O3'	2.08	0.53
33:i:92:PRO:HB3	33:i:134:SER:HA	1.89	0.53
39:o:30:ARG:HG3	39:o:102:ARG:HD2	1.89	0.53
51:1:737:C:H2'	51:1:738:G:H8	1.72	0.53
51:1:2092:U:C5	51:1:2199:A:H2	2.26	0.53
51:1:2276:G:O2'	51:1:2277:G:H5'	2.09	0.53
58:B1:290:ILE:HG21	61:NG:93:ILE:O	2.09	0.53
7:G:68:PHE:HA	7:G:161:PHE:HB3	1.90	0.53
7:G:210:THR:HA	7:G:213:LEU:HB2	1.90	0.53
8:H:179:ALA:HB1	8:H:202:PHE:HE1	1.73	0.53
10:J:53:ARG:CZ	53:3:1071:C:H5'	2.39	0.53
16:P:124:LYS:HA	26:Z:34:ARG:HE	1.73	0.53
29:d:63:LYS:HE3	51:1:2060:A:H3'	1.91	0.53
51:1:231:A:H2'	51:1:232:G:O4'	2.08	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
51:1:2048:G:H3'	51:1:2049:G:H5''	1.91	0.53
53:3:36:C:H2'	53:3:37:U:H6	1.73	0.53
58:B1:111:THR:HG22	58:B1:300:GLN:NE2	2.23	0.53
65:0:223:ILE:HG13	65:0:237:TYR:HE1	1.74	0.53
8:H:135:ARG:HH12	59:B2:905:ILE:CG2	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:120:ARG:HG2	53:3:37:U:H5'	1.89	0.53
20:T:2:LEU:HD11	20:T:30:LEU:HD11	1.90	0.53
27:b:231:HIS:ND1	51:1:1826:G:OP1	2.38	0.53
29:d:45:ALA:HB3	51:1:38:A:H4'	1.91	0.53
38:n:39:PRO:CG	51:1:1651:G:H5'	2.33	0.53
51:1:533:G:H1	51:1:560:C:H42	1.56	0.53
51:1:1229:C:H2'	51:1:1230:A:H8	1.74	0.53
51:1:1352:U:O2'	51:1:1353:A:H5'	2.08	0.53
51:1:2638:G:H1	51:1:2775:G:H2'	1.74	0.53
53:3:299:G:N2	53:3:565:U:H3	2.06	0.53
53:3:563:A:H4'	53:3:566:G:O2'	2.09	0.53
53:3:601:G:H2'	53:3:602:A:C8	2.44	0.53
58:B1:39:LYS:O	58:B1:273:ILE:HG23	2.08	0.53
59:B2:628:HIS:HB3	59:B2:647:ARG:HH21	1.74	0.53
59:B2:684:ASN:OD1	59:B2:687:ARG:NH2	2.41	0.53
64:a:194:VAL:HA	64:a:197:LYS:HB2	1.89	0.53
12:L:63:VAL:HA	12:L:66:GLU:HG2	1.91	0.53
14:N:97:LEU:O	14:N:102:PHE:N	2.39	0.53
51:1:133:U:H3	51:1:146:A:H61	1.57	0.53
51:1:351:C:H2'	51:1:352:A:H8	1.74	0.53
51:1:1303:G:H2'	51:1:1304:A:H8	1.74	0.53
51:1:2699:C:H2'	51:1:2700:A:C8	2.44	0.53
53:3:224:U:H2'	53:3:225:C:C6	2.44	0.53
58:B1:633:ALA:HB2	59:B2:808:ASN:N	2.19	0.53
8:H:18:ASN:HA	8:H:55:VAL:HG22	1.91	0.53
10:J:154:ALA:O	10:J:158:LYS:NZ	2.41	0.53
12:L:12:LEU:HD13	53:3:1374:A:OP1	2.09	0.53
12:L:92:PRO:HA	12:L:95:ARG:CG	2.37	0.53
13:M:9:MET:HE1	13:M:35:ILE:HD13	1.91	0.53
14:N:64:ILE:HG21	14:N:78:ILE:HG13	1.91	0.53
36:l:29:LYS:HA	51:1:810:U:C5	2.44	0.53
40:p:19:PHE:HE2	40:p:46:VAL:HG21	1.74	0.53
41:q:48:ASP:HA	41:q:51:GLN:HB3	1.89	0.53
49:y:21:LEU:HA	49:y:25:GLN:HB3	1.90	0.53
51:1:1065:U:H3'	51:1:1066:U:H5''	1.91	0.53
51:1:1361:G:H2'	51:1:1362:C:H6	1.74	0.53
51:1:1592:C:H2'	51:1:1593:A:C8	2.44	0.53
51:1:1656:C:H2'	51:1:1657:U:C6	2.44	0.53
53:3:1064:G:O3'	53:3:1065:U:H4'	2.09	0.53
53:3:1077:G:N2	53:3:1079:G:H3'	2.23	0.53
57:A2:100:LEU:HD23	57:A2:115:ILE:HG21	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:68:TYR:CA	58:B1:75:TYR:HE2	2.22	0.53
58:B1:209:ASN:HA	58:B1:214:ARG:HH21	1.74	0.53
4:D:13:ASN:HB3	51:1:125:A:C4'	2.39	0.52
19:S:8:ARG:HB2	19:S:62:ARG:HH12	1.74	0.52
28:c:23:PRO:HB3	51:1:2682:A:C2	2.43	0.52
28:c:144:GLY:HA2	51:1:2578:G:H1'	1.91	0.52
51:1:772:C:H5''	51:1:1356:G:H5'	1.90	0.52
59:B2:246:LEU:HB3	59:B2:269:ILE:HD13	1.91	0.52
65:0:136:PRO:HG2	65:0:287:PRO:HG3	1.90	0.52
9:I:13:ARG:NH2	9:I:37:PRO:O	2.42	0.52
14:N:45:MET:HE3	14:N:49:GLN:HA	1.90	0.52
38:n:8:ARG:NH2	38:n:43:GLU:OE1	2.42	0.52
43:s:4:ILE:HG23	43:s:106:VAL:HG22	1.91	0.52
51:1:1082:U:H3	51:1:1086:A:H2	1.56	0.52
51:1:1433:A:H2'	51:1:1434:A:C1'	2.38	0.52
51:1:2124:G:N1	51:1:2175:C:O2	2.42	0.52
51:1:2125:G:H5'	64:a:39:VAL:C	2.34	0.52
51:1:2345:G:N3	51:1:2381:A:H2'	2.24	0.52
51:1:2694:G:H2'	51:1:2695:U:O4'	2.09	0.52
52:2:30:C:C2'	52:2:31:C:H5'	2.40	0.52
53:3:67:C:H2'	53:3:68:G:C8	2.44	0.52
53:3:358:U:H2'	53:3:359:G:C8	2.44	0.52
53:3:1406:U:H2'	53:3:1407:C:O4'	2.10	0.52
58:B1:975:ILE:HD11	58:B1:1003:LEU:HD11	1.91	0.52
59:B2:1117:LEU:HD12	59:B2:1195:ILE:HG12	1.89	0.52
62:5:38:A:H2'	62:5:39:U:H4'	1.91	0.52
65:0:415:VAL:H	65:0:461:MET:HA	1.73	0.52
65:0:530:ASN:ND2	65:0:535:GLU:OE1	2.42	0.52
15:O:15:HIS:CD2	53:3:1152:A:H5'	2.44	0.52
17:Q:6:LEU:HD21	17:Q:11:ARG:HH21	1.73	0.52
22:V:11:VAL:HG23	22:V:55:GLY:H	1.74	0.52
25:Y:67:HIS:HD2	25:Y:69:ASN:HB2	1.73	0.52
31:f:2:ARG:HG2	51:1:2751:G:C4	2.43	0.52
32:g:2:GLN:HB3	32:g:18:GLN:HB3	1.91	0.52
33:i:101:SER:OG	33:i:102:ARG:N	2.42	0.52
35:k:64:ARG:O	35:k:83:ALA:N	2.42	0.52
36:l:85:VAL:HG22	36:l:86:GLU:HG2	1.92	0.52
37:m:27:SER:OG	37:m:66:ARG:NH1	2.42	0.52
49:y:44:LYS:HE2	49:y:48:ARG:HG3	1.91	0.52
51:1:351:C:H2'	51:1:352:A:C8	2.44	0.52
52:2:33:G:H2'	52:2:34:A:O4'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:36:C:H2'	53:3:37:U:C6	2.44	0.52
53:3:1479:C:H2'	53:3:1480:A:O4'	2.09	0.52
19:S:82:LYS:HA	19:S:85:GLU:HB2	1.92	0.52
22:V:46:HIS:HB2	22:V:70:LYS:HD3	1.91	0.52
30:e:33:ILE:HD12	30:e:155:ILE:HG22	1.90	0.52
36:l:29:LYS:HE3	51:1:566:U:H5''	1.90	0.52
42:r:77:PHE:HD1	42:r:84:ARG:HB3	1.73	0.52
53:3:369:G:H22	53:3:393:A:H1'	1.75	0.52
53:3:1366:C:H2'	53:3:1367:C:H6	1.72	0.52
57:A2:28:LEU:HD22	57:A2:201:LEU:HD23	1.90	0.52
59:B2:714:VAL:HB	59:B2:787:PRO:HD2	1.92	0.52
7:G:67:LEU:HD11	7:G:157:PRO:HG3	1.91	0.52
8:H:181:ILE:HD11	8:H:200:TRP:HB3	1.91	0.52
28:c:15:PHE:HB3	40:p:78:PRO:HD3	1.89	0.52
30:e:23:SER:HB3	30:e:26:GLN:HB2	1.91	0.52
35:k:21:CYS:HA	35:k:41:ILE:HA	1.92	0.52
38:n:32:GLU:HG2	38:n:115:LEU:HD13	1.92	0.52
51:1:1635:A:H2	51:1:1761:C:O2'	1.92	0.52
51:1:2507:C:H6	51:1:2507:C:O5'	1.93	0.52
53:3:737:C:H2'	53:3:738:C:H6	1.74	0.52
53:3:1274:A:C2'	53:3:1275:A:H5''	2.39	0.52
16:P:87:GLY:O	16:P:92:ARG:NH1	2.43	0.52
38:n:103:ARG:HB3	38:n:108:ALA:H	1.74	0.52
42:r:29:THR:HA	42:r:63:VAL:HG23	1.92	0.52
51:1:25:U:H2'	51:1:26:G:O4'	2.10	0.52
51:1:803:U:O2'	51:1:804:A:H5'	2.09	0.52
51:1:1864:U:H5''	51:1:2410:G:O2'	2.10	0.52
52:2:102:G:H2'	52:2:103:U:O4'	2.08	0.52
53:3:90:C:H2'	53:3:91:U:C6	2.45	0.52
53:3:153:C:H2'	53:3:154:U:C4'	2.39	0.52
53:3:722:G:H1	53:3:733:G:H1	1.56	0.52
57:A1:100:LEU:HD21	57:A1:121:VAL:HG11	1.90	0.52
57:A2:43:LEU:HD13	57:A2:217:ILE:HD11	1.90	0.52
58:B1:832:LYS:HB3	58:B1:1242:ARG:NH1	2.24	0.52
65:0:520:ILE:HB	65:0:576:ILE:HD11	1.90	0.52
21:U:55:ASP:OD1	21:U:55:ASP:N	2.41	0.52
27:b:36:ASN:HB3	27:b:38:LYS:HG2	1.91	0.52
51:1:155:A:H2'	51:1:156:A:C8	2.44	0.52
51:1:203:A:H3'	51:1:204:A:C5'	2.39	0.52
51:1:413:C:N4	51:1:2410:G:H1	1.96	0.52
51:1:1674:G:N2	51:1:1677:A:H61	2.07	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1767:G:O5'	51:1:1767:G:H8	1.93	0.52
51:1:1903:G:C2	51:1:1904:G:C8	2.98	0.52
53:3:1169:A:H2'	53:3:1170:A:O4'	2.09	0.52
14:N:114:LYS:HE3	53:3:1188:A:P	2.49	0.52
14:N:122:ARG:NH1	53:3:1350:A:OP1	2.43	0.52
16:P:17:ASP:N	16:P:17:ASP:OD1	2.42	0.52
27:b:7:PRO:HB3	27:b:13:ARG:HA	1.92	0.52
28:c:161:MET:HE1	51:1:2050:C:H1'	1.91	0.52
51:1:277:G:H4'	51:1:278:A:C8	2.44	0.52
51:1:958:U:H2'	52:2:89:U:C1'	2.39	0.52
51:1:1655:A:H2'	51:1:1656:C:H5'	1.91	0.52
51:1:1841:U:H2'	51:1:1842:G:H8	1.73	0.52
51:1:2577:A:H2'	51:1:2614:A:H61	1.75	0.52
53:3:265:G:H2'	53:3:267:C:H5	1.75	0.52
53:3:1225:A:H2'	53:3:1225:A:N3	2.25	0.52
58:B1:750:PRO:CB	59:B2:549:ASP:OD2	2.45	0.52
64:a:63:THR:HG21	64:a:195:ALA:HB1	1.90	0.52
65:0:53:MET:O	65:0:57:GLN:NE2	2.43	0.52
65:0:541:LYS:NZ	65:0:579:HIS:O	2.41	0.52
5:E:48:MET:SD	5:E:48:MET:N	2.79	0.52
8:H:9:ILE:HG13	8:H:177:LEU:HD21	1.91	0.52
11:K:47:LEU:HD21	11:K:55:HIS:HA	1.92	0.52
28:c:133:THR:OG1	28:c:134:HIS:N	2.38	0.52
34:j:135:GLN:HE22	51:1:7:G:H1'	1.75	0.52
39:o:29:HIS:HB3	39:o:36:TYR:HD2	1.74	0.52
41:q:57:ARG:NH2	51:1:1154:G:OP2	2.43	0.52
51:1:745:G:H2'	51:1:746:U:O4'	2.09	0.52
51:1:1357:C:H42	51:1:1374:G:H1	1.57	0.52
51:1:1954:G:H1	51:1:1986:C:H5''	1.75	0.52
51:1:2022:U:O2'	51:1:2617:U:H5'	2.10	0.52
51:1:2061:G:H8	51:1:2501:C:H4'	1.73	0.52
51:1:2272:U:H5''	51:1:2273:A:OP1	2.10	0.52
51:1:2402:U:O2'	51:1:2403:C:H5''	2.09	0.52
53:3:112:G:N2	53:3:354:G:H5'	2.02	0.52
53:3:731:G:O2'	53:3:732:C:H5'	2.10	0.52
14:N:11:ARG:HH11	14:N:105:ARG:HH12	1.57	0.52
17:Q:28:GLN:HB2	53:3:363:A:H1'	1.92	0.52
17:Q:45:ASN:OD1	17:Q:45:ASN:N	2.43	0.52
18:R:89:ARG:NH2	18:R:95:PRO:O	2.34	0.52
30:e:32:LYS:O	30:e:156:THR:OG1	2.27	0.52
32:g:94:ILE:HD12	32:g:99:ILE:HD13	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:j:69:ARG:NH1	34:j:90:GLU:OE2	2.38	0.52
39:o:110:ALA:HB1	39:o:115:LEU:HD12	1.92	0.52
51:1:1187:G:O5'	51:1:1187:G:H8	1.93	0.52
51:1:1505:A:H2'	51:1:1506:U:O4'	2.10	0.52
53:3:1496:C:H2'	53:3:1497:G:O4'	2.10	0.52
58:B1:412:LEU:HD23	58:B1:416:ILE:HG13	1.92	0.52
59:B2:125:GLY:HA2	59:B2:499:SER:HB2	1.92	0.52
59:B2:786:GLY:N	59:B2:789:THR:OG1	2.41	0.52
64:a:183:ASP:OD1	64:a:183:ASP:N	2.43	0.52
8:H:38:VAL:O	8:H:42:LEU:N	2.43	0.51
42:r:61:ALA:HB1	42:r:96:VAL:HB	1.92	0.51
51:1:755:U:H2'	51:1:756:A:H8	1.75	0.51
51:1:1409:U:H2'	51:1:1410:G:C8	2.46	0.51
51:1:1536:C:H4'	51:1:1537:G:C2	2.44	0.51
51:1:1710:G:H2'	51:1:1711:A:H8	1.74	0.51
51:1:1755:A:C2'	51:1:1756:G:H5'	2.40	0.51
53:3:19:A:H1'	53:3:864:A:C2	2.45	0.51
53:3:148:G:H1	53:3:174:A:H61	1.58	0.51
53:3:174:A:C2'	53:3:175:C:H5'	2.40	0.51
53:3:955:U:H2'	53:3:956:U:H6	1.74	0.51
57:A1:205:MET:HE3	57:A1:213:PRO:HB3	1.91	0.51
58:B1:99:ARG:HG3	58:B1:99:ARG:HH11	1.73	0.51
58:B1:201:LEU:HD12	58:B1:224:LEU:HD12	1.92	0.51
65:0:217:GLU:O	65:0:220:GLN:NE2	2.41	0.51
65:0:295:ILE:HG13	65:0:309:ARG:HB2	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	1.91	0.51
41:q:24:TYR:OH	51:1:2020:A:O3'	2.25	0.51
51:1:526:A:N6	51:1:2626:C:H4'	2.25	0.51
51:1:622:G:O2'	51:1:623:C:H5'	2.10	0.51
53:3:135:C:H2'	53:3:136:C:H5'	1.92	0.51
53:3:410:G:H21	53:3:432:A:H62	1.57	0.51
53:3:977:A:H2'	53:3:977:A:N3	2.25	0.51
53:3:1485:U:O2'	53:3:1486:G:H5'	2.10	0.51
65:0:107:ASP:OD1	65:0:107:ASP:N	2.40	0.51
19:S:7:ALA:HB1	53:3:994:A:O2'	2.09	0.51
30:e:117:SER:HB3	30:e:177:ARG:HH21	1.75	0.51
51:1:1867:G:H1	51:1:1874:C:N4	2.08	0.51
51:1:2660:A:OP1	65:0:675:LYS:HD2	2.10	0.51
53:3:49:U:O2'	53:3:50:A:H2'	2.10	0.51
53:3:207:C:C3'	53:3:208:U:H5''	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1271:A:H5'	53:3:1314:C:H5''	1.91	0.51
58:B1:205:LEU:HG	58:B1:217:LEU:HB3	1.90	0.51
58:B1:375:GLU:HG2	59:B2:1245:ALA:O	2.10	0.51
59:B2:524:ILE:HG21	59:B2:708:VAL:HG13	1.92	0.51
65:0:473:MET:HA	65:0:477:PHE:HB2	1.91	0.51
2:B:54:ILE:HG13	2:B:56:LYS:H	1.76	0.51
25:Y:10:ALA:O	25:Y:13:SER:OG	2.28	0.51
36:l:9:ALA:HB3	36:l:12:SER:HB3	1.91	0.51
51:1:1394:U:H4'	51:1:1603:A:H4'	1.93	0.51
51:1:1410:G:O2'	51:1:1411:U:H5'	2.10	0.51
51:1:2656:U:H2'	51:1:2657:A:H8	1.75	0.51
53:3:884:U:OP2	53:3:884:U:H6	1.92	0.51
53:3:1251:A:H2'	53:3:1252:A:C8	2.46	0.51
58:B1:99:ARG:HA	58:B1:248:ASP:HB2	1.92	0.51
58:B1:144:TYR:CE1	58:B1:162:GLU:CD	2.88	0.51
58:B1:215:LYS:HA	58:B1:218:THR:HG22	1.92	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''	1.93	0.51
12:L:114:SER:O	12:L:118:ARG:N	2.38	0.51
24:X:35:ARG:HB2	53:3:1320:C:N4	2.25	0.51
38:n:64:ARG:HD3	51:1:2706:A:O2'	2.10	0.51
51:1:178:G:O2'	51:1:179:C:H5'	2.10	0.51
51:1:1332:G:N3	51:1:1332:G:H5'	2.25	0.51
51:1:2082:A:H2'	51:1:2083:G:O4'	2.10	0.51
51:1:2248:C:H3'	51:1:2249:U:C6	2.46	0.51
53:3:302:G:H2'	53:3:303:A:H8	1.74	0.51
53:3:437:U:H2'	53:3:438:U:H5'	1.91	0.51
53:3:574:A:N3	53:3:883:C:H1'	2.25	0.51
53:3:1239:A:H5''	53:3:1240:U:C5	2.44	0.51
58:B1:112:ALA:HA	58:B1:238:ILE:HA	1.91	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
7:G:187:ASP:OD1	7:G:187:ASP:N	2.42	0.51
14:N:33:SER:OG	14:N:34:LEU:N	2.43	0.51
27:b:31:PRO:HG2	27:b:32:LEU:HD12	1.92	0.51
32:g:131:SER:OG	32:g:140:ALA:O	2.28	0.51
40:p:93:LYS:HE2	51:1:1754:A:OP1	2.11	0.51
40:p:102:ARG:HH22	51:1:1755:A:P	2.34	0.51
51:1:44:A:H2'	51:1:45:G:H5'	1.93	0.51
51:1:216:A:O2'	51:1:217:A:H5'	2.11	0.51
51:1:233:A:H2'	51:1:234:U:H5'	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:243:U:O2'	51:1:244:A:H5'	2.11	0.51
51:1:532:A:H2'	51:1:532:A:N3	2.24	0.51
51:1:1470:A:H61	51:1:1521:G:H1'	1.75	0.51
51:1:2489:U:H2'	51:1:2490:G:O4'	2.11	0.51
53:3:218:U:H2'	53:3:219:U:O4'	2.09	0.51
53:3:515:G:O2'	53:3:516:U:H5'	2.10	0.51
53:3:1421:G:C2'	53:3:1422:G:H4'	2.40	0.51
55:8:13:DT:OP2	58:B1:791:ALA:CB	2.59	0.51
59:B2:974:ARG:HD2	59:B2:1014:LEU:HD21	1.92	0.51
60:W0:3:ARG:NH1	60:W0:55:GLU:OE2	2.40	0.51
8:H:67:ILE:N	8:H:101:ASN:O	2.42	0.51
16:P:22:ILE:HD13	16:P:83:VAL:HG13	1.93	0.51
29:d:67:ARG:O	51:1:1255:U:H5	1.94	0.51
33:i:4:VAL:HB	51:1:1055:G:OP2	2.10	0.51
51:1:1333:G:H2'	51:1:1334:G:H8	1.75	0.51
51:1:2616:C:H2'	51:1:2617:U:H6	1.76	0.51
53:3:1105:A:H2'	53:3:1106:G:H8	1.74	0.51
58:B1:390:LEU:N	58:B1:390:LEU:CD1	2.73	0.51
9:I:18:LEU:HB3	9:I:20:LEU:HD22	1.91	0.51
32:g:22:LYS:HB2	51:1:2094:A:OP1	2.11	0.51
51:1:216:A:H2'	51:1:217:A:O4'	2.11	0.51
51:1:286:U:H2'	51:1:287:G:C8	2.46	0.51
51:1:548:G:H2'	51:1:549:G:O4'	2.10	0.51
51:1:1550:C:H2'	51:1:1551:A:C8	2.46	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
51:1:2656:U:H5''	65:0:146:ARG:NH2	2.25	0.51
53:3:379:C:H2'	53:3:380:G:O4'	2.10	0.51
58:B1:289:ASP:H	61:NG:104:SER:CB	2.23	0.51
58:B1:902:ASP:HB3	58:B1:905:ARG:HB2	1.93	0.51
1:A:8:LYS:O	1:A:27:THR:OG1	2.28	0.51
15:O:8:ILE:HB	15:O:74:VAL:HB	1.92	0.51
21:U:1:MET:SD	21:U:24:SER:OG	2.64	0.51
28:c:177:VAL:HA	28:c:189:VAL:HA	1.93	0.51
51:1:12:U:H2'	51:1:13:A:H5'	1.92	0.51
51:1:376:G:H2'	51:1:377:G:H8	1.74	0.51
51:1:1210:G:P	51:1:1212:G:H5'	2.51	0.51
51:1:1963:U:C2'	51:1:1964:G:H5''	2.41	0.51
51:1:2545:G:H2'	51:1:2546:U:O4'	2.11	0.51
52:2:29:A:H2'	52:2:30:C:O4'	2.11	0.51
53:3:1400:C:N4	63:6:34:C:H1'	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:505:ASP:OD2	59:B2:812:PHE:HA	2.11	0.51
59:B2:400:VAL:HG21	59:B2:452:ARG:HE	1.76	0.51
65:0:194:ASN:OD1	65:0:200:VAL:N	2.44	0.51
7:G:72:LYS:HZ2	7:G:74:ALA:HB3	1.76	0.51
15:O:59:LYS:HE3	53:3:972:C:C5'	2.41	0.51
18:R:89:ARG:HB3	18:R:96:VAL:HG22	1.93	0.51
19:S:78:LEU:HD13	19:S:82:LYS:HB3	1.92	0.51
39:o:100:HIS:O	39:o:104:GLN:NE2	2.44	0.51
43:s:40:ASN:OD1	43:s:40:ASN:N	2.40	0.51
51:1:866:A:H61	51:1:913:U:H1'	1.76	0.51
51:1:1951:U:C2	51:1:1953:A:OP2	2.63	0.51
53:3:554:A:H2'	53:3:555:U:H5'	1.93	0.51
53:3:678:U:H2'	53:3:679:C:O4'	2.11	0.51
53:3:1351:U:H3	53:3:1371:G:H1	1.59	0.51
58:B1:437:PHE:HZ	58:B1:453:VAL:HG11	1.76	0.51
58:B1:850:LYS:HB2	58:B1:857:LEU:HB2	1.91	0.51
59:B2:255:ILE:HB	59:B2:263:VAL:HB	1.92	0.51
8:H:135:ARG:HH11	59:B2:902:LEU:HG	1.75	0.50
15:O:54:SER:O	19:S:80:ARG:NH2	2.44	0.50
29:d:1:MET:N	29:d:14:VAL:O	2.35	0.50
29:d:58:LYS:HE2	51:1:676:A:OP1	2.11	0.50
36:l:51:GLU:HG3	36:l:56:PRO:HB3	1.93	0.50
41:q:23:TYR:HD1	51:1:533:G:H5'	1.75	0.50
44:t:55:VAL:O	44:t:88:LYS:NZ	2.37	0.50
51:1:3:U:H2'	51:1:4:U:C6	2.45	0.50
51:1:543:G:H3'	51:1:544:C:H5''	1.92	0.50
51:1:558:U:H2'	51:1:559:G:C8	2.46	0.50
51:1:1597:A:H4'	51:1:1598:A:H8	1.76	0.50
51:1:1913:A:H61	53:3:1493:A:H2'	1.76	0.50
51:1:1917:U:O2'	51:1:1918:A:H5'	2.11	0.50
51:1:1977:A:H2'	51:1:1978:A:O4'	2.12	0.50
51:1:2415:G:H2'	51:1:2416:C:H6	1.75	0.50
57:A2:140:ILE:HD12	57:A2:142:MET:HE3	1.92	0.50
7:G:53:LEU:HD11	7:G:215:ALA:HB1	1.92	0.50
7:G:210:THR:O	7:G:214:GLY:N	2.40	0.50
10:J:36:THR:OG1	10:J:37:VAL:N	2.38	0.50
13:M:11:THR:OG1	53:3:876:C:H1'	2.10	0.50
13:M:16:GLY:O	13:M:64:TYR:OH	2.28	0.50
31:f:151:ARG:HG3	31:f:160:GLY:HA2	1.92	0.50
33:i:113:ALA:HB2	33:i:121:ILE:HD11	1.93	0.50
48:x:14:GLY:HA3	48:x:28:PHE:HE1	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:x:57:VAL:O	48:x:61:LYS:NZ	2.44	0.50
51:1:403:U:O3'	51:1:404:A:H4'	2.11	0.50
51:1:1268:A:H2'	51:1:1269:A:H8	1.74	0.50
51:1:1439:A:H2'	51:1:1440:U:H5'	1.94	0.50
51:1:1810:A:H2'	51:1:1811:G:O4'	2.12	0.50
51:1:2372:U:H2'	51:1:2373:G:C8	2.46	0.50
53:3:894:G:H2'	53:3:895:G:H8	1.75	0.50
53:3:1516:G:H2'	53:3:1518:A:OP2	2.10	0.50
62:5:34:G:H5''	62:5:35:A:C8	2.47	0.50
65:0:499:THR:HG23	65:0:500:ASP:N	2.23	0.50
9:I:146:GLU:HA	9:I:149:LYS:HE2	1.92	0.50
9:I:173:ASP:OD1	9:I:173:ASP:N	2.44	0.50
25:Y:4:LYS:HB3	25:Y:6:ALA:H	1.76	0.50
28:c:27:ILE:HD11	28:c:187:LEU:HD23	1.93	0.50
31:f:126:THR:OG1	31:f:127:GLN:N	2.44	0.50
38:n:107:ASN:HD22	51:1:2009:A:H4'	1.74	0.50
44:t:61:LEU:HD21	44:t:82:LYS:HD2	1.92	0.50
51:1:402:A:H2'	51:1:403:U:O4'	2.12	0.50
51:1:838:C:H2'	51:1:839:U:H6	1.75	0.50
51:1:839:U:H2'	51:1:840:C:C6	2.47	0.50
51:1:990:A:N6	51:1:1186:G:H1'	2.27	0.50
51:1:1599:U:H2'	51:1:1600:C:H6	1.75	0.50
53:3:284:C:O2'	53:3:285:C:H5'	2.11	0.50
53:3:945:G:H2'	53:3:945:G:N3	2.27	0.50
53:3:1230:C:H5'	63:6:30:G:H5''	1.93	0.50
59:B2:1070:HIS:NE2	59:B2:1114:GLU:OE1	2.36	0.50
65:0:490:TYR:HB2	65:0:569:TYR:CD1	2.46	0.50
9:I:96:ARG:NE	9:I:132:ALA:O	2.44	0.50
26:Z:16:ARG:HG3	26:Z:19:LYS:HB2	1.94	0.50
32:g:8:LYS:NZ	32:g:11:ASN:O	2.44	0.50
42:r:76:LYS:HZ1	42:r:85:LYS:HE2	1.76	0.50
51:1:375:G:C2'	51:1:376:G:H5'	2.42	0.50
51:1:1040:A:H2'	51:1:1041:G:C8	2.47	0.50
51:1:1042:G:H2'	51:1:1043:C:C6	2.46	0.50
51:1:1473:G:H1	51:1:1518:C:N4	2.00	0.50
51:1:1783:A:N6	51:1:2587:A:N3	2.59	0.50
51:1:1794:A:H1'	51:1:1900:A:C2	2.46	0.50
51:1:2358:A:H2'	51:1:2359:C:O4'	2.11	0.50
51:1:2372:U:H2'	51:1:2373:G:H8	1.77	0.50
51:1:2850:A:H2'	51:1:2851:A:O4'	2.11	0.50
52:2:24:G:H4'	52:2:25:U:H5	1.73	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:793:U:O2	53:3:1516:G:H4'	2.11	0.50
53:3:1267:C:H2'	53:3:1268:G:O4'	2.11	0.50
58:B1:749:LYS:HB3	58:B1:755:ILE:HD11	1.93	0.50
58:B1:972:LYS:HD2	58:B1:1004:ALA:HA	1.93	0.50
65:0:70:ALA:HB3	65:0:84:ILE:HB	1.94	0.50
14:N:96:GLU:O	14:N:100:ALA:N	2.41	0.50
14:N:118:ARG:NH2	53:3:1366:C:OP1	2.44	0.50
35:k:71:ARG:HG3	35:k:77:ILE:HD11	1.92	0.50
51:1:2297:A:N1	51:1:2321:U:H5	2.09	0.50
51:1:2375:G:C2'	51:1:2376:A:H5''	2.38	0.50
52:2:87:U:H5''	52:2:88:C:H5	1.74	0.50
53:3:162:A:C2'	53:3:163:C:H5'	2.42	0.50
53:3:650:G:H2'	53:3:651:C:C6	2.47	0.50
53:3:993:G:N3	53:3:993:G:H2'	2.25	0.50
53:3:1271:A:H4'	53:3:1314:C:OP1	2.10	0.50
59:B2:870:ILE:HB	59:B2:944:ARG:HD3	1.93	0.50
65:0:105:VAL:HG23	65:0:106:LEU:HD12	1.93	0.50
65:0:141:VAL:HB	65:0:266:CYS:HA	1.92	0.50
65:0:419:ALA:HA	65:0:457:ILE:HA	1.93	0.50
9:I:103:ARG:HH11	9:I:165:GLU:HG3	1.76	0.50
24:X:76:THR:HG21	53:3:1221:G:H4'	1.94	0.50
28:c:160:LYS:HD2	51:1:2513:A:OP1	2.12	0.50
43:s:16:LYS:HE3	51:1:1266:G:N7	2.27	0.50
43:s:42:LYS:HB2	51:1:2010:G:H5''	1.94	0.50
51:1:475:C:H4'	51:1:510:C:H5'	1.93	0.50
51:1:801:G:H3'	51:1:802:A:H5'	1.92	0.50
51:1:1390:U:O2'	51:1:1391:U:H5'	2.11	0.50
51:1:2040:G:H2'	51:1:2041:U:O4'	2.12	0.50
53:3:559:A:H4'	53:3:560:A:H3'	1.94	0.50
53:3:599:C:H2'	53:3:600:A:H8	1.77	0.50
59:B2:400:VAL:HG11	59:B2:452:ARG:HD2	1.93	0.50
11:K:68:GLN:NE2	53:3:738:C:O3'	2.44	0.50
12:L:92:PRO:C	12:L:95:ARG:HG3	2.36	0.50
12:L:107:ALA:HB1	12:L:115:MET:HE1	1.94	0.50
17:Q:33:CYS:HA	17:Q:54:VAL:HG22	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
29:d:195:GLN:HE22	29:d:199:MET:HE2	1.77	0.50
42:r:80:ARG:HD3	51:1:566:U:C5	2.47	0.50
45:u:73:ASN:HD22	45:u:76:THR:H	1.60	0.50
51:1:598:U:H2'	51:1:599:A:H8	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:704:G:H1'	51:1:726:G:N2	2.27	0.50
51:1:2416:C:H2'	51:1:2417:C:C6	2.47	0.50
51:1:2549:G:H2'	51:1:2550:G:H8	1.76	0.50
53:3:1327:C:O2'	53:3:1328:C:H5'	2.12	0.50
58:B1:421:VAL:O	58:B1:436:ALA:HA	2.12	0.50
59:B2:93:SER:HA	59:B2:128:PRO:HA	1.93	0.50
59:B2:232:ILE:HG12	59:B2:237:LEU:HG	1.94	0.50
65:0:631:VAL:O	65:0:635:LEU:N	2.42	0.50
5:E:35:LYS:HE2	5:E:39:ARG:HE	1.76	0.50
15:O:37:ARG:HG2	15:O:77:VAL:HB	1.93	0.50
40:p:28:LYS:HD3	40:p:82:SER:HB3	1.93	0.50
41:q:10:ARG:NH1	51:1:1216:G:H5''	2.25	0.50
47:w:52:ASP:HB2	47:w:54:THR:HG23	1.94	0.50
51:1:871:U:H2'	51:1:872:U:C6	2.47	0.50
51:1:1581:G:H2'	51:1:1582:C:O4'	2.12	0.50
51:1:2417:C:H2'	51:1:2418:A:H8	1.76	0.50
52:2:88:C:H4'	52:2:90:C:N3	2.27	0.50
53:3:953:G:H2'	53:3:954:G:O4'	2.12	0.50
53:3:1012:A:H5'	53:3:1012:A:H8	1.77	0.50
65:0:501:VAL:HG12	65:0:607:LYS:HZ1	1.77	0.50
2:B:28:SER:HG	2:B:39:ARG:HH21	1.57	0.50
14:N:3:ASN:N	14:N:88:GLU:OE1	2.45	0.50
18:R:24:VAL:HA	53:3:1329:A:H5''	1.94	0.50
26:Z:27:VAL:HG22	26:Z:31:VAL:HB	1.93	0.50
30:e:129:MET:HG3	30:e:153:ILE:HB	1.94	0.50
31:f:2:ARG:HD3	51:1:2751:G:OP2	2.12	0.50
33:i:30:GLN:HG3	33:i:60:VAL:HG11	1.93	0.50
51:1:594:U:H2'	51:1:595:C:H6	1.77	0.50
51:1:737:C:H2'	51:1:738:G:C8	2.47	0.50
51:1:1934:C:H2'	51:1:1935:G:O4'	2.12	0.50
51:1:2124:G:HO2'	64:a:41:SER:CB	2.21	0.50
51:1:2259:U:C5	51:1:2427:C:N4	2.80	0.50
53:3:62:U:H2'	53:3:63:C:C6	2.46	0.50
53:3:162:A:C2	53:3:348:G:H4'	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	2.47	0.50
53:3:812:G:OP1	53:3:903:G:H1'	2.12	0.50
53:3:967:C:H2'	53:3:968:A:N7	2.26	0.50
53:3:1017:U:H2'	53:3:1018:G:O4'	2.11	0.50
53:3:1049:U:H4'	53:3:1050:G:H5''	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:1371:ARG:HE	58:B1:1372:ARG:NH1	2.10	0.50
59:B2:554:HIS:HD2	59:B2:558:VAL:HB	1.77	0.50
4:D:13:ASN:HB3	51:1:125:A:H4'	1.93	0.49
10:J:37:VAL:HG11	10:J:113:VAL:HA	1.93	0.49
12:L:14:ASP:OD1	12:L:43:TYR:OH	2.24	0.49
14:N:26:LYS:HG2	14:N:61:ASP:HB2	1.93	0.49
21:U:5:ARG:NH1	21:U:26:ASN:O	2.43	0.49
33:i:9:LYS:HD3	51:1:1060:U:OP2	2.12	0.49
34:j:108:MET:HB3	51:1:1006:C:O2'	2.11	0.49
40:p:102:ARG:NH2	51:1:1755:A:H5'	2.26	0.49
42:r:8:GLY:HA3	42:r:23:GLU:HG3	1.94	0.49
46:v:58:SER:OG	46:v:59:GLU:OE1	2.30	0.49
51:1:45:G:C5'	51:1:46:G:H5'	2.25	0.49
51:1:227:A:O2'	51:1:228:C:H4'	2.11	0.49
51:1:1686:C:H2'	51:1:1687:G:O4'	2.12	0.49
51:1:1937:A:C2'	51:1:1938:A:H5'	2.41	0.49
51:1:1984:G:H2'	51:1:1985:C:C6	2.47	0.49
51:1:2235:G:H2'	51:1:2236:U:O4'	2.12	0.49
53:3:138:G:H2'	53:3:139:A:C8	2.46	0.49
53:3:579:A:H2'	53:3:580:C:C6	2.47	0.49
53:3:903:G:H2'	53:3:904:U:O4'	2.11	0.49
9:I:131:ILE:HD12	53:3:620:C:C2	2.47	0.49
11:K:17:GLN:O	11:K:21:MET:N	2.44	0.49
14:N:62:LEU:HD12	14:N:64:ILE:HD11	1.92	0.49
14:N:108:ARG:HB3	53:3:1347:G:C8	2.47	0.49
15:O:19:ASP:OD1	15:O:19:ASP:N	2.45	0.49
20:T:27:GLN:HE21	20:T:31:LEU:HG	1.77	0.49
31:f:171:LYS:NZ	51:1:2529:G:OP2	2.40	0.49
34:j:60:ASP:OD1	34:j:60:ASP:N	2.41	0.49
42:r:10:LYS:HE2	51:1:994:C:O2'	2.12	0.49
51:1:198:C:O2'	51:1:199:A:H5'	2.12	0.49
51:1:341:C:H2'	51:1:342:A:C8	2.46	0.49
51:1:864:G:O5'	51:1:864:G:H8	1.95	0.49
51:1:1326:U:H2'	51:1:1327:A:H8	1.77	0.49
51:1:2549:G:H2'	51:1:2550:G:C8	2.47	0.49
52:2:53:A:C2	52:2:54:G:H1'	2.47	0.49
53:3:860:A:H2'	53:3:861:G:O4'	2.12	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
59:B2:9:LYS:HG2	59:B2:1171:ARG:HH12	1.77	0.49
65:0:73:SER:O	65:0:73:SER:OG	2.29	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:0:169:LEU:HD11	65:0:186:VAL:HG13	1.94	0.49
66:h:6:5OH:N	66:h:6:5OH:CS	2.75	0.49
3:C:16:THR:OG1	3:C:17:GLY:N	2.44	0.49
9:I:59:LYS:O	9:I:63:ILE:N	2.44	0.49
15:O:47:GLU:HG3	53:3:1254:A:OP1	2.12	0.49
19:S:9:GLU:HA	19:S:12:ARG:HE	1.76	0.49
22:V:4:ILE:HD11	22:V:61:ARG:HD3	1.94	0.49
30:e:65:LEU:HD22	52:2:42:C:C5	2.47	0.49
35:k:1:MET:HE1	51:1:1664:A:H2	1.77	0.49
41:q:10:ARG:HH11	51:1:1216:G:H5'	1.78	0.49
41:q:62:ALA:O	41:q:66:ALA:N	2.43	0.49
51:1:90:U:H1'	51:1:456:C:H42	1.77	0.49
51:1:376:G:H2'	51:1:377:G:C8	2.47	0.49
51:1:1424:G:H2'	51:1:1425:G:O4'	2.12	0.49
51:1:1620:G:O2'	51:1:1621:U:H5'	2.13	0.49
51:1:1700:A:H2'	51:1:1701:A:H5'	1.93	0.49
51:1:1952:A:H2'	51:1:1953:A:O4'	2.13	0.49
53:3:25:C:H2'	53:3:26:A:H8	1.78	0.49
53:3:128:G:H2'	53:3:129:A:H8	1.76	0.49
53:3:803:G:H2'	53:3:804:U:C6	2.47	0.49
58:B1:275:ARG:HH12	58:B1:278:ARG:NH1	2.09	0.49
58:B1:395:LYS:NZ	58:B1:399:LYS:CD	2.74	0.49
58:B1:1361:THR:OG1	59:B2:1282:GLY:O	2.28	0.49
65:0:92:HIS:CD2	65:0:464:LEU:HD21	2.47	0.49
65:0:128:ARG:HA	65:0:131:ASN:HD22	1.77	0.49
65:0:530:ASN:ND2	65:0:532:LYS:O	2.45	0.49
1:A:36:VAL:HG13	1:A:40:CYS:HB3	1.94	0.49
7:G:71:THR:OG1	7:G:72:LYS:N	2.45	0.49
9:I:12:ARG:HG3	9:I:37:PRO:HG3	1.94	0.49
10:J:79:THR:OG1	10:J:80:LEU:N	2.44	0.49
14:N:72:SER:O	14:N:76:GLY:N	2.45	0.49
36:l:46:VAL:HG21	51:1:832:U:H4'	1.94	0.49
37:m:12:MET:H	37:m:72:PRO:HG2	1.77	0.49
43:s:10:ALA:N	43:s:101:SER:O	2.43	0.49
44:t:58:VAL:HG22	44:t:85:VAL:HG22	1.94	0.49
48:x:7:THR:HG23	48:x:9:LYS:HG3	1.95	0.49
51:1:123:G:H2'	51:1:124:G:H8	1.77	0.49
51:1:739:A:H8	51:1:739:A:O5'	1.95	0.49
53:3:269:C:H2'	53:3:270:A:H8	1.77	0.49
53:3:505:G:H2'	53:3:506:G:C8	2.47	0.49
53:3:1231:G:H2'	53:3:1232:U:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:4:1:A:H2'	54:4:2:U:H6	1.78	0.49
13:M:89:ASP:OD1	13:M:89:ASP:N	2.37	0.49
19:S:1:ALA:N	19:S:66:THR:O	2.45	0.49
36:l:65:GLY:HA2	51:1:631:A:O2'	2.12	0.49
51:1:306:U:H3	51:1:310:A:H62	1.61	0.49
51:1:1937:A:C3'	51:1:1938:A:H5'	2.41	0.49
52:2:49:C:H2'	52:2:50:A:C8	2.48	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'	1.95	0.49
53:3:1382:C:H3'	53:3:1382:C:O2	2.13	0.49
53:3:1489:G:H2'	53:3:1490:U:C6	2.48	0.49
58:B1:683:ILE:HD12	58:B1:754:ILE:HG21	1.93	0.49
59:B2:18:ARG:HE	59:B2:620:ASN:HA	1.77	0.49
9:I:7:LYS:HB3	9:I:20:LEU:HG	1.94	0.49
12:L:34:LYS:HE2	53:3:1290:G:H4'	1.95	0.49
41:q:65:ASN:HD21	41:q:69:ARG:HH11	1.61	0.49
43:s:72:THR:OG1	43:s:73:LYS:N	2.45	0.49
47:w:10:ARG:HD2	51:1:2258:C:OP1	2.12	0.49
48:x:2:ARG:CG	48:x:32:LEU:HD12	2.41	0.49
51:1:210:C:H2'	51:1:211:C:C6	2.48	0.49
51:1:458:G:N2	51:1:469:G:H2'	2.27	0.49
51:1:1366:A:H2'	51:1:1367:A:O4'	2.12	0.49
51:1:1658:C:O5'	51:1:1658:C:H6	1.95	0.49
51:1:1963:U:H2'	51:1:1964:G:H5''	1.93	0.49
53:3:23:C:H2'	53:3:24:U:C6	2.48	0.49
53:3:570:G:H2'	53:3:571:U:O4'	2.11	0.49
53:3:666:G:H5'	53:3:725:G:N2	2.27	0.49
57:A1:18:GLN:HA	57:A1:24:ALA:HA	1.94	0.49
59:B2:565:GLU:HA	59:B2:569:ILE:HG12	1.95	0.49
64:a:46:VAL:HG11	64:a:196:LEU:HD13	1.94	0.49
6:F:1:MET:CG	51:1:2742:G:H5'	2.43	0.49
20:T:88:ARG:HH22	51:1:715:A:H5''	1.76	0.49
25:Y:54:GLN:HE22	53:3:193:C:H1'	1.75	0.49
37:m:18:ARG:O	37:m:97:GLN:NE2	2.46	0.49
51:1:108:G:O2'	51:1:109:C:H5'	2.12	0.49
51:1:1130:U:H5	51:1:2026:U:P	2.35	0.49
51:1:1528:A:H2'	51:1:1529:G:C5'	2.40	0.49
51:1:2194:U:H2'	51:1:2195:U:H6	1.77	0.49
53:3:153:C:C2'	53:3:154:U:H5''	2.43	0.49
31:f:91:VAL:CG2	51:1:2657:A:H4'	2.43	0.49
32:g:80:ILE:HG13	32:g:102:ALA:HB1	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:k:65:THR:HG23	35:k:68:GLY:H	1.78	0.49
38:n:68:ALA:HA	51:1:2707:U:O2'	2.13	0.49
51:1:937:C:H2'	51:1:938:G:H8	1.78	0.49
51:1:1378:A:H1'	51:1:1379:U:C5	2.48	0.49
51:1:2716:C:O2'	51:1:2717:C:H5'	2.13	0.49
51:1:2786:U:H2'	51:1:2787:C:C6	2.48	0.49
53:3:17:U:H2'	53:3:18:C:C6	2.48	0.49
53:3:1424:U:H3	53:3:1476:A:N6	2.05	0.49
58:B1:1179:PRO:HD2	58:B1:1184:ASP:HA	1.93	0.49
3:C:35:LEU:CD2	51:1:2286:G:H22	2.26	0.49
8:H:127:VAL:CG2	59:B2:906:PHE:HA	2.34	0.49
11:K:73:GLU:O	11:K:76:THR:OG1	2.31	0.49
14:N:8:THR:H	14:N:84:ARG:HB2	1.78	0.49
23:W:49:LYS:NZ	53:3:836:G:OP1	2.45	0.49
30:e:132:ARG:NH1	30:e:148:VAL:O	2.46	0.49
34:j:47:HIS:CG	51:1:536:G:H21	2.30	0.49
37:m:61:GLY:HA3	37:m:105:MET:HE1	1.95	0.49
44:t:34:VAL:HG11	44:t:43:ILE:HD13	1.93	0.49
45:u:5:ARG:HH11	51:1:84:A:H5''	1.77	0.49
47:w:65:PHE:CD2	51:1:857:G:H5'	2.48	0.49
51:1:157:C:H2'	51:1:158:U:O4'	2.13	0.49
51:1:664:G:O2'	51:1:940:G:H5''	2.12	0.49
51:1:1289:C:O2'	51:1:1330:C:H4'	2.12	0.49
51:1:1595:C:H2'	51:1:1596:A:C8	2.48	0.49
51:1:2807:U:H3	51:1:2891:U:H3	1.61	0.49
52:2:3:C:C3'	52:2:4:C:H5''	2.42	0.49
53:3:423:G:C2	53:3:424:G:H1'	2.48	0.49
59:B2:529:ARG:HH11	59:B2:572:ILE:HG22	1.77	0.49
65:0:390:ASP:OD1	65:0:390:ASP:N	2.44	0.49
65:0:659:PRO:HB2	65:0:662:GLU:HB2	1.93	0.49
27:b:48:ILE:HG22	51:1:779:U:OP2	2.13	0.49
27:b:155:ARG:CZ	51:1:1818:U:H5	2.26	0.49
33:i:10:LEU:HD11	51:1:1070:A:C2	2.41	0.49
37:m:28:PHE:N	37:m:104:GLU:OE1	2.44	0.49
51:1:1178:C:H2'	51:1:1179:G:C8	2.48	0.49
51:1:1893:C:H2'	51:1:1894:C:O4'	2.13	0.49
51:1:2247:A:H2'	51:1:2248:C:O4'	2.13	0.49
51:1:2600:A:H2'	51:1:2601:C:C6	2.48	0.49
51:1:2638:G:H1'	51:1:2778:A:H61	1.78	0.49
53:3:454:G:H2'	53:3:455:G:H8	1.77	0.49
53:3:955:U:H2'	53:3:956:U:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1349:A:H2'	53:3:1350:A:O4'	2.13	0.49
53:3:1354:U:H2'	53:3:1355:G:H8	1.78	0.49
57:A1:100:LEU:HB2	57:A1:144:ILE:HG23	1.94	0.49
58:B1:102:MET:HG2	58:B1:246:PRO:HD3	1.95	0.49
58:B1:550:VAL:O	58:B1:569:LEU:HA	2.13	0.49
62:5:51:U:H2'	62:5:52:G:C8	2.48	0.49
9:I:32:LYS:HB3	53:3:429:U:OP2	2.12	0.48
17:Q:58:ASN:OD1	17:Q:58:ASN:N	2.46	0.48
30:e:21:TYR:OH	30:e:164:GLU:OE1	2.31	0.48
31:f:8:VAL:O	31:f:49:LEU:N	2.43	0.48
32:g:50:ARG:O	32:g:55:GLU:N	2.38	0.48
51:1:532:A:N1	51:1:2020:A:H1'	2.27	0.48
51:1:1036:G:H1	51:1:1119:U:H3	1.60	0.48
51:1:2364:C:H2'	51:1:2365:G:O4'	2.13	0.48
53:3:83:C:O2'	53:3:84:U:H3'	2.13	0.48
53:3:1253:G:H2'	53:3:1254:A:H8	1.78	0.48
58:B1:124:ILE:HG23	58:B1:128:LEU:HD12	1.94	0.48
59:B2:318:SER:OG	59:B2:320:ASP:OD1	2.31	0.48
63:6:26:G:H3'	63:6:27:U:C5'	2.42	0.48
12:L:78:ARG:NH1	12:L:82:SER:O	2.46	0.48
14:N:87:MET:HA	14:N:90:ASP:HB3	1.94	0.48
14:N:113:LYS:NZ	53:3:1368:A:OP2	2.39	0.48
19:S:96:LYS:HZ3	19:S:97:LYS:H	1.61	0.48
29:d:2:GLU:HA	29:d:13:THR:HA	1.96	0.48
44:t:36:LYS:NZ	44:t:79:ASP:OD1	2.38	0.48
51:1:1807:G:H2'	51:1:1808:A:H5'	1.95	0.48
51:1:1912:A:N7	51:1:1917:U:H5	2.11	0.48
51:1:2803:G:H2'	51:1:2804:U:C6	2.48	0.48
53:3:513:C:H2'	53:3:514:C:O4'	2.13	0.48
58:B1:809:VAL:HG21	58:B1:909:ILE:HG12	1.95	0.48
59:B2:857:VAL:HG13	59:B2:919:ARG:HH21	1.78	0.48
5:E:32:LEU:HD12	5:E:32:LEU:HA	1.73	0.48
27:b:59:GLN:NE2	51:1:1567:G:OP1	2.46	0.48
33:i:75:ALA:HA	33:i:78:LEU:HB2	1.96	0.48
51:1:1005:C:H2'	51:1:1006:C:H6	1.78	0.48
51:1:1999:C:O2'	51:1:2000:C:H5'	2.12	0.48
51:1:2262:U:H2'	51:1:2263:C:H6	1.71	0.48
9:I:12:ARG:NH1	9:I:36:ALA:O	2.46	0.48
17:Q:76:HIS:O	65:0:425:LYS:NZ	2.45	0.48
19:S:19:TYR:HB3	19:S:23:ARG:HH21	1.77	0.48
19:S:75:LYS:HZ1	53:3:1357:A:H5''	1.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:z:30:ARG:HG2	50:z:33:HIS:HB2	1.94	0.48
51:1:93:G:O2'	51:1:94:A:H5'	2.12	0.48
51:1:153:U:O2'	51:1:154:U:H5'	2.13	0.48
51:1:511:U:H2'	51:1:512:G:H5'	1.95	0.48
51:1:1258:U:H2'	51:1:1259:G:C8	2.48	0.48
51:1:2556:C:H2'	51:1:2557:G:H5'	1.96	0.48
53:3:701:U:O4'	53:3:703:G:H1'	2.14	0.48
55:8:3:DC:H2''	55:8:4:DT:C7	2.42	0.48
55:8:14:DC:H2'	55:8:15:DC:H6	1.79	0.48
58:B1:103:GLY:H	58:B1:244:VAL:HG22	1.79	0.48
58:B1:190:LYS:HB2	58:B1:190:LYS:HE3	1.41	0.48
65:0:157:GLN:HE22	65:0:161:ARG:HE	1.61	0.48
65:0:501:VAL:HG11	65:0:604:GLY:CA	2.43	0.48
7:G:100:LEU:HD11	7:G:160:LEU:HD13	1.95	0.48
17:Q:36:VAL:HG13	17:Q:73:LEU:HD11	1.96	0.48
24:X:76:THR:HG21	53:3:1221:G:O2'	2.13	0.48
29:d:23:PHE:H	29:d:114:ARG:HH22	1.60	0.48
31:f:85:LYS:NZ	31:f:129:GLU:OE1	2.41	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
42:r:4:VAL:HG22	42:r:13:ARG:HA	1.95	0.48
51:1:387:U:H4'	51:1:388:G:O4'	2.14	0.48
51:1:404:A:H2	51:1:421:C:N3	2.11	0.48
51:1:445:C:O2	51:1:450:G:H1'	2.14	0.48
51:1:821:A:H5''	51:1:822:G:C8	2.49	0.48
51:1:1810:A:H2'	51:1:1811:G:H5'	1.95	0.48
51:1:2298:A:H2'	51:1:2299:U:O4'	2.13	0.48
51:1:2339:C:H2'	51:1:2340:A:C8	2.45	0.48
51:1:2810:A:H62	51:1:2890:G:N2	2.11	0.48
53:3:554:A:C2'	53:3:555:U:H5'	2.43	0.48
58:B1:115:TRP:O	58:B1:1333:THR:HG21	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
4:D:3:ARG:O	4:D:6:GLN:NE2	2.40	0.48
11:K:91:ARG:O	11:K:93:LYS:NZ	2.39	0.48
41:q:84:LYS:HB3	41:q:115:ALA:HB1	1.94	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
51:1:1657:U:H2'	51:1:1658:C:C6	2.48	0.48
51:1:2834:G:H2'	51:1:2879:A:N6	2.29	0.48
53:3:714:G:H2'	53:3:715:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
57:A1:182:ARG:O	57:A1:205:MET:HA	2.14	0.48
58:B1:968:ASN:HA	58:B1:1117:SER:HB2	1.96	0.48
58:B1:1261:LEU:HD12	58:B1:1304:ARG:HH21	1.78	0.48
65:0:530:ASN:HD22	65:0:532:LYS:HB2	1.79	0.48
1:A:26:SER:OG	1:A:27:THR:N	2.47	0.48
15:O:15:HIS:HA	15:O:18:ILE:HG22	1.96	0.48
22:V:11:VAL:HA	22:V:22:VAL:HA	1.95	0.48
24:X:32:THR:O	24:X:56:HIS:NE2	2.45	0.48
27:b:146:LYS:HB2	27:b:149:LYS:HB2	1.94	0.48
32:g:71:LYS:HD3	32:g:71:LYS:HA	1.66	0.48
37:m:65:ILE:HG22	37:m:67:VAL:H	1.78	0.48
37:m:111:GLU:HA	37:m:114:ARG:HB3	1.96	0.48
51:1:175:G:H2'	51:1:176:A:C8	2.49	0.48
51:1:443:A:H2	51:1:1246:A:H1'	1.78	0.48
51:1:445:C:H2'	51:1:446:G:H5'	1.94	0.48
51:1:999:U:H5''	51:1:1154:G:O6	2.13	0.48
51:1:2314:A:H2'	51:1:2315:G:C8	2.48	0.48
53:3:483:C:H3'	53:3:484:G:H5'	1.94	0.48
53:3:1414:U:H2'	53:3:1415:G:H8	1.79	0.48
58:B1:145:VAL:HG12	58:B1:184:ALA:HB1	1.94	0.48
58:B1:201:LEU:HD11	58:B1:220:ARG:HG2	1.95	0.48
59:B2:411:ARG:NH2	59:B2:427:ASP:OD2	2.44	0.48
65:0:99:VAL:HG11	65:0:126:VAL:HG12	1.95	0.48
22:V:56:ASP:HB3	22:V:80:LYS:HA	1.94	0.48
29:d:67:ARG:NH2	51:1:1257:C:H5''	2.29	0.48
34:j:7:LYS:HE2	51:1:539:G:H5'	1.95	0.48
35:k:65:THR:OG1	35:k:66:LYS:N	2.44	0.48
48:x:4:CYS:SG	48:x:5:GLN:N	2.86	0.48
51:1:80:G:H2'	51:1:81:G:C8	2.49	0.48
51:1:459:U:H2'	51:1:460:A:O4'	2.13	0.48
51:1:1018:U:H2'	51:1:1019:U:O4'	2.13	0.48
51:1:1103:A:H2'	51:1:1103:A:N3	2.29	0.48
51:1:1219:U:H2'	51:1:1220:G:H8	1.78	0.48
51:1:2828:G:O2'	51:1:2829:A:H5'	2.13	0.48
53:3:770:C:O2'	53:3:771:G:H5'	2.12	0.48
53:3:792:A:H4'	53:3:793:U:H5''	1.95	0.48
57:A1:33:ARG:HE	57:A1:33:ARG:HB3	1.56	0.48
57:A2:102:LEU:HD12	57:A2:115:ILE:HG12	1.96	0.48
58:B1:255:LEU:HD23	58:B1:261:ALA:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:487:LEU:HD22	59:B2:487:LEU:HA	1.77	0.48
63:6:36:U:H2'	63:6:37:A:C8	2.48	0.48
9:I:37:PRO:HD2	9:I:41:GLY:HA3	1.96	0.48
10:J:23:THR:HG21	53:3:15:G:N3	2.29	0.48
10:J:24:VAL:HG13	10:J:26:GLY:H	1.79	0.48
10:J:87:VAL:HA	10:J:92:ARG:HA	1.96	0.48
11:K:92:THR:OG1	11:K:94:HIS:O	2.29	0.48
23:W:32:ILE:HD12	23:W:36:GLY:HA2	1.95	0.48
28:c:134:HIS:CD2	51:1:1675:C:H42	2.32	0.48
36:l:41:ARG:HG2	51:1:806:C:H41	1.78	0.48
41:q:24:TYR:N	51:1:533:G:OP1	2.38	0.48
51:1:1710:G:H2'	51:1:1711:A:C8	2.49	0.48
51:1:1993:U:H2'	51:1:1994:C:O4'	2.14	0.48
53:3:27:G:H2'	53:3:28:A:C8	2.49	0.48
53:3:153:C:H2'	53:3:154:U:H5''	1.95	0.48
53:3:316:C:H2'	53:3:317:U:H6	1.79	0.48
53:3:563:A:H5'	53:3:566:G:C2	2.49	0.48
55:8:14:DC:H2'	55:8:15:DC:C6	2.48	0.48
58:B1:86:GLU:O	58:B1:87:LYS:C	2.57	0.48
58:B1:1036:ARG:HE	58:B1:1081:VAL:HG11	1.79	0.48
16:P:83:VAL:HG11	16:P:96:ILE:HG12	1.95	0.48
20:T:19:ASN:HB2	53:3:750:C:C4'	2.43	0.48
28:c:8:LYS:HB2	28:c:201:LEU:HD11	1.96	0.48
40:p:1:SER:N	51:1:2876:G:OP1	2.44	0.48
51:1:189:G:N2	51:1:206:U:C5	2.82	0.48
51:1:319:G:H2'	51:1:320:A:O4'	2.13	0.48
51:1:1225:G:O2'	51:1:1226:A:H5'	2.13	0.48
51:1:1343:G:N3	51:1:1343:G:H2'	2.28	0.48
51:1:2654:A:H8	51:1:2654:A:OP1	1.97	0.48
52:2:45:A:H2'	52:2:46:A:O4'	2.13	0.48
53:3:483:C:C3'	53:3:484:G:H5'	2.44	0.48
53:3:865:A:H8	53:3:865:A:O5'	1.96	0.48
53:3:1274:A:H2'	53:3:1275:A:H5''	1.96	0.48
53:3:1465:A:H2'	53:3:1466:C:C6	2.48	0.48
53:3:1491:G:C2	66:h:2:DPP:HB3	2.49	0.48
21:U:8:ARG:NH1	53:3:391:G:H5''	2.29	0.47
33:i:9:LYS:HZ2	51:1:1059:G:P	2.36	0.47
33:i:65:SER:OG	33:i:66:PHE:N	2.46	0.47
34:j:49:ASP:N	34:j:49:ASP:OD1	2.39	0.47
37:m:22:GLN:HE21	51:1:864:G:P	2.36	0.47
51:1:367:G:H2'	51:1:368:A:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1414:C:H2'	51:1:1415:U:H5'	1.95	0.47
51:1:2257:U:O2'	51:1:2258:C:H5'	2.14	0.47
51:1:2884:U:O2	51:1:2884:U:H3'	2.14	0.47
53:3:193:C:H2'	53:3:194:C:C5	2.49	0.47
58:B1:833:GLU:N	58:B1:1242:ARG:HH12	2.12	0.47
59:B2:363:LEU:HB3	59:B2:381:ALA:HB1	1.96	0.47
65:0:498:VAL:HG22	65:0:499:THR:H	1.79	0.47
3:C:5:ARG:NH2	3:C:23:THR:O	2.48	0.47
7:G:18:GLN:NE2	7:G:189:ASN:HB3	2.30	0.47
17:Q:87:LYS:HB3	17:Q:87:LYS:HE3	1.69	0.47
20:T:74:VAL:HA	20:T:77:TYR:HB3	1.96	0.47
25:Y:34:VAL:HG22	25:Y:49:ALA:HB1	1.95	0.47
31:f:84:LYS:HD2	31:f:84:LYS:HA	1.78	0.47
37:m:42:THR:N	37:m:45:GLN:OE1	2.40	0.47
45:u:8:ASP:O	45:u:23:LYS:NZ	2.45	0.47
47:w:45:ALA:N	47:w:77:SER:OG	2.42	0.47
49:y:43:LEU:HD21	49:y:47:ARG:HH11	1.79	0.47
51:1:166:U:H2'	51:1:167:A:H8	1.78	0.47
51:1:833:A:H2'	51:1:834:G:H8	1.78	0.47
51:1:1463:C:H2'	51:1:1464:G:C8	2.48	0.47
51:1:2276:G:C2'	51:1:2277:G:H5'	2.44	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
58:B1:1060:VAL:HG13	58:B1:1106:ILE:HG12	1.96	0.47
58:B1:1347:LEU:HG	58:B1:1357:ILE:HG23	1.96	0.47
59:B2:836:LEU:HD13	59:B2:1054:LEU:HD13	1.95	0.47
65:0:22:GLY:N	67:0:801:GDP:O1B	2.47	0.47
18:R:27:THR:HG22	53:3:1328:C:H5''	1.96	0.47
19:S:12:ARG:HH22	19:S:60:ARG:H	1.61	0.47
36:l:30:THR:O	36:l:33:ARG:N	2.46	0.47
36:l:42:SER:O	36:l:42:SER:OG	2.32	0.47
36:l:43:GLY:N	51:1:671:C:OP1	2.47	0.47
38:n:34:ILE:HA	51:1:1279:G:OP1	2.13	0.47
51:1:118:A:H5'	51:1:119:A:H8	1.79	0.47
51:1:881:G:H1	51:1:895:U:H3	1.61	0.47
51:1:1414:C:H42	51:1:1588:G:H1	1.62	0.47
51:1:1924:C:H3'	51:1:1925:C:C5	2.49	0.47
51:1:2515:C:O2'	51:1:2516:A:H5'	2.15	0.47
51:1:2531:A:H2'	51:1:2532:G:H5'	1.95	0.47
51:1:2813:A:H2'	51:1:2814:A:H8	1.78	0.47
53:3:129:A:O2'	53:3:130:A:H5''	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:631:C:H5''	53:3:632:U:O4'	2.15	0.47
53:3:1268:G:H21	53:3:1327:C:H1'	1.79	0.47
58:B1:1146:GLU:OE2	58:B1:1310:THR:HG22	2.14	0.47
59:B2:1311:GLY:O	60:W0:31:GLN:NE2	2.47	0.47
65:0:319:ALA:HB3	65:0:397:LEU:HB2	1.96	0.47
65:0:422:PRO:HG3	65:0:428:GLN:HB2	1.97	0.47
2:B:2:VAL:O	51:1:2615:U:C4	2.67	0.47
5:E:57:VAL:O	5:E:61:LEU:N	2.41	0.47
10:J:83:PRO:HD3	10:J:97:PRO:HG3	1.96	0.47
24:X:39:ILE:HD11	24:X:70:LEU:HD23	1.96	0.47
30:e:31:GLU:HG2	30:e:32:LYS:H	1.80	0.47
31:f:107:GLY:O	51:1:2666:C:N4	2.47	0.47
35:k:89:ASN:OD1	35:k:89:ASN:N	2.45	0.47
50:z:18:LYS:O	50:z:22:THR:OG1	2.31	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
51:1:1680:U:H2'	51:1:1681:G:C5'	2.40	0.47
51:1:2143:C:H3'	51:1:2144:G:C8	2.49	0.47
51:1:2316:G:O2'	51:1:2317:A:H5'	2.14	0.47
51:1:2521:C:H42	51:1:2544:G:H1	1.62	0.47
51:1:2721:A:H2'	51:1:2722:G:O4'	2.14	0.47
52:2:30:C:H2'	52:2:31:C:H5'	1.95	0.47
53:3:92:U:H2'	53:3:93:U:H5'	1.96	0.47
53:3:751:U:C2'	53:3:752:G:H5'	2.44	0.47
53:3:1015:G:H2'	53:3:1016:A:O4'	2.14	0.47
65:0:330:VAL:HG11	65:0:386:ILE:HD11	1.96	0.47
3:C:6:GLU:HG2	3:C:26:LYS:HD3	1.96	0.47
3:C:8:ILE:HD11	3:C:50:GLU:HB2	1.96	0.47
4:D:24:THR:HG23	4:D:27:GLY:H	1.78	0.47
7:G:66:ILE:HD11	7:G:161:PHE:HB2	1.96	0.47
11:K:86:ARG:NH2	53:3:673:A:O3'	2.48	0.47
27:b:15:VAL:HB	27:b:205:GLY:HA3	1.95	0.47
29:d:178:VAL:HA	29:d:181:ILE:HG22	1.95	0.47
34:j:47:HIS:CD2	51:1:536:G:H21	2.32	0.47
34:j:116:ARG:HH22	51:1:528:A:H8	1.60	0.47
37:m:22:GLN:NE2	51:1:864:G:OP1	2.47	0.47
46:v:21:ARG:HH12	52:2:77:U:H5''	1.80	0.47
51:1:145:C:H2'	51:1:146:A:C8	2.49	0.47
51:1:215:G:O3'	51:1:216:A:H4'	2.15	0.47
51:1:514:A:N3	51:1:581:C:O2'	2.45	0.47
51:1:858:G:H5'	51:1:859:G:OP2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1085:A:H2'	51:1:1086:A:N7	2.30	0.47
51:1:1810:A:C2'	51:1:1811:G:H5'	2.44	0.47
51:1:1900:A:H5'	51:1:1970:A:H5'	1.96	0.47
53:3:840:C:C2'	53:3:841:C:H5''	2.41	0.47
53:3:1000:A:H2'	53:3:1001:C:O4'	2.15	0.47
53:3:1465:A:H2'	53:3:1466:C:H6	1.80	0.47
58:B1:141:PHE:CE2	58:B1:296:LYS:CB	2.94	0.47
58:B1:220:ARG:HG2	58:B1:220:ARG:NH1	2.26	0.47
58:B1:395:LYS:NZ	58:B1:399:LYS:CE	2.78	0.47
58:B1:526:VAL:HG12	58:B1:549:LYS:HB2	1.96	0.47
59:B2:1314:GLN:HB2	60:W0:28:ARG:HH12	1.79	0.47
8:H:30:ASP:OD1	8:H:30:ASP:N	2.47	0.47
12:L:91:ARG:HG2	12:L:91:ARG:HH11	1.78	0.47
13:M:4:ASP:OD2	13:M:76:ARG:NH2	2.47	0.47
15:O:64:GLN:HB3	19:S:98:ALA:HB3	1.96	0.47
36:l:18:ARG:NE	51:1:1249:U:C5	2.79	0.47
51:1:593:U:H2'	51:1:594:U:C6	2.49	0.47
51:1:1587:G:H2'	51:1:1588:G:C8	2.50	0.47
51:1:1943:U:OP1	51:1:1943:U:H6	1.98	0.47
51:1:2475:C:H2'	51:1:2476:A:H5'	1.97	0.47
53:3:1059:C:H2'	53:3:1060:U:C6	2.49	0.47
53:3:1161:C:H2'	53:3:1162:C:H6	1.78	0.47
59:B2:732:ILE:HD11	59:B2:769:PRO:HB3	1.95	0.47
7:G:17:HIS:CE1	7:G:187:ASP:HB2	2.50	0.47
8:H:147:GLY:HA2	8:H:170:GLY:HA3	1.97	0.47
15:O:21:ALA:HB2	15:O:93:ALA:HB2	1.97	0.47
27:b:158:GLY:HA3	51:1:1820:U:C5	2.49	0.47
27:b:240:GLY:HA2	51:1:2597:G:H5''	1.97	0.47
29:d:112:LEU:O	29:d:117:ARG:N	2.43	0.47
30:e:22:ASN:ND2	30:e:26:GLN:OE1	2.48	0.47
42:r:80:ARG:HD3	51:1:566:U:H5	1.80	0.47
43:s:47:VAL:O	43:s:51:LEU:N	2.39	0.47
44:t:67:VAL:HG12	44:t:76:ARG:HA	1.96	0.47
44:t:89:GLU:OE1	44:t:91:GLN:NE2	2.48	0.47
47:w:56:PHE:HE2	51:1:2365:G:H5'	1.80	0.47
51:1:680:C:H42	51:1:797:G:H1	1.63	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
51:1:1265:A:N6	51:1:2013:A:H5''	2.27	0.47
51:1:2153:C:H3'	51:1:2154:A:H8	1.78	0.47
53:3:138:G:H2'	53:3:139:A:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
53:3:343:U:O2'	53:3:344:A:H2'	2.14	0.47
53:3:344:A:OP1	65:0:38:HIS:NE2	2.48	0.47
53:3:1093:A:H2'	53:3:1094:G:H5'	1.96	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
53:3:1382:C:H2'	53:3:1383:C:C6	2.50	0.47
53:3:1486:G:H2'	53:3:1487:G:O4'	2.15	0.47
58:B1:29:MET:HG2	59:B2:1336:ASN:ND2	2.29	0.47
58:B1:198:CYS:HA	58:B1:221:ILE:CD1	2.45	0.47
58:B1:352:ARG:CD	59:B2:1268:GLN:NE2	2.67	0.47
59:B2:207:THR:OG1	59:B2:354:ASP:OD2	2.32	0.47
65:0:494:ILE:HG21	65:0:605:PHE:CD1	2.50	0.47
1:A:8:LYS:NZ	1:A:10:GLU:OE1	2.45	0.47
2:B:37:HIS:HB3	2:B:43:THR:HG22	1.97	0.47
18:R:23:GLY:HA2	18:R:68:LEU:HD13	1.97	0.47
19:S:41:TRP:HZ2	24:X:10:ILE:HG22	1.79	0.47
25:Y:76:ALA:O	25:Y:79:THR:OG1	2.27	0.47
36:l:109:LYS:HB3	51:1:636:G:O6	2.15	0.47
51:1:744:U:H5''	51:1:1658:C:H5''	1.96	0.47
51:1:1595:C:H2'	51:1:1596:A:H8	1.79	0.47
51:1:2248:C:C2'	51:1:2249:U:H5'	2.45	0.47
51:1:2682:A:O2'	51:1:2683:C:H5'	2.15	0.47
53:3:1435:G:H1	53:3:1466:C:H42	1.63	0.47
53:3:1478:U:H2'	53:3:1479:C:C6	2.49	0.47
58:B1:891:ASP:OD2	58:B1:1290:ARG:NH2	2.47	0.47
62:5:50:U:H2'	62:5:51:U:C6	2.49	0.47
63:6:62:C:H5'	64:a:53:ARG:CZ	2.45	0.47
65:0:24:THR:HG21	65:0:62:THR:HG21	1.97	0.47
8:H:32:LEU:HD21	19:S:78:LEU:HD11	1.97	0.47
13:M:63:LYS:HG2	13:M:70:VAL:HG21	1.95	0.47
27:b:210:ALA:HA	27:b:213:ARG:HG3	1.96	0.47
28:c:55:LYS:HG3	28:c:77:ARG:HB3	1.97	0.47
28:c:119:ALA:C	51:1:1655:A:H4'	2.40	0.47
51:1:524:G:O2'	51:1:525:U:H5'	2.14	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
53:3:857:C:H2'	53:3:858:G:O4'	2.14	0.47
53:3:1441:A:N3	53:3:1441:A:H2'	2.30	0.47
58:B1:128:LEU:HD21	58:B1:188:LEU:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:375:GLU:HB3	59:B2:1245:ALA:HB3	1.97	0.47
58:B1:770:LEU:CD1	59:B2:618:GLN:HG3	2.36	0.47
58:B1:1221:LEU:HD22	58:B1:1306:LEU:HB2	1.96	0.47
65:0:420:VAL:HB	65:0:458:ILE:HD11	1.97	0.47
13:M:102:VAL:HB	13:M:126:CYS:HB3	1.96	0.47
16:P:23:HIS:HB3	16:P:30:ILE:HG23	1.96	0.47
33:i:47:SER:O	33:i:47:SER:OG	2.31	0.47
51:1:696:G:O2'	51:1:697:G:H5'	2.15	0.47
51:1:1333:G:H2'	51:1:1334:G:C8	2.49	0.47
51:1:1663:G:O2'	51:1:1664:A:H8	1.98	0.47
51:1:1868:C:C2'	51:1:1869:G:H5'	2.42	0.47
53:3:325:A:H2'	53:3:326:G:O4'	2.14	0.47
53:3:545:C:O2'	53:3:546:A:H5'	2.14	0.47
57:A1:35:PHE:HA	57:A1:38:THR:HG22	1.97	0.47
58:B1:43:THR:HG22	58:B1:57:PHE:HE1	1.80	0.47
58:B1:1027:VAL:HB	58:B1:1121:LEU:HB2	1.96	0.47
58:B1:1357:ILE:HD13	59:B2:1279:GLU:HG2	1.97	0.47
59:B2:800:MET:HB2	59:B2:800:MET:HE3	1.69	0.47
7:G:53:LEU:HA	7:G:56:LEU:HB2	1.97	0.46
8:H:39:ARG:HA	8:H:42:LEU:HB3	1.97	0.46
18:R:53:ASP:OD1	18:R:53:ASP:N	2.48	0.46
27:b:250:GLN:HB3	27:b:254:LYS:HD2	1.96	0.46
29:d:173:THR:OG1	29:d:174:GLY:N	2.48	0.46
32:g:68:ARG:O	32:g:72:ILE:N	2.48	0.46
32:g:93:SER:HB3	32:g:121:VAL:HG12	1.97	0.46
51:1:233:A:H5'	51:1:233:A:C8	2.50	0.46
51:1:940:G:H2'	51:1:941:A:H5''	1.97	0.46
51:1:1306:C:O2'	51:1:1307:A:H5'	2.13	0.46
51:1:1580:A:H2'	51:1:1581:G:O4'	2.14	0.46
51:1:2531:A:C2'	51:1:2532:G:H5'	2.45	0.46
51:1:2845:U:H2'	51:1:2846:G:C8	2.50	0.46
52:2:116:G:O2'	52:2:117:G:H5'	2.15	0.46
53:3:520:A:H62	53:3:529:G:N2	2.11	0.46
58:B1:1219:ASP:O	58:B1:1223:LEU:HB2	2.16	0.46
5:E:7:ARG:NH2	51:1:245:G:N7	2.63	0.46
12:L:66:GLU:HA	12:L:69:ARG:HG3	1.96	0.46
17:Q:11:ARG:NH1	53:3:563:A:H2	2.13	0.46
17:Q:83:GLY:H	53:3:552:U:H4'	1.80	0.46
25:Y:22:SER:HB2	53:3:1458:G:H4'	1.98	0.46
27:b:86:ARG:HB3	27:b:88:ALA:H	1.80	0.46
31:f:88:LEU:O	31:f:128:THR:OG1	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:k:31:ARG:HH12	51:1:2676:C:P	2.38	0.46
37:m:43:ALA:HB2	37:m:69:PRO:HG3	1.96	0.46
46:v:13:GLY:N	52:2:76:G:OP1	2.39	0.46
51:1:340:A:C2'	51:1:341:C:H5'	2.43	0.46
51:1:341:C:H2'	51:1:342:A:H8	1.79	0.46
51:1:1136:G:H2'	51:1:1137:G:H8	1.80	0.46
51:1:1826:G:H2'	51:1:1827:U:C6	2.50	0.46
51:1:2080:A:C6	51:1:2081:U:C4	3.04	0.46
51:1:2861:U:O2'	51:1:2862:G:H5'	2.15	0.46
58:B1:1150:PRO:HG3	58:B1:1214:PRO:HB2	1.96	0.46
62:5:29:G:H3'	62:5:30:G:C8	2.50	0.46
12:L:91:ARG:HG2	12:L:91:ARG:NH1	2.30	0.46
12:L:101:ARG:HH22	53:3:940:C:P	2.37	0.46
25:Y:79:THR:HA	25:Y:82:ILE:HB	1.98	0.46
33:i:79:LEU:HD22	33:i:131:THR:HG23	1.97	0.46
51:1:435:C:H2'	51:1:436:C:C5'	2.37	0.46
51:1:742:A:O2'	51:1:743:A:H5'	2.15	0.46
51:1:1388:G:H2'	51:1:1389:G:C8	2.50	0.46
51:1:1639:C:H2'	51:1:1640:A:H5'	1.98	0.46
51:1:2134:A:C5	51:1:2157:G:H4'	2.51	0.46
51:1:2135:A:H8	51:1:2156:G:H21	1.64	0.46
52:2:51:G:N3	52:2:52:A:H1'	2.30	0.46
53:3:835:U:C3'	53:3:836:G:H5''	2.46	0.46
54:4:1:A:H2'	54:4:2:U:C6	2.50	0.46
59:B2:103:VAL:HG12	59:B2:117:ILE:HG22	1.97	0.46
59:B2:689:ALA:HB2	59:B2:1233:LEU:HD23	1.97	0.46
65:0:376:GLU:OE1	65:0:378:ARG:NE	2.48	0.46
65:0:474:LYS:HD3	65:0:474:LYS:HA	1.72	0.46
9:I:140:ASP:O	9:I:181:PHE:N	2.46	0.46
11:K:18:VAL:HG13	11:K:19:PRO:HD3	1.97	0.46
51:1:139:U:H2'	51:1:140:C:C5	2.49	0.46
51:1:141:G:C8	51:1:142:A:H1'	2.51	0.46
51:1:175:G:H2'	51:1:176:A:H8	1.81	0.46
51:1:433:C:O2'	51:1:434:U:H5'	2.15	0.46
51:1:912:C:O2'	51:1:913:U:H5'	2.15	0.46
51:1:1790:C:H2'	51:1:1791:A:C5	2.51	0.46
51:1:1933:G:H2'	51:1:1934:C:H6	1.80	0.46
51:1:2491:U:C2'	51:1:2492:U:H5'	2.41	0.46
53:3:250:A:O4'	53:3:252:U:H1'	2.15	0.46
58:B1:105:ILE:HD12	58:B1:242:LEU:CD2	2.44	0.46
58:B1:209:ASN:HA	58:B1:214:ARG:NH2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:420:PRO:HA	58:B1:437:PHE:O	2.15	0.46
62:5:8:U:H2'	62:5:13:C:N4	2.30	0.46
62:5:26:A:H61	62:5:44:G:H22	1.64	0.46
2:B:14:MET:HG2	51:1:15:G:O2'	2.16	0.46
8:H:2:GLN:NE2	53:3:1062:U:O4	2.48	0.46
8:H:51:VAL:HA	8:H:69:THR:HA	1.97	0.46
11:K:53:LYS:HD3	11:K:53:LYS:HA	1.75	0.46
28:c:49:GLN:HE21	28:c:79:LEU:HB3	1.79	0.46
33:i:9:LYS:HZ3	51:1:1059:G:H5'	1.80	0.46
46:v:7:GLU:HG3	46:v:41:GLU:HB3	1.97	0.46
48:x:16:ASN:HB2	48:x:24:THR:HB	1.97	0.46
51:1:690:G:H2'	51:1:691:C:H5'	1.98	0.46
51:1:786:C:O2'	51:1:787:C:H5'	2.16	0.46
51:1:1321:A:C2	51:1:1322:A:H1'	2.50	0.46
51:1:1485:U:H2'	51:1:1486:U:C6	2.50	0.46
51:1:2450:A:OP1	51:1:2497:A:O2'	2.31	0.46
51:1:2741:A:H61	51:1:2763:G:H1'	1.80	0.46
51:1:2751:G:O2'	51:1:2752:C:H5'	2.16	0.46
53:3:211:G:H3'	53:3:211:G:N3	2.29	0.46
53:3:994:A:H3'	53:3:994:A:OP2	2.15	0.46
58:B1:352:ARG:HB2	59:B2:1268:GLN:NE2	2.30	0.46
58:B1:1167:LYS:NZ	58:B1:1170:LYS:HB2	2.30	0.46
65:0:463:GLU:O	65:0:467:ASP:N	2.42	0.46
6:F:15:LYS:N	6:F:26:ILE:O	2.40	0.46
14:N:72:SER:HA	14:N:75:ALA:HB3	1.98	0.46
19:S:55:SER:OG	19:S:57:SER:OG	2.30	0.46
31:f:85:LYS:HE2	31:f:129:GLU:HB3	1.97	0.46
31:f:91:VAL:HG21	51:1:2657:A:H4'	1.97	0.46
45:u:88:ASP:OD1	45:u:88:ASP:N	2.47	0.46
51:1:820:A:O2'	51:1:821:A:H5'	2.15	0.46
51:1:824:U:H2'	51:1:825:A:O4'	2.15	0.46
51:1:1196:C:O2'	51:1:1197:G:H5'	2.15	0.46
51:1:2259:U:C6	51:1:2427:C:C5	3.04	0.46
51:1:2537:U:H2'	51:1:2538:C:H6	1.78	0.46
53:3:131:A:H2'	53:3:132:C:C6	2.51	0.46
53:3:859:G:O2'	53:3:860:A: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:B1:772:TYR:HE2	59:B2:561:ILE:HG21	1.80	0.46
59:B2:1314:GLN:HA	60:W0:28:ARG:HH22	1.80	0.46
65:0:136:PRO:HB3	65:0:256:VAL:HG12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:135:ARG:NH1	59:B2:902:LEU:HG	2.31	0.46
9:I:103:ARG:HD2	9:I:167:PRO:HG3	1.97	0.46
14:N:40:ARG:NE	53:3:1292:G:H5'	2.31	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
33:i:7:TYR:CE1	51:1:1058:U:H5'	2.50	0.46
33:i:94:LYS:HD3	33:i:94:LYS:HA	1.72	0.46
39:o:6:ALA:HA	39:o:9:ARG:HE	1.81	0.46
51:1:365:U:H2'	51:1:366:C:O4'	2.16	0.46
51:1:704:G:N3	51:1:726:G:C2	2.84	0.46
51:1:1313:U:O2	51:1:1313:U:C2'	2.64	0.46
51:1:1470:A:N6	51:1:1521:G:H1'	2.31	0.46
51:1:1569:A:H2'	51:1:1570:A:C8	2.51	0.46
51:1:1642:G:O2'	51:1:1643:G:H5'	2.15	0.46
51:1:1661:G:O2'	51:1:1662:U:H5'	2.16	0.46
53:3:528:C:H4'	53:3:535:A:C6	2.51	0.46
58:B1:108:ALA:HB1	58:B1:279:LEU:HD22	1.96	0.46
58:B1:343:LEU:HD11	58:B1:1324:SER:HB3	1.98	0.46
58:B1:842:ARG:HH22	58:B1:1250:ASP:HB2	1.80	0.46
59:B2:1286:THR:O	59:B2:1290:MET:HB2	2.14	0.46
62:5:8:U:H2'	62:5:13:C:H41	1.81	0.46
64:a:193:LEU:O	64:a:197:LYS:N	2.42	0.46
65:0:369:ASN:OD1	65:0:369:ASN:N	2.48	0.46
15:O:36:VAL:HG22	15:O:38:GLY:H	1.80	0.46
15:O:36:VAL:HA	15:O:76:ILE:HA	1.97	0.46
16:P:97:ARG:HA	16:P:100:ASN:HD22	1.81	0.46
20:T:50:HIS:ND1	53:3:667:G:H4'	2.31	0.46
43:s:82:MET:HE1	51:1:1322:A:H4'	1.97	0.46
51:1:393:C:H2'	51:1:394:C:H6	1.81	0.46
51:1:1572:A:O2'	51:1:1573:G:H5'	2.15	0.46
51:1:1614:A:C2'	51:1:1615:C:H5'	2.46	0.46
51:1:1695:G:H2'	51:1:1696:G:O4'	2.15	0.46
51:1:1842:G:O2'	51:1:1843:C:H5'	2.15	0.46
51:1:1858:A:N6	51:1:1884:G:O2'	2.48	0.46
51:1:2695:U:H2'	51:1:2696:U:C6	2.51	0.46
52:2:118:C:C2'	52:2:119:A:H4'	2.33	0.46
53:3:10:A:H2'	53:3:11:G:C8	2.51	0.46
53:3:144:G:H2'	53:3:145:G:O4'	2.16	0.46
53:3:556:C:O2'	53:3:557:G:H5'	2.16	0.46
53:3:962:C:H1'	53:3:1201:A:C6	2.51	0.46
53:3:1018:G:O2'	53:3:1019:A:H5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1260:G:H4'	53:3:1284:C:H5'	1.98	0.46
59:B2:872:TYR:HA	59:B2:944:ARG:HH22	1.81	0.46
59:B2:1002:LEU:HD21	59:B2:1007:LYS:HB2	1.98	0.46
60:W0:25:ARG:NH1	60:W0:61:ASN:OD1	2.49	0.46
62:5:70:G:H2'	62:5:71:G:C8	2.51	0.46
4:D:1:MET:HE3	4:D:3:ARG:HH21	1.80	0.46
8:H:49:ALA:O	8:H:69:THR:OG1	2.34	0.46
10:J:156:ARG:NH1	13:M:98:LEU:O	2.49	0.46
12:L:79:VAL:O	12:L:79:VAL:HG12	2.16	0.46
14:N:30:ASN:N	14:N:64:ILE:O	2.48	0.46
16:P:115:ILE:HD12	16:P:116:PRO:HD2	1.98	0.46
25:Y:60:GLN:HA	25:Y:63:LYS:HD2	1.98	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
49:y:10:SER:HA	49:y:13:GLU:HB3	1.98	0.46
51:1:441:U:H2'	51:1:442:G:H8	1.81	0.46
51:1:2099:U:H2'	51:1:2100:G:C8	2.51	0.46
51:1:2643:G:O2'	51:1:2644:G:H5'	2.16	0.46
53:3:113:G:O2'	53:3:353:A:H4'	2.16	0.46
53:3:271:C:H2'	53:3:272:C:C6	2.51	0.46
53:3:1361:G:H2'	53:3:1362:A:O4'	2.16	0.46
55:8:13:DT:C6	58:B1:791:ALA:HA	2.51	0.46
57:A2:64:VAL:HG11	57:A2:78:ILE:HG21	1.97	0.46
59:B2:400:VAL:HG22	59:B2:584:TYR:HB3	1.96	0.46
65:0:533:GLY:HA3	65:0:572:VAL:HG22	1.97	0.46
7:G:132:GLU:OE2	7:G:136:ARG:NE	2.47	0.46
17:Q:120:ARG:HG2	53:3:37:U:C5'	2.46	0.46
20:T:80:LEU:O	20:T:84:LEU:N	2.42	0.46
21:U:4:ILE:HD13	21:U:21:VAL:HA	1.99	0.46
27:b:6:LYS:HD2	27:b:7:PRO:HD2	1.98	0.46
27:b:155:ARG:CZ	51:1:1818:U:C5	2.99	0.46
29:d:123:LYS:HE2	29:d:123:LYS:HB3	1.80	0.46
32:g:30:LEU:HA	32:g:35:LYS:HE3	1.97	0.46
33:i:52:LEU:HD13	33:i:77:VAL:HG13	1.97	0.46
41:q:36:GLN:OE1	51:1:1252:G:N2	2.38	0.46
51:1:107:G:H2'	51:1:108:G:C8	2.51	0.46
51:1:191:A:H2'	51:1:192:C:H6	1.81	0.46
53:3:973:G:H2'	53:3:974:A:C8	2.52	0.46
53:3:1121:U:H2'	53:3:1122:U:C6	2.51	0.46
59:B2:24:VAL:HG11	59:B2:704:MET:HE1	1.98	0.46
65:0:15:ILE:O	65:0:89:THR:OG1	2.35	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:0:618:LYS:N	65:0:683:GLU:O	2.49	0.46
1:A:9:TYR:HE1	30:e:61:GLY:H	1.63	0.45
3:C:35:LEU:HD21	51:1:2286:G:H22	1.81	0.45
15:O:47:GLU:OE2	15:O:69:THR:OG1	2.29	0.45
27:b:107:LYS:N	27:b:193:GLU:O	2.49	0.45
28:c:61:THR:HB	28:c:63:PRO:HD2	1.96	0.45
32:g:94:ILE:HD12	32:g:99:ILE:HG21	1.98	0.45
34:j:7:LYS:HG2	34:j:10:THR:HG23	1.97	0.45
34:j:57:LEU:HD11	34:j:130:HIS:HD2	1.82	0.45
43:s:82:MET:HB2	43:s:98:LYS:HB2	1.97	0.45
45:u:5:ARG:NH1	51:1:84:A:H5''	2.31	0.45
51:1:864:G:H2'	51:1:865:C:O4'	2.16	0.45
53:3:1289:A:H2'	53:3:1290:G:H5'	1.98	0.45
55:8:20:DA:H4'	59:B2:143:ARG:NH1	2.31	0.45
57:A2:80:GLU:HG3	59:B2:694:ARG:HH22	1.81	0.45
58:B1:115:TRP:HB3	58:B1:1333:THR:CG2	2.46	0.45
58:B1:288:PRO:HB3	61:NG:105:ASP:H	1.81	0.45
58:B1:847:ASP:N	58:B1:847:ASP:OD1	2.49	0.45
59:B2:176:ILE:HD11	59:B2:428:VAL:HG21	1.98	0.45
8:H:10:ARG:HA	8:H:13:ILE:HD11	1.97	0.45
15:O:15:HIS:CG	53:3:1152:A:H5'	2.51	0.45
26:Z:44:ARG:HD3	26:Z:44:ARG:HA	1.77	0.45
51:1:388:G:H2'	51:1:390:U:H5	1.81	0.45
51:1:468:G:C2'	51:1:469:G:H5'	2.46	0.45
51:1:2869:G:H2'	51:1:2870:C:O4'	2.16	0.45
53:3:280:C:H5''	53:3:281:G:OP2	2.16	0.45
53:3:460:A:H2'	53:3:461:A:C8	2.51	0.45
53:3:556:C:H2'	53:3:557:G:O4'	2.15	0.45
53:3:951:G:H2'	53:3:952:U:H6	1.79	0.45
53:3:1069:C:H4'	53:3:1192:C:O2	2.16	0.45
58:B1:75:TYR:CD2	58:B1:75:TYR:O	2.70	0.45
58:B1:385:LEU:HD23	58:B1:390:LEU:HB2	1.97	0.45
14:N:56:MET:HB2	14:N:60:LEU:HB2	1.97	0.45
17:Q:34:THR:HG22	17:Q:76:HIS:CD2	2.51	0.45
31:f:88:LEU:HB3	31:f:128:THR:HA	1.97	0.45
37:m:27:SER:H	37:m:104:GLU:CD	2.24	0.45
48:x:57:VAL:HG12	48:x:61:LYS:HZ1	1.80	0.45
51:1:91:A:H8	51:1:91:A:OP1	1.99	0.45
51:1:252:G:H2'	51:1:253:C:H6	1.81	0.45
51:1:817:C:O2'	51:1:839:U:H5''	2.16	0.45
51:1:845:A:N3	51:1:845:A:H3'	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1792:G:H1	51:1:1827:U:H3	1.65	0.45
51:1:2190:G:H2'	51:1:2191:A:O4'	2.16	0.45
51:1:2646:C:H2'	51:1:2647:U:O4'	2.16	0.45
51:1:2680:U:O2'	51:1:2681:C:H5'	2.16	0.45
52:2:30:C:H2'	52:2:31:C:C5'	2.47	0.45
55:8:1:DC:H2''	55:8:2:DC:C6	2.51	0.45
57:A1:185:TYR:HA	57:A1:202:VAL:O	2.16	0.45
57:A1:212:ASP:OD1	57:A1:212:ASP:N	2.48	0.45
59:B2:28:LEU:HD21	59:B2:524:ILE:HG13	1.98	0.45
62:5:27:G:H1	62:5:43:C:H42	1.64	0.45
65:0:520:ILE:HD12	65:0:576:ILE:HD11	1.99	0.45
2:B:49:ARG:NH2	51:1:2884:U:H1'	2.32	0.45
13:M:86:LYS:HD2	13:M:86:LYS:HA	1.73	0.45
15:O:59:LYS:HD3	53:3:972:C:O3'	2.17	0.45
22:V:21:VAL:HG22	22:V:44:HIS:HA	1.98	0.45
29:d:22:ASP:OD1	29:d:22:ASP:N	2.48	0.45
29:d:43:THR:O	51:1:38:A:H1'	2.17	0.45
31:f:94:ARG:HA	31:f:127:GLN:HB2	1.99	0.45
35:k:56:ASP:N	35:k:56:ASP:OD1	2.49	0.45
51:1:1573:G:H2'	51:1:1574:C:O4'	2.17	0.45
51:1:1954:G:H21	51:1:1956:U:H3	1.65	0.45
51:1:2599:G:H2'	51:1:2600:A:H8	1.80	0.45
53:3:437:U:C2'	53:3:438:U:H5'	2.46	0.45
53:3:1104:G:H2'	53:3:1105:A:O4'	2.16	0.45
53:3:1448:C:O2	53:3:1448:C:H2'	2.15	0.45
58:B1:375:GLU:O	59:B2:1247:SER:HB3	2.16	0.45
58:B1:484:MET:CE	59:B2:1278:LEU:HD21	2.47	0.45
58:B1:770:LEU:HD13	59:B2:618:GLN:CD	2.42	0.45
58:B1:1158:GLU:HA	58:B1:1223:LEU:HD21	1.99	0.45
58:B1:1227:HIS:HA	58:B1:1230:THR:HG22	1.99	0.45
62:5:6:G:H2'	62:5:7:A:C8	2.51	0.45
65:0:17:ALA:H	65:0:23:LYS:HZ3	1.64	0.45
65:0:171:LEU:HD11	65:0:218:TRP:HD1	1.82	0.45
13:M:104:SER:OG	53:3:642:A:N3	2.48	0.45
16:P:71:ASP:OD1	16:P:71:ASP:N	2.43	0.45
16:P:105:ARG:HD2	16:P:105:ARG:HA	1.84	0.45
23:W:37:LYS:HE2	23:W:37:LYS:HB2	1.73	0.45
29:d:131:THR:HA	29:d:134:LEU:HB3	1.98	0.45
42:r:38:VAL:HG21	42:r:57:GLY:HA3	1.97	0.45
51:1:233:A:H5'	51:1:233:A:H8	1.81	0.45
51:1:717:C:H2'	51:1:718:A:H5'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1337:G:O2'	51:1:1338:G:H5'	2.17	0.45
51:1:1841:U:H2'	51:1:1842:G:C8	2.51	0.45
51:1:2061:G:C2'	51:1:2501:C:HO2'	2.25	0.45
51:1:2101:A:H2'	51:1:2102:G:C8	2.50	0.45
53:3:37:U:H2'	53:3:38:G:H5'	1.97	0.45
53:3:684:U:H3	53:3:706:A:H61	1.63	0.45
53:3:1316:G:H2'	53:3:1317:C:H5''	1.99	0.45
57:A1:231:PHE:O	57:A2:218:ARG:NH1	2.50	0.45
58:B1:506:VAL:HG23	58:B1:628:GLY:HA3	1.98	0.45
65:0:145:ASP:OD1	65:0:273:LYS:NZ	2.45	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
12:L:140:VAL:O	12:L:144:ALA:N	2.46	0.45
16:P:114:PRO:O	26:Z:28:LEU:HD21	2.17	0.45
20:T:38:LEU:HD23	20:T:55:LEU:HD12	1.98	0.45
27:b:73:ILE:HG12	51:1:1490:A:H2	1.79	0.45
42:r:49:ILE:HG22	42:r:54:VAL:HG22	1.98	0.45
50:z:19:HIS:CD2	50:z:50:VAL:HG12	2.52	0.45
51:1:44:A:C2'	51:1:45:G:H5'	2.45	0.45
51:1:866:A:H61	51:1:913:U:C1'	2.28	0.45
51:1:1177:G:C2'	51:1:1178:C:H5''	2.45	0.45
51:1:1786:A:O2'	51:1:1787:A:H5'	2.17	0.45
51:1:2123:G:N3	51:1:2176:A:N6	2.65	0.45
51:1:2183:A:H2'	51:1:2184:A:C8	2.52	0.45
51:1:2457:U:O2'	51:1:2458:G:H5'	2.15	0.45
52:2:16:G:N2	52:2:69:G:H1'	2.31	0.45
53:3:323:U:H3	53:3:327:A:H62	1.64	0.45
53:3:384:G:H2'	53:3:385:C:C6	2.52	0.45
53:3:478:A:H2'	53:3:479:U:C4'	2.46	0.45
53:3:771:G:H2'	53:3:772:U:C6	2.51	0.45
53:3:792:A:H4'	53:3:793:U:C5'	2.47	0.45
53:3:1096:C:H2'	53:3:1097:C:H6	1.80	0.45
53:3:1198:G:H2'	53:3:1199:U:C6	2.51	0.45
57:A1:59:VAL:HG22	57:A1:144:ILE:HA	1.97	0.45
59:B2:230:PHE:HB2	59:B2:333:ILE:HB	1.97	0.45
65:0:565:PRO:HD3	65:0:602:LYS:HZ2	1.81	0.45
65:0:600:ALA:HA	65:0:603:GLU:HB2	1.98	0.45
8:H:63:ILE:HG23	8:H:98:ALA:HA	1.98	0.45
24:X:46:LEU:HD12	24:X:48:ILE:HD11	1.99	0.45
39:o:94:ARG:NH2	39:o:98:GLN:OE1	2.50	0.45
40:p:28:LYS:HB2	40:p:82:SER:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:y:38:GLN:O	51:1:95:A:H4'	2.16	0.45
50:z:37:ARG:NH1	51:1:928:A:O2'	2.50	0.45
51:1:642:U:H2'	51:1:644:A:OP2	2.16	0.45
51:1:1028:A:N6	51:1:1125:G:H2'	2.31	0.45
51:1:1086:A:H1'	51:1:1103:A:H2	1.81	0.45
51:1:1094:U:H2'	51:1:1096:A:OP2	2.17	0.45
51:1:2125:G:C5'	64:a:39:VAL:HG22	2.47	0.45
51:1:2226:C:H2'	51:1:2227:A:O4'	2.17	0.45
51:1:2785:C:H2'	51:1:2786:U:C6	2.51	0.45
53:3:1173:U:H2'	53:3:1174:G:C8	2.48	0.45
58:B1:201:LEU:CD1	58:B1:224:LEU:HD12	2.46	0.45
58:B1:213:LYS:HA	58:B1:213:LYS:HE3	1.99	0.45
65:0:144:MET:HG2	65:0:266:CYS:HB2	1.99	0.45
7:G:20:ARG:HD2	53:3:831:A:H5''	1.98	0.45
16:P:24:ALA:N	16:P:86:LYS:O	2.39	0.45
19:S:75:LYS:HZ3	53:3:1357:A:H5''	1.81	0.45
24:X:71:GLY:HA3	53:3:1320:C:C2	2.51	0.45
29:d:153:LEU:HD11	29:d:158:PHE:HB2	1.98	0.45
30:e:35:LEU:HD22	30:e:151:LEU:HD21	1.99	0.45
48:x:31:ASN:ND2	48:x:52:ALA:HB3	2.32	0.45
51:1:708:G:O2'	51:1:709:U:H5'	2.17	0.45
51:1:878:A:H3'	51:1:879:G:H8	1.82	0.45
51:1:1069:A:H2'	51:1:1073:A:C5	2.51	0.45
51:1:2073:C:O5'	51:1:2073:C:H6	1.99	0.45
51:1:2127:G:H2'	51:1:2128:G:C8	2.52	0.45
53:3:20:U:O2'	53:3:21:G:H5'	2.17	0.45
53:3:962:C:H42	53:3:973:G:H1	1.65	0.45
53:3:1147:C:H2'	53:3:1148:U:C6	2.52	0.45
58:B1:201:LEU:HD11	58:B1:220:ARG:NH1	2.32	0.45
62:5:49:C:H2'	62:5:50:U:C6	2.52	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	0.45
10:J:161:GLU:HA	10:J:164:LEU:HD12	1.98	0.45
11:K:11:HIS:HB3	11:K:14:GLN:HB2	1.99	0.45
14:N:16:ALA:HA	14:N:66:VAL:HA	1.98	0.45
17:Q:11:ARG:HH11	53:3:563:A:H2	1.64	0.45
17:Q:57:THR:HG21	53:3:362:G:H5''	1.99	0.45
29:d:37:ALA:HB1	29:d:94:GLN:H	1.82	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
32:g:98:ASP:O	32:g:102:ALA:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:n:73:ASN:O	38:n:77:ALA:N	2.50	0.45
40:p:74:GLN:NE2	51:1:2683:C:O2'	2.49	0.45
44:t:17:SER:OG	44:t:20:ALA:N	2.48	0.45
51:1:162:U:H6	51:1:163:C:H5	1.64	0.45
51:1:598:U:H2'	51:1:599:A:C8	2.52	0.45
51:1:1429:G:C2	51:1:1568:G:C2	3.05	0.45
53:3:607:A:H2'	53:3:608:A:O4'	2.17	0.45
53:3:946:A:H4'	53:3:1333:A:O2'	2.17	0.45
53:3:946:A:H4'	53:3:1333:A:HO2'	1.82	0.45
53:3:1255:G:H1	53:3:1282:C:H42	1.64	0.45
58:B1:141:PHE:HE2	58:B1:296:LYS:CB	2.23	0.45
58:B1:213:LYS:HE3	58:B1:213:LYS:CA	2.47	0.45
58:B1:1357:ILE:HG22	58:B1:1359:ALA:H	1.82	0.45
59:B2:517:GLN:HB3	59:B2:760:ASN:H	1.79	0.45
62:5:22:G:H2'	62:5:23:A:C8	2.52	0.45
1:A:41:HIS:HD2	30:e:108:PRO:HA	1.82	0.45
6:F:28:SER:OG	6:F:29:ALA:N	2.50	0.45
7:G:115:ASP:OD1	7:G:115:ASP:N	2.42	0.45
9:I:96:ARG:HG2	9:I:133:SER:HA	1.99	0.45
18:R:107:THR:HG21	53:3:1307:U:H4'	1.99	0.45
20:T:19:ASN:O	53:3:750:C:H1'	2.16	0.45
28:c:2:ILE:HG12	28:c:90:PHE:HZ	1.82	0.45
28:c:194:PRO:HA	51:1:2680:U:C5'	2.46	0.45
33:i:52:LEU:HD11	33:i:81:LYS:HD3	1.99	0.45
38:n:40:LYS:O	38:n:44:LEU:N	2.48	0.45
39:o:18:LEU:HD23	39:o:21:LEU:HD12	1.99	0.45
40:p:105:LYS:HG2	53:3:1464:U:OP1	2.17	0.45
41:q:25:GLY:O	41:q:29:ARG:NH1	2.50	0.45
51:1:224:U:H2'	51:1:225:C:O4'	2.17	0.45
51:1:776:G:C8	51:1:793:A:C2	3.05	0.45
51:1:952:G:H3'	51:1:953:G:H5''	1.98	0.45
51:1:1276:A:H61	51:1:1294:U:H3	1.64	0.45
51:1:1954:G:N2	51:1:1956:U:H3	2.15	0.45
53:3:433:G:H2'	53:3:434:U:C6	2.51	0.45
53:3:757:U:H2'	53:3:758:C:H5'	1.99	0.45
53:3:925:G:H1'	53:3:1502:A:C4	2.52	0.45
53:3:962:C:H1'	53:3:1201:A:N1	2.32	0.45
53:3:1436:U:H2'	53:3:1437:A:C8	2.45	0.45
59:B2:674:ASP:OD2	59:B2:1070:HIS:ND1	2.50	0.45
59:B2:735:LYS:HA	59:B2:748:ILE:HG22	1.97	0.45
59:B2:746:ALA:O	59:B2:974:ARG:NH2	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:15:LYS:HA	5:E:21:PHE:HA	1.99	0.44
7:G:136:ARG:O	7:G:140:LEU:N	2.47	0.44
10:J:72:ASN:OD1	10:J:72:ASN:N	2.50	0.44
16:P:25:SER:HG	16:P:28:ASN:H	1.64	0.44
19:S:2:LYS:HG2	19:S:4:SER:H	1.81	0.44
19:S:61:ASN:HB3	19:S:72:PHE:CE2	2.52	0.44
27:b:84:PRO:HG3	51:1:1568:G:OP1	2.16	0.44
33:i:9:LYS:HA	33:i:57:VAL:HA	1.99	0.44
33:i:126:ARG:O	33:i:130:GLY:N	2.50	0.44
40:p:48:ALA:N	40:p:59:THR:OG1	2.50	0.44
51:1:397:U:O5'	51:1:397:U:H6	2.00	0.44
51:1:918:A:H4'	52:2:97:C:O2	2.16	0.44
51:1:927:A:H2'	51:1:928:A:O4'	2.17	0.44
51:1:1024:G:O5'	51:1:1025:G:H5''	2.16	0.44
51:1:1093:G:H22	51:1:1097:U:H3'	1.82	0.44
51:1:1541:C:H2'	51:1:1542:U:O4'	2.18	0.44
51:1:1656:C:H2'	51:1:1657:U:H6	1.82	0.44
51:1:1979:U:O5'	51:1:1979:U:H6	1.99	0.44
53:3:782:A:O3'	53:3:1515:G:H4'	2.16	0.44
53:3:1098:C:H2'	53:3:1099:G:O4'	2.17	0.44
55:8:16:DT:H2'	55:8:17:DC:C6	2.52	0.44
58:B1:128:LEU:CD2	58:B1:188:LEU:HB3	2.47	0.44
58:B1:731:ARG:HB3	59:B2:1105:SER:HB2	2.00	0.44
59:B2:11:ILE:HG22	59:B2:1172:LEU:HD11	1.99	0.44
14:N:28:VAL:HG13	14:N:63:TYR:HA	1.99	0.44
15:O:70:HIS:HD2	15:O:72:ARG:HH22	1.64	0.44
19:S:23:ARG:HH12	19:S:27:LYS:HB3	1.82	0.44
27:b:252:LYS:HA	27:b:252:LYS:HD3	1.80	0.44
28:c:94:GLN:H	28:c:94:GLN:HG3	1.59	0.44
31:f:98:LYS:HD2	31:f:98:LYS:HA	1.78	0.44
34:j:134:ALA:HB1	51:1:2898:U:O2	2.17	0.44
36:l:135:ILE:HG23	36:l:140:GLY:HA3	1.99	0.44
45:u:65:GLN:CD	51:1:328:U:H4'	2.42	0.44
51:1:138:U:H3'	51:1:139:U:H5'	1.99	0.44
51:1:146:A:H2'	51:1:147:C:H6	1.81	0.44
51:1:753:A:H2'	51:1:754:U:C6	2.52	0.44
51:1:1130:U:C5	51:1:2025:C:H5''	2.53	0.44
51:1:2007:U:O5'	51:1:2007:U:H6	2.01	0.44
53:3:152:A:H2'	53:3:153:C:H5'	1.99	0.44
53:3:675:A:C2	53:3:676:A:H1'	2.52	0.44
62:5:69:G:H2'	62:5:70:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
65:0:97:ILE:HD13	65:0:412:PRO:HG3	1.99	0.44
7:G:33:ALA:HB3	7:G:37:VAL:HB	1.99	0.44
8:H:153:SER:O	8:H:196:GLY:N	2.50	0.44
9:I:47:LEU:HD22	53:3:510:A:OP1	2.17	0.44
12:L:57:GLU:HG3	12:L:58:LEU:HD12	1.99	0.44
21:U:26:ASN:HD21	21:U:31:ARG:N	2.15	0.44
22:V:64:ARG:CB	53:3:130:A:H8	2.31	0.44
29:d:5:LEU:HG	29:d:120:VAL:HG13	2.00	0.44
45:u:27:VAL:HA	45:u:33:VAL:HG13	1.99	0.44
51:1:623:C:H2'	51:1:624:C:C6	2.52	0.44
51:1:1300:G:N7	51:1:1626:A:H2'	2.32	0.44
53:3:68:G:H2'	53:3:69:G:O4'	2.17	0.44
53:3:723:U:O2	53:3:855:U:H4'	2.17	0.44
53:3:768:A:C2	53:3:1512:U:H4'	2.52	0.44
53:3:969:A:H2'	53:3:970:C:O4'	2.18	0.44
53:3:1490:U:H2'	53:3:1491:G:O4'	2.17	0.44
58:B1:67:ASP:OD1	58:B1:67:ASP:O	2.35	0.44
58:B1:388:ARG:HG2	58:B1:388:ARG:NH1	2.32	0.44
65:0:13:ILE:HG22	65:0:86:ILE:HA	1.98	0.44
65:0:392:THR:OG1	65:0:395:ASP:OD2	2.31	0.44
65:0:618:LYS:H	65:0:684:PHE:HA	1.82	0.44
3:C:45:HIS:ND1	51:1:2372:U:H4'	2.32	0.44
10:J:50:GLY:HA3	10:J:62:ALA:HB2	1.99	0.44
31:f:41:GLU:N	31:f:52:GLY:O	2.49	0.44
43:s:13:SER:OG	43:s:14:ALA:N	2.50	0.44
51:1:233:A:C2'	51:1:234:U:H5'	2.48	0.44
51:1:648:G:H2'	51:1:649:G:H8	1.82	0.44
51:1:740:C:H5'	51:1:740:C:C6	2.46	0.44
51:1:974:G:O2'	51:1:989:G:N2	2.51	0.44
51:1:1087:G:H1	51:1:1102:C:H42	1.64	0.44
51:1:1147:A:O2'	51:1:1148:U:H5'	2.17	0.44
51:1:1432:G:H2'	51:1:1433:A:C8	2.52	0.44
51:1:2073:C:O2'	51:1:2074:U:H5'	2.17	0.44
51:1:2270:A:H2'	51:1:2271:G:O4'	2.18	0.44
51:1:2737:G:H2'	51:1:2738:A:C8	2.52	0.44
53:3:334:C:H2'	53:3:335:C:O4'	2.16	0.44
53:3:347:G:H2'	53:3:348:G:O4'	2.17	0.44
53:3:569:C:H4'	53:3:574:A:N7	2.31	0.44
53:3:806:C:H2'	53:3:807:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1312:G:H2'	53:3:1313:U:C6	2.52	0.44
58:B1:109:SER:HB2	58:B1:296:LYS:HG2	1.98	0.44
58:B1:804:ALA:HB2	58:B1:1256:ILE:CD1	2.48	0.44
58:B1:1033:GLY:HA3	58:B1:1081:VAL:O	2.18	0.44
64:a:50:ILE:HG12	64:a:169:GLY:HA2	1.99	0.44
6:F:1:MET:N	51:1:2526:G:H1'	2.32	0.44
11:K:3:HIS:ND1	11:K:65:GLU:HB2	2.33	0.44
12:L:67:ASN:HB3	12:L:129:ASN:HD21	1.83	0.44
14:N:47:VAL:HG12	14:N:78:ILE:HG21	2.00	0.44
14:N:125:GLN:HG3	53:3:1232:U:H5''	1.99	0.44
16:P:57:SER:O	16:P:57:SER:OG	2.34	0.44
18:R:94:LEU:HD12	18:R:95:PRO:HD2	2.00	0.44
23:W:58:ILE:O	23:W:62:ARG:N	2.49	0.44
25:Y:4:LYS:NZ	53:3:332:G:P	2.91	0.44
25:Y:16:ALA:O	25:Y:20:ASN:N	2.45	0.44
27:b:212:TRP:NE1	51:1:1566:A:O4'	2.50	0.44
27:b:227:VAL:HG11	51:1:784:G:C2	2.52	0.44
28:c:197:THR:HG23	51:1:2820:A:C6	2.52	0.44
29:d:136:GLN:HA	29:d:139:LYS:HB2	1.99	0.44
35:k:62:VAL:HA	35:k:84:CYS:HA	2.00	0.44
47:w:30:GLY:N	47:w:57:ALA:O	2.33	0.44
47:w:56:PHE:HE1	47:w:58:LYS:HE2	1.83	0.44
51:1:754:U:O5'	51:1:754:U:H6	2.01	0.44
51:1:861:A:H2'	51:1:862:G:O4'	2.18	0.44
51:1:1177:G:H2'	51:1:1178:C:C5'	2.48	0.44
51:1:1565:C:O2'	51:1:1566:A:H2'	2.16	0.44
51:1:2066:C:H2'	51:1:2067:G:H8	1.81	0.44
51:1:2560:A:O2'	51:1:2561:U:H5'	2.17	0.44
51:1:2762:C:H2'	51:1:2763:G:H5'	2.00	0.44
53:3:505:G:C6	53:3:535:A:C2	3.05	0.44
53:3:563:A:H5'	53:3:566:G:N2	2.33	0.44
53:3:563:A:H2'	53:3:563:A:N3	2.32	0.44
58:B1:33:TRP:HZ2	59:B2:1336:ASN:OD1	2.00	0.44
58:B1:472:LEU:CD1	59:B2:1294:LYS:HG2	2.47	0.44
58:B1:515:ARG:NH2	58:B1:718:SER:O	2.48	0.44
59:B2:562:GLU:OE1	59:B2:662:SER:OG	2.28	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
65:0:365:GLN:N	65:0:372:GLU:O	2.38	0.44
8:H:135:ARG:NH2	59:B2:905:ILE:HG22	2.30	0.44
14:N:6:TYR:OH	53:3:1148:U:H5'	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:50:LYS:HA	17:Q:50:LYS:HD2	1.86	0.44
28:c:5:VAL:HG22	28:c:202:ILE:HG12	2.00	0.44
39:o:90:VAL:HG23	39:o:117:PHE:HB3	2.00	0.44
41:q:32:ARG:HB2	51:1:581:C:OP1	2.18	0.44
51:1:885:C:H2'	51:1:891:G:H22	1.83	0.44
51:1:2102:G:H2'	51:1:2103:C:O4'	2.18	0.44
52:2:6:G:O2'	52:2:7:G:H5'	2.17	0.44
52:2:115:A:H2'	52:2:116:G:C8	2.53	0.44
53:3:240:G:H2'	53:3:241:G:C8	2.53	0.44
53:3:894:G:H2'	53:3:895:G:C8	2.53	0.44
57:A1:78:ILE:HA	57:A1:81:ILE:HG22	2.00	0.44
58:B1:1108:GLN:HG3	58:B1:1109:LEU:HD12	1.99	0.44
35:k:61:VAL:O	35:k:85:VAL:N	2.47	0.44
37:m:71:LYS:HD3	37:m:72:PRO:HD2	2.00	0.44
37:m:81:ARG:NH1	51:1:2251:G:OP1	2.51	0.44
40:p:25:VAL:HG21	40:p:83:ILE:HG22	1.99	0.44
45:u:14:THR:OG1	45:u:15:GLY:N	2.51	0.44
51:1:514:A:O2'	51:1:515:A:H5'	2.17	0.44
51:1:1028:A:C2	51:1:2487:G:H1'	2.52	0.44
51:1:1744:A:H3'	51:1:1745:A:H8	1.83	0.44
53:3:272:C:H2'	53:3:273:U:H6	1.83	0.44
53:3:994:A:H61	53:3:1047:G:C4'	2.30	0.44
53:3:1494:G:H2'	53:3:1495:U:C6	2.53	0.44
58:B1:161:THR:H	58:B1:164:GLN:HB2	1.82	0.44
58:B1:395:LYS:NZ	58:B1:399:LYS:HE2	2.32	0.44
58:B1:434:ILE:HD11	59:B2:1274:GLU:HG3	2.00	0.44
59:B2:712:SER:OG	59:B2:713:GLY:N	2.49	0.44
65:0:338:VAL:HG13	65:0:380:GLY:H	1.83	0.44
65:0:423:LYS:HA	65:0:482:ASN:HD21	1.83	0.44
8:H:6:PRO:O	8:H:10:ARG:NE	2.41	0.44
9:I:145:ARG:HB3	9:I:148:ALA:HB3	1.99	0.44
27:b:57:HIS:CE1	51:1:1567:G:H4'	2.52	0.44
27:b:120:ASP:OD1	27:b:120:ASP:N	2.49	0.44
31:f:62:ALA:HA	51:1:2748:A:O2'	2.18	0.44
34:j:116:ARG:HH21	51:1:528:A:H5''	1.81	0.44
36:l:29:LYS:HA	51:1:810:U:H5	1.81	0.44
51:1:368:A:C2'	51:1:369:U:H5'	2.47	0.44
51:1:960:A:H5''	51:1:961:C:OP1	2.17	0.44
51:1:1630:A:H2'	51:1:1631:G:H5'	2.00	0.44
51:1:1783:A:N1	51:1:2587:A:N3	2.63	0.44
51:1:2703:C:H2'	51:1:2704:C:H6	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:182:A:N1	53:3:224:U:H5'	2.33	0.44
53:3:253:A:O4'	53:3:276:G:H1'	2.18	0.44
53:3:964:A:H2'	53:3:965:U:H5'	2.00	0.44
53:3:1475:G:C2	53:3:1476:A:H1'	2.52	0.44
53:3:1491:G:H2'	66:h:6:5OH:O	2.17	0.44
57:A1:192:VAL:HG12	57:A1:193:GLU:H	1.83	0.44
58:B1:1046:ILE:HG22	58:B1:1061:VAL:HA	2.00	0.44
59:B2:557:ARG:HB3	59:B2:587:LEU:HD13	2.00	0.44
59:B2:1088:ASP:OD1	59:B2:1088:ASP:N	2.51	0.44
62:5:13:C:H42	62:5:46:G:N2	2.16	0.44
62:5:63:G:H2'	62:5:64:A:C8	2.53	0.44
16:P:25:SER:HG	16:P:28:ASN:N	2.16	0.44
21:U:13:LYS:CD	53:3:392:C:H5'	2.48	0.44
23:W:71:ASP:OD1	23:W:71:ASP:N	2.50	0.44
27:b:155:ARG:NH1	51:1:1818:U:C5	2.81	0.44
30:e:135:ILE:HA	30:e:140:ILE:HD11	1.99	0.44
37:m:68:PHE:CE2	51:1:871:U:H5''	2.53	0.44
51:1:537:G:H22	51:1:555:G:H2'	1.83	0.44
51:1:608:A:H2'	51:1:609:A:O4'	2.18	0.44
51:1:728:G:O2'	51:1:730:A:H8	2.01	0.44
51:1:862:G:H2'	51:1:863:A:O4'	2.18	0.44
51:1:1056:G:H1'	51:1:1103:A:N6	2.33	0.44
51:1:1086:A:H3'	51:1:1086:A:N3	2.33	0.44
51:1:1747:U:H2'	51:1:1748:C:C6	2.52	0.44
51:1:2069:G:H2'	51:1:2070:A:H8	1.82	0.44
51:1:2259:U:C2	51:1:2427:C:C4	3.06	0.44
51:1:2723:C:H2'	51:1:2724:U: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
53:3:570:G:H5'	53:3:820:U:O4'	2.17	0.44
53:3:599:C:H2'	53:3:600:A:C8	2.53	0.44
53:3:1508:A:H61	53:3:1527:U:H3	1.66	0.44
58:B1:45:ASN:HD22	58:B1:48:THR:H	1.65	0.44
58:B1:68:TYR:HB3	58:B1:75:TYR:HE2	1.81	0.44
58:B1:107:LEU:HA	58:B1:276:ASN:ND2	2.33	0.44
58:B1:478:LEU:HD21	60:W0:47:THR:HG23	1.99	0.44
59:B2:896:THR:HB	59:B2:897:PRO:HD2	1.99	0.44
62:5:37:A:H2'	62:5:38:A:C8	2.53	0.44
13:M:45:ILE:HG12	13:M:60:LEU:HD23	2.00	0.43
30:e:134:GLN:NE2	30:e:147:ARG:O	2.41	0.43
33:i:128:ILE:HA	33:i:131:THR:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:j:81:ILE:HG21	51:1:2514:U:H4'	1.99	0.43
51:1:74:A:H2'	51:1:74:A:N3	2.33	0.43
51:1:330:A:H8	51:1:1210:G:C5	2.36	0.43
51:1:1020:A:C1'	51:1:1021:A:OP2	2.61	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
51:1:2065:C:H2'	51:1:2066:C:C6	2.53	0.43
51:1:2194:U:H2'	51:1:2195:U:C6	2.52	0.43
53:3:160:A:H2'	53:3:161:A:O4'	2.19	0.43
53:3:622:A:H2'	53:3:623:C:H5'	1.99	0.43
53:3:865:A:H2'	53:3:866:C:C6	2.52	0.43
53:3:1195:C:O5'	53:3:1195:C:H6	2.01	0.43
57:A1:68:TYR:HE1	57:A1:79:LEU:HD13	1.82	0.43
58:B1:62:PHE:N	58:B1:62:PHE:CD1	2.85	0.43
58:B1:111:THR:HG21	58:B1:303:VAL:HB	1.99	0.43
58:B1:824:PRO:HD3	58:B1:835:LEU:HD12	2.00	0.43
59:B2:811:ASN:ND2	59:B2:1098:LEU:O	2.51	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
65:0:75:MET:HG3	65:0:279:LEU:HD11	1.99	0.43
65:0:334:THR:HG1	65:0:385:ALA:H	1.65	0.43
8:H:68:HIS:HE2	8:H:105:VAL:HB	1.81	0.43
26:Z:66:ARG:O	53:3:1088:G:O2'	2.35	0.43
41:q:51:GLN:O	41:q:55:GLN:N	2.48	0.43
42:r:17:GLY:H	42:r:98:ILE:HB	1.83	0.43
47:w:58:LYS:HD3	51:1:2366:A:H4'	1.99	0.43
48:x:17:ARG:HA	48:x:17:ARG:HD3	1.72	0.43
51:1:118:A:H5'	51:1:119:A:C8	2.53	0.43
51:1:578:G:H21	51:1:1252:G:N2	2.16	0.43
51:1:755:U:H2'	51:1:756:A:C8	2.52	0.43
51:1:1308:A:N6	51:1:1608:A:H61	2.16	0.43
51:1:1984:G:H2'	51:1:1985:C:H6	1.82	0.43
51:1:2338:C:H6	51:1:2338:C:O5'	2.01	0.43
51:1:2599:G:H2'	51:1:2600:A:C8	2.53	0.43
51:1:2757:A:H2'	51:1:2757:A:N3	2.32	0.43
53:3:1489:G:H2'	53:3:1490:U:H6	1.84	0.43
58:B1:388:ARG:HG2	58:B1:388:ARG:HH11	1.84	0.43
58:B1:978:ARG:HD3	58:B1:999:TYR:H	1.83	0.43
59:B2:300:ASP:OD1	59:B2:313:ALA:N	2.52	0.43
59:B2:444:ASP:OD1	59:B2:444:ASP:N	2.51	0.43
65:0:122:GLN:O	65:0:125:THR:OG1	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:33:LEU:HD21	51:1:2286:G:C5	2.53	0.43
9:I:33:ILE:HG23	9:I:34:GLU:HG2	1.99	0.43
11:K:45:ARG:N	11:K:57:ALA:O	2.44	0.43
12:L:34:LYS:NZ	53:3:1289:A:C2	2.86	0.43
14:N:129:ARG:NH1	63:6:32:C:OP2	2.50	0.43
27:b:106:PRO:HD2	27:b:109:LEU:HD22	1.99	0.43
34:j:80:HIS:CD2	51:1:2642:G:H5'	2.53	0.43
34:j:118:MET:HE3	34:j:118:MET:HB2	1.76	0.43
37:m:46:ILE:O	37:m:50:ARG:N	2.45	0.43
39:o:56:LYS:HA	39:o:59:ALA:HB3	2.01	0.43
40:p:59:THR:HG22	40:p:72:VAL:HG23	2.00	0.43
42:r:34:GLU:HB2	42:r:58:VAL:HB	1.99	0.43
43:s:36:LEU:HD23	43:s:48:LYS:HB2	2.01	0.43
51:1:298:G:C2	51:1:339:U:H5	2.36	0.43
51:1:1044:C:O5'	51:1:1044:C:H6	2.00	0.43
51:1:1794:A:O2'	51:1:1795:C:H5'	2.18	0.43
51:1:1815:A:O4'	51:1:1817:G:H1'	2.18	0.43
51:1:1823:G:C6	51:1:1824:G:C6	3.06	0.43
51:1:2061:G:C8	51:1:2501:C:H4'	2.53	0.43
51:1:2102:G:H1	51:1:2187:U:H3	1.65	0.43
51:1:2267:A:H5''	51:1:2268:A:H5'	2.01	0.43
51:1:2524:G:C3'	51:1:2525:G:H5''	2.48	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
52:2:4:C:H6	52:2:4:C:C5'	2.31	0.43
53:3:1057:G:H2'	53:3:1058:G:O4'	2.18	0.43
53:3:1242:G:H4'	53:3:1304:G:OP1	2.18	0.43
58:B1:362:ARG:HB2	58:B1:364:HIS:HD2	1.83	0.43
58:B1:926:PRO:HB2	58:B1:1241:TYR:HE1	1.82	0.43
58:B1:1079:LYS:HD3	58:B1:1098:GLN:HB3	1.99	0.43
59:B2:557:ARG:NH2	59:B2:607:SER:O	2.49	0.43
59:B2:646:SER:OG	59:B2:647:ARG:N	2.51	0.43
64:a:203:GLN:HG2	64:a:205:LYS:H	1.82	0.43
8:H:66:THR:HA	8:H:101:ASN:HB2	1.99	0.43
14:N:45:MET:HA	14:N:48:ARG:HH21	1.82	0.43
29:d:131:THR:HG21	51:1:320:A:H2'	1.99	0.43
32:g:27:ARG:NH2	48:x:55:MET:HB3	2.32	0.43
39:o:55:GLU:OE2	52:2:116:G:H5''	2.17	0.43
48:x:9:LYS:HB3	48:x:30:PRO:CB	2.48	0.43
50:z:18:LYS:HE2	50:z:18:LYS:HB3	1.89	0.43
51:1:152:A:H2'	51:1:153:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:984:A:P	51:1:985:C:H5	2.41	0.43
51:1:1368:G:H2'	51:1:1369:G:C8	2.51	0.43
53:3:296:U:H2'	53:3:297:G:O4'	2.19	0.43
53:3:971:G:H4'	53:3:972:C:H5''	1.99	0.43
53:3:1095:U:OP1	53:3:1108:G:N2	2.52	0.43
53:3:1364:U:O2'	53:3:1365:G:H5'	2.19	0.43
3:C:35:LEU:HD12	3:C:35:LEU:HA	1.91	0.43
14:N:11:ARG:O	14:N:14:SER:OG	2.32	0.43
27:b:209:ALA:HA	27:b:212:TRP:CE2	2.54	0.43
29:d:134:LEU:HD11	29:d:161:ALA:HB2	1.99	0.43
34:j:41:LYS:HB2	34:j:41:LYS:HE3	1.86	0.43
35:k:51:LYS:HD3	35:k:51:LYS:HA	1.75	0.43
38:n:36:THR:HG22	51:1:1278:C:OP1	2.18	0.43
43:s:84:ARG:NH1	51:1:1322:A:O2'	2.51	0.43
51:1:793:A:OP2	51:1:793:A:H8	2.01	0.43
51:1:812:C:H1'	51:1:1250:G:C2	2.53	0.43
51:1:960:A:O3'	51:1:961:C:H3'	2.18	0.43
51:1:974:G:C6	51:1:1186:G:C6	3.06	0.43
51:1:1057:A:H5''	51:1:1058:U:O2	2.18	0.43
51:1:1716:U:C2'	51:1:1717:A:H5'	2.49	0.43
51:1:2672:U:C3'	51:1:2673:G:H5''	2.48	0.43
53:3:640:A:H2'	53:3:641:U:H5'	2.01	0.43
53:3:1014:A:C2	53:3:1219:A:H1'	2.54	0.43
53:3:1158:C:H2'	53:3:1159:U:H4'	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	2.59	0.43
58:B1:76:LYS:NZ	58:B1:76:LYS:HB3	2.32	0.43
58:B1:245:LEU:CG	58:B1:246:PRO:HD2	2.47	0.43
58:B1:568:SER:HB3	58:B1:570:LYS:NZ	2.34	0.43
58:B1:894:VAL:HG22	58:B1:1258:ARG:HH11	1.83	0.43
59:B2:515:MET:HE2	59:B2:515:MET:HB3	1.82	0.43
59:B2:829:THR:HG23	59:B2:1059:ARG:HG2	2.00	0.43
9:I:69:ARG:HH11	9:I:72:ARG:HH22	1.67	0.43
10:J:25:LYS:HG3	53:3:923:A:C5'	2.49	0.43
12:L:91:ARG:O	12:L:92:PRO:C	2.59	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
24:X:38:THR:HG23	24:X:69:LYS:HD3	2.00	0.43
26:Z:6:ARG:HA	26:Z:6:ARG:HD2	1.61	0.43
29:d:129:PRO:HG3	29:d:156:ASN:HA	2.00	0.43
38:n:72:ASP:O	38:n:76:VAL:HG23	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:170:U:H2'	51:1:171:U:C6	2.53	0.43
51:1:597:G:H2'	51:1:598:U:O4'	2.18	0.43
51:1:786:C:H2'	51:1:787:C:H6	1.83	0.43
51:1:974:G:C8	51:1:989:G:C2	3.07	0.43
51:1:1404:C:O5'	51:1:1404:C:H6	2.01	0.43
51:1:1412:U:H2'	51:1:1413:A:O4'	2.18	0.43
51:1:1771:C:H2'	51:1:1772:A:O4'	2.19	0.43
51:1:2845:U:H2'	51:1:2846:G:H8	1.83	0.43
53:3:1134:G:H1	53:3:1140:C:H42	1.66	0.43
53:3:1423:G:H1	53:3:1477:U:H3	1.65	0.43
58:B1:220:ARG:NH1	58:B1:220:ARG:CG	2.82	0.43
58:B1:1026:PRO:HB2	58:B1:1028:ILE:HG23	2.00	0.43
59:B2:27:LEU:O	59:B2:528:ARG:NH1	2.43	0.43
65:0:112:VAL:HG12	65:0:140:PHE:HB3	2.00	0.43
65:0:159:LYS:HG3	65:0:166:PRO:HD2	2.00	0.43
65:0:173:ILE:HD13	65:0:173:ILE:HA	1.90	0.43
35:k:49:ARG:HH22	53:3:1423:G:H5'	1.84	0.43
39:o:57:ALA:O	39:o:61:GLN:NE2	2.52	0.43
50:z:11:SER:OG	51:1:988:A:H5''	2.18	0.43
51:1:728:G:H3'	51:1:729:G:H5'	2.00	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
51:1:1037:G:O2'	51:1:1038:G:H5'	2.18	0.43
51:1:1998:A:H4'	51:1:2724:U:O2'	2.19	0.43
51:1:2101:A:H2'	51:1:2102:G:H8	1.84	0.43
51:1:2489:U:O2'	51:1:2490:G:H5'	2.18	0.43
53:3:1382:C:H2'	53:3:1383:C:C5	2.54	0.43
58:B1:24:LEU:HD21	58:B1:116:PHE:CE2	2.54	0.43
65:0:129:GLN:HG3	65:0:132:LYS:HE2	1.99	0.43
65:0:634:ASP:O	65:0:638:ARG:NH1	2.52	0.43
12:L:29:LEU:HD23	12:L:104:VAL:HG23	2.01	0.43
14:N:7:GLY:HA3	14:N:85:ALA:HB2	2.00	0.43
18:R:78:ARG:HD3	24:X:64:GLU:HG2	2.01	0.43
28:c:118:PHE:O	51:1:1655:A:H5'	2.18	0.43
28:c:120:GLY:H	28:c:123:LYS:HB2	1.82	0.43
34:j:130:HIS:HB2	34:j:132:HIS:HD2	1.84	0.43
35:k:47:ILE:HD13	35:k:47:ILE:HA	1.85	0.43
38:n:73:ASN:HB3	51:1:1453:A:C8	2.54	0.43
38:n:90:ARG:NH2	51:1:2880:C:O2'	2.48	0.43
51:1:252:G:H2'	51:1:253:C:C6	2.53	0.43
51:1:666:A:H2'	51:1:667:U:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:784:G:N7	51:1:792:A:C5	2.87	0.43
51:1:832:U:C5	51:1:944:C:N4	2.87	0.43
51:1:1060:U:OP2	51:1:1060:U:H3'	2.19	0.43
51:1:1064:C:H5''	51:1:1065:U:C5	2.54	0.43
51:1:1123:C:O2'	51:1:1124:G:H5'	2.18	0.43
51:1:1428:C:C5	51:1:1569:A:H5''	2.53	0.43
51:1:1794:A:H1'	51:1:1900:A:N3	2.34	0.43
51:1:1931:U:H2'	51:1:1932:A:C8	2.54	0.43
51:1:2248:C:H3'	51:1:2249:U:H6	1.82	0.43
51:1:2311:A:H3'	51:1:2312:U:C6	2.54	0.43
51:1:2577:A:H2'	51:1:2614:A:N6	2.33	0.43
51:1:2626:C:O2'	51:1:2627:G:H5'	2.19	0.43
53:3:37:U:C2'	53:3:38:G:H5'	2.48	0.43
53:3:1042:A:H2'	53:3:1043:G:H4'	2.00	0.43
53:3:1210:C:H2'	53:3:1211:U:H5'	2.00	0.43
53:3:1233:G:O2'	53:3:1365:G:H5''	2.18	0.43
53:3:1252:A:H2'	53:3:1253:G:O4'	2.19	0.43
55:8:15:DC:H5'	59:B2:1269:ARG:HD3	2.01	0.43
59:B2:125:GLY:H	59:B2:495:ALA:HB1	1.84	0.43
59:B2:866:ASP:C	59:B2:868:SER:N	2.76	0.43
59:B2:998:LEU:HG	59:B2:1011:LEU:HB3	2.00	0.43
64:a:193:LEU:HG	64:a:197:LYS:HG3	2.00	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
10:J:123:LEU:HD22	53:3:7:A:H2'	1.99	0.43
11:K:89:VAL:HG23	53:3:737:C:C5'	2.48	0.43
14:N:18:VAL:HG21	14:N:81:GLY:HA3	2.01	0.43
14:N:58:GLU:HG2	14:N:59:LYS:HG3	2.00	0.43
18:R:13:HIS:HB3	18:R:15:VAL:HG12	2.00	0.43
20:T:60:SER:HB2	53:3:581:G:C5'	2.48	0.43
27:b:73:ILE:HA	27:b:74:PRO:HD3	1.90	0.43
30:e:88:VAL:HA	52:2:42:C:O2	2.19	0.43
31:f:9:VAL:HA	31:f:48:THR:HA	2.01	0.43
32:g:63:ALA:HA	32:g:66:ASN:HD22	1.84	0.43
38:n:9:GLN:HB2	51:1:1653:G:C6	2.54	0.43
38:n:107:ASN:HD22	51:1:2009:A:C4'	2.31	0.43
51:1:824:U:H1'	51:1:2358:A:N7	2.34	0.43
51:1:1962:C:H1'	51:1:1963:U:C5	2.53	0.43
51:1:2564:A:C2	51:1:2647:U:H4'	2.54	0.43
51:1:2617:U:H2'	51:1:2618:G:H5'	2.01	0.43
53:3:439:U:O2'	53:3:440:C:H5'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:635:A:H2'	53:3:636:U:C6	2.53	0.43
53:3:777:A:C2	53:3:778:G:H1'	2.52	0.43
55:8:12:DG:OP1	58:B1:795:TYR:CE1	2.71	0.43
56:9:12:DC:H3'	58:B1:47:ARG:HH12	1.83	0.43
58:B1:68:TYR:O	58:B1:75:TYR:CD2	2.70	0.43
11:K:89:VAL:HG23	53:3:737:C:C4'	2.49	0.43
36:l:37:GLY:H	36:l:41:ARG:HH22	1.66	0.43
37:m:33:LEU:HD12	37:m:117:PHE:HB3	2.00	0.43
44:t:1:MET:HG3	51:1:136:G:H21	1.84	0.43
51:1:194:G:H2'	51:1:195:A:O4'	2.19	0.43
51:1:272:A:H2'	51:1:273:G:C8	2.54	0.43
51:1:481:G:H2'	51:1:507:A:N1	2.34	0.43
51:1:533:G:H5''	51:1:533:G:H8	1.83	0.43
51:1:571:U:C4	51:1:575:A:C5	3.07	0.43
51:1:690:G:C2'	51:1:691:C:H5'	2.49	0.43
51:1:1135:C:O2	51:1:1135:C:H2'	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
53:3:304:U:O2'	53:3:305:G:H5'	2.19	0.43
53:3:778:G:H2'	53:3:779:C:O4'	2.19	0.43
58:B1:211:GLU:CG	58:B1:215:LYS:HE3	2.44	0.43
58:B1:375:GLU:HB3	59:B2:1245:ALA:CB	2.48	0.43
58:B1:515:ARG:HH12	58:B1:724:MET:HG2	1.83	0.43
58:B1:559:ALA:HB3	58:B1:562:GLU:HB3	2.01	0.43
58:B1:1106:ILE:O	58:B1:1123:ARG:N	2.45	0.43
62:5:9:A:H1'	62:5:45:U:H2'	2.01	0.43
65:0:498:VAL:HG22	65:0:499:THR:N	2.33	0.43
8:H:79:LYS:HB2	8:H:79:LYS:HE2	1.33	0.42
13:M:10:LEU:HD13	13:M:74:ILE:HG13	2.00	0.42
23:W:25:ILE:HA	23:W:28:LEU:HD12	2.01	0.42
43:s:29:VAL:HG21	43:s:55:ILE:HG21	2.01	0.42
46:v:88:HIS:CE1	52:2:75:G:H21	2.37	0.42
48:x:31:ASN:ND2	48:x:52:ALA:HB2	2.34	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
51:1:1943:U:OP1	51:1:1943:U:C6	2.71	0.42
51:1:2234:G:O2'	51:1:2235:G:H5'	2.19	0.42
53:3:405:U:O2	53:3:498:A:H2'	2.19	0.42
53:3:633:G:H2'	53:3:634:C:C6	2.54	0.42
53:3:865:A:H5'	53:3:1078:U:O4	2.19	0.42
53:3:927:G:H4'	53:3:1503:A:N7	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1305:G:HO2'	53:3:1306:A:H8	1.62	0.42
57:A1:211:ILE:HD12	57:A1:211:ILE:HA	1.92	0.42
58:B1:71:LEU:HD23	58:B1:71:LEU:HA	1.75	0.42
58:B1:850:LYS:HB3	58:B1:855:ASP:HB2	2.00	0.42
59:B2:22:LEU:HB3	59:B2:655:VAL:HG11	2.01	0.42
59:B2:741:MET:HE3	59:B2:974:ARG:HH12	1.84	0.42
64:a:48:LEU:HB3	64:a:50:ILE:HG23	2.01	0.42
4:D:10:LEU:HD13	51:1:125:A:C2	2.54	0.42
9:I:12:ARG:NH2	9:I:36:ALA:H	2.17	0.42
9:I:119:HIS:HA	53:3:439:U:H5''	2.01	0.42
9:I:200:VAL:HG11	10:J:103:GLY:HA2	2.00	0.42
12:L:138:GLU:HA	12:L:141:HIS:HB2	2.00	0.42
21:U:31:ARG:HB2	53:3:310:G:H5''	2.00	0.42
22:V:29:LYS:HE2	22:V:29:LYS:HB3	1.83	0.42
28:c:140:HIS:NE2	51:1:1658:C:OP1	2.52	0.42
28:c:183:GLU:OE2	28:c:184:ARG:NE	2.53	0.42
33:i:105:LEU:HD13	33:i:128:ILE:HG23	2.01	0.42
35:k:40:LYS:HZ2	35:k:57:VAL:HG12	1.85	0.42
38:n:99:LYS:HB3	38:n:99:LYS:HE3	1.72	0.42
44:t:29:THR:HG22	44:t:86:THR:HA	2.01	0.42
51:1:39:G:H2'	51:1:40:U:C6	2.54	0.42
51:1:828:U:H2'	51:1:829:A:N7	2.30	0.42
51:1:1797:G:C4	51:1:1798:U:C6	3.07	0.42
51:1:2556:C:H2'	51:1:2557:G:O4'	2.19	0.42
51:1:2656:U:H2'	51:1:2657:A:C8	2.55	0.42
52:2:79:G:H2'	52:2:80:U:O4'	2.19	0.42
53:3:250:A:H4'	53:3:251:G:O5'	2.19	0.42
53:3:1199:U:H2'	53:3:1200:C:H5'	2.01	0.42
53:3:1236:A:H2'	53:3:1237:C:O4'	2.19	0.42
58:B1:111:THR:CG2	58:B1:300:GLN:HA	2.48	0.42
59:B2:616:ILE:HG13	59:B2:652:TYR:HB2	2.01	0.42
59:B2:861:ALA:HB1	59:B2:882:ILE:HD13	2.02	0.42
60:W0:58:LEU:HD12	60:W0:59:ILE:HG12	2.00	0.42
65:0:493:THR:OG1	65:0:525:LEU:CD1	2.68	0.42
66:h:2:DPP:NG	66:h:3:SER:N	2.65	0.42
5:E:44:ARG:NH2	51:1:2349:G:OP1	2.48	0.42
7:G:56:LEU:HD23	7:G:56:LEU:HA	1.93	0.42
9:I:110:ARG:O	9:I:114:ARG:N	2.52	0.42
10:J:155:LYS:NZ	13:M:70:VAL:O	2.44	0.42
10:J:158:LYS:HA	10:J:158:LYS:HD3	1.73	0.42
14:N:13:SER:HG	53:3:1251:A:H5'	1.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:48:LEU:HD12	17:Q:48:LEU:HA	1.85	0.42
31:f:85:LYS:HE3	31:f:131:VAL:HG22	2.00	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:18:ARG:NE	51:1:1249:U:C4	2.88	0.42
39:o:40:ILE:HD13	39:o:40:ILE:HA	1.92	0.42
51:1:343:C:C2'	51:1:344:A:H5'	2.49	0.42
51:1:441:U:O2'	51:1:442:G:H5'	2.19	0.42
51:1:842:U:H2'	51:1:843:G:O4'	2.19	0.42
51:1:1177:G:C3'	51:1:1178:C:H5''	2.49	0.42
51:1:1191:G:H2'	51:1:1192:G:C8	2.51	0.42
51:1:1229:C:H2'	51:1:1230:A:C8	2.53	0.42
51:1:1313:U:O2	51:1:1313:U:H2'	2.19	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
53:3:264:C:H2'	53:3:265:G:O4'	2.19	0.42
53:3:596:A:H61	53:3:644:U:H3	1.66	0.42
53:3:1469:C:C2'	53:3:1470:U:H5'	2.50	0.42
58:B1:96:LYS:NZ	59:B2:1298:VAL:HG11	2.34	0.42
58:B1:126:LEU:H	58:B1:126:LEU:HG	1.67	0.42
58:B1:647:PRO:HG3	58:B1:697:MET:HB3	2.01	0.42
58:B1:797:THR:HG22	58:B1:924:GLY:HA3	2.01	0.42
58:B1:950:ILE:HB	58:B1:1018:ALA:HB3	2.01	0.42
65:0:68:THR:N	65:0:86:ILE:O	2.46	0.42
2:B:24:VAL:H	43:s:35:ILE:HD11	1.84	0.42
2:B:41:HIS:HD2	38:n:101:GLY:HA2	1.84	0.42
6:F:38:GLY:OXT	51:1:1124:G:H1'	2.18	0.42
8:H:3:LYS:HA	8:H:3:LYS:HD3	1.95	0.42
8:H:168:ARG:NH1	53:3:1106:G:O2'	2.53	0.42
11:K:12:PRO:O	11:K:15:SER:OG	2.32	0.42
15:O:30:LYS:HB3	15:O:30:LYS:HE3	1.64	0.42
18:R:22:TYR:HD2	18:R:65:GLU:HA	1.84	0.42
18:R:77:LYS:HB2	18:R:77:LYS:HE3	1.88	0.42
23:W:35:SER:OG	23:W:37:LYS:NZ	2.37	0.42
34:j:93:ILE:HD12	34:j:93:ILE:HA	1.72	0.42
39:o:10:ARG:HE	39:o:10:ARG:HB2	1.61	0.42
41:q:47:ARG:NH2	51:1:560:C:O2'	2.52	0.42
47:w:56:PHE:HB2	47:w:57:ALA:H	1.73	0.42
51:1:917:A:H5''	51:1:2268:A:N6	2.30	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1373:A:H2'	51:1:1374:G:O4'	2.19	0.42
51:1:1854:A:H2'	51:1:1855:U:H5'	2.02	0.42
51:1:2060:A:O2'	51:1:2061:G:OP2	2.35	0.42
51:1:2350:C:H2'	51:1:2351:G:O4'	2.19	0.42
51:1:2575:C:O5'	51:1:2575:C:H6	2.03	0.42
51:1:2596:U:H2'	51:1:2597:G:O4'	2.19	0.42
53:3:316:C:H2'	53:3:317:U:C6	2.55	0.42
58:B1:102:MET:HG2	58:B1:246:PRO:CG	2.49	0.42
58:B1:201:LEU:CB	58:B1:221:ILE:HD13	2.47	0.42
58:B1:586:GLY:HA3	58:B1:612:LEU:HD11	2.01	0.42
59:B2:524:ILE:HD12	59:B2:712:SER:HB2	2.02	0.42
5:E:28:LEU:HD12	5:E:32:LEU:HD11	2.01	0.42
7:G:53:LEU:HD23	7:G:56:LEU:HD12	2.01	0.42
10:J:24:VAL:N	10:J:27:GLY:O	2.51	0.42
13:M:15:ASN:HB3	53:3:827:U:C4'	2.48	0.42
15:O:68:ARG:HA	15:O:68:ARG:HD3	1.68	0.42
21:U:71:VAL:HA	21:U:74:LEU:HB2	2.02	0.42
26:Z:24:LYS:HD3	26:Z:24:LYS:HA	1.81	0.42
27:b:218:THR:HG22	51:1:1790:C:OP1	2.19	0.42
31:f:28:LYS:HE3	31:f:28:LYS:HB2	1.86	0.42
51:1:1363:C:O2'	51:1:1809:A:H1'	2.20	0.42
51:1:1741:C:H2'	51:1:1742:U:H5'	2.01	0.42
51:1:2521:C:C2'	51:1:2522:U:H5'	2.50	0.42
51:1:2556:C:C2'	51:1:2557:G:H5'	2.48	0.42
53:3:301:G:H2'	53:3:302:G:H8	1.83	0.42
53:3:1119:C:O2'	53:3:1120:C:H5'	2.20	0.42
58:B1:144:TYR:CE1	58:B1:162:GLU:OE1	2.73	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:B1:434:ILE:HD11	59:B2:1274:GLU:CG	2.49	0.42
58:B1:1024:THR:HG23	58:B1:1123:ARG:HA	2.00	0.42
59:B2:50:GLU:HG2	59:B2:73:TYR:HE1	1.85	0.42
11:K:47:LEU:CD2	11:K:55:HIS:HA	2.49	0.42
14:N:53:LEU:HD12	14:N:54:VAL:HG13	2.00	0.42
14:N:113:LYS:HA	14:N:120:ALA:HB2	2.02	0.42
15:O:40:ILE:HD11	53:3:1124:G:H4'	2.01	0.42
18:R:105:ALA:HB3	18:R:109:LYS:HE3	2.02	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
27:b:204:LEU:O	27:b:206:LYS:N	2.48	0.42
27:b:219:VAL:HG21	51:1:782:A:N7	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:k:38:ILE:HG22	35:k:61:VAL:HG22	2.01	0.42
36:l:90:VAL:HG22	36:l:122:VAL:HA	2.02	0.42
49:y:9:LYS:HD3	49:y:10:SER:H	1.84	0.42
51:1:813:U:H2'	51:1:814:C:C6	2.54	0.42
51:1:981:A:H1'	51:1:2037:A:H1'	2.00	0.42
51:1:2688:G:N1	51:1:2720:U:OP2	2.40	0.42
53:3:58:C:H2'	53:3:59:A:H5'	2.01	0.42
53:3:182:A:H2'	53:3:183:C:H5''	2.01	0.42
53:3:973:G:H2'	53:3:974:A:H8	1.84	0.42
53:3:1061:G:H2'	53:3:1062:U:O4'	2.19	0.42
53:3:1194:U:H2'	53:3:1195:C:C6	2.54	0.42
53:3:1271:A:H5'	53:3:1314:C:H5'	2.01	0.42
58:B1:137:ARG:HA	58:B1:142:GLU:HG2	2.02	0.42
58:B1:820:ILE:HG12	58:B1:884:SER:HB2	2.01	0.42
59:B2:148:GLN:NE2	59:B2:535:PRO:O	2.40	0.42
59:B2:1275:VAL:HG13	59:B2:1287:LEU:HD11	2.01	0.42
59:B2:1313:HIS:CD2	60:W0:31:GLN:HE22	2.37	0.42
65:0:493:THR:OG1	65:0:525:LEU:HD11	2.20	0.42
65:0:607:LYS:HE2	65:0:607:LYS:HB2	1.84	0.42
8:H:174:LEU:HB3	53:3:1108:G:OP1	2.19	0.42
10:J:126:ALA:H	53:3:9:G:P	2.43	0.42
19:S:52:ARG:HD3	53:3:1317:C:N3	2.35	0.42
20:T:3:SER:OG	20:T:4:THR:N	2.53	0.42
21:U:5:ARG:NH2	53:3:377:G:H5''	2.35	0.42
24:X:32:THR:OG1	24:X:33:TRP:N	2.53	0.42
27:b:17:LYS:HE3	27:b:17:LYS:HB3	1.80	0.42
28:c:161:MET:CE	51:1:2050:C:H1'	2.49	0.42
37:m:55:ARG:HA	37:m:58:LYS:HA	2.02	0.42
38:n:106:ASP:OD2	51:1:1287:A:C5	2.72	0.42
46:v:76:ASP:H	46:v:90:ASP:HB3	1.85	0.42
49:y:1:MET:HA	49:y:4:LYS:HE2	2.02	0.42
51:1:76:C:H42	51:1:110:G:H1	1.68	0.42
51:1:516:C:H2'	51:1:517:C:H5'	2.02	0.42
51:1:820:A:H5'	51:1:837:C:O2'	2.19	0.42
51:1:2475:C:H42	51:1:2529:G:H22	1.66	0.42
51:1:2544:G:H2'	51:1:2545:G:C8	2.55	0.42
51:1:2581:G:N1	51:1:2610:C:O2'	2.52	0.42
53:3:7:A:H5'	53:3:298:A:O4'	2.19	0.42
53:3:540:G:H2'	53:3:541:G:O4'	2.20	0.42
53:3:1005:A:C2'	53:3:1006:G:H5'	2.49	0.42
53:3:1229:A:H2'	53:3:1230:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1405:G:H21	53:3:1518:A:H8	1.66	0.42
59:B2:699:LEU:HG	59:B2:799:ASN:HD22	1.85	0.42
59:B2:898:GLU:H	59:B2:898:GLU:HG3	1.60	0.42
7:G:26:MET:HG3	7:G:29:PHE:HB2	2.00	0.42
20:T:27:GLN:O	20:T:27:GLN:NE2	2.52	0.42
21:U:50:THR:HB	21:U:78:VAL:HB	2.02	0.42
24:X:44:ILE:HD12	24:X:44:ILE:HA	1.92	0.42
27:b:204:LEU:HD23	27:b:204:LEU:HA	1.90	0.42
28:c:47:ALA:HA	28:c:84:LEU:HG	2.01	0.42
28:c:152:PRO:HA	51:1:1130:U:O2	2.19	0.42
38:n:51:LEU:HD23	38:n:79:LEU:HD11	2.02	0.42
39:o:11:ALA:HB1	39:o:14:ALA:HB3	2.01	0.42
51:1:382:A:C2	51:1:393:C:N3	2.88	0.42
51:1:445:C:O2'	51:1:446:G:H5'	2.20	0.42
51:1:481:G:H1'	51:1:506:G:H22	1.82	0.42
51:1:503:A:H4'	51:1:505:A:H5''	2.02	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
51:1:1145:C:H2'	51:1:1146:C:C6	2.54	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
51:1:2305:U:H2'	51:1:2306:C:H5'	2.02	0.42
51:1:2670:A:H2'	51:1:2671:G:C8	2.55	0.42
53:3:269:C:H2'	53:3:270:A:C8	2.55	0.42
53:3:1327:C:H2'	53:3:1328:C:H6	1.84	0.42
59:B2:538:LEU:HD13	59:B2:543:ALA:HB2	2.01	0.42
65:0:520:ILE:HG22	65:0:578:LEU:HA	2.02	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
9:I:160:LEU:HA	9:I:163:GLN:HE22	1.85	0.42
15:O:82:LYS:HD2	15:O:82:LYS:HA	1.53	0.42
16:P:25:SER:OG	16:P:28:ASN:N	2.48	0.42
18:R:64:VAL:H	18:R:67:ASP:HB3	1.85	0.42
27:b:144:GLU:HA	27:b:151:GLY:HA2	2.00	0.42
28:c:170:VAL:HG13	28:c:194:PRO:HG3	2.01	0.42
31:f:14:VAL:HG12	31:f:27:GLY:HA2	2.01	0.42
37:m:82:MET:HE2	37:m:82:MET:HB2	1.80	0.42
46:v:44:HIS:CE1	46:v:86:LEU:H	2.37	0.42
51:1:8:C:H2'	51:1:9:G:O4'	2.20	0.42
51:1:172:A:H2'	51:1:173:A:C8	2.54	0.42
51:1:751:A:H62	51:1:789:A:H62	1.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1050:A:O2'	51:1:2752:C:H1'	2.19	0.42
51:1:1086:A:C1'	51:1:1103:A:H2	2.33	0.42
51:1:1741:C:C2'	51:1:1742:U:H5'	2.50	0.42
51:1:1972:G:H2'	51:1:1973:G:H8	1.85	0.42
51:1:2114:A:N6	51:1:2119:A:H61	2.18	0.42
51:1:2498:C:O2'	51:1:2499:C:H5'	2.20	0.42
51:1:2553:G:C3'	51:1:2554:U:H5''	2.47	0.42
51:1:2733:A:H2'	51:1:2734:A:H8	1.81	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
55:8:3:DC:N1	55:8:4:DT:H72	2.34	0.42
58:B1:242:LEU:C	58:B1:242:LEU:HD23	2.44	0.42
58:B1:513:MET:HG3	58:B1:544:LEU:HD11	2.01	0.42
58:B1:1289:ASN:O	58:B1:1293:GLU:HB2	2.20	0.42
58:B1:1350:ASN:HA	58:B1:1353:VAL:HG12	2.01	0.42
59:B2:469:VAL:HA	59:B2:472:GLU:HG2	2.02	0.42
65:0:211:MET:HE2	65:0:211:MET:HB3	1.63	0.42
7:G:95:TRP:HZ3	7:G:99:MET:HE2	1.85	0.42
8:H:24:ASN:OD1	8:H:25:THR:N	2.53	0.42
8:H:74:ILE:HG22	59:B2:867:GLU:HA	2.01	0.42
8:H:113:LYS:HA	8:H:113:LYS:HD2	1.88	0.42
10:J:13:LYS:NZ	10:J:14:LEU:O	2.53	0.42
13:M:46:GLU:O	13:M:61:THR:OG1	2.28	0.42
19:S:96:LYS:HA	19:S:96:LYS:HD2	1.79	0.42
27:b:170:TYR:HB3	27:b:182:LYS:HB3	2.02	0.42
28:c:116:LYS:HB2	28:c:165:MET:HB3	2.02	0.42
29:d:50:ALA:HB2	51:1:801:G:C8	2.55	0.42
29:d:93:SER:O	29:d:93:SER:OG	2.32	0.42
33:i:3:LYS:HB3	51:1:1055:G:O5'	2.19	0.42
42:r:1:MET:N	42:r:42:ALA:O	2.42	0.42
51:1:527:C:OP2	51:1:2779:U:N3	2.51	0.42
51:1:809:G:O4'	51:1:1254:A:H1'	2.19	0.42
51:1:976:G:H5'	51:1:1156:A:N6	2.35	0.42
51:1:1716:U:O2'	51:1:1717:A:H5'	2.20	0.42
51:1:2654:A:H1'	51:1:2656:U:C6	2.55	0.42
53:3:627:G:H2'	53:3:628:G:C8	2.54	0.42
53:3:1007:U:H2'	53:3:1008:U:C5	2.54	0.42
53:3:1368:A:O2'	53:3:1369:C:H5'	2.19	0.42
58:B1:59:ALA:HB1	58:B1:90:VAL:HG23	2.01	0.42
58:B1:202:ARG:HH11	58:B1:202:ARG:CG	2.14	0.42
58:B1:390:LEU:N	58:B1:390:LEU:HD13	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:590:PRO:HB2	59:B2:655:VAL:HG21	2.01	0.42
64:a:42:VAL:HG13	64:a:175:ILE:HG13	2.02	0.42
65:0:281:ALA:O	65:0:285:TYR:N	2.53	0.42
6:F:32:LYS:HD2	51:1:2478:A:OP1	2.20	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
28:c:80:TRP:CD1	28:c:202:ILE:HD11	2.55	0.41
29:d:46:GLN:HE21	29:d:86:ALA:HA	1.84	0.41
29:d:85:PHE:CG	51:1:588:U:H1'	2.55	0.41
39:o:35:ILE:HD13	39:o:35:ILE:HA	1.94	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
51:1:191:A:N3	51:1:192:C:C6	2.88	0.41
51:1:736:C:H42	51:1:760:G:H1	1.67	0.41
51:1:1512:C:O5'	51:1:1512:C:H6	2.03	0.41
51:1:2114:A:C5	51:1:2115:G:H1'	2.55	0.41
51:1:2259:U:H1'	51:1:2427:C:H2'	2.02	0.41
51:1:2402:U:H2'	51:1:2403:C:C5'	2.42	0.41
51:1:2472:G:H5''	51:1:2473:U:OP2	2.20	0.41
53:3:224:U:H2'	53:3:225:C:C5	2.55	0.41
53:3:228:A:H2'	53:3:229:U:O4'	2.20	0.41
53:3:426:U:H2'	53:3:427:U:C6	2.54	0.41
53:3:668:G:H2'	53:3:669:G:C8	2.55	0.41
53:3:866:C:N3	53:3:867:G:H1'	2.35	0.41
53:3:957:U:H2'	53:3:959:A:OP2	2.20	0.41
53:3:1153:G:H2'	53:3:1154:G:O4'	2.20	0.41
53:3:1292:G:H2'	53:3:1293:C:C6	2.55	0.41
53:3:1422:G:N2	53:3:1479:C:N4	2.68	0.41
57:A1:76:GLU:HB3	57:A1:80:GLU:HB3	2.01	0.41
58:B1:175:GLU:H	58:B1:175:GLU:HG3	1.66	0.41
58:B1:616:PRO:HA	58:B1:619:ILE:HG22	2.02	0.41
64:a:54:LYS:NZ	64:a:56:ASP:OD1	2.53	0.41
64:a:211:LYS:HE2	64:a:211:LYS:HB2	1.58	0.41
65:0:324:ILE:HA	65:0:334:THR:HA	2.01	0.41
7:G:218:ALA:HA	7:G:221:ARG:HE	1.85	0.41
9:I:201:GLU:OE1	10:J:111:ARG:NH1	2.53	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:38:PHE:HZ	21:U:48:GLU:HG3	1.84	0.41
23:W:62:ARG:NH1	53:3:718:A:N6	2.69	0.41
29:d:29:HIS:CE1	36:l:8:PRO:HB3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:67:SER:HB2	51:1:327:G:H21	1.85	0.41
45:u:96:LYS:HE2	51:1:300:A:P	2.60	0.41
51:1:72:U:C4	51:1:112:U:H4'	2.55	0.41
51:1:458:G:H21	51:1:469:G:H2'	1.84	0.41
51:1:1158:C:O5'	51:1:1158:C:H6	2.02	0.41
51:1:1379:U:H2'	51:1:1380:G:H5'	2.02	0.41
51:1:1388:G:H2'	51:1:1389:G:H8	1.84	0.41
51:1:2638:G:H1'	51:1:2778:A:N6	2.34	0.41
51:1:2676:C:O5'	51:1:2676:C:H6	2.03	0.41
53:3:909:A:H2'	53:3:910:C:O4'	2.20	0.41
53:3:1032:G:H21	53:3:1033:G:H4'	1.85	0.41
58:B1:141:PHE:CD2	58:B1:297:ARG:HB2	2.54	0.41
58:B1:839:VAL:HG12	58:B1:864:LEU:HD12	2.02	0.41
58:B1:848:VAL:HB	58:B1:858:VAL:HG22	2.02	0.41
62:5:4:C:H2'	62:5:5:G:C8	2.55	0.41
65:0:169:LEU:HD12	65:0:185:LEU:HB3	2.01	0.41
65:0:499:THR:CG2	65:0:500:ASP:H	2.23	0.41
2:B:53:VAL:HG23	2:B:54:ILE:HG23	2.02	0.41
9:I:149:LYS:HG2	9:I:150:LYS:HG2	2.02	0.41
13:M:110:MET:HE2	13:M:110:MET:HB3	1.84	0.41
14:N:68:GLY:O	14:N:74:GLN:NE2	2.37	0.41
15:O:58:ASN:HD21	53:3:1061:G:H4'	1.85	0.41
30:e:65:LEU:N	30:e:87:LYS:O	2.53	0.41
37:m:42:THR:HA	37:m:93:VAL:HA	2.02	0.41
51:1:711:G:H2'	51:1:712:G:O4'	2.21	0.41
51:1:777:G:N7	51:1:793:A:C2	2.78	0.41
51:1:1024:G:P	51:1:1025:G:H3'	2.60	0.41
51:1:1592:C:H2'	51:1:1593:A:H8	1.83	0.41
51:1:1625:C:H2'	51:1:1626:A:O4'	2.20	0.41
51:1:2469:A:H2'	51:1:2470:G:O4'	2.20	0.41
51:1:2520:C:H1'	51:1:2565:A:O2'	2.19	0.41
51:1:2553:G:H2'	51:1:2554:U:C4'	2.49	0.41
51:1:2633:G:C2'	51:1:2634:A:H5''	2.47	0.41
53:3:107:G:H2'	53:3:108:G:O4'	2.20	0.41
53:3:262:A:H2'	53:3:263:A:C8	2.55	0.41
53:3:458:U:H2'	53:3:459:A:C8	2.55	0.41
53:3:938:A:H1'	53:3:1376:U:O2'	2.20	0.41
53:3:971:G:N7	53:3:1233:G:H1'	2.34	0.41
53:3:1386:G:O2'	53:3:1387:G:H5'	2.20	0.41
57:A1:48:LEU:HD12	57:A1:48:LEU:HA	1.79	0.41
1:A:11:GLU:HG2	1:A:25:ARG:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:10:LEU:HD21	51:1:2477:U:H5	1.82	0.41
9:I:57:LYS:NZ	9:I:68:GLU:OE1	2.43	0.41
13:M:3:GLN:HE21	53:3:878:A:H1'	1.86	0.41
28:c:117:GLY:H	28:c:164:GLN:HE22	1.68	0.41
28:c:209:ALA:OXT	51:1:2733:A:C2	2.74	0.41
29:d:85:PHE:CE2	51:1:587:C:H5'	2.54	0.41
30:e:63:LYS:O	52:2:42:C:H1'	2.21	0.41
38:n:24:MET:O	38:n:28:LEU:N	2.54	0.41
51:1:538:A:H2'	51:1:539:G:O4'	2.20	0.41
51:1:1183:U:O2'	51:1:1184:U:H5'	2.20	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
51:1:2138:G:N1	51:1:2154:A:O2'	2.47	0.41
51:1:2302:U:H2'	51:1:2303:G:C8	2.55	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
53:3:1315:U:H2'	53:3:1316:G:O4'	2.21	0.41
58:B1:1050:THR:HG23	58:B1:1057:SER:HB3	2.03	0.41
62:5:17:C:H6	62:5:17:C:H2'	1.69	0.41
65:0:495:ARG:HG3	65:0:495:ARG:NH1	2.36	0.41
65:0:569:TYR:HA	65:0:570:PRO:HD3	1.93	0.41
7:G:23:ASN:H	7:G:189:ASN:HA	1.86	0.41
18:R:52:ILE:HD12	18:R:52:ILE:HA	1.96	0.41
20:T:84:LEU:HD12	20:T:84:LEU:HA	1.93	0.41
25:Y:15:LYS:HE2	25:Y:15:LYS:HB3	1.92	0.41
28:c:59:ARG:HA	28:c:59:ARG:HD2	1.85	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
34:j:114:LEU:O	34:j:118:MET:N	2.54	0.41
51:1:19:A:H2'	51:1:20:C:C6	2.55	0.41
51:1:151:C:H5''	51:1:1360:G:OP1	2.21	0.41
51:1:692:C:H2'	51:1:693:A: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
51:1:1310:G:C3'	51:1:1311:G:H5'	2.50	0.41
51:1:1354:A:H2'	51:1:1355:G:O4'	2.20	0.41
51:1:1974:C:H2'	51:1:1975:G:C8	2.55	0.41
51:1:2013:A:H61	51:1:2613:U:H3	1.68	0.41
51:1:2139:U:H2'	51:1:2140:G:H8	1.85	0.41
51:1:2140:G:H1	51:1:2151:U:H3	1.69	0.41
51:1:2448:A:H3'	51:1:2449:U:H2'	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2611:C:H2'	51:1:2612:C:H6	1.85	0.41
52:2:53:A:H2'	52:2:54:G:O4'	2.20	0.41
53:3:68:G:C2	53:3:69:G:H1'	2.55	0.41
53:3:461:A:H2'	53:3:462:G:C8	2.56	0.41
53:3:762:U:H2'	53:3:763:G:C8	2.55	0.41
55:8:14:DC:C2	55:8:15:DC:C5	3.09	0.41
57:A1:205:MET:HE1	57:A1:217:ILE:HG13	2.02	0.41
64:a:167:LYS:HE2	64:a:167:LYS:HB3	1.52	0.41
65:0:64:THR:HG23	65:0:472:ARG:HH22	1.86	0.41
65:0:520:ILE:HD13	65:0:557:ILE:HD11	2.01	0.41
2:B:6:LYS:NZ	51:1:1262:A:C2	2.89	0.41
12:L:138:GLU:O	12:L:142:ARG:N	2.52	0.41
16:P:86:LYS:HG3	16:P:114:PRO:HD3	2.03	0.41
18:R:88:LEU:HD21	18:R:92:ARG:HE	1.86	0.41
28:c:91:THR:H	28:c:94:GLN:HE21	1.66	0.41
30:e:32:LYS:H	30:e:32:LYS:HG2	1.68	0.41
34:j:27:ARG:NH2	51:1:1142:A:H4'	2.36	0.41
36:l:4:ASN:OD1	51:1:1203:U:O2	2.39	0.41
39:o:24:THR:HB	39:o:90:VAL:HG12	2.02	0.41
47:w:56:PHE:HE2	51:1:2365:G:C5'	2.34	0.41
48:x:57:VAL:HG13	51:1:372:G:H5'	2.03	0.41
51:1:140:C:C6	51:1:141:G:H4'	2.55	0.41
51:1:324:A:H2'	51:1:325:G:H5'	2.01	0.41
51:1:1444:G:H2'	51:1:1445:G:O4'	2.21	0.41
51:1:2073:C:O2	51:1:2437:G:C2	2.74	0.41
51:1:2139:U:H2'	51:1:2140:G:C8	2.54	0.41
58:B1:109:SER:CB	58:B1:296:LYS:HG2	2.51	0.41
58:B1:515:ARG:HG2	58:B1:516:ASP:H	1.85	0.41
58:B1:576:ARG:HD3	58:B1:593:ASN:HA	2.03	0.41
58:B1:609:TYR:HD2	58:B1:610:ARG:NH1	2.17	0.41
58:B1:1177:ILE:HD12	58:B1:1186:TYR:HE2	1.86	0.41
59:B2:738:GLU:HA	59:B2:741:MET:HE2	2.03	0.41
59:B2:979:LEU:HD11	59:B2:1011:LEU:HD11	2.03	0.41
1:A:26:SER:HB2	30:e:101:ARG:HH11	1.84	0.41
3:C:13:SER:OG	3:C:47:ILE:O	2.27	0.41
5:E:7:ARG:NH1	51:1:254:G:H22	2.18	0.41
8:H:12:GLY:N	8:H:15:LYS:O	2.35	0.41
14:N:21:LYS:HZ1	14:N:63:TYR:H	1.67	0.41
24:X:20:LYS:O	24:X:24:SER:OG	2.38	0.41
26:Z:27:VAL:O	26:Z:31:VAL:N	2.54	0.41
31:f:97:VAL:HG12	31:f:124:CYS:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:l:78:ARG:HE	36:l:111:ILE:HD11	1.86	0.41
44:t:49:LYS:HD2	44:t:49:LYS:HA	1.75	0.41
51:1:838:C:C2	51:1:941:A:C6	3.09	0.41
51:1:986:C:H6	51:1:986:C:O5'	2.04	0.41
51:1:1054:A:H2	51:1:1105:U:H3	1.69	0.41
51:1:1639:C:C2'	51:1:1640:A:H5'	2.51	0.41
51:1:2041:U:H2'	51:1:2042:A:H8	1.81	0.41
51:1:2049:G:N2	51:1:2620:C:C2	2.89	0.41
51:1:2559:C:H2'	51:1:2560:A:H8	1.86	0.41
53:3:79:G:H2'	53:3:80:A:H5'	2.03	0.41
53:3:111:G:O2'	53:3:389:A:H1'	2.20	0.41
53:3:678:U:H2'	53:3:679:C:C6	2.55	0.41
53:3:1389:C:H2'	53:3:1390:U:O4'	2.21	0.41
58:B1:279:LEU:HD13	58:B1:299:LEU:HD13	2.02	0.41
58:B1:395:LYS:HE3	58:B1:395:LYS:HB3	1.45	0.41
59:B2:310:ILE:HG21	59:B2:325:LEU:HB3	2.03	0.41
59:B2:478:ARG:HD2	59:B2:492:MET:HA	2.02	0.41
59:B2:657:THR:HG21	59:B2:1188:ASP:HB2	2.03	0.41
65:0:320:LEU:HD12	65:0:320:LEU:HA	1.85	0.41
65:0:494:ILE:HB	65:0:608:ALA:HB1	2.03	0.41
10:J:83:PRO:HB3	10:J:97:PRO:HD3	2.02	0.41
11:K:88:MET:HB2	23:W:63:TYR:HE2	1.86	0.41
14:N:6:TYR:CZ	53:3:1147:C:H4'	2.56	0.41
19:S:99:SER:HG	53:3:1187:G:H21	1.69	0.41
27:b:145:MET:HE3	27:b:153:LEU:HD11	2.02	0.41
27:b:153:LEU:HA	51:1:1799:G:N2	2.35	0.41
27:b:240:GLY:CA	51:1:2597:G:H5''	2.51	0.41
32:g:101:ASP:O	32:g:105:ALA:N	2.46	0.41
51:1:1:G:H2'	51:1:2:G:C8	2.55	0.41
51:1:4:U:H2'	51:1:5:A:O4'	2.20	0.41
51:1:272:A:H2'	51:1:273:G:H8	1.86	0.41
51:1:1063:G:OP2	51:1:1070:A:C4'	2.69	0.41
51:1:1752:C:O2'	51:1:1753:G:H5'	2.21	0.41
51:1:1900:A:H5'	51:1:1970:A:C5'	2.50	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
51:1:2201:G:H2'	51:1:2202:U:O4'	2.21	0.41
51:1:2588:G:C2'	51:1:2589:A:H5'	2.50	0.41
53:3:520:A:H61	53:3:533:A:H61	1.67	0.41
53:3:862:C:O2'	53:3:863:U:H5'	2.20	0.41
53:3:1264:U:H3	53:3:1271:A:H61	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1409:C:H2'	53:3:1410:A:C8	2.56	0.41
57:A1:224:LEU:HD23	57:A2:228:LEU:HD21	2.03	0.41
58:B1:71:LEU:HB2	58:B1:90:VAL:HG11	2.03	0.41
58:B1:239:LEU:HD23	58:B1:239:LEU:N	2.36	0.41
58:B1:472:LEU:HD11	59:B2:1294:LYS:HG2	2.02	0.41
59:B2:213:LEU:HD13	59:B2:422:LYS:HG2	2.03	0.41
65:O:18:HIS:ND1	65:O:120:GLN:HB3	2.36	0.41
14:N:21:LYS:HE2	14:N:21:LYS:HB2	1.85	0.41
16:P:25:SER:HA	16:P:88:PRO:HD2	2.02	0.41
17:Q:9:LYS:HE2	17:Q:9:LYS:HB2	1.85	0.41
20:T:3:SER:OG	20:T:5:GLU:OE1	2.33	0.41
21:U:12:LYS:HB3	53:3:392:C:OP2	2.20	0.41
21:U:60:TRP:HB3	21:U:65:ALA:HB2	2.03	0.41
22:V:46:HIS:CG	22:V:66:LEU:HD22	2.56	0.41
24:X:77:ARG:HH11	53:3:1225:A:H4'	1.83	0.41
27:b:7:PRO:HB3	27:b:13:ARG:HG3	2.03	0.41
27:b:71:ASP:OD2	27:b:188:ARG:NH2	2.46	0.41
27:b:145:MET:SD	51:1:1800:C:H5''	2.61	0.41
28:c:55:LYS:HE3	28:c:60:VAL:HG22	2.03	0.41
28:c:113:SER:HB3	28:c:194:PRO:HB3	2.03	0.41
28:c:179:ARG:HB3	28:c:188:LEU:HB2	2.03	0.41
33:i:123:ALA:CB	51:1:1081:U:H4'	2.50	0.41
35:k:1:MET:HE3	51:1:1665:A:H1'	2.02	0.41
36:l:2:ARG:O	36:l:5:THR:OG1	2.36	0.41
37:m:11:LYS:O	51:1:910:A:N6	2.54	0.41
37:m:62:LYS:HD2	37:m:62:LYS:HA	1.91	0.41
41:q:30:VAL:HG11	51:1:580:U:H4'	2.02	0.41
41:q:94:LEU:HA	41:q:97:ILE:HG22	2.03	0.41
51:1:375:G:H2'	51:1:376: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
51:1:740:C:O2'	51:1:741:U:H5'	2.21	0.41
51:1:958:U:C2'	52:2:89:U:H1'	2.47	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
51:1:2081:U:H2'	51:1:2082:A:H8	1.85	0.41
51:1:2534:A:C2	51:1:2535:G:H1'	2.56	0.41
51:1:2830:C:O2	51:1:2883:A:H2	2.03	0.41
53:3:26:A:H61	53:3:558:G:H1'	1.86	0.41
53:3:153:C:H2'	53:3:154:U:C5'	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:204:G:H2'	53:3:205:A:C8	2.56	0.41
53:3:795:C:C5	53:3:796:C:C5	3.09	0.41
57:A1:44:ARG:HA	57:A1:183:ILE:HD12	2.03	0.41
57:A2:42:ALA:HB1	57:A2:224:LEU:HD11	2.03	0.41
57:A2:57:THR:HG23	57:A2:158:ARG:HH21	1.86	0.41
58:B1:87:LYS:H	58:B1:87:LYS:HG2	1.65	0.41
58:B1:144:TYR:N	58:B1:144:TYR:CD1	2.88	0.41
58:B1:907:HIS:ND1	58:B1:908:ILE:O	2.53	0.41
59:B2:741:MET:SD	59:B2:974:ARG:NH2	2.93	0.41
59:B2:866:ASP:C	59:B2:868:SER:H	2.28	0.41
59:B2:886:LYS:HE2	59:B2:918:LEU:HD13	2.03	0.41
64:a:41:SER:OG	64:a:43:ASP:OD2	2.32	0.41
65:0:534:TYR:HB2	65:0:561:LEU:HD11	2.03	0.41
65:0:632:ILE:O	65:0:636:SER:OG	2.36	0.41
4:D:24:THR:OG1	4:D:25:LYS:N	2.53	0.41
4:D:39:ARG:CZ	51:1:469:G:O6	2.69	0.41
9:I:155:LYS:HD2	9:I:155:LYS:HA	1.86	0.41
13:M:126:CYS:SG	13:M:127:TYR:N	2.94	0.41
14:N:82:ILE:HA	14:N:85:ALA:HB3	2.03	0.41
15:O:45:ARG:NH1	15:O:47:GLU:OE1	2.53	0.41
17:Q:23:LEU:HA	17:Q:23:LEU:HD23	1.82	0.41
27:b:110:LYS:HD2	27:b:110:LYS:HA	1.90	0.41
27:b:255:LYS:HD3	51:1:1844:C:H5''	2.02	0.41
31:f:123:GLU:HB2	31:f:131:VAL:HB	2.03	0.41
32:g:9:VAL:HG12	32:g:11:ASN:H	1.86	0.41
39:o:25:ARG:HG3	39:o:40:ILE:HB	2.03	0.41
42:r:78:ARG:HH22	51:1:975:A:H4'	1.86	0.41
45:u:73:ASN:ND2	45:u:76:THR:H	2.19	0.41
45:u:84:PHE:HB2	51:1:297:G:O3'	2.21	0.41
46:v:78:GLN:HB3	46:v:88:HIS:HB3	2.03	0.41
51:1:121:G:H2'	51:1:122:G:H8	1.86	0.41
51:1:395:U:H2'	51:1:396:G:H8	1.80	0.41
51:1:772:C:H5''	51:1:1356:G:C5'	2.50	0.41
51:1:1698:A:N7	51:1:1700:A:C8	2.89	0.41
51:1:1787:A:H2'	51:1:1787:A:N3	2.36	0.41
51:1:1801:A:H5'	51:1:1801:A:H8	1.86	0.41
51:1:1853:A:H2'	51:1:1854:A:H8	1.82	0.41
51:1:2136:G:N1	51:1:2137:U:O2	2.54	0.41
51:1:2255:G:H2'	51:1:2256:G:C8	2.56	0.41
51:1:2746:U:H2'	51:1:2747:G:O4'	2.21	0.41
52:2:102:G:H2'	52:2:103:U:C1'	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
53:3:1536:C:H2'	53:3:1537:U:C6	2.56	0.41
55:8:2:DC:C6	55:8:2:DC:H5'	2.56	0.41
57:A2:104:LYS:HG2	57:A2:110:VAL:HG22	2.03	0.41
58:B1:68:TYR:CB	58:B1:75:TYR:HE2	2.34	0.41
58:B1:243:PRO:HG2	59:B2:1332:SER:C	2.44	0.41
58:B1:390:LEU:HD13	58:B1:390:LEU:H	1.85	0.41
58:B1:930:LEU:HA	58:B1:1244:GLN:HG3	2.02	0.41
65:0:446:ARG:HB3	65:0:459:ALA:HB3	2.02	0.41
15:O:53:ILE:HD12	19:S:84:ARG:HD2	2.03	0.40
25:Y:30:PHE:O	25:Y:34:VAL:N	2.52	0.40
27:b:121:ALA:HA	27:b:129:LEU:HD13	2.02	0.40
28:c:149:ASN:ND2	51:1:2572:A:C8	2.89	0.40
28:c:209:ALA:OXT	51:1:2733:A:N3	2.54	0.40
33:i:21:PRO:HB2	33:i:22:PRO:HD3	2.03	0.40
36:l:29:LYS:HA	36:l:29:LYS:HD2	1.71	0.40
41:q:14:LYS:HA	41:q:14:LYS:HD3	1.88	0.40
49:y:31:GLN:HB3	49:y:37:LEU:HD12	2.02	0.40
51:1:226:A:H2'	51:1:227:A:O4'	2.21	0.40
51:1:1146:C:O2'	51:1:1147:A:H5'	2.21	0.40
51:1:2070:A:C2	51:1:2071:A:C4	3.08	0.40
51:1:2356:U:H3'	51:1:2357:G:H5''	2.03	0.40
53:3:562:U:H4'	53:3:563:A:O5'	2.20	0.40
53:3:794:A:O2'	53:3:795:C:H5'	2.20	0.40
53:3:1283:U:O2'	53:3:1284:C:H5'	2.21	0.40
66:h:5:UAL:C	66:h:6:5OH:HS	2.51	0.40
2:B:39:ARG:CZ	51:1:2884:U:H3	2.34	0.40
2:B:42:ILE:HG22	2:B:48:TYR:HB2	2.03	0.40
7:G:17:HIS:HB2	7:G:202:ASN:HD22	1.86	0.40
10:J:37:VAL:HG21	10:J:113:VAL:HG13	2.02	0.40
13:M:4:ASP:HB3	13:M:7:ALA:HB3	2.02	0.40
15:O:46:LYS:HB3	53:3:1253:G:OP1	2.21	0.40
16:P:66:ALA:HA	16:P:69:CYS:HB3	2.04	0.40
17:Q:56:LEU:HD13	17:Q:56:LEU:HA	1.91	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
27:b:269:ARG:HA	27:b:269:ARG:HD2	1.84	0.40
28:c:19:GLY:HA2	40:p:78:PRO:HD2	2.02	0.40
30:e:78:ILE:HD11	30:e:82:TYR:HB3	2.03	0.40
31:f:97:VAL:HG11	31:f:123:GLU:HA	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:i:71:LYS:HD3	33:i:116:MET:HE2	2.03	0.40
33:i:91:LYS:HD2	33:i:91:LYS:HA	1.93	0.40
41:q:23:TYR:HD1	51:1:533:G:C5'	2.35	0.40
51:1:191:A:H2'	51:1:192:C:C6	2.56	0.40
51:1:677:A:C6	51:1:802:A:C6	3.09	0.40
51:1:940:G:C3'	51:1:941:A:H5''	2.51	0.40
51:1:1047:G:N2	51:1:1110:G:H2'	2.36	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
51:1:1831:G:C2	51:1:1975:G:C2	3.10	0.40
51:1:2313:C:H2'	51:1:2314:A:C8	2.56	0.40
51:1:2656:U:OP1	65:0:146:ARG:NH2	2.52	0.40
51:1:2811:G:O2'	51:1:2812:G:H5'	2.21	0.40
53:3:220:G:O2'	53:3:221:C:H5'	2.21	0.40
53:3:1346:A:N1	53:3:1374:A:H5''	2.35	0.40
54:4:37:G:H5'	59:B2:688:GLN:HE22	1.85	0.40
63:6:33:U:H2'	63:6:35:A:OP2	2.21	0.40
63:6:62:C:H5'	64:a:53:ARG:NE	2.36	0.40
9:I:49:ASP:OD1	9:I:49:ASP:N	2.54	0.40
19:S:4:SER:OG	53:3:1216:A:H5''	2.21	0.40
24:X:46:LEU:HB3	24:X:48:ILE:HG12	2.03	0.40
27:b:77:VAL:HB	27:b:112:GLY:H	1.86	0.40
27:b:116:GLN:NE2	27:b:120:ASP:OD2	2.54	0.40
27:b:159:THR:OG1	27:b:160:TYR:N	2.54	0.40
38:n:20:MET:HE2	38:n:20:MET:HB3	1.74	0.40
40:p:17:PRO:HD2	40:p:83:ILE:HB	2.03	0.40
48:x:1:SER:OG	51:1:1365:A:H5'	2.20	0.40
49:y:31:GLN:HG2	49:y:37:LEU:HB2	2.03	0.40
51:1:43:G:H2'	51:1:44:A:O4'	2.22	0.40
51:1:1169:A:H2'	51:1:1170:C:O4'	2.22	0.40
51:1:1955:U:H6	51:1:1955:U:H5'	1.86	0.40
51:1:2798:U:H4'	51:1:2799:A:C6	2.56	0.40
52:2:78:A:H2'	52:2:79:G:O4'	2.20	0.40
52:2:112:G:H2'	52:2:113:C:C6	2.56	0.40
53:3:392:C:H2'	53:3:393:A:O4'	2.21	0.40
53:3:408:A:N6	53:3:434:U:H3	2.18	0.40
53:3:492:C:H2'	53:3:493:A:H8	1.83	0.40
53:3:517:G:H4'	53:3:519:C:C2	2.56	0.40
53:3:904:U:H2'	53:3:905:U:C6	2.56	0.40
53:3:990:C:H2'	53:3:991:U:O4'	2.21	0.40
53:3:1093:A:O2'	53:3:1094:G:H5'	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1221:G:O2'	53:3:1222:G:H5'	2.21	0.40
64:a:48:LEU:HB2	64:a:169:GLY:O	2.21	0.40
65:0:158:ILE:HG23	65:0:162:LEU:HB2	2.03	0.40
65:0:375:LYS:HE2	65:0:375:LYS:HB2	1.89	0.40
3:C:10:LEU:HB2	3:C:20:TYR:HB2	2.04	0.40
18:R:70:ARG:NE	30:e:141:ASP:O	2.53	0.40
19:S:1:ALA:HB1	53:3:1049:U:C4	2.56	0.40
25:Y:21:ALA:HA	25:Y:24:ARG:HD3	2.02	0.40
44:t:36:LYS:HA	44:t:36:LYS:HD2	1.86	0.40
51:1:277:G:H2'	51:1:361:G:O6	2.21	0.40
51:1:375:G:O2'	51:1:376:G:H5'	2.21	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
51:1:1601:G:O2'	51:1:1602:U:H5'	2.22	0.40
51:1:1642:G:H2'	51:1:1643:G:O4'	2.21	0.40
51:1:1679:A:H4'	51:1:1990:C:H4'	2.03	0.40
51:1:1843:C:H2'	51:1:1844:C:H6	1.82	0.40
51:1:1967:C:H2'	51:1:1968:G:O4'	2.22	0.40
51:1:2140:G:H2'	51:1:2141:G:C8	2.56	0.40
51:1:2356:U:C3'	51:1:2357:G:H5''	2.52	0.40
51:1:2533:U:H2'	51:1:2534:A:O4'	2.21	0.40
51:1:2741:A:N6	51:1:2763:G:H1'	2.37	0.40
53:3:79:G:C2'	53:3:80:A:H5'	2.51	0.40
53:3:883:C:H2'	53:3:884:U:C6	2.56	0.40
53:3:944:G:N1	53:3:1338:G:OP2	2.50	0.40
53:3:962:C:H1'	53:3:1201:A:N6	2.36	0.40
58:B1:26:SER:HB3	58:B1:29:MET:H	1.87	0.40
58:B1:245:LEU:HD13	59:B2:1329:GLU:HA	2.04	0.40
58:B1:820:ILE:HD11	58:B1:822:MET:HE2	2.02	0.40
59:B2:22:LEU:HD22	59:B2:603:ILE:HG21	2.02	0.40
59:B2:998:LEU:HD21	59:B2:1015:ALA:HB2	2.02	0.40
65:0:32:PHE:HA	65:0:37:ASN:HB2	2.03	0.40
7:G:33:ALA:N	7:G:37:VAL:O	2.46	0.40
8:H:148:ILE:HG23	8:H:169:GLU:HB3	2.03	0.40
9:I:2:ARG:HD3	53:3:405:U:OP2	2.22	0.40
32:g:1:MET:HE3	32:g:1:MET:HB3	1.90	0.40
32:g:78:VAL:HG21	32:g:103:VAL:HG23	2.04	0.40
35:k:71:ARG:HH22	40:p:79:VAL:HG11	1.86	0.40
38:n:23:ASN:HD21	51:1:1294:U:H1'	1.87	0.40
47:w:58:LYS:HB2	47:w:58:LYS:HE3	1.76	0.40
51:1:126:A:C6	51:1:127:A:C2	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1521:G:H2'	51:1:1522:A:C8	2.56	0.40
51:1:1923:U:H2'	51:1:1924:C:C6	2.53	0.40
51:1:2108:A:OP1	64:a:3:LYS:HB3	2.22	0.40
51:1:2112:G:O6	51:1:2167:U:O2'	2.37	0.40
52:2:4:C:H2'	52:2:5:U:H6	1.83	0.40
53:3:42:G:H1	53:3:400:C:H42	1.70	0.40
53:3:581:G:N2	53:3:761:G:C6	2.89	0.40
53:3:866:C:C2	53:3:867:G:H1'	2.57	0.40
53:3:986:U:H2'	53:3:987:G:O4'	2.21	0.40
57:A1:51:MET:HA	57:A1:52:PRO:HD3	1.93	0.40
58:B1:111:THR:HG23	58:B1:300:GLN:HA	2.03	0.40
58:B1:351:GLY:O	58:B1:467:ALA:HA	2.21	0.40
62:5:37:A:H3'	62:5:38:A:C8	2.56	0.40
63:6:25:C:H2'	63:6:26:G:H8	1.85	0.40
63:6:27:U:H6	63:6:27:U:H5'	1.87	0.40
65:0:340:SER:HA	65:0:379:ALA:HB1	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	37
6	F	36/38 (95%)	29 (81%)	7 (19%)	0	100	100
7	G	216/241 (90%)	182 (84%)	34 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	204/233 (88%)	186 (91%)	18 (9%)	0	100	100
9	I	203/206 (98%)	171 (84%)	31 (15%)	1 (0%)	24	63
10	J	155/167 (93%)	129 (83%)	26 (17%)	0	100	100
11	K	98/135 (73%)	81 (83%)	17 (17%)	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%)	81 (84%)	15 (16%)	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	53
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
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%)	165 (94%)	10 (6%)	0	100	100
31	f	174/177 (98%)	157 (90%)	17 (10%)	0	100	100
32	g	147/149 (99%)	124 (84%)	23 (16%)	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	79 (86%)	13 (14%)	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	214/329 (65%)	195 (91%)	19 (9%)	0	100	100
57	A2	217/329 (66%)	207 (95%)	10 (5%)	0	100	100
58	B1	1329/1407 (94%)	1205 (91%)	120 (9%)	4 (0%)	36	71
59	B2	1338/1342 (100%)	1206 (90%)	126 (9%)	6 (0%)	30	67
60	W0	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
61	NG	84/181 (46%)	77 (92%)	6 (7%)	1 (1%)	10	43
64	a	128/234 (55%)	105 (82%)	23 (18%)	0	100	100
65	0	695/716 (97%)	618 (89%)	72 (10%)	5 (1%)	18	55
66	h	2/6 (33%)	1 (50%)	1 (50%)	0	100	100
All	All	9784/10690 (92%)	8648 (88%)	1117 (11%)	19 (0%)	44	77

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
58	B1	121	PRO
59	B2	897	PRO
59	B2	43	PRO
59	B2	918	LEU
61	NG	102	PRO
65	0	199	GLY
59	B2	888	THR
65	0	298	ILE
65	0	299	LEU

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Mol	Chain	Res	Type
17	Q	87	LYS
58	B1	43	THR
58	B1	193	ASP
65	0	196	ALA
5	E	16	THR
58	B1	1325	PHE
59	B2	905	ILE
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	32
5	E	51/52 (98%)	46 (90%)	5 (10%)	7	24
6	F	34/34 (100%)	33 (97%)	1 (3%)	37	58
7	G	180/199 (90%)	172 (96%)	8 (4%)	25	47
8	H	170/190 (90%)	158 (93%)	12 (7%)	13	35
9	I	171/173 (99%)	166 (97%)	5 (3%)	37	58
10	J	119/126 (94%)	113 (95%)	6 (5%)	22	43
11	K	87/116 (75%)	82 (94%)	5 (6%)	18	41
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%)	77 (90%)	9 (10%)	6	22
16	P	89/99 (90%)	88 (99%)	1 (1%)	65	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	73
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	12
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	79
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	76
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%)	87 (94%)	6 (6%)	15	37
44	t	80/84 (95%)	77 (96%)	3 (4%)	29	51
45	u	83/85 (98%)	82 (99%)	1 (1%)	63	73
46	v	78/78 (100%)	77 (99%)	1 (1%)	61	72
47	w	57/63 (90%)	57 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	40
57	A2	186/286 (65%)	182 (98%)	4 (2%)	45	64
58	B1	1110/1168 (95%)	1020 (92%)	90 (8%)	11	31
59	B2	1150/1157 (99%)	1115 (97%)	35 (3%)	36	57
60	W0	70/75 (93%)	68 (97%)	2 (3%)	37	58
64	a	109/181 (60%)	98 (90%)	11 (10%)	7	23
65	o	574/588 (98%)	554 (96%)	20 (4%)	32	53
66	h	2/2 (100%)	2 (100%)	0	100	100
All	All	8119/8683 (94%)	7831 (96%)	288 (4%)	32	53

All (288) 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

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Mol	Chain	Res	Type
8	H	63	ILE
8	H	65	VAL
8	H	76	ILE
8	H	78	LYS
8	H	79	LYS
8	H	81	GLU
8	H	134	LYS
8	H	135	ARG
9	I	27	ILE
9	I	128	VAL
9	I	163	GLN
9	I	165	GLU
9	I	166	LYS
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	53	LYS
11	K	54	LEU
11	K	55	HIS
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	30	LYS
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

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Mol	Chain	Res	Type
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
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	76	VAL
43	s	92	ARG

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Mol	Chain	Res	Type
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
57	A2	93	GLN
57	A2	95	LYS
57	A2	96	ASP
58	B1	24	LEU
58	B1	40	LYS
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

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Mol	Chain	Res	Type
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
58	B1	190	LYS
58	B1	193	ASP
58	B1	196	GLN
58	B1	210	SER
58	B1	212	THR
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
59	B2	857	VAL
59	B2	866	ASP
59	B2	887	VAL
59	B2	890	LYS
59	B2	893	THR
59	B2	894	GLN
59	B2	895	LEU
59	B2	897	PRO
59	B2	898	GLU
59	B2	899	GLU
59	B2	900	LYS
59	B2	901	LEU
59	B2	902	LEU
59	B2	903	ARG
59	B2	905	ILE
59	B2	912	ASP
59	B2	913	VAL
59	B2	915	ASP
59	B2	918	LEU
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
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

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Mol	Chain	Res	Type
65	0	301	ASP
65	0	303	LYS
65	0	338	VAL
65	0	390	ASP
65	0	504	LYS
65	0	507	LYS
65	0	508	GLN
65	0	512	ARG
65	0	514	GLN
65	0	517	HIS
65	0	519	VAL
65	0	611	VAL
65	0	662	GLU
65	0	663	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (157) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
3	C	45	HIS
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
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	163	GLN
9	I	195	ASN
9	I	197	HIS

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Mol	Chain	Res	Type
10	J	69	ASN
10	J	121	ASN
10	J	147	ASN
11	K	52	ASN
11	K	94	HIS
12	L	8	GLN
12	L	27	ASN
12	L	96	ASN
13	M	3	GLN
13	M	15	ASN
13	M	20	ASN
14	N	3	ASN
16	P	21	HIS
16	P	27	ASN
16	P	80	ASN
17	Q	28	GLN
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	67	HIS
25	Y	74	HIS
25	Y	81	GLN
25	Y	83	ASN
26	Z	55	HIS
27	b	14	HIS
27	b	24	HIS
27	b	85	ASN
27	b	142	ASN
28	c	32	ASN
28	c	36	GLN
28	c	49	GLN
28	c	67	HIS

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Mol	Chain	Res	Type
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
32	g	18	GLN
32	g	33	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	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
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	66	HIS

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Mol	Chain	Res	Type
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	364	HIS
58	B1	424	ASN
58	B1	450	HIS
58	B1	469	HIS
58	B1	805	GLN
58	B1	865	HIS
58	B1	1195	GLN
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	1080	ASN
59	B2	1237	HIS
59	B2	1268	GLN
59	B2	1313	HIS
60	W0	7	GLN
60	W0	31	GLN
60	W0	62	GLN
64	a	24	ASN
64	a	172	HIS
65	0	85	ASN
65	0	92	HIS
65	0	157	GLN
65	0	170	GLN
65	0	259	ASN
65	0	272	ASN

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Mol	Chain	Res	Type
65	0	276	GLN
65	0	351	ASN
65	0	455	GLN
65	0	487	GLN
65	0	514	GLN
65	0	530	ASN
65	0	584	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	1	2902/2904 (99%)	439 (15%)	6 (0%)
52	2	119/120 (99%)	18 (15%)	0
53	3	1538/1542 (99%)	193 (12%)	1 (0%)
54	4	20/38 (52%)	9 (45%)	1 (5%)
62	5	75/76 (98%)	45 (60%)	10 (13%)
63	6	76/77 (98%)	14 (18%)	0
All	All	4730/4757 (99%)	718 (15%)	18 (0%)

All (718) 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
51	1	120	U
51	1	125	A
51	1	126	A
51	1	139	U
51	1	140	C

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Mol	Chain	Res	Type
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	355	U
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
51	1	431	U
51	1	451	U
51	1	455	C
51	1	456	C

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Mol	Chain	Res	Type
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
51	1	775	G
51	1	776	G
51	1	782	A
51	1	783	A

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Mol	Chain	Res	Type
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
51	1	1021	A
51	1	1022	G
51	1	1025	G
51	1	1026	G

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Mol	Chain	Res	Type
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
51	1	1180	U
51	1	1206	G
51	1	1212	G
51	1	1225	G

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Mol	Chain	Res	Type
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
51	1	1555	G
51	1	1559	U
51	1	1566	A
51	1	1569	A

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Mol	Chain	Res	Type
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
51	1	1938	A
51	1	1939	U
51	1	1955	U
51	1	1963	U

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Mol	Chain	Res	Type
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
51	1	2134	A
51	1	2135	A
51	1	2138	G
51	1	2143	C

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Mol	Chain	Res	Type
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
51	1	2350	C
51	1	2357	G
51	1	2361	G
51	1	2371	G

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Mol	Chain	Res	Type
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
51	1	2578	G
51	1	2585	U
51	1	2602	A
51	1	2603	G

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Mol	Chain	Res	Type
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
51	1	2880	C
51	1	2883	A
51	1	2884	U
51	1	2893	A

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Mol	Chain	Res	Type
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
53	3	100	G
53	3	110	C
53	3	134	G
53	3	154	U

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Mol	Chain	Res	Type
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
53	3	497	G
53	3	509	A
53	3	510	A
53	3	511	C

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Mol	Chain	Res	Type
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
53	3	841	C
53	3	843	U
53	3	844	G
53	3	846	G

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Mol	Chain	Res	Type
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
53	3	1139	G
53	3	1159	U
53	3	1168	U
53	3	1182	G

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Mol	Chain	Res	Type
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	1492	A
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

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Mol	Chain	Res	Type
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	30	G
62	5	2	C
62	5	7	A
62	5	8	U
62	5	9	A
62	5	11	C
62	5	13	C
62	5	15	G
62	5	17	C
62	5	18	G
62	5	19	G
62	5	20	U
62	5	21	A
62	5	26	A
62	5	28	G
62	5	29	G
62	5	30	G
62	5	32	U
62	5	33	U
62	5	34	G
62	5	35	A
62	5	36	A
62	5	37	A
62	5	39	U
62	5	40	C
62	5	41	C
62	5	43	C
62	5	44	G
62	5	46	G
62	5	47	U
62	5	48	C
62	5	49	C
62	5	52	G

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Mol	Chain	Res	Type
62	5	53	G
62	5	55	U
62	5	56	C
62	5	57	G
62	5	58	A
62	5	59	U
62	5	60	U
62	5	61	C
62	5	66	U
62	5	73	A
62	5	74	C
62	5	75	C
62	5	76	A
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 (18) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	1	858	G
51	1	1020	A
51	1	1106	G
51	1	1801	A
51	1	2326	C
51	1	2756	U
53	3	413	G
54	4	10	C
62	5	7	A
62	5	29	G
62	5	32	U

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Mol	Chain	Res	Type
62	5	35	A
62	5	39	U
62	5	48	C
62	5	57	G
62	5	60	U
62	5	73	A
62	5	75	C

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
66	KBE	h	1	66	8,8,9	0.59	0	6,8,10	1.19	0
66	UAL	h	5	66	6,8,9	2.35	2 (33%)	4,9,11	1.87	1 (25%)
66	5OH	h	6	66	7,12,13	0.74	0	4,16,18	1.35	1 (25%)
66	DPP	h	2	66	4,5,6	0.51	0	1,5,7	0.06	0

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
66	KBE	h	1	66	-	0/7/7/8	-
66	UAL	h	5	66	-	0/3/7/9	-
66	5OH	h	6	66	-	0/2/18/20	0/1/1/1
66	DPP	h	2	66	-	0/2/4/6	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	h	5	UAL	C1-N1	-4.91	1.32	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	h	5	UAL	C-CA	-2.80	1.40	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
66	h	5	UAL	O-C-CA	-3.28	121.27	125.39
66	h	6	5OH	CR-CB-CA	-2.43	110.03	112.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
66	h	5	UAL	2	0
66	h	6	5OH	5	0
66	h	2	DPP	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
67	GDP	0	801	-	29,30,30	1.17	3 (10%)	45,47,47	1.88	8 (17%)
68	PO4	0	802	-	4,4,4	1.01	0	6,6,6	0.50	0

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	GDP	0	801	-	-	2/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	0	801	GDP	C5-C4	2.77	1.46	1.38
67	0	801	GDP	C6-N1	-2.63	1.33	1.38
67	0	801	GDP	C4-N9	-2.01	1.33	1.38

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	0	801	GDP	C5-C4-N3	-5.99	118.85	128.39
67	0	801	GDP	C2-N3-C4	5.06	121.02	112.30
67	0	801	GDP	N9-C4-N3	4.47	134.90	125.95
67	0	801	GDP	C6-C5-N7	3.60	136.85	130.29
67	0	801	GDP	C4-C5-N7	-2.75	106.31	110.67
67	0	801	GDP	C2'-C1'-N9	-2.12	107.36	113.25
67	0	801	GDP	O6-C6-C5	-2.10	120.99	126.53
67	0	801	GDP	C5-C6-N1	2.03	118.43	113.25

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
67	0	801	GDP	C5'-O5'-PA-O3A
67	0	801	GDP	C5'-O5'-PA-O1A

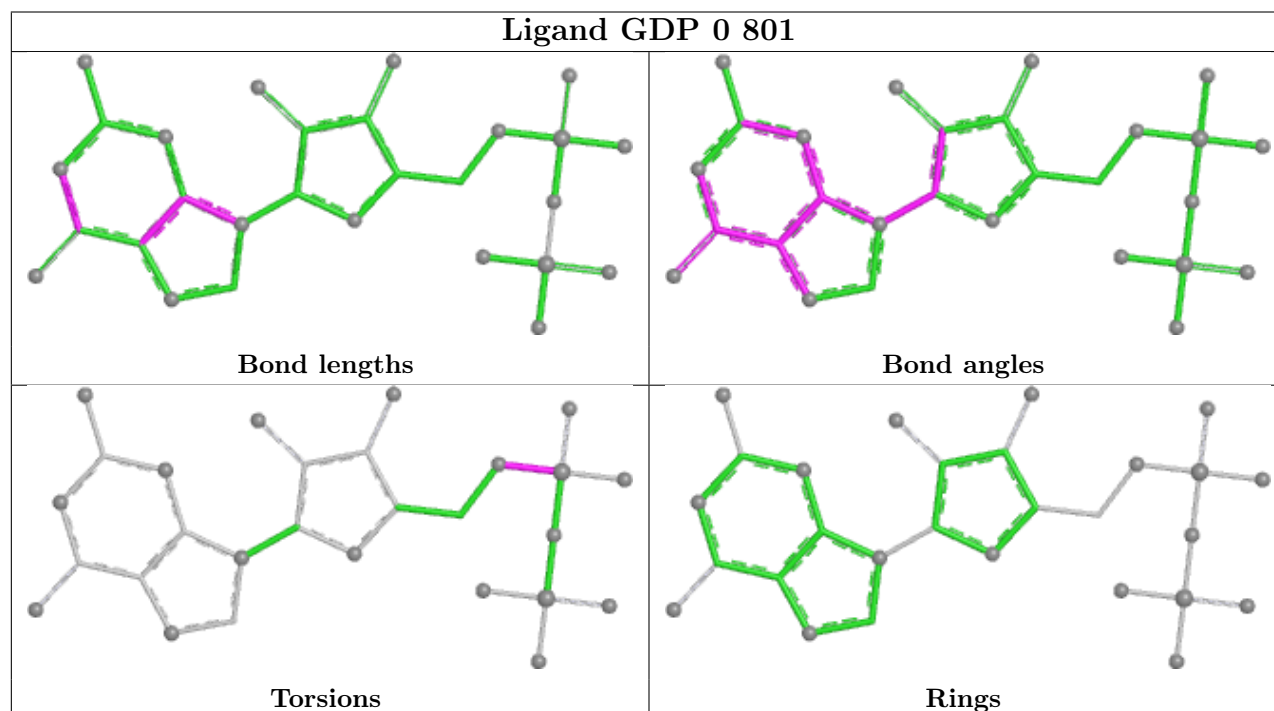
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
67	0	801	GDP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

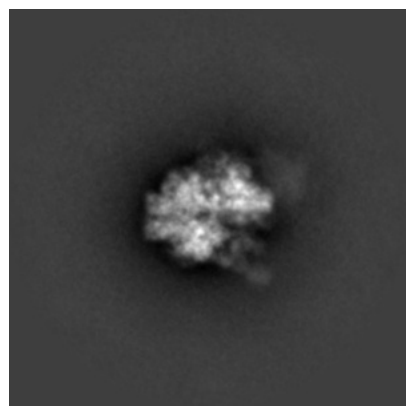
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38943. These allow visual inspection of the internal detail of the map and identification of artifacts.

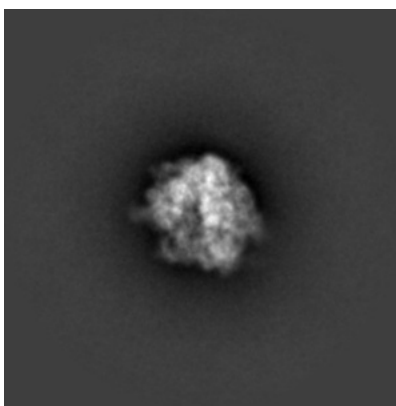
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

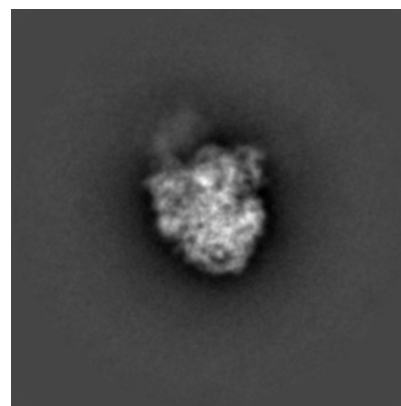
6.1.1 Primary map



X

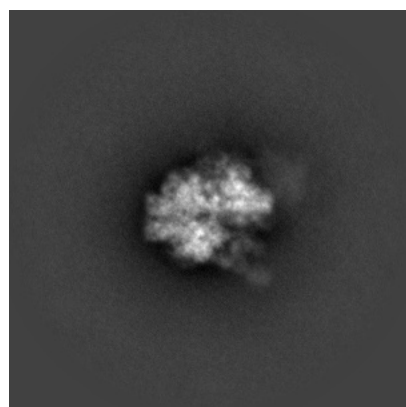


Y

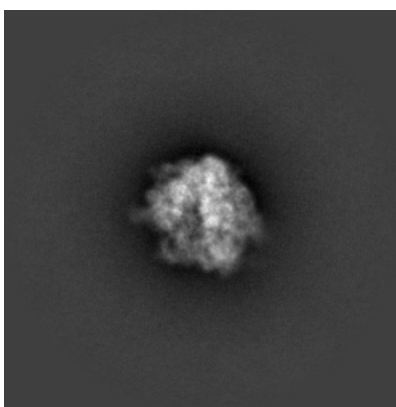


Z

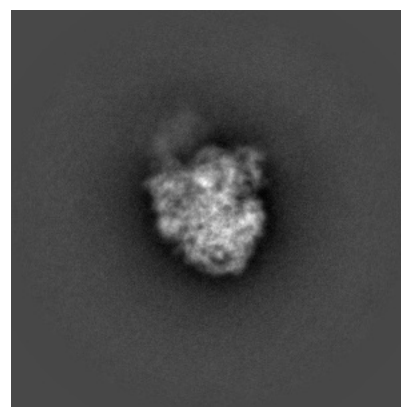
6.1.2 Raw map



X



Y

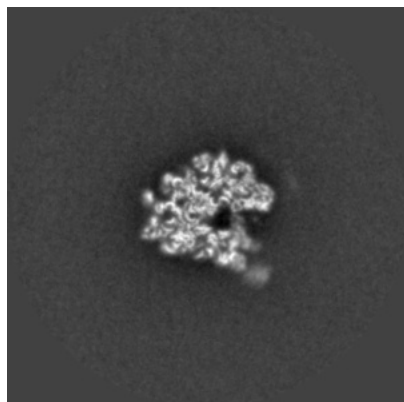


Z

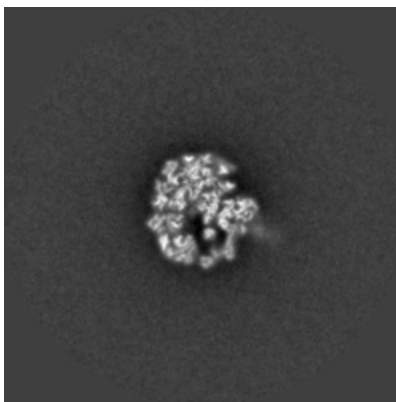
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

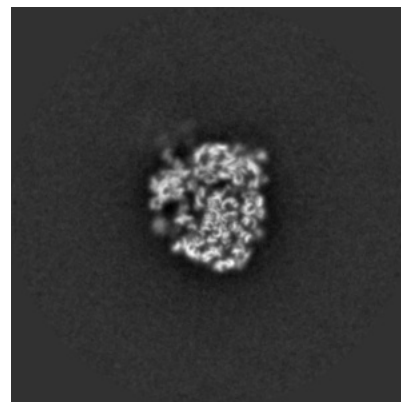
6.2.1 Primary map



X Index: 240

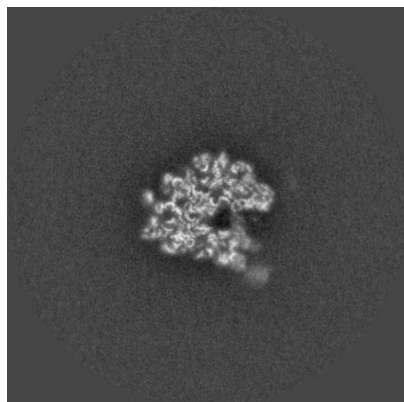


Y Index: 240

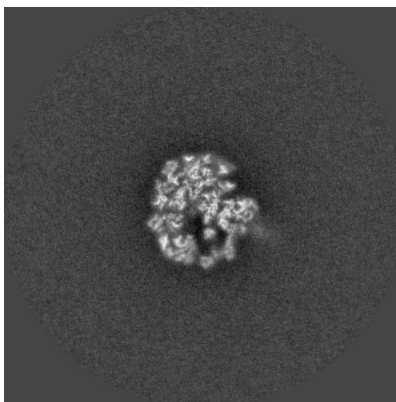


Z Index: 240

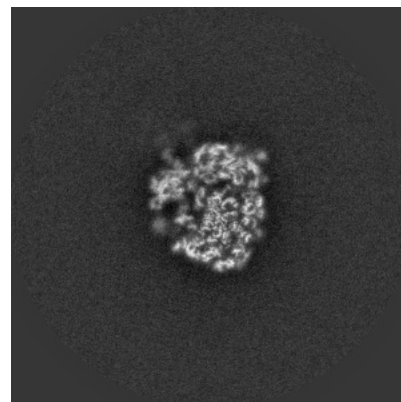
6.2.2 Raw map



X Index: 240



Y Index: 240

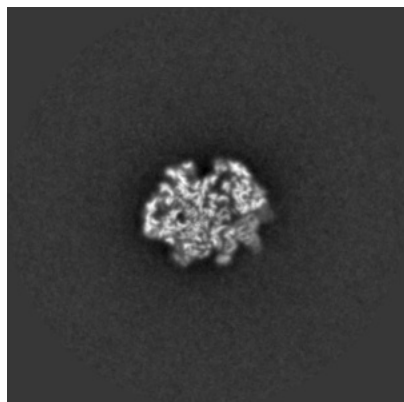


Z Index: 240

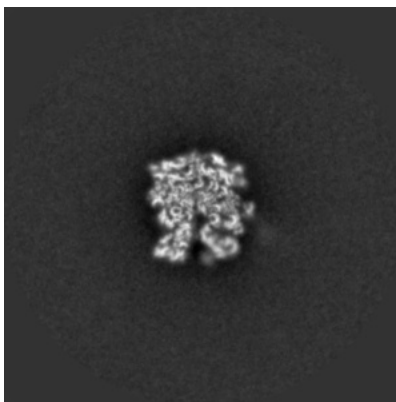
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

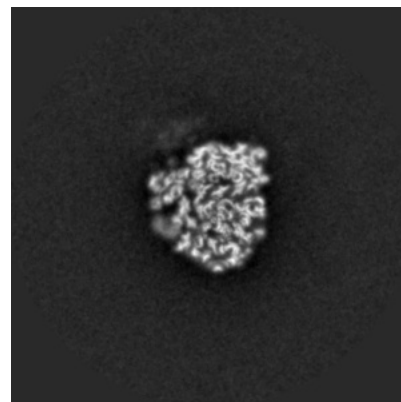
6.3.1 Primary map



X Index: 263

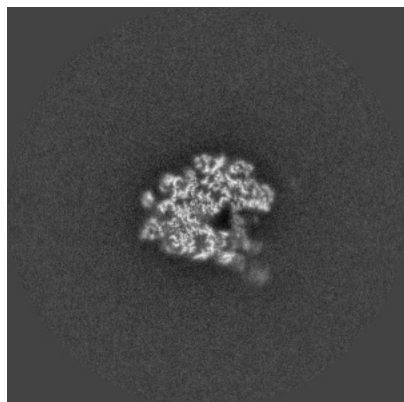


Y Index: 225

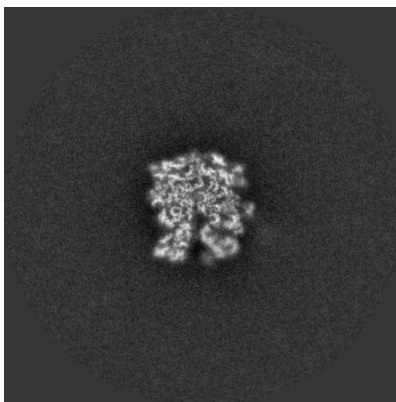


Z Index: 245

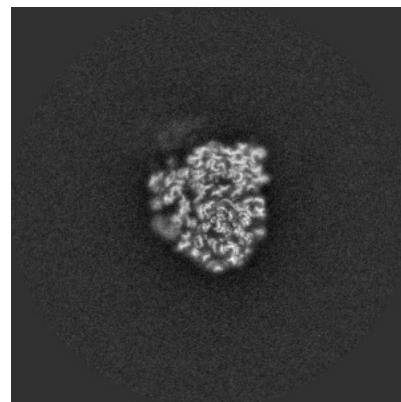
6.3.2 Raw map



X Index: 243



Y Index: 225

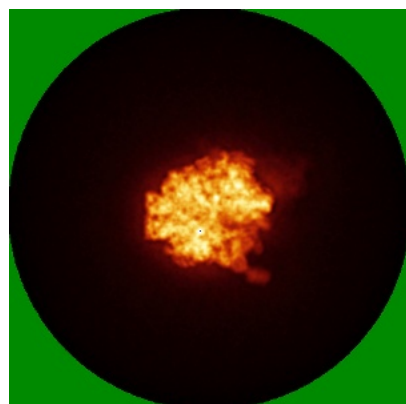


Z Index: 246

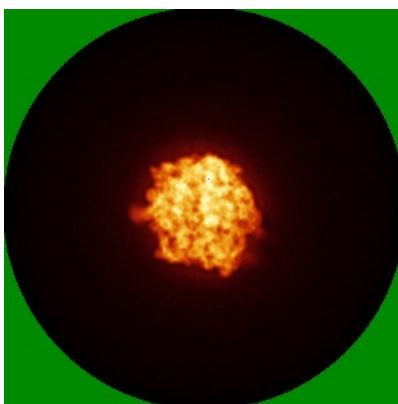
The images above show the largest variance slices of the map in three orthogonal directions.

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

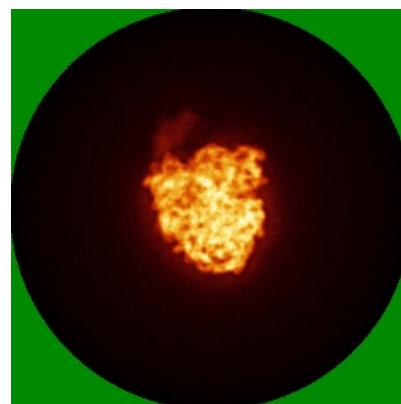
6.4.1 Primary map



X

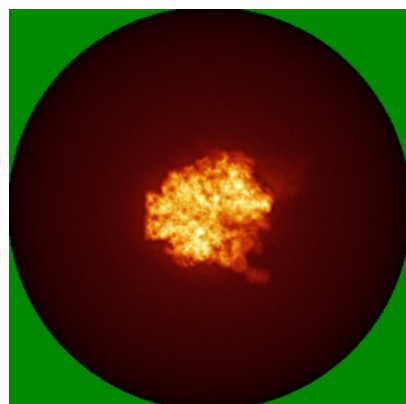


Y

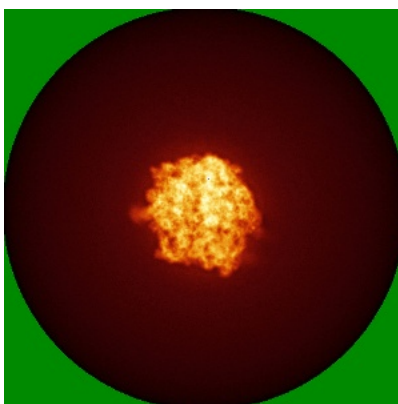


Z

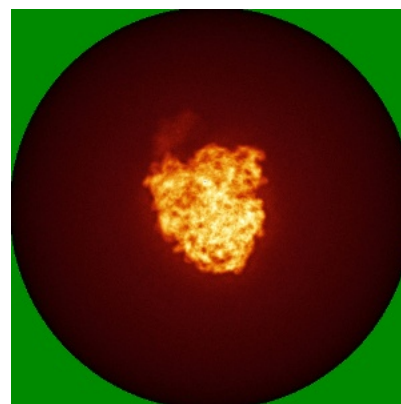
6.4.2 Raw map



X



Y

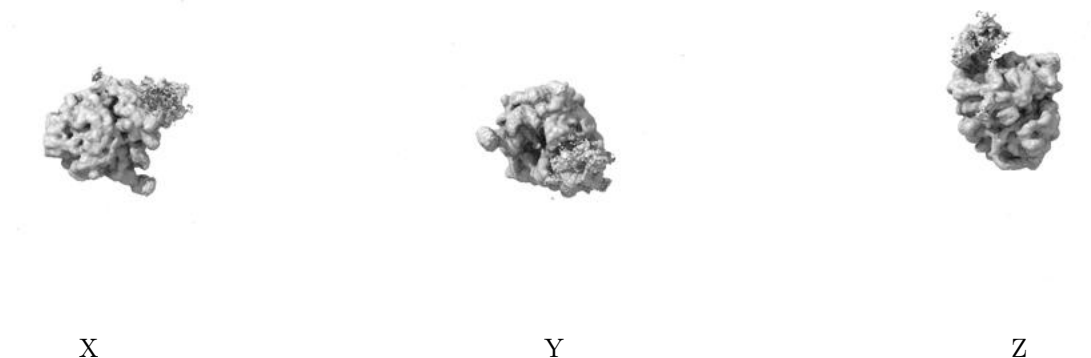


Z

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

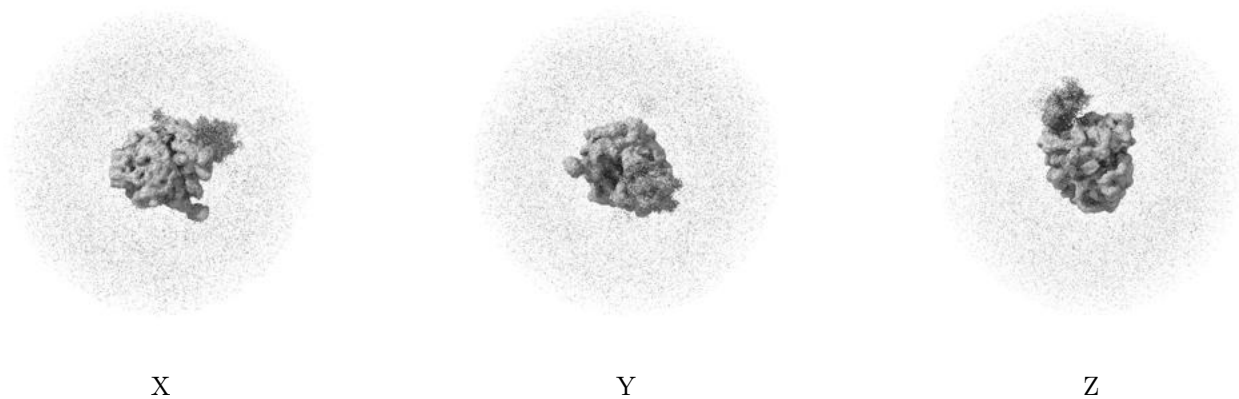
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

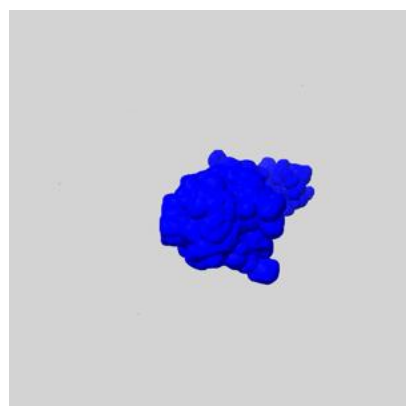
6.6 Mask visualisation [i](#)

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

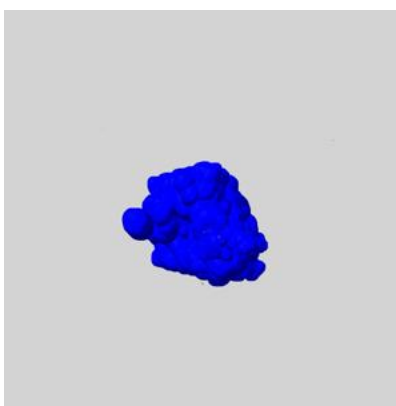
A mask typically either:

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

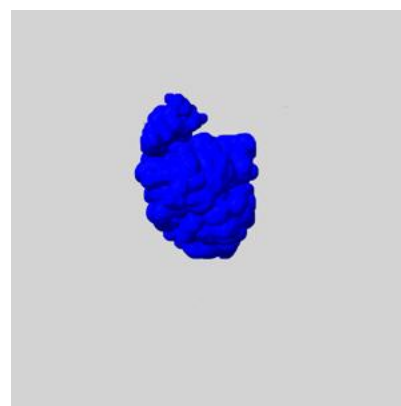
6.6.1 emd_38943_msk_1.map [i](#)



X



Y

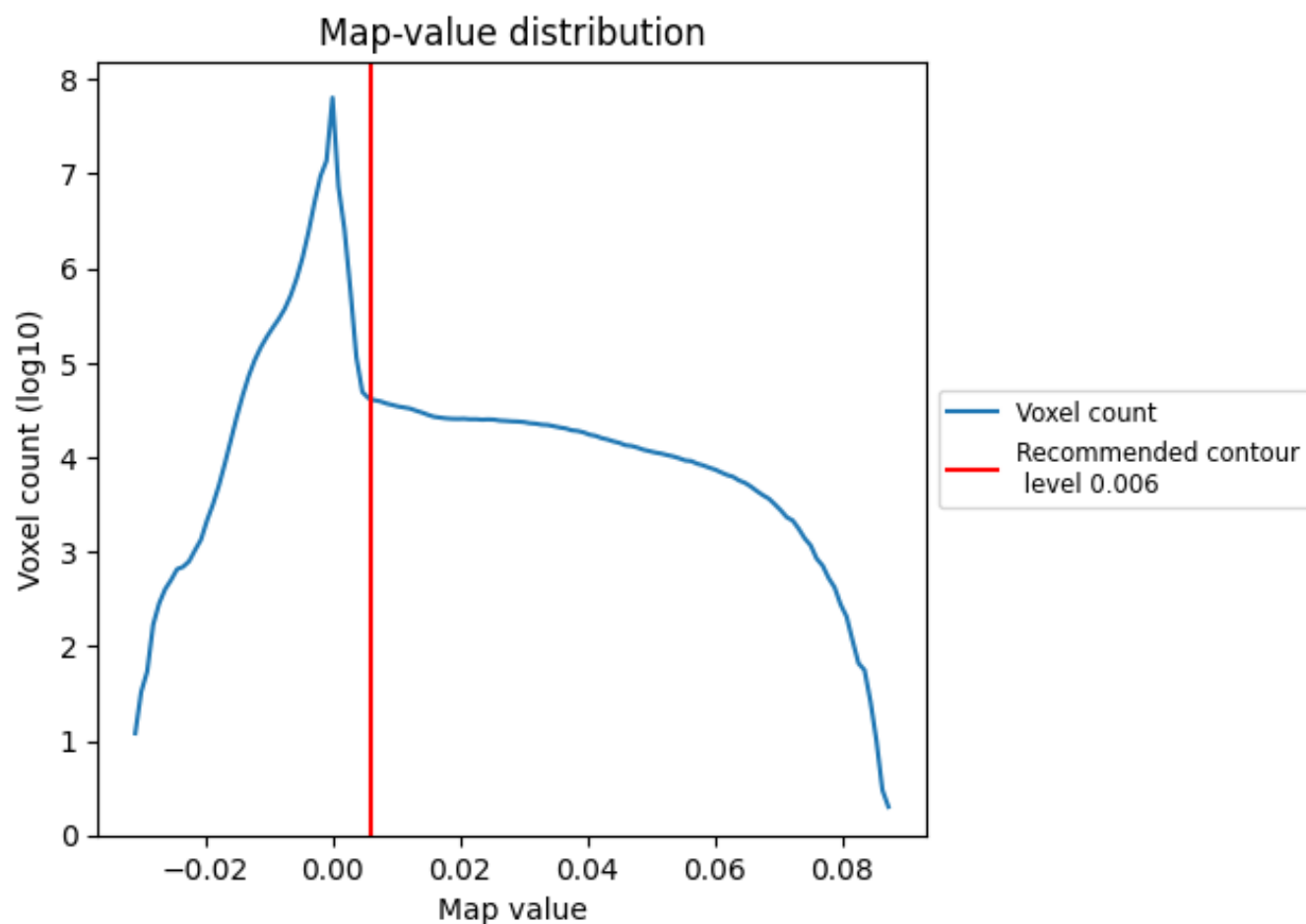


Z

7 Map analysis [i](#)

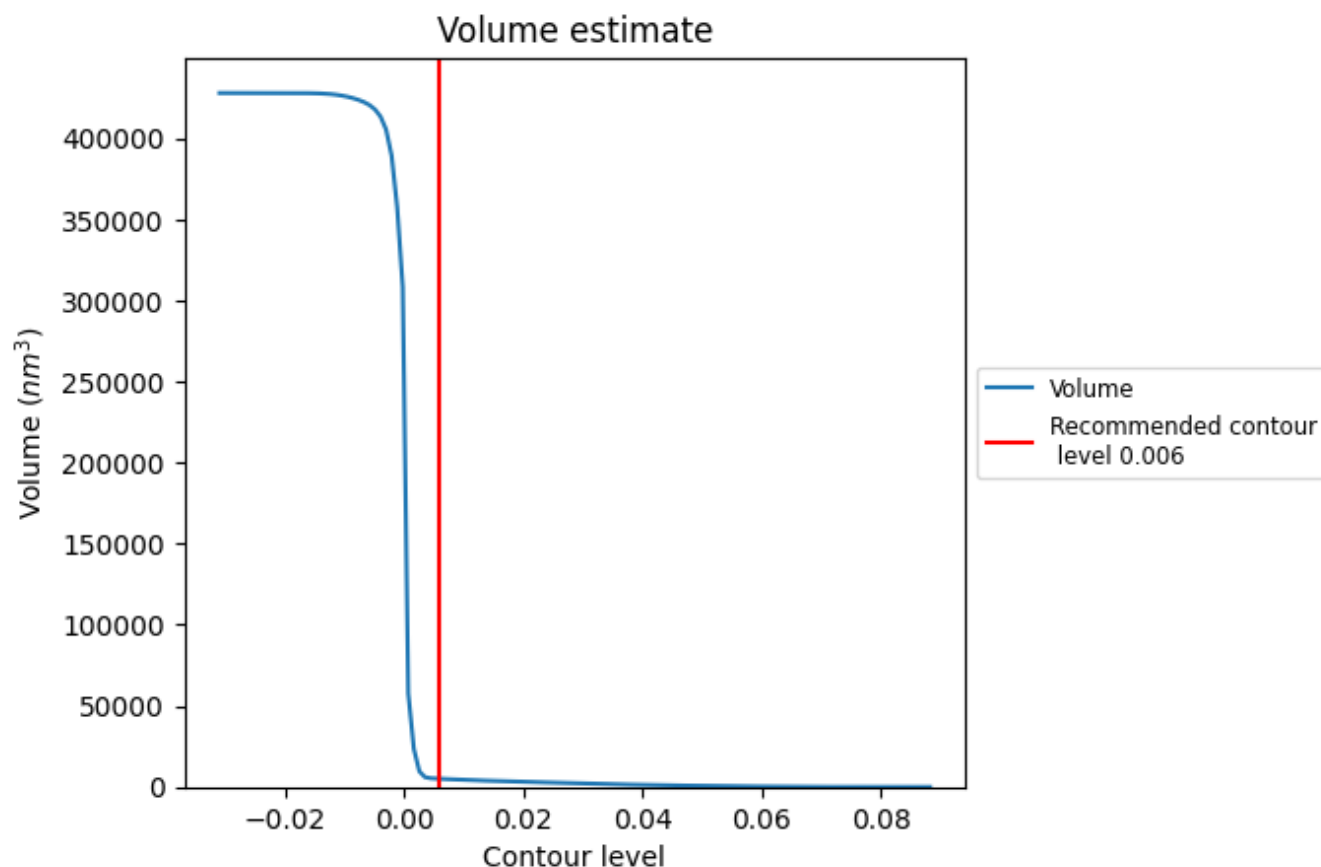
This section contains the results of statistical analysis of the map.

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.

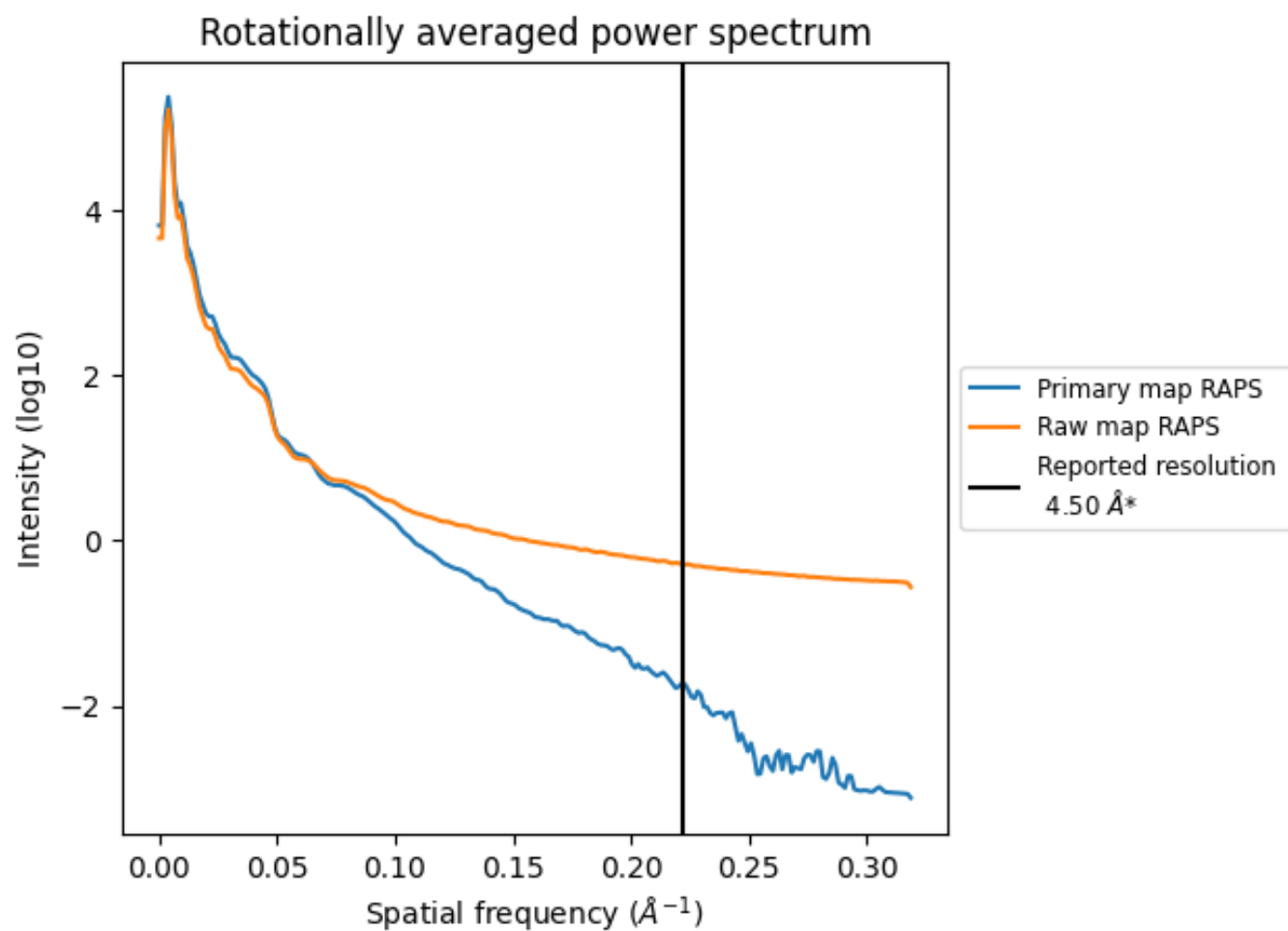
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5051 nm^3 ; this corresponds to an approximate mass of 4562 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 ⓘ

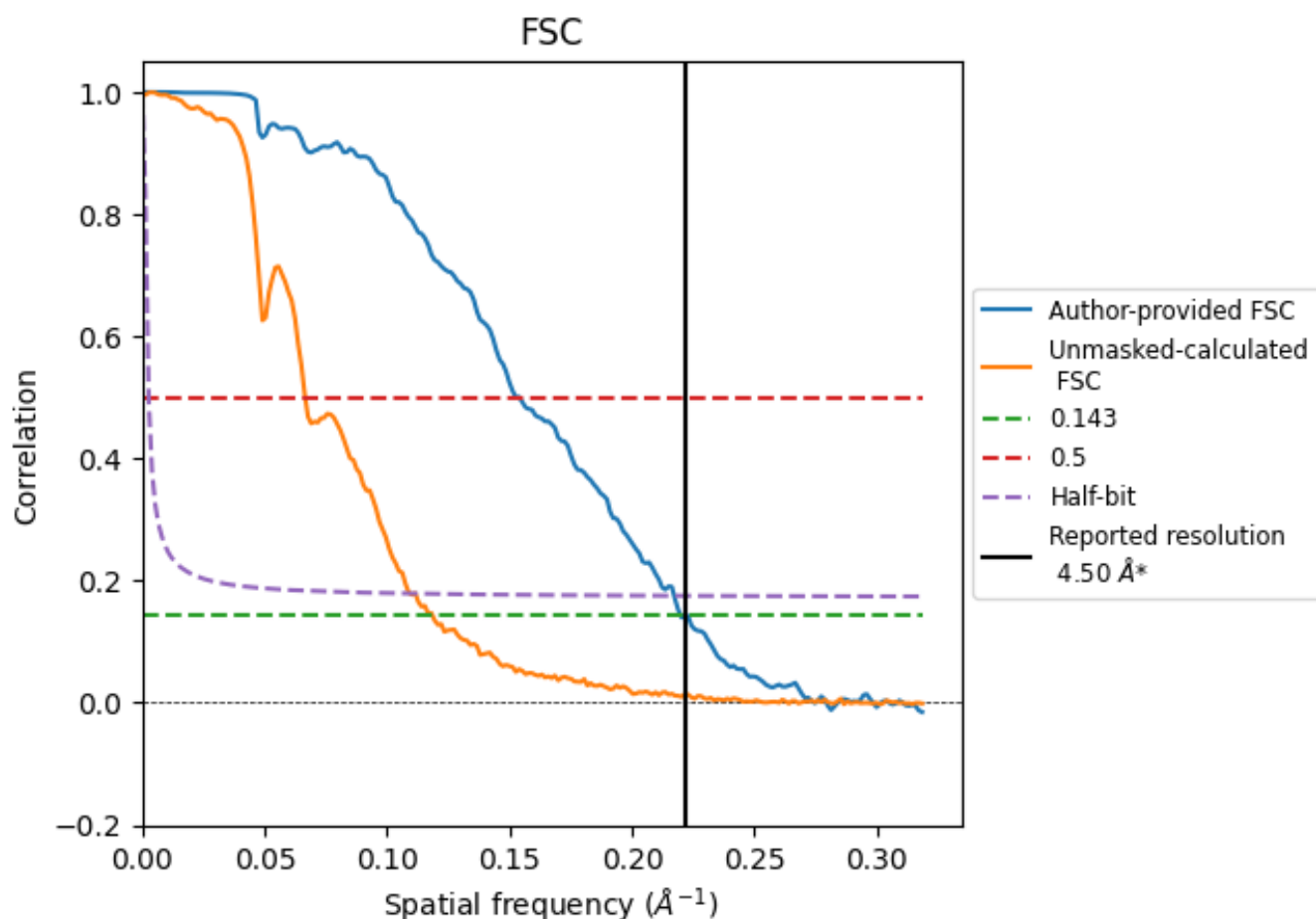


*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

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 0.222 Å⁻¹

8.2 Resolution estimates [i](#)

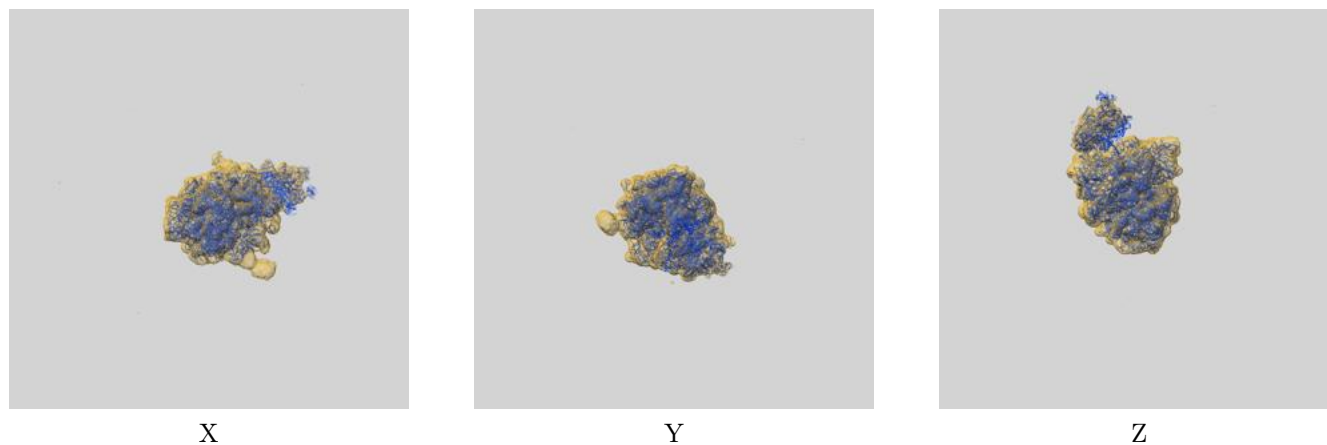
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.55	6.49	4.60
Unmasked-calculated*	8.44	15.02	9.13

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.44 differs from the reported value 4.5 by more than 10 %

9 Map-model fit [i](#)

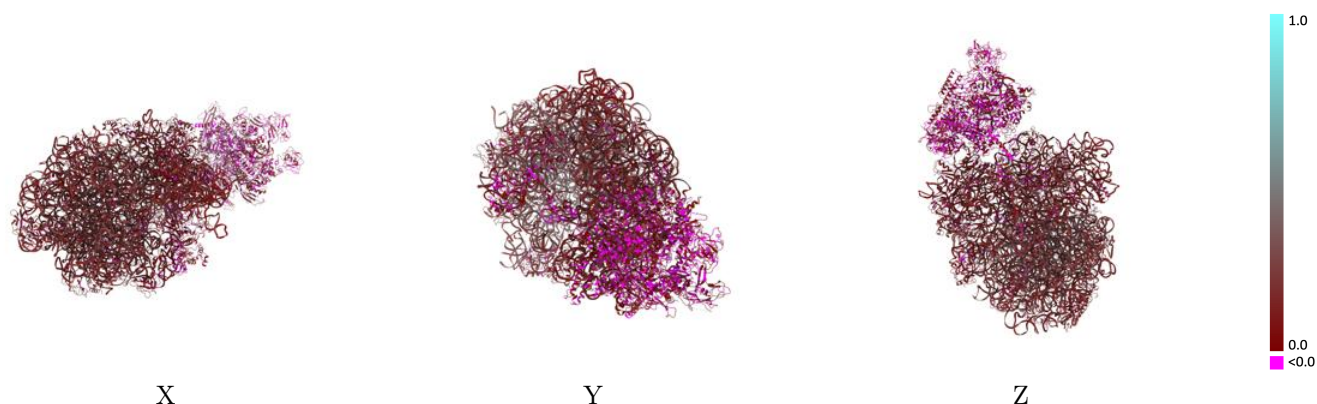
This section contains information regarding the fit between EMDB map EMD-38943 and PDB model 8Y5N. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



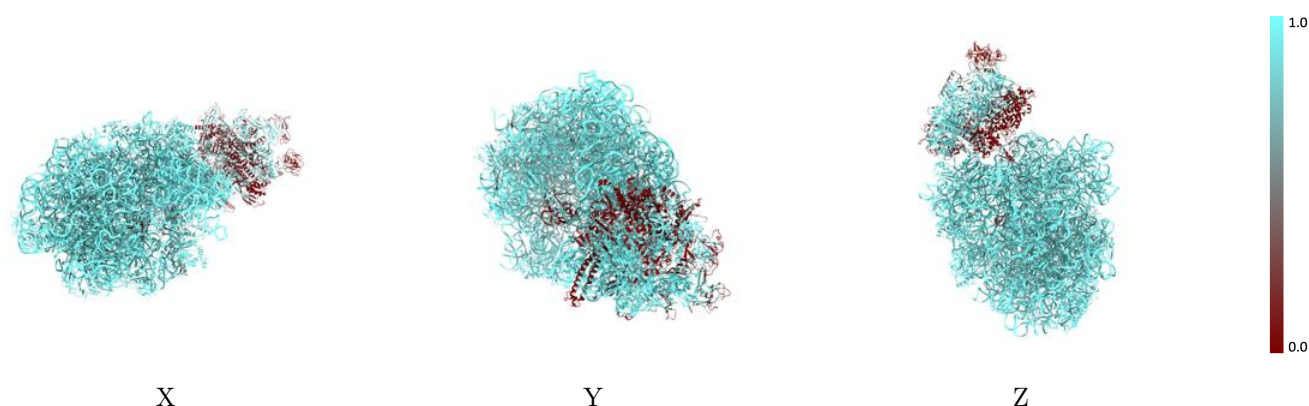
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



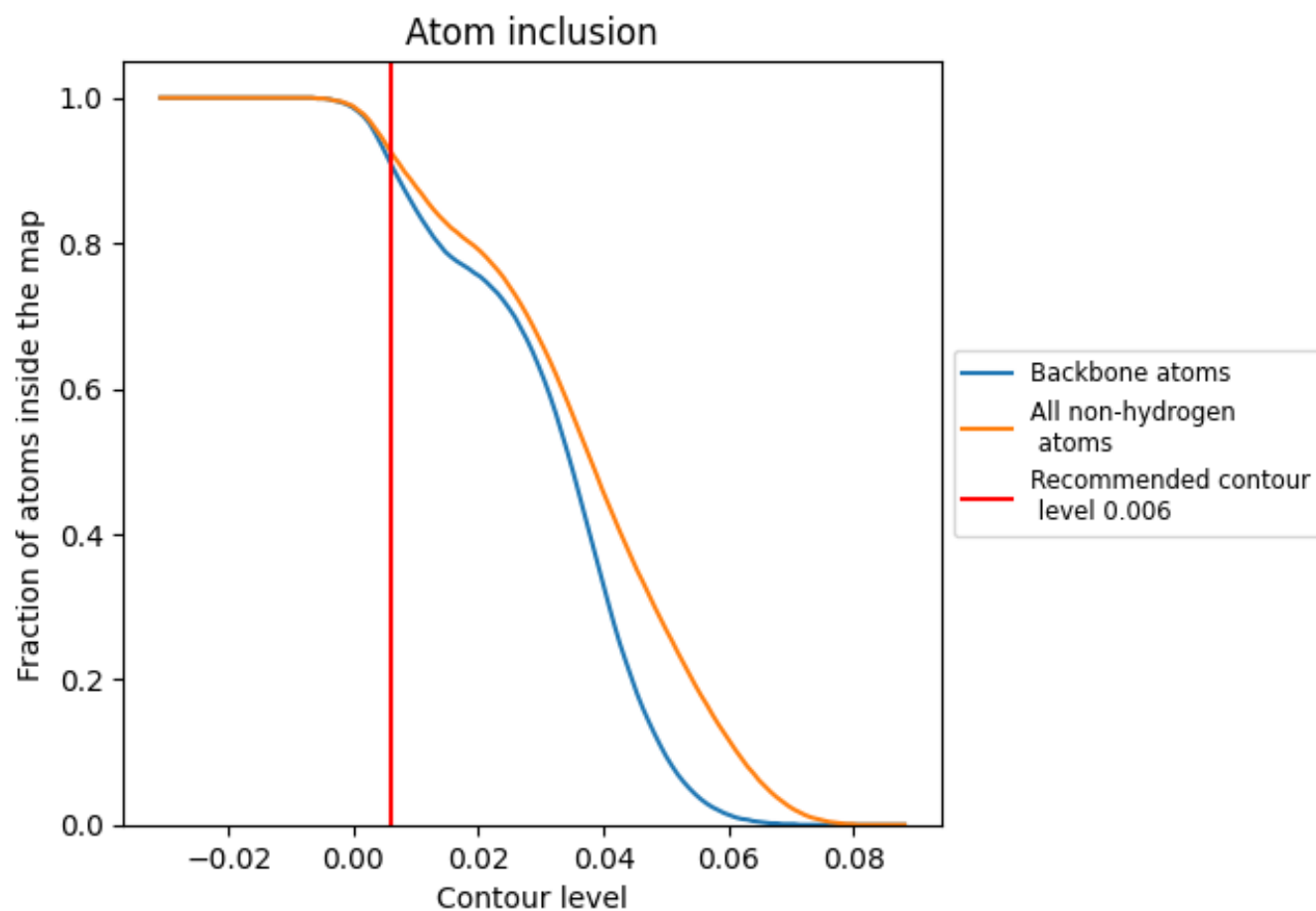
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.006).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 92% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9250	 0.1580
0	 0.8730	 0.0920
1	 1.0000	 0.2110
2	 1.0000	 0.1580
3	 1.0000	 0.1800
4	 0.9380	 0.1350
5	 0.5650	 0.0810
6	 0.9960	 0.1750
8	 0.8160	 0.0890
9	 0.7410	 0.0960
A	 0.9970	 0.1060
A1	 0.5740	 0.0740
A2	 0.6060	 0.0320
B	 0.9950	 0.1630
B1	 0.4920	 0.0580
B2	 0.6440	 0.0520
C	 0.9750	 0.1480
D	 0.9920	 0.1470
E	 1.0000	 0.1420
F	 1.0000	 0.1290
G	 0.9950	 0.1450
H	 0.9980	 0.1450
I	 0.9970	 0.1280
J	 1.0000	 0.1360
K	 0.9950	 0.1540
L	 0.9900	 0.1350
M	 0.9880	 0.1100
N	 0.9880	 0.1030
NG	 0.0230	 0.1060
O	 0.9990	 0.1210
P	 0.9950	 0.1590
Q	 0.9700	 0.1500
R	 0.9910	 0.1360
S	 1.0000	 0.1200
T	 0.9990	 0.1430



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Chain	Atom inclusion	Q-score
U	 1.0000	 0.1030
V	 0.9970	 0.1060
W	 1.0000	 0.1440
W0	 0.0680	 0.0080
X	 1.0000	 0.1200
Y	 0.9830	 0.1080
Z	 0.9540	 0.1430
a	 0.9890	 0.1000
b	 0.9930	 0.1830
c	 0.9970	 0.1710
d	 0.9970	 0.1500
e	 0.9700	 0.1160
f	 0.9950	 0.1360
g	 0.9380	 0.1300
h	 1.0000	 0.1970
i	 0.9090	 0.0490
j	 1.0000	 0.1690
k	 0.9810	 0.1920
l	 0.9990	 0.1440
m	 0.9800	 0.1540
n	 1.0000	 0.1640
o	 1.0000	 0.1020
p	 0.9940	 0.1790
q	 0.9990	 0.1360
r	 0.9990	 0.1520
s	 0.9950	 0.1750
t	 0.9990	 0.1480
u	 0.9920	 0.1380
v	 0.9970	 0.1450
w	 0.9960	 0.1140
x	 1.0000	 0.1720
y	 0.9980	 0.1500
z	 0.9930	 0.1490