



## Full wwPDB EM Validation Report ⓘ

Aug 18, 2025 – 04:52 PM JST

PDB ID : 8YDH / pdb\_00008ydh  
EMDB ID : EMD-39171  
Title : E.coli transcription translation coupling complex in TTC-P state 1 (subclass1) containing mRNA with 39-mer spacer, NusG, NusA, fMet-tRNA(iMet), Phe-tRNA(Phe), and viomycin  
Authors : Zhang, J.; Lu, G.; Wang, C.; Lin, J.  
Deposited on : 2024-02-20  
Resolution : 4.55 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev126  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.45.1

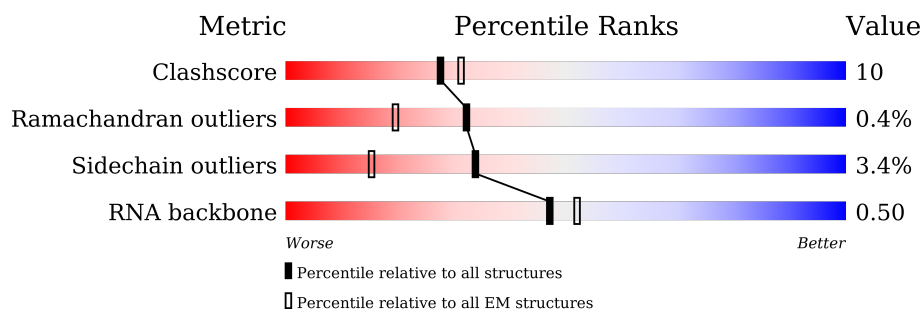
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.55 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	 81% 13% 6%
2	B	57	 81% 16% . .
3	C	55	 84% 7% 9%
4	D	46	 76% 24%
5	E	65	 89% 9% .
6	F	38	 66% 32% .
7	G	241	 67% 22% . 10%

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Mol	Chain	Length	Quality of chain
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	
29	d	201	
30	e	179	
31	f	177	
32	g	149	

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Mol	Chain	Length	Quality of chain
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	
54	4	47	
55	8	37	
56	9	37	
57	A1	329	

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Mol	Chain	Length	Quality of chain
57	A2	329	
58	B1	1407	
59	B2	1342	
60	W0	91	
61	NA	495	
62	NG	181	
63	5	76	
64	6	77	
64	7	77	
65	h	6	

## 2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 177388 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	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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



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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	52	Total	C	N	O	S	0	0
			400	256	73	70	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	35	Total	C	N	O	P	0	0
			729	326	105	263	35		

- 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 NusA.

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
63	5	76	Total	C	N	O	P	0	0
			1622	723	290	533	76		

- Molecule 64 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
64	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
64	7	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 65 is a protein (with D amino acids) called tRNA(fMet).

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

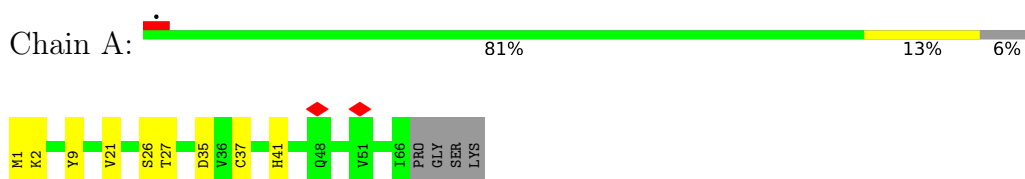
- Molecule 66 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

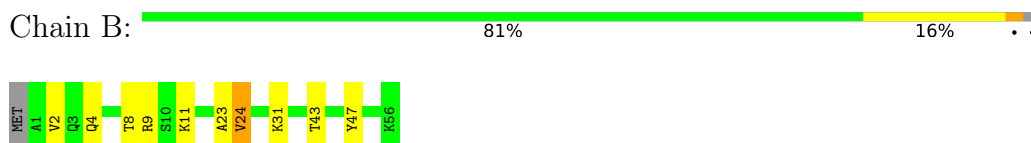
### 3 Residue-property plots [i](#)

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.

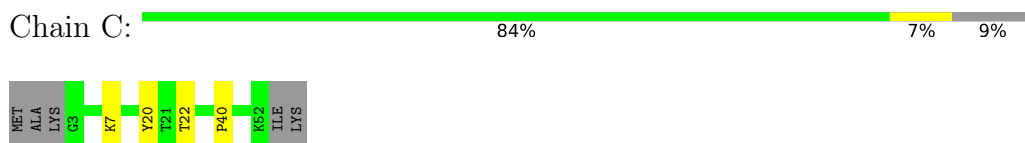
- Molecule 1: 50S ribosomal protein L31



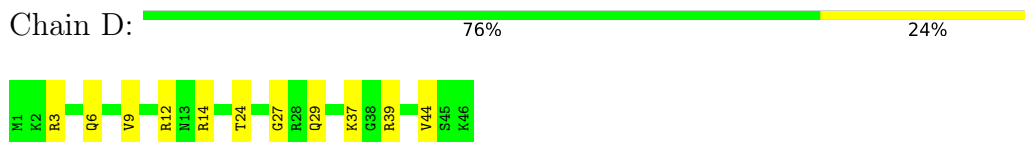
- Molecule 2: 50S ribosomal protein L32



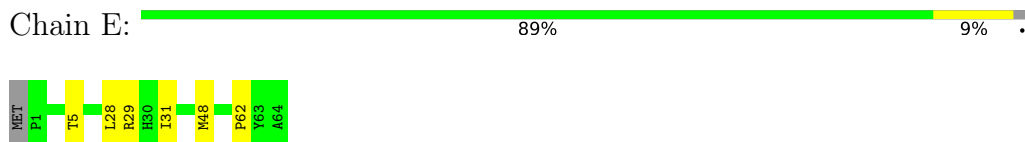
- Molecule 3: 50S ribosomal protein L33



- Molecule 4: 50S ribosomal protein L34




- Molecule 5: 50S ribosomal protein L35



- Molecule 6: 50S ribosomal protein L36

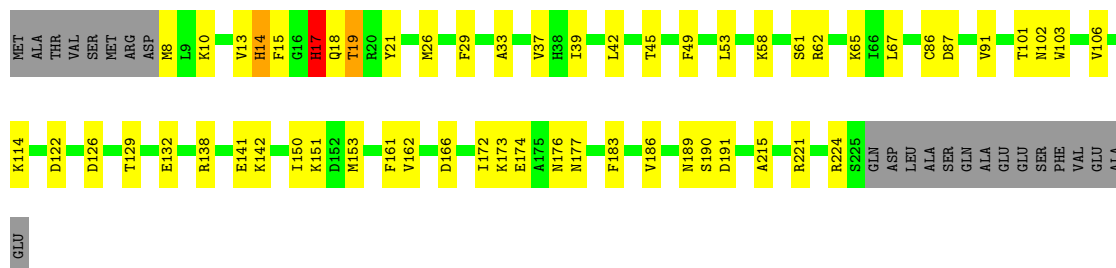


Chain F:  66% 32% .



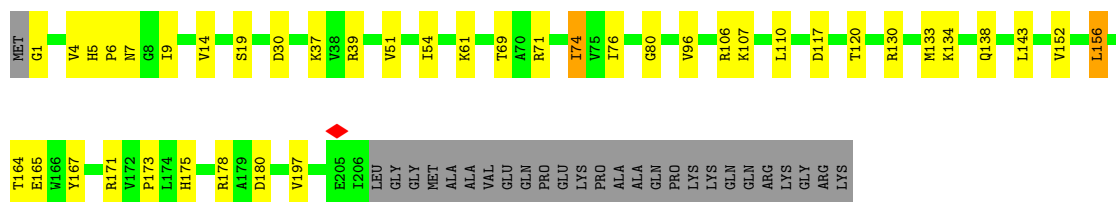
- Molecule 7: 30S ribosomal protein S2

Chain G:  67% 22% . 10%




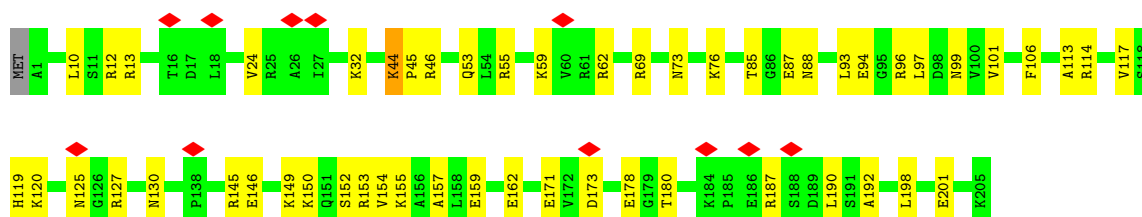
- Molecule 8: 30S ribosomal protein S3

Chain H:  71% 17% . 12%



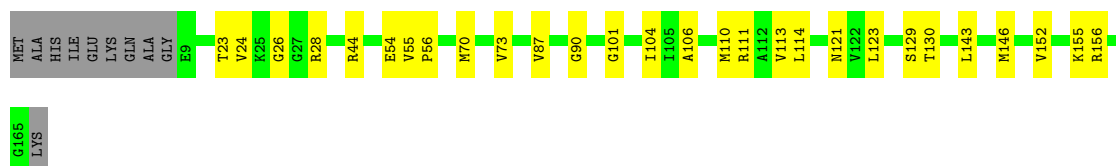
- Molecule 9: 30S ribosomal protein S4

Chain I:  5% 74% 25%



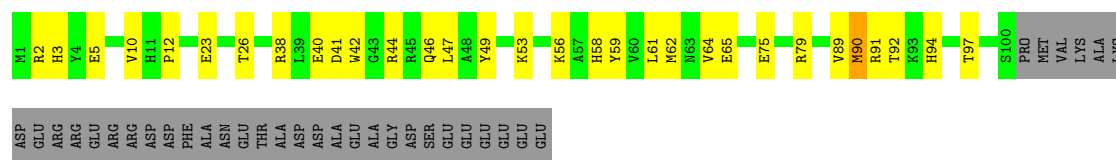
- Molecule 10: 30S ribosomal protein S5

Chain J:  77% 17% 6%



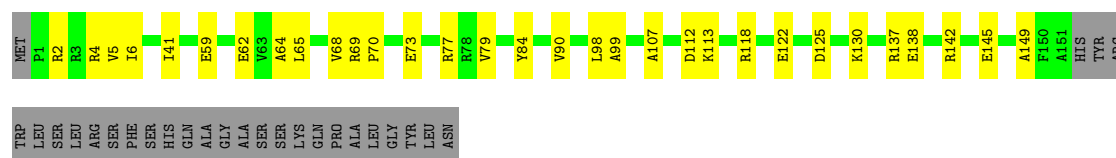
- Molecule 11: 30S ribosomal protein S6, fully modified isoform

Chain K: 




- Molecule 12: 30S ribosomal protein S7

Chain L: 



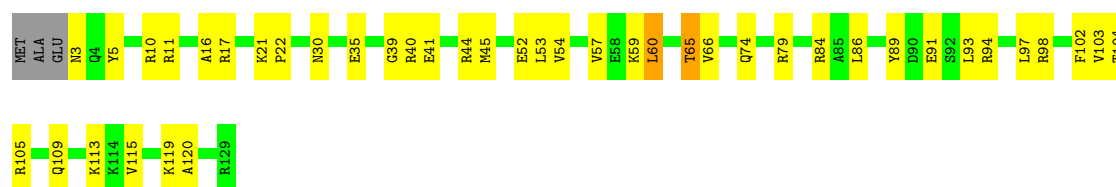
- Molecule 13: 30S ribosomal protein S8

Chain M: 



- Molecule 14: 30S ribosomal protein S9

Chain N: 



- Molecule 15: 30S ribosomal protein S10

Chain O: 



- Molecule 16: 30S ribosomal protein S11

Chain P: 





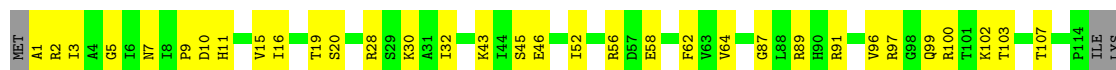
- Molecule 17: 30S ribosomal protein S12

Chain Q: 65% 33%



- Molecule 18: 30S ribosomal protein S13

Chain R: 69% 28%



- Molecule 19: 30S ribosomal protein S14

Chain S: 84% 15%



- Molecule 20: 30S ribosomal protein S15

Chain T: 84% 15%



- Molecule 21: 30S ribosomal protein S16

Chain U: 77% 22%



- Molecule 22: 30S ribosomal protein S17

Chain V: 74% 20% 5%



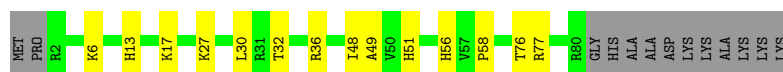
- Molecule 23: 30S ribosomal protein S18

Chain W: 65% 20% 13%



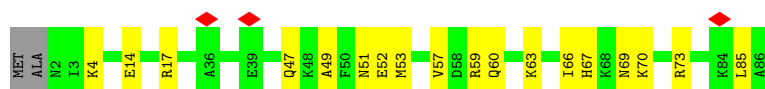
- Molecule 24: 30S ribosomal protein S19

Chain X: 71% 15% 14%



- Molecule 25: 30S ribosomal protein S20

Chain Y: 77% 21% 2%



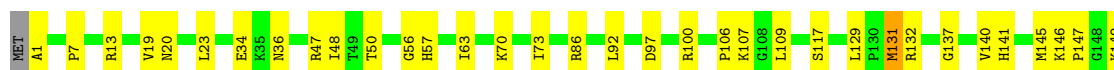
- Molecule 26: 30S ribosomal protein S21

Chain Z: 58% 30% 8%



- Molecule 27: 50S ribosomal protein L2

Chain b: 78% 21% 1%



- Molecule 28: 50S ribosomal protein L3

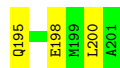
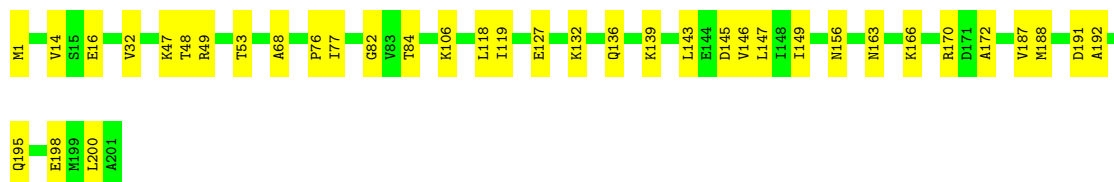
Chain c: 84% 16% 0%





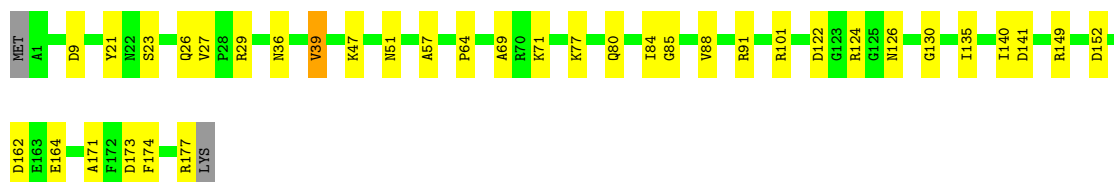
- Molecule 29: 50S ribosomal protein L4

Chain d: 82% 18%



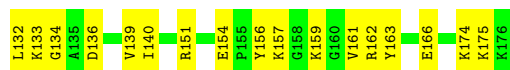
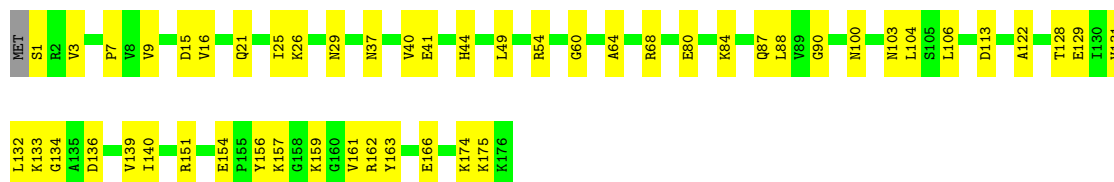
- Molecule 30: 50S ribosomal protein L5

Chain e: 79% 20% ..



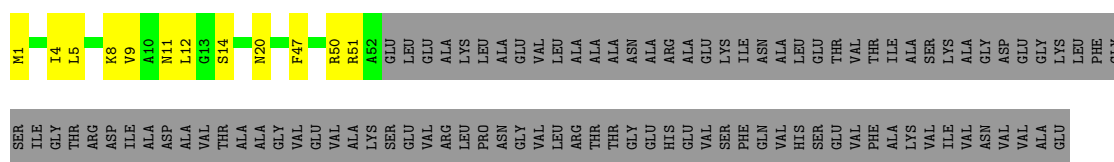
- Molecule 31: 50S ribosomal protein L6

Chain f: 71% 28% .



- Molecule 32: 50S ribosomal protein L9

Chain g: 27% 8% 65%



- Molecule 33: 50S ribosomal protein L11

Chain i: 9% 65% 33% ..





- Molecule 34: 50S ribosomal protein L13

Chain j: 82% 18%



- Molecule 35: 50S ribosomal protein L14

Chain k: 80% 20%



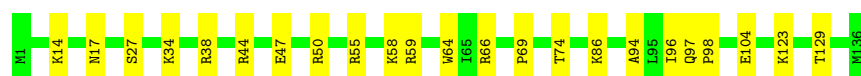
- Molecule 36: 50S ribosomal protein L15

Chain l: 86% 13%



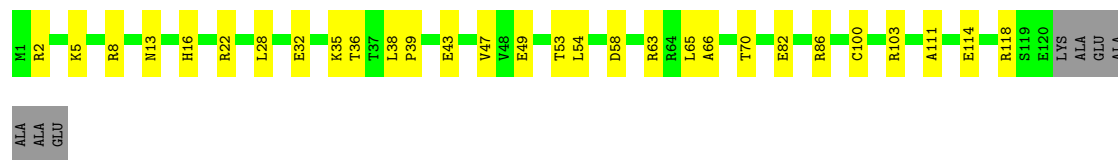
- Molecule 37: 50S ribosomal protein L16

Chain m: 83% 17%



- Molecule 38: 50S ribosomal protein L17

Chain n: 72% 23% 6%




- Molecule 39: 50S ribosomal protein L18

Chain o: 81% 18%




- Molecule 40: 50S ribosomal protein L19

Chain p:  83% 17% .



- Molecule 41: 50S ribosomal protein L20

Chain q:  83% 15% ..




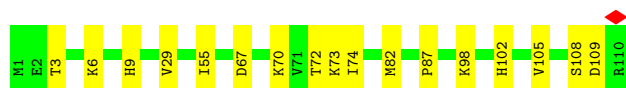
- Molecule 42: 50S ribosomal protein L21

Chain r:  73% 26% .



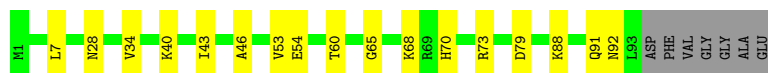
- Molecule 43: 50S ribosomal protein L22

Chain s:  85% 15%



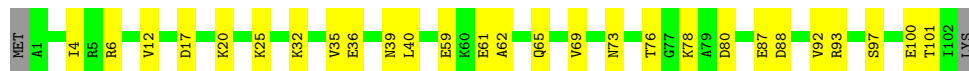
- Molecule 44: 50S ribosomal protein L23

Chain t:  76% 17% 7%




- Molecule 45: 50S ribosomal protein L24

Chain u:  72% 26% .



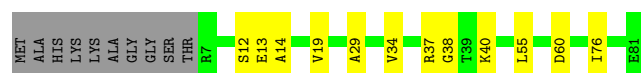
- Molecule 46: 50S ribosomal protein L25

Chain v:  86% 14%




- Molecule 47: 50S ribosomal protein L27

Chain w:  74% 14% 12%




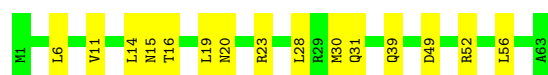
- Molecule 48: 50S ribosomal protein L28

Chain x:  76% 22% ..



- Molecule 49: 50S ribosomal protein L29

Chain y:  76% 24%



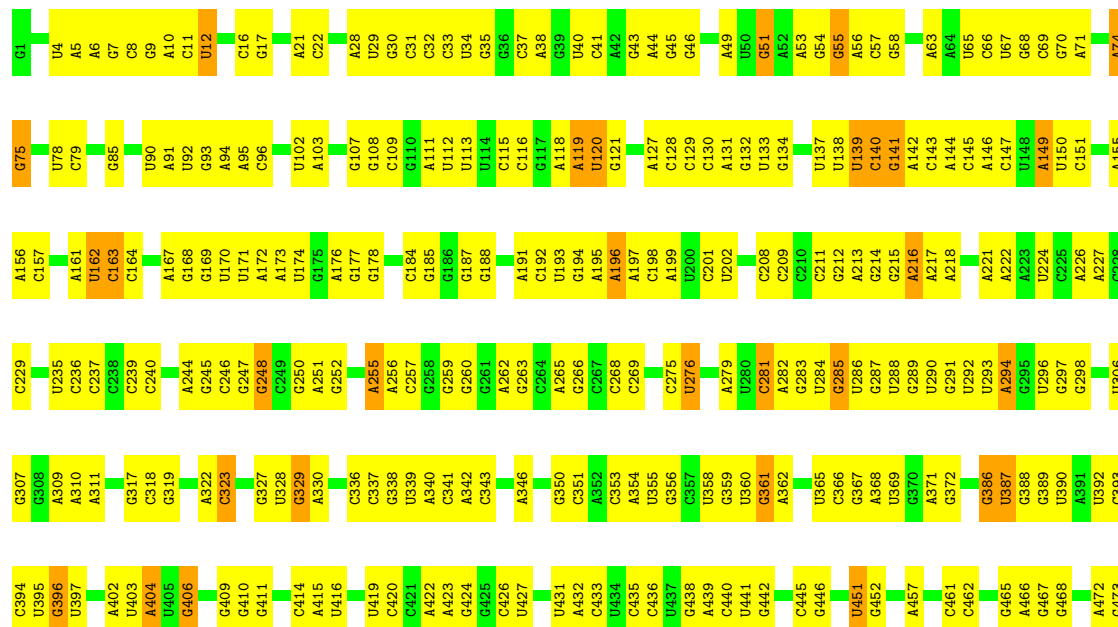
- Molecule 50: 50S ribosomal protein L30

Chain z:  76% 22% .



- Molecule 51: 23S rRNA

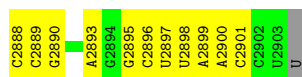
Chain 1:  42% 51% 6%





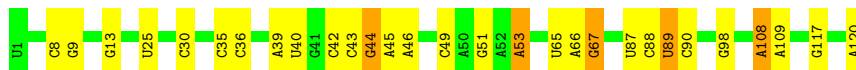
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A1579	C1511	G1430	G1338	A1431	G1177	G1107	C1045	A959	A886	G713	G629	C550	G476
A1580	C1512	A1432	G1339	U1271	C1178	U1108	A1046	C961	U887	U810	G630	U551	G481
C1582	A1515	A1433	G1343	U1273	U1179	G1109	G1047	C968	C889	A718	A633	G553	G482
A1583	G1516	A1434	U1344	A1274	U1181	A1111	C1049	C968	C890	C719	C634	U554	C485
	G1517	G1435	C1345	A1275	U1182	U1112	A1050		C891	U720	C635	U555	C486
G1588	C1518	G1436	G1346	U1276	U1183	U1113		A972	C892	C721	C636	A556	
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A1590	U1520	U1438	A1348	U1279	U1185	G1115	G1056	G974	C894	C723	G638	G488	
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C1592	A1522	U1440	G1352	G1281	U1187	C1117	A1057		U895	G725	C640	C490	
	U1523	G1441	U1352	U1282	U1188	C1118	U1058	A979	A896	G736	U641	A563	C491
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U1597	A1528	G1450	G1368	A1287	U1196	U1330	G1063	A984	C901		G647	U569	
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A1603	C1536	C1456	G1381	U1293	A1204	G1136	A1069	C994	G907	A752	A655	A575	A504
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C1607	G1540	A1460	A1385	C1298	G1211	U1141	G1073	A1009	G914	A760	G669	U511	G512
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G2876	U2584	U2585	U2586	U2462	G2374	U2295	G2215	C2150	C2073	A1978	A1901	G1816	G1743
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G2886	G2614	U2615	U2616	U2471	A2388	C2306	A2226						



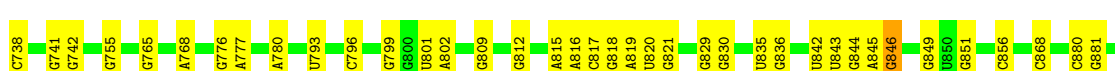
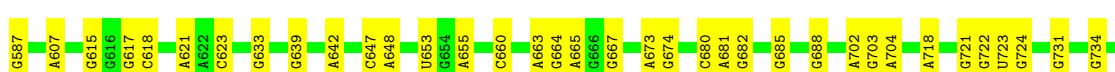
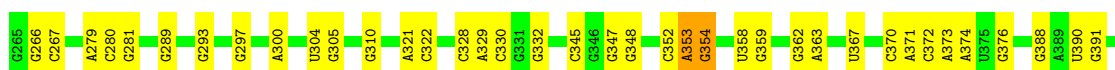
• Molecule 52: 5S rRNA

Chain 2: 76% 20%

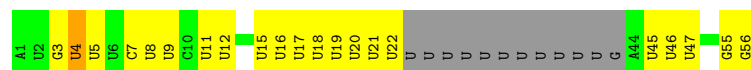


• Molecule 53: 16S rRNA

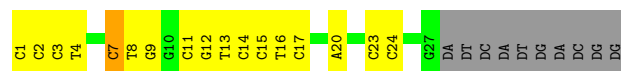
Chain 3: 69% 28%



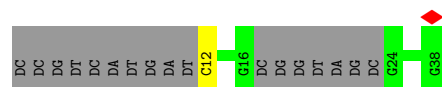
- Molecule 54: mRNA



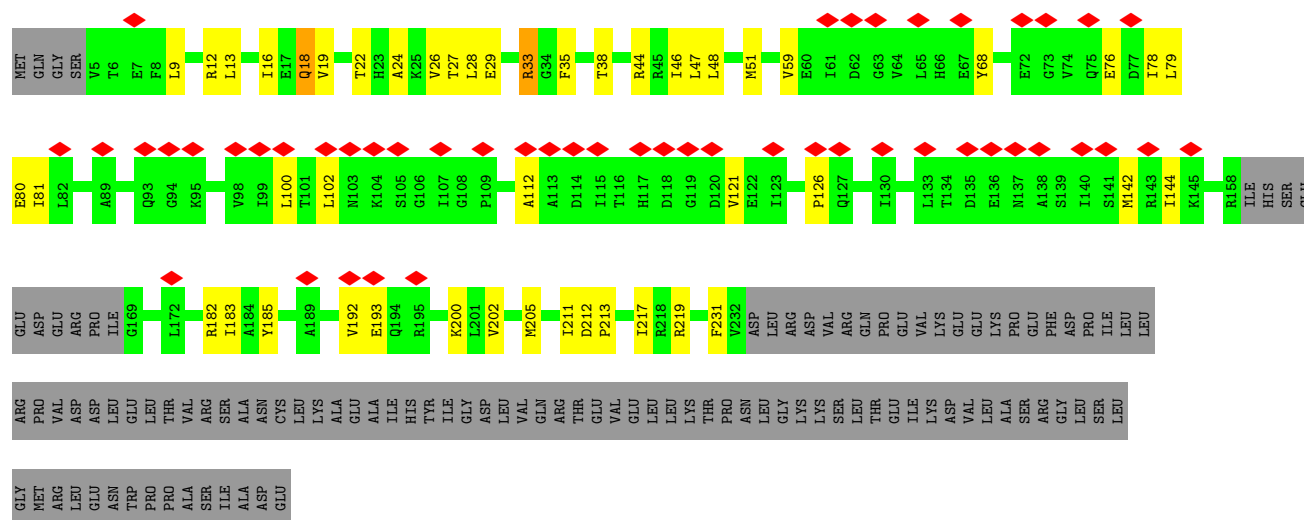
- Molecule 55: template DNA strand



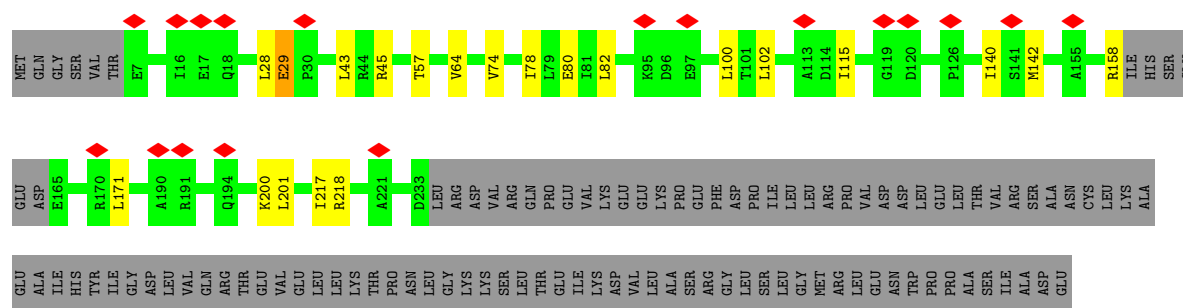
- Molecule 56: non-template DNA strand



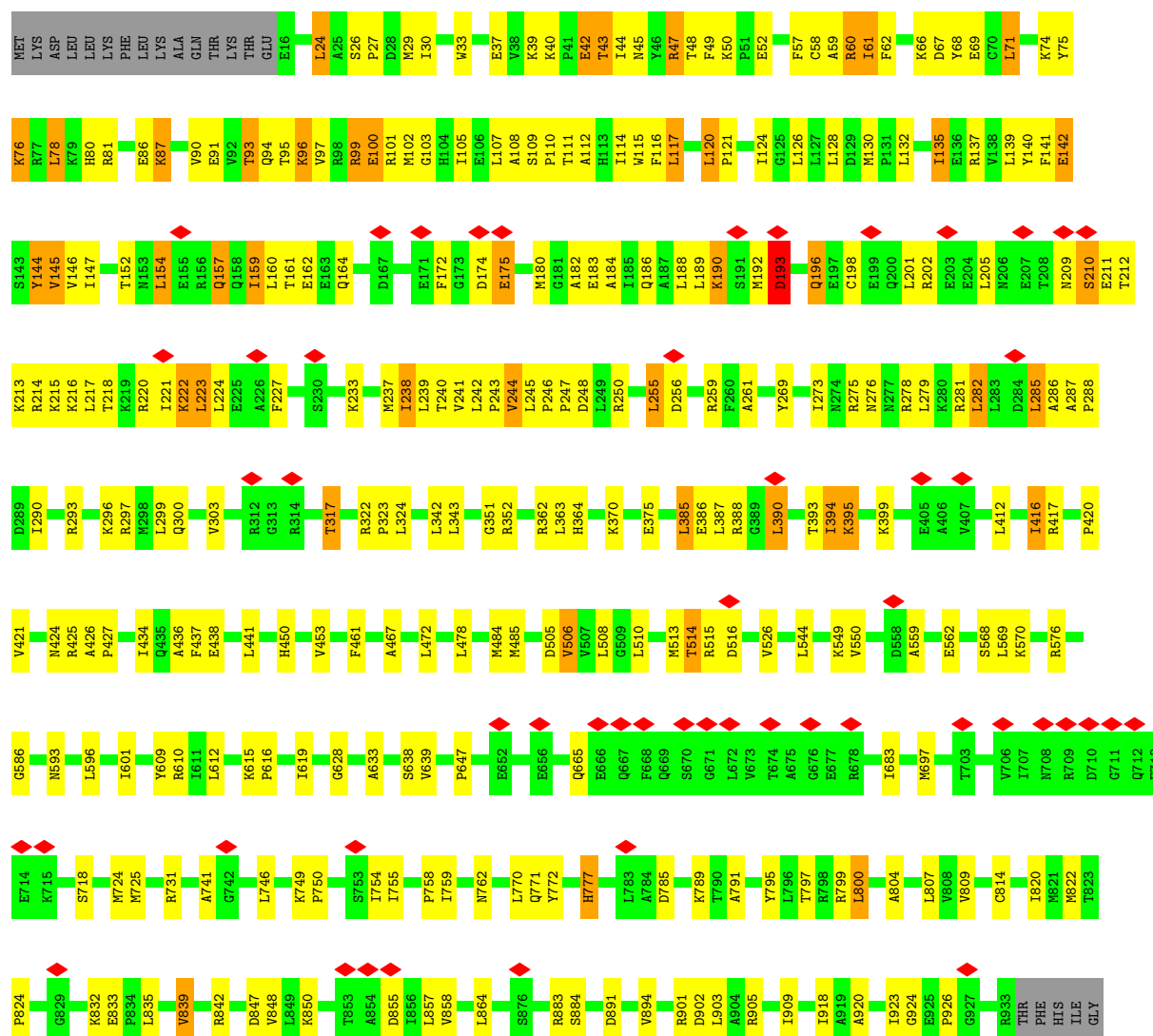
- Molecule 57: DNA-directed RNA polymerase subunit alpha



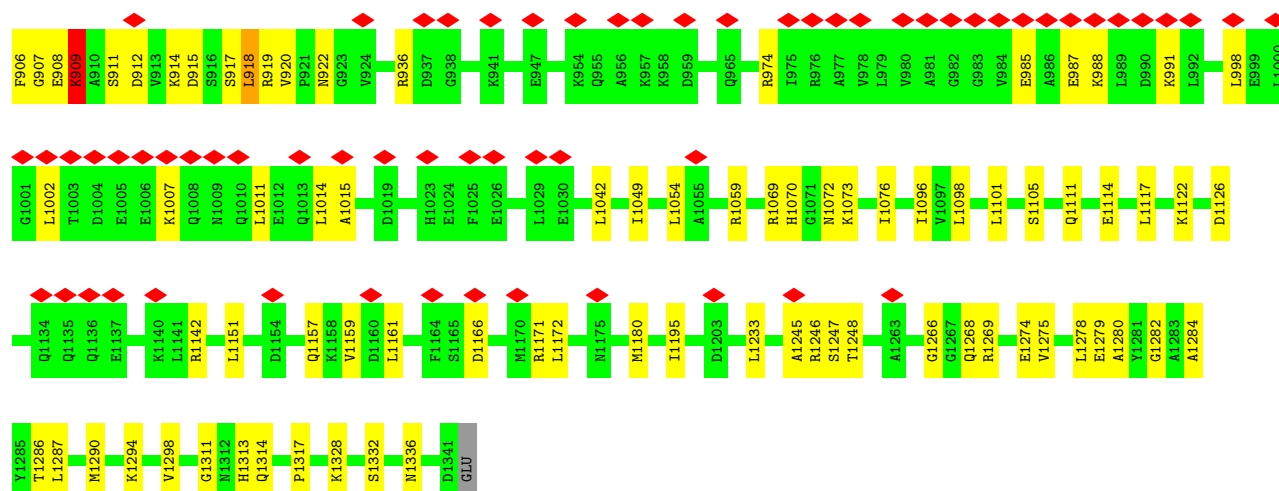
- Molecule 57: DNA-directed RNA polymerase subunit alpha



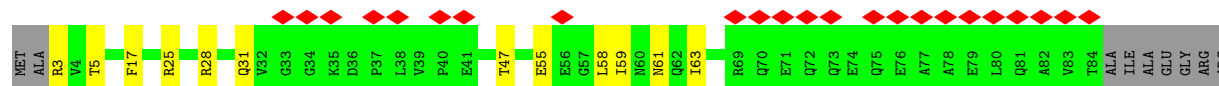
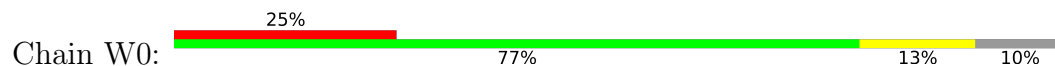
• Molecule 58: DNA-directed RNA polymerase subunit beta'



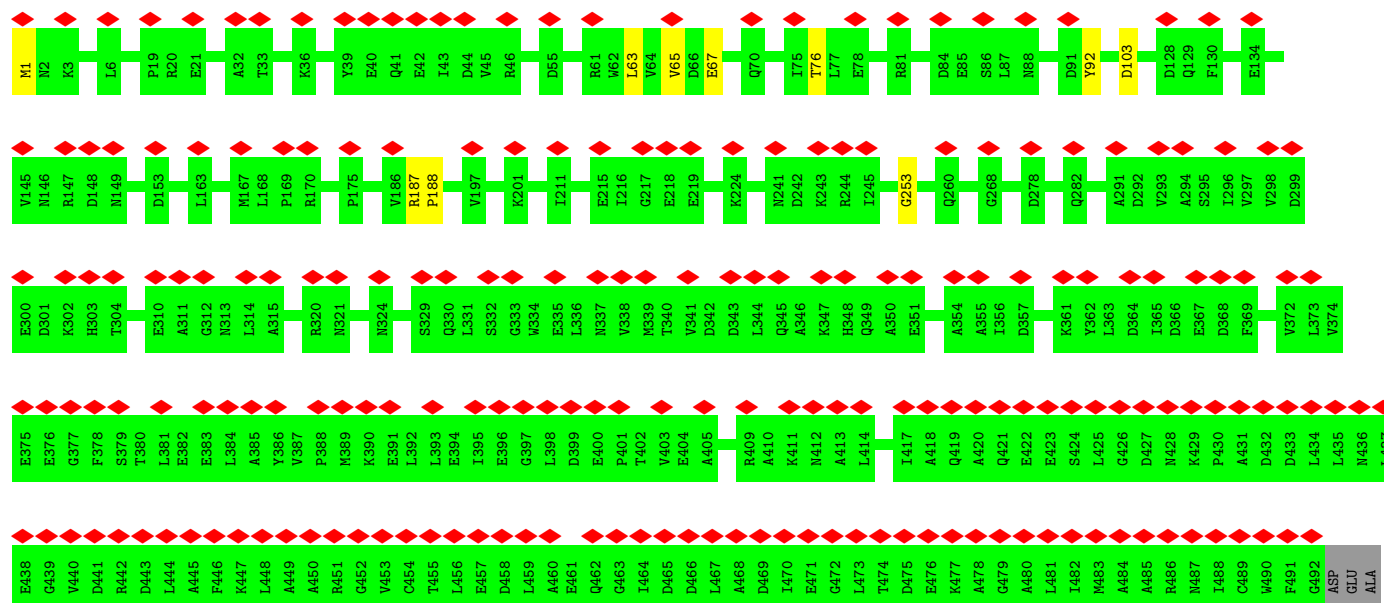
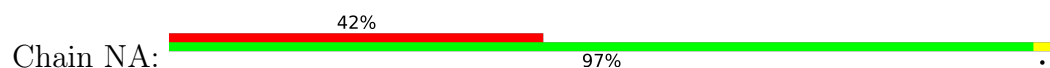




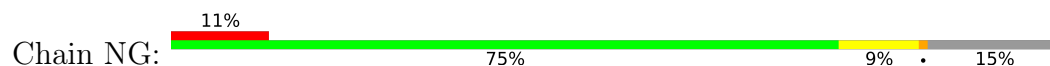
- Molecule 60: DNA-directed RNA polymerase subunit omega

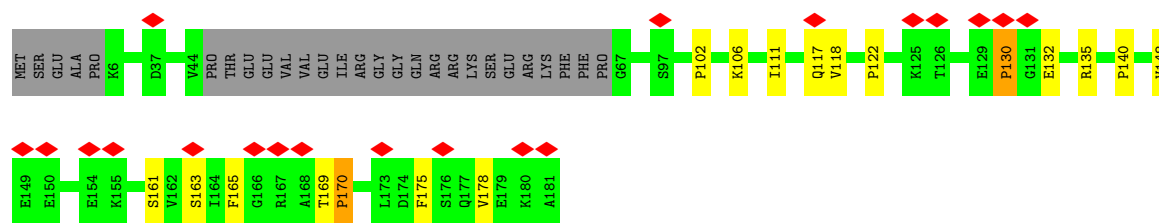


- Molecule 61: Transcription termination/antitermination protein NusA



- Molecule 62: Transcription termination/antitermination protein NusG





• Molecule 63: tRNA(Phe)

Chain 5: 21% 47% 30% .



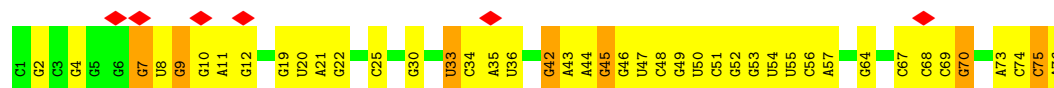
• Molecule 64: tRNA(fMet)

Chain 6: 77% 19% .



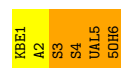
• Molecule 64: tRNA(fMet)

Chain 7: 8% 44% 47% 9%



• Molecule 65: tRNA(fMet)

Chain h: 33% 67%





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23023	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	0.188	Depositor
Minimum map value	-0.085	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.011	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: MG, KBE, DPP, 5OH, 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	0.27	0/531	0.54	0/709
2	B	0.41	0/450	0.60	2/599 (0.3%)
3	C	0.28	0/416	0.52	0/554
4	D	0.47	0/380	0.69	0/498
5	E	0.53	0/513	0.60	0/676
6	F	0.57	0/303	0.65	0/397
7	G	0.37	0/1735	0.64	0/2338
8	H	0.34	0/1651	0.55	0/2225
9	I	0.35	0/1665	0.71	0/2227
10	J	0.38	0/1169	0.68	2/1573 (0.1%)
11	K	0.46	0/835	0.77	0/1128
12	L	0.31	0/1195	0.66	3/1602 (0.2%)
13	M	0.35	0/989	0.53	0/1326
14	N	0.41	0/1034	0.77	0/1375
15	O	0.50	0/796	0.78	2/1077 (0.2%)
16	P	0.45	0/885	0.64	1/1195 (0.1%)
17	Q	0.50	0/969	0.85	2/1300 (0.2%)
18	R	0.33	0/892	0.73	2/1193 (0.2%)
19	S	0.33	0/817	0.61	0/1088
20	T	0.49	0/722	0.65	0/964
21	U	0.30	0/659	0.71	2/884 (0.2%)
22	V	0.44	0/657	0.71	0/881
23	W	0.54	0/544	0.74	1/731 (0.1%)
24	X	0.28	0/652	0.55	0/877
25	Y	0.28	0/671	0.52	0/888
26	Z	0.67	0/550	1.01	2/728 (0.3%)
27	b	0.49	0/2121	0.64	0/2852
28	c	0.42	0/1586	0.59	2/2134 (0.1%)
29	d	0.43	0/1571	0.62	0/2113
30	e	0.38	0/1434	0.60	2/1926 (0.1%)
31	f	0.29	0/1343	0.55	0/1816
32	g	0.32	0/405	0.75	0/544

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	i	0.31	0/1046	0.77	3/1410 (0.2%)
34	j	0.42	0/1152	0.56	1/1551 (0.1%)
35	k	0.45	0/947	0.66	0/1268
36	l	0.40	0/1054	0.63	0/1403
37	m	0.56	0/1093	0.74	0/1460
38	n	0.46	0/973	0.72	1/1301 (0.1%)
39	o	0.32	0/902	0.51	0/1209
40	p	0.42	0/929	0.62	0/1242
41	q	0.52	0/960	0.62	1/1278 (0.1%)
42	r	0.47	0/829	0.66	0/1107
43	s	0.44	0/864	0.58	0/1156
44	t	0.33	0/744	0.52	0/994
45	u	0.45	0/787	0.75	0/1051
46	v	0.34	0/766	0.51	0/1025
47	w	0.40	0/582	0.52	0/769
48	x	0.43	0/635	0.63	1/848 (0.1%)
49	y	0.29	0/510	0.64	0/677
50	z	0.41	0/453	0.54	0/605
51	1	0.51	0/69796	0.62	20/108888 (0.0%)
52	2	0.44	0/2872	0.46	0/4479
53	3	0.42	0/36963	0.43	1/57662 (0.0%)
54	4	0.53	0/808	0.67	0/1251
55	8	0.56	0/599	0.70	1/919 (0.1%)
56	9	0.49	0/468	0.53	0/719
57	A1	0.49	0/1696	0.69	0/2298
57	A2	0.43	0/1718	0.63	0/2328
58	B1	0.57	4/10510 (0.0%)	0.75	8/14196 (0.1%)
59	B2	0.46	0/10714	0.67	1/14459 (0.0%)
60	W0	0.30	0/652	0.61	0/879
61	NA	0.87	0/2431	1.26	1/3385 (0.0%)
62	NG	1.11	0/756	1.03	0/1048
63	5	0.57	0/1812	0.86	3/2823 (0.1%)
64	6	0.41	0/1832	0.48	0/2855
64	7	0.39	0/1832	0.57	1/2855 (0.0%)
65	h	3.17	2/11 (18.2%)	0.75	0/13
All	All	0.48	6/190836 (0.0%)	0.62	66/281829 (0.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	h	3	SER	CA-C	-6.73	1.38	1.52
65	h	4	SER	CA-C	-6.15	1.40	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	B1	1350	ASN	CG-ND2	-5.24	1.22	1.33
58	B1	1108	GLN	CD-OE1	5.09	1.33	1.23
58	B1	424	ASN	CG-ND2	-5.06	1.22	1.33
58	B1	665	GLN	CD-OE1	5.04	1.33	1.23

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	P	73	VAL	N-CA-C	-9.04	104.53	113.20
41	q	33	VAL	N-CA-C	-8.79	104.73	112.12
12	L	64	ALA	N-CA-C	-7.70	105.05	114.75
51	1	1130	U	C2'-C3'-O3'	7.58	120.87	109.50
64	7	33	U	C2'-C3'-O3'	7.24	120.35	109.50
51	1	2326	C	C2'-C3'-O3'	7.22	120.33	109.50
58	B1	450	HIS	CB-CG-CD2	-6.56	122.67	131.20
51	1	761	A	C4'-C3'-O3'	-6.51	103.24	113.00
58	B1	777	HIS	CB-CG-CD2	-6.37	122.92	131.20
58	B1	61	ILE	CA-C-N	-6.33	114.05	121.64
58	B1	61	ILE	C-N-CA	-6.33	114.05	121.64
59	B2	855	PRO	N-CA-C	6.12	120.24	111.13
28	c	147	GLY	CA-C-N	-6.03	115.27	122.44
28	c	147	GLY	C-N-CA	-6.03	115.27	122.44
63	5	39	U	C3'-C2'-O2'	5.88	119.53	110.70
58	B1	450	HIS	CB-CG-ND1	5.68	131.22	122.70
51	1	1790	C	N1-C1'-C2'	5.62	120.43	112.00
51	1	2060	A	C2'-C3'-O3'	5.62	117.92	109.50
26	Z	35	GLU	CA-C-N	5.60	132.24	121.54
26	Z	35	GLU	C-N-CA	5.60	132.24	121.54
15	O	57	VAL	CA-C-N	5.59	132.21	121.54
15	O	57	VAL	C-N-CA	5.59	132.21	121.54
10	J	155	LYS	N-CA-C	-5.54	107.77	114.75
38	n	47	VAL	N-CA-C	-5.51	107.49	112.12
51	1	1020	A	C2'-C3'-O3'	5.46	117.69	109.50
51	1	960	A	N9-C1'-C2'	5.46	120.19	112.00
51	1	1451	C	N1-C1'-C2'	5.45	120.17	112.00
51	1	1905	C	C4'-C3'-O3'	-5.43	104.85	113.00
51	1	1696	G	N9-C1'-C2'	5.42	120.12	112.00
58	B1	777	HIS	CB-CG-ND1	5.41	130.82	122.70
55	8	7	DC	C2'-C3'-O3'	-5.33	103.50	111.50
51	1	2428	G	N9-C1'-C2'	5.31	119.97	112.00
51	1	1782	U	N1-C1'-C2'	5.31	119.96	112.00
12	L	5	VAL	CA-C-N	5.30	127.81	120.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	5	VAL	C-N-CA	5.30	127.81	120.49
33	i	24	GLY	N-CA-C	5.29	123.13	112.34
61	NA	253	GLY	CA-C-O	-5.28	118.35	122.52
63	5	39	U	C4'-C3'-O3'	5.28	120.92	113.00
58	B1	27	PRO	N-CA-C	-5.27	106.17	113.81
30	e	141	ASP	CA-C-N	5.26	131.60	121.54
30	e	141	ASP	C-N-CA	5.26	131.60	121.54
53	3	1302	C	O3'-P-O5'	5.26	111.89	104.00
34	j	110	PRO	N-CA-C	5.24	120.74	113.98
51	1	2055	C	N1-C1'-C2'	5.24	119.86	112.00
51	1	980	A	N9-C1'-C2'	5.23	119.84	112.00
63	5	57	G	C4'-C3'-O3'	5.20	117.19	109.40
51	1	2576	G	N9-C1'-C2'	5.19	119.79	112.00
10	J	87	VAL	N-CA-C	5.14	116.03	109.30
21	U	78	VAL	CA-C-N	5.14	129.58	121.56
21	U	78	VAL	C-N-CA	5.14	129.58	121.56
51	1	2430	A	N9-C1'-C2'	5.13	119.70	112.00
51	1	1328	A	N9-C1'-C2'	5.13	119.69	112.00
23	W	14	ALA	N-CA-C	-5.12	106.12	112.93
18	R	3	ILE	CA-C-N	5.12	131.31	121.54
18	R	3	ILE	C-N-CA	5.12	131.31	121.54
17	Q	42	LYS	CA-C-N	5.10	129.63	121.62
17	Q	42	LYS	C-N-CA	5.10	129.63	121.62
51	1	2777	G	N9-C1'-C2'	5.10	119.65	112.00
51	1	1565	C	N1-C1'-C2'	5.09	119.64	112.00
33	i	71	LYS	CA-C-N	5.07	134.17	121.80
33	i	71	LYS	C-N-CA	5.07	134.17	121.80
48	x	25	LYS	N-CA-C	5.05	121.56	110.80
51	1	972	A	N9-C1'-C2'	5.03	119.55	112.00
58	B1	61	ILE	CA-C-O	-5.02	115.72	120.95
2	B	24	VAL	CA-C-N	5.01	131.11	121.54
2	B	24	VAL	C-N-CA	5.01	131.11	121.54

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [\(i\)](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	522	0	524	7	0
2	B	444	0	461	8	0
3	C	409	0	440	3	0
4	D	377	0	418	9	0
5	E	504	0	574	3	0
6	F	302	0	343	7	0
7	G	1704	0	1732	35	0
8	H	1624	0	1699	28	0
9	I	1643	0	1710	32	0
10	J	1156	0	1199	18	0
11	K	817	0	808	17	0
12	L	1181	0	1240	19	0
13	M	979	0	1034	9	0
14	N	1022	0	1070	25	0
15	O	786	0	828	16	0
16	P	869	0	878	22	0
17	Q	955	0	1019	29	0
18	R	883	0	944	19	0
19	S	805	0	847	10	0
20	T	714	0	737	6	0
21	U	649	0	666	14	0
22	V	648	0	691	10	0
23	W	535	0	552	9	0
24	X	637	0	665	9	0
25	Y	665	0	714	11	0
26	Z	544	0	579	13	0
27	b	2082	0	2157	46	0
28	c	1565	0	1616	29	0
29	d	1552	0	1619	27	0
30	e	1410	0	1447	23	0
31	f	1323	0	1374	34	0
32	g	400	0	423	6	0
33	i	1032	0	1088	40	0
34	j	1129	0	1162	22	0
35	k	938	0	1012	17	0
36	l	1045	0	1117	16	0
37	m	1074	0	1157	13	0
38	n	960	0	1000	20	0
39	o	892	0	923	15	0
40	p	917	0	965	18	0
41	q	947	0	1022	10	0
42	r	816	0	839	17	0
43	s	857	0	922	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	t	738	0	807	9	0
45	u	779	0	834	14	0
46	v	753	0	780	8	0
47	w	575	0	592	8	0
48	x	625	0	655	11	0
49	y	509	0	543	11	0
50	z	449	0	491	8	0
51	1	62317	0	31346	1468	0
52	2	2568	0	1303	15	0
53	3	33012	0	16618	180	0
54	4	729	0	364	7	0
55	8	539	0	305	27	0
56	9	417	0	224	1	0
57	A1	1677	0	1713	25	0
57	A2	1698	0	1718	13	0
58	B1	10353	0	10548	327	0
59	B2	10546	0	10550	169	0
60	W0	650	0	658	10	0
61	NA	2432	0	1171	4	0
62	NG	758	0	334	16	0
63	5	1622	0	821	29	0
64	6	1640	0	837	7	0
64	7	1640	0	837	20	0
65	h	48	0	40	7	0
66	B1	1	0	0	0	0
All	All	177388	0	126304	2824	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 10.

All (2824) 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)
40:p:52:ARG:HH21	51:1:2720:U:H5''	0.95	1.08
51:1:275:C:H2'	51:1:276:U:H4'	1.37	1.07
51:1:1666:G:H2'	51:1:1667:G:H5'	1.41	1.03
51:1:2713:U:H3'	51:1:2714:G:H5'	1.41	1.03
51:1:1672:A:C2	51:1:2582:G:H5'	1.95	1.02
58:B1:750:PRO:HB3	59:B2:549:ASP:OD2	1.60	1.01
51:1:1807:G:H2'	51:1:1808:A:H5'	1.44	1.00
51:1:1082:U:H3'	51:1:1083:U:H5''	1.41	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:111:THR:HG23	58:B1:300:GLN:CD	1.86	0.98
40:p:52:ARG:NH2	51:1:2720:U:H5''	1.79	0.98
58:B1:352:ARG:HD2	59:B2:1268:GLN:NE2	1.79	0.97
51:1:1847:A:HO2'	51:1:1848:A:H8	1.07	0.97
58:B1:68:TYR:O	58:B1:75:TYR:CE2	2.20	0.95
51:1:2713:U:H3'	51:1:2714:G:C5'	1.98	0.94
51:1:2156:G:H2'	51:1:2157:G:H5'	1.47	0.94
51:1:655:A:H4'	51:1:656:G:H5'	1.50	0.94
51:1:644:A:H2'	51:1:645:C:H5''	1.50	0.93
30:e:84:ILE:HD13	51:1:2312:U:H5'	1.51	0.93
51:1:1102:C:H2'	51:1:1103:A:H8	1.35	0.91
30:e:130:GLY:HA3	51:1:2305:U:H5''	1.51	0.91
54:4:56:G:H21	58:B1:427:PRO:HD3	1.34	0.90
51:1:890:C:H2'	51:1:891:G:H5'	1.53	0.90
58:B1:68:TYR:C	58:B1:75:TYR:HE2	1.80	0.90
58:B1:202:ARG:HG2	58:B1:202:ARG:HH11	1.34	0.90
51:1:1702:G:H2'	51:1:1703:G:H5''	1.51	0.89
58:B1:317:THR:HA	58:B1:323:PRO:HA	1.54	0.89
51:1:1019:U:H3	51:1:1142:A:H62	1.17	0.89
51:1:1668:A:H4'	51:1:1669:A:H5'	1.54	0.89
14:N:3:ASN:N	14:N:5:TYR:HH	1.69	0.89
17:Q:40:THR:HG21	65:h:6:5OH:OS	1.72	0.89
63:5:9:A:H2'	63:5:11:C:H41	1.38	0.88
51:1:11:C:H2'	51:1:12:U:H5''	1.54	0.88
51:1:2097:A:H2'	51:1:2098:U:C6	2.08	0.88
51:1:1060:U:H4'	51:1:1061:U:H5''	1.55	0.87
2:B:8:THR:HB	51:1:2020:A:H5'	1.56	0.87
31:f:174:LYS:HG3	51:1:2529:G:H4'	1.56	0.86
51:1:1387:A:H5'	51:1:1469:A:H1'	1.58	0.86
51:1:2333:A:H5'	51:1:2334:U:H2'	1.57	0.86
40:p:52:ARG:HH21	51:1:2720:U:C5'	1.86	0.85
58:B1:68:TYR:HB3	58:B1:75:TYR:OH	1.76	0.85
51:1:1869:G:H3'	51:1:1870:C:H5'	1.58	0.85
51:1:475:C:H4'	51:1:510:C:H5'	1.59	0.84
51:1:2792:A:H2'	51:1:2793:C:H5''	1.59	0.84
17:Q:69:GLU:HG3	53:3:521:G:H4'	1.59	0.84
51:1:1175:A:H3'	51:1:1176:U:H5'	1.59	0.84
51:1:1666:G:C2'	51:1:1667:G:H5'	2.07	0.83
58:B1:68:TYR:O	58:B1:75:TYR:HE2	1.58	0.83
51:1:849:A:H2'	51:1:850:U:C6	2.14	0.83
51:1:2584:U:H2'	51:1:2585:U:H5'	1.58	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:8:1:DC:H5''	58:B1:210:SER:OG	1.80	0.82
51:1:757:G:H2'	51:1:758:C:H5'	1.61	0.81
51:1:1141:U:H4'	51:1:1142:A:O4'	1.80	0.81
33:i:119:ALA:HB2	51:1:1082:U:H5'	1.60	0.81
58:B1:141:PHE:HE2	58:B1:296:LYS:HB2	1.45	0.81
58:B1:633:ALA:HB2	59:B2:808:ASN:H	1.41	0.81
51:1:279:A:H61	51:1:361:G:H1'	1.46	0.81
51:1:2360:G:H2'	51:1:2361:G:H5'	1.62	0.81
51:1:2224:G:H4'	51:1:2226:C:C2	2.16	0.81
58:B1:141:PHE:CE2	58:B1:296:LYS:HB2	2.16	0.81
3:C:40:PRO:HG3	51:1:2348:U:H4'	1.62	0.81
38:n:36:THR:HG22	51:1:1278:C:OP1	1.80	0.81
58:B1:770:LEU:HD13	59:B2:618:GLN:HG3	1.61	0.81
51:1:1197:G:O2'	51:1:1198:U:H5'	1.81	0.80
51:1:2799:A:H2'	51:1:2800:A:H5'	1.63	0.80
51:1:545:U:C2	51:1:546:U:H1'	2.16	0.80
58:B1:111:THR:HG23	58:B1:300:GLN:OE1	1.81	0.80
51:1:2112:G:H2'	51:1:2113:U:H5'	1.63	0.80
58:B1:144:TYR:HE1	58:B1:162:GLU:OE2	1.64	0.80
64:7:46:G:H2'	64:7:47:U:H5'	1.64	0.80
51:1:1087:G:N2	51:1:1103:A:H1'	1.97	0.80
58:B1:37:GLU:O	58:B1:61:ILE:HD11	1.81	0.80
51:1:784:G:H5'	51:1:785:G:OP1	1.81	0.80
51:1:1071:G:O2'	51:1:1089:A:H2'	1.82	0.79
51:1:1064:C:H41	51:1:1069:A:H5''	1.47	0.79
58:B1:186:GLN:HG3	58:B1:238:ILE:HG13	1.65	0.79
7:G:18:GLN:HG3	7:G:189:ASN:HB3	1.65	0.78
51:1:1536:C:H4'	51:1:1537:G:C2	2.18	0.78
51:1:1775:U:H2'	51:1:1776:G:H5'	1.64	0.78
51:1:2130:U:H2'	51:1:2131:U:H5''	1.65	0.78
51:1:2286:G:H4'	51:1:2287:A:O4'	1.82	0.78
51:1:2792:A:C3'	51:1:2793:C:H5''	2.14	0.78
28:c:114:LYS:HB2	51:1:2680:U:OP1	1.84	0.78
33:i:55:PRO:HG3	51:1:1060:U:OP2	1.83	0.78
35:k:6:THR:HG22	51:1:1666:G:O2'	1.83	0.78
61:NA:63:LEU:HA	61:NA:92:TYR:HA	1.65	0.77
51:1:1275:A:N6	51:1:1296:G:H4'	2.00	0.77
51:1:1297:C:OP1	51:1:2710:C:H4'	1.83	0.77
51:1:2215:C:H2'	51:1:2216:G:C8	2.18	0.77
51:1:1310:G:C2'	51:1:1311:G:H5'	2.14	0.77
51:1:275:C:H2'	51:1:276:U:C4'	2.14	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1702:G:C2'	51:1:1703:G:H5''	2.13	0.77
51:1:2156:G:C2'	51:1:2157:G:H5'	2.14	0.77
51:1:1736:U:H2'	51:1:1737:G:O4'	1.85	0.77
51:1:310:A:O2'	51:1:311:A:H2'	1.84	0.77
51:1:368:A:H2'	51:1:369:U:H5'	1.66	0.77
51:1:1063:G:H1	51:1:1075:C:N4	1.83	0.76
51:1:548:G:H2'	51:1:549:G:O4'	1.84	0.76
55:8:13:DT:H72	58:B1:791:ALA:HB2	1.66	0.76
51:1:1394:U:H4'	51:1:1603:A:H4'	1.66	0.76
51:1:2097:A:H2'	51:1:2098:U:H6	1.50	0.75
55:8:15:DC:H1'	58:B1:426:ALA:HB1	1.67	0.75
51:1:2792:A:C2'	51:1:2793:C:H5''	2.16	0.75
51:1:1555:G:H5'	51:1:1555:G:H8	1.51	0.75
51:1:1020:A:H5'	51:1:1021:A:C8	2.22	0.74
51:1:958:U:H2'	52:2:89:U:O2	1.87	0.74
51:1:1083:U:H2'	51:1:1085:A:OP2	1.86	0.74
58:B1:110:PRO:HG2	58:B1:183:GLU:HG3	1.68	0.74
51:1:275:C:H3'	51:1:276:U:H5''	1.66	0.74
51:1:1773:A:H2'	51:1:1774:C:H5'	1.68	0.74
51:1:1061:U:H3'	51:1:1062:G:C5'	2.18	0.74
51:1:1425:G:H2'	51:1:1426:G:C8	2.23	0.74
51:1:2432:A:H1'	64:7:75:C:O4'	1.86	0.74
53:3:456:A:H61	53:3:476:U:H3	1.36	0.74
51:1:543:G:H2'	51:1:544:C:H5''	1.68	0.74
55:8:3:DC:H2'	55:8:4:DT:H72	1.69	0.73
58:B1:211:GLU:HG2	58:B1:215:LYS:HE3	1.70	0.73
51:1:2611:C:O2	51:1:2611:C:H2'	1.86	0.73
51:1:481:G:H1'	51:1:506:G:N2	2.04	0.73
51:1:545:U:H2'	51:1:546:U:O4'	1.88	0.73
51:1:2834:G:H2'	51:1:2879:A:H61	1.54	0.73
37:m:14:LYS:NZ	51:1:956:G:N7	2.35	0.73
51:1:1942:C:H3'	51:1:1943:U:H2'	1.70	0.73
51:1:322:A:H5'	51:1:340:A:C1'	2.19	0.73
51:1:1433:A:H2'	51:1:1434:A:O4'	1.89	0.73
51:1:1670:C:H2'	51:1:1671:U:H5'	1.70	0.73
58:B1:282:LEU:HA	58:B1:286:ALA:HA	1.70	0.73
51:1:1310:G:H2'	51:1:1311:G:H5'	1.69	0.72
55:8:3:DC:C2'	55:8:4:DT:H72	2.19	0.72
58:B1:157:GLN:OE1	58:B1:157:GLN:HA	1.89	0.72
58:B1:220:ARG:HG2	58:B1:220:ARG:HH11	1.55	0.72
59:B2:903:ARG:HA	59:B2:907:GLY:HA2	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:404:A:H1'	51:1:406:G:C4	2.23	0.72
51:1:864:G:O2'	51:1:865:C:H5'	1.89	0.72
51:1:2036:C:H2'	51:1:2037:A:C8	2.23	0.72
58:B1:107:LEU:HD11	58:B1:242:LEU:HB2	1.70	0.72
51:1:2713:U:C3'	51:1:2714:G:C5'	2.67	0.72
64:7:50:U:H2'	64:7:51:C:C4	2.24	0.72
51:1:2671:G:H2'	51:1:2672:U:C6	2.25	0.72
53:3:452:A:H61	53:3:480:U:H3	1.37	0.72
31:f:15:ASP:HB3	31:f:26:LYS:H	1.54	0.72
17:Q:33:CYS:HA	17:Q:54:VAL:HG12	1.70	0.72
51:1:1795:C:H2'	51:1:1796:U:O4'	1.90	0.72
51:1:1872:A:H2'	51:1:1873:G:O4'	1.89	0.72
58:B1:105:ILE:HD12	58:B1:242:LEU:HD22	1.71	0.71
36:l:59:ARG:HD2	51:1:250:G:H4'	1.71	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
51:1:1858:A:H1'	51:1:1885:A:C2	2.26	0.71
58:B1:202:ARG:HG2	58:B1:202:ARG:NH1	1.99	0.71
51:1:890:C:C2'	51:1:891:G:H5'	2.21	0.71
51:1:1441:G:H2'	51:1:1442:U:C6	2.25	0.71
53:3:663:A:H61	53:3:742:G:H1	1.39	0.71
51:1:394:C:H2'	51:1:395:U:O4'	1.90	0.71
51:1:1102:C:H2'	51:1:1103:A:C8	2.22	0.70
51:1:1386:C:H2'	51:1:1387:A:H8	1.56	0.70
58:B1:142:GLU:HG3	58:B1:142:GLU:O	1.89	0.70
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE22	1.55	0.70
51:1:2151:U:H2'	51:1:2152:G:H8	1.56	0.70
51:1:2297:A:N1	51:1:2321:U:H5	1.90	0.70
51:1:2267:A:H5''	51:1:2268:A:H5''	1.74	0.70
51:1:633:A:H2'	51:1:634:C:H5'	1.72	0.70
51:1:1983:G:O2'	51:1:1984:G:H5'	1.91	0.70
58:B1:128:LEU:HD11	58:B1:189:LEU:HG	1.73	0.70
59:B2:65:ASN:HB3	59:B2:105:TYR:HB2	1.74	0.70
51:1:723:C:H2'	51:1:724:U:C6	2.27	0.70
51:1:1292:G:H2'	51:1:1293:C:C6	2.27	0.70
51:1:368:A:C2'	51:1:369:U:H5'	2.21	0.70
51:1:612:G:H2'	51:1:614:A:C8	2.26	0.70
65:h:6:5OH:N	65:h:6:5OH:HS	2.07	0.70
51:1:2151:U:H2'	51:1:2152:G:C8	2.27	0.70
51:1:1019:U:H3	51:1:1142:A:N6	1.89	0.70
51:1:1670:C:C2'	51:1:1671:U:H5'	2.21	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:r:79:ARG:NH1	51:1:572:A:OP2	2.25	0.70
27:b:47:ARG:NH2	51:1:774:G:H5''	2.07	0.69
51:1:319:G:H1	51:1:323:C:H5	1.40	0.69
51:1:419:U:H2'	51:1:420:C:C6	2.27	0.69
51:1:940:G:H2'	51:1:941:A:H5''	1.73	0.69
51:1:1337:G:H2'	51:1:1338:G:H8	1.58	0.69
51:1:2114:A:H2	51:1:2167:U:H1'	1.58	0.69
34:j:7:LYS:HG2	51:1:538:A:H4'	1.73	0.69
58:B1:93:THR:HB	58:B1:97:VAL:HG21	1.73	0.69
51:1:282:A:H2'	51:1:283:G:H8	1.57	0.69
51:1:1555:G:H5'	51:1:1555:G:C8	2.27	0.69
65:h:4:SER:O	65:h:5:UAL:N1	2.26	0.69
8:H:117:ASP:HA	8:H:120:THR:HG22	1.75	0.69
51:1:644:A:H2'	51:1:645:C:C5'	2.22	0.69
58:B1:832:LYS:C	58:B1:1242:ARG:HH12	2.01	0.69
51:1:322:A:H5'	51:1:340:A:H1'	1.73	0.69
51:1:1889:A:H2'	51:1:1890:A:H8	1.58	0.69
51:1:2626:C:O2'	51:1:2627:G:H5'	1.92	0.69
58:B1:243:PRO:HG2	59:B2:1332:SER:O	1.93	0.69
51:1:392:U:H2'	51:1:393:C:H6	1.58	0.69
51:1:1137:G:O2'	51:1:1138:G:H5'	1.92	0.69
51:1:2092:U:H4'	51:1:2093:G:H5''	1.75	0.69
36:l:30:THR:HG22	51:1:810:U:O4	1.93	0.68
50:z:38:GLU:OE2	51:1:928:A:H5'	1.94	0.68
51:1:2510:C:N4	51:1:2511:U:O4	2.27	0.68
51:1:402:A:H2'	51:1:403:U:H5'	1.74	0.68
51:1:894:U:H2'	51:1:895:U:O4'	1.93	0.68
52:2:65:U:H3'	52:2:108:A:H61	1.59	0.68
51:1:2403:C:O2'	51:1:2404:U:H5'	1.92	0.68
51:1:2869:G:H2'	51:1:2870:C:C6	2.28	0.68
51:1:528:A:C8	51:1:528:A:H3'	2.27	0.68
51:1:1063:G:H1	51:1:1075:C:H41	1.42	0.68
51:1:849:A:H2'	51:1:850:U:H6	1.58	0.68
51:1:1999:C:H5''	51:1:2723:C:O2'	1.94	0.68
51:1:419:U:H2'	51:1:420:C:H6	1.58	0.68
51:1:905:A:C2'	51:1:906:U:H5'	2.23	0.68
51:1:1702:G:C3'	51:1:1703:G:H5''	2.24	0.68
51:1:2758:A:H2'	51:1:2759:G:H5'	1.75	0.68
58:B1:39:LYS:O	58:B1:273:ILE:CG2	2.41	0.68
51:1:1061:U:H3'	51:1:1062:G:H5'	1.76	0.68
51:1:1082:U:H3'	51:1:1083:U:C5'	2.22	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2747:G:O6	51:1:2755:C:H5''	1.93	0.68
58:B1:117:LEU:HD12	58:B1:117:LEU:O	1.94	0.68
48:x:16:ASN:ND2	48:x:26:ARG:HB3	2.09	0.67
58:B1:141:PHE:CD2	58:B1:293:ARG:O	2.47	0.67
51:1:1078:U:H2'	51:1:1088:A:OP1	1.94	0.67
51:1:1270:C:H5''	51:1:1271:G:H5'	1.77	0.67
51:1:1889:A:H2'	51:1:1890:A:C8	2.29	0.67
51:1:2157:G:H2'	51:1:2158:A:H2	1.59	0.67
9:I:73:ASN:HA	9:I:76:LYS:HB2	1.77	0.67
51:1:1432:G:O2'	51:1:1433:A:H5'	1.94	0.67
51:1:1717:A:H2'	51:1:1718:G:H5'	1.77	0.67
36:I:39:LYS:NZ	51:1:942:G:OP2	2.28	0.67
51:1:1438:U:O2'	51:1:1439:A:H5'	1.94	0.67
51:1:1484:U:H2'	51:1:1485:U:C6	2.30	0.67
45:u:25:LYS:HD3	45:u:36:GLU:HB3	1.75	0.67
51:1:2233:U:H2'	51:1:2234:G:H8	1.59	0.67
51:1:2278:A:C3'	51:1:2279:G:H5''	2.25	0.67
51:1:2595:G:N2	51:1:2598:A:OP2	2.23	0.67
51:1:2898:U:H2'	51:1:2899:A:C8	2.29	0.67
58:B1:161:THR:HG22	58:B1:164:GLN:HB2	1.75	0.67
51:1:226:A:H2'	51:1:227:A:O4'	1.93	0.67
51:1:466:A:H2'	51:1:467:G:H5'	1.76	0.67
53:3:437:U:H3	53:3:495:A:H62	1.41	0.67
55:8:3:DC:C6	55:8:4:DT:H72	2.29	0.67
63:5:47:U:H4'	63:5:48:C:H5'	1.75	0.67
17:Q:109:ARG:HH21	17:Q:112:ALA:HB3	1.59	0.67
51:1:703:U:C2'	51:1:704:G:H5'	2.25	0.67
51:1:1020:A:H1'	51:1:1021:A:OP2	1.95	0.67
51:1:2221:G:O2'	51:1:2222:C:H5'	1.95	0.67
55:8:23:DC:H2''	55:8:24:DC:C5	2.30	0.67
51:1:1176:U:H2'	51:1:1177:G:C8	2.29	0.66
51:1:673:C:H2'	51:1:674:G:H5'	1.77	0.66
51:1:905:A:H2'	51:1:906:U:H5'	1.78	0.66
51:1:2555:U:H2'	51:1:2556:C:H5'	1.78	0.66
51:1:246:C:H2'	51:1:247:G:H5'	1.76	0.66
51:1:414:C:H2'	51:1:415:A:C8	2.31	0.66
51:1:2233:U:H2'	51:1:2234:G:C8	2.30	0.66
58:B1:108:ALA:CB	58:B1:279:LEU:HD22	2.25	0.66
51:1:707:G:O2'	51:1:708:G:H5'	1.94	0.66
51:1:1733:G:O2'	51:1:1734:G:H5'	1.95	0.66
51:1:2516:A:O2'	51:1:2517:C:H5'	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:984:LEU:HB3	58:B1:993:GLU:HB2	1.77	0.66
4:D:37:LYS:HD3	4:D:39:ARG:HD3	1.77	0.66
51:1:528:A:H3'	51:1:528:A:H8	1.59	0.66
51:1:2013:A:H5''	51:1:2013:A:H8	1.59	0.66
51:1:2733:A:O2'	51:1:2734:A:H5'	1.96	0.66
55:8:13:DT:OP2	58:B1:791:ALA:HB1	1.96	0.66
28:c:4:LEU:HD23	28:c:29:VAL:HG11	1.77	0.66
58:B1:978:ARG:HG2	58:B1:1197:ASN:HD21	1.61	0.66
33:i:27:LEU:HD22	33:i:32:VAL:HG21	1.78	0.66
51:1:2278:A:H3'	51:1:2279:G:H5''	1.78	0.66
51:1:2844:G:H2'	51:1:2845:U:C6	2.31	0.66
38:n:63:ARG:NE	51:1:1454:C:H5'	2.10	0.66
51:1:644:A:C2'	51:1:645:C:H5''	2.22	0.66
51:1:1098:A:H2'	51:1:1099:G:H5'	1.77	0.66
58:B1:68:TYR:C	58:B1:75:TYR:CE2	2.65	0.66
58:B1:111:THR:CG2	58:B1:300:GLN:CD	2.67	0.66
51:1:112:U:H2'	51:1:113:U:H5'	1.76	0.66
51:1:870:U:C2'	51:1:871:U:H5'	2.26	0.66
51:1:1270:C:H5''	51:1:1271:G:C5'	2.25	0.66
51:1:1788:C:O2'	51:1:1789:A:H5'	1.96	0.66
51:1:1064:C:N4	51:1:1069:A:H5''	2.10	0.66
51:1:1746:A:H2'	51:1:1747:U:C6	2.31	0.66
51:1:2625:G:H2'	51:1:2626:C:C6	2.30	0.66
58:B1:461:PHE:HD2	59:B2:813:GLU:HB2	1.62	0.66
51:1:521:U:H2'	51:1:522:A:C8	2.30	0.65
51:1:1666:G:H2'	51:1:1667:G:C5'	2.24	0.65
58:B1:108:ALA:HB3	58:B1:279:LEU:HD22	1.77	0.65
7:G:67:LEU:HD12	7:G:153:MET:HE1	1.77	0.65
43:s:6:LYS:HB2	51:1:494:G:H4'	1.78	0.65
51:1:1796:U:H2'	51:1:1797:G:H8	1.61	0.65
17:Q:47:ALA:HB3	17:Q:49:ARG:HE	1.60	0.65
51:1:359:G:O2'	51:1:360:U:H5'	1.97	0.65
51:1:635:C:H2'	51:1:636:G:C8	2.31	0.65
51:1:2052:A:O2'	51:1:2053:G:H5'	1.96	0.65
51:1:2193:G:H2'	51:1:2194:U:C6	2.32	0.65
58:B1:141:PHE:HD2	58:B1:293:ARG:O	1.79	0.65
51:1:65:U:H2'	51:1:66:C:H6	1.59	0.65
51:1:536:G:H2'	51:1:537:G:H5'	1.79	0.65
51:1:2170:A:H2'	51:1:2171:A:O4'	1.97	0.65
51:1:2760:C:O2'	51:1:2761:A:H5'	1.96	0.65
58:B1:1355:ARG:NH1	58:B1:1369:ARG:HH12	1.92	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:488:G:N2	51:1:491:G:H5''	2.11	0.65
51:1:1572:A:O2'	51:1:1573:G:H5'	1.97	0.65
51:1:543:G:H2'	51:1:544:C:C5'	2.26	0.65
51:1:1098:A:C2'	51:1:1099:G:H5'	2.27	0.65
58:B1:975:ILE:HG22	58:B1:977:SER:H	1.62	0.65
51:1:613:A:H5''	51:1:614:A:C8	2.32	0.65
19:S:38:GLU:HA	19:S:41:TRP:HB3	1.79	0.65
27:b:227:VAL:HG11	51:1:784:G:C2	2.31	0.65
28:c:149:ASN:HB3	51:1:2572:A:OP2	1.97	0.65
51:1:1857:G:H22	51:1:1884:G:H2'	1.62	0.65
51:1:2290:G:H2'	51:1:2291:U:C6	2.32	0.65
51:1:2834:G:O2'	51:1:2835:A:H5'	1.97	0.65
16:P:19:VAL:HG22	16:P:82:GLU:HB2	1.79	0.65
58:B1:68:TYR:HB3	58:B1:75:TYR:CE2	2.32	0.64
58:B1:285:LEU:HD13	58:B1:285:LEU:H	1.62	0.64
51:1:1853:A:H2'	51:1:1854:A:C8	2.32	0.64
51:1:2792:A:H3'	51:1:2793:C:H5''	1.79	0.64
11:K:38:ARG:HE	11:K:97:THR:HA	1.62	0.64
51:1:306:U:H2'	51:1:307:G:O4'	1.98	0.64
51:1:703:U:H2'	51:1:704:G:H5'	1.77	0.64
51:1:1766:G:O2'	51:1:1767:G:H5'	1.98	0.64
58:B1:918:ILE:HG22	59:B2:1280:ALA:HB1	1.79	0.64
4:D:24:THR:HG23	4:D:27:GLY:H	1.61	0.64
27:b:106:PRO:HD2	27:b:109:LEU:HD22	1.79	0.64
31:f:154:GLU:HG3	31:f:156:TYR:H	1.61	0.64
58:B1:193:ASP:HB3	58:B1:196:GLN:HB2	1.78	0.64
59:B2:1282:GLY:HA3	60:W0:17:PHE:HE1	1.63	0.64
58:B1:1037:PHE:HB3	58:B1:1040:MET:HB2	1.78	0.64
51:1:201:C:O2'	51:1:202:U:H5'	1.97	0.64
53:3:85:U:H5''	53:3:86:G:H5'	1.78	0.64
59:B2:314:ASN:HD21	59:B2:348:SER:HA	1.62	0.64
59:B2:891:GLY:H	59:B2:914:LYS:H	1.43	0.64
51:1:256:A:O2'	51:1:257:C:H5'	1.98	0.64
51:1:622:G:O2'	51:1:623:C:H5'	1.98	0.64
51:1:870:U:H2'	51:1:871:U:H5'	1.80	0.64
51:1:2404:U:O2'	51:1:2405:G:H5'	1.97	0.64
51:1:65:U:H2'	51:1:66:C:C6	2.33	0.64
12:L:59:GLU:HA	12:L:62:GLU:HB3	1.80	0.64
51:1:1161:C:H2'	51:1:1162:G:H8	1.61	0.64
51:1:2073:C:O2'	51:1:2074:U:H5'	1.98	0.64
51:1:905:A:O2'	51:1:906:U:H5'	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:940:G:C3'	51:1:941:A:H5''	2.28	0.63
51:1:2112:G:C2'	51:1:2113:U:H5'	2.27	0.63
51:1:2114:A:N7	51:1:2115:G:H1'	2.12	0.63
55:8:3:DC:C2'	55:8:4:DT:C7	2.75	0.63
26:Z:65:ARG:NH2	53:3:1087:G:N3	2.47	0.63
51:1:2811:G:O2'	51:1:2812:G:H5'	1.97	0.63
51:1:317:G:H2'	51:1:318:C:H6	1.64	0.63
51:1:2799:A:C2'	51:1:2800:A:H5'	2.27	0.63
26:Z:32:ARG:HG2	26:Z:33:ARG:HG3	1.80	0.63
51:1:161:A:N7	51:1:162:U:H5	1.96	0.63
51:1:1181:U:H2'	51:1:1182:G:C8	2.33	0.63
58:B1:395:LYS:HZ2	58:B1:399:LYS:CD	2.11	0.63
51:1:1280:G:O2'	51:1:1281:G:H5'	1.99	0.63
51:1:2469:A:H2'	51:1:2470:G:O4'	1.98	0.63
51:1:1909:C:H2'	51:1:1910:G:H8	1.64	0.63
51:1:2636:C:H2'	51:1:2637:U:H6	1.64	0.63
58:B1:245:LEU:HG	58:B1:246:PRO:HD2	1.80	0.63
58:B1:1357:ILE:HD11	59:B2:1287:LEU:HD13	1.80	0.63
51:1:1164:C:O2'	51:1:1165:A:H5'	1.99	0.63
9:I:152:SER:H	9:I:155:LYS:HD3	1.63	0.63
17:Q:40:THR:OG1	65:h:6:5OH:HR	1.99	0.63
51:1:815:C:C2	51:1:1193:G:N2	2.66	0.63
51:1:1921:G:O2'	51:1:1922:G:H5'	1.98	0.63
51:1:2314:A:H2'	51:1:2315:G:C8	2.33	0.63
16:P:87:GLY:H	16:P:113:THR:HG22	1.62	0.62
34:j:45:THR:HB	34:j:48:VAL:HG22	1.81	0.62
51:1:872:U:O2'	51:1:873:C:H5'	1.99	0.62
51:1:1524:G:H2'	51:1:1525:A:H8	1.63	0.62
53:3:373:A:H61	53:3:391:G:H1'	1.64	0.62
58:B1:162:GLU:HA	58:B1:162:GLU:OE1	1.97	0.62
51:1:2898:U:H2'	51:1:2899:A:H8	1.64	0.62
55:8:13:DT:C7	58:B1:791:ALA:HB2	2.29	0.62
51:1:212:G:O2'	51:1:213:A:H5'	1.99	0.62
57:A1:211:ILE:HG12	57:A1:219:ARG:HH12	1.65	0.62
58:B1:201:LEU:HB2	58:B1:221:ILE:HD13	1.80	0.62
51:1:37:C:O2'	51:1:38:A:H5'	1.99	0.62
51:1:445:C:H2'	51:1:446:G:O4'	1.98	0.62
58:B1:1355:ARG:NH1	58:B1:1369:ARG:NH1	2.47	0.62
59:B2:528:ARG:NH2	59:B2:576:SER:O	2.30	0.62
51:1:1935:G:H1'	51:1:1964:G:N2	2.15	0.62
51:1:2298:A:H2'	51:1:2299:U:O4'	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:MET:HG2	52:2:43:C:H5''	1.82	0.62
7:G:173:LYS:O	7:G:177:ASN:ND2	2.32	0.62
16:P:58:THR:HG22	16:P:60:PHE:H	1.65	0.62
44:t:53:VAL:HG12	44:t:92:ASN:HD22	1.65	0.62
51:1:161:A:H3'	51:1:162:U:H5''	1.81	0.62
51:1:1038:G:H2'	51:1:1039:A:C8	2.33	0.62
51:1:1149:G:H2'	51:1:1150:C:C6	2.33	0.62
51:1:1448:G:H2'	51:1:1449:G:H8	1.64	0.62
61:NA:67:GLU:HA	61:NA:76:THR:HA	1.81	0.62
16:P:45:THR:HG23	16:P:48:GLY:H	1.65	0.62
51:1:236:C:H2'	51:1:237:C:H6	1.64	0.62
51:1:554:U:H2'	51:1:555:G:O4'	1.99	0.62
51:1:889:C:H2'	51:1:890:C:O4'	1.99	0.62
51:1:2092:U:H5	51:1:2199:A:H2	1.48	0.62
51:1:723:C:H2'	51:1:724:U:H6	1.64	0.62
51:1:1086:A:H5'	51:1:1103:A:H2	1.65	0.62
51:1:2097:A:H2'	51:1:2098:U:O4'	2.00	0.62
51:1:2637:U:H2'	51:1:2638:G:H5'	1.82	0.62
58:B1:395:LYS:NZ	58:B1:399:LYS:HD3	2.15	0.62
64:7:46:G:C2'	64:7:47:U:H5'	2.29	0.62
28:c:181:ASP:HB3	28:c:186:LEU:HB2	1.82	0.62
57:A1:38:THR:HB	57:A2:45:ARG:HD3	1.82	0.62
31:f:174:LYS:HG3	51:1:2529:G:C4'	2.29	0.62
51:1:1503:A:H3'	51:1:1504:A:H5''	1.81	0.62
51:1:2734:A:H2'	51:1:2735:G:H5'	1.82	0.62
55:8:1:DC:H2''	55:8:2:DC:C5	2.35	0.62
7:G:15:PHE:HB2	7:G:39:ILE:HG23	1.82	0.61
51:1:1680:U:H2'	51:1:1681:G:O4'	2.00	0.61
58:B1:111:THR:CG2	58:B1:300:GLN:NE2	2.63	0.61
33:i:135:MET:HE2	51:1:1062:G:H21	1.65	0.61
51:1:590:A:O2'	51:1:591:U:H5'	2.00	0.61
34:j:3:THR:N	51:1:995:C:N3	2.48	0.61
34:j:132:HIS:CD2	51:1:7:G:H5'	2.35	0.61
51:1:322:A:H5'	51:1:340:A:O4'	2.00	0.61
51:1:941:A:H2'	51:1:942:G:O4'	2.00	0.61
51:1:2345:G:N3	51:1:2381:A:H2'	2.15	0.61
51:1:2404:U:H2'	51:1:2405:G:O4'	2.01	0.61
58:B1:770:LEU:HD13	59:B2:618:GLN:CG	2.30	0.61
59:B2:55:SER:OG	59:B2:465:ARG:NH1	2.33	0.61
22:V:30:HIS:HD2	22:V:33:TYR:H	1.48	0.61
30:e:9:ASP:OD1	30:e:9:ASP:N	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:940:G:C2'	51:1:941:A:H5''	2.30	0.61
58:B1:68:TYR:HB3	58:B1:75:TYR:CZ	2.35	0.61
7:G:86:CYS:SG	7:G:87:ASP:N	2.74	0.61
58:B1:128:LEU:HA	58:B1:192:MET:HE1	1.81	0.61
58:B1:633:ALA:HA	59:B2:806:PRO:O	2.01	0.61
45:u:87:GLU:HG2	45:u:92:VAL:HG21	1.82	0.61
51:1:547:A:H3'	51:1:547:A:N3	2.16	0.61
51:1:1775:U:C2'	51:1:1776:G:H5'	2.30	0.61
51:1:1948:G:H21	53:3:1418:A:H2	1.49	0.61
51:1:1954:G:H1'	51:1:1956:U:O4	2.01	0.61
58:B1:223:LEU:HG	58:B1:223:LEU:O	2.00	0.61
32:g:50:ARG:HH22	32:g:51:ARG:HH21	1.48	0.61
34:j:39:LYS:HE3	51:1:1009:A:OP1	2.01	0.61
51:1:414:C:H2'	51:1:415:A:H8	1.63	0.61
51:1:1775:U:H2'	51:1:1776:G:C5'	2.29	0.61
55:8:3:DC:H2'	55:8:4:DT:C7	2.30	0.61
58:B1:100:GLU:HA	59:B2:1328:LYS:HE2	1.82	0.61
58:B1:342:LEU:HD23	58:B1:1352:ILE:HG23	1.83	0.61
63:5:39:U:H2'	63:5:40:C:C6	2.36	0.61
37:m:17:ASN:O	37:m:38:ARG:NH1	2.34	0.61
51:1:172:A:H2'	51:1:173:A:H8	1.66	0.61
51:1:2812:G:H2'	51:1:2813:A:C8	2.36	0.61
4:D:3:ARG:O	4:D:6:GLN:NE2	2.33	0.60
59:B2:120:GLN:NE2	59:B2:490:GLN:OE1	2.32	0.60
51:1:11:C:C2'	51:1:12:U:H5''	2.29	0.60
51:1:558:U:H6	51:1:558:U:O5'	1.84	0.60
51:1:2852:G:O2'	51:1:2853:C:H5'	2.01	0.60
39:o:4:LYS:HD3	39:o:7:ARG:HH21	1.65	0.60
51:1:1040:A:H2	51:1:1115:G:H22	1.48	0.60
51:1:1287:A:C5	51:1:1288:G:C6	2.89	0.60
51:1:1717:A:C2'	51:1:1718:G:H5'	2.31	0.60
51:1:2188:U:H2'	51:1:2189:U:O4'	2.01	0.60
51:1:2386:A:O2'	51:1:2387:U:H5'	2.01	0.60
53:3:1351:U:H3	53:3:1371:G:H1	1.49	0.60
29:d:149:ILE:HG23	29:d:188:MET:HB3	1.83	0.60
21:U:70:ARG:HH22	53:3:451:A:H5'	1.66	0.60
27:b:153:LEU:HD23	51:1:1799:G:C2	2.37	0.60
51:1:198:C:H42	51:1:248:G:H1	1.49	0.60
51:1:435:C:H2'	51:1:436:C:H5'	1.82	0.60
51:1:893:C:H2'	51:1:894:U:C6	2.36	0.60
51:1:1508:A:H2'	51:1:1509:A:O4'	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:w:38:GLY:HA2	51:1:2330:G:H21	1.66	0.60
51:1:1071:G:H1'	51:1:1089:A:C8	2.37	0.60
51:1:2137:U:H2'	51:1:2138:G:H8	1.67	0.60
51:1:2187:U:O2'	51:1:2188:U:H5'	2.02	0.60
58:B1:1161:GLY:HA3	58:B1:1179:PRO:HA	1.82	0.60
51:1:851:C:H2'	51:1:852:U:C6	2.36	0.60
58:B1:395:LYS:HZ2	58:B1:399:LYS:HD3	1.66	0.60
51:1:1183:U:H2'	51:1:1184:U:C6	2.37	0.60
51:1:1198:U:H2'	51:1:1199:U:C6	2.37	0.60
53:3:1032:G:H21	53:3:1033:G:H4'	1.65	0.60
51:1:841:G:O2'	51:1:842:U:H5'	2.02	0.60
51:1:1171:G:H2'	51:1:1172:C:O4'	2.02	0.60
51:1:1437:C:H2'	51:1:1438:U:C6	2.36	0.60
51:1:2093:G:O2'	51:1:2094:A:H5'	2.01	0.60
51:1:2717:C:C4	51:1:2718:G:N7	2.70	0.60
51:1:2749:A:OP2	51:1:2751:G:H5''	2.02	0.60
58:B1:99:ARG:NH1	58:B1:99:ARG:HG3	2.17	0.60
51:1:854:C:O2'	51:1:855:G:H5'	2.01	0.60
51:1:1538:G:H2'	51:1:1539:U:C6	2.37	0.60
51:1:1857:G:N2	51:1:1884:G:H2'	2.17	0.60
51:1:2327:A:H2'	51:1:2328:A:C8	2.35	0.60
53:3:1133:G:H1	53:3:1141:C:H42	1.48	0.60
29:d:68:ALA:HA	51:1:1255:U:C5	2.37	0.59
45:u:40:LEU:HD12	45:u:59:GLU:HG2	1.84	0.59
51:1:2643:G:H2'	51:1:2644:G:H5'	1.84	0.59
58:B1:201:LEU:HD11	58:B1:220:ARG:HH11	1.67	0.59
58:B1:370:LYS:HG2	58:B1:441:LEU:HD23	1.84	0.59
58:B1:926:PRO:HG2	58:B1:1248:ILE:HD11	1.84	0.59
14:N:40:ARG:NH2	14:N:41:GLU:OE2	2.34	0.59
18:R:102:LYS:HG2	18:R:103:THR:HG23	1.83	0.59
51:1:1670:C:H2'	51:1:1671:U:C5'	2.31	0.59
51:1:2804:U:H2'	51:1:2805:C:C6	2.36	0.59
55:8:7:DC:H2''	55:8:8:DT:H71	1.84	0.59
58:B1:144:TYR:CE1	58:B1:162:GLU:OE2	2.51	0.59
58:B1:154:LEU:HD21	58:B1:160:LEU:HD21	1.83	0.59
58:B1:951:GLN:NE2	58:B1:1014:GLY:O	2.35	0.59
9:I:69:ARG:NH1	53:3:401:C:OP2	2.36	0.59
37:m:86:LYS:NZ	51:1:955:U:OP1	2.33	0.59
51:1:215:G:H4'	51:1:216:A:H4'	1.85	0.59
55:8:11:DC:H2'	55:8:12:DG:C8	2.37	0.59
59:B2:1072:ASN:ND2	59:B2:1111:GLN:OE1	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2165:C:H2'	51:1:2166:U:C6	2.38	0.59
51:1:2743:U:H3'	51:1:2744:G:H5''	1.84	0.59
53:3:1040:U:H2'	53:3:1041:G:H8	1.67	0.59
29:d:77:ILE:HG23	51:1:1256:G:H21	1.68	0.59
51:1:283:G:H2'	51:1:284:U:H5'	1.83	0.59
51:1:1110:G:HO2'	51:1:1111:A:H8	1.50	0.59
51:1:2812:G:H2'	51:1:2813:A:H8	1.67	0.59
30:e:51:ASN:OD1	30:e:149:ARG:NH1	2.34	0.59
47:w:40:LYS:HE3	51:1:2330:G:O2'	2.03	0.59
6:F:14:CYS:SG	6:F:33:HIS:ND1	2.75	0.59
22:V:11:VAL:HA	22:V:22:VAL:HA	1.83	0.59
42:r:4:VAL:HG22	42:r:40:MET:HG2	1.85	0.59
51:1:1725:U:H2'	51:1:1726:C:C6	2.38	0.59
55:8:9:DG:H4'	58:B1:120:LEU:HG	1.84	0.59
58:B1:412:LEU:HD22	58:B1:441:LEU:HD21	1.84	0.59
59:B2:1142:ARG:NH1	59:B2:1161:LEU:O	2.36	0.59
14:N:17:ARG:HB2	14:N:65:THR:HG23	1.83	0.59
53:3:422:C:O2'	53:3:423:G:N2	2.36	0.59
58:B1:161:THR:HG23	58:B1:164:GLN:H	1.68	0.59
58:B1:438:GLU:HG3	58:B1:485:MET:HE1	1.84	0.59
51:1:1026:G:H2'	51:1:1027:A:H8	1.67	0.59
51:1:1337:G:H2'	51:1:1338:G:C8	2.38	0.59
58:B1:97:VAL:HG11	58:B1:101:ARG:NH2	2.18	0.59
59:B2:707:ALA:O	59:B2:711:ASP:HB2	2.03	0.59
24:X:30:LEU:HB2	24:X:48:ILE:HG22	1.84	0.59
29:d:77:ILE:CG2	51:1:1256:G:H21	2.15	0.59
51:1:246:C:C2'	51:1:247:G:H5'	2.33	0.59
51:1:1469:A:H2'	51:1:1470:A:C8	2.38	0.59
51:1:2183:A:H2'	51:1:2184:A:C4	2.38	0.59
51:1:2360:G:C2'	51:1:2361:G:H5'	2.31	0.59
25:Y:73:ARG:NH2	53:3:261:U:OP2	2.36	0.58
51:1:794:A:H2'	51:1:795:C:O4'	2.02	0.58
51:1:1773:A:C2'	51:1:1774:C:H5'	2.31	0.58
57:A1:112:ALA:HB3	57:A1:126:PRO:HA	1.83	0.58
58:B1:514:THR:HG21	58:B1:596:LEU:HD12	1.84	0.58
27:b:141:HIS:ND1	27:b:192:GLY:O	2.36	0.58
51:1:49:A:H5''	51:1:51:G:O4'	2.02	0.58
51:1:1042:G:H2'	51:1:1043:C:C6	2.37	0.58
51:1:1098:A:H2'	51:1:1099:G:C5'	2.33	0.58
51:1:1511:G:H2'	51:1:1512:C:C6	2.38	0.58
51:1:1524:G:H2'	51:1:1525:A:C8	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1845:G:O2'	51:1:1846:G:H5'	2.02	0.58
51:1:2091:C:H5	51:1:2092:U:HO2'	1.50	0.58
58:B1:725:MET:SD	59:B2:1101:LEU:HD23	2.42	0.58
58:B1:1361:THR:HB	59:B2:1284:ALA:HB3	1.86	0.58
59:B2:69:GLN:HE21	59:B2:101:ARG:HD2	1.67	0.58
14:N:79:ARG:HH21	14:N:102:PHE:HA	1.67	0.58
23:W:49:LYS:HA	23:W:52:ARG:HH21	1.68	0.58
51:1:528:A:C8	51:1:528:A:C3'	2.86	0.58
51:1:1077:A:C8	51:1:1078:U:H1'	2.37	0.58
51:1:1463:C:H2'	51:1:1464:G:H8	1.68	0.58
51:1:2533:U:H2'	51:1:2534:A:H5'	1.85	0.58
53:3:409:U:H3	53:3:433:G:H1	1.51	0.58
59:B2:918:LEU:O	59:B2:918:LEU:HD23	2.02	0.58
33:i:25:PRO:HG2	51:1:1068:G:H21	1.67	0.58
37:m:66:ARG:NH1	37:m:104:GLU:OE2	2.36	0.58
51:1:2789:C:H2'	51:1:2893:A:N7	2.18	0.58
51:1:2834:G:H2'	51:1:2879:A:N6	2.17	0.58
53:3:148:G:H1'	53:3:1447:A:H1'	1.84	0.58
9:I:201:GLU:O	53:3:8:A:N6	2.36	0.58
51:1:621:A:H2'	51:1:622:G:H5'	1.86	0.58
51:1:1561:C:H2'	51:1:1562:U:C6	2.39	0.58
51:1:1893:C:H2'	51:1:1894:C:H5'	1.86	0.58
51:1:2215:C:H2'	51:1:2216:G:H8	1.65	0.58
58:B1:638:SER:OG	58:B1:639:VAL:N	2.36	0.58
27:b:34:GLU:HG3	27:b:63:ILE:HD11	1.84	0.58
28:c:129:THR:OG1	28:c:140:HIS:O	2.22	0.58
51:1:1579:A:H2'	51:1:1580:A:C8	2.38	0.58
51:1:2845:U:H2'	51:1:2846:G:H8	1.69	0.58
53:3:1125:U:H2'	53:3:1126:U:H2'	1.86	0.58
33:i:22:PRO:HA	51:1:1067:A:O2'	2.04	0.58
50:z:4:ILE:HD11	50:z:58:GLU:HG2	1.85	0.58
51:1:640:C:O2'	51:1:641:U:H5'	2.04	0.58
27:b:157:ALA:O	51:1:1820:U:C2	2.56	0.58
51:1:327:G:O2'	51:1:328:U:H5'	2.04	0.58
51:1:673:C:C2'	51:1:674:G:H5'	2.34	0.58
29:d:1:MET:HG2	29:d:16:GLU:HG2	1.86	0.58
51:1:834:G:H2'	51:1:835:C:O4'	2.04	0.58
51:1:1565:C:O2'	51:1:1566:A:H8	1.87	0.58
51:1:2153:C:H2'	51:1:2154:A:H5'	1.85	0.58
58:B1:241:VAL:O	58:B1:241:VAL:HG12	2.04	0.58
58:B1:750:PRO:CB	59:B2:549:ASP:OD2	2.45	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:n:63:ARG:CZ	51:1:1454:C:H5'	2.34	0.57
39:o:56:LYS:NZ	52:2:117:G:OP1	2.36	0.57
51:1:323:C:H3'	51:1:323:C:OP2	2.05	0.57
51:1:2636:C:H2'	51:1:2637:U:C6	2.39	0.57
51:1:2762:C:H2'	51:1:2763:G:H5'	1.86	0.57
58:B1:160:LEU:HD22	58:B1:164:GLN:HB3	1.86	0.57
58:B1:615:LYS:HG2	60:W0:5:THR:HG21	1.85	0.57
38:n:22:ARG:HG3	38:n:70:THR:HA	1.86	0.57
51:1:32:C:H2'	51:1:33:C:C6	2.39	0.57
51:1:2186:G:O2'	51:1:2187:U:H5'	2.04	0.57
51:1:2570:G:H2'	51:1:2571:U:H5'	1.85	0.57
51:1:2897:U:H2'	51:1:2898:U:C6	2.39	0.57
57:A2:28:LEU:HB2	57:A2:201:LEU:HB3	1.85	0.57
58:B1:275:ARG:NH1	58:B1:278:ARG:NH1	2.51	0.57
1:A:26:SER:OG	1:A:27:THR:N	2.37	0.57
27:b:220:ARG:NH1	51:1:1789:A:OP2	2.38	0.57
40:p:1:SER:OG	40:p:2:ASN:N	2.37	0.57
51:1:655:A:H4'	51:1:656:G:C5'	2.30	0.57
51:1:877:A:N1	51:1:899:A:H2'	2.20	0.57
51:1:1333:G:O2'	51:1:1334:G:H5'	2.03	0.57
51:1:2092:U:H4'	51:1:2093:G:C5'	2.34	0.57
57:A2:82:LEU:HD11	57:A2:171:LEU:HD23	1.86	0.57
14:N:35:GLU:HA	14:N:39:GLY:HA3	1.85	0.57
30:e:47:LYS:O	30:e:51:ASN:ND2	2.37	0.57
31:f:151:ARG:HB3	31:f:161:VAL:HG23	1.86	0.57
51:1:235:U:H2'	51:1:236:C:C6	2.39	0.57
16:P:92:ARG:NH2	16:P:111:ASP:OD1	2.38	0.57
38:n:54:LEU:HD23	38:n:66:ALA:HB2	1.86	0.57
39:o:25:ARG:NH1	52:2:8:C:O3'	2.37	0.57
51:1:2899:A:O2'	51:1:2900:A:H5'	2.05	0.57
58:B1:741:ALA:O	58:B1:762:ASN:ND2	2.37	0.57
15:O:46:LYS:HG2	15:O:68:ARG:HG2	1.84	0.57
27:b:259:ASN:ND2	27:b:262:THR:OG1	2.38	0.57
28:c:55:LYS:NZ	28:c:59:ARG:O	2.36	0.57
59:B2:13:LYS:HB2	59:B2:1180:MET:HE2	1.86	0.57
19:S:5:MET:HE1	53:3:981:U:H5''	1.86	0.57
28:c:63:PRO:HG3	51:1:2787:C:H1'	1.85	0.57
31:f:174:LYS:HE2	51:1:2529:G:H4'	1.86	0.57
41:q:30:VAL:HG13	51:1:580:U:O3'	2.04	0.57
51:1:146:A:H2'	51:1:147:C:C6	2.39	0.57
51:1:1275:A:C6	51:1:1296:G:H4'	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1526:C:H2'	51:1:1527:G:O4'	2.04	0.57
59:B2:1122:LYS:NZ	59:B2:1126:ASP:OD1	2.38	0.57
31:f:44:HIS:HA	31:f:49:LEU:HG	1.87	0.57
51:1:635:C:H2'	51:1:636:G:H8	1.70	0.57
51:1:1173:U:C5	51:1:1174:U:H1'	2.40	0.57
58:B1:247:PRO:HA	58:B1:250:ARG:HG3	1.87	0.57
7:G:114:LYS:HE3	7:G:151:LYS:HB2	1.85	0.57
9:I:10:LEU:HD23	9:I:62:ARG:HB3	1.86	0.57
31:f:40:VAL:O	31:f:54:ARG:NH2	2.38	0.57
51:1:163:C:H2'	51:1:164:C:O4'	2.04	0.57
51:1:593:U:H2'	51:1:594:U:C6	2.40	0.57
51:1:1108:U:H2'	51:1:1109:C:C2	2.40	0.57
51:1:1400:U:O2'	51:1:1401:G:H5'	2.04	0.57
51:1:1590:A:O2'	51:1:1591:A:H5'	2.05	0.57
58:B1:198:CYS:HA	58:B1:221:ILE:HD11	1.86	0.57
10:J:54:GLU:HG2	10:J:56:PRO:HD2	1.86	0.57
34:j:116:ARG:NH2	51:1:529:A:OP2	2.32	0.57
49:y:39:GLN:HG2	51:1:96:C:OP1	2.04	0.57
53:3:202:G:H21	53:3:466:A:H61	1.53	0.57
59:B2:839:VAL:HG12	59:B2:1049:ILE:HG12	1.87	0.57
51:1:366:C:O2'	51:1:367:G:H5'	2.04	0.56
58:B1:130:MET:HE2	58:B1:135:ILE:HG12	1.87	0.56
58:B1:1046:ILE:HD12	58:B1:1059:LEU:HB3	1.86	0.56
19:S:26:LEU:HA	19:S:30:ILE:HD12	1.87	0.56
25:Y:59:ARG:NH1	53:3:177:G:OP1	2.37	0.56
28:c:18:ASP:N	28:c:18:ASP:OD1	2.35	0.56
51:1:78:U:H2'	51:1:79:C:C6	2.40	0.56
51:1:503:A:H4'	51:1:505:A:H5''	1.87	0.56
51:1:1520:U:O2'	51:1:1521:G:H5'	2.05	0.56
51:1:1678:A:H2'	51:1:1679:A:H5'	1.86	0.56
51:1:2457:U:O2'	51:1:2458:G:H5'	2.04	0.56
16:P:111:ASP:HB2	26:Z:16:ARG:HH22	1.68	0.56
17:Q:8:ARG:NH2	53:3:880:C:OP1	2.36	0.56
39:o:52:SER:OG	39:o:53:THR:N	2.39	0.56
45:u:36:GLU:HA	45:u:61:GLU:HG2	1.86	0.56
46:v:57:TYR:OH	46:v:79:ARG:NH2	2.38	0.56
51:1:287:G:H2'	51:1:288:U:C6	2.40	0.56
51:1:727:A:H2'	51:1:728:G:C8	2.40	0.56
51:1:1319:C:O2'	51:1:1320:C:H5'	2.05	0.56
51:1:1485:U:H2'	51:1:1486:U:C6	2.41	0.56
51:1:1528:A:H2'	51:1:1529:G:H5'	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1917:U:O2'	51:1:1918:A:H5'	2.05	0.56
58:B1:102:MET:HG2	58:B1:246:PRO:HG3	1.87	0.56
62:NG:130:PRO:C	62:NG:132:GLU:H	2.13	0.56
51:1:69:C:H2'	51:1:70:G:H8	1.70	0.56
58:B1:804:ALA:HA	58:B1:1259:GLN:HG3	1.88	0.56
58:B1:1166:GLY:HA3	58:B1:1174:ARG:HB2	1.88	0.56
8:H:39:ARG:NH1	8:H:54:ILE:O	2.39	0.56
51:1:359:G:C2'	51:1:360:U:H5'	2.36	0.56
51:1:885:C:N4	51:1:886:A:H62	2.03	0.56
51:1:2395:C:H42	51:1:2421:G:H1	1.54	0.56
53:3:49:U:H3	53:3:362:G:H1'	1.71	0.56
59:B2:902:LEU:HD23	59:B2:908:GLU:HB2	1.86	0.56
64:7:52:G:H2'	64:7:53:G:H8	1.69	0.56
18:R:100:ARG:NH1	18:R:103:THR:OG1	2.38	0.56
51:1:288:U:H2'	51:1:289:G:H8	1.71	0.56
51:1:1097:U:H2'	51:1:1098:A:O4'	2.06	0.56
51:1:1182:G:H2'	51:1:1183:U:O4'	2.06	0.56
51:1:2584:U:C2'	51:1:2585:U:H5'	2.34	0.56
51:1:2626:C:H2'	51:1:2627:G:O4'	2.06	0.56
53:3:158:G:N2	53:3:163:C:O2	2.36	0.56
59:B2:854:ILE:CG2	59:B2:917:SER:HB3	2.36	0.56
7:G:58:LYS:O	7:G:62:ARG:NH1	2.38	0.56
19:S:52:ARG:O	19:S:58:ARG:NH1	2.39	0.56
28:c:134:HIS:CE1	51:1:1675:C:C4	2.94	0.56
51:1:1597:A:H5''	51:1:1598:A:H5'	1.87	0.56
59:B2:818:VAL:HG22	59:B2:1096:ILE:HG12	1.87	0.56
10:J:44:ARG:NH2	10:J:70:MET:SD	2.78	0.56
12:L:4:ARG:HB3	12:L:6:ILE:HG23	1.88	0.56
49:y:49:ASP:OD1	49:y:52:ARG:NH2	2.39	0.56
51:1:74:A:H4'	51:1:75:G:O5'	2.05	0.56
51:1:780:G:H21	51:1:783:A:H62	1.54	0.56
51:1:1120:G:O2'	51:1:1121:C:H5'	2.05	0.56
51:1:1130:U:O2'	51:1:1131:G:OP1	2.20	0.56
51:1:1485:U:H2'	51:1:1486:U:H6	1.70	0.56
51:1:2533:U:C2'	51:1:2534:A:H5'	2.36	0.56
53:3:503:C:H2'	53:3:504:C:C6	2.41	0.56
57:A2:29:GLU:HG3	57:A2:200:LYS:HG3	1.88	0.56
58:B1:42:GLU:HB3	58:B1:52:GLU:HG3	1.86	0.56
26:Z:44:ARG:NH1	53:3:722:G:OP2	2.39	0.56
51:1:613:A:H2'	51:1:613:A:N3	2.21	0.56
51:1:1772:A:H5'	51:1:1773:A:OP2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2662:A:H2'	51:1:2663:G:O4'	2.05	0.56
11:K:12:PRO:HB2	11:K:44:ARG:HH21	1.70	0.56
16:P:63:GLN:HG3	16:P:98:ALA:HB2	1.88	0.56
27:b:216:ARG:NH2	51:1:781:A:OP1	2.38	0.56
35:k:76:VAL:H	40:p:72:VAL:HG22	1.71	0.56
51:1:133:U:O2'	51:1:134:G:H5'	2.06	0.56
51:1:184:C:H2'	51:1:185:G:C8	2.41	0.56
51:1:1553:A:HO2'	51:1:1554:U:H5	1.54	0.56
53:3:1036:A:H2'	53:3:1037:C:H5'	1.88	0.56
58:B1:37:GLU:O	58:B1:61:ILE:CD1	2.52	0.56
4:D:9:VAL:HG22	51:1:1309:G:OP1	2.06	0.55
11:K:2:ARG:NH1	53:3:738:C:OP1	2.39	0.55
17:Q:40:THR:CG2	65:h:6:5OH:OS	2.51	0.55
29:d:84:THR:HG21	51:1:586:A:H5'	1.87	0.55
49:y:28:LEU:HA	49:y:31:GLN:HB2	1.88	0.55
51:1:296:U:H2'	51:1:297:G:C8	2.41	0.55
51:1:358:U:H2'	51:1:359:G:C8	2.40	0.55
51:1:1670:C:O5'	51:1:1670:C:H6	1.90	0.55
51:1:184:C:H2'	51:1:185:G:H8	1.70	0.55
53:3:1040:U:H2'	53:3:1041:G:C8	2.42	0.55
57:A1:29:GLU:HB3	57:A1:200:LYS:HG3	1.87	0.55
58:B1:39:LYS:O	58:B1:273:ILE:HG21	2.06	0.55
58:B1:1175:LEU:HD22	58:B1:1190:ILE:HD11	1.88	0.55
63:5:38:A:C8	63:5:39:U:H1'	2.40	0.55
8:H:76:ILE:HD11	54:4:20:U:H4'	1.87	0.55
33:i:5:GLN:O	33:i:30:GLN:NE2	2.40	0.55
51:1:317:G:H2'	51:1:318:C:C6	2.42	0.55
51:1:543:G:H2'	51:1:544:C:O4'	2.05	0.55
51:1:633:A:C2'	51:1:634:C:H5'	2.35	0.55
51:1:757:G:H2'	51:1:758:C:C5'	2.35	0.55
51:1:2236:U:H2'	51:1:2237:G:H5'	1.88	0.55
58:B1:99:ARG:CG	58:B1:99:ARG:HH11	2.17	0.55
51:1:112:U:C2'	51:1:113:U:H5'	2.37	0.55
51:1:1506:U:H2'	51:1:1507:C:C6	2.41	0.55
51:1:1697:G:H4'	51:1:1978:A:H5''	1.89	0.55
51:1:2845:U:H2'	51:1:2846:G:C8	2.42	0.55
51:1:2850:A:N1	51:1:2869:G:H4'	2.21	0.55
59:B2:103:VAL:HB	59:B2:114:VAL:HG11	1.89	0.55
35:k:65:THR:HG23	35:k:68:GLY:H	1.69	0.55
38:n:2:ARG:HA	38:n:5:LYS:HD3	1.88	0.55
43:s:98:LYS:HD3	51:1:2012:G:OP1	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:118:A:OP2	51:1:119:A:H5''	2.06	0.55
51:1:155:A:H2'	51:1:156:A:C8	2.41	0.55
51:1:1410:G:H2'	51:1:1411:U:C6	2.41	0.55
51:1:2488:G:O2'	51:1:2489:U:H5'	2.07	0.55
58:B1:510:LEU:HD22	58:B1:601:ILE:HD12	1.86	0.55
7:G:91:VAL:HG22	7:G:150:ILE:HD11	1.88	0.55
30:e:23:SER:HB3	30:e:26:GLN:HB2	1.87	0.55
51:1:1745:A:O2'	51:1:1746:A:H5'	2.07	0.55
51:1:2510:C:C4	51:1:2511:U:C4	2.94	0.55
51:1:2545:G:O2'	51:1:2546:U:H5'	2.07	0.55
59:B2:633:LEU:HD13	59:B2:644:LEU:HD23	1.89	0.55
36:l:89:VAL:HG23	36:l:121:THR:HG23	1.88	0.55
51:1:461:C:H2'	51:1:462:C:C6	2.42	0.55
51:1:720:U:H2'	51:1:721:A:C8	2.41	0.55
51:1:1048:A:H2'	51:1:1049:C:H5'	1.88	0.55
51:1:1909:C:H2'	51:1:1910:G:C8	2.41	0.55
54:4:4:U:H3	63:5:36:A:H61	1.55	0.55
58:B1:144:TYR:HE1	58:B1:162:GLU:CD	2.14	0.55
51:1:439:A:H2'	51:1:440:C:C6	2.42	0.55
51:1:1083:U:H2'	51:1:1084:A:H3'	1.89	0.55
51:1:2637:U:C2'	51:1:2638:G:H5'	2.36	0.55
58:B1:145:VAL:HG23	58:B1:159:ILE:HG22	1.89	0.55
59:B2:985:GLU:HB3	59:B2:988:LYS:HB2	1.89	0.55
59:B2:1142:ARG:NH2	59:B2:1166:ASP:OD1	2.38	0.55
63:5:40:C:H2'	63:5:41:C:C6	2.41	0.55
19:S:84:ARG:NH2	53:3:1059:C:O3'	2.40	0.55
33:i:10:LEU:HA	51:1:1061:U:C2	2.42	0.55
46:v:83:LYS:HD3	46:v:85:LYS:HZ1	1.72	0.55
51:1:877:A:C2'	51:1:878:A:H5''	2.37	0.55
51:1:1448:G:H2'	51:1:1449:G:C8	2.42	0.55
51:1:1545:A:H2'	51:1:1546:G:O4'	2.06	0.55
53:3:159:G:N2	53:3:162:A:OP2	2.34	0.55
53:3:505:G:H5''	53:3:534:U:H2'	1.89	0.55
64:7:9:G:C2	64:7:45:G:O6	2.60	0.55
25:Y:60:GLN:HA	25:Y:63:LYS:HB3	1.89	0.55
27:b:250:GLN:NE2	27:b:251:THR:O	2.38	0.55
51:1:128:C:H2'	51:1:129:C:H6	1.71	0.55
51:1:543:G:H2'	51:1:544:C:C4'	2.37	0.55
51:1:613:A:H5''	51:1:614:A:N7	2.22	0.55
51:1:759:G:H2'	51:1:760:G:C8	2.41	0.55
51:1:2217:G:O2'	51:1:2218:G:H5'	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:830:G:H1	53:3:856:C:H42	1.53	0.55
58:B1:508:LEU:HD22	59:B2:1101:LEU:HD21	1.88	0.55
7:G:19:THR:HA	7:G:37:VAL:HA	1.88	0.54
12:L:73:GLU:HG2	12:L:90:VAL:HG22	1.88	0.54
16:P:86:LYS:HG3	16:P:114:PRO:HD3	1.89	0.54
35:k:70:ARG:HG2	35:k:76:VAL:HG12	1.88	0.54
51:1:172:A:H2'	51:1:173:A:C8	2.40	0.54
51:1:1086:A:H5'	51:1:1103:A:C2	2.41	0.54
51:1:2195:U:O2'	51:1:2196:C:H5'	2.06	0.54
51:1:2743:U:C3'	51:1:2744:G:H5''	2.37	0.54
51:1:2827:C:O2'	51:1:2828:G:H5'	2.07	0.54
58:B1:833:GLU:HB2	58:B1:1242:ARG:NH1	2.22	0.54
59:B2:855:PRO:HB3	61:NA:103:ASP:CB	2.37	0.54
8:H:71:ARG:HB3	8:H:74:ILE:HD13	1.89	0.54
49:y:15:ASN:O	49:y:19:LEU:N	2.41	0.54
49:y:19:LEU:O	49:y:23:ARG:N	2.35	0.54
51:1:358:U:H2'	51:1:359:G:H8	1.71	0.54
51:1:825:A:O2'	51:1:826:U:H5'	2.07	0.54
51:1:1511:G:H2'	51:1:1512:C:H6	1.73	0.54
51:1:1541:C:O2'	51:1:1542:U:H5'	2.06	0.54
58:B1:759:ILE:HG23	58:B1:771:GLN:HB3	1.89	0.54
7:G:45:THR:O	7:G:49:PHE:N	2.35	0.54
10:J:23:THR:HA	10:J:28:ARG:HA	1.88	0.54
29:d:76:PRO:HA	29:d:82:GLY:HA3	1.90	0.54
36:l:20:GLY:HA2	36:l:28:GLY:HA2	1.90	0.54
36:l:80:SER:HB3	36:l:114:GLY:HA3	1.89	0.54
51:1:8:C:H2'	51:1:9:G:H8	1.73	0.54
51:1:1091:G:H2'	51:1:1092:C:C6	2.43	0.54
51:1:2114:A:C8	51:1:2115:G:H1'	2.42	0.54
59:B2:360:LEU:HD13	59:B2:378:ARG:HH11	1.72	0.54
59:B2:684:ASN:OD1	59:B2:687:ARG:NH2	2.41	0.54
31:f:103:ASN:ND2	31:f:113:ASP:OD1	2.41	0.54
51:1:141:G:H3'	51:1:142:A:O4'	2.07	0.54
51:1:143:C:H2'	51:1:144:A:H8	1.72	0.54
51:1:296:U:H2'	51:1:297:G:H8	1.71	0.54
51:1:1601:G:C2'	51:1:1602:U:H5'	2.37	0.54
7:G:138:ARG:NH1	7:G:141:GLU:OE2	2.40	0.54
38:n:35:LYS:NZ	38:n:100:CYS:SG	2.81	0.54
50:z:15:ARG:HE	50:z:52:PHE:HE2	1.53	0.54
51:1:340:A:H2'	51:1:341:C:O4'	2.06	0.54
51:1:392:U:H2'	51:1:393:C:C6	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1297:C:H2'	51:1:1298:C:C6	2.43	0.54
51:1:1748:C:H2'	51:1:1749:A:H8	1.73	0.54
51:1:2114:A:C2	51:1:2167:U:H1'	2.41	0.54
57:A2:100:LEU:HD23	57:A2:115:ILE:HG21	1.89	0.54
58:B1:814:CYS:SG	58:B1:883:ARG:NH2	2.81	0.54
7:G:53:LEU:HD21	7:G:215:ALA:HB1	1.88	0.54
51:1:53:A:H2'	51:1:54:G:H5'	1.89	0.54
51:1:1068:G:N2	51:1:1096:A:H1'	2.23	0.54
51:1:1530:G:H22	51:1:1542:U:H1'	1.73	0.54
53:3:923:A:N6	53:3:1392:G:O6	2.40	0.54
59:B2:29:SER:O	59:B2:33:ASP:HB2	2.07	0.54
51:1:359:G:H2'	51:1:360:U:O4'	2.07	0.54
51:1:1063:G:N1	51:1:1075:C:N4	2.52	0.54
51:1:1310:G:O2'	51:1:1311:G:H5'	2.06	0.54
51:1:2345:G:H5'	51:1:2347:C:H5'	1.89	0.54
58:B1:58:CYS:SG	58:B1:59:ALA:N	2.80	0.54
27:b:227:VAL:HG11	51:1:784:G:N1	2.23	0.54
39:o:69:ASP:N	39:o:69:ASP:OD1	2.36	0.54
51:1:402:A:C2'	51:1:403:U:H5'	2.38	0.54
51:1:472:A:H2'	51:1:473:G:H5'	1.89	0.54
51:1:1014:A:H2'	51:1:1015:U:C6	2.43	0.54
51:1:1111:A:H2'	51:1:1112:G:H4'	1.90	0.54
58:B1:799:ARG:HG2	58:B1:1325:PHE:HZ	1.72	0.54
58:B1:1155:ILE:HG13	58:B1:1210:ILE:HB	1.89	0.54
7:G:102:ASN:ND2	53:3:1073:U:O2	2.39	0.54
51:1:923:G:O2'	51:1:924:G:H5'	2.07	0.54
51:1:2734:A:C2'	51:1:2735:G:H5'	2.38	0.54
51:1:21:A:O2'	51:1:22:C:H5'	2.08	0.54
51:1:268:C:H2'	51:1:269:C:H6	1.73	0.54
51:1:1288:G:C6	51:1:1327:A:C2	2.95	0.54
51:1:1528:A:C2'	51:1:1529:G:H5'	2.38	0.54
51:1:2297:A:N1	51:1:2321:U:C5	2.75	0.54
58:B1:800:LEU:HB3	58:B1:920:ALA:HB1	1.89	0.54
59:B2:903:ARG:HB3	61:NA:1:MET:HA	1.89	0.54
48:x:29:LEU:HD12	51:1:2230:G:H5''	1.91	0.53
51:1:752:A:H62	51:1:2609:U:H3	1.56	0.53
51:1:784:G:C5'	51:1:785:G:OP1	2.54	0.53
51:1:973:A:H5'	51:1:1188:U:H1'	1.90	0.53
51:1:1389:G:O2'	51:1:1390:U:H5'	2.07	0.53
51:1:1601:G:O2'	51:1:1602:U:H5'	2.08	0.53
51:1:2190:G:O2'	51:1:2191:A:H5'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:2:40:U:N3	52:2:44:G:OP2	2.40	0.53
58:B1:633:ALA:HB2	59:B2:808:ASN:N	2.19	0.53
64:7:11:A:H2'	64:7:12:G:H8	1.72	0.53
25:Y:66:ILE:HG21	25:Y:70:LYS:HB3	1.91	0.53
42:r:75:VAL:HG23	42:r:86:GLN:HG2	1.90	0.53
51:1:481:G:H1'	51:1:506:G:H21	1.71	0.53
51:1:682:G:N2	51:1:796:C:O2	2.41	0.53
51:1:2644:G:O2'	51:1:2645:G:H5'	2.09	0.53
64:7:25:C:H42	64:7:45:G:H22	1.56	0.53
3:C:20:TYR:OH	51:1:2348:U:H5'	2.09	0.53
7:G:126:ASP:OD1	7:G:126:ASP:N	2.41	0.53
12:L:113:LYS:O	53:3:1239:A:O2'	2.22	0.53
23:W:52:ARG:NH2	53:3:835:U:OP1	2.41	0.53
30:e:21:TYR:OH	30:e:164:GLU:OE1	2.26	0.53
51:1:57:C:H2'	51:1:58:G:O4'	2.08	0.53
53:3:959:A:HO2'	53:3:984:C:HO2'	1.52	0.53
57:A2:43:LEU:HD13	57:A2:217:ILE:HD11	1.90	0.53
59:B2:628:HIS:HB3	59:B2:647:ARG:HH21	1.73	0.53
34:j:2:LYS:HA	51:1:995:C:N3	2.23	0.53
37:m:27:SER:H	37:m:66:ARG:HH12	1.54	0.53
51:1:894:U:O2'	51:1:895:U:H5'	2.09	0.53
51:1:1278:C:O2'	51:1:1279:G:H5'	2.09	0.53
51:1:2742:G:O2'	51:1:2743:U:H5'	2.08	0.53
51:1:2850:A:C2	51:1:2869:G:H4'	2.44	0.53
60:W0:3:ARG:NH1	60:W0:55:GLU:OE2	2.40	0.53
9:I:55:ARG:O	9:I:59:LYS:N	2.41	0.53
13:M:92:PRO:O	13:M:116:ARG:NH2	2.42	0.53
17:Q:64:SER:OG	17:Q:65:TYR:N	2.41	0.53
35:k:42:THR:HG22	35:k:57:VAL:HG12	1.91	0.53
41:q:90:ASP:OD1	41:q:90:ASP:N	2.37	0.53
51:1:176:A:O2'	51:1:177:G:H5'	2.08	0.53
51:1:1005:C:H6	51:1:1005:C:O5'	1.90	0.53
51:1:1856:U:H2'	51:1:1857:G:O4'	2.08	0.53
51:1:2123:G:H2'	51:1:2124:G:H8	1.73	0.53
51:1:2758:A:H2'	51:1:2759:G:C5'	2.39	0.53
53:3:1023:U:H2'	53:3:1024:G:C8	2.43	0.53
57:A1:205:MET:HE3	57:A1:213:PRO:HB3	1.91	0.53
58:B1:39:LYS:O	58:B1:273:ILE:HG23	2.08	0.53
58:B1:111:THR:HG22	58:B1:300:GLN:NE2	2.23	0.53
59:B2:243:PRO:HB2	59:B2:274:ILE:HG23	1.90	0.53
33:i:53:PRO:HD2	33:i:77:VAL:HG11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:268:C:H2'	51:1:269:C:C6	2.44	0.53
51:1:876:C:H2'	51:1:877:A:O4'	2.08	0.53
51:1:925:A:O2'	51:1:926:G:H5'	2.08	0.53
51:1:1530:G:N2	51:1:1542:U:H1'	2.23	0.53
51:1:2290:G:H2'	51:1:2291:U:H6	1.74	0.53
51:1:2328:A:H8	51:1:2328:A:O5'	1.91	0.53
51:1:2625:G:O2'	51:1:2626:C:H5'	2.09	0.53
59:B2:1117:LEU:HD12	59:B2:1195:ILE:HG12	1.90	0.53
63:5:38:A:H2'	63:5:39:U:H4'	1.91	0.53
9:I:154:VAL:HA	9:I:157:ALA:HB3	1.91	0.53
10:J:104:ILE:O	10:J:111:ARG:NH1	2.41	0.53
25:Y:47:GLN:NE2	25:Y:51:ASN:OD1	2.40	0.53
39:o:31:THR:HG23	39:o:34:HIS:H	1.73	0.53
42:r:38:VAL:HG11	42:r:57:GLY:HA3	1.90	0.53
51:1:44:A:O2'	51:1:45:G:H5'	2.08	0.53
51:1:441:U:O2'	51:1:442:G:H5'	2.07	0.53
51:1:878:A:H2'	51:1:879:G:O4'	2.09	0.53
51:1:995:C:H6	51:1:995:C:H5'	1.74	0.53
51:1:1789:A:H2'	51:1:1790:C:O4'	2.09	0.53
51:1:2092:U:C5	51:1:2199:A:C2	2.97	0.53
51:1:2092:U:C5	51:1:2199:A:H2	2.26	0.53
51:1:2762:C:C2'	51:1:2763:G:H5'	2.39	0.53
58:B1:209:ASN:HA	58:B1:214:ARG:HH21	1.74	0.53
58:B1:832:LYS:HB3	58:B1:1242:ARG:NH1	2.24	0.53
58:B1:975:ILE:HD11	58:B1:1003:LEU:HD11	1.91	0.53
12:L:77:ARG:NH2	53:3:1381:U:O2	2.41	0.53
21:U:69:ASP:OD1	21:U:69:ASP:N	2.38	0.53
31:f:174:LYS:CG	51:1:2529:G:H4'	2.34	0.53
39:o:40:ILE:HD12	39:o:44:GLY:HA2	1.91	0.53
44:t:54:GLU:HB3	44:t:88:LYS:HE3	1.90	0.53
51:1:53:A:C2'	51:1:54:G:H5'	2.39	0.53
51:1:1386:C:H2'	51:1:1387:A:C8	2.41	0.53
51:1:1678:A:H2'	51:1:1679:A:C5'	2.38	0.53
51:1:1827:U:H2'	51:1:1828:G:H5'	1.89	0.53
51:1:2631:G:O2'	51:1:2632:A:H5'	2.09	0.53
58:B1:30:ILE:HG21	58:B1:241:VAL:O	2.08	0.53
1:A:35:ASP:OD1	18:R:2:ARG:NH1	2.42	0.53
31:f:7:PRO:O	31:f:68:ARG:NH2	2.38	0.53
50:z:36:GLU:O	50:z:37:ARG:NH1	2.42	0.53
51:1:213:A:O2'	51:1:214:G:H5'	2.09	0.53
51:1:2425:A:H4'	51:1:2426:A:H5''	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:A2:28:LEU:HD22	57:A2:201:LEU:HD23	1.90	0.53
59:B2:786:GLY:N	59:B2:789:THR:OG1	2.41	0.53
14:N:115:VAL:HG23	53:3:1367:C:H5''	1.91	0.53
16:P:15:VAL:HG12	16:P:76:TYR:HB3	1.90	0.53
29:d:76:PRO:HD2	51:1:673:C:H5''	1.89	0.53
30:e:162:ASP:OD1	30:e:162:ASP:N	2.37	0.53
37:m:64:TRP:HB2	37:m:104:GLU:HB2	1.89	0.53
51:1:1175:A:H3'	51:1:1176:U:C5'	2.37	0.53
51:1:1409:U:H2'	51:1:1410:G:C8	2.44	0.53
51:1:1565:C:HO2'	51:1:1566:A:H8	1.53	0.53
51:1:1599:U:H2'	51:1:1600:C:C6	2.43	0.53
51:1:2092:U:C4'	51:1:2093:G:H5''	2.37	0.53
51:1:2194:U:H2'	51:1:2195:U:C6	2.44	0.53
58:B1:746:LEU:HG	58:B1:758:PRO:HG3	1.90	0.53
28:c:114:LYS:HZ1	51:1:2723:C:P	2.32	0.52
33:i:27:LEU:HD13	33:i:32:VAL:HG11	1.90	0.52
51:1:279:A:N6	51:1:361:G:H1'	2.21	0.52
51:1:723:C:O2'	51:1:724:U:H5'	2.09	0.52
51:1:1558:C:O4'	51:1:1560:G:C8	2.62	0.52
51:1:1794:A:O2'	51:1:1795:C:H5'	2.09	0.52
51:1:2529:G:H5''	51:1:2530:A:H5''	1.91	0.52
53:3:1023:U:H2'	53:3:1024:G:H8	1.74	0.52
53:3:1244:G:H1	53:3:1293:C:H42	1.57	0.52
57:A1:100:LEU:HD21	57:A1:121:VAL:HG11	1.90	0.52
58:B1:112:ALA:HA	58:B1:238:ILE:HA	1.91	0.52
58:B1:785:ASP:O	58:B1:789:LYS:HB2	2.08	0.52
17:Q:49:ARG:NH1	17:Q:88:ASP:OD2	2.42	0.52
27:b:257:ARG:NH2	27:b:262:THR:OG1	2.42	0.52
51:1:543:G:C2'	51:1:544:C:H5''	2.37	0.52
51:1:729:G:H5''	51:1:730:A:H5''	1.92	0.52
53:3:458:U:H3	53:3:474:G:H1	1.56	0.52
26:Z:28:LEU:HA	26:Z:31:VAL:HG12	1.90	0.52
28:c:23:PRO:HB3	51:1:2682:A:N3	2.24	0.52
33:i:25:PRO:HG2	51:1:1068:G:N2	2.24	0.52
34:j:38:GLY:HA3	34:j:50:THR:HG23	1.90	0.52
42:r:4:VAL:HG12	42:r:13:ARG:HA	1.91	0.52
51:1:341:C:O2'	51:1:342:A:H5'	2.08	0.52
51:1:2102:G:H2'	51:1:2103:C:O4'	2.09	0.52
53:3:203:G:N2	53:3:204:G:O6	2.43	0.52
58:B1:205:LEU:HG	58:B1:217:LEU:HB3	1.90	0.52
9:I:12:ARG:NH1	9:I:32:LYS:O	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:92:LEU:HD11	27:b:100:ARG:HB3	1.91	0.52
51:1:519:U:H2'	51:1:520:G:H8	1.75	0.52
51:1:2470:G:O2'	51:1:2471:A:H5'	2.10	0.52
51:1:2758:A:C2'	51:1:2759:G:H5'	2.40	0.52
58:B1:99:ARG:HG3	58:B1:99:ARG:HH11	1.73	0.52
7:G:61:SER:OG	7:G:62:ARG:NH1	2.42	0.52
8:H:107:LYS:HB3	8:H:110:LEU:HD23	1.92	0.52
47:w:55:LEU:HD12	47:w:76:ILE:HD12	1.89	0.52
51:1:140:C:H2'	51:1:141:G:H5'	1.90	0.52
51:1:611:C:H2'	51:1:612:G:O4'	2.09	0.52
51:1:1560:G:H2'	51:1:1560:G:N3	2.24	0.52
51:1:1662:U:H2'	51:1:1663:G:O4'	2.09	0.52
51:1:1722:A:O2'	51:1:1723:G:H5'	2.10	0.52
51:1:1722:A:H62	51:1:1738:G:H1'	1.74	0.52
51:1:1917:U:C2'	51:1:1918:A:H5'	2.39	0.52
51:1:2707:U:H2'	51:1:2708:G:C8	2.44	0.52
58:B1:201:LEU:HD12	58:B1:224:LEU:HD12	1.92	0.52
64:7:43:A:H2'	64:7:44:A:C8	2.44	0.52
1:A:9:TYR:OH	30:e:101:ARG:NH2	2.41	0.52
51:1:215:G:C4'	51:1:216:A:H4'	2.39	0.52
51:1:1161:C:H2'	51:1:1162:G:C8	2.44	0.52
51:1:1171:G:H2'	51:1:1172:C:C4'	2.38	0.52
51:1:1782:U:H2'	51:1:1783:A:H5''	1.90	0.52
57:A1:47:LEU:HD23	57:A1:51:MET:HG3	1.90	0.52
58:B1:78:LEU:O	58:B1:78:LEU:HD13	2.08	0.52
58:B1:390:LEU:N	58:B1:390:LEU:CD1	2.73	0.52
7:G:14:HIS:HB3	7:G:42:LEU:HD21	1.91	0.52
8:H:30:ASP:OD1	8:H:30:ASP:N	2.41	0.52
10:J:152:VAL:HG21	13:M:98:LEU:HD13	1.91	0.52
11:K:23:GLU:HA	11:K:26:THR:HG22	1.91	0.52
51:1:40:U:H2'	51:1:41:C:C6	2.43	0.52
51:1:368:A:H2'	51:1:369:U:C5'	2.39	0.52
51:1:820:A:O2'	51:1:821:A:H5'	2.08	0.52
51:1:1338:G:H2'	51:1:1339:G:H8	1.74	0.52
51:1:2216:G:H2'	51:1:2217:G:H8	1.74	0.52
51:1:2731:G:H2'	51:1:2732:G:C8	2.45	0.52
57:A1:16:ILE:HG23	57:A1:26:VAL:HG22	1.91	0.52
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE21	1.68	0.52
59:B2:125:GLY:HA2	59:B2:499:SER:HB2	1.92	0.52
51:1:49:A:O5'	51:1:51:G:H5'	2.09	0.52
51:1:597:G:H2'	51:1:598:U:C6	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1503:A:C3'	51:1:1504:A:H5''	2.40	0.52
51:1:2204:G:H2'	51:1:2205:A:C8	2.44	0.52
51:1:2617:U:H2'	51:1:2618:G:H5'	1.91	0.52
53:3:460:A:H2'	53:3:461:A:H8	1.75	0.52
58:B1:68:TYR:CA	58:B1:75:TYR:HE2	2.22	0.52
58:B1:99:ARG:HA	58:B1:248:ASP:HB2	1.92	0.52
58:B1:215:LYS:HA	58:B1:218:THR:HG22	1.92	0.52
59:B2:811:ASN:HA	59:B2:815:SER:HB2	1.90	0.52
43:s:109:ASP:OD1	43:s:109:ASP:N	2.42	0.52
51:1:870:U:O2'	51:1:871:U:H5'	2.10	0.52
51:1:1534:U:H2'	51:1:1536:C:O4'	2.10	0.52
51:1:1878:G:O2'	51:1:1879:C:H5'	2.09	0.52
51:1:1923:U:H2'	51:1:1924:C:C6	2.45	0.52
51:1:1930:G:C2'	51:1:1931:U:OP2	2.58	0.52
51:1:2670:A:H2'	51:1:2671:G:H8	1.75	0.52
51:1:2747:G:O6	51:1:2754:U:H2'	2.09	0.52
59:B2:714:VAL:HB	59:B2:787:PRO:HD2	1.92	0.52
8:H:133:MET:HE3	8:H:167:TYR:HB2	1.91	0.52
39:o:40:ILE:HG22	39:o:47:VAL:HG12	1.91	0.52
51:1:138:U:C5	51:1:139:U:H5	2.28	0.52
51:1:386:G:H3'	51:1:387:U:H5''	1.92	0.52
51:1:736:C:H42	51:1:760:G:H1	1.58	0.52
51:1:1047:G:N2	51:1:1110:G:H2'	2.25	0.52
51:1:1507:C:H2'	51:1:1508:A:C4'	2.40	0.52
51:1:1574:C:H2'	51:1:1575:C:H6	1.74	0.52
51:1:1910:G:H1	51:1:1920:C:H42	1.58	0.52
51:1:2651:C:O2'	51:1:2652:C:H5'	2.10	0.52
57:A2:140:ILE:HD12	57:A2:142:MET:HE3	1.91	0.52
58:B1:683:ILE:HD12	58:B1:754:ILE:HG21	1.92	0.52
58:B1:1167:LYS:HZ2	58:B1:1170:LYS:HB2	1.75	0.52
4:D:3:ARG:NH1	51:1:752:A:OP1	2.43	0.51
51:1:69:C:H2'	51:1:70:G:C8	2.46	0.51
9:I:150:LYS:O	9:I:155:LYS:NZ	2.42	0.51
15:O:24:GLU:HA	15:O:27:GLU:HB2	1.93	0.51
30:e:69:ALA:O	30:e:80:GLN:NE2	2.43	0.51
33:i:56:VAL:HB	33:i:68:PHE:HB2	1.92	0.51
40:p:28:LYS:HB3	40:p:39:LEU:HD21	1.91	0.51
51:1:2236:U:C2'	51:1:2237:G:H5'	2.39	0.51
51:1:2463:C:O2'	51:1:2464:G:H5'	2.10	0.51
51:1:2776:A:C6	51:1:2782:G:H1'	2.45	0.51
58:B1:144:TYR:CE1	58:B1:162:GLU:CD	2.88	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:412:LEU:HD23	58:B1:416:ILE:HG13	1.92	0.51
58:B1:850:LYS:HB2	58:B1:857:LEU:HB2	1.91	0.51
10:J:106:ALA:O	10:J:111:ARG:NH2	2.43	0.51
10:J:123:LEU:HD12	53:3:7:A:H2'	1.92	0.51
51:1:291:G:O2'	51:1:292:U:H5'	2.11	0.51
51:1:492:A:H2'	51:1:493:G:O4'	2.09	0.51
51:1:1112:G:H2'	51:1:1113:U:O4'	2.10	0.51
51:1:1678:A:C2'	51:1:1679:A:H5'	2.40	0.51
53:3:816:A:OP1	53:3:1526:G:O2'	2.28	0.51
15:O:5:ARG:N	15:O:76:ILE:O	2.43	0.51
17:Q:36:VAL:HG21	17:Q:73:LEU:HB3	1.91	0.51
21:U:25:ARG:O	53:3:110:C:O2'	2.28	0.51
51:1:1403:A:H2'	51:1:1404:C:C6	2.45	0.51
51:1:1542:U:O2'	51:1:1543:G:H5'	2.09	0.51
6:F:19:ARG:HB2	6:F:24:ARG:HD2	1.92	0.51
51:1:8:C:H2'	51:1:9:G:C8	2.45	0.51
51:1:286:U:H2'	51:1:287:G:H8	1.75	0.51
51:1:2013:A:H5''	51:1:2013:A:C8	2.43	0.51
53:3:202:G:H1	53:3:215:C:H42	1.57	0.51
64:6:1:C:H2'	64:6:2:G:H8	1.75	0.51
15:O:81:GLU:HG2	58:B1:87:LYS:HE2	1.93	0.51
21:U:6:LEU:HD22	21:U:17:TYR:HB3	1.91	0.51
51:1:2570:G:C2'	51:1:2571:U:H5'	2.40	0.51
51:1:2670:A:H2'	51:1:2671:G:C8	2.45	0.51
53:3:517:G:N2	53:3:533:A:OP2	2.34	0.51
64:6:43:A:H2'	64:6:44:A:C8	2.45	0.51
2:B:2:VAL:HG23	51:1:2015:A:C6	2.46	0.51
15:O:39:PRO:HD2	53:3:1123:U:H4'	1.92	0.51
23:W:71:ASP:N	23:W:71:ASP:OD1	2.44	0.51
31:f:136:ASP:HB3	31:f:139:VAL:HG12	1.92	0.51
36:l:42:SER:HB2	51:1:672:C:H5	1.76	0.51
46:v:77:VAL:HG23	46:v:89:ILE:HG12	1.92	0.51
51:1:439:A:H2'	51:1:440:C:H6	1.75	0.51
51:1:800:A:H4'	51:1:801:G:H3'	1.92	0.51
51:1:2105:U:N3	51:1:2184:A:C2	2.78	0.51
51:1:2555:U:O2	51:1:2555:U:O4'	2.29	0.51
53:3:1077:G:N2	53:3:1080:A:OP2	2.40	0.51
58:B1:972:LYS:HD2	58:B1:1004:ALA:HA	1.93	0.51
64:7:9:G:O4'	64:7:46:G:N3	2.43	0.51
4:D:14:ARG:NH1	51:1:1377:G:O3'	2.44	0.51
8:H:130:ARG:NH2	8:H:165:GLU:OE1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:89:TYR:HB3	14:N:93:LEU:HD21	1.92	0.51
33:i:126:ARG:HD2	51:1:1080:A:H4'	1.93	0.51
35:k:31:ARG:NH2	51:1:2676:C:OP2	2.43	0.51
35:k:75:SER:OG	40:p:72:VAL:O	2.26	0.51
37:m:38:ARG:HB3	37:m:98:PRO:HD3	1.92	0.51
51:1:251:A:H2'	51:1:252:G:O4'	2.10	0.51
51:1:1717:A:H2'	51:1:1718:G:C5'	2.40	0.51
58:B1:1179:PRO:HD2	58:B1:1184:ASP:HA	1.93	0.51
59:B2:524:ILE:HG21	59:B2:708:VAL:HG13	1.92	0.51
22:V:60:ILE:HA	22:V:74:LEU:HA	1.93	0.51
27:b:50:THR:HG23	51:1:1813:G:H21	1.76	0.51
29:d:191:ASP:O	29:d:195:GLN:NE2	2.44	0.51
51:1:355:U:H2'	51:1:356:G:C8	2.45	0.51
51:1:707:G:H2'	51:1:708:G:O4'	2.11	0.51
51:1:1415:U:H1'	51:1:1588:G:N2	2.26	0.51
51:1:1468:U:H2'	51:1:1522:A:N6	2.26	0.51
51:1:1528:A:H2'	51:1:1529:G:O4'	2.11	0.51
51:1:2618:G:H2'	51:1:2619:C:O4'	2.11	0.51
58:B1:505:ASP:OD2	59:B2:812:PHE:HA	2.11	0.51
59:B2:411:ARG:NH2	59:B2:427:ASP:OD2	2.44	0.51
10:J:23:THR:HG22	10:J:28:ARG:HB3	1.91	0.51
42:r:51:VAL:HG22	42:r:52:PRO:HD2	1.92	0.51
44:t:65:GLY:N	44:t:79:ASP:OD1	2.43	0.51
51:1:1416:G:H2'	51:1:1417:C:C6	2.46	0.51
51:1:2815:C:O2'	51:1:2816:G:H5'	2.11	0.51
59:B2:246:LEU:HB3	59:B2:269:ILE:HD13	1.91	0.51
8:H:175:HIS:ND1	53:3:1109:C:OP2	2.44	0.50
20:T:2:LEU:HD22	20:T:34:GLN:HB2	1.92	0.50
28:c:161:MET:HE1	51:1:2050:C:O2	2.11	0.50
51:1:386:G:H3'	51:1:387:U:C5'	2.41	0.50
51:1:2052:A:C2'	51:1:2053:G:H5'	2.40	0.50
51:1:2285:C:O2'	51:1:2286:G:H5'	2.11	0.50
51:1:2611:C:O2	51:1:2611:C:C2'	2.58	0.50
53:3:1178:G:N2	53:3:1181:G:OP2	2.43	0.50
58:B1:902:ASP:HB3	58:B1:905:ARG:HB2	1.93	0.50
59:B2:255:ILE:HB	59:B2:263:VAL:HB	1.92	0.50
3:C:7:LYS:HD3	51:1:2420:C:H5''	1.93	0.50
30:e:27:VAL:O	30:e:29:ARG:NH1	2.41	0.50
51:1:145:C:H2'	51:1:146:A:C8	2.46	0.50
51:1:630:G:H4'	51:1:640:C:H4'	1.93	0.50
51:1:724:U:O2'	51:1:725:G:H5'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:891:G:H2'	51:1:892:A:C8	2.46	0.50
51:1:928:A:O2'	51:1:929:U:H5'	2.10	0.50
51:1:2687:U:H2'	51:1:2688:G:O4'	2.11	0.50
59:B2:854:ILE:HG22	59:B2:857:VAL:HG22	1.93	0.50
62:NG:130:PRO:C	62:NG:132:GLU:N	2.69	0.50
15:O:29:ALA:O	15:O:33:GLY:N	2.42	0.50
27:b:206:LYS:HD2	51:1:729:G:C8	2.46	0.50
27:b:207:ALA:HB2	51:1:1790:C:O2'	2.12	0.50
28:c:13:ARG:NH2	40:p:74:GLN:OE1	2.43	0.50
51:1:246:C:H2'	51:1:247:G:C5'	2.40	0.50
51:1:438:G:H2'	51:1:439:A:H8	1.76	0.50
51:1:1441:G:H2'	51:1:1442:U:H6	1.71	0.50
58:B1:437:PHE:HZ	58:B1:453:VAL:HG11	1.76	0.50
59:B2:974:ARG:HD2	59:B2:1014:LEU:HD21	1.92	0.50
59:B2:1070:HIS:NE2	59:B2:1114:GLU:OE1	2.36	0.50
62:NG:161:SER:HA	62:NG:170:PRO:HA	1.92	0.50
19:S:68:ARG:NH2	53:3:974:A:OP1	2.45	0.50
30:e:91:ARG:NH2	52:2:43:C:O2	2.36	0.50
48:x:64:ASP:N	48:x:64:ASP:OD1	2.43	0.50
51:1:1539:U:H2'	51:1:1540:G:H8	1.77	0.50
51:1:2248:C:H2'	51:1:2249:U:H5'	1.93	0.50
51:1:2348:U:O2'	51:1:2349:G:H5'	2.12	0.50
51:1:2593:U:O2'	51:1:2594:C:H5'	2.11	0.50
59:B2:400:VAL:HG21	59:B2:452:ARG:HE	1.76	0.50
59:B2:562:GLU:OE1	59:B2:662:SER:OG	2.28	0.50
12:L:65:LEU:O	12:L:69:ARG:N	2.43	0.50
29:d:77:ILE:HG23	51:1:1256:G:N2	2.26	0.50
33:i:25:PRO:HG3	51:1:1095:A:C2	2.46	0.50
45:u:73:ASN:ND2	45:u:80:ASP:OD2	2.43	0.50
51:1:208:C:O5'	51:1:208:C:H6	1.93	0.50
51:1:282:A:H2'	51:1:283:G:C8	2.42	0.50
51:1:580:U:O5'	51:1:580:U:H6	1.94	0.50
51:1:1293:C:H2'	51:1:1294:U:C6	2.46	0.50
51:1:1676:A:H8	51:1:1676:A:O5'	1.95	0.50
55:8:13:DT:OP2	58:B1:791:ALA:CB	2.59	0.50
1:A:35:ASP:OD1	1:A:35:ASP:N	2.42	0.50
8:H:4:VAL:HG21	8:H:9:ILE:HD13	1.93	0.50
11:K:41:ASP:OD1	11:K:58:HIS:NE2	2.39	0.50
27:b:147:PRO:HG3	27:b:184:GLU:HG2	1.92	0.50
27:b:257:ARG:HH22	27:b:262:THR:HG1	1.57	0.50
51:1:155:A:H2'	51:1:156:A:H8	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1270:C:H5''	51:1:1271:G:H5''	1.93	0.50
51:1:1345:C:H6	51:1:1345:C:H5'	1.77	0.50
51:1:1348:C:C5	51:1:1349:C:C5	3.00	0.50
51:1:2888:C:H2'	51:1:2889:C:H6	1.77	0.50
58:B1:86:GLU:OE1	62:NG:140:PRO:HA	2.11	0.50
58:B1:749:LYS:HB3	58:B1:755:ILE:HD11	1.94	0.50
59:B2:9:LYS:HG2	59:B2:1171:ARG:HH12	1.77	0.50
33:i:110:GLN:HG2	33:i:121:ILE:HD13	1.93	0.50
43:s:67:ASP:OD1	43:s:67:ASP:N	2.39	0.50
51:1:1754:A:C6	51:1:1755:A:C6	2.98	0.50
28:c:176:ASP:OD1	28:c:176:ASP:N	2.44	0.50
30:e:135:ILE:HG23	30:e:140:ILE:HD11	1.93	0.50
38:n:49:GLU:O	38:n:53:THR:OG1	2.29	0.50
51:1:288:U:H2'	51:1:289:G:C8	2.47	0.50
51:1:521:U:H2'	51:1:522:A:H8	1.73	0.50
51:1:539:G:O2'	51:1:540:C:H5'	2.11	0.50
51:1:757:G:C2'	51:1:758:C:H5'	2.38	0.50
51:1:1668:A:C4'	51:1:1669:A:H5'	2.36	0.50
51:1:2286:G:H21	51:1:2287:A:N6	2.09	0.50
53:3:494:G:H2'	53:3:496:A:H8	1.76	0.50
58:B1:375:GLU:HG2	59:B2:1245:ALA:O	2.10	0.50
59:B2:529:ARG:HH11	59:B2:572:ILE:HG22	1.77	0.50
7:G:221:ARG:HG2	7:G:224:ARG:HH11	1.77	0.50
15:O:42:LEU:HB3	15:O:71:LEU:HB2	1.94	0.50
21:U:5:ARG:HB3	53:3:376:G:H5''	1.93	0.50
33:i:25:PRO:HB3	51:1:1095:A:N1	2.27	0.50
51:1:197:A:H2	51:1:2434:A:N6	2.10	0.50
51:1:840:C:O2'	51:1:841:G:H5'	2.12	0.50
51:1:1593:A:H2'	51:1:1594:U:C6	2.47	0.50
51:1:2525:G:N2	51:1:2539:C:C2	2.79	0.50
53:3:664:G:H22	53:3:741:G:H1	1.60	0.50
53:3:1013:G:N2	53:3:1016:A:OP2	2.35	0.50
64:7:9:G:C2	64:7:45:G:C6	3.00	0.50
7:G:103:TRP:HA	7:G:106:VAL:HG12	1.93	0.49
20:T:23:SER:OG	20:T:25:GLU:OE1	2.30	0.49
31:f:41:GLU:HG2	31:f:54:ARG:HH21	1.77	0.49
34:j:2:LYS:HG2	51:1:995:C:N4	2.27	0.49
38:n:8:ARG:HH21	38:n:43:GLU:HG3	1.77	0.49
46:v:51:GLN:OE1	46:v:79:ARG:NH2	2.40	0.49
51:1:30:G:H2'	51:1:31:C:C6	2.47	0.49
51:1:131:A:H2'	51:1:132:G:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:262:A:H2'	51:1:263:G:O4'	2.12	0.49
51:1:286:U:H2'	51:1:287:G:C8	2.47	0.49
51:1:488:G:H22	51:1:491:G:H5''	1.77	0.49
51:1:644:A:H2'	51:1:645:C:C4'	2.42	0.49
51:1:898:C:H2'	51:1:899:A:O4'	2.12	0.49
51:1:1061:U:H4'	51:1:1070:A:H1'	1.93	0.49
51:1:1084:A:O2'	51:1:1105:U:H4'	2.12	0.49
51:1:1614:A:H2'	51:1:1615:C:H5'	1.94	0.49
53:3:1538:C:O2'	53:3:1539:C:H5'	2.11	0.49
59:B2:18:ARG:HE	59:B2:620:ASN:HA	1.77	0.49
64:7:9:G:O4'	64:7:46:G:C2	2.65	0.49
21:U:36:VAL:HG12	21:U:53:ASP:HB3	1.94	0.49
25:Y:53:MET:HE2	25:Y:57:VAL:HG21	1.94	0.49
27:b:50:THR:HG23	51:1:1813:G:N2	2.27	0.49
27:b:137:GLY:O	27:b:162:GLN:NE2	2.45	0.49
28:c:81:GLU:HG3	51:1:2636:C:O5'	2.13	0.49
44:t:7:LEU:HD13	44:t:46:ALA:HA	1.94	0.49
51:1:16:C:H2'	51:1:17:G:H8	1.77	0.49
51:1:78:U:H2'	51:1:79:C:H6	1.77	0.49
51:1:173:A:H2'	51:1:174:U:C6	2.47	0.49
51:1:886:A:C5	51:1:887:U:H1'	2.47	0.49
51:1:2250:G:H8	51:1:2250:G:O5'	1.95	0.49
51:1:2257:U:O2'	51:1:2258:C:H5'	2.13	0.49
51:1:2302:U:O2'	51:1:2303:G:H5'	2.12	0.49
51:1:2533:U:H2'	51:1:2534:A:C5'	2.42	0.49
51:1:2670:A:O2'	51:1:2671:G:H5'	2.12	0.49
58:B1:421:VAL:O	58:B1:436:ALA:HA	2.12	0.49
59:B2:93:SER:HA	59:B2:128:PRO:HA	1.92	0.49
25:Y:59:ARG:O	25:Y:63:LYS:N	2.46	0.49
27:b:92:LEU:HD21	27:b:100:ARG:HD3	1.93	0.49
51:1:673:C:H2'	51:1:674:G:C5'	2.41	0.49
51:1:905:A:H2'	51:1:906:U:C5'	2.41	0.49
51:1:1087:G:H2'	51:1:1089:A:H5'	1.94	0.49
51:1:1144:A:H2'	51:1:1145:C:C6	2.47	0.49
51:1:1310:G:H2'	51:1:1311:G:C5'	2.38	0.49
51:1:2241:A:O2'	51:1:2242:G:H5'	2.12	0.49
58:B1:275:ARG:HH12	58:B1:278:ARG:NH1	2.09	0.49
27:b:70:LYS:O	27:b:117:SER:OG	2.30	0.49
27:b:146:LYS:HB2	27:b:149:LYS:HB2	1.93	0.49
28:c:56:LYS:NZ	51:1:2830:C:H5''	2.28	0.49
33:i:134:SER:OG	51:1:1062:G:N2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1388:G:O2'	51:1:1389:G:H5'	2.12	0.49
51:1:1748:C:H2'	51:1:1749:A:C8	2.47	0.49
51:1:2836:U:H2'	51:1:2837:A:C8	2.47	0.49
59:B2:232:ILE:HG12	59:B2:237:LEU:HG	1.94	0.49
11:K:42:TRP:HB2	11:K:59:TYR:HB2	1.93	0.49
13:M:29:SER:OG	13:M:30:LYS:N	2.44	0.49
51:1:187:G:C6	51:1:188:G:N7	2.80	0.49
51:1:1796:U:H2'	51:1:1797:G:C8	2.45	0.49
53:3:1137:C:H4'	53:3:1138:G:H5'	1.95	0.49
55:8:3:DC:H2''	55:8:4:DT:C7	2.42	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	1.94	0.49
58:B1:395:LYS:NZ	58:B1:399:LYS:CD	2.74	0.49
17:Q:97:VAL:HG12	17:Q:99:GLY:H	1.78	0.49
51:1:367:G:H2'	51:1:368:A:O4'	2.13	0.49
51:1:900:A:H2'	51:1:901:C:H5'	1.94	0.49
51:1:2553:G:H22	63:5:75:C:H42	1.60	0.49
51:1:2634:A:O2'	51:1:2635:A:H5'	2.12	0.49
58:B1:145:VAL:HG12	58:B1:184:ALA:HB1	1.94	0.49
7:G:101:THR:HG23	7:G:174:GLU:HG3	1.95	0.49
17:Q:120:ARG:HH12	53:3:500:G:H5'	1.78	0.49
30:e:84:ILE:HD11	51:1:2311:A:H1'	1.94	0.49
31:f:87:GLN:NE2	31:f:129:GLU:OE2	2.46	0.49
51:1:355:U:H2'	51:1:356:G:H8	1.77	0.49
51:1:554:U:O2'	51:1:555:G:H5'	2.13	0.49
51:1:609:A:H2'	51:1:610:C:O4'	2.11	0.49
51:1:1465:G:H2'	51:1:1466:U:O4'	2.13	0.49
51:1:1668:A:N3	51:1:1670:C:N4	2.60	0.49
51:1:1916:A:H2'	51:1:1917:U:O4'	2.12	0.49
53:3:481:G:O2'	53:3:483:C:N4	2.46	0.49
58:B1:1371:ARG:HE	58:B1:1372:ARG:NH1	2.10	0.49
11:K:46:GLN:HA	11:K:56:LYS:HB3	1.94	0.49
15:O:89:ARG:HH22	62:NG:165:PHE:H	1.60	0.49
48:x:71:ARG:NH2	48:x:77:TYR:OH	2.42	0.49
51:1:69:C:O2'	51:1:70:G:H5'	2.13	0.49
51:1:121:G:H4'	51:1:149:A:H5'	1.95	0.49
51:1:236:C:H2'	51:1:237:C:C6	2.46	0.49
51:1:898:C:C2'	51:1:899:A:H5'	2.43	0.49
51:1:1534:U:H4'	51:1:1535:A:N1	2.27	0.49
53:3:890:G:O2'	53:3:906:A:N6	2.46	0.49
53:3:927:G:O2'	53:3:1503:A:N7	2.38	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:201:LEU:HD11	58:B1:220:ARG:HG2	1.95	0.49
59:B2:533:LEU:HD13	59:B2:540:ARG:HH21	1.77	0.49
59:B2:857:VAL:HG13	59:B2:919:ARG:HH21	1.78	0.49
62:NG:130:PRO:HA	62:NG:148:VAL:O	2.13	0.49
63:5:51:U:H2'	63:5:52:G:C8	2.48	0.49
30:e:57:ALA:HB2	30:e:64:PRO:HD3	1.95	0.49
40:p:59:THR:HG22	40:p:72:VAL:HG12	1.95	0.49
42:r:71:LYS:HA	42:r:90:ARG:HG2	1.95	0.49
51:1:54:G:H2'	51:1:55:G:O4'	2.12	0.49
51:1:482:A:H1'	51:1:498:G:N2	2.27	0.49
51:1:519:U:H2'	51:1:520:G:C8	2.48	0.49
51:1:1645:G:H5''	51:1:1646:C:H5'	1.94	0.49
51:1:2180:U:O2'	51:1:2181:U:H5'	2.13	0.49
51:1:2843:G:O2'	51:1:2844:G:H5'	2.13	0.49
53:3:113:G:N3	53:3:353:A:O2'	2.42	0.49
53:3:401:C:O2'	53:3:621:A:N3	2.45	0.49
53:3:768:A:N3	53:3:1512:U:O2'	2.46	0.49
13:M:83:ARG:NH2	53:3:587:G:OP1	2.44	0.49
35:k:5:GLN:HE21	51:1:1668:A:H5''	1.78	0.49
45:u:88:ASP:OD1	45:u:88:ASP:N	2.43	0.49
51:1:553:G:H2'	51:1:554:U:O4'	2.13	0.49
51:1:940:G:H2'	51:1:941:A:C5'	2.41	0.49
51:1:1400:U:H2'	51:1:1401:G:H8	1.78	0.49
51:1:2126:A:H5'	51:1:2127:G:O5'	2.12	0.49
51:1:2510:C:N4	51:1:2511:U:C4	2.81	0.49
51:1:2527:C:O2'	51:1:2528:U:H5'	2.13	0.49
51:1:2734:A:H2'	51:1:2735:G:C5'	2.42	0.49
53:3:776:G:N2	53:3:802:A:OP2	2.39	0.49
58:B1:115:TRP:O	58:B1:1333:THR:HG21	2.13	0.49
58:B1:220:ARG:HG2	58:B1:220:ARG:NH1	2.25	0.49
59:B2:732:ILE:HD11	59:B2:769:PRO:HB3	1.95	0.49
12:L:2:ARG:NH2	53:3:933:G:O6	2.46	0.48
14:N:10:ARG:NH2	53:3:1119:C:OP2	2.46	0.48
27:b:56:GLY:HA2	27:b:212:TRP:HA	1.94	0.48
33:i:79:LEU:HD13	33:i:132:ALA:HB2	1.94	0.48
48:x:1:SER:O	48:x:49:ARG:NH1	2.46	0.48
51:1:92:U:H2'	51:1:93:G:H5'	1.95	0.48
51:1:360:U:H2'	51:1:361:G:C1'	2.43	0.48
51:1:1111:A:H2'	51:1:1111:A:N3	2.28	0.48
51:1:1119:U:O2'	51:1:1120:G:H5'	2.13	0.48
51:1:1266:G:O2'	51:1:2012:G:O6	2.25	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1871:A:H2'	51:1:1872:A:O4'	2.13	0.48
51:1:2281:A:O2'	51:1:2282:G:H5'	2.12	0.48
51:1:2298:A:O2'	51:1:2299:U:H5'	2.12	0.48
55:8:14:DC:H2'	55:8:15:DC:C6	2.48	0.48
58:B1:550:VAL:O	58:B1:569:LEU:HA	2.13	0.48
59:B2:400:VAL:HG11	59:B2:452:ARG:HD2	1.94	0.48
18:R:1:ALA:H1	18:R:52:ILE:HD13	1.78	0.48
37:m:74:THR:HG21	37:m:86:LYS:HG2	1.94	0.48
40:p:2:ASN:HD21	51:1:2876:G:H4'	1.79	0.48
41:q:103:VAL:HA	41:q:106:THR:HG22	1.94	0.48
46:v:79:ARG:HA	46:v:86:LEU:HA	1.94	0.48
51:1:718:A:H2'	51:1:719:C:O4'	2.12	0.48
51:1:841:G:C2	51:1:938:G:C2	3.01	0.48
51:1:1910:G:N2	51:1:1911:U:C2	2.81	0.48
51:1:2329:U:H2'	51:1:2330:G:H8	1.78	0.48
51:1:2367:G:O2'	51:1:2368:C:H5'	2.13	0.48
53:3:898:G:N2	53:3:901:A:OP2	2.46	0.48
9:I:153:ARG:NH2	53:3:435:A:N3	2.61	0.48
14:N:44:ARG:HG2	14:N:45:MET:HE2	1.95	0.48
51:1:118:A:H2'	51:1:120:U:O4	2.13	0.48
51:1:481:G:C2'	51:1:482:A:OP2	2.61	0.48
51:1:1537:G:H3'	51:1:1537:G:N3	2.28	0.48
51:1:2393:U:H2'	51:1:2394:C:H5'	1.94	0.48
15:O:58:ASN:ND2	53:3:1061:G:O2'	2.45	0.48
42:r:68:ARG:O	42:r:90:ARG:NH2	2.46	0.48
49:y:16:THR:O	49:y:20:ASN:ND2	2.46	0.48
51:1:1324:G:O2'	51:1:1326:U:OP2	2.29	0.48
51:1:2214:C:H2'	51:1:2215:C:O4'	2.14	0.48
53:3:1064:G:O2'	53:3:1190:G:N2	2.46	0.48
53:3:1223:C:H5'	53:3:1224:U:H5''	1.96	0.48
57:A1:18:GLN:HA	57:A1:24:ALA:HA	1.94	0.48
58:B1:124:ILE:HG23	58:B1:128:LEU:HD12	1.94	0.48
59:B2:554:HIS:HD2	59:B2:558:VAL:HB	1.77	0.48
59:B2:565:GLU:HA	59:B2:569:ILE:HG12	1.95	0.48
14:N:91:GLU:HA	14:N:94:ARG:HB2	1.94	0.48
26:Z:55:HIS:HA	26:Z:58:LYS:HD2	1.95	0.48
28:c:136:ASN:OD1	51:1:2579:C:O2'	2.32	0.48
33:i:85:ILE:HD12	33:i:97:VAL:HG12	1.95	0.48
44:t:70:HIS:N	44:t:73:ARG:O	2.45	0.48
51:1:67:U:H2'	51:1:68:G:H8	1.77	0.48
51:1:1257:C:O5'	51:1:1257:C:H6	1.97	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2283:C:H2'	51:1:2284:A:O4'	2.11	0.48
16:P:96:ILE:HD13	16:P:109:ILE:HD13	1.94	0.48
17:Q:70:GLY:O	17:Q:107:LYS:NZ	2.44	0.48
17:Q:110:LYS:HG3	17:Q:121:PRO:HG3	1.94	0.48
21:U:18:GLN:HA	21:U:38:PHE:HA	1.95	0.48
27:b:156:SER:OG	27:b:157:ALA:N	2.44	0.48
31:f:122:ALA:HB2	31:f:132:LEU:HD23	1.94	0.48
31:f:163:TYR:HB2	31:f:166:GLU:HB2	1.95	0.48
39:o:15:ARG:NH2	52:2:8:C:OP1	2.47	0.48
45:u:39:ASN:HB3	45:u:62:ALA:HB3	1.95	0.48
51:1:572:A:H8	51:1:572:A:O5'	1.97	0.48
51:1:1387:A:C5'	51:1:1469:A:H1'	2.38	0.48
51:1:1785:A:O2'	51:1:1786:A:H8	1.96	0.48
51:1:2649:C:O2'	51:1:2650:U:H5'	2.13	0.48
6:F:6:SER:O	6:F:6:SER:OG	2.31	0.48
17:Q:82:ARG:O	17:Q:95:HIS:N	2.47	0.48
51:1:129:C:H2'	51:1:130:C:H6	1.79	0.48
51:1:1077:A:H8	51:1:1078:U:H1'	1.77	0.48
51:1:1729:U:H5	51:1:1731:G:N2	2.12	0.48
53:3:358:U:H2'	53:3:359:G:H8	1.78	0.48
58:B1:103:GLY:H	58:B1:244:VAL:HG22	1.79	0.48
58:B1:141:PHE:HE2	58:B1:296:LYS:CB	2.23	0.48
58:B1:809:VAL:HG21	58:B1:909:ILE:HG12	1.95	0.48
58:B1:1261:LEU:HD12	58:B1:1304:ARG:HH21	1.79	0.48
58:B1:1347:LEU:HG	58:B1:1357:ILE:HG23	1.96	0.48
14:N:86:LEU:HD12	14:N:97:LEU:HD11	1.95	0.48
51:1:107:G:O2'	51:1:108:G:H5'	2.14	0.48
51:1:415:A:H2'	51:1:416:U:C6	2.48	0.48
51:1:476:G:H4'	51:1:502:A:N1	2.28	0.48
51:1:706:A:H2'	51:1:707:G:H5'	1.95	0.48
51:1:852:U:H2'	51:1:853:C:C6	2.49	0.48
51:1:1026:G:OP2	51:1:1134:A:H1'	2.13	0.48
51:1:2208:C:H2'	51:1:2209:G:C8	2.48	0.48
53:3:880:C:H2'	53:3:881:G:H8	1.78	0.48
53:3:1531:A:O2'	53:3:1532:U:H5'	2.14	0.48
59:B2:886:LYS:HB3	59:B2:918:LEU:HD22	1.96	0.48
59:B2:1314:GLN:HB2	60:W0:28:ARG:HH12	1.79	0.48
12:L:41:ILE:HD11	53:3:1240:U:H5'	1.95	0.48
51:1:214:G:H2'	51:1:215:G:C8	2.48	0.48
51:1:217:A:H2'	51:1:218:A:O4'	2.13	0.48
51:1:898:C:O2'	51:1:899:A:H5'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1019:U:N3	51:1:1142:A:N6	2.57	0.48
51:1:1087:G:O6	51:1:1089:A:C2	2.67	0.48
51:1:1437:C:H2'	51:1:1438:U:H6	1.78	0.48
51:1:1509:A:H2'	51:1:1510:G:C8	2.49	0.48
51:1:1536:C:H5''	51:1:1537:G:C4	2.48	0.48
51:1:2895:G:H2'	51:1:2896:C:C6	2.49	0.48
53:3:19:A:O2'	53:3:572:A:N1	2.46	0.48
65:h:6:5OH:N	65:h:6:5OH:CS	2.75	0.48
14:N:94:ARG:HG2	14:N:97:LEU:HD12	1.95	0.48
51:1:473:G:O2'	51:1:474:G:H5'	2.13	0.48
51:1:813:U:C2	51:1:1195:G:N2	2.82	0.48
51:1:2016:U:O5'	51:1:2016:U:H6	1.97	0.48
51:1:2362:C:O5'	51:1:2362:C:H6	1.97	0.48
51:1:2547:A:H61	51:1:2561:U:H3	1.62	0.48
53:3:673:A:H2'	53:3:674:G:C8	2.49	0.48
53:3:1266:G:N2	53:3:1269:A:OP2	2.29	0.48
7:G:129:THR:HB	7:G:132:GLU:HB2	1.96	0.47
9:I:94:GLU:HG3	9:I:190:LEU:HD21	1.95	0.47
28:c:190:LYS:HE2	51:1:2729:G:H4'	1.95	0.47
29:d:143:LEU:HD13	29:d:146:VAL:HG11	1.94	0.47
29:d:149:ILE:HD11	29:d:172:ALA:HA	1.96	0.47
33:i:20:SER:HA	33:i:24:GLY:HA3	1.95	0.47
40:p:105:LYS:O	40:p:108:ARG:NH2	2.42	0.47
42:r:7:SER:OG	42:r:8:GLY:N	2.47	0.47
51:1:40:U:H2'	51:1:41:C:H6	1.78	0.47
51:1:214:G:O2'	51:1:215:G:H5'	2.14	0.47
51:1:1117:C:H2'	51:1:1118:C:H6	1.78	0.47
51:1:1409:U:H2'	51:1:1410:G:H8	1.76	0.47
51:1:1807:G:C2'	51:1:1808:A:H5'	2.29	0.47
57:A2:102:LEU:HD12	57:A2:115:ILE:HG12	1.96	0.47
59:B2:363:LEU:HB3	59:B2:381:ALA:HB1	1.96	0.47
62:NG:161:SER:CA	62:NG:170:PRO:HA	2.43	0.47
12:L:107:ALA:HA	12:L:122:GLU:HG3	1.95	0.47
33:i:8:VAL:HG21	33:i:26:ALA:HB1	1.96	0.47
51:1:5:A:H2'	51:1:6:A:C8	2.49	0.47
51:1:2050:C:N4	51:1:2051:A:C6	2.81	0.47
53:3:780:A:N6	53:3:801:U:OP2	2.42	0.47
58:B1:255:LEU:HD23	58:B1:261:ALA:HB2	1.95	0.47
58:B1:526:VAL:HG12	58:B1:549:LYS:HB2	1.96	0.47
59:B2:836:LEU:HD13	59:B2:1054:LEU:HD13	1.95	0.47
1:A:37:CYS:O	1:A:41:HIS:N	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:34:THR:OG1	16:P:35:ASP:N	2.47	0.47
17:Q:114:SER:O	53:3:35:G:O2'	2.30	0.47
27:b:152:GLN:HB3	51:1:1818:U:N3	2.29	0.47
49:y:15:ASN:OD1	49:y:16:THR:N	2.48	0.47
51:1:149:A:H2'	51:1:150:U:C6	2.49	0.47
51:1:1285:A:H2'	51:1:1286:A:H5'	1.96	0.47
51:1:1742:U:O2'	51:1:1743:G:H5'	2.14	0.47
51:1:2098:U:H2'	51:1:2099:U:O4'	2.14	0.47
51:1:2149:U:H2'	51:1:2150:C:C6	2.49	0.47
57:A1:182:ARG:O	57:A1:205:MET:HA	2.14	0.47
58:B1:891:ASP:OD2	58:B1:1290:ARG:NH2	2.47	0.47
58:B1:1146:GLU:OE2	58:B1:1310:THR:HG22	2.14	0.47
64:7:50:U:H2'	64:7:51:C:C5	2.49	0.47
9:I:171:GLU:HB3	9:I:180:THR:HG22	1.97	0.47
12:L:79:VAL:HB	12:L:84:TYR:HD2	1.80	0.47
29:d:48:THR:OG1	29:d:49:ARG:N	2.47	0.47
33:i:79:LEU:HD21	33:i:105:LEU:HD21	1.96	0.47
36:l:129:LYS:HG2	51:1:636:G:OP1	2.14	0.47
51:1:596:U:C2	51:1:662:G:N2	2.82	0.47
51:1:820:A:H2'	51:1:821:A:O4'	2.14	0.47
51:1:1020:A:C1'	51:1:1021:A:OP2	2.61	0.47
51:1:1400:U:H2'	51:1:1401:G:C8	2.50	0.47
51:1:1464:G:H2'	51:1:1465:G:C8	2.49	0.47
51:1:1680:U:O2'	51:1:1681:G:H5'	2.13	0.47
51:1:2286:G:H21	51:1:2287:A:H61	1.62	0.47
51:1:2554:U:H2'	51:1:2555:U:O2	2.15	0.47
53:3:410:G:H21	53:3:432:A:H62	1.62	0.47
58:B1:99:ARG:NH1	58:B1:99:ARG:CG	2.76	0.47
58:B1:968:ASN:HA	58:B1:1117:SER:HB2	1.96	0.47
63:5:29:G:H3'	63:5:30:G:C8	2.50	0.47
6:F:27:CYS:HG	6:F:33:HIS:HD1	1.55	0.47
12:L:112:ASP:HB2	12:L:118:ARG:HG2	1.96	0.47
34:j:65:THR:HG22	51:1:1141:U:OP2	2.14	0.47
47:w:19:VAL:HA	47:w:34:VAL:HG22	1.96	0.47
51:1:435:C:C2'	51:1:436:C:H5'	2.44	0.47
51:1:555:G:O2'	51:1:556:A:H8	1.96	0.47
51:1:712:G:H2'	51:1:713:G:H5'	1.96	0.47
51:1:1098:A:O2'	51:1:1099:G:H5'	2.15	0.47
51:1:1491:G:H2'	51:1:1492:G:H8	1.80	0.47
51:1:1702:G:H2'	51:1:1703:G:C5'	2.35	0.47
51:1:2259:U:H2'	51:1:2260:C:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2445:G:C6	51:1:2446:G:C6	3.02	0.47
51:1:2679:A:O2'	51:1:2680:U:H5'	2.15	0.47
51:1:2828:G:O2'	51:1:2829:A:H5'	2.14	0.47
52:2:51:G:H22	52:2:53:A:H62	1.61	0.47
58:B1:190:LYS:HE3	58:B1:190:LYS:HB2	1.41	0.47
59:B2:1311:GLY:O	60:W0:31:GLN:NE2	2.47	0.47
63:5:37:A:H3'	63:5:38:A:C8	2.49	0.47
31:f:87:GLN:HB3	31:f:162:ARG:HG3	1.96	0.47
38:n:100:CYS:H	38:n:111:ALA:HA	1.79	0.47
47:w:29:ALA:N	47:w:60:ASP:OD1	2.48	0.47
51:1:143:C:H2'	51:1:144:A:C8	2.49	0.47
51:1:708:G:H2'	51:1:709:U:C6	2.49	0.47
51:1:1068:G:H2'	51:1:1069:A:H4'	1.96	0.47
51:1:1090:A:H61	51:1:1101:U:H3	1.62	0.47
51:1:1219:U:O2'	51:1:1220:G:H5'	2.15	0.47
51:1:1267:U:H2'	51:1:1267:U:O2	2.14	0.47
51:1:1389:G:C2	51:1:1390:U:C2	3.02	0.47
51:1:2047:C:O5'	51:1:2047:C:H6	1.98	0.47
51:1:2298:A:C2'	51:1:2299:U:H5'	2.45	0.47
58:B1:1150:PRO:HG3	58:B1:1214:PRO:HB2	1.97	0.47
58:B1:1167:LYS:NZ	58:B1:1170:LYS:HB2	2.30	0.47
58:B1:1221:LEU:HD22	58:B1:1306:LEU:HB2	1.96	0.47
59:B2:318:SER:OG	59:B2:320:ASP:OD1	2.31	0.47
63:5:50:U:H2'	63:5:51:U:C6	2.49	0.47
20:T:38:LEU:HD22	20:T:55:LEU:HD13	1.96	0.47
21:U:25:ARG:NH1	53:3:230:G:O2'	2.48	0.47
27:b:131:MET:HE2	27:b:187:CYS:HB2	1.96	0.47
29:d:119:ILE:HB	29:d:187:VAL:HG12	1.95	0.47
31:f:100:ASN:OD1	31:f:100:ASN:N	2.47	0.47
32:g:8:LYS:HD3	32:g:14:SER:HA	1.95	0.47
32:g:47:PHE:HA	32:g:51:ARG:HB2	1.96	0.47
33:i:54:ILE:HD12	33:i:73:PRO:HD3	1.95	0.47
36:l:39:LYS:HG2	51:1:832:U:OP1	2.15	0.47
51:1:156:A:H2'	51:1:157:C:C6	2.50	0.47
51:1:297:G:H2'	51:1:298:G:O4'	2.14	0.47
51:1:877:A:O2'	51:1:878:A:H5''	2.14	0.47
51:1:900:A:C2'	51:1:901:C:H5'	2.45	0.47
51:1:1090:A:C2	51:1:1102:C:H1'	2.50	0.47
51:1:1105:U:H2'	51:1:1106:G:H8	1.80	0.47
51:1:1435:G:O2'	51:1:1436:G:H5'	2.15	0.47
51:1:1463:C:H2'	51:1:1464:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1464:G:H2'	51:1:1465:G:H8	1.78	0.47
51:1:2155:U:H2'	51:1:2156:G:O4'	2.15	0.47
51:1:2194:U:O2'	51:1:2195:U:H5'	2.14	0.47
51:1:2295:C:O2'	51:1:2296:U:H5'	2.15	0.47
51:1:2899:A:H2'	51:1:2900:A:O4'	2.15	0.47
53:3:38:G:H22	53:3:397:A:H5'	1.78	0.47
53:3:512:U:H2'	53:3:513:C:C6	2.50	0.47
53:3:1305:G:N2	53:3:1331:G:H2'	2.29	0.47
58:B1:395:LYS:NZ	58:B1:399:LYS:CE	2.77	0.47
58:B1:833:GLU:N	58:B1:1242:ARG:HH12	2.12	0.47
58:B1:1036:ARG:HE	58:B1:1081:VAL:HG11	1.79	0.47
58:B1:1060:VAL:HG13	58:B1:1106:ILE:HG12	1.96	0.47
59:B2:103:VAL:HG12	59:B2:117:ILE:HG22	1.97	0.47
59:B2:689:ALA:HB2	59:B2:1233:LEU:HD23	1.97	0.47
64:7:48:C:H5''	64:7:50:U:OP1	2.15	0.47
4:D:29:GLN:O	4:D:29:GLN:NE2	2.47	0.47
5:E:5:THR:HG22	5:E:62:PRO:HD2	1.97	0.47
11:K:10:VAL:HG23	11:K:58:HIS:HB3	1.97	0.47
12:L:149:ALA:HB1	16:P:58:THR:HG21	1.97	0.47
18:R:15:VAL:HG11	18:R:30:LYS:HG2	1.97	0.47
31:f:16:VAL:HA	31:f:25:ILE:HG12	1.96	0.47
51:1:538:A:O2'	51:1:539:G:H5'	2.14	0.47
51:1:762:U:N3	51:1:1431:A:OP1	2.47	0.47
51:1:1036:G:O2'	51:1:1037:G:H5'	2.15	0.47
51:1:1141:U:H4'	51:1:1142:A:C1'	2.45	0.47
51:1:1297:C:H2'	51:1:1298:C:H6	1.79	0.47
51:1:1874:C:H2'	51:1:1875:G:O4'	2.15	0.47
51:1:1927:A:H2'	51:1:1928:A:C8	2.50	0.47
51:1:2563:U:H2'	51:1:2565:A:OP2	2.15	0.47
54:4:3:G:H1	64:6:34:C:H42	1.63	0.47
26:Z:19:LYS:H	26:Z:19:LYS:HG3	1.53	0.47
31:f:88:LEU:HD21	31:f:104:LEU:HD23	1.97	0.47
46:v:26:PHE:HE2	46:v:89:ILE:HG13	1.80	0.47
51:1:30:G:C5	51:1:31:C:C4	3.03	0.47
51:1:551:G:O2'	51:1:552:U:H5'	2.15	0.47
51:1:554:U:C2'	51:1:555:G:H5'	2.45	0.47
51:1:1465:G:HO2'	51:1:1466:U:H5'	1.80	0.47
51:1:1873:G:O2'	51:1:1874:C:H5'	2.15	0.47
51:1:1922:G:O2'	51:1:1923:U:H5'	2.15	0.47
51:1:2156:G:C3'	51:1:2157:G:H5'	2.44	0.47
58:B1:395:LYS:HB3	58:B1:395:LYS:HE3	1.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:171:ARG:HG2	8:H:173:PRO:HD3	1.96	0.47
11:K:49:TYR:H	23:W:65:SER:HG	1.63	0.47
12:L:142:ARG:HA	12:L:145:GLU:HG3	1.97	0.47
19:S:32:ASP:O	19:S:34:ASN:ND2	2.48	0.47
24:X:32:THR:OG1	24:X:49:ALA:O	2.31	0.47
27:b:184:GLU:HG3	27:b:186:ASP:H	1.80	0.47
31:f:29:ASN:ND2	31:f:80:GLU:O	2.48	0.47
45:u:6:ARG:HB2	51:1:85:G:P	2.55	0.47
51:1:848:C:H2'	51:1:849:A:H8	1.80	0.47
51:1:854:C:H2'	51:1:855:G:H8	1.79	0.47
51:1:859:G:C2'	51:1:860:U:OP2	2.62	0.47
51:1:1367:A:H3'	51:1:1368:G:O4'	2.15	0.47
51:1:1768:C:H42	51:1:1984:G:H1	1.62	0.47
51:1:2294:G:O2'	51:1:2295:C:H5'	2.15	0.47
51:1:2395:C:H2'	51:1:2396:G:O4'	2.15	0.47
51:1:2625:G:H2'	51:1:2626:C:H6	1.76	0.47
51:1:2626:C:H2'	51:1:2627:G:H8	1.80	0.47
53:3:1225:A:H2'	53:3:1225:A:N3	2.30	0.47
58:B1:108:ALA:HB1	58:B1:279:LEU:HD22	1.96	0.47
58:B1:842:ARG:HH22	58:B1:1250:ASP:HB2	1.80	0.47
58:B1:1027:VAL:HB	58:B1:1121:LEU:HB2	1.95	0.47
9:I:159:GLU:HA	9:I:162:GLU:HB2	1.97	0.46
12:L:137:ARG:NH1	12:L:138:GLU:OE2	2.48	0.46
27:b:145:MET:HE1	51:1:1800:C:H2'	1.98	0.46
33:i:115:ASP:OD2	51:1:1059:G:H4'	2.14	0.46
39:o:68:LYS:HE3	52:2:49:C:H5''	1.97	0.46
51:1:1726:C:H2'	51:1:1727:C:C6	2.50	0.46
51:1:1922:G:H2'	51:1:1923:U:C6	2.50	0.46
53:3:617:G:H1	53:3:623:C:H42	1.63	0.46
53:3:1035:A:H1'	53:3:1036:A:O5'	2.16	0.46
57:A1:59:VAL:HG22	57:A1:144:ILE:HA	1.97	0.46
58:B1:29:MET:HG2	59:B2:1336:ASN:ND2	2.29	0.46
58:B1:420:PRO:HA	58:B1:437:PHE:O	2.15	0.46
59:B2:28:LEU:HD21	59:B2:524:ILE:HG13	1.97	0.46
59:B2:735:LYS:HA	59:B2:748:ILE:HG22	1.97	0.46
14:N:11:ARG:NH2	53:3:1347:G:O6	2.49	0.46
26:Z:29:ALA:O	26:Z:32:ARG:NH1	2.49	0.46
51:1:275:C:C3'	51:1:276:U:H5''	2.40	0.46
51:1:283:G:C2'	51:1:284:U:H5'	2.45	0.46
51:1:979:A:H2'	51:1:982:C:H42	1.81	0.46
51:1:1851:U:OP1	64:7:4:G:H4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1913:A:N7	53:3:1494:G:H4'	2.29	0.46
51:1:1930:G:HO2'	51:1:1931:U:P	2.37	0.46
51:1:2241:A:H2'	51:1:2242:G:C8	2.50	0.46
51:1:2455:G:C6	51:1:2456:C:N4	2.83	0.46
58:B1:43:THR:HG22	58:B1:57:PHE:HE1	1.80	0.46
58:B1:285:LEU:HD23	62:NG:111:ILE:HA	1.97	0.46
58:B1:343:LEU:HD11	58:B1:1324:SER:HB3	1.97	0.46
58:B1:770:LEU:CD1	59:B2:618:GLN:HG3	2.36	0.46
17:Q:72:ASN:HD21	17:Q:103:CYS:HA	1.81	0.46
20:T:48:ASP:OD1	53:3:667:G:O2'	2.25	0.46
35:k:47:ILE:HG22	35:k:49:ARG:H	1.80	0.46
48:x:38:TRP:NE1	48:x:40:GLU:OE1	2.41	0.46
51:1:555:G:HO2'	51:1:556:A:H8	1.62	0.46
51:1:686:U:H6	51:1:788:A:H61	1.61	0.46
51:1:1067:A:H2'	51:1:1068:G:C8	2.49	0.46
51:1:1146:C:O2'	51:1:1147:A:H5'	2.16	0.46
51:1:1517:G:O2'	51:1:1518:C:H5'	2.15	0.46
51:1:1528:A:H2'	51:1:1529:G:C5'	2.44	0.46
51:1:1536:C:H5''	51:1:1537:G:C5	2.50	0.46
51:1:2180:U:H2'	51:1:2181:U:O4'	2.14	0.46
52:2:39:A:O2'	52:2:46:A:N1	2.47	0.46
54:4:56:G:OP1	59:B2:1073:LYS:NZ	2.35	0.46
58:B1:141:PHE:CE2	58:B1:296:LYS:CB	2.94	0.46
58:B1:772:TYR:HE2	59:B2:561:ILE:HG21	1.80	0.46
58:B1:1219:ASP:O	58:B1:1223:LEU:HB2	2.15	0.46
17:Q:70:GLY:O	17:Q:98:ARG:NH2	2.47	0.46
20:T:37:HIS:HD2	20:T:38:LEU:HD12	1.80	0.46
28:c:170:VAL:HG21	51:1:2679:A:H5'	1.97	0.46
31:f:1:SER:HA	51:1:2749:A:OP1	2.15	0.46
31:f:90:GLY:HA2	31:f:159:LYS:HG2	1.98	0.46
34:j:2:LYS:HA	51:1:995:C:C4	2.50	0.46
48:x:14:GLY:HA3	48:x:28:PHE:HE1	1.81	0.46
51:1:93:G:O2'	51:1:94:A:H5'	2.16	0.46
51:1:466:A:H2'	51:1:467:G:C5'	2.44	0.46
51:1:569:U:H1'	51:1:947:A:O4'	2.16	0.46
51:1:570:G:H5'	51:1:983:A:C2	2.51	0.46
51:1:1209:U:O3'	51:1:1212:G:H5'	2.16	0.46
51:1:1344:U:H3'	51:1:1345:C:H5'	1.97	0.46
51:1:1480:C:H2'	51:1:1481:U:C6	2.49	0.46
51:1:2315:G:H2'	51:1:2316:G:H8	1.80	0.46
53:3:1200:C:H5''	53:3:1201:A:H3'	1.97	0.46

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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	0.46
59:B2:207:THR:OG1	59:B2:354:ASP:OD2	2.32	0.46
59:B2:517:GLN:HB3	59:B2:760:ASN:H	1.79	0.46
51:1:338:G:O2'	51:1:339:U:H5'	2.14	0.46
51:1:389:G:O2'	51:1:390:U:H5'	2.15	0.46
51:1:438:G:O2'	51:1:439:A:H5'	2.16	0.46
51:1:688:U:H5'	51:1:1780:A:C2	2.51	0.46
51:1:1516:G:O2'	51:1:1517:G:H5'	2.15	0.46
51:1:2743:U:H2'	51:1:2744:G:O4'	2.16	0.46
51:1:2858:C:H2'	51:1:2859:G:O4'	2.15	0.46
11:K:5:GLU:HB2	11:K:90:MET:HB2	1.98	0.46
16:P:127:ARG:HB2	26:Z:34:ARG:HH22	1.81	0.46
17:Q:23:LEU:HD12	17:Q:29:LYS:HD2	1.97	0.46
51:1:28:A:O2'	51:1:29:U:H5'	2.16	0.46
51:1:289:G:H2'	51:1:290:U:C6	2.50	0.46
51:1:848:C:H2'	51:1:849:A:C8	2.51	0.46
51:1:1338:G:H2'	51:1:1339:G:C8	2.51	0.46
51:1:1381:G:H2'	51:1:1382:G:H5'	1.98	0.46
51:1:1572:A:H2'	51:1:1573:G:O4'	2.16	0.46
51:1:2360:G:H2'	51:1:2361:G:C5'	2.40	0.46
53:3:459:A:H2'	53:3:460:A:C8	2.50	0.46
55:8:13:DT:C6	58:B1:791:ALA:HA	2.51	0.46
57:A1:33:ARG:HE	57:A1:33:ARG:HB3	1.56	0.46
58:B1:68:TYR:HB3	58:B1:75:TYR:HE2	1.81	0.46
58:B1:385:LEU:HD23	58:B1:390:LEU:HB2	1.97	0.46
59:B2:1286:THR:O	59:B2:1290:MET:HB2	2.14	0.46
63:5:8:U:H2'	63:5:13:C:N4	2.30	0.46
64:6:21:A:H62	64:6:47:U:H1'	1.81	0.46
8:H:152:VAL:HG12	8:H:197:VAL:HG22	1.98	0.46
15:O:100:ILE:O	62:NG:170:PRO:O	2.33	0.46
18:R:7:ASN:HD22	18:R:20:SER:HB2	1.80	0.46
36:l:69:ARG:NH1	51:1:2406:A:C2	2.84	0.46
51:1:1287:A:O2'	51:1:1288:G:H5'	2.16	0.46
51:1:1486:U:O2'	51:1:1487:U:H5'	2.14	0.46
51:1:2247:A:H2'	51:1:2248:C:H6	1.81	0.46
51:1:2329:U:H2'	51:1:2330:G:C8	2.51	0.46
55:8:14:DC:H2'	55:8:15:DC:H6	1.79	0.46
58:B1:198:CYS:HA	58:B1:221:ILE:CD1	2.45	0.46
59:B2:400:VAL:HG22	59:B2:584:TYR:HB3	1.96	0.46
62:NG:135:ARG:O	62:NG:178:VAL:HA	2.16	0.46
63:5:26:A:H61	63:5:44:G:H22	1.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:73:VAL:HG11	10:J:143:LEU:HB3	1.98	0.46
18:R:97:ARG:HB2	18:R:99:GLN:HE22	1.81	0.46
28:c:4:LEU:HD11	28:c:100:LEU:HD21	1.98	0.46
33:i:109:ALA:HA	33:i:112:LYS:HB2	1.98	0.46
35:k:70:ARG:NH1	51:1:2684:U:O4'	2.49	0.46
51:1:409:G:H2'	51:1:410:G:C8	2.50	0.46
51:1:637:A:C6	51:1:652:U:H4'	2.50	0.46
51:1:1117:C:H2'	51:1:1118:C:C6	2.50	0.46
51:1:1183:U:H2'	51:1:1184:U:H6	1.80	0.46
51:1:1923:U:O2'	51:1:1924:C:H5'	2.16	0.46
51:1:2528:U:O2'	51:1:2529:G:H3'	2.16	0.46
58:B1:220:ARG:HH11	58:B1:220:ARG:CG	2.26	0.46
58:B1:288:PRO:HB3	62:NG:106:LYS:H	1.79	0.46
6:F:33:HIS:O	6:F:34:LYS:C	2.58	0.46
37:m:34:LYS:N	37:m:129:THR:O	2.47	0.46
51:1:44:A:H2'	51:1:45:G:O4'	2.15	0.46
51:1:540:C:O2'	51:1:541:A:H5'	2.16	0.46
51:1:853:C:O2'	51:1:854:C:H5'	2.16	0.46
51:1:1087:G:H22	51:1:1103:A:H1'	1.75	0.46
51:1:1574:C:H2'	51:1:1575:C:C6	2.50	0.46
51:1:1766:G:C2'	51:1:1767:G:H5'	2.45	0.46
51:1:2030:A:N3	51:1:2499:C:H5''	2.31	0.46
51:1:2290:G:O2'	51:1:2291:U:H5'	2.16	0.46
51:1:2813:A:O2'	51:1:2814:A:H5'	2.15	0.46
53:3:618:C:N4	53:3:621:A:OP2	2.49	0.46
57:A2:64:VAL:HG11	57:A2:78:ILE:HG21	1.97	0.46
58:B1:128:LEU:HD21	58:B1:188:LEU:HB3	1.97	0.46
58:B1:352:ARG:HB2	59:B2:1268:GLN:NE2	2.30	0.46
60:W0:25:ARG:NH1	60:W0:61:ASN:OD1	2.49	0.46
7:G:18:GLN:HG3	7:G:189:ASN:CB	2.41	0.46
9:I:114:ARG:HA	9:I:117:VAL:HG22	1.98	0.46
11:K:75:GLU:O	11:K:79:ARG:N	2.47	0.46
29:d:132:LYS:HG2	29:d:136:GLN:HE22	1.81	0.46
35:k:121:GLU:HG2	35:k:122:VAL:HG23	1.97	0.46
43:s:72:THR:OG1	43:s:73:LYS:N	2.48	0.46
51:1:360:U:H2'	51:1:361:G:H1'	1.98	0.46
51:1:438:G:H2'	51:1:439:A:C8	2.51	0.46
51:1:536:G:H2'	51:1:537:G:C5'	2.43	0.46
51:1:1520:U:H2'	51:1:1521:G:O4'	2.16	0.46
51:1:2496:C:H2'	51:1:2497:A:O4'	2.16	0.46
51:1:2581:G:H2'	51:1:2581:G:N3	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2642:G:O5'	51:1:2642:G:H8	1.98	0.46
53:3:112:G:N2	53:3:354:G:O5'	2.48	0.46
55:8:1:DC:H2''	55:8:2:DC:C6	2.51	0.46
58:B1:375:GLU:O	59:B2:1247:SER:HB3	2.16	0.46
59:B2:515:MET:HE2	59:B2:515:MET:HB3	1.82	0.46
63:5:6:G:H2'	63:5:7:A:C8	2.51	0.46
9:I:173:ASP:HB3	9:I:178:GLU:HB3	1.98	0.45
19:S:58:ARG:HH21	53:3:980:C:H4'	1.81	0.45
39:o:29:HIS:HB3	39:o:36:TYR:HB2	1.98	0.45
51:1:239:C:H2'	51:1:240:C:O4'	2.16	0.45
51:1:519:U:C2	51:1:520:G:C8	3.03	0.45
51:1:2101:A:H2'	51:1:2102:G:H8	1.81	0.45
51:1:2339:C:H2'	51:1:2340:A:H8	1.81	0.45
51:1:2648:G:C2	51:1:2649:C:C2	3.04	0.45
51:1:2651:C:H2'	51:1:2652:C:H6	1.82	0.45
58:B1:175:GLU:H	58:B1:175:GLU:HG3	1.65	0.45
63:5:22:G:H2'	63:5:23:A:C8	2.51	0.45
2:B:8:THR:OG1	2:B:9:ARG:N	2.49	0.45
9:I:93:LEU:O	9:I:99:ASN:ND2	2.39	0.45
27:b:1:ALA:N	27:b:19:VAL:O	2.41	0.45
28:c:151:THR:O	51:1:1130:U:C4	2.70	0.45
33:i:112:LYS:HD2	33:i:128:ILE:HD12	1.97	0.45
34:j:108:MET:CE	51:1:1138:G:H21	2.29	0.45
47:w:37:ARG:HA	47:w:37:ARG:HD3	1.70	0.45
51:1:595:C:C2	51:1:596:U:C5	3.04	0.45
51:1:607:U:O4	51:1:620:G:H5'	2.17	0.45
51:1:1034:G:C5	51:1:1035:U:C4	3.04	0.45
51:1:1869:G:H3'	51:1:1870:C:C5'	2.38	0.45
51:1:2122:U:H2'	51:1:2123:G:O4'	2.16	0.45
51:1:2141:G:H1	51:1:2151:U:H3	1.63	0.45
51:1:2636:C:O2'	51:1:2637:U:H5'	2.16	0.45
51:1:2844:G:H2'	51:1:2845:U:O4'	2.16	0.45
53:3:1253:G:H2'	53:3:1254:A:C8	2.52	0.45
57:A1:231:PHE:O	57:A2:218:ARG:NH1	2.50	0.45
58:B1:201:LEU:CD1	58:B1:224:LEU:HD12	2.47	0.45
59:B2:557:ARG:NH2	59:B2:607:SER:O	2.50	0.45
2:B:31:LYS:HG2	51:1:2885:G:N2	2.31	0.45
11:K:3:HIS:HA	11:K:65:GLU:HA	1.97	0.45
32:g:1:MET:HE3	32:g:1:MET:HB3	1.77	0.45
34:j:85:LYS:NZ	51:1:2768:U:OP1	2.49	0.45
51:1:6:A:H2'	51:1:7:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:290:U:O2'	51:1:291:G:H5'	2.16	0.45
51:1:355:U:H6	51:1:355:U:O5'	1.99	0.45
51:1:367:G:O2'	51:1:368:A:H5'	2.17	0.45
51:1:1140:C:H2'	51:1:1141:U:H5'	1.98	0.45
51:1:1412:U:H2'	51:1:1413:A:H8	1.81	0.45
51:1:1710:G:H2'	51:1:1711:A:C8	2.51	0.45
51:1:1923:U:H5''	64:6:24:U:O2'	2.17	0.45
51:1:2085:U:O2'	51:1:2086:U:H5'	2.16	0.45
51:1:2661:G:O2'	51:1:2662:A:H5'	2.16	0.45
63:5:49:C:H2'	63:5:50:U:C6	2.52	0.45
7:G:166:ASP:HB3	7:G:190:SER:HB2	1.99	0.45
10:J:28:ARG:NH2	53:3:1397:C:OP2	2.38	0.45
23:W:33:THR:OG1	23:W:34:GLU:N	2.49	0.45
43:s:82:MET:HE1	51:1:1322:A:H5''	1.98	0.45
51:1:342:A:H2'	51:1:343:C:O4'	2.16	0.45
51:1:1049:C:C2'	51:1:1050:A:H5'	2.47	0.45
51:1:1488:C:H2'	51:1:1489:C:C6	2.51	0.45
51:1:1550:C:O2'	51:1:1551:A:H5'	2.17	0.45
51:1:2204:G:H2'	51:1:2205:A:H8	1.81	0.45
53:3:647:C:H2'	53:3:648:A:H8	1.81	0.45
58:B1:115:TRP:HB3	58:B1:1333:THR:CG2	2.46	0.45
59:B2:24:VAL:HG11	59:B2:704:MET:HE1	1.98	0.45
7:G:65:LYS:HG2	7:G:153:MET:HG3	1.98	0.45
9:I:13:ARG:NH1	53:3:542:G:O3'	2.50	0.45
10:J:101:GLY:H	10:J:121:ASN:HB3	1.81	0.45
12:L:142:ARG:HH21	64:7:42:G:H4'	1.81	0.45
29:d:136:GLN:HA	29:d:139:LYS:HE2	1.99	0.45
35:k:5:GLN:NE2	51:1:1668:A:H5''	2.31	0.45
51:1:111:A:O2'	51:1:112:U:H5'	2.17	0.45
51:1:654:A:N3	51:1:654:A:H5''	2.31	0.45
51:1:1173:U:C6	51:1:1174:U:H1'	2.51	0.45
51:1:1863:G:H2'	51:1:1864:U:C6	2.51	0.45
51:1:2783:U:H2'	51:1:2784:U:C6	2.51	0.45
57:A1:35:PHE:HA	57:A1:38:THR:HG22	1.98	0.45
64:7:7:G:H3'	64:7:49:G:OP2	2.16	0.45
4:D:12:ARG:NH1	51:1:465:G:OP1	2.49	0.45
22:V:11:VAL:HG13	22:V:58:VAL:HG21	1.98	0.45
31:f:175:LYS:HD3	31:f:175:LYS:HA	1.70	0.45
33:i:135:MET:CE	51:1:1062:G:H21	2.30	0.45
48:x:30:PRO:HG2	48:x:32:LEU:HD11	1.98	0.45
51:1:198:C:N4	51:1:248:G:H1	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:707:G:C2'	51:1:708:G:H5'	2.47	0.45
51:1:1239:G:O2'	51:1:1240:U:H5'	2.17	0.45
51:1:1868:C:H2'	51:1:1869:G:C8	2.51	0.45
51:1:2047:C:O2'	51:1:2048:G:H5'	2.16	0.45
51:1:2201:G:H2'	51:1:2202:U:O4'	2.17	0.45
51:1:2350:C:H2'	51:1:2351:G:O4'	2.16	0.45
51:1:2364:C:O2'	51:1:2365:G:H5'	2.17	0.45
51:1:2658:C:H2'	51:1:2659:G:O4'	2.16	0.45
51:1:2889:C:O2'	51:1:2890:G:H5'	2.17	0.45
58:B1:67:ASP:OD1	58:B1:67:ASP:O	2.35	0.45
58:B1:388:ARG:HG2	58:B1:388:ARG:NH1	2.32	0.45
58:B1:484:MET:CE	59:B2:1278:LEU:HD21	2.47	0.45
58:B1:847:ASP:N	58:B1:847:ASP:OD1	2.49	0.45
59:B2:230:PHE:HB2	59:B2:333:ILE:HB	1.98	0.45
59:B2:674:ASP:OD2	59:B2:1070:HIS:ND1	2.50	0.45
7:G:172:ILE:O	7:G:176:ASN:ND2	2.50	0.45
14:N:40:ARG:NH2	53:3:1291:U:O3'	2.38	0.45
17:Q:45:ASN:ND2	17:Q:88:ASP:OD2	2.39	0.45
51:1:1210:G:P	51:1:1212:G:H5'	2.56	0.45
51:1:1288:G:C5	51:1:1327:A:C2	3.04	0.45
51:1:1715:G:HO2'	51:1:1716:U:H6	1.60	0.45
51:1:2137:U:H2'	51:1:2138:G:C8	2.50	0.45
51:1:2849:U:H4'	51:1:2868:A:C2	2.51	0.45
53:3:1376:U:H2'	53:3:1377:A:C8	2.52	0.45
58:B1:109:SER:HB2	58:B1:296:LYS:HG2	1.98	0.45
59:B2:1314:GLN:HA	60:W0:28:ARG:HH22	1.80	0.45
63:5:8:U:H2'	63:5:13:C:H41	1.81	0.45
64:6:46:G:H5''	64:6:47:U:OP2	2.17	0.45
8:H:5:HIS:CE1	8:H:7:ASN:HB3	2.51	0.45
16:P:124:LYS:HB3	26:Z:34:ARG:HB3	1.98	0.45
19:S:44:VAL:O	19:S:48:GLN:NE2	2.50	0.45
33:i:10:LEU:HD21	33:i:27:LEU:HD21	1.99	0.45
50:z:30:ARG:HG2	50:z:33:HIS:HB2	1.99	0.45
51:1:639:U:H2'	51:1:640:C:C6	2.52	0.45
51:1:1140:C:C2'	51:1:1141:U:H5'	2.47	0.45
51:1:1832:C:O5'	51:1:1832:C:H6	2.00	0.45
51:1:1952:A:H2'	51:1:1953:A:C8	2.51	0.45
53:3:142:G:O2'	53:3:196:A:N1	2.45	0.45
53:3:1498:U:H4'	53:3:1519:A:H2	1.82	0.45
55:8:20:DA:H4'	59:B2:143:ARG:NH1	2.31	0.45
57:A1:185:TYR:HA	57:A1:202:VAL:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:1227:HIS:HA	58:B1:1230:THR:HG22	1.99	0.45
59:B2:854:ILE:HG23	59:B2:917:SER:HB3	1.99	0.45
63:5:70:G:H2'	63:5:71:G:C8	2.51	0.45
21:U:28:ARG:NH1	53:3:390:U:O2'	2.46	0.45
22:V:10:ARG:NE	22:V:55:GLY:O	2.48	0.45
29:d:32:VAL:HG21	36:l:6:LEU:HD13	1.99	0.45
30:e:71:LYS:HA	30:e:71:LYS:HD2	1.78	0.45
30:e:122:ASP:OD2	30:e:126:ASN:ND2	2.42	0.45
51:1:195:A:H3'	51:1:196:A:H4'	1.99	0.45
51:1:395:U:H2'	51:1:396:G:C8	2.52	0.45
51:1:1170:C:H2'	51:1:1171:G:C8	2.51	0.45
51:1:1800:C:O2	51:1:1802:A:C8	2.70	0.45
57:A1:212:ASP:OD1	57:A1:212:ASP:N	2.48	0.45
57:A2:80:GLU:HG3	59:B2:694:ARG:HH22	1.82	0.45
58:B1:75:TYR:CD2	58:B1:75:TYR:O	2.70	0.45
58:B1:1357:ILE:HD13	59:B2:1279:GLU:HG2	1.97	0.45
16:P:35:ASP:OD1	16:P:39:ASN:N	2.50	0.45
37:m:96:ILE:HD13	37:m:96:ILE:HA	1.82	0.45
41:q:82:LEU:HD22	41:q:87:VAL:HB	1.98	0.45
51:1:167:A:H2'	51:1:168:G:O4'	2.16	0.45
51:1:1680:U:C2'	51:1:1681:G:H5'	2.47	0.45
51:1:1807:G:H2'	51:1:1808:A:C5'	2.30	0.45
51:1:2241:A:H2'	51:1:2242:G:H8	1.82	0.45
51:1:2312:U:O2'	51:1:2313:C:H5'	2.17	0.45
51:1:2402:U:O2'	51:1:2403:C:H3'	2.17	0.45
51:1:2741:A:H2'	51:1:2742:G:H5'	1.98	0.45
53:3:1200:C:O2'	53:3:1205:U:O4	2.34	0.45
57:A1:68:TYR:HE1	57:A1:79:LEU:HD13	1.82	0.45
58:B1:111:THR:HG21	58:B1:303:VAL:HB	1.99	0.45
58:B1:209:ASN:HA	58:B1:214:ARG:NH2	2.30	0.45
58:B1:395:LYS:NZ	58:B1:399:LYS:HE2	2.32	0.45
65:h:2:DPP:NG	65:h:3:SER:N	2.65	0.45
8:H:5:HIS:HE1	8:H:7:ASN:HB3	1.82	0.44
9:I:120:LYS:HG2	9:I:130:ASN:HB3	1.98	0.44
12:L:113:LYS:HB3	53:3:1297:G:H21	1.82	0.44
16:P:17:ASP:OD1	16:P:17:ASP:N	2.44	0.44
33:i:9:LYS:HD2	51:1:1061:U:OP1	2.17	0.44
44:t:34:VAL:HG21	44:t:43:ILE:HD11	1.99	0.44
51:1:402:A:H2'	51:1:403:U:C5'	2.44	0.44
51:1:432:A:O2'	51:1:433:C:H5'	2.17	0.44
51:1:1500:G:O2'	51:1:1501:G:H5'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2869:G:H2'	51:1:2870:C:O4'	2.17	0.44
58:B1:213:LYS:HA	58:B1:213:LYS:HE3	1.99	0.44
58:B1:515:ARG:NH2	58:B1:718:SER:O	2.48	0.44
58:B1:1158:GLU:HA	58:B1:1223:LEU:HD21	1.99	0.44
59:B2:176:ILE:HD11	59:B2:428:VAL:HG21	1.98	0.44
59:B2:998:LEU:HG	59:B2:1011:LEU:HB3	1.99	0.44
7:G:142:LYS:NZ	53:3:1098:C:OP1	2.49	0.44
10:J:24:VAL:HG23	10:J:26:GLY:H	1.82	0.44
14:N:104:THR:HG23	53:3:1180:A:H5'	1.99	0.44
28:c:150:GLN:HE22	51:1:2032:G:H1'	1.81	0.44
31:f:132:LEU:HB3	31:f:140:ILE:HD11	1.99	0.44
31:f:133:LYS:NZ	31:f:134:GLY:O	2.44	0.44
40:p:88:ARG:HH11	40:p:114:ASN:HD21	1.65	0.44
51:1:1020:A:C2	51:1:1141:U:C2	3.05	0.44
51:1:1280:G:C2'	51:1:1281:G:H5'	2.46	0.44
51:1:1452:G:H2'	51:1:1453:A:OP2	2.17	0.44
51:1:1866:A:H2'	51:1:1867:G:O4'	2.17	0.44
51:1:1882:U:O2'	51:1:1883:U:H5'	2.17	0.44
51:1:1893:C:C2'	51:1:1894:C:H5'	2.47	0.44
51:1:1922:G:H2'	51:1:1923:U:O4'	2.18	0.44
51:1:2717:C:N3	51:1:2718:G:N7	2.65	0.44
58:B1:770:LEU:HD13	59:B2:618:GLN:CD	2.42	0.44
12:L:70:PRO:HG3	12:L:98:LEU:HD23	1.97	0.44
15:O:29:ALA:HB2	15:O:87:LEU:HD11	1.99	0.44
21:U:79:ASN:HB2	21:U:82:ALA:HB3	1.99	0.44
28:c:59:ARG:HA	28:c:59:ARG:HD3	1.83	0.44
45:u:76:THR:HB	45:u:78:LYS:HE3	1.99	0.44
47:w:12:SER:OG	47:w:13:GLU:N	2.51	0.44
48:x:51:SER:OG	48:x:54:GLY:N	2.48	0.44
51:1:30:G:H2'	51:1:31:C:O4'	2.17	0.44
51:1:336:C:O2'	51:1:337:C:H5'	2.18	0.44
51:1:893:C:H2'	51:1:894:U:O4'	2.17	0.44
51:1:940:G:H3'	51:1:941:A:H5''	1.97	0.44
51:1:1605:C:H2'	51:1:1606:C:H5'	1.98	0.44
51:1:1717:A:C2	51:1:1718:G:H1'	2.53	0.44
51:1:2411:A:H2'	51:1:2412:A:C8	2.53	0.44
51:1:2626:C:H2'	51:1:2627:G:C8	2.51	0.44
51:1:2880:C:O2	51:1:2880:C:H2'	2.17	0.44
53:3:490:C:H2'	53:3:491:G:C8	2.53	0.44
53:3:530:G:N1	53:3:1492:A:N1	2.60	0.44
58:B1:33:TRP:HZ2	59:B2:1336:ASN:OD1	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:120:LEU:HD22	58:B1:120:LEU:HA	1.77	0.44
59:B2:1002:LEU:HD21	59:B2:1007:LYS:HB2	1.98	0.44
2:B:4:GLN:HG3	51:1:2054:A:C2	2.52	0.44
7:G:26:MET:HE1	7:G:186:VAL:HB	1.99	0.44
31:f:106:LEU:O	31:f:151:ARG:NH2	2.38	0.44
45:u:17:ASP:HA	45:u:20:LYS:HE2	2.00	0.44
51:1:107:G:H2'	51:1:108:G:H8	1.82	0.44
51:1:974:G:H1'	51:1:975:A:C8	2.53	0.44
51:1:1199:U:H2'	51:1:1200:C:C6	2.52	0.44
51:1:1507:C:H2'	51:1:1508:A:H4'	1.99	0.44
53:3:477:C:H2'	53:3:478:A:C8	2.52	0.44
53:3:908:A:H2'	53:3:909:A:H8	1.83	0.44
58:B1:45:ASN:HD22	58:B1:48:THR:H	1.65	0.44
58:B1:161:THR:H	58:B1:164:GLN:HB2	1.82	0.44
58:B1:850:LYS:HB3	58:B1:855:ASP:HB2	1.99	0.44
58:B1:1046:ILE:HG22	58:B1:1061:VAL:HA	2.00	0.44
59:B2:11:ILE:HG22	59:B2:1172:LEU:HD11	1.99	0.44
59:B2:856:ASN:HB2	59:B2:919:ARG:HH22	1.82	0.44
1:A:2:LYS:NZ	52:2:42:C:OP2	2.39	0.44
14:N:84:ARG:NH2	53:3:1119:C:OP1	2.48	0.44
38:n:103:ARG:HH11	51:1:1287:A:H5'	1.83	0.44
42:r:1:MET:HE3	42:r:101:ILE:HB	1.99	0.44
45:u:32:LYS:HG2	45:u:65:GLN:HA	1.99	0.44
49:y:6:LEU:HD13	49:y:56:LEU:HD22	1.98	0.44
51:1:169:G:O2'	51:1:170:U:H5'	2.18	0.44
51:1:354:A:H2'	51:1:355:U:O4'	2.17	0.44
51:1:473:G:C2'	51:1:474:G:H5'	2.48	0.44
51:1:500:G:N2	51:1:502:A:H3'	2.32	0.44
51:1:704:G:H1'	51:1:727:A:H62	1.83	0.44
51:1:854:C:H2'	51:1:855:G:C8	2.52	0.44
51:1:1232:G:H2'	51:1:1233:C:C6	2.53	0.44
51:1:1536:C:H4'	51:1:1537:G:N1	2.32	0.44
51:1:1749:A:H2'	51:1:1750:G:H8	1.82	0.44
52:2:66:A:H4'	52:2:67:G:C8	2.53	0.44
53:3:765:G:H1	53:3:812:G:HO2'	1.63	0.44
55:8:16:DT:H2'	55:8:17:DC:C6	2.52	0.44
63:5:69:G:H2'	63:5:70:G:C8	2.52	0.44
4:D:12:ARG:HH12	51:1:465:G:P	2.41	0.44
7:G:33:ALA:HB3	7:G:37:VAL:HG12	1.99	0.44
27:b:107:LYS:HE2	27:b:107:LYS:HB2	1.88	0.44
40:p:52:ARG:NH2	51:1:2720:U:OP1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:p:92:ARG:H	40:p:92:ARG:HG2	1.60	0.44
51:1:350:G:H2'	51:1:351:C:O4'	2.18	0.44
51:1:388:G:N7	51:1:390:U:H2'	2.33	0.44
51:1:720:U:H2'	51:1:721:A:H8	1.82	0.44
51:1:1465:G:O2'	51:1:1466:U:H5'	2.17	0.44
51:1:1507:C:H2'	51:1:1508:A:O4'	2.18	0.44
51:1:1672:A:N3	51:1:2582:G:H5'	2.27	0.44
51:1:2713:U:C3'	51:1:2714:G:H5'	2.27	0.44
51:1:2805:C:O2'	51:1:2806:C:H5'	2.18	0.44
58:B1:128:LEU:CD2	58:B1:188:LEU:HB3	2.47	0.44
63:5:63:G:H2'	63:5:64:A:C8	2.53	0.44
8:H:134:LYS:HB3	8:H:134:LYS:HE2	1.84	0.44
14:N:74:GLN:OE1	53:3:1249:C:O2'	2.35	0.44
18:R:1:ALA:HB3	18:R:56:ARG:HH22	1.83	0.44
18:R:107:THR:OG1	53:3:947:G:O3'	2.35	0.44
24:X:76:THR:OG1	24:X:77:ARG:N	2.51	0.44
28:c:106:LYS:HA	28:c:176:ASP:HA	1.99	0.44
41:q:47:ARG:NH2	41:q:51:GLN:OE1	2.51	0.44
51:1:68:G:H2'	51:1:69:C:O4'	2.18	0.44
51:1:131:A:H2'	51:1:132:G:C8	2.53	0.44
51:1:696:G:H2'	51:1:697:G:O4'	2.17	0.44
51:1:819:A:H5'	51:1:973:A:N1	2.33	0.44
51:1:1010:A:H1'	51:1:1153:C:H1'	1.99	0.44
51:1:1173:U:H5	51:1:1174:U:H1'	1.81	0.44
51:1:1761:C:H2'	51:1:1762:A:O4'	2.18	0.44
51:1:1998:A:O2'	51:1:1999:C:H5'	2.18	0.44
51:1:2226:C:C5	51:1:2227:A:N7	2.86	0.44
53:3:560:A:H5''	53:3:561:U:H5'	2.00	0.44
53:3:1053:G:H4'	53:3:1054:C:H3'	2.00	0.44
53:3:1513:A:H2'	53:3:1514:G:H8	1.83	0.44
58:B1:201:LEU:HD11	58:B1:220:ARG:NH1	2.32	0.44
63:5:27:G:H1	63:5:43:C:H42	1.64	0.44
7:G:67:LEU:HD21	7:G:91:VAL:HG23	2.00	0.44
10:J:110:MET:HE3	10:J:110:MET:HB2	1.79	0.44
17:Q:72:ASN:OD1	17:Q:72:ASN:N	2.50	0.44
33:i:131:THR:HB	51:1:1060:U:O4	2.18	0.44
42:r:19:THR:OG1	42:r:95:ASP:OD1	2.35	0.44
45:u:12:VAL:HA	45:u:69:VAL:HG12	1.99	0.44
48:x:1:SER:OG	51:1:1365:A:OP2	2.35	0.44
49:y:20:ASN:HA	49:y:23:ARG:HB2	1.99	0.44
51:1:150:U:H2'	51:1:151:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:255:A:H2'	51:1:256:A:O4'	2.18	0.44
51:1:293:U:H2'	51:1:294:A:H5''	1.99	0.44
51:1:327:G:H2'	51:1:328:U:O4'	2.18	0.44
51:1:1539:U:H2'	51:1:1540:G:C8	2.53	0.44
53:3:75:G:H2'	53:3:76:G:C8	2.53	0.44
55:8:12:DG:OP1	58:B1:795:TYR:CE1	2.71	0.44
58:B1:111:THR:CG2	58:B1:300:GLN:HA	2.48	0.44
58:B1:375:GLU:HB3	59:B2:1245:ALA:CB	2.48	0.44
58:B1:800:LEU:HD12	58:B1:800:LEU:HA	1.79	0.44
58:B1:1357:ILE:HG22	58:B1:1359:ALA:H	1.82	0.44
5:E:48:MET:HE3	5:E:48:MET:HB3	1.86	0.44
7:G:122:ASP:N	7:G:122:ASP:OD1	2.51	0.44
8:H:76:ILE:HB	8:H:80:GLY:HA2	2.00	0.44
10:J:104:ILE:HD11	10:J:114:LEU:HD13	1.99	0.44
11:K:62:MET:HB3	11:K:64:VAL:HG13	1.98	0.44
18:R:43:LYS:HB2	18:R:46:GLU:HG2	2.00	0.44
23:W:33:THR:HG22	23:W:37:LYS:H	1.83	0.44
25:Y:67:HIS:O	25:Y:69:ASN:ND2	2.51	0.44
27:b:153:LEU:HD23	51:1:1799:G:N2	2.33	0.44
51:1:150:U:O2'	51:1:151:C:H5'	2.18	0.44
51:1:208:C:O2'	51:1:209:C:H5'	2.18	0.44
51:1:721:A:H2'	51:1:722:A:C8	2.53	0.44
51:1:1287:A:H3'	51:1:1288:G:N2	2.33	0.44
51:1:1915:U:O2	51:1:1915:U:O4'	2.33	0.44
58:B1:76:LYS:NZ	58:B1:76:LYS:HB3	2.32	0.44
58:B1:105:ILE:HD12	58:B1:242:LEU:CD2	2.44	0.44
58:B1:894:VAL:HG22	58:B1:1258:ARG:HH11	1.83	0.44
58:B1:926:PRO:HB2	58:B1:1241:TYR:HE1	1.82	0.44
58:B1:1033:GLY:HA3	58:B1:1081:VAL:O	2.18	0.44
59:B2:557:ARG:HB3	59:B2:587:LEU:HD13	2.00	0.44
62:NG:161:SER:CB	62:NG:170:PRO:HA	2.47	0.44
9:I:85:THR:HA	9:I:88:ASN:HB2	2.00	0.43
36:l:39:LYS:HZ3	51:1:942:G:P	2.39	0.43
51:1:192:C:H2'	51:1:193:U:H5'	1.99	0.43
51:1:365:U:H2'	51:1:366:C:C6	2.53	0.43
51:1:518:G:O2'	51:1:519:U:H5'	2.18	0.43
51:1:623:C:O2'	51:1:624:C:H5'	2.17	0.43
51:1:684:G:C2	51:1:794:A:C2	3.06	0.43
51:1:1426:G:C6	51:1:1427:A:C6	3.06	0.43
51:1:1571:A:H2'	51:1:1572:A:C8	2.53	0.43
51:1:1710:G:O2'	51:1:1711:A:H5'	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2236:U:H2'	51:1:2237:G:C5'	2.46	0.43
51:1:2285:C:C2'	51:1:2286:G:H5'	2.48	0.43
51:1:2671:G:C2	51:1:2672:U:C2	3.06	0.43
53:3:501:C:H2'	53:3:502:A:C8	2.53	0.43
57:A1:192:VAL:HG12	57:A1:193:GLU:H	1.82	0.43
58:B1:62:PHE:N	58:B1:62:PHE:CD1	2.86	0.43
58:B1:1026:PRO:HB2	58:B1:1028:ILE:HG23	2.00	0.43
2:B:4:GLN:NE2	51:1:2056:G:O2'	2.51	0.43
2:B:8:THR:HG23	2:B:11:LYS:H	1.82	0.43
8:H:134:LYS:HG2	8:H:138:GLN:HE21	1.82	0.43
14:N:105:ARG:NH1	14:N:109:GLN:OE1	2.49	0.43
17:Q:3:VAL:HA	17:Q:6:LEU:HD12	2.00	0.43
17:Q:113:ARG:NH1	53:3:36:C:O2'	2.51	0.43
21:U:70:ARG:O	21:U:74:LEU:N	2.47	0.43
24:X:6:LYS:NZ	53:3:1314:C:OP1	2.51	0.43
33:i:129:GLU:HG3	33:i:139:VAL:HG21	2.00	0.43
36:l:95:LEU:HD22	36:l:100:ILE:HD11	2.00	0.43
37:m:17:ASN:OD1	37:m:97:GLN:NE2	2.51	0.43
51:1:161:A:C5	51:1:162:U:H5	2.36	0.43
51:1:163:C:O2'	51:1:164:C:H5'	2.17	0.43
51:1:545:U:O2	51:1:546:U:H1'	2.17	0.43
51:1:648:G:H5''	51:1:2352:A:H5''	2.00	0.43
51:1:1565:C:C5	51:1:1567:G:C6	3.06	0.43
51:1:1625:C:H2'	51:1:1626:A:O4'	2.18	0.43
51:1:1741:C:O2'	51:1:1742:U:H5'	2.18	0.43
51:1:1993:U:O2	51:1:1993:U:H2'	2.18	0.43
51:1:2643:G:C2'	51:1:2644:G:H5'	2.49	0.43
51:1:2839:G:O2'	51:1:2840:C:H5'	2.18	0.43
53:3:146:G:N2	53:3:177:G:N7	2.66	0.43
53:3:162:A:C5	53:3:163:C:H1'	2.53	0.43
53:3:1253:G:H2'	53:3:1254:A:H8	1.83	0.43
57:A1:78:ILE:HA	57:A1:81:ILE:HG22	2.00	0.43
58:B1:213:LYS:HE3	58:B1:213:LYS:CA	2.47	0.43
58:B1:287:ALA:HB1	58:B1:288:PRO:HD2	1.99	0.43
58:B1:362:ARG:HB2	58:B1:364:HIS:HD2	1.83	0.43
58:B1:506:VAL:HG23	58:B1:628:GLY:HA3	1.99	0.43
58:B1:731:ARG:HB3	59:B2:1105:SER:HB2	2.00	0.43
58:B1:1024:THR:HG23	58:B1:1123:ARG:HA	2.00	0.43
59:B2:646:SER:OG	59:B2:647:ARG:N	2.51	0.43
59:B2:811:ASN:ND2	59:B2:1098:LEU:O	2.51	0.43
59:B2:854:ILE:HG23	59:B2:855:PRO:HD2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:1246:ARG:HH11	59:B2:1266:GLY:HA2	1.82	0.43
9:I:125:ASN:HB2	9:I:127:ARG:HD3	2.01	0.43
14:N:98:ARG:HG2	14:N:103:VAL:HG21	2.01	0.43
16:P:115:ILE:HD12	16:P:116:PRO:HD2	1.99	0.43
27:b:20:ASN:HB3	27:b:23:LEU:HD13	2.01	0.43
27:b:86:ARG:HA	27:b:86:ARG:HD3	1.84	0.43
29:d:147:LEU:HD11	29:d:170:ARG:HG2	1.98	0.43
34:j:34:ARG:NH2	34:j:39:LYS:O	2.51	0.43
35:k:38:ILE:HG22	35:k:61:VAL:HB	2.00	0.43
39:o:40:ILE:HA	39:o:47:VAL:HA	1.99	0.43
43:s:74:ILE:HB	43:s:105:VAL:HG23	1.99	0.43
48:x:36:ARG:NH2	51:1:2200:C:OP2	2.52	0.43
51:1:29:U:O5'	51:1:29:U:H6	2.01	0.43
51:1:1087:G:H5''	51:1:1088:A:OP2	2.18	0.43
51:1:1095:A:H3'	51:1:1096:A:H8	1.83	0.43
51:1:1670:C:O2'	51:1:1671:U:H5'	2.16	0.43
51:1:1751:U:H2'	51:1:1752:C:C6	2.54	0.43
51:1:2314:A:H2'	51:1:2315:G:H8	1.77	0.43
53:3:490:C:H2'	53:3:491:G:H8	1.84	0.43
53:3:1442:G:H1	53:3:1460:C:H42	1.66	0.43
58:B1:96:LYS:NZ	59:B2:1298:VAL:HG11	2.34	0.43
58:B1:478:LEU:HD21	60:W0:47:THR:HG23	1.99	0.43
58:B1:978:ARG:HD3	58:B1:999:TYR:H	1.83	0.43
59:B2:538:LEU:HD13	59:B2:543:ALA:HB2	2.00	0.43
59:B2:854:ILE:HG12	59:B2:887:VAL:HG22	1.99	0.43
10:J:110:MET:HA	10:J:113:VAL:HG12	2.00	0.43
13:M:24:VAL:HG23	13:M:60:LEU:HB2	2.00	0.43
14:N:119:LYS:NZ	53:3:1350:A:N7	2.64	0.43
15:O:88:MET:HE3	15:O:88:MET:HB3	1.70	0.43
22:V:44:HIS:HB3	22:V:70:LYS:HG2	1.99	0.43
27:b:48:ILE:HG12	51:1:779:U:OP2	2.18	0.43
27:b:97:ASP:N	27:b:97:ASP:OD1	2.44	0.43
28:c:62:LYS:NZ	51:1:2810:A:H5''	2.34	0.43
29:d:68:ALA:HA	51:1:1255:U:C6	2.52	0.43
38:n:39:PRO:HG2	51:1:1651:G:H4'	2.01	0.43
39:o:33:ARG:O	39:o:65:THR:OG1	2.28	0.43
40:p:113:LEU:HD13	40:p:113:LEU:HA	1.86	0.43
51:1:30:G:O2'	51:1:31:C:H5'	2.18	0.43
51:1:156:A:O2'	51:1:157:C:H5'	2.18	0.43
51:1:993:G:O2'	51:1:994:C:H5'	2.19	0.43
51:1:1383:A:H2	51:1:1406:U:H1'	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1747:U:H2'	51:1:1748:C:C6	2.53	0.43
51:1:1864:U:O5'	51:1:1864:U:H6	2.01	0.43
51:1:2152:G:N3	51:1:2152:G:H2'	2.33	0.43
51:1:2660:A:H2'	51:1:2661:G:O4'	2.18	0.43
51:1:2700:A:O2'	51:1:2701:U:H5'	2.17	0.43
59:B2:1072:ASN:OD1	59:B2:1072:ASN:N	2.52	0.43
63:5:13:C:H42	63:5:46:G:N2	2.16	0.43
8:H:37:LYS:HA	8:H:37:LYS:HD3	1.81	0.43
8:H:51:VAL:HA	8:H:69:THR:HG22	2.00	0.43
9:I:44:LYS:HA	9:I:44:LYS:HD2	1.55	0.43
11:K:38:ARG:HH11	11:K:61:LEU:HD21	1.83	0.43
21:U:31:ARG:HB2	53:3:310:G:H5''	2.01	0.43
34:j:47:HIS:CG	51:1:536:G:H21	2.37	0.43
38:n:65:LEU:HD11	51:1:2870:C:H5''	1.99	0.43
41:q:83:LYS:HE2	41:q:83:LYS:HB3	1.72	0.43
42:r:80:ARG:HD3	51:1:566:U:O4	2.17	0.43
51:1:43:G:H2'	51:1:44:A:C8	2.53	0.43
51:1:1054:A:H2'	51:1:1055:G:C8	2.53	0.43
51:1:2836:U:H2'	51:1:2837:A:H8	1.81	0.43
53:3:958:A:N3	53:3:985:C:O2'	2.48	0.43
58:B1:472:LEU:CD1	59:B2:1294:LYS:HG2	2.47	0.43
58:B1:515:ARG:HH12	58:B1:724:MET:HG2	1.84	0.43
13:M:52:GLY:HA3	13:M:56:PRO:HA	2.01	0.43
17:Q:50:LYS:HE2	17:Q:70:GLY:HA2	2.01	0.43
17:Q:67:GLY:O	17:Q:98:ARG:NH1	2.52	0.43
25:Y:4:LYS:HA	25:Y:4:LYS:HD3	1.85	0.43
25:Y:49:ALA:HA	25:Y:52:GLU:HG3	2.00	0.43
27:b:140:VAL:HG12	27:b:191:LEU:HD23	2.01	0.43
36:l:109:LYS:HE2	51:1:636:G:N7	2.34	0.43
38:n:58:ASP:OD1	38:n:63:ARG:NH2	2.44	0.43
51:1:28:A:H2'	51:1:29:U:C6	2.53	0.43
51:1:108:G:O2'	51:1:109:C:H5'	2.19	0.43
51:1:705:A:C2	51:1:727:A:H1'	2.54	0.43
51:1:841:G:C2'	51:1:842:U:H5'	2.49	0.43
51:1:864:G:C2'	51:1:865:C:H5'	2.48	0.43
11:K:47:LEU:HG	11:K:56:LYS:HA	2.01	0.43
18:R:28:ARG:HH21	18:R:62:PHE:HB2	1.84	0.43
51:1:629:G:H2'	51:1:630:G:O4'	2.19	0.43
51:1:1172:C:H2'	51:1:1173:U:O4'	2.19	0.43
51:1:1258:U:H2'	51:1:1259:G:C8	2.54	0.43
51:1:1306:C:H41	51:1:1606:C:H2'	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:422:C:H4'	53:3:423:G:C2	2.54	0.43
53:3:680:C:H2'	53:3:681:A:H8	1.84	0.43
53:3:959:A:O2'	53:3:984:C:O2'	2.25	0.43
58:B1:107:LEU:HA	58:B1:276:ASN:ND2	2.33	0.43
58:B1:139:LEU:HD23	58:B1:139:LEU:HA	1.89	0.43
58:B1:434:ILE:HD11	59:B2:1274:GLU:HG3	1.99	0.43
58:B1:513:MET:HG3	58:B1:544:LEU:HD11	2.01	0.43
58:B1:804:ALA:HB2	58:B1:1256:ILE:CD1	2.47	0.43
58:B1:1079:LYS:HD3	58:B1:1098:GLN:HB3	2.00	0.43
59:B2:1157:GLN:HG3	59:B2:1159:VAL:HG13	2.00	0.43
59:B2:1275:VAL:HG13	59:B2:1287:LEU:HD11	2.01	0.43
60:W0:58:LEU:HD12	60:W0:59:ILE:HG12	2.00	0.43
17:Q:31:GLY:HA2	17:Q:56:LEU:HA	2.01	0.43
25:Y:14:GLU:OE1	25:Y:17:ARG:NH2	2.52	0.43
29:d:188:MET:HB2	29:d:192:ALA:HB3	1.99	0.43
30:e:171:ALA:C	30:e:173:ASP:H	2.26	0.43
34:j:47:HIS:CG	51:1:536:G:N2	2.87	0.43
34:j:109:LEU:HD23	34:j:109:LEU:HA	1.85	0.43
51:1:541:A:H2'	51:1:542:C:O4'	2.19	0.43
51:1:595:C:H2'	51:1:596:U:C6	2.54	0.43
51:1:918:A:H2'	51:1:919:U:O4'	2.19	0.43
51:1:1092:C:H2'	51:1:1093:G:O4'	2.18	0.43
51:1:1306:C:N4	51:1:1606:C:H2'	2.34	0.43
51:1:2106:U:H2'	51:1:2107:G:O4'	2.18	0.43
51:1:2462:C:H2'	51:1:2463:C:C6	2.54	0.43
51:1:2736:A:O2'	51:1:2737:G:H5'	2.19	0.43
58:B1:434:ILE:HD11	59:B2:1274:GLU:CG	2.49	0.43
59:B2:903:ARG:HA	59:B2:907:GLY:CA	2.44	0.43
9:I:53:GLN:HA	9:I:198:LEU:HD12	2.01	0.43
18:R:16:ILE:O	18:R:19:THR:OG1	2.26	0.43
33:i:91:LYS:HB2	33:i:91:LYS:HE3	1.72	0.43
34:j:51:GLY:HA3	34:j:121:LYS:HE2	2.00	0.43
42:r:62:GLU:HG3	42:r:97:LYS:HB3	2.01	0.43
51:1:467:G:O2'	51:1:468:G:H5'	2.19	0.43
51:1:572:A:O5'	51:1:572:A:C8	2.72	0.43
51:1:1487:U:H2'	51:1:1488:C:C6	2.54	0.43
51:1:2305:U:O2'	51:1:2306:C:H5'	2.19	0.43
51:1:2562:U:C2'	51:1:2563:U:H5'	2.49	0.43
51:1:2834:G:C2'	51:1:2835:A:H5'	2.49	0.43
51:1:2870:C:H2'	51:1:2871:U:H5'	2.01	0.43
53:3:987:G:H2'	53:3:988:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1348:U:H2'	53:3:1349:A:H8	1.84	0.43
53:3:1492:A:H1'	54:4:5:U:O2'	2.18	0.43
58:B1:242:LEU:C	58:B1:242:LEU:HD23	2.44	0.43
58:B1:245:LEU:CG	58:B1:246:PRO:HD2	2.48	0.43
58:B1:282:LEU:HA	58:B1:282:LEU:HD12	1.79	0.43
58:B1:568:SER:HB3	58:B1:570:LYS:NZ	2.34	0.43
8:H:61:LYS:HE2	8:H:96:VAL:HG12	2.01	0.43
23:W:47:ARG:HD3	23:W:47:ARG:HA	1.80	0.43
29:d:47:LYS:HE2	51:1:451:U:H4'	2.00	0.43
36:l:69:ARG:CZ	51:1:2406:A:N3	2.82	0.43
51:1:528:A:C2	51:1:2043:C:H4'	2.53	0.43
51:1:648:G:H2'	51:1:649:G:H8	1.83	0.43
51:1:2216:G:H2'	51:1:2217:G:C8	2.54	0.43
51:1:2371:G:O2'	51:1:2372:U:H5'	2.19	0.43
51:1:2584:U:O5'	51:1:2584:U:H6	2.02	0.43
58:B1:222:LYS:HA	58:B1:222:LYS:HD2	1.33	0.43
58:B1:820:ILE:HG12	58:B1:884:SER:HB2	2.01	0.43
58:B1:824:PRO:HD3	58:B1:835:LEU:HD12	2.00	0.43
58:B1:1108:GLN:HG3	58:B1:1109:LEU:HD12	2.00	0.43
59:B2:300:ASP:OD1	59:B2:313:ALA:N	2.51	0.43
9:I:152:SER:HB3	53:3:436:C:H4'	2.00	0.42
14:N:30:ASN:HD21	14:N:66:VAL:H	1.66	0.42
33:i:106:GLN:OE1	33:i:125:THR:OG1	2.31	0.42
51:1:870:U:H2'	51:1:871:U:C5'	2.48	0.42
51:1:2092:U:H5	51:1:2199:A:C2	2.30	0.42
51:1:2701:U:H3'	51:1:2702:G:H5''	2.01	0.42
53:3:460:A:H2'	53:3:461:A:C8	2.54	0.42
58:B1:24:LEU:HD21	58:B1:116:PHE:CE2	2.54	0.42
58:B1:243:PRO:HG2	59:B2:1332:SER:C	2.44	0.42
58:B1:244:VAL:HA	58:B1:269:TYR:OH	2.19	0.42
59:B2:444:ASP:OD1	59:B2:444:ASP:N	2.51	0.42
59:B2:1313:HIS:CD2	60:W0:31:GLN:HE22	2.37	0.42
9:I:101:VAL:HG22	9:I:106:PHE:HB2	2.01	0.42
18:R:87:GLY:O	18:R:91:ARG:N	2.52	0.42
21:U:4:ILE:HG12	21:U:21:VAL:HG22	2.00	0.42
27:b:206:LYS:HB2	51:1:729:G:C5	2.54	0.42
27:b:244:VAL:HG12	27:b:250:GLN:HA	2.01	0.42
29:d:127:GLU:O	29:d:156:ASN:ND2	2.51	0.42
33:i:123:ALA:HB1	51:1:1081:U:H4'	2.00	0.42
33:i:127:SER:OG	51:1:1059:G:N2	2.51	0.42
51:1:783:A:C8	51:1:783:A:H3'	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1601:G:H2'	51:1:1602:U:H5'	2.01	0.42
51:1:2102:G:H1	51:1:2187:U:H3	1.66	0.42
53:3:1209:C:O2'	53:3:1214:C:N4	2.52	0.42
53:3:1238:A:OP1	53:3:1335:U:O2'	2.35	0.42
55:8:15:DC:H5'	59:B2:1269:ARG:HD3	2.01	0.42
56:9:12:DC:H3'	58:B1:47:ARG:HH12	1.84	0.42
57:A1:76:GLU:HB3	57:A1:80:GLU:HB3	2.01	0.42
58:B1:58:CYS:SG	58:B1:60:ARG:HG2	2.59	0.42
58:B1:59:ALA:HB1	58:B1:90:VAL:HG23	2.01	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:B1:506:VAL:H	58:B1:506:VAL:HG12	1.59	0.42
58:B1:1350:ASN:HA	58:B1:1353:VAL:HG12	2.01	0.42
59:B2:590:PRO:HB2	59:B2:655:VAL:HG21	2.01	0.42
59:B2:805:MET:HE3	59:B2:805:MET:HB2	1.86	0.42
63:5:17:C:H6	63:5:17:C:H2'	1.69	0.42
14:N:113:LYS:HA	14:N:120:ALA:HB2	2.01	0.42
18:R:11:HIS:HA	18:R:43:LYS:HD2	2.01	0.42
24:X:51:HIS:HB2	24:X:56:HIS:CE1	2.55	0.42
27:b:7:PRO:HB3	27:b:13:ARG:HG3	2.00	0.42
49:y:30:MET:HE3	49:y:30:MET:HB3	1.83	0.42
51:1:128:C:H2'	51:1:129:C:C6	2.53	0.42
51:1:712:G:C2'	51:1:713:G:H5'	2.49	0.42
51:1:871:U:H2'	51:1:872:U:C6	2.54	0.42
51:1:908:C:O2'	51:1:909:A:H5'	2.19	0.42
51:1:1230:A:H2'	51:1:1231:U:O4'	2.19	0.42
51:1:1327:A:H2'	51:1:1328:A:H5'	2.01	0.42
51:1:2098:U:C2'	51:1:2099:U:H5'	2.49	0.42
51:1:2144:G:H1'	51:1:2147:A:N6	2.33	0.42
9:I:119:HIS:O	9:I:145:ARG:NH2	2.52	0.42
29:d:106:LYS:HG3	29:d:200:LEU:HD13	2.01	0.42
35:k:17:ARG:HD3	35:k:47:ILE:HD11	2.02	0.42
38:n:28:LEU:O	38:n:32:GLU:N	2.38	0.42
49:y:11:VAL:HA	49:y:14:LEU:HB2	2.00	0.42
51:1:8:C:C2	51:1:9:G:C8	3.07	0.42
51:1:281:C:H2'	51:1:282:A:C8	2.54	0.42
51:1:481:G:H2'	51:1:482:A:OP2	2.18	0.42
51:1:2073:C:C2'	51:1:2074:U:H5'	2.49	0.42
51:1:2812:G:O2'	51:1:2813:A:H5'	2.19	0.42
53:3:1243:C:H2'	53:3:1244:G:H8	1.85	0.42
55:8:3:DC:N1	55:8:4:DT:H72	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:388:ARG:HG2	58:B1:388:ARG:HH11	1.84	0.42
58:B1:616:PRO:HA	58:B1:619:ILE:HG22	2.02	0.42
62:NG:135:ARG:O	62:NG:178:VAL:CA	2.68	0.42
64:7:11:A:H2'	64:7:12:G:C8	2.51	0.42
6:F:8:LYS:NZ	51:1:2467:C:OP1	2.37	0.42
7:G:162:VAL:N	7:G:183:PHE:O	2.38	0.42
8:H:106:ARG:HG2	8:H:107:LYS:HG3	2.01	0.42
10:J:146:MET:HE2	10:J:146:MET:HB3	1.76	0.42
18:R:91:ARG:HD2	51:1:888:C:OP1	2.18	0.42
31:f:84:LYS:HD2	31:f:84:LYS:HA	1.87	0.42
34:j:13:ARG:NH1	34:j:49:ASP:O	2.41	0.42
42:r:24:LYS:HE2	42:r:24:LYS:HB3	1.89	0.42
51:1:90:U:H2'	51:1:91:A:C8	2.55	0.42
51:1:94:A:H2'	51:1:95:A:C8	2.54	0.42
51:1:532:A:H2'	51:1:532:A:N3	2.34	0.42
51:1:644:A:C3'	51:1:645:C:H5''	2.49	0.42
51:1:809:G:C6	51:1:810:U:C4	3.08	0.42
51:1:955:U:H2'	51:1:956:G:H5'	2.02	0.42
51:1:1020:A:O5'	51:1:1020:A:H8	2.02	0.42
51:1:1381:G:C2'	51:1:1382:G:H5'	2.49	0.42
51:1:2628:C:H3'	51:1:2629:U:H5'	2.01	0.42
51:1:2852:G:H2'	51:1:2853:C:O4'	2.20	0.42
53:3:322:C:O2	53:3:332:G:N2	2.52	0.42
53:3:1531:A:C2'	53:3:1532:U:H5'	2.50	0.42
59:B2:478:ARG:HD2	59:B2:492:MET:HA	2.02	0.42
31:f:151:ARG:HD3	31:f:151:ARG:HA	1.88	0.42
50:z:38:GLU:CD	51:1:928:A:H5'	2.43	0.42
51:1:12:U:O2	51:1:12:U:H2'	2.18	0.42
51:1:115:C:O2'	51:1:116:C:H5'	2.19	0.42
51:1:431:U:O5'	51:1:431:U:H6	2.03	0.42
51:1:510:C:OP1	51:1:510:C:H3'	2.20	0.42
51:1:892:A:O2'	51:1:893:C:H5'	2.19	0.42
51:1:1246:A:H2'	51:1:1247:A:O4'	2.19	0.42
51:1:1433:A:H2'	51:1:1434:A:C1'	2.49	0.42
51:1:1488:C:H2'	51:1:1489:C:H6	1.84	0.42
51:1:1901:A:C2	51:1:1902:C:C5	3.08	0.42
51:1:1914:C:O2	51:1:1914:C:O4'	2.37	0.42
51:1:2024:G:H2'	51:1:2025:C:C6	2.54	0.42
64:6:69:C:H2'	64:6:70:G:H8	1.83	0.42
7:G:173:LYS:HE3	7:G:173:LYS:HB2	1.76	0.42
33:i:25:PRO:HG3	51:1:1095:A:N1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:l:108:ALA:HB3	36:l:125:LEU:HG	2.01	0.42
37:m:69:PRO:HA	37:m:94:ALA:HB2	2.01	0.42
43:s:87:PRO:HG3	51:1:1615:C:C6	2.54	0.42
51:1:422:A:H2'	51:1:423:A:O4'	2.20	0.42
51:1:535:G:O2'	51:1:536:G:H5'	2.19	0.42
51:1:623:C:H2'	51:1:624:C:H6	1.85	0.42
51:1:1049:C:H2'	51:1:1050:A:H5'	1.99	0.42
51:1:1197:G:C2'	51:1:1198:U:H5'	2.50	0.42
51:1:1204:A:H4'	51:1:1205:A:H5''	2.02	0.42
51:1:1520:U:C2'	51:1:1521:G:H5'	2.49	0.42
51:1:1642:G:H2'	51:1:1643:G:O4'	2.20	0.42
51:1:1739:A:H2'	51:1:1740:G:O4'	2.18	0.42
51:1:1886:U:O2'	51:1:1887:C:H5'	2.20	0.42
51:1:1907:G:C5	51:1:1908:C:C4	3.07	0.42
51:1:1931:U:C5	51:1:1968:G:N2	2.88	0.42
51:1:2091:C:H5	51:1:2092:U:O2'	2.02	0.42
51:1:2482:A:H2'	51:1:2483:C:C6	2.54	0.42
51:1:2741:A:H2'	51:1:2742:G:C5'	2.50	0.42
53:3:1513:A:H2'	53:3:1514:G:C8	2.55	0.42
54:4:55:G:H5'	59:B2:688:GLN:HE22	1.85	0.42
58:B1:137:ARG:HA	58:B1:142:GLU:HG2	2.02	0.42
58:B1:141:PHE:CD2	58:B1:297:ARG:HB2	2.54	0.42
58:B1:1064:SER:OG	58:B1:1168:GLU:OE1	2.31	0.42
58:B1:1289:ASN:O	58:B1:1293:GLU:HB2	2.20	0.42
59:B2:125:GLY:H	59:B2:495:ALA:HB1	1.84	0.42
59:B2:741:MET:HE3	59:B2:974:ARG:HH12	1.85	0.42
59:B2:998:LEU:HD21	59:B2:1015:ALA:HB2	2.02	0.42
16:P:126:ARG:O	53:3:796:C:H5''	2.19	0.42
18:R:89:ARG:HB2	18:R:96:VAL:HG22	2.01	0.42
24:X:27:LYS:HB3	24:X:27:LYS:HE2	1.77	0.42
24:X:36:ARG:HB3	53:3:1320:C:N4	2.35	0.42
28:c:90:PHE:HD1	28:c:94:GLN:HG2	1.83	0.42
38:n:16:HIS:CD2	51:1:1275:A:C2	3.07	0.42
51:1:4:U:O2'	51:1:5:A:H5'	2.20	0.42
51:1:758:C:H2'	51:1:759:G:H8	1.84	0.42
51:1:1314:C:H42	51:1:1338:G:H1	1.68	0.42
58:B1:279:LEU:HD13	58:B1:299:LEU:HD13	2.02	0.42
58:B1:385:LEU:CD2	58:B1:390:LEU:HB2	2.50	0.42
58:B1:394:ILE:O	58:B1:394:ILE:HG13	2.19	0.42
58:B1:797:THR:HG22	58:B1:924:GLY:HA3	2.01	0.42
59:B2:800:MET:HE3	59:B2:800:MET:HB2	1.69	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:124:LYS:H	16:P:124:LYS:HG3	1.58	0.42
29:d:53:THR:HB	51:1:452:G:H8	1.85	0.42
47:w:14:ALA:HB1	51:1:2271:G:OP1	2.19	0.42
51:1:56:A:H1'	51:1:127:A:C2	2.55	0.42
51:1:191:A:C2	51:1:192:C:C4	3.08	0.42
51:1:196:A:N3	51:1:196:A:H2'	2.35	0.42
51:1:256:A:C2'	51:1:257:C:H5'	2.50	0.42
51:1:1034:G:C6	51:1:1035:U:N3	2.88	0.42
51:1:1213:A:C1'	51:1:1237:A:C2	3.03	0.42
51:1:1316:U:O2'	51:1:1317:G:H5'	2.20	0.42
51:1:1343:G:N3	51:1:1343:G:H2'	2.35	0.42
51:1:1589:U:H2'	51:1:1590:A:C8	2.55	0.42
51:1:1710:G:H2'	51:1:1711:A:H8	1.85	0.42
51:1:2287:A:C4	51:1:2289:G:N7	2.87	0.42
51:1:2741:A:N6	51:1:2742:G:C2	2.88	0.42
51:1:2848:G:C2	51:1:2867:G:C4	3.08	0.42
53:3:297:G:N2	53:3:300:A:OP2	2.39	0.42
59:B2:524:ILE:HD12	59:B2:712:SER:HB2	2.02	0.42
59:B2:829:THR:HG23	59:B2:1059:ARG:HG2	2.00	0.42
8:H:5:HIS:HA	8:H:6:PRO:HD3	1.94	0.42
13:M:42:GLU:HG2	13:M:100:ILE:HG21	2.02	0.42
17:Q:29:LYS:HA	17:Q:29:LYS:HD3	1.65	0.42
18:R:7:ASN:CG	18:R:9:PRO:HD2	2.45	0.42
39:o:16:ARG:HD3	39:o:16:ARG:HA	1.84	0.42
51:1:466:A:C2'	51:1:467:G:H5'	2.46	0.42
51:1:552:U:O2'	51:1:553:G:H5'	2.20	0.42
51:1:598:U:H2'	51:1:599:A:C8	2.54	0.42
51:1:1500:G:H2'	51:1:1501:G:H8	1.83	0.42
51:1:1600:C:H2'	51:1:1601:G:C8	2.55	0.42
51:1:1964:G:H4'	51:1:1965:C:OP2	2.19	0.42
51:1:2292:U:H2'	51:1:2293:G:C8	2.55	0.42
51:1:2389:G:H5''	51:1:2390:U:H5'	2.01	0.42
51:1:2583:G:H8	51:1:2583:G:O5'	2.03	0.42
53:3:73:C:H2'	53:3:74:A:C8	2.55	0.42
53:3:440:C:H2'	53:3:441:A:H8	1.85	0.42
53:3:944:G:N1	53:3:1338:G:OP2	2.34	0.42
58:B1:220:ARG:NH1	58:B1:220:ARG:CG	2.82	0.42
58:B1:647:PRO:HG3	58:B1:697:MET:HB3	2.01	0.42
8:H:1:GLY:HA2	53:3:1060:U:C5	2.54	0.41
11:K:40:GLU:HB3	11:K:61:LEU:HB3	2.02	0.41
22:V:7:LEU:N	22:V:59:GLU:OE2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:c:128:ARG:HE	28:c:128:ARG:HB2	1.63	0.41
32:g:11:ASN:ND2	51:1:2095:A:OP1	2.53	0.41
40:p:63:ILE:HA	40:p:68:GLY:HA2	2.01	0.41
43:s:9:HIS:H	43:s:102:HIS:CE1	2.38	0.41
43:s:70:LYS:N	43:s:108:SER:O	2.45	0.41
50:z:57:GLU:OE1	50:z:57:GLU:N	2.53	0.41
51:1:170:U:H2'	51:1:171:U:C6	2.55	0.41
51:1:397:U:O5'	51:1:397:U:H6	2.03	0.41
51:1:673:C:O2'	51:1:674:G:H5'	2.19	0.41
51:1:903:C:H2'	51:1:904:G:H8	1.86	0.41
51:1:1176:U:H2'	51:1:1177:G:N9	2.35	0.41
51:1:1335:C:H2'	51:1:1336:A:H8	1.84	0.41
51:1:1336:A:H2'	51:1:1337:G:H8	1.84	0.41
51:1:2193:G:H2'	51:1:2194:U:H6	1.83	0.41
51:1:2612:C:O5'	51:1:2612:C:H6	2.04	0.41
51:1:2697:G:C2	51:1:2711:A:C2	3.08	0.41
53:3:75:G:H1	53:3:95:C:H42	1.67	0.41
53:3:1005:A:OP2	53:3:1024:G:N2	2.48	0.41
53:3:1124:G:H1	53:3:1149:C:H42	1.68	0.41
55:8:14:DC:C2	55:8:15:DC:C5	3.08	0.41
58:B1:144:TYR:CE1	58:B1:162:GLU:OE1	2.73	0.41
58:B1:515:ARG:HG2	58:B1:516:ASP:H	1.85	0.41
58:B1:559:ALA:HB3	58:B1:562:GLU:HB3	2.01	0.41
58:B1:609:TYR:HD2	58:B1:610:ARG:NH1	2.17	0.41
59:B2:741:MET:SD	59:B2:974:ARG:NH2	2.93	0.41
63:5:20:U:H6	63:5:20:U:H2'	1.72	0.41
7:G:190:SER:OG	7:G:191:ASP:N	2.54	0.41
15:O:12:ALA:HB2	15:O:96:VAL:HG13	2.03	0.41
15:O:46:LYS:HE3	15:O:46:LYS:HB2	1.88	0.41
26:Z:39:LYS:HA	26:Z:42:THR:HB	2.02	0.41
38:n:114:GLU:OE1	38:n:118:ARG:NH1	2.50	0.41
41:q:23:TYR:HB3	41:q:27:ARG:HB2	2.02	0.41
41:q:54:ARG:HD3	51:1:1155:A:H5''	2.01	0.41
44:t:40:LYS:HE3	44:t:60:THR:HG22	2.01	0.41
46:v:14:LYS:HB2	52:2:98:G:H1	1.84	0.41
46:v:58:SER:OG	46:v:59:GLU:OE1	2.36	0.41
51:1:49:A:P	51:1:51:G:H5'	2.60	0.41
51:1:837:C:O5'	51:1:837:C:H6	2.02	0.41
51:1:1812:U:H5''	51:1:1812:U:H6	1.85	0.41
51:1:2411:A:O2'	51:1:2412:A:H5'	2.20	0.41
53:3:497:G:H2'	53:3:498:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1228:C:H2'	53:3:1229:A:C8	2.55	0.41
58:B1:586:GLY:HA3	58:B1:612:LEU:HD11	2.01	0.41
59:B2:22:LEU:HB3	59:B2:655:VAL:HG11	2.01	0.41
59:B2:133:ASN:O	59:B2:527:LYS:NZ	2.42	0.41
59:B2:310:ILE:HG21	59:B2:325:LEU:HB3	2.03	0.41
63:5:4:C:H2'	63:5:5:G:C8	2.55	0.41
8:H:19:SER:HB2	8:H:39:ARG:HH21	1.85	0.41
23:W:23:LYS:HE2	23:W:23:LYS:HB2	1.82	0.41
23:W:24:ASP:OD1	23:W:24:ASP:N	2.53	0.41
27:b:70:LYS:HD2	27:b:73:ILE:HD12	2.02	0.41
27:b:209:ALA:HA	27:b:212:TRP:CE2	2.55	0.41
29:d:145:ASP:HA	29:d:166:LYS:HB3	2.02	0.41
35:k:7:MET:HE2	35:k:18:ARG:HD3	2.01	0.41
51:1:127:A:H5''	51:1:128:C:O4'	2.21	0.41
51:1:191:A:H2'	51:1:192:C:C6	2.56	0.41
51:1:197:A:H2	51:1:2434:A:H62	1.69	0.41
51:1:439:A:H2'	51:1:440:C:O4'	2.19	0.41
51:1:518:G:H2'	51:1:519:U:C6	2.55	0.41
51:1:722:A:H2'	51:1:723:C:C6	2.56	0.41
51:1:1070:A:H5'	51:1:1072:C:OP1	2.20	0.41
51:1:1107:G:H2'	51:1:1108:U:O4'	2.20	0.41
51:1:2160:C:H2'	51:1:2161:C:O4'	2.20	0.41
51:1:2248:C:C2'	51:1:2249:U:H5'	2.49	0.41
51:1:2743:U:H2'	51:1:2744:G:C4'	2.50	0.41
53:3:842:U:H5''	53:3:846:G:C6	2.55	0.41
58:B1:282:LEU:CA	58:B1:286:ALA:HA	2.45	0.41
58:B1:352:ARG:CD	59:B2:1268:GLN:NE2	2.67	0.41
58:B1:848:VAL:HB	58:B1:858:VAL:HG22	2.02	0.41
58:B1:950:ILE:HB	58:B1:1018:ALA:HB3	2.01	0.41
58:B1:1177:ILE:HD12	58:B1:1186:TYR:HE2	1.85	0.41
59:B2:469:VAL:HA	59:B2:472:GLU:HG2	2.01	0.41
59:B2:699:LEU:HG	59:B2:799:ASN:HD22	1.85	0.41
18:R:32:ILE:HG23	18:R:58:GLU:HB3	2.02	0.41
21:U:68:SER:OG	21:U:69:ASP:N	2.53	0.41
22:V:11:VAL:HG23	22:V:55:GLY:H	1.85	0.41
29:d:49:ARG:NH2	51:1:673:C:OP1	2.48	0.41
30:e:124:ARG:NH2	51:1:2315:G:N3	2.68	0.41
51:1:573:U:O2'	51:1:574:A:H3'	2.20	0.41
51:1:724:U:H2'	51:1:725:G:C8	2.55	0.41
51:1:1727:C:O2'	51:1:1728:C:H5'	2.20	0.41
51:1:2224:G:H4'	51:1:2226:C:N3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2335:A:N7	51:1:2337:G:C5	2.88	0.41
51:1:2379:G:H2'	51:1:2380:C:C6	2.56	0.41
58:B1:144:TYR:CD1	58:B1:144:TYR:N	2.88	0.41
58:B1:1050:THR:HG23	58:B1:1057:SER:HB3	2.03	0.41
59:B2:487:LEU:HA	59:B2:487:LEU:HD22	1.77	0.41
7:G:17:HIS:C	7:G:19:THR:H	2.28	0.41
12:L:68:VAL:HG23	12:L:99:ALA:HB1	2.02	0.41
24:X:13:HIS:O	24:X:17:LYS:N	2.49	0.41
31:f:157:LYS:HD3	51:1:2658:C:H5''	2.02	0.41
33:i:77:VAL:HA	33:i:80:LYS:HE2	2.02	0.41
42:r:81:LYS:NZ	51:1:568:U:O4	2.54	0.41
44:t:68:LYS:HD3	44:t:68:LYS:HA	1.83	0.41
51:1:137:U:H3	51:1:142:A:H61	1.68	0.41
51:1:1020:A:H5'	51:1:1021:A:N7	2.35	0.41
51:1:1024:G:H21	51:1:1144:A:C4'	2.33	0.41
51:1:1410:G:H2'	51:1:1411:U:H6	1.85	0.41
51:1:1416:G:H2'	51:1:1417:C:H6	1.82	0.41
51:1:1719:G:O2'	51:1:1720:U:H5'	2.20	0.41
51:1:1721:G:H1'	51:1:1739:A:N6	2.35	0.41
51:1:1917:U:H2'	51:1:1918:A:H5'	2.01	0.41
51:1:2600:A:H8	51:1:2600:A:O5'	2.03	0.41
58:B1:68:TYR:O	58:B1:75:TYR:CD2	2.70	0.41
58:B1:109:SER:CB	58:B1:296:LYS:HG2	2.51	0.41
62:NG:175:PHE:O	62:NG:178:VAL:O	2.38	0.41
8:H:156:LEU:H	8:H:156:LEU:HG	1.65	0.41
20:T:66:LEU:HB3	20:T:77:TYR:HE1	1.84	0.41
27:b:131:MET:H	27:b:131:MET:HG2	1.57	0.41
50:z:31:ILE:HD11	51:1:989:G:P	2.61	0.41
51:1:543:G:C3'	51:1:544:C:H5''	2.51	0.41
51:1:630:G:N2	51:1:634:C:C4	2.88	0.41
51:1:849:A:H2'	51:1:850:U:C5	2.54	0.41
51:1:1045:C:H1'	51:1:1047:G:C2	2.56	0.41
51:1:1418:G:H1'	51:1:1581:G:N2	2.36	0.41
51:1:1591:A:H2'	51:1:1592:C:C6	2.56	0.41
51:1:1767:G:N2	51:1:1986:C:C2	2.89	0.41
53:3:146:G:H2'	53:3:147:G:C8	2.56	0.41
53:3:373:A:N1	53:3:391:G:O2'	2.49	0.41
57:A1:205:MET:HE1	57:A1:217:ILE:HG13	2.03	0.41
58:B1:161:THR:CG2	58:B1:164:GLN:HB2	2.49	0.41
58:B1:820:ILE:HD11	58:B1:822:MET:HE2	2.02	0.41
59:B2:854:ILE:HG21	59:B2:917:SER:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:NG:117:GLN:O	62:NG:118:VAL:C	2.63	0.41
8:H:110:LEU:HD21	8:H:143:LEU:HB3	2.02	0.41
8:H:178:ARG:NH1	53:3:1112:C:O2'	2.54	0.41
15:O:89:ARG:NH2	62:NG:165:PHE:H	2.18	0.41
17:Q:98:ARG:HA	17:Q:103:CYS:HB2	2.02	0.41
27:b:36:ASN:OD1	27:b:36:ASN:N	2.54	0.41
28:c:4:LEU:HD21	28:c:98:VAL:HA	2.03	0.41
31:f:128:THR:OG1	31:f:129:GLU:OE2	2.35	0.41
33:i:100:ILE:HB	33:i:139:VAL:HG12	2.03	0.41
41:q:57:ARG:NH1	51:1:1154:G:OP2	2.52	0.41
45:u:4:ILE:HD13	45:u:69:VAL:HG23	2.03	0.41
51:1:191:A:C6	51:1:192:C:N4	2.88	0.41
51:1:211:C:O2'	51:1:212:G:H5'	2.21	0.41
51:1:638:G:H2'	51:1:639:U:C6	2.55	0.41
51:1:724:U:H2'	51:1:725:G:O4'	2.21	0.41
51:1:1063:G:N2	51:1:1075:C:H41	2.18	0.41
51:1:1160:G:C6	51:1:1161:C:C4	3.09	0.41
51:1:1452:G:C2'	51:1:1453:A:OP2	2.68	0.41
51:1:1782:U:C2'	51:1:1783:A:H5''	2.51	0.41
51:1:2467:C:N4	51:1:2468:A:C6	2.89	0.41
51:1:2757:A:H2'	51:1:2758:A:H5''	2.03	0.41
52:2:65:U:H3'	52:2:108:A:N6	2.30	0.41
53:3:202:G:H2'	53:3:203:G:C8	2.55	0.41
58:B1:71:LEU:HB2	58:B1:90:VAL:HG11	2.03	0.41
58:B1:839:VAL:HG12	58:B1:864:LEU:HD12	2.02	0.41
59:B2:861:ALA:HB1	59:B2:882:ILE:HD13	2.02	0.41
2:B:43:THR:HG1	2:B:47:TYR:N	2.19	0.41
6:F:30:GLU:HA	6:F:31:PRO:HD3	1.91	0.41
12:L:125:ASP:HB2	12:L:130:LYS:HG3	2.02	0.41
16:P:30:ILE:HG23	16:P:45:THR:HB	2.02	0.41
30:e:36:ASN:HB3	30:e:152:ASP:HB3	2.03	0.41
31:f:21:GLN:NE2	31:f:37:ASN:O	2.54	0.41
33:i:41:PHE:O	33:i:45:THR:N	2.54	0.41
33:i:78:LEU:HA	33:i:81:LYS:HB3	2.02	0.41
39:o:24:THR:HB	39:o:42:PRO:HG3	2.03	0.41
51:1:706:A:H2'	51:1:707:G:C5'	2.51	0.41
51:1:724:U:C4	51:1:725:G:C6	3.08	0.41
51:1:940:G:H2'	51:1:941:A:C4'	2.51	0.41
51:1:1077:A:H3'	51:1:1078:U:H4'	2.02	0.41
51:1:1092:C:O2'	51:1:1093:G:H5'	2.21	0.41
51:1:1150:C:C2	51:1:1151:A:C8	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1239:G:H2'	51:1:1240:U:O4'	2.21	0.41
51:1:1334:G:C6	51:1:1335:C:C4	3.09	0.41
51:1:1412:U:H2'	51:1:1413:A:C8	2.56	0.41
51:1:1482:G:H2'	51:1:1483:G:H8	1.85	0.41
51:1:1614:A:C8	51:1:1614:A:O5'	2.73	0.41
51:1:2895:G:H2'	51:1:2896:C:H6	1.85	0.41
53:3:370:C:H2'	53:3:371:A:H8	1.86	0.41
58:B1:390:LEU:H	58:B1:390:LEU:HD13	1.85	0.41
58:B1:1361:THR:OG1	59:B2:1282:GLY:O	2.28	0.41
9:I:10:LEU:HG	9:I:62:ARG:HD2	2.03	0.41
9:I:24:VAL:HG22	53:3:409:U:H4'	2.02	0.41
9:I:87:GLU:N	9:I:87:GLU:OE2	2.53	0.41
14:N:22:PRO:HA	14:N:60:LEU:HA	2.03	0.41
15:O:57:VAL:HG22	15:O:58:ASN:H	1.85	0.41
26:Z:9:GLU:HB3	26:Z:10:PRO:HD3	2.03	0.41
26:Z:15:LEU:HD23	26:Z:15:LEU:HA	1.80	0.41
27:b:57:HIS:ND1	51:1:1567:G:H5'	2.35	0.41
28:c:169:ARG:O	51:1:2773:C:H4'	2.21	0.41
30:e:39:VAL:HG12	30:e:85:GLY:HA2	2.03	0.41
34:j:17:VAL:HG13	34:j:137:PRO:HB2	2.03	0.41
34:j:138:GLN:H	34:j:138:GLN:HG2	1.63	0.41
35:k:34:GLY:N	35:k:37:ASP:OD2	2.41	0.41
37:m:123:LYS:HE2	51:1:2467:C:O2	2.20	0.41
42:r:48:LYS:HD2	42:r:48:LYS:HA	1.78	0.41
45:u:6:ARG:N	51:1:85:G:OP1	2.52	0.41
51:1:79:C:O2	51:1:346:A:H2	2.03	0.41
51:1:426:C:O2'	51:1:427:U:H5'	2.21	0.41
51:1:490:C:O2'	51:1:491:G:P	2.79	0.41
51:1:511:U:H2'	51:1:512:G:H5'	2.03	0.41
51:1:518:G:C2	51:1:519:U:C2	3.08	0.41
51:1:859:G:HO2'	51:1:860:U:P	2.43	0.41
51:1:1048:A:C2'	51:1:1049:C:H5'	2.49	0.41
51:1:1107:G:H2'	51:1:1108:U:C6	2.56	0.41
51:1:1279:G:H2'	51:1:1280:G:C8	2.56	0.41
51:1:1283:G:H22	51:1:1286:A:P	2.44	0.41
51:1:1333:G:C2'	51:1:1334:G:H5'	2.51	0.41
51:1:1467:U:C4	51:1:1468:U:C4	3.08	0.41
51:1:1594:U:O2'	51:1:1595:C:H5'	2.20	0.41
51:1:1750:G:H2'	51:1:1751:U:C6	2.56	0.41
51:1:1930:G:O2'	51:1:1931:U:P	2.79	0.41
51:1:1955:U:H5	51:1:2557:G:N2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1991:U:H2'	51:1:1992:G:H5'	2.02	0.41
51:1:2293:G:O2'	51:1:2294:G:H5'	2.21	0.41
51:1:2393:U:C2'	51:1:2394:C:H5'	2.51	0.41
51:1:2437:G:O4'	51:1:2598:A:C2	2.73	0.41
51:1:2646:C:H2'	51:1:2647:U:O4'	2.21	0.41
51:1:2660:A:H2'	51:1:2661:G:C8	2.56	0.41
57:A1:44:ARG:HA	57:A1:183:ILE:HD12	2.03	0.41
58:B1:224:LEU:HD23	58:B1:224:LEU:HA	1.89	0.41
58:B1:390:LEU:N	58:B1:390:LEU:HD13	2.35	0.41
58:B1:777:HIS:CD2	59:B2:550:VAL:HG13	2.56	0.41
58:B1:923:ILE:O	58:B1:1241:TYR:OH	2.32	0.41
59:B2:213:LEU:HD13	59:B2:422:LYS:HG2	2.03	0.41
59:B2:616:ILE:HG13	59:B2:652:TYR:HB2	2.01	0.41
59:B2:678:ARG:HD3	59:B2:678:ARG:HA	1.83	0.41
63:5:9:A:H1'	63:5:45:U:H2'	2.01	0.41
7:G:18:GLN:HB3	7:G:21:TYR:HB2	2.03	0.41
7:G:161:PHE:HA	7:G:183:PHE:HB2	2.02	0.41
10:J:156:ARG:HE	13:M:42:GLU:HG3	1.86	0.41
18:R:10:ASP:HB3	18:R:45:SER:HB3	2.03	0.41
30:e:64:PRO:HA	30:e:88:VAL:HG22	2.03	0.41
51:1:244:A:H2'	51:1:245:G:O4'	2.20	0.41
51:1:759:G:H2'	51:1:760:G:H8	1.83	0.41
51:1:1042:G:H2'	51:1:1043:C:H6	1.85	0.41
51:1:1328:A:H2'	51:1:1330:C:C4	2.56	0.41
51:1:1505:A:O2'	51:1:1506:U:H5'	2.19	0.41
51:1:1722:A:H2'	51:1:1723:G:O4'	2.21	0.41
51:1:1868:C:H2'	51:1:1869:G:H8	1.86	0.41
51:1:1936:A:N6	51:1:1963:U:H3	2.18	0.41
51:1:2061:G:H2'	51:1:2501:C:O2'	2.21	0.41
51:1:2098:U:H2'	51:1:2099:U:C5'	2.51	0.41
51:1:2105:U:C2	51:1:2184:A:H2	2.39	0.41
51:1:2210:U:H6	51:1:2210:U:OP1	2.04	0.41
51:1:2575:C:H2'	51:1:2578:G:O6	2.21	0.41
53:3:685:G:N1	53:3:704:A:OP2	2.52	0.41
59:B2:909:LYS:HD3	59:B2:909:LYS:HA	1.58	0.41
59:B2:936:ARG:HB2	59:B2:1042:LEU:HD12	2.03	0.41
59:B2:1069:ARG:NH2	59:B2:1114:GLU:OE2	2.44	0.41
14:N:21:LYS:HE2	14:N:21:LYS:HB3	1.93	0.40
38:n:22:ARG:HH22	51:1:2709:G:H5'	1.86	0.40
43:s:29:VAL:HG21	43:s:55:ILE:HG21	2.03	0.40
44:t:28:ASN:HD21	44:t:91:GLN:HB3	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:194:G:O6	51:1:195:A:C6	2.74	0.40
51:1:259:G:O2'	51:1:260:G:H5'	2.20	0.40
51:1:284:U:H2'	51:1:285:G:C8	2.55	0.40
51:1:597:G:H2'	51:1:598:U:H6	1.85	0.40
51:1:688:U:O5'	51:1:688:U:H6	2.03	0.40
51:1:877:A:H2'	51:1:878:A:H5''	2.02	0.40
51:1:1116:G:O2'	51:1:1117:C:H5'	2.22	0.40
51:1:1152:C:H2'	51:1:1153:C:C6	2.55	0.40
51:1:1165:A:O2'	51:1:1166:G:H5'	2.21	0.40
51:1:1283:G:N2	51:1:1285:A:H3'	2.35	0.40
51:1:1430:G:O2'	51:1:1431:A:H5'	2.21	0.40
51:1:1599:U:H2'	51:1:1600:C:H6	1.85	0.40
51:1:1822:C:H2'	51:1:1823:G:H8	1.85	0.40
51:1:1930:G:O2'	51:1:1931:U:OP2	2.33	0.40
51:1:2326:C:H42	51:1:2389:G:H1	1.69	0.40
51:1:2585:U:O2	51:1:2585:U:O4'	2.39	0.40
51:1:2776:A:C6	51:1:2778:A:C6	3.09	0.40
51:1:2828:G:N1	51:1:2829:A:C5	2.90	0.40
53:3:202:G:H2'	53:3:203:G:H8	1.85	0.40
58:B1:351:GLY:O	58:B1:467:ALA:HA	2.21	0.40
64:7:10:G:OP1	64:7:46:G:H4'	2.21	0.40
5:E:29:ARG:HD3	5:E:29:ARG:HA	1.91	0.40
9:I:146:GLU:HA	9:I:149:LYS:HZ3	1.86	0.40
9:I:150:LYS:HD2	9:I:155:LYS:HD2	2.04	0.40
10:J:90:GLY:O	10:J:129:SER:OG	2.36	0.40
16:P:99:LEU:HA	16:P:102:ALA:HB3	2.03	0.40
41:q:86:SER:O	42:r:52:PRO:HD3	2.21	0.40
51:1:55:G:N2	51:1:116:C:C2	2.90	0.40
51:1:309:A:N3	51:1:329:G:O2'	2.53	0.40
51:1:481:G:H1'	51:1:506:G:H22	1.84	0.40
51:1:679:C:H2'	51:1:680:C:C6	2.56	0.40
51:1:924:G:O2'	51:1:925:A:H5'	2.21	0.40
51:1:1048:A:N6	51:1:1111:A:C8	2.89	0.40
51:1:1430:G:H2'	51:1:1431:A:O4'	2.21	0.40
51:1:1553:A:O2'	51:1:1554:U:H5	2.02	0.40
51:1:1827:U:C2'	51:1:1828:G:H5'	2.51	0.40
51:1:2106:U:H3'	51:1:2107:G:H8	1.86	0.40
51:1:2221:G:H2'	51:1:2222:C:C6	2.56	0.40
58:B1:108:ALA:HB2	58:B1:276:ASN:OD1	2.21	0.40
59:B2:987:GLU:HG2	59:B2:991:LYS:HE3	2.03	0.40
8:H:14:VAL:HG11	8:H:180:ASP:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:24:ILE:HG23	22:V:41:THR:HB	2.03	0.40
29:d:163:ASN:HD21	51:1:322:A:P	2.44	0.40
32:g:1:MET:N	32:g:20:ASN:OD1	2.39	0.40
35:k:13:ASN:HB3	35:k:100:PHE:CZ	2.57	0.40
38:n:38:LEU:HD23	38:n:38:LEU:HA	1.93	0.40
40:p:110:LYS:HE3	40:p:110:LYS:HB3	1.91	0.40
51:1:120:U:C2	51:1:149:A:C6	3.10	0.40
51:1:914:G:H5'	51:1:915:C:OP2	2.22	0.40
51:1:955:U:H2'	51:1:956:G:C5'	2.52	0.40
51:1:1346:G:O2'	51:1:1347:A:H5'	2.22	0.40
51:1:1605:C:H2'	51:1:1606:C:C5'	2.52	0.40
51:1:2049:G:O2'	51:1:2050:C:H5'	2.21	0.40
51:1:2648:G:O2'	51:1:2649:C:H5'	2.21	0.40
51:1:2680:U:O2'	51:1:2681:C:H5'	2.21	0.40
51:1:2833:U:O2'	51:1:2834:G:H5'	2.22	0.40
53:3:146:G:H2'	53:3:147:G:H8	1.86	0.40
53:3:304:U:H2'	53:3:305:G:C8	2.56	0.40
58:B1:140:TYR:HD1	58:B1:140:TYR:HA	1.79	0.40
58:B1:182:ALA:HB1	58:B1:238:ILE:CG2	2.52	0.40
58:B1:1106:ILE:O	58:B1:1123:ARG:N	2.45	0.40
59:B2:546:GLU:H	59:B2:546:GLU:HG3	1.53	0.40
63:5:17:C:H2'	63:5:18:G:C8	2.56	0.40
64:7:69:C:H2'	64:7:70:G:C8	2.56	0.40
9:I:101:VAL:HG13	9:I:113:ALA:HB1	2.03	0.40
9:I:187:ARG:HH22	9:I:192:ALA:HA	1.86	0.40
19:S:15:LEU:HB3	19:S:54:SER:HB3	2.03	0.40
31:f:60:GLY:O	31:f:64:ALA:N	2.54	0.40
34:j:78:THR:HB	51:1:2641:G:H5''	2.04	0.40
38:n:82:GLU:O	38:n:86:ARG:N	2.47	0.40
40:p:84:SER:O	40:p:86:LYS:NZ	2.55	0.40
51:1:1783:A:N1	51:1:2587:A:H2'	2.37	0.40
51:1:1944:U:H3'	51:1:1945:G:H5'	2.03	0.40
51:1:2098:U:H2'	51:1:2099:U:H5'	2.03	0.40
51:1:2649:C:N3	51:1:2650:U:C4	2.89	0.40
53:3:195:A:H2'	53:3:196:A:C8	2.56	0.40
57:A2:57:THR:HG23	57:A2:158:ARG:HH21	1.86	0.40
58:B1:26:SER:HB3	58:B1:29:MET:H	1.86	0.40
58:B1:242:LEU:HA	58:B1:243:PRO:HD3	1.95	0.40
59:B2:50:GLU:HG2	59:B2:73:TYR:HE1	1.85	0.40
59:B2:159:SER:HB2	59:B2:442:VAL:HG11	2.04	0.40
11:K:53:LYS:HE2	11:K:53:LYS:HB2	1.95	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:26:MET:HE2	13:M:26:MET:HB3	1.96	0.40
14:N:16:ALA:HA	14:N:66:VAL:HA	2.03	0.40
16:P:17:ASP:HB3	16:P:80:ASN:HD21	1.87	0.40
22:V:52:CYS:HB3	22:V:58:VAL:HG11	2.03	0.40
24:X:49:ALA:HA	24:X:58:PRO:HA	2.03	0.40
30:e:77:LYS:HE2	30:e:77:LYS:HB2	1.89	0.40
31:f:3:VAL:HG13	51:1:2751:G:H4'	2.02	0.40
51:1:224:U:O4	51:1:420:C:H5'	2.21	0.40
51:1:485:C:O2'	51:1:486:C:H5'	2.22	0.40
51:1:510:C:H2'	51:1:511:U:H6	1.85	0.40
51:1:570:G:O2'	51:1:571:U:H5'	2.22	0.40
51:1:935:C:H2'	51:1:936:A:C8	2.56	0.40
51:1:1420:A:C2	51:1:2211:A:N1	2.90	0.40
51:1:1722:A:N6	51:1:1738:G:H1'	2.36	0.40
51:1:1749:A:C4	51:1:1750:G:C8	3.10	0.40
51:1:1783:A:C8	51:1:1783:A:H5'	2.57	0.40
51:1:2038:G:H2'	51:1:2039:U:O4'	2.21	0.40
51:1:2093:G:N7	51:1:2225:A:H2'	2.37	0.40
51:1:2514:U:H2'	51:1:2515:C:C6	2.57	0.40
51:1:2667:C:O5'	51:1:2667:C:H6	2.03	0.40
51:1:2788:C:H2'	51:1:2789:C:C6	2.56	0.40
57:A1:102:LEU:HB3	57:A1:142:MET:HG2	2.04	0.40
57:A1:211:ILE:HD12	57:A1:211:ILE:HA	1.92	0.40
58:B1:68:TYR:CB	58:B1:75:TYR:HE2	2.34	0.40
58:B1:111:THR:HG23	58:B1:300:GLN:HA	2.03	0.40
58:B1:576:ARG:HD3	58:B1:593:ASN:HA	2.03	0.40
59:B2:1247:SER:OG	59:B2:1248:THR:N	2.55	0.40
63:5:23:A:H2'	63:5:24:G:C8	2.56	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	64/70 (91%)	59 (92%)	5 (8%)	0	100	100
2	B	54/57 (95%)	48 (89%)	4 (7%)	2 (4%)	2	20
3	C	48/55 (87%)	41 (85%)	7 (15%)	0	100	100
4	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
5	E	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
6	F	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	4	24
7	G	216/241 (90%)	187 (87%)	27 (12%)	2 (1%)	14	51
8	H	204/233 (88%)	194 (95%)	10 (5%)	0	100	100
9	I	203/206 (98%)	172 (85%)	30 (15%)	1 (0%)	25	64
10	J	155/167 (93%)	138 (89%)	17 (11%)	0	100	100
11	K	98/135 (73%)	85 (87%)	13 (13%)	0	100	100
12	L	149/179 (83%)	129 (87%)	20 (13%)	0	100	100
13	M	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
14	N	125/130 (96%)	104 (83%)	21 (17%)	0	100	100
15	O	96/103 (93%)	87 (91%)	8 (8%)	1 (1%)	13	49
16	P	114/129 (88%)	100 (88%)	13 (11%)	1 (1%)	14	51
17	Q	121/124 (98%)	94 (78%)	27 (22%)	0	100	100
18	R	112/118 (95%)	98 (88%)	13 (12%)	1 (1%)	14	51
19	S	98/101 (97%)	83 (85%)	15 (15%)	0	100	100
20	T	86/89 (97%)	75 (87%)	11 (13%)	0	100	100
21	U	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
22	V	78/84 (93%)	69 (88%)	8 (10%)	1 (1%)	10	42
23	W	63/75 (84%)	56 (89%)	5 (8%)	2 (3%)	3	21
24	X	77/92 (84%)	71 (92%)	6 (8%)	0	100	100
25	Y	83/87 (95%)	78 (94%)	5 (6%)	0	100	100
26	Z	63/71 (89%)	44 (70%)	18 (29%)	1 (2%)	8	38
27	b	269/273 (98%)	244 (91%)	25 (9%)	0	100	100
28	c	207/209 (99%)	189 (91%)	18 (9%)	0	100	100
29	d	199/201 (99%)	186 (94%)	13 (6%)	0	100	100
30	e	175/179 (98%)	157 (90%)	18 (10%)	0	100	100
31	f	174/177 (98%)	158 (91%)	16 (9%)	0	100	100
32	g	50/149 (34%)	44 (88%)	5 (10%)	1 (2%)	6	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	i	139/142 (98%)	116 (84%)	23 (16%)	0	100	100
34	j	140/142 (99%)	128 (91%)	12 (9%)	0	100	100
35	k	120/123 (98%)	106 (88%)	14 (12%)	0	100	100
36	l	141/144 (98%)	129 (92%)	12 (8%)	0	100	100
37	m	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
38	n	118/127 (93%)	103 (87%)	15 (13%)	0	100	100
39	o	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
40	p	112/115 (97%)	103 (92%)	9 (8%)	0	100	100
41	q	115/118 (98%)	110 (96%)	3 (3%)	2 (2%)	7	36
42	r	101/103 (98%)	89 (88%)	12 (12%)	0	100	100
43	s	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
44	t	91/100 (91%)	82 (90%)	9 (10%)	0	100	100
45	u	100/104 (96%)	84 (84%)	15 (15%)	1 (1%)	13	49
46	v	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
47	w	73/85 (86%)	67 (92%)	6 (8%)	0	100	100
48	x	75/78 (96%)	72 (96%)	2 (3%)	1 (1%)	10	42
49	y	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
50	z	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
57	A1	214/329 (65%)	195 (91%)	19 (9%)	0	100	100
57	A2	217/329 (66%)	206 (95%)	11 (5%)	0	100	100
58	B1	1329/1407 (94%)	1203 (90%)	122 (9%)	4 (0%)	37	72
59	B2	1338/1342 (100%)	1207 (90%)	126 (9%)	5 (0%)	30	68
60	W0	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
61	NA	490/495 (99%)	451 (92%)	36 (7%)	3 (1%)	22	60
62	NG	150/181 (83%)	131 (87%)	13 (9%)	6 (4%)	2	18
65	h	2/6 (33%)	1 (50%)	1 (50%)	0	100	100
All	All	9440/10235 (92%)	8500 (90%)	904 (10%)	36 (0%)	32	68

All (36) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
48	x	25	LYS
58	B1	121	PRO

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Mol	Chain	Res	Type
61	NA	187	ARG
61	NA	188	PRO
62	NG	102	PRO
62	NG	130	PRO
6	F	34	LYS
59	B2	43	PRO
62	NG	122	PRO
62	NG	163	SER
59	B2	888	THR
2	B	23	ALA
7	G	19	THR
18	R	5	GLY
23	W	13	THR
32	g	12	LEU
41	q	23	TYR
58	B1	43	THR
58	B1	193	ASP
59	B2	909	LYS
7	G	17	HIS
15	O	58	ASN
22	V	50	ASN
45	u	97	SER
58	B1	1325	PHE
59	B2	911	SER
9	I	45	PRO
23	W	17	VAL
62	NG	169	THR
62	NG	170	PRO
61	NA	65	VAL
26	Z	10	PRO
41	q	6	GLY
59	B2	1317	PRO
2	B	24	VAL
16	P	88	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	59/62 (95%)	58 (98%)	1 (2%)	56	72
2	B	47/48 (98%)	47 (100%)	0	100	100
3	C	45/49 (92%)	44 (98%)	1 (2%)	47	65
4	D	38/38 (100%)	37 (97%)	1 (3%)	41	60
5	E	51/52 (98%)	49 (96%)	2 (4%)	27	49
6	F	34/34 (100%)	30 (88%)	4 (12%)	4	17
7	G	180/199 (90%)	174 (97%)	6 (3%)	33	54
8	H	170/190 (90%)	167 (98%)	3 (2%)	54	71
9	I	172/173 (99%)	168 (98%)	4 (2%)	45	64
10	J	119/126 (94%)	117 (98%)	2 (2%)	56	72
11	K	87/116 (75%)	82 (94%)	5 (6%)	17	39
12	L	124/147 (84%)	124 (100%)	0	100	100
13	M	104/105 (99%)	103 (99%)	1 (1%)	73	81
14	N	105/107 (98%)	98 (93%)	7 (7%)	13	34
15	O	86/90 (96%)	78 (91%)	8 (9%)	7	23
16	P	89/99 (90%)	86 (97%)	3 (3%)	32	53
17	Q	103/104 (99%)	98 (95%)	5 (5%)	21	42
18	R	92/96 (96%)	91 (99%)	1 (1%)	70	80
19	S	83/84 (99%)	83 (100%)	0	100	100
20	T	76/77 (99%)	73 (96%)	3 (4%)	27	49
21	U	65/65 (100%)	64 (98%)	1 (2%)	60	75
22	V	74/78 (95%)	72 (97%)	2 (3%)	40	60
23	W	56/65 (86%)	52 (93%)	4 (7%)	12	32
24	X	70/79 (89%)	70 (100%)	0	100	100
25	Y	65/66 (98%)	64 (98%)	1 (2%)	60	75
26	Z	55/61 (90%)	47 (86%)	8 (14%)	2	13
27	b	216/218 (99%)	212 (98%)	4 (2%)	52	69
28	c	164/164 (100%)	164 (100%)	0	100	100
29	d	165/165 (100%)	162 (98%)	3 (2%)	54	71
30	e	148/150 (99%)	145 (98%)	3 (2%)	50	68
31	f	137/138 (99%)	135 (98%)	2 (2%)	60	75
32	g	41/114 (36%)	38 (93%)	3 (7%)	11	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	i	109/110 (99%)	108 (99%)	1 (1%)	75	83
34	j	116/116 (100%)	116 (100%)	0	100	100
35	k	103/104 (99%)	102 (99%)	1 (1%)	73	81
36	l	102/103 (99%)	101 (99%)	1 (1%)	73	81
37	m	109/109 (100%)	103 (94%)	6 (6%)	18	40
38	n	100/103 (97%)	99 (99%)	1 (1%)	73	81
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%)	86 (97%)	3 (3%)	32	53
42	r	84/84 (100%)	80 (95%)	4 (5%)	21	43
43	s	93/93 (100%)	92 (99%)	1 (1%)	70	80
44	t	80/84 (95%)	80 (100%)	0	100	100
45	u	83/85 (98%)	79 (95%)	4 (5%)	21	43
46	v	78/78 (100%)	77 (99%)	1 (1%)	65	77
47	w	57/63 (90%)	57 (100%)	0	100	100
48	x	67/68 (98%)	67 (100%)	0	100	100
49	y	55/55 (100%)	55 (100%)	0	100	100
50	z	48/49 (98%)	46 (96%)	2 (4%)	25	47
57	A1	185/286 (65%)	174 (94%)	11 (6%)	16	38
57	A2	186/286 (65%)	184 (99%)	2 (1%)	70	80
58	B1	1110/1168 (95%)	1017 (92%)	93 (8%)	9	28
59	B2	1150/1157 (99%)	1116 (97%)	34 (3%)	36	56
60	W0	70/75 (93%)	69 (99%)	1 (1%)	62	76
65	h	2/2 (100%)	2 (100%)	0	100	100
All	All	7381/7914 (93%)	7127 (97%)	254 (3%)	34	53

All (254) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	VAL
3	C	22	THR
4	D	44	VAL
5	E	28	LEU
5	E	31	ILE

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Mol	Chain	Res	Type
6	F	34	LYS
6	F	35	GLN
6	F	36	ARG
6	F	37	GLN
7	G	8	MET
7	G	10	LYS
7	G	13	VAL
7	G	14	HIS
7	G	17	HIS
7	G	29	PHE
8	H	74	ILE
8	H	156	LEU
8	H	164	THR
9	I	44	LYS
9	I	46	ARG
9	I	96	ARG
9	I	97	LEU
10	J	55	VAL
10	J	130	THR
11	K	89	VAL
11	K	90	MET
11	K	91	ARG
11	K	92	THR
11	K	94	HIS
13	M	102	VAL
14	N	52	GLU
14	N	53	LEU
14	N	54	VAL
14	N	57	VAL
14	N	59	LYS
14	N	60	LEU
14	N	65	THR
15	O	16	ARG
15	O	82	LYS
15	O	83	THR
15	O	87	LEU
15	O	88	MET
15	O	89	ARG
15	O	91	ASP
15	O	92	LEU
16	P	120	CYS
16	P	121	ARG

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Mol	Chain	Res	Type
16	P	124	LYS
17	Q	15	VAL
17	Q	17	LYS
17	Q	20	VAL
17	Q	29	LYS
17	Q	34	THR
18	R	64	VAL
20	T	82	GLU
20	T	86	LEU
20	T	88	ARG
21	U	36	VAL
22	V	47	ASP
22	V	52	CYS
23	W	15	GLU
23	W	17	VAL
23	W	18	GLN
23	W	70	THR
25	Y	85	LEU
26	Z	3	ILE
26	Z	4	LYS
26	Z	5	VAL
26	Z	12	ASP
26	Z	15	LEU
26	Z	19	LYS
26	Z	20	ARG
26	Z	27	VAL
27	b	129	LEU
27	b	131	MET
27	b	132	ARG
27	b	203	VAL
29	d	14	VAL
29	d	118	LEU
29	d	198	GLU
30	e	39	VAL
30	e	174	PHE
30	e	177	ARG
31	f	9	VAL
31	f	131	VAL
32	g	4	ILE
32	g	5	LEU
32	g	9	VAL
33	i	22	PRO

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Mol	Chain	Res	Type
35	k	58	LEU
36	l	85	VAL
37	m	44	ARG
37	m	47	GLU
37	m	50	ARG
37	m	55	ARG
37	m	58	LYS
37	m	59	ARG
38	n	13	ASN
41	q	4	LYS
41	q	5	ARG
41	q	28	SER
42	r	51	VAL
42	r	53	PHE
42	r	55	ASP
42	r	58	VAL
43	s	3	THR
45	u	35	VAL
45	u	93	ARG
45	u	100	GLU
45	u	101	THR
46	v	72	VAL
50	z	16	LEU
50	z	40	THR
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	74	VAL
58	B1	24	LEU
58	B1	40	LYS
58	B1	42	GLU
58	B1	44	ILE
58	B1	47	ARG

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Mol	Chain	Res	Type
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	87	LYS
58	B1	91	GLU
58	B1	93	THR
58	B1	94	GLN
58	B1	95	THR
58	B1	96	LYS
58	B1	99	ARG
58	B1	100	GLU
58	B1	114	ILE
58	B1	117	LEU
58	B1	120	LEU
58	B1	126	LEU
58	B1	132	LEU
58	B1	135	ILE
58	B1	142	GLU
58	B1	144	TYR
58	B1	145	VAL
58	B1	146	VAL
58	B1	147	ILE
58	B1	152	THR
58	B1	154	LEU
58	B1	157	GLN
58	B1	159	ILE
58	B1	172	PHE
58	B1	174	ASP
58	B1	175	GLU
58	B1	180	MET
58	B1	190	LYS
58	B1	193	ASP
58	B1	196	GLN
58	B1	210	SER

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Mol	Chain	Res	Type
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
58	B1	256	ASP
58	B1	259	ARG
58	B1	281	ARG
58	B1	282	LEU
58	B1	285	LEU
58	B1	290	ILE
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

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Mol	Chain	Res	Type
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
59	B2	856	ASN
59	B2	857	VAL
59	B2	859	GLU
59	B2	887	VAL
59	B2	890	LYS
59	B2	892	GLU
59	B2	895	LEU
59	B2	896	THR
59	B2	898	GLU
59	B2	899	GLU
59	B2	900	LYS
59	B2	901	LEU
59	B2	905	ILE
59	B2	906	PHE
59	B2	909	LYS
59	B2	912	ASP
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	63	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (127) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	33	ASN
1	A	61	ASN
2	B	4	GLN
3	C	44	GLN
4	D	16	HIS
6	F	35	GLN
7	G	14	HIS
7	G	119	GLN
7	G	121	GLN
7	G	167	HIS
8	H	7	ASN
8	H	68	HIS
8	H	99	GLN
8	H	122	GLN
8	H	138	GLN
8	H	139	ASN
9	I	151	GLN
9	I	197	HIS
10	J	121	ASN
12	L	85	GLN
12	L	96	ASN
12	L	121	ASN
12	L	147	ASN
13	M	37	ASN
13	M	66	GLN
14	N	4	GLN
14	N	30	ASN
15	O	20	GLN
15	O	35	GLN
15	O	58	ASN
16	P	80	ASN
17	Q	4	ASN
17	Q	71	HIS
18	R	7	ASN
18	R	99	GLN
19	S	59	GLN
20	T	19	ASN
20	T	39	GLN
22	V	30	HIS
24	X	68	HIS
25	Y	2	ASN
25	Y	77	ASN

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Mol	Chain	Res	Type
26	Z	8	ASN
27	b	24	HIS
27	b	69	ASN
27	b	89	ASN
27	b	142	ASN
27	b	259	ASN
28	c	49	GLN
28	c	134	HIS
28	c	150	GLN
28	c	164	GLN
28	c	173	GLN
29	d	41	GLN
29	d	90	GLN
29	d	94	GLN
29	d	165	HIS
30	e	4	HIS
30	e	80	GLN
31	f	47	ASN
32	g	2	GLN
33	i	29	GLN
33	i	30	GLN
34	j	58	ASN
34	j	135	GLN
35	k	5	GLN
35	k	93	GLN
36	l	4	ASN
36	l	99	ASN
36	l	104	GLN
37	m	13	HIS
38	n	13	ASN
40	p	2	ASN
40	p	114	ASN
41	q	55	GLN
41	q	58	GLN
42	r	18	GLN
42	r	82	HIS
43	s	7	HIS
44	t	28	ASN
44	t	59	ASN
44	t	92	ASN
45	u	52	ASN
46	v	87	GLN

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Mol	Chain	Res	Type
47	w	53	HIS
48	x	16	ASN
48	x	33	HIS
49	y	31	GLN
49	y	38	GLN
49	y	41	HIS
49	y	45	GLN
50	z	8	GLN
57	A1	66	HIS
57	A1	84	ASN
57	A1	117	HIS
57	A1	128	HIS
57	A1	227	GLN
57	A2	23	HIS
57	A2	227	GLN
58	B1	45	ASN
58	B1	196	GLN
58	B1	364	HIS
58	B1	424	ASN
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	688	GLN
59	B2	762	ASN
59	B2	808	ASN
59	B2	856	ASN
59	B2	1008	GLN
59	B2	1237	HIS
59	B2	1268	GLN
59	B2	1313	HIS
60	W0	7	GLN
60	W0	31	GLN
60	W0	62	GLN

## 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	1	2902/2904 (99%)	398 (13%)	16 (0%)
52	2	119/120 (99%)	17 (14%)	1 (0%)
53	3	1538/1542 (99%)	255 (16%)	4 (0%)
54	4	33/47 (70%)	16 (48%)	2 (6%)
63	5	75/76 (98%)	43 (57%)	7 (9%)
64	6	76/77 (98%)	10 (13%)	0
64	7	76/77 (98%)	27 (35%)	2 (2%)
All	All	4819/4843 (99%)	766 (15%)	32 (0%)

All (766) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	1	10	A
51	1	12	U
51	1	34	U
51	1	35	G
51	1	46	G
51	1	51	G
51	1	55	G
51	1	63	A
51	1	71	A
51	1	74	A
51	1	75	G
51	1	102	U
51	1	103	A
51	1	119	A
51	1	120	U
51	1	139	U
51	1	140	C
51	1	141	G
51	1	149	A
51	1	162	U
51	1	163	C
51	1	178	G
51	1	196	A
51	1	199	A
51	1	216	A
51	1	221	A
51	1	222	A
51	1	229	C
51	1	248	G

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Mol	Chain	Res	Type
51	1	255	A
51	1	265	A
51	1	266	G
51	1	276	U
51	1	281	C
51	1	285	G
51	1	294	A
51	1	323	C
51	1	329	G
51	1	330	A
51	1	353	C
51	1	361	G
51	1	362	A
51	1	371	A
51	1	372	G
51	1	386	G
51	1	387	U
51	1	396	G
51	1	404	A
51	1	406	G
51	1	411	G
51	1	424	G
51	1	451	U
51	1	457	A
51	1	481	G
51	1	482	A
51	1	491	G
51	1	504	A
51	1	505	A
51	1	526	A
51	1	529	A
51	1	531	C
51	1	532	A
51	1	533	G
51	1	544	C
51	1	545	U
51	1	546	U
51	1	547	A
51	1	562	U
51	1	563	A
51	1	573	U
51	1	574	A

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Mol	Chain	Res	Type
51	1	575	A
51	1	603	A
51	1	614	A
51	1	616	A
51	1	627	A
51	1	637	A
51	1	646	U
51	1	647	G
51	1	654	A
51	1	669	G
51	1	671	C
51	1	677	A
51	1	686	U
51	1	687	C
51	1	695	G
51	1	730	A
51	1	745	G
51	1	747	C
51	1	758	C
51	1	764	A
51	1	765	C
51	1	775	G
51	1	782	A
51	1	784	G
51	1	785	G
51	1	789	A
51	1	791	C
51	1	792	A
51	1	801	G
51	1	805	G
51	1	812	C
51	1	819	A
51	1	827	U
51	1	828	U
51	1	829	A
51	1	830	G
51	1	845	A
51	1	846	U
51	1	858	G
51	1	860	U
51	1	878	A
51	1	887	U

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Mol	Chain	Res	Type
51	1	896	A
51	1	910	A
51	1	911	A
51	1	932	U
51	1	941	A
51	1	946	C
51	1	961	C
51	1	968	C
51	1	974	G
51	1	981	A
51	1	983	A
51	1	985	C
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	1031	G
51	1	1033	U
51	1	1045	C
51	1	1046	A
51	1	1047	G
51	1	1057	A
51	1	1058	U
51	1	1060	U
51	1	1061	U
51	1	1063	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	1075	C
51	1	1078	U
51	1	1083	U
51	1	1084	A
51	1	1086	A
51	1	1088	A

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Mol	Chain	Res	Type
51	1	1104	C
51	1	1111	A
51	1	1131	G
51	1	1132	U
51	1	1133	A
51	1	1135	C
51	1	1139	G
51	1	1142	A
51	1	1143	A
51	1	1157	G
51	1	1175	A
51	1	1177	G
51	1	1178	C
51	1	1180	U
51	1	1186	G
51	1	1212	G
51	1	1225	G
51	1	1253	A
51	1	1256	G
51	1	1271	G
51	1	1272	A
51	1	1273	U
51	1	1289	C
51	1	1294	U
51	1	1300	G
51	1	1301	A
51	1	1345	C
51	1	1352	U
51	1	1365	A
51	1	1378	A
51	1	1379	U
51	1	1383	A
51	1	1406	U
51	1	1416	G
51	1	1419	A
51	1	1420	A
51	1	1427	A
51	1	1429	G
51	1	1452	G
51	1	1453	A
51	1	1461	C
51	1	1482	G

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Mol	Chain	Res	Type
51	1	1490	A
51	1	1491	G
51	1	1497	U
51	1	1504	A
51	1	1515	A
51	1	1524	G
51	1	1533	C
51	1	1535	A
51	1	1536	C
51	1	1537	G
51	1	1555	G
51	1	1560	G
51	1	1565	C
51	1	1569	A
51	1	1578	U
51	1	1583	A
51	1	1608	A
51	1	1616	A
51	1	1634	A
51	1	1647	U
51	1	1648	U
51	1	1674	G
51	1	1698	A
51	1	1699	G
51	1	1703	G
51	1	1715	G
51	1	1716	U
51	1	1729	U
51	1	1730	C
51	1	1732	C
51	1	1738	G
51	1	1758	U
51	1	1764	C
51	1	1773	A
51	1	1783	A
51	1	1784	A
51	1	1786	A
51	1	1800	C
51	1	1801	A
51	1	1802	A
51	1	1808	A
51	1	1809	A

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Mol	Chain	Res	Type
51	1	1816	C
51	1	1829	A
51	1	1833	C
51	1	1834	U
51	1	1870	C
51	1	1871	A
51	1	1901	A
51	1	1906	G
51	1	1913	A
51	1	1914	C
51	1	1929	G
51	1	1931	U
51	1	1936	A
51	1	1937	A
51	1	1938	A
51	1	1939	U
51	1	1943	U
51	1	1955	U
51	1	1967	C
51	1	1970	A
51	1	1971	U
51	1	1972	G
51	1	1990	C
51	1	1993	U
51	1	1997	C
51	1	2020	A
51	1	2022	U
51	1	2023	C
51	1	2024	G
51	1	2027	G
51	1	2030	A
51	1	2031	A
51	1	2033	A
51	1	2034	U
51	1	2043	C
51	1	2052	A
51	1	2055	C
51	1	2056	G
51	1	2060	A
51	1	2061	G
51	1	2069	G
51	1	2093	G

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Mol	Chain	Res	Type
51	1	2096	C
51	1	2100	G
51	1	2110	G
51	1	2111	U
51	1	2118	U
51	1	2119	A
51	1	2123	G
51	1	2128	G
51	1	2131	U
51	1	2132	U
51	1	2133	G
51	1	2134	A
51	1	2137	U
51	1	2141	G
51	1	2145	C
51	1	2149	U
51	1	2162	G
51	1	2164	C
51	1	2166	U
51	1	2172	U
51	1	2173	A
51	1	2174	C
51	1	2189	U
51	1	2192	U
51	1	2198	A
51	1	2204	G
51	1	2211	A
51	1	2213	U
51	1	2225	A
51	1	2238	G
51	1	2239	G
51	1	2243	U
51	1	2268	A
51	1	2275	C
51	1	2279	G
51	1	2283	C
51	1	2287	A
51	1	2288	A
51	1	2305	U
51	1	2309	A
51	1	2325	G
51	1	2326	C

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Mol	Chain	Res	Type
51	1	2327	A
51	1	2333	A
51	1	2334	U
51	1	2345	G
51	1	2350	C
51	1	2382	G
51	1	2383	G
51	1	2385	C
51	1	2392	A
51	1	2402	U
51	1	2406	A
51	1	2407	A
51	1	2423	U
51	1	2426	A
51	1	2427	C
51	1	2429	G
51	1	2430	A
51	1	2435	A
51	1	2436	G
51	1	2440	C
51	1	2441	U
51	1	2445	G
51	1	2447	G
51	1	2448	A
51	1	2476	A
51	1	2482	A
51	1	2491	U
51	1	2492	U
51	1	2498	C
51	1	2502	G
51	1	2505	G
51	1	2506	U
51	1	2507	C
51	1	2518	A
51	1	2547	A
51	1	2554	U
51	1	2566	A
51	1	2567	G
51	1	2572	A
51	1	2573	C
51	1	2582	G
51	1	2602	A

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Mol	Chain	Res	Type
51	1	2609	U
51	1	2613	U
51	1	2629	U
51	1	2630	G
51	1	2642	G
51	1	2646	C
51	1	2689	U
51	1	2690	U
51	1	2714	G
51	1	2726	A
51	1	2732	G
51	1	2744	G
51	1	2748	A
51	1	2751	G
51	1	2758	A
51	1	2764	A
51	1	2765	A
51	1	2778	A
51	1	2779	U
51	1	2793	C
51	1	2798	U
51	1	2799	A
51	1	2800	A
51	1	2801	G
51	1	2820	A
51	1	2861	U
51	1	2867	G
51	1	2868	A
51	1	2872	A
51	1	2879	A
51	1	2880	C
51	1	2884	U
51	1	2901	C
52	2	9	G
52	2	13	G
52	2	25	U
52	2	30	C
52	2	35	C
52	2	36	C
52	2	44	G
52	2	45	A
52	2	53	A

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Mol	Chain	Res	Type
52	2	67	G
52	2	87	U
52	2	88	C
52	2	89	U
52	2	90	C
52	2	108	A
52	2	109	A
52	2	120	A
53	3	4	U
53	3	5	U
53	3	6	G
53	3	7	A
53	3	9	G
53	3	22	G
53	3	32	A
53	3	39	G
53	3	47	C
53	3	48	C
53	3	51	A
53	3	71	A
53	3	75	G
53	3	77	A
53	3	78	A
53	3	80	A
53	3	83	C
53	3	84	U
53	3	87	C
53	3	88	U
53	3	94	G
53	3	95	C
53	3	100	G
53	3	108	G
53	3	116	A
53	3	121	U
53	3	127	G
53	3	130	A
53	3	144	G
53	3	163	C
53	3	183	C
53	3	197	A
53	3	206	C
53	3	208	U

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Mol	Chain	Res	Type
53	3	210	C
53	3	211	G
53	3	212	G
53	3	222	C
53	3	226	G
53	3	240	G
53	3	245	U
53	3	247	G
53	3	251	G
53	3	263	A
53	3	264	C
53	3	266	G
53	3	267	C
53	3	279	A
53	3	280	C
53	3	281	G
53	3	289	G
53	3	293	G
53	3	321	A
53	3	328	C
53	3	329	A
53	3	330	C
53	3	345	C
53	3	347	G
53	3	348	G
53	3	352	C
53	3	353	A
53	3	354	G
53	3	363	A
53	3	367	U
53	3	372	C
53	3	374	A
53	3	388	G
53	3	397	A
53	3	398	U
53	3	405	U
53	3	406	G
53	3	412	A
53	3	413	G
53	3	422	C
53	3	423	G
53	3	428	G

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Mol	Chain	Res	Type
53	3	429	U
53	3	446	G
53	3	453	G
53	3	467	U
53	3	468	A
53	3	472	U
53	3	479	U
53	3	480	U
53	3	481	G
53	3	484	G
53	3	485	U
53	3	486	U
53	3	487	A
53	3	496	A
53	3	497	G
53	3	505	G
53	3	508	U
53	3	509	A
53	3	511	C
53	3	518	C
53	3	521	G
53	3	522	C
53	3	531	U
53	3	532	A
53	3	533	A
53	3	536	C
53	3	547	A
53	3	561	U
53	3	562	U
53	3	564	C
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	607	A
53	3	615	G
53	3	633	G
53	3	639	G
53	3	642	A
53	3	653	U

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Mol	Chain	Res	Type
53	3	655	A
53	3	660	C
53	3	665	A
53	3	682	G
53	3	688	G
53	3	702	A
53	3	703	G
53	3	718	A
53	3	721	G
53	3	723	U
53	3	724	G
53	3	731	G
53	3	734	G
53	3	755	G
53	3	777	A
53	3	793	U
53	3	799	G
53	3	809	G
53	3	815	A
53	3	817	C
53	3	818	G
53	3	819	A
53	3	820	U
53	3	821	G
53	3	829	G
53	3	836	G
53	3	843	U
53	3	844	G
53	3	845	A
53	3	846	G
53	3	849	G
53	3	851	G
53	3	868	C
53	3	902	G
53	3	914	A
53	3	934	C
53	3	935	A
53	3	960	U
53	3	961	U
53	3	966	G
53	3	969	A
53	3	971	G

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Mol	Chain	Res	Type
53	3	975	A
53	3	976	G
53	3	977	A
53	3	991	U
53	3	992	U
53	3	993	G
53	3	1004	A
53	3	1020	G
53	3	1028	C
53	3	1031	C
53	3	1032	G
53	3	1033	G
53	3	1034	G
53	3	1036	A
53	3	1053	G
53	3	1054	C
53	3	1055	A
53	3	1085	U
53	3	1094	G
53	3	1095	U
53	3	1099	G
53	3	1101	A
53	3	1108	G
53	3	1133	G
53	3	1136	C
53	3	1137	C
53	3	1139	G
53	3	1158	C
53	3	1159	U
53	3	1168	U
53	3	1171	A
53	3	1182	G
53	3	1183	U
53	3	1184	G
53	3	1195	C
53	3	1196	A
53	3	1197	A
53	3	1202	U
53	3	1206	G
53	3	1224	U
53	3	1225	A
53	3	1226	C

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Mol	Chain	Res	Type
53	3	1227	A
53	3	1237	C
53	3	1238	A
53	3	1240	U
53	3	1241	G
53	3	1250	A
53	3	1256	A
53	3	1260	G
53	3	1261	A
53	3	1275	A
53	3	1278	G
53	3	1280	A
53	3	1281	C
53	3	1282	C
53	3	1286	U
53	3	1287	A
53	3	1290	G
53	3	1300	G
53	3	1302	C
53	3	1303	C
53	3	1305	G
53	3	1312	G
53	3	1317	C
53	3	1322	C
53	3	1331	G
53	3	1335	U
53	3	1336	C
53	3	1340	A
53	3	1363	A
53	3	1370	G
53	3	1379	G
53	3	1394	A
53	3	1400	C
53	3	1404	C
53	3	1419	G
53	3	1429	A
53	3	1446	A
53	3	1448	C
53	3	1452	C
53	3	1453	G
53	3	1487	G
53	3	1491	G

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Mol	Chain	Res	Type
53	3	1492	A
53	3	1497	G
53	3	1499	A
53	3	1503	A
53	3	1506	U
53	3	1507	A
53	3	1517	G
53	3	1518	A
53	3	1519	A
53	3	1529	G
53	3	1530	G
54	4	4	U
54	4	7	C
54	4	8	U
54	4	9	U
54	4	11	U
54	4	12	U
54	4	15	U
54	4	16	U
54	4	17	U
54	4	18	U
54	4	19	U
54	4	21	U
54	4	22	U
54	4	45	U
54	4	46	U
54	4	47	U
63	5	2	C
63	5	7	A
63	5	8	U
63	5	9	A
63	5	11	C
63	5	13	C
63	5	15	G
63	5	17	C
63	5	18	G
63	5	19	G
63	5	20	U
63	5	21	A
63	5	26	A
63	5	28	G
63	5	29	G

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Mol	Chain	Res	Type
63	5	30	G
63	5	32	U
63	5	33	U
63	5	34	G
63	5	35	A
63	5	36	A
63	5	37	A
63	5	39	U
63	5	40	C
63	5	41	C
63	5	43	C
63	5	44	G
63	5	46	G
63	5	47	U
63	5	48	C
63	5	49	C
63	5	52	G
63	5	53	G
63	5	55	U
63	5	57	G
63	5	58	A
63	5	59	U
63	5	60	U
63	5	61	C
63	5	66	U
63	5	73	A
63	5	74	C
63	5	76	A
64	6	2	G
64	6	9	G
64	6	18	G
64	6	19	G
64	6	20	U
64	6	46	G
64	6	47	U
64	6	59	A
64	6	74	C
64	6	76	A
64	7	2	G
64	7	7	G
64	7	8	U
64	7	9	G

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Mol	Chain	Res	Type
64	7	19	G
64	7	20	U
64	7	21	A
64	7	22	G
64	7	30	G
64	7	33	U
64	7	34	C
64	7	35	A
64	7	36	U
64	7	42	G
64	7	45	G
64	7	54	U
64	7	55	U
64	7	56	C
64	7	57	A
64	7	64	G
64	7	67	C
64	7	68	C
64	7	70	G
64	7	73	A
64	7	74	C
64	7	75	C
64	7	76	A

All (32) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	1	481	G
51	1	490	C
51	1	685	A
51	1	764	A
51	1	784	G
51	1	827	U
51	1	859	G
51	1	1020	A
51	1	1130	U
51	1	1715	G
51	1	1783	A
51	1	1801	A
51	1	1930	G
51	1	2275	C
51	1	2326	C

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Mol	Chain	Res	Type
51	1	2732	G
52	2	88	C
53	3	4	U
53	3	1035	A
53	3	1139	G
53	3	1224	U
54	4	11	U
54	4	16	U
63	5	7	A
63	5	29	G
63	5	32	U
63	5	39	U
63	5	48	C
63	5	57	G
63	5	60	U
64	7	33	U
64	7	56	C

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

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	$\# Z  > 2$
65	DPP	h	2	65	3,5,6	0.56	0	1,5,7	0.09	0
65	UAL	h	5	65	7,8,9	2.31	3 (42%)	5,9,11	2.90	2 (40%)
65	5OH	h	6	65	8,12,13	0.76	0	3,16,18	1.53	1 (33%)
65	KBE	h	1	65	8,8,9	0.61	0	7,8,10	1.21	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
65	DPP	h	2	65	-	0/2/4/6	-
65	UAL	h	5	65	-	0/3/7/9	-
65	5OH	h	6	65	-	0/2/18/20	0/1/1/1
65	KBE	h	1	65	-	0/7/7/8	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	h	5	UAL	C1-N1	-4.92	1.32	1.40
65	h	5	UAL	C-CA	-2.87	1.40	1.45
65	h	5	UAL	CA-N	2.01	1.40	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	h	5	UAL	CA-CB-N1	-5.28	115.65	125.60
65	h	5	UAL	O-C-CA	-3.23	121.28	125.39
65	h	6	5OH	CR-CB-CA	-2.40	110.02	112.61
65	h	1	KBE	CB-CA-C	-2.07	109.21	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
65	h	2	DPP	1	0
65	h	5	UAL	1	0
65	h	6	5OH	5	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.



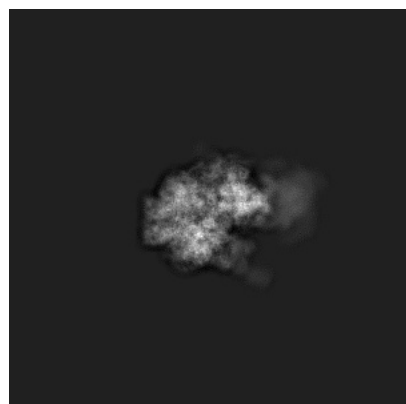
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39171. These allow visual inspection of the internal detail of the map and identification of artifacts.

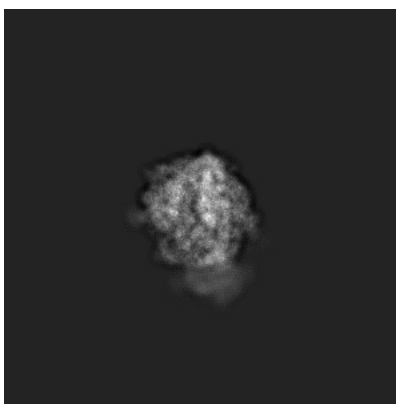
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

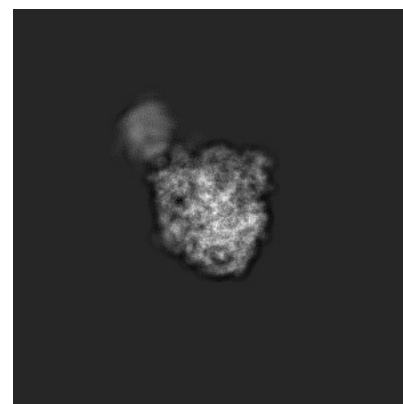
#### 6.1.1 Primary map



X

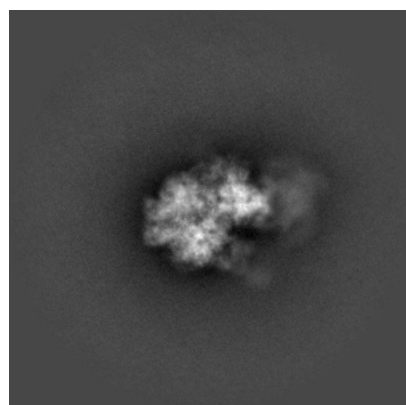


Y

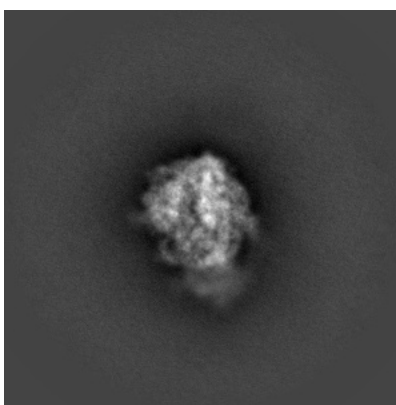


Z

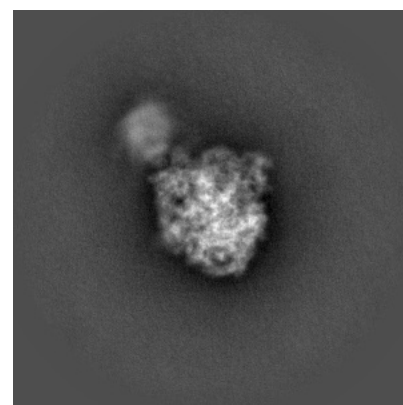
#### 6.1.2 Raw map



X



Y

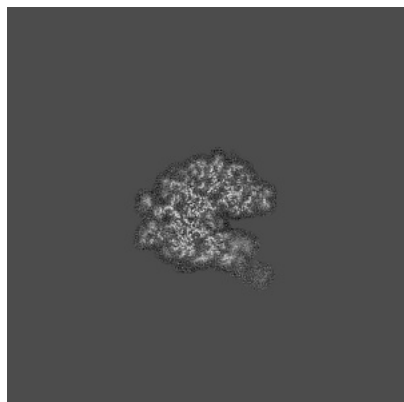


Z

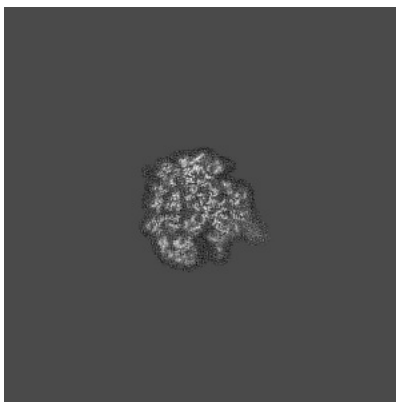
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

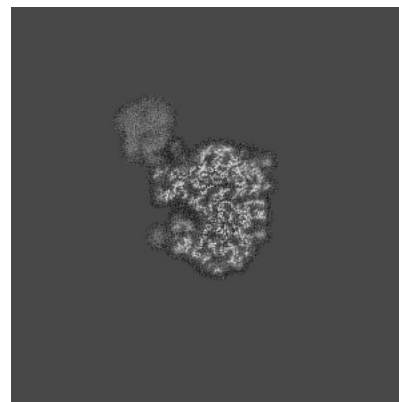
### 6.2.1 Primary map



X Index: 240

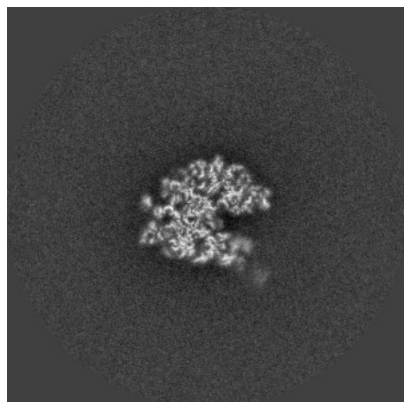


Y Index: 240

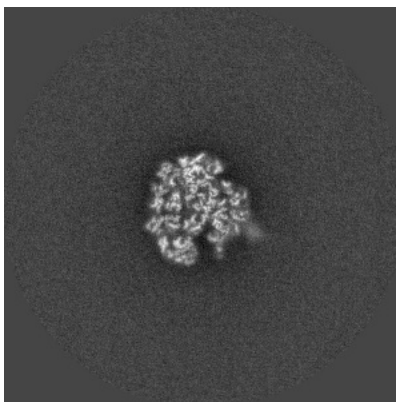


Z Index: 240

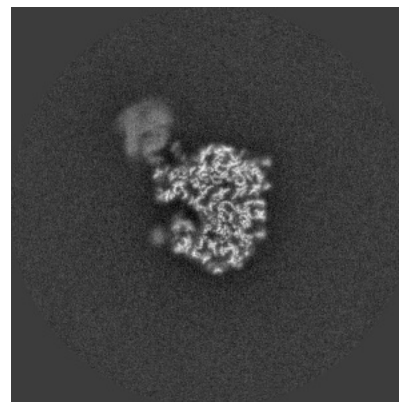
### 6.2.2 Raw map



X Index: 240



Y Index: 240

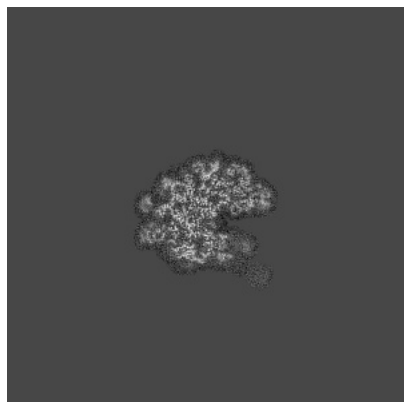


Z Index: 240

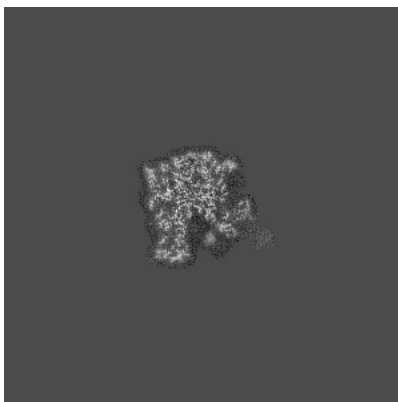
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

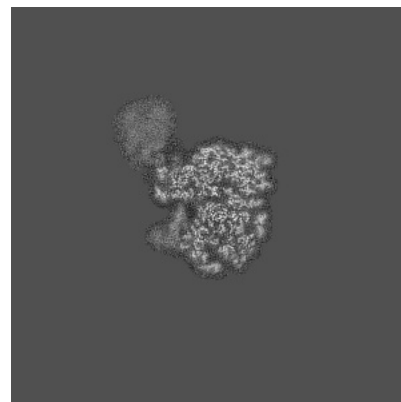
### 6.3.1 Primary map



X Index: 243

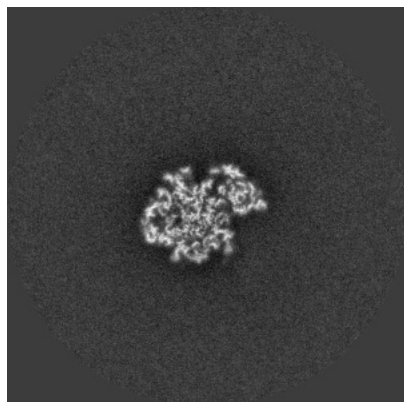


Y Index: 228

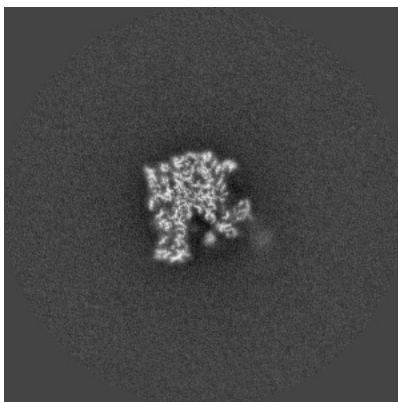


Z Index: 245

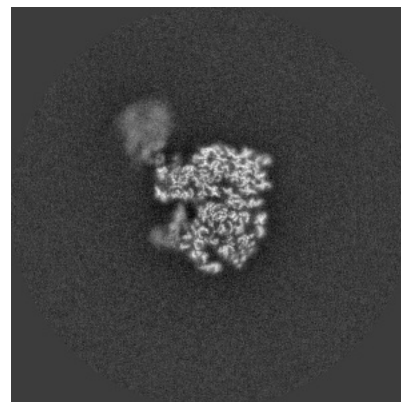
### 6.3.2 Raw map



X Index: 265



Y Index: 228

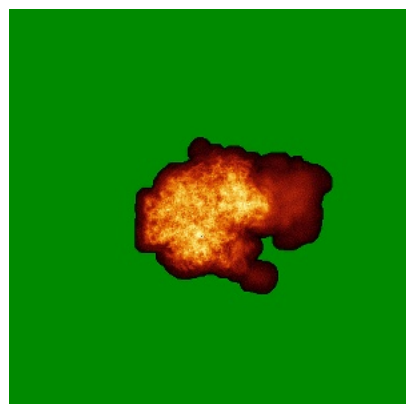


Z Index: 245

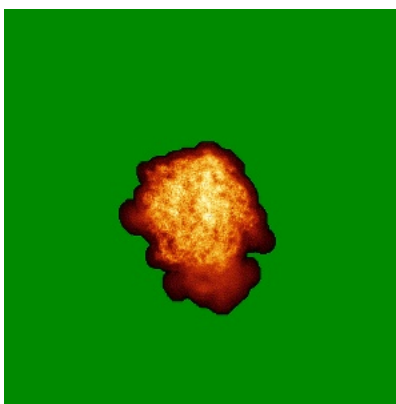
The images above show the largest variance slices of the map in three orthogonal directions.

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

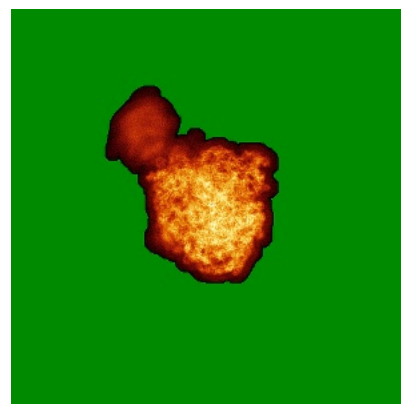
### 6.4.1 Primary map



X

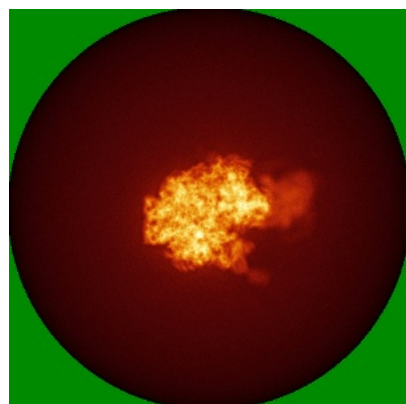


Y

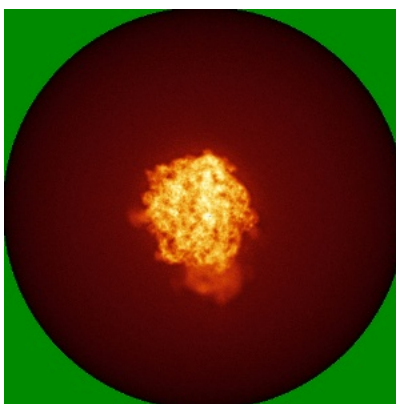


Z

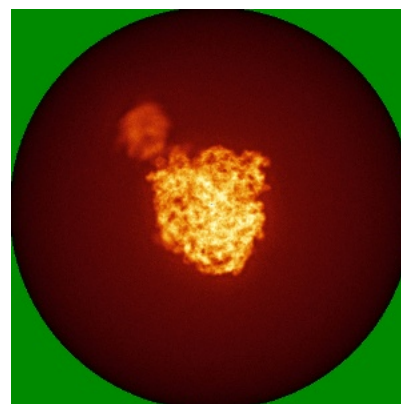
### 6.4.2 Raw map



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.

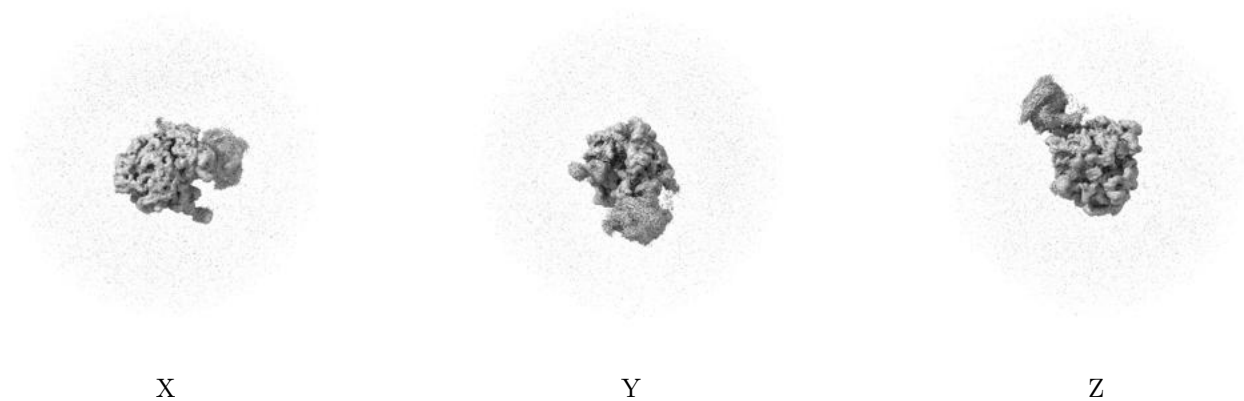
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.011. 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.

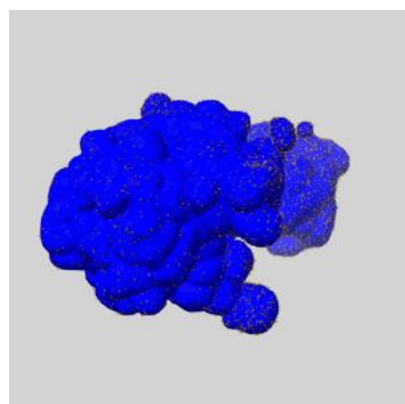
## 6.6 Mask visualisation [i](#)

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

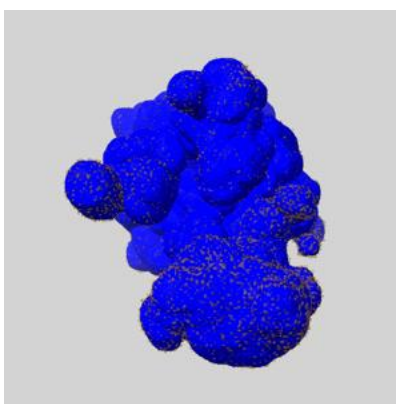
A mask typically either:

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

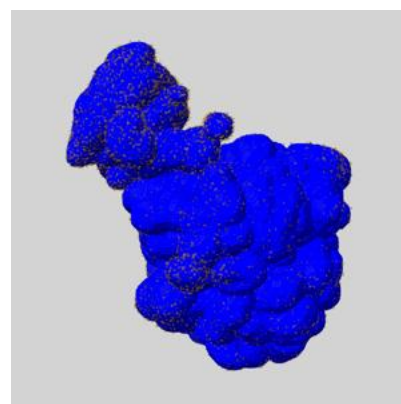
### 6.6.1 emd\_39171\_msk\_1.map [i](#)



X



Y

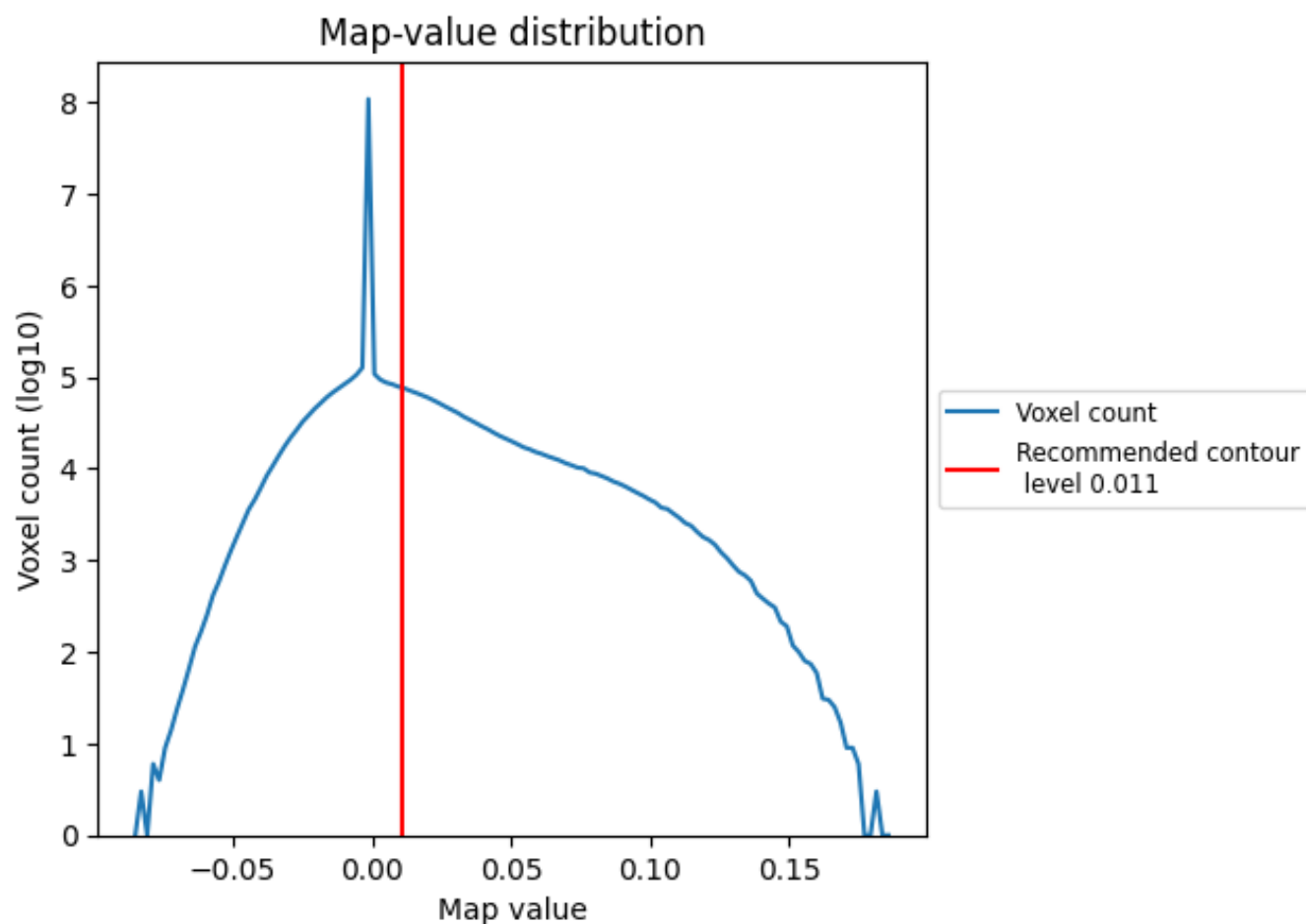


Z

## 7 Map analysis [i](#)

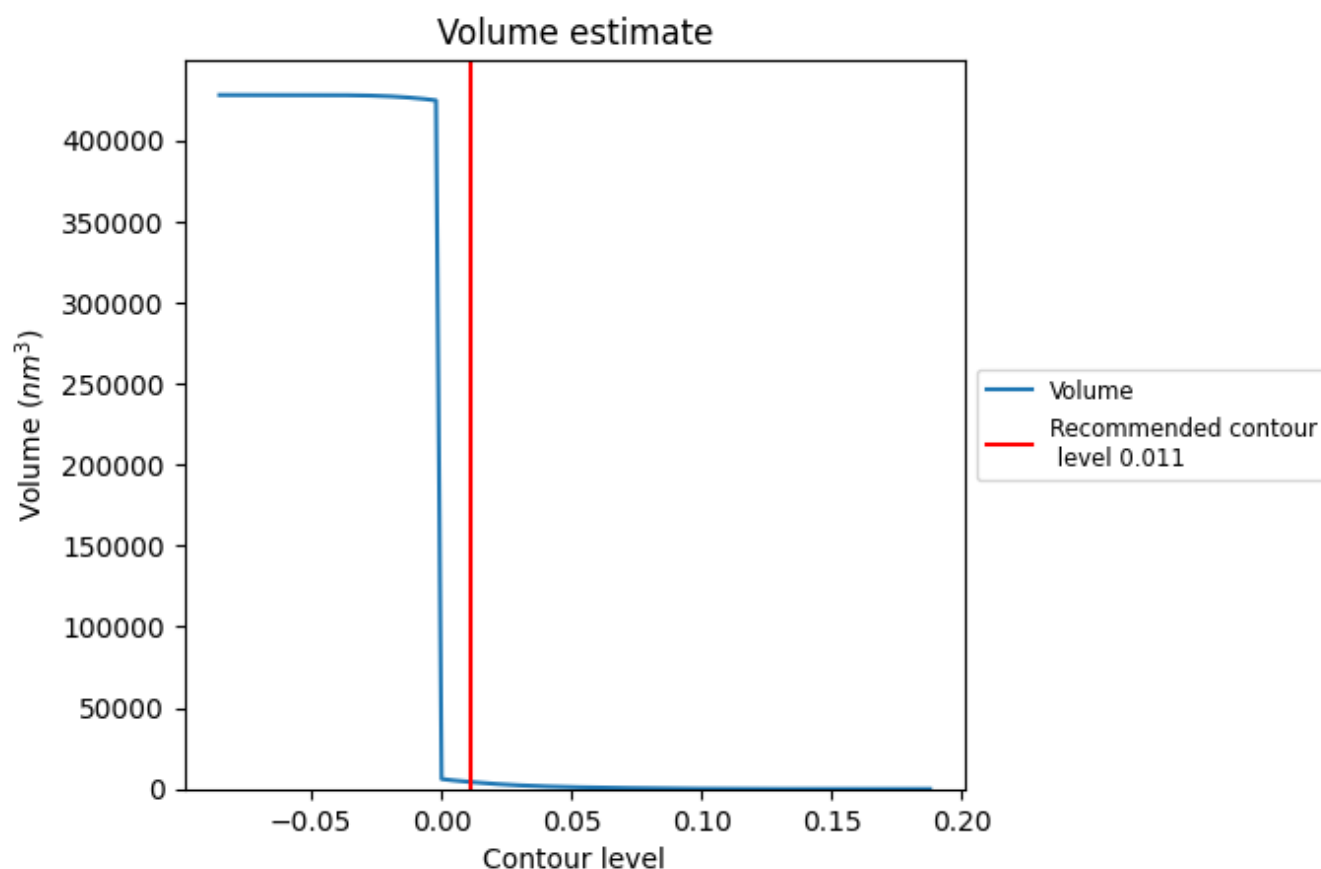
This section contains the results of statistical analysis of the map.

### 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](#)

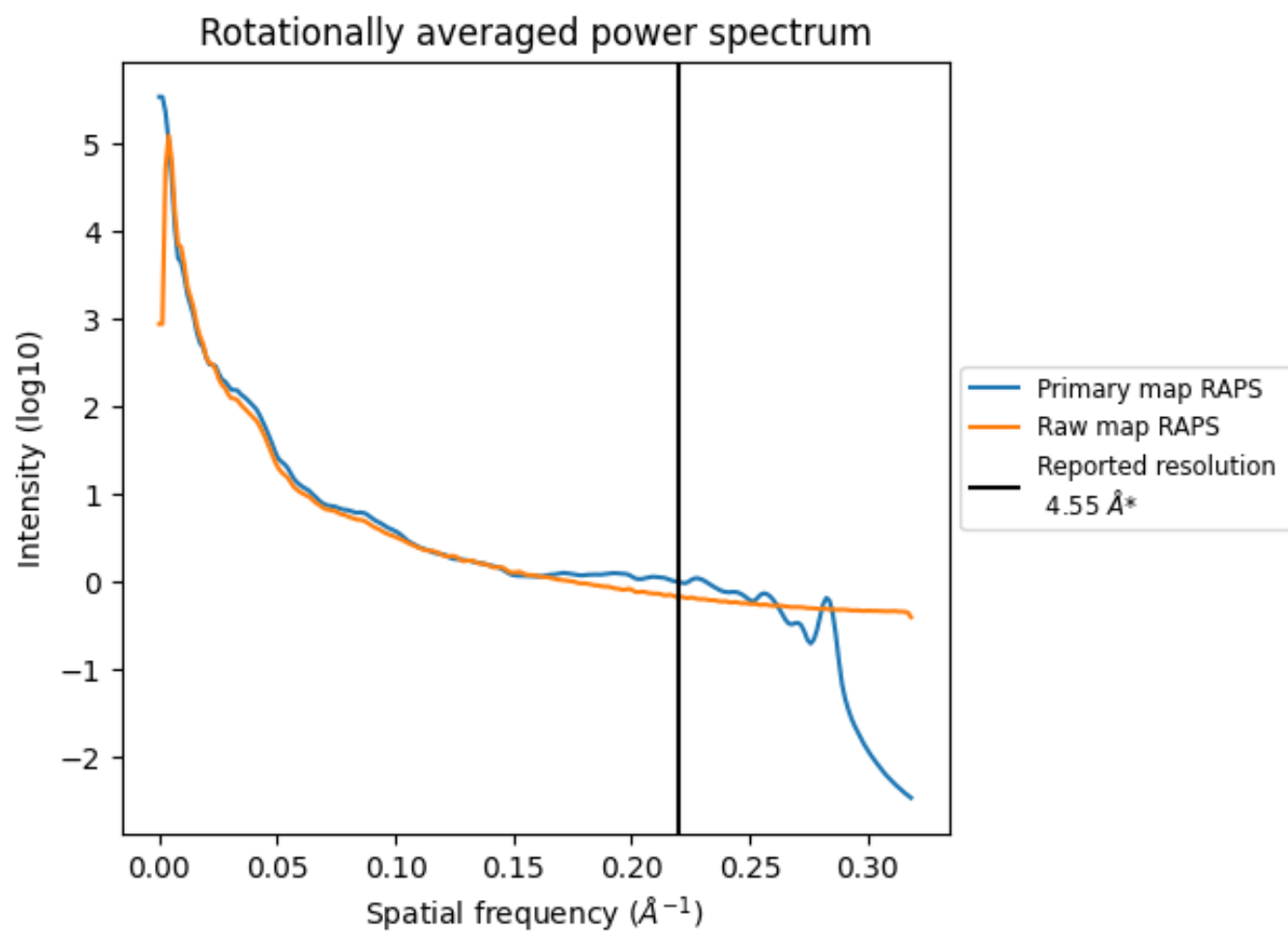


The volume at the recommended contour level is 4328  $\text{nm}^3$ ; this corresponds to an approximate mass of 3910 kDa.

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 ⓘ

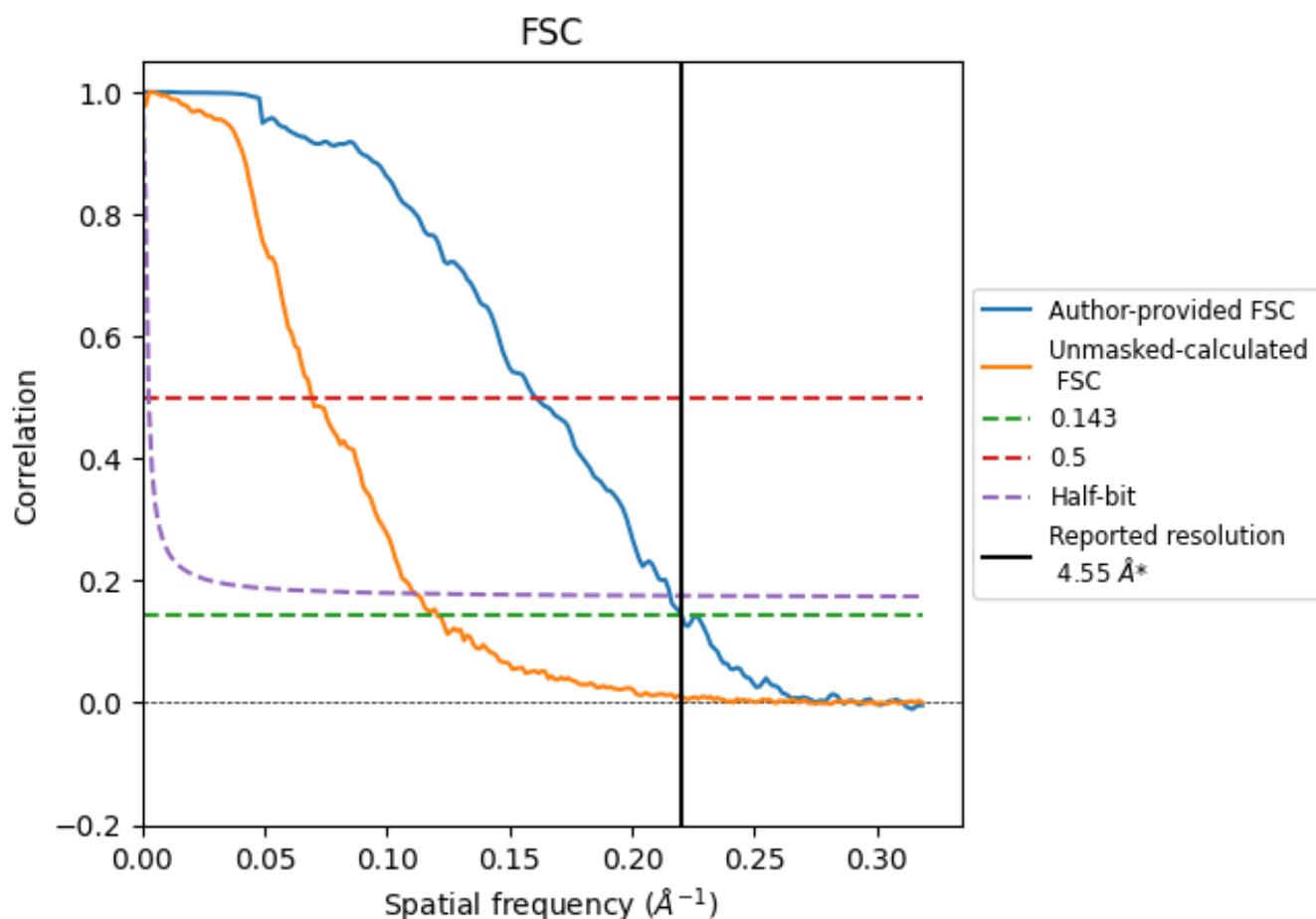


\*Reported resolution corresponds to spatial frequency of 0.220 Å<sup>-1</sup>

## 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 0.220  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

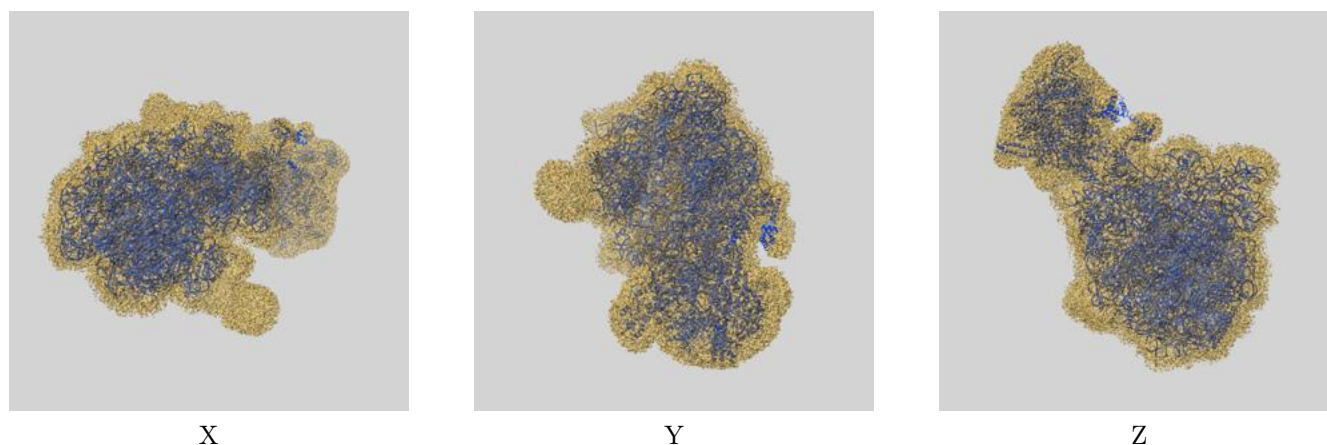
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.55	-	-
Author-provided FSC curve	4.54	6.23	4.64
Unmasked-calculated*	8.29	14.43	8.99

\*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 8.29 differs from the reported value 4.55 by more than 10 %

## 9 Map-model fit [i](#)

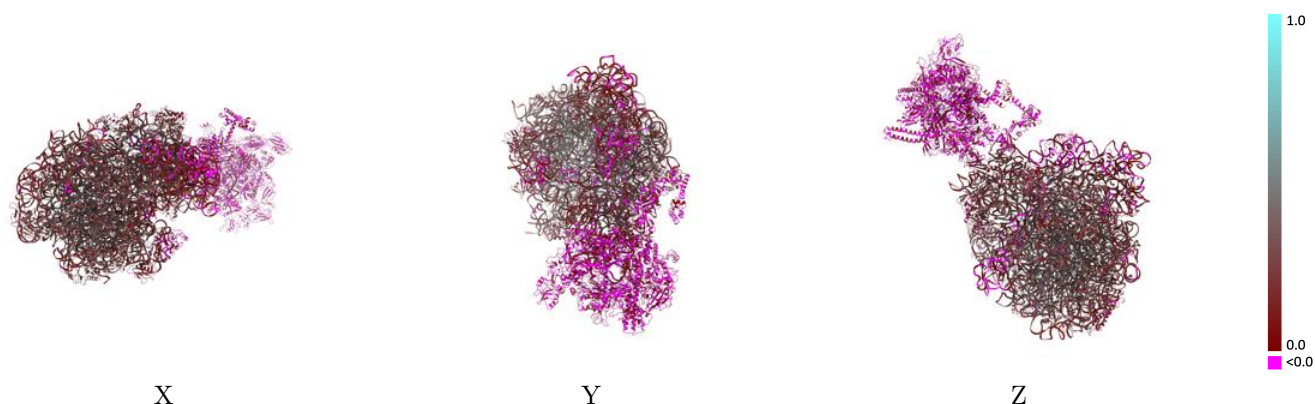
This section contains information regarding the fit between EMDB map EMD-39171 and PDB model 8YDH. Per-residue inclusion information can be found in section [3](#) on page [16](#).

### 9.1 Map-model overlay [i](#)



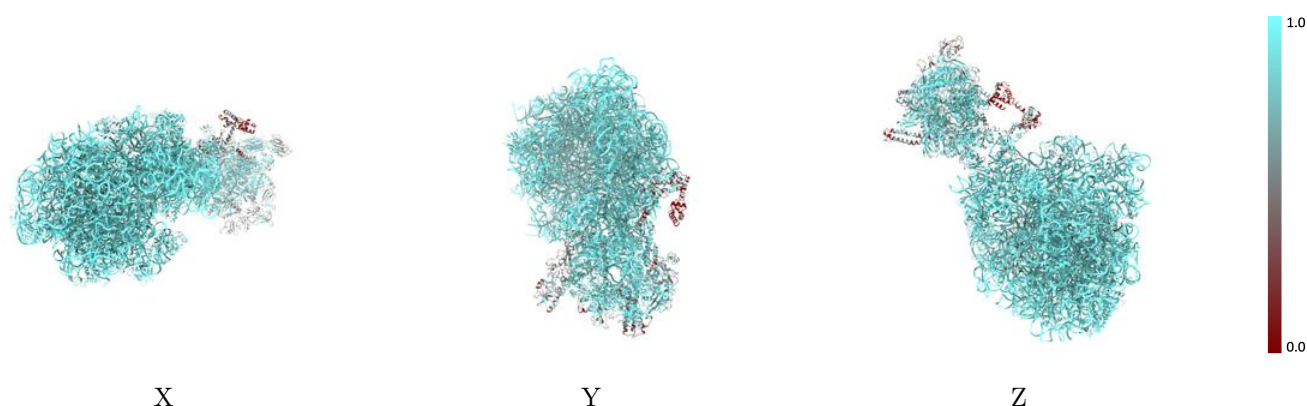
The images above show the 3D surface view of the map at the recommended contour level 0.011 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



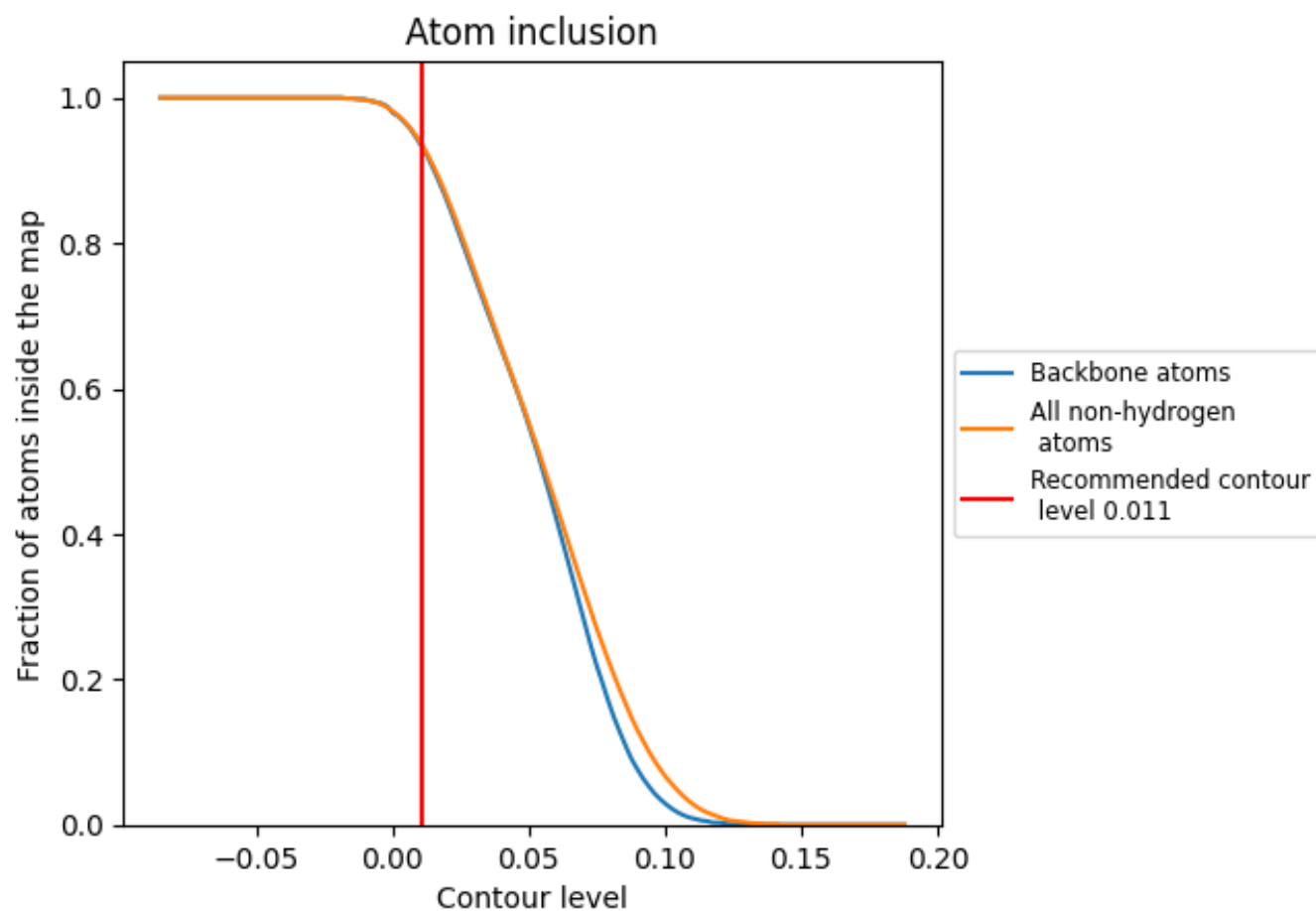
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.011).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 93% 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 (0.011) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9340	 0.2260
1	 0.9900	 0.3100
2	 0.9910	 0.2590
3	 0.9830	 0.2500
4	 0.8270	 0.0830
5	 0.9240	 0.1000
6	 0.9870	 0.3050
7	 0.7770	 0.0540
8	 0.8570	 0.0020
9	 0.9230	 0.0700
A	 0.8900	 0.1890
A1	 0.6540	 -0.0010
A2	 0.7980	 0.0170
B	 0.9600	 0.3140
B1	 0.7830	 0.0090
B2	 0.7870	 0.0140
C	 0.9300	 0.2990
D	 0.9490	 0.3370
E	 0.9490	 0.3470
F	 0.9280	 0.2270
G	 0.9270	 0.1850
H	 0.9190	 0.2580
I	 0.8260	 0.0500
J	 0.9500	 0.2820
K	 0.9360	 0.2160
L	 0.9290	 0.2040
M	 0.9430	 0.2750
N	 0.9540	 0.1940
NA	 0.5560	 0.0200
NG	 0.8290	 0.0140
O	 0.9240	 0.1910
P	 0.9440	 0.2610
Q	 0.8950	 0.2090
R	 0.9540	 0.2150
S	 0.9470	 0.2240



*Continued on next page...*

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Chain	Atom inclusion	Q-score
T	 0.9460	 0.2380
U	 0.8740	 0.1020
V	 0.8970	 0.1510
W	 0.9610	 0.2360
W0	 0.5790	 0.0370
X	 0.9400	 0.1940
Y	 0.9010	 0.1440
Z	 0.8700	 0.1690
b	 0.9530	 0.3590
c	 0.9380	 0.2780
d	 0.9570	 0.2770
e	 0.9550	 0.2630
f	 0.9550	 0.1620
g	 0.9520	 0.2110
h	 0.9380	 0.2200
i	 0.8340	 0.0160
j	 0.9620	 0.2990
k	 0.8860	 0.2660
l	 0.9680	 0.3070
m	 0.9300	 0.2990
n	 0.9630	 0.2950
o	 0.9660	 0.2310
p	 0.9200	 0.2140
q	 0.9600	 0.3200
r	 0.9690	 0.2970
s	 0.9230	 0.2970
t	 0.9240	 0.1900
u	 0.9610	 0.2110
v	 0.9580	 0.2300
w	 0.9360	 0.3050
x	 0.9530	 0.3240
y	 0.9540	 0.1810
z	 0.9630	 0.2960