



Full wwPDB EM Validation Report ⓘ

Aug 18, 2025 – 02:52 PM JST

PDB ID : 8YDE / pdb_00008yde
EMDB ID : EMD-39168
Title : E.coli transcription translation coupling complex in TTC-B state 1 (subclass 3) 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 : 5.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

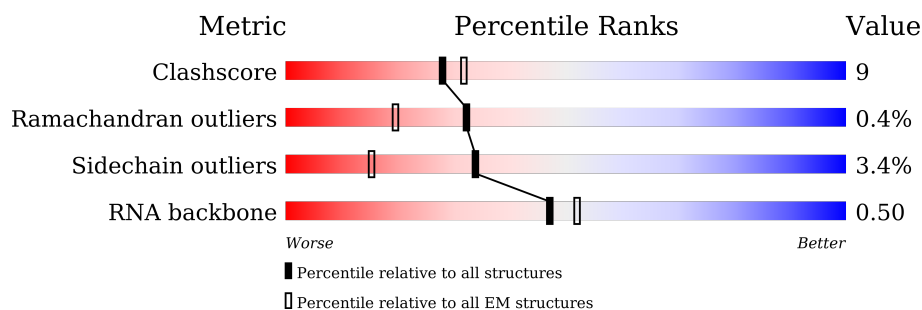
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.00 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 ≥ 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	<div> <div>6%</div> <div> <div></div> <div>81%</div> <div>13%</div> <div>6%</div> </div> </div>
2	B	57	<div> <div>79%</div> <div>19%</div> <div>.</div> </div>
3	C	55	<div> <div>80%</div> <div>11%</div> <div>9%</div> </div>
4	D	46	<div> <div>76%</div> <div>22%</div> <div>.</div> </div>
5	E	65	<div> <div>89%</div> <div>9%</div> <div>.</div> </div>
6	F	38	<div> <div>66%</div> <div>32%</div> <div>.</div> </div>
7	G	241	<div> <div>66%</div> <div>23%</div> <div>.</div> <div>10%</div> </div>

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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	56	
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	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
65	5OH	h	6	-	-	X	-

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 178130 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	301	Total	C	N	O	S	0	0
			2088	1293	380	409	6		
57	A2	288	Total	C	N	O	S	0	0
			2029	1257	366	400	6		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
59	B2	1340	Total	C	N	O	S	0	0
			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 Viomycin.

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

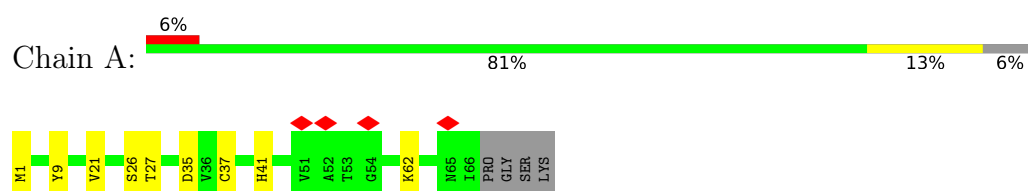
- Molecule 66 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

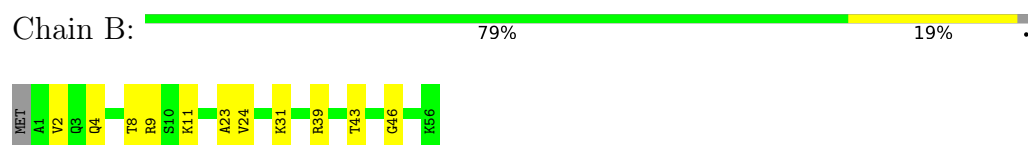
3 Residue-property plots [i](#)

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.

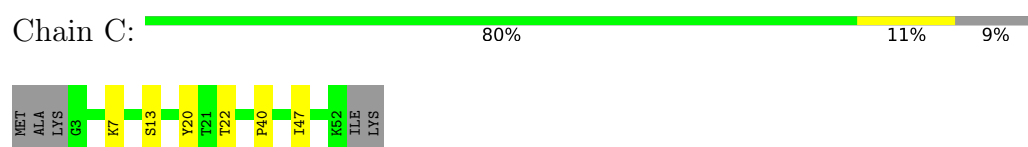
- Molecule 1: 50S ribosomal protein L31



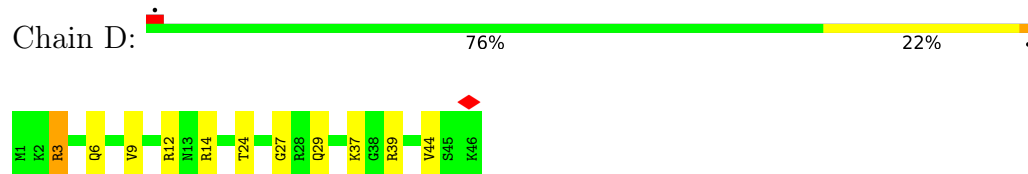
- Molecule 2: 50S ribosomal protein L32



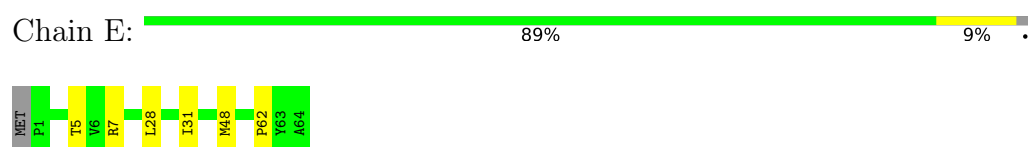
- Molecule 3: 50S ribosomal protein L33



- Molecule 4: 50S ribosomal protein L34



- Molecule 5: 50S ribosomal protein L35



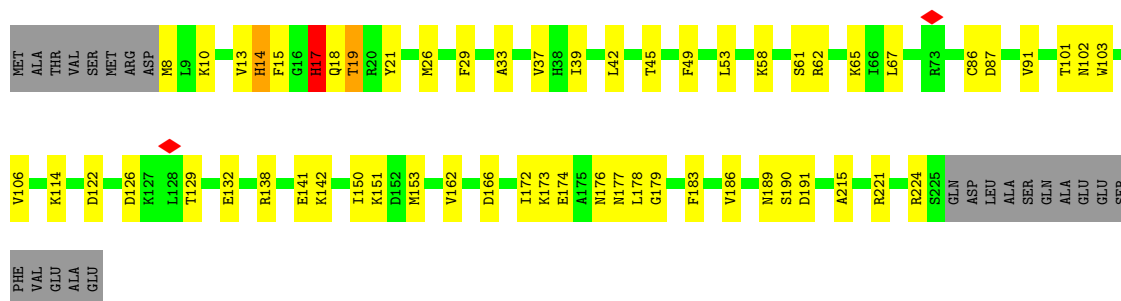
- Molecule 6: 50S ribosomal protein L36

Chain F:  66% 32% .



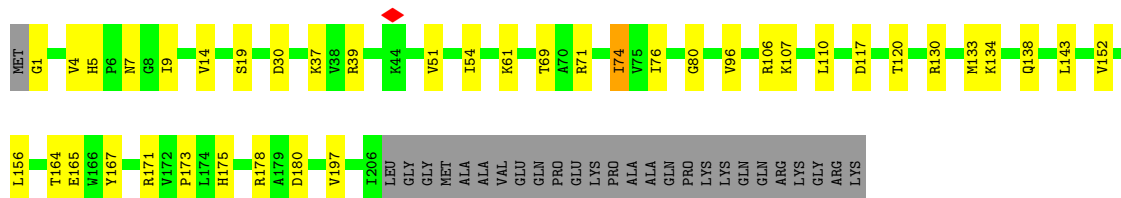
- Molecule 7: 30S ribosomal protein S2

Chain G:  66% 23% 10%




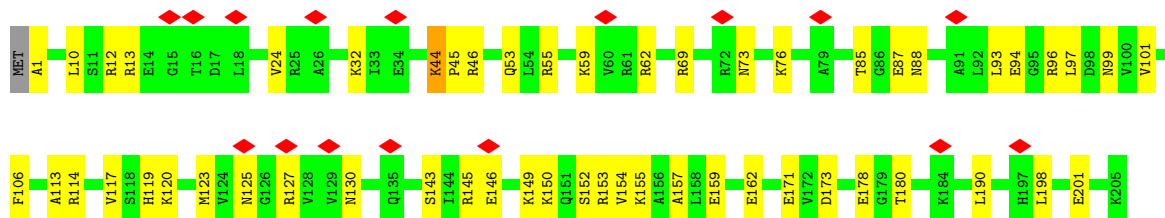
- Molecule 8: 30S ribosomal protein S3

Chain H:  71% 17% 12%



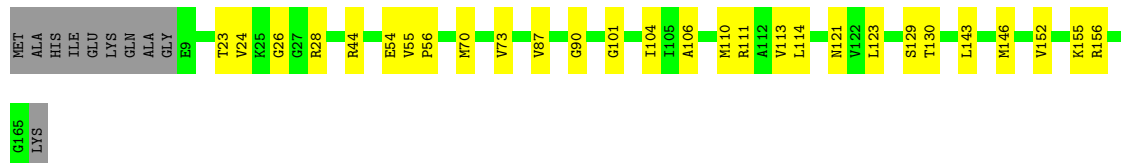
- Molecule 9: 30S ribosomal protein S4

Chain I:  8% 73% 26%

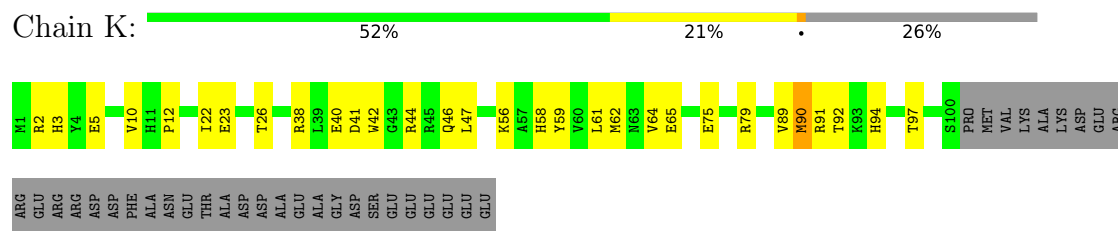


- Molecule 10: 30S ribosomal protein S5

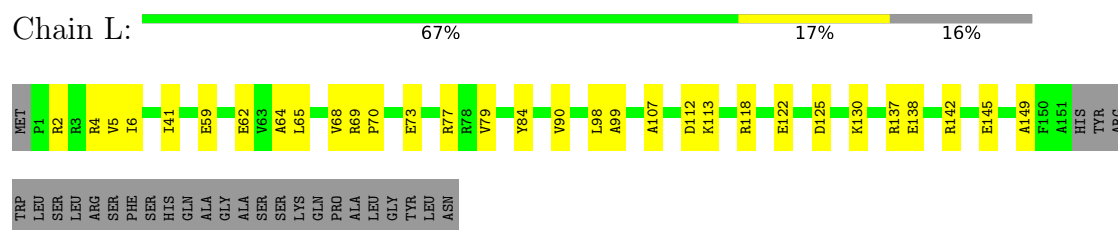
Chain J:  77% 17% 6%



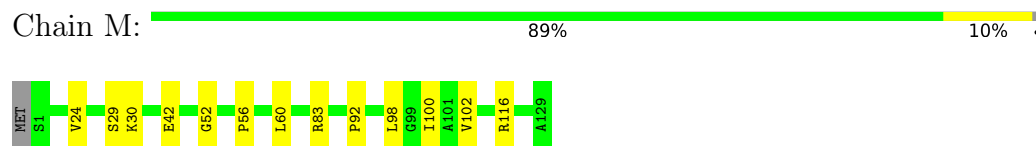
- Molecule 11: 30S ribosomal protein S6, fully modified isoform



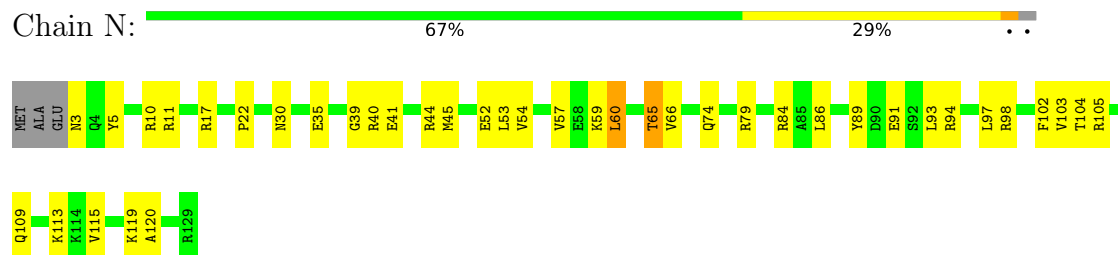
- Molecule 12: 30S ribosomal protein S7



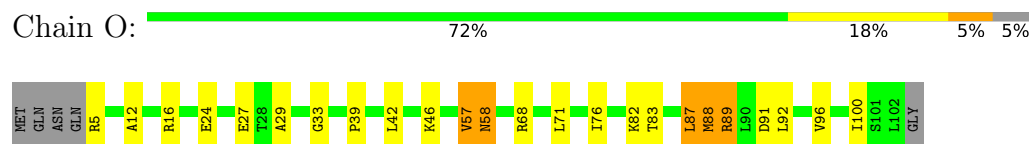
- Molecule 13: 30S ribosomal protein S8



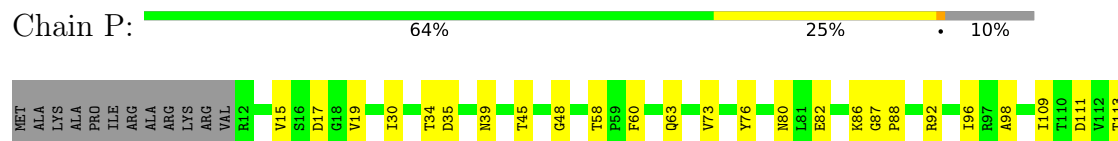
- Molecule 14: 30S ribosomal protein S9

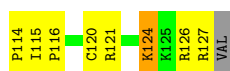


- Molecule 15: 30S ribosomal protein S10



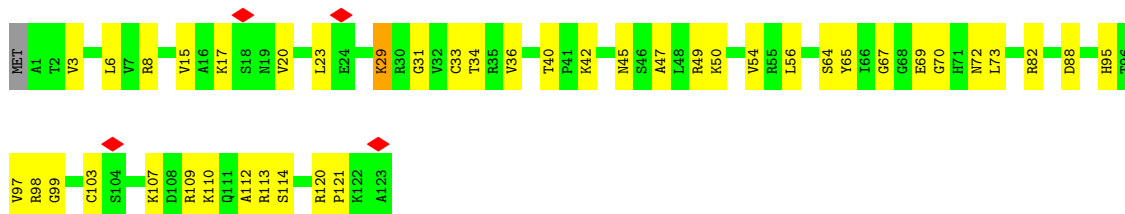
- Molecule 16: 30S ribosomal protein S11





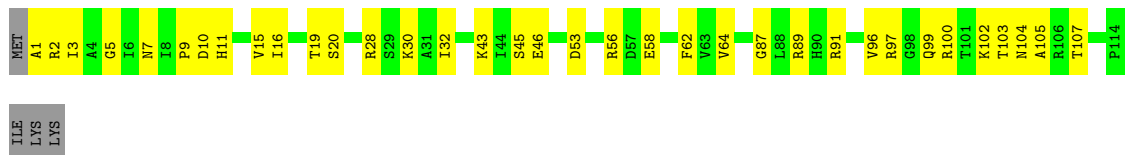
- Molecule 17: 30S ribosomal protein S12

Chain Q: 65% 33%



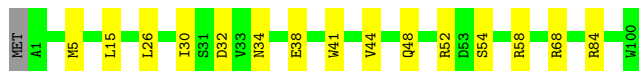
- Molecule 18: 30S ribosomal protein S13

Chain R: 67% 30%



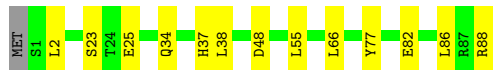
- Molecule 19: 30S ribosomal protein S14

Chain S: 84% 15%



- Molecule 20: 30S ribosomal protein S15

Chain T: 84% 15%



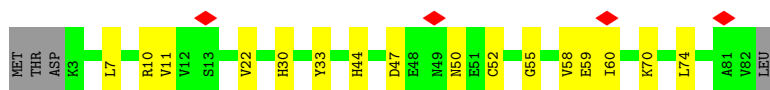
- Molecule 21: 30S ribosomal protein S16

Chain U: 7% 76% 23%



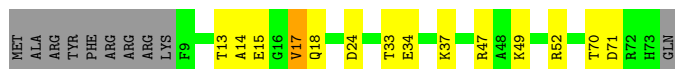
- Molecule 22: 30S ribosomal protein S17

Chain V: 5% 76% 19% 5%



- Molecule 23: 30S ribosomal protein S18

Chain W: 68% 17% 13%



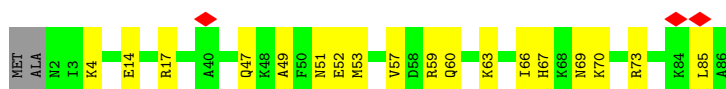
- Molecule 24: 30S ribosomal protein S19

Chain X: 74% 12% 14%



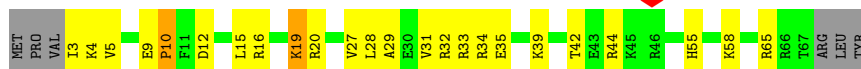
- Molecule 25: 30S ribosomal protein S20

Chain Y: 77% 21% 2%



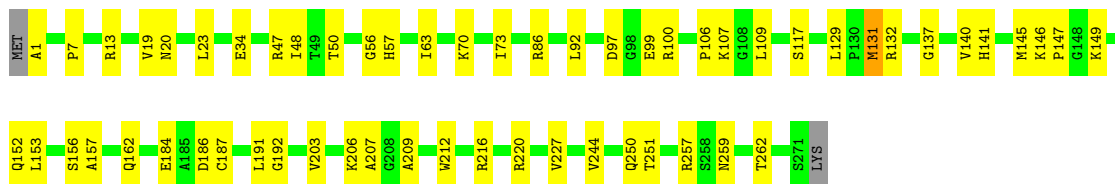
- Molecule 26: 30S ribosomal protein S21

Chain Z: 58% 31% 8%



- Molecule 27: 50S ribosomal protein L2

Chain b: 78% 21% 1%



- Molecule 28: 50S ribosomal protein L3

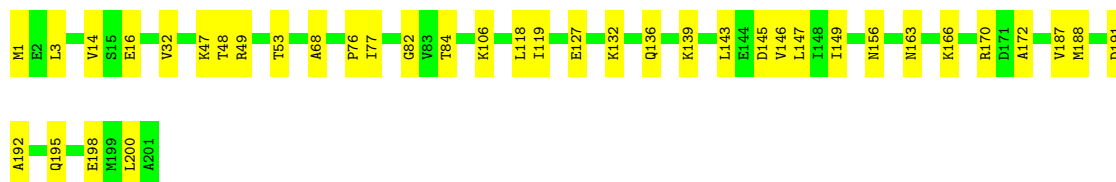
Chain c: 85% 15%





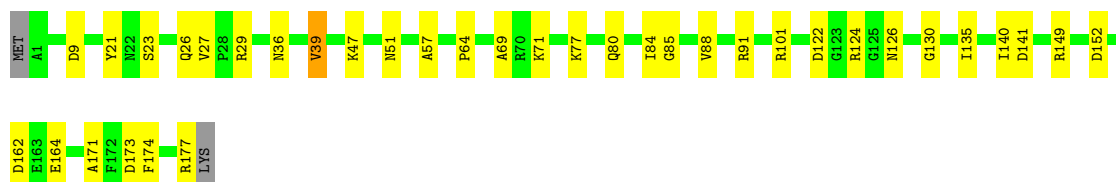
- Molecule 29: 50S ribosomal protein L4

Chain d: 81% 19%



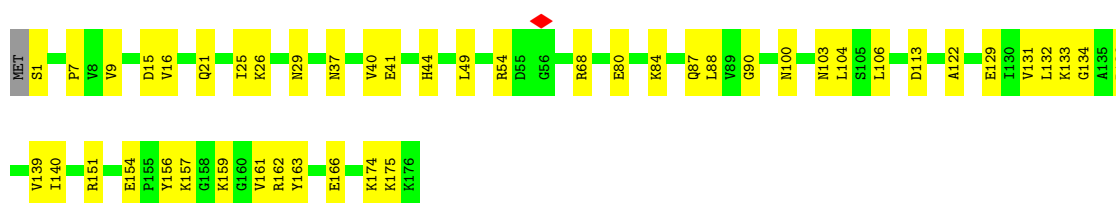
- Molecule 30: 50S ribosomal protein L5

Chain e: 79% 20% ..



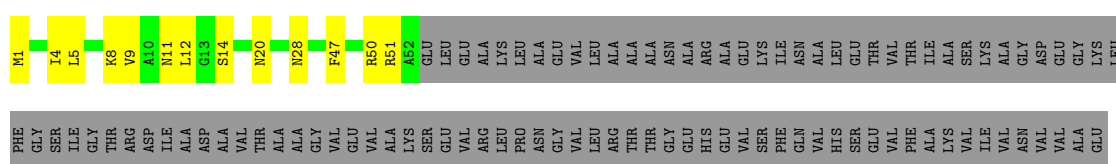
- Molecule 31: 50S ribosomal protein L6

Chain f: 73% 26% .



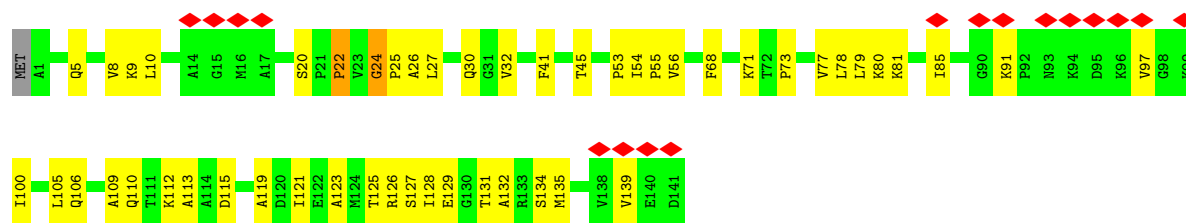
- Molecule 32: 50S ribosomal protein L9

Chain g: 26% 9% 65%



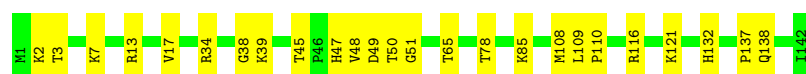
- Molecule 33: 50S ribosomal protein L11

Chain i: 12% 64% 34% ..



- Molecule 34: 50S ribosomal protein L13

Chain j: 82% 18%



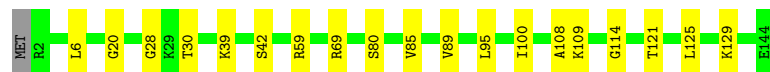
- Molecule 35: 50S ribosomal protein L14

Chain k: 81% 18%



- Molecule 36: 50S ribosomal protein L15

Chain l: 86% 13%



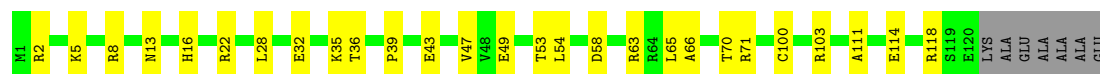
- Molecule 37: 50S ribosomal protein L16

Chain m: 83% 17%



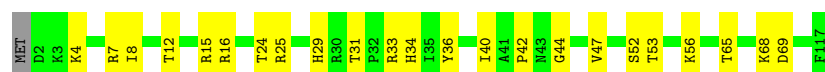
- Molecule 38: 50S ribosomal protein L17

Chain n: 73% 21% 6%




- Molecule 39: 50S ribosomal protein L18

Chain o: 79% 20%




- Molecule 40: 50S ribosomal protein L19

Chain p:  84% 15%



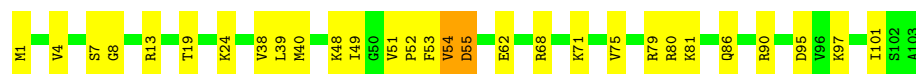
- Molecule 41: 50S ribosomal protein L20

Chain q:  84% 14%




- Molecule 42: 50S ribosomal protein L21

Chain r:  72% 26%



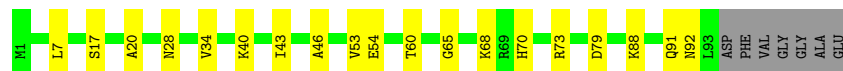
- Molecule 43: 50S ribosomal protein L22

Chain s:  85% 15%



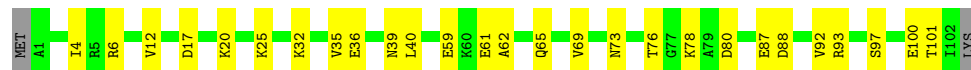
- Molecule 44: 50S ribosomal protein L23

Chain t:  74% 19% 7%




- Molecule 45: 50S ribosomal protein L24

Chain u:  72% 26%



- Molecule 46: 50S ribosomal protein L25

Chain v:  85% 15%



- Molecule 47: 50S ribosomal protein L27

Chain w:  74% 14% 12%




- Molecule 48: 50S ribosomal protein L28

Chain x:  74% 23% ..



- Molecule 49: 50S ribosomal protein L29

Chain y:  76% 24%



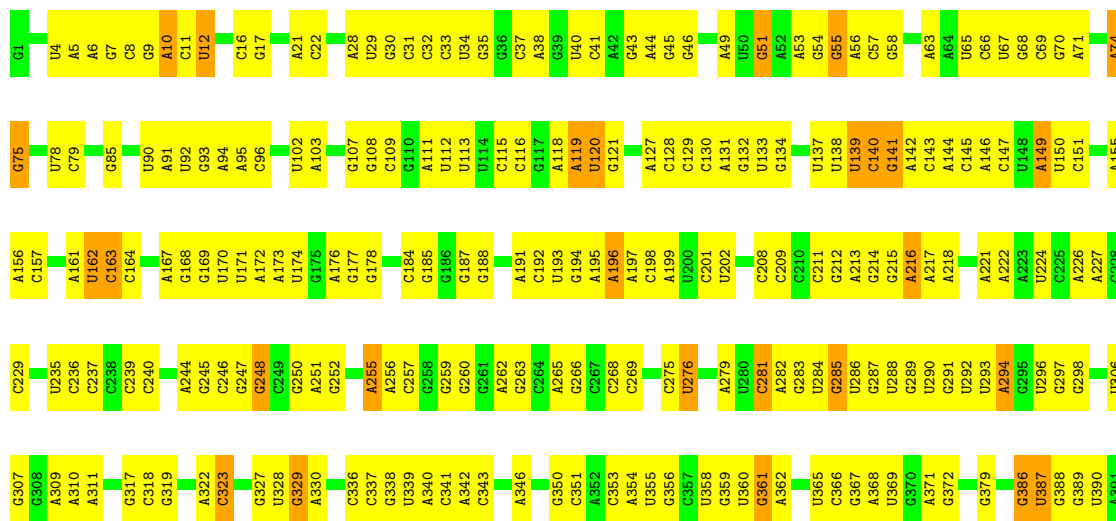
- Molecule 50: 50S ribosomal protein L30

Chain z:  76% 22% .



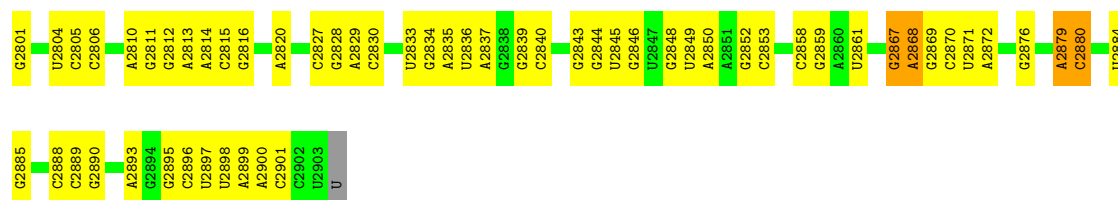
- Molecule 51: 23S rRNA

Chain 1:  42% 51% 7%



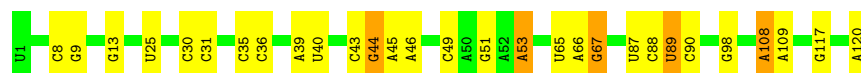
C1507	G1436	G1334	G1266	U1173	G1106	G1044	U958	A877	A800	G707	C624	U546	A472	U392
A1508	A1427	C1335	U1267	U1174	G1107	C1045	A959	A878	G801	G708	C627	A547	G473	C393
A1509	C1428	A1336	G1287	A1175	U1108	A1046	A960	G879	G805	U709	A627	G548	G474	C394
G1510	G1429	G1337	G1270	U1176	C1109	G1047	C961	G885	G809	G712	G628	G550	G475	U395
C1511	G1430	G1338	C1271	G1177	G1110	A1048	C968	C886	U810	G713	G629	C551	G396	G396
C1512	A1431	G1339	A1272	C1178	A1111	A1049	C968	U887	G809	G713	G630	U552	U397	
	G1432		U1273	G1179	G1112	A1050	A972	C888	U811	A718	A633	U553	G481	
A1515	A1433	G1343	A1274	U1180	C1113		A973	C889	G812	C719	C634	U554	A482	A402
G1516	A1434	U1344	U1275	U1181	G1114	A1054	A974	C890	C813	U720	C635	U555	C485	A403
G1517	G1435	C1345	A1276	U1182	G1115	G1055	A975	C891	U813	U721	C636	A556	U405	A404
C1518	G1436	G1346	G1278	U1183	G1116	G1056	A976	C892	C814	A721	C637	C557	G487	U406
G1519	C1437	A1347	C1279	U1184	C1117	A1057	A977	A892	C815	A722	A637	U558	G488	
U1520	G1438	G1348	G1279	U1185	C1118	U1058	A979	C893	A819	C723	G638		G489	G409
G1521	C1349	U1349	G1280	U1186	U1119	G1059	A880	U894	A821	U724	U639	U562	C490	G410
A1522			U1281	G1187	G1120	U1060	C982	U895	A822	G725	U641	A563	C491	G411
U1523	U1440	U1352	U1282	U1188	C1121	U1061	A984	A896	A823	A727			A492	
G1524	U1442		G1283	G1193	G1123	G1062	A984	C897	A824				G493	
A1525	A1284	A1365	A1284	G1194	C1124	G1063	C985	C898	A825	A728	A644	U566	G494	C414
C1526	A1285	A1366	A1285	A1194	G1124	C1064	C985	A899	U826	G729	C645	U567	A415	A415
G1527	A1286	A1367	A1286	G1195		U1065	G989	A900	U827	A730	C646	U568	U416	U416
A1528	A1287	A1368	A1287	U1196	U1130	U1066		C901	U828		C647	U569	U419	U419
G1529	G1288	G1369	G1288	G1197	G1131	A1067	G993	C902	A829	C736	G648	U570	U499	C420
G1530	C1289	C1289	C1289	U1198	U1132	G1068	C994	C903	G830		G649	U571	G500	
				U1199	A1133	A1069	C995	A904	U831	G745	U652	A572	A501	C421
				C1200	A1134	A1070	C996	A905	U832	U746	U653	U573	A502	A422
C1533	G1292	C1293	G1292	U1201	C1135	G1071	A996	U906	A833	C747	U654	A574	A503	A423
U1534	C1293	C1293	C1293	A1204	G1136	A1072	C1005	G907	G834		U655	A575	A504	G424
A1535	U1294	U1294	U1294	A1205	U1137	C1073	C1006	C908	C835	A752	A654	U580	A505	G425
C1536	G1295	G1295	G1295	U1206	G1138	A1074	A1009	A909	G836	G757	G656	U580	G506	C426
G1537	C1296	C1296	C1296	G1210	U1141	U1075	A1010	A910	C837		G662	A586	C510	U427
C1538	G1297	G1297	G1297	U1209	U1142	C1076	G1011	A911	C840	G759	U669	A590	U511	U431
U1539	C1298	C1298	C1298	G1211	A1143	U1077	G1012	G914	G841	G760	A670	U591	U512	A432
G1540	A1386	A1387	G1299	U1210	U1144	U1078	C1013	C915	U842	A761	U671	A592	G518	U433
U1466	G1300	G1300	G1300	G1212	A1145	C1079	U1014	A918	A845	G763	C672	U593	U519	C435
C1541	C1301	C1301	C1301	A1213	A1144	U1080	U1015	U919	U846	A764	C673	U594	G520	C436
U1468				U1219	A1145	U1081	A1020	G923	U847	C765	G674	C595	U521	U437
G1543	C1306	C1306	C1306	G1220	A1147	U1082	A1021	G924	C848	G774	A677	U596	A522	G438
A1544				U1225	U1148	U1083	G1031	G925	C849	G775	C678	G597	A526	A439
U1545	G1309	G1310	G1310	G1226	G1149	A1084	U1033	A926	U850	U779	C679	U599	C527	C440
G1546	G1311	G1311	G1311	U1230	C1150	A1085	G1034	G927	U851	U780	C680	A603	A528	C442
				U1231	A1151	A1086	U1035	A941	C852	A781	G681		G529	C445
A1551	C1314	C1314	C1314	G1232	C1152	G1087	G1036	G942	U853	A782	U683	U607	C531	G446
A1552	U1315	U1315	U1315	C1233	C1153	A1088	G1037	G943	C854	G785	G682	A608	U451	U451
U1554	G1316	G1316	G1316	U1237	G1155	A1089	G1038	G946	C855		G683	A609	U534	C452
G1555	U1317	U1317	U1317	G1238	A1156	A1090	G1039	A947	U856		G684	C610	G535	
				U1239	U1157	C1091	U1040	U955	G858		G685	C611	G536	A457
				U1240	G1157	C1092	A1041	U956	U859		G686	C612	G537	
				U1241	G1160	G1093	U1042	U957	U860		G687	A613	G538	C461
				A1246	C1161	U1094	G1043	G940			U688	A614	G539	C462
				A1247	G1162	A1095	U1044	A941	G864		G695	U615	G540	C463
					G1163	A1096	U1045	G942	C865		G696	A616	C541	C464
				A1253	C1164	U1097	G1046	G943	U870		G697		C542	G465
				U1254	A1165	A1098	G1047	G944	U871				C543	A466
				U1255	G1166	G1099	A1048	A947	U872				G544	G467
				U1256	U1101	G1100	A1049		U873					
				G1257	C1102	U1101	A1040		U874					
				U1258	A1103	U1102	G1041		U875					
				G1259	C1104	U1103	G1042		C876					
					C1172	U1105	C1043							





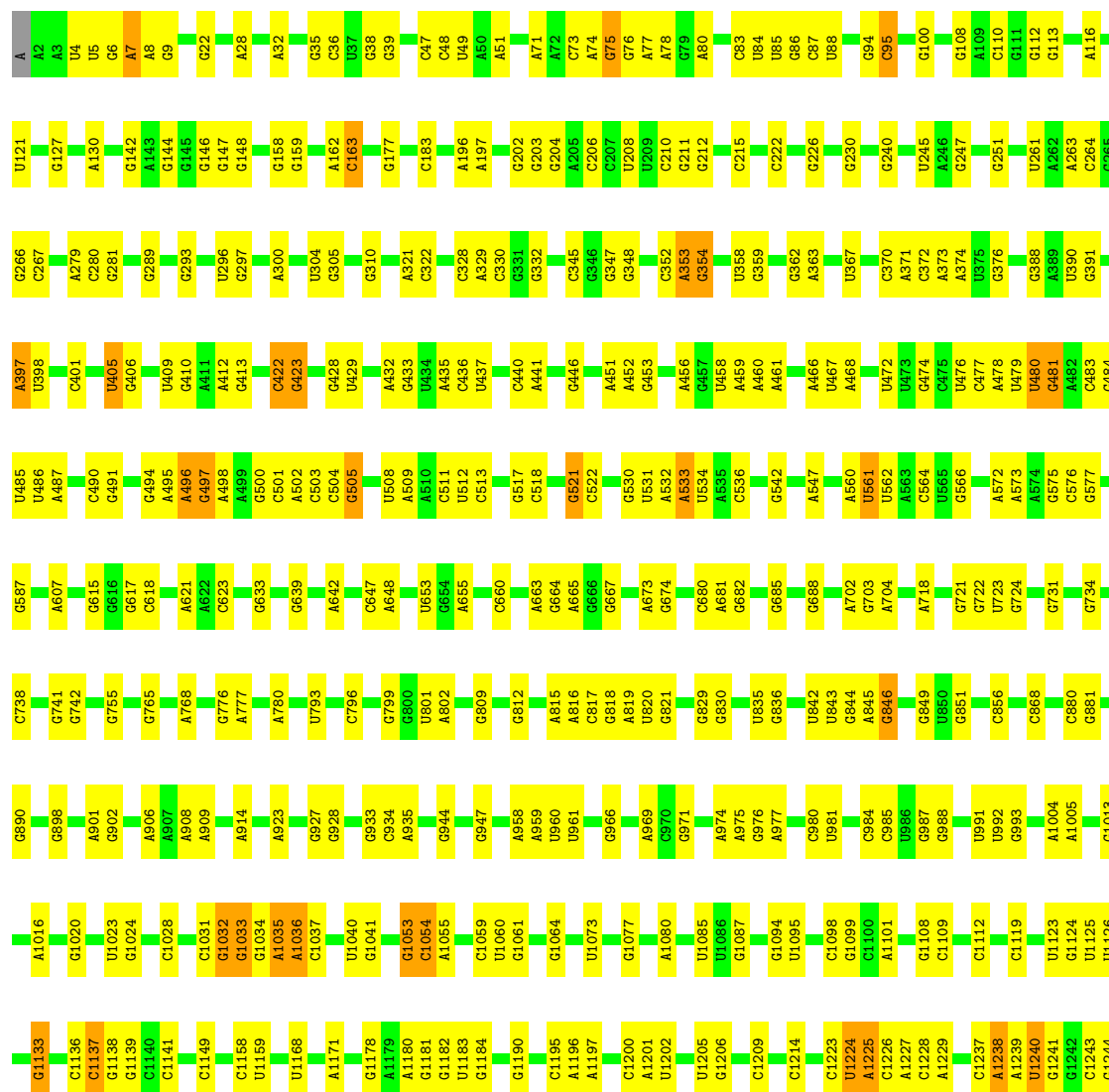
• Molecule 52: 5S rRNA

Chain 2: 76% 20% •

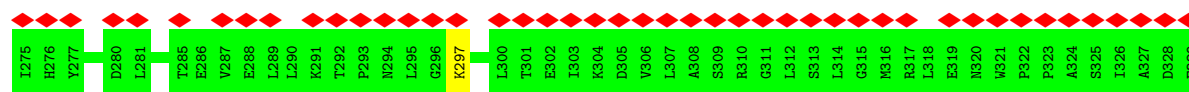


• Molecule 53: 16S rRNA

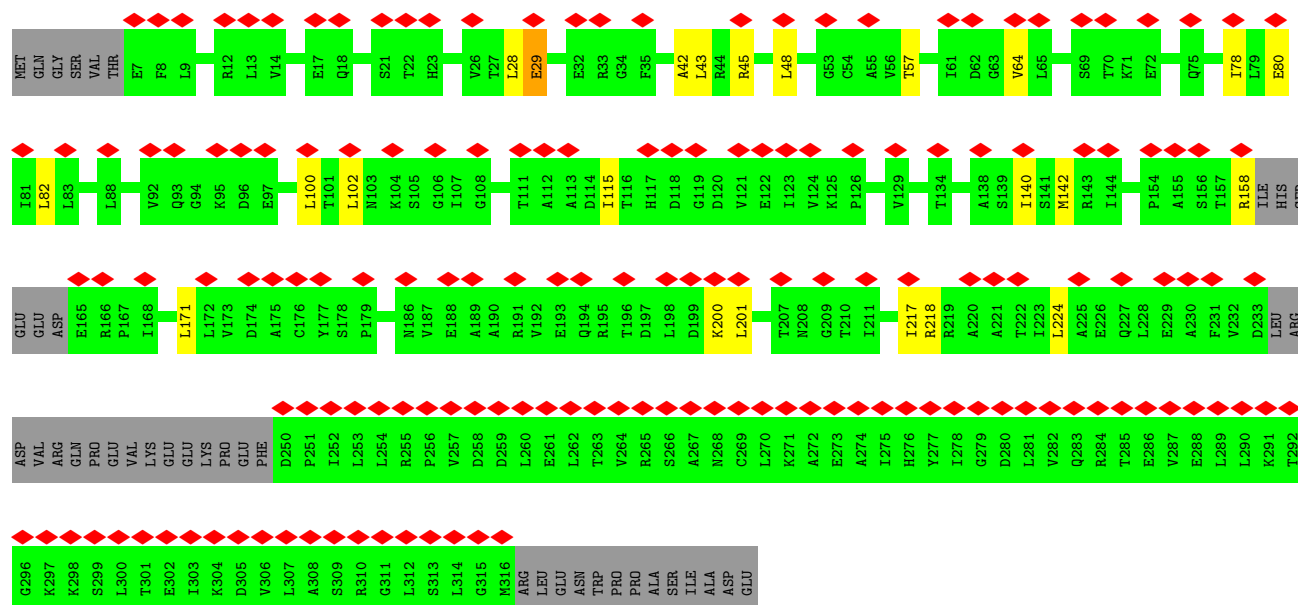
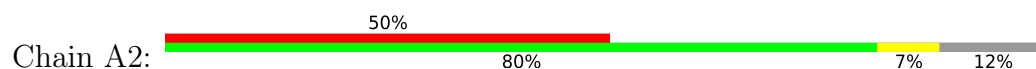
Chain 3: 68% 29% •



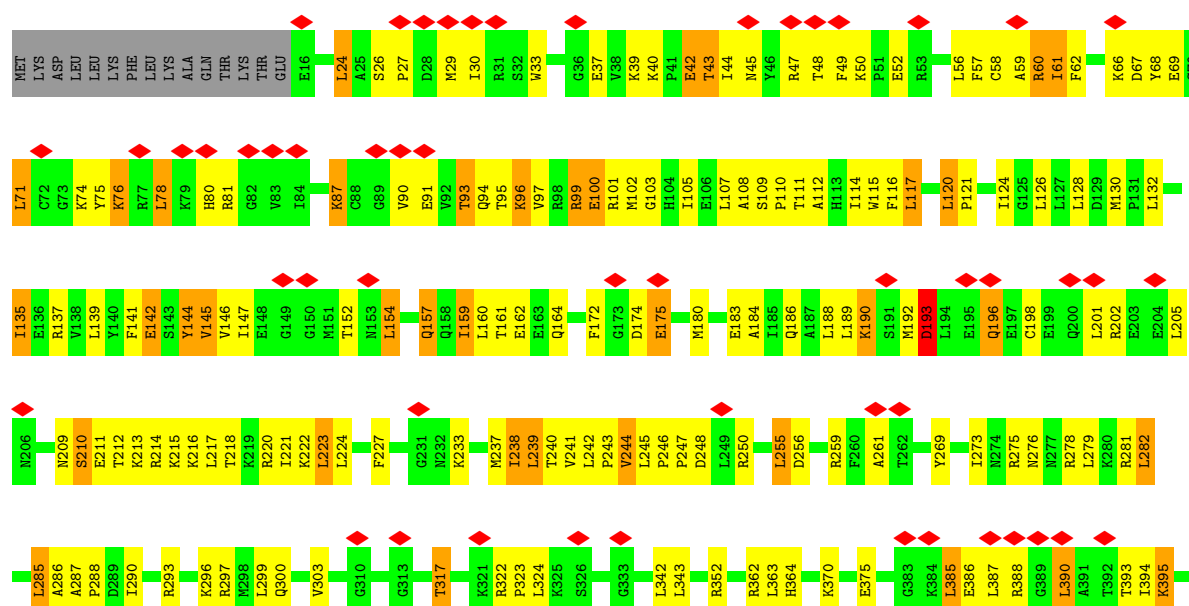


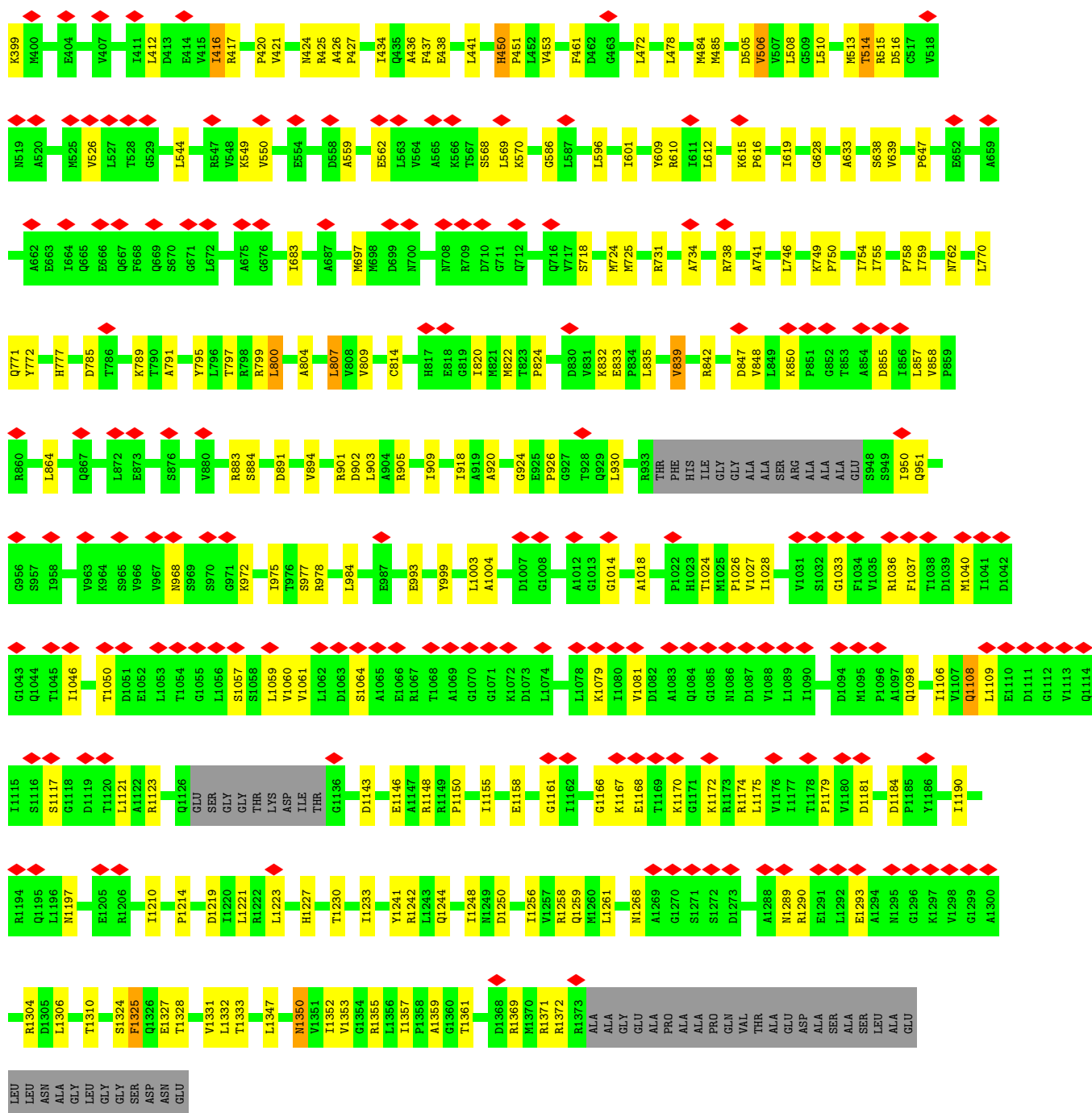


• Molecule 57: DNA-directed RNA polymerase subunit alpha

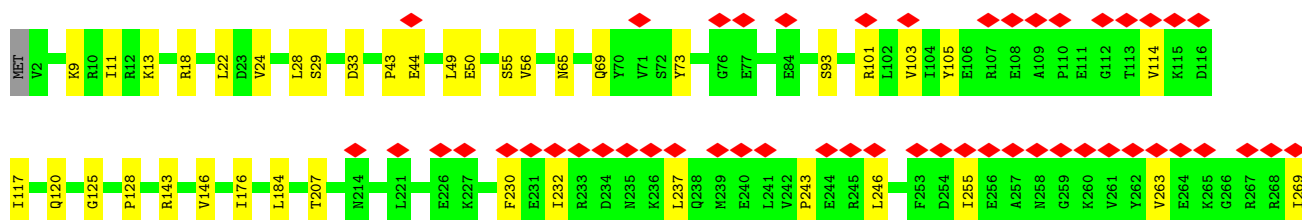
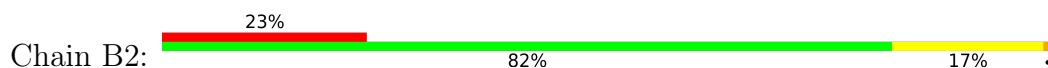


• Molecule 58: DNA-directed RNA polymerase subunit beta'



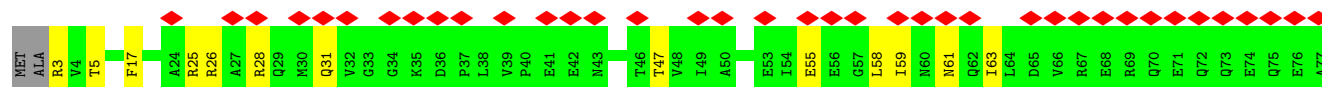
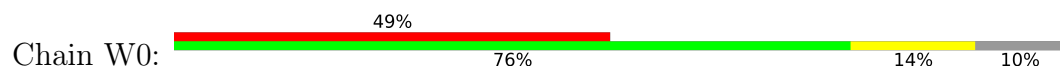


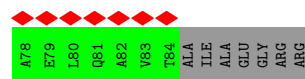
• Molecule 59: DNA-directed RNA polymerase subunit beta



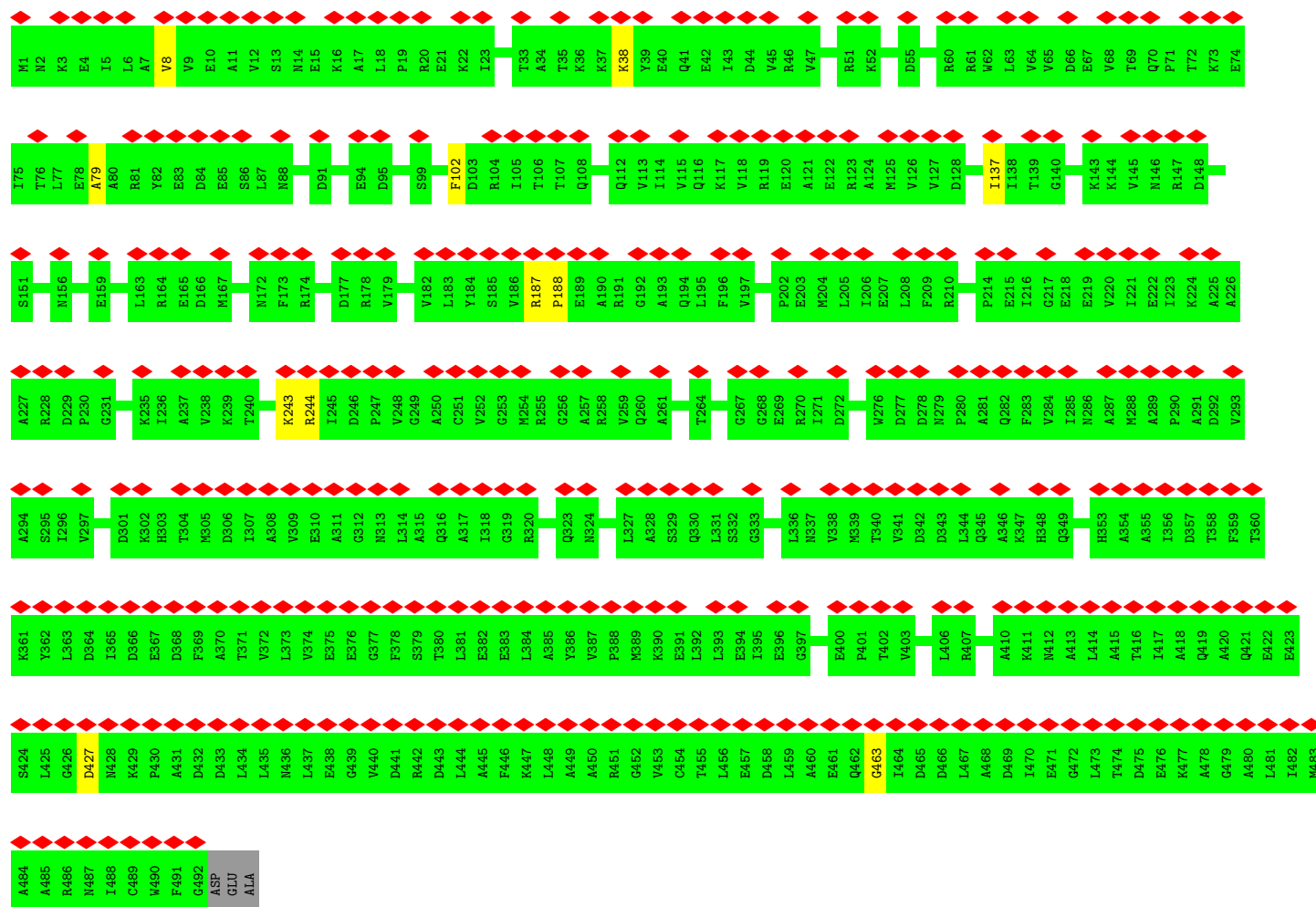


- Molecule 60: DNA-directed RNA polymerase subunit omega

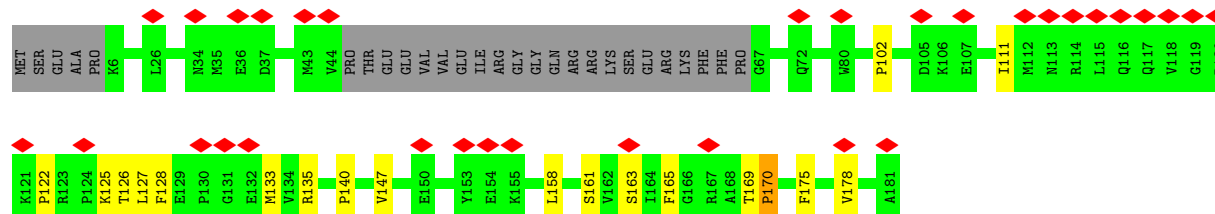
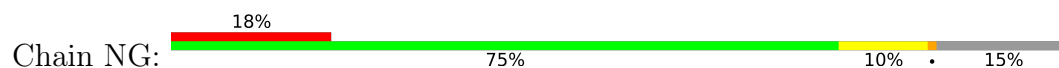




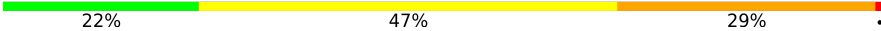
• Molecule 61: Transcription termination/antitermination protein NusA

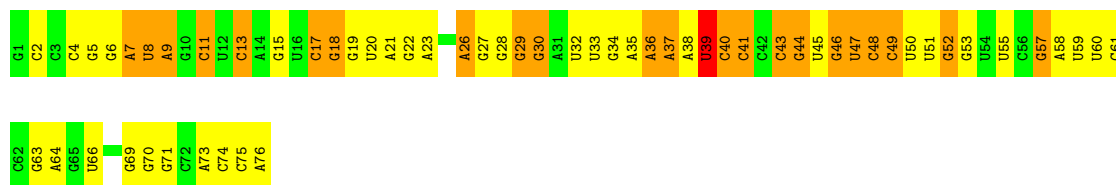


• Molecule 62: Transcription termination/antitermination protein NusG




• Molecule 63: tRNA(Phe)

Chain 5:  22% 47% 29% .



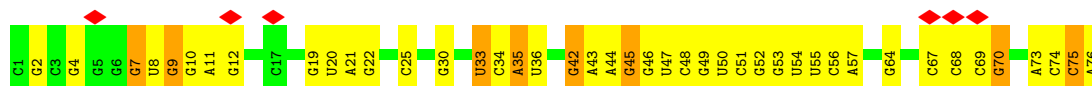
• Molecule 64: tRNA(fMet)

Chain 6:  77% 19% .



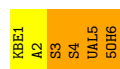
• Molecule 64: tRNA(fMet)

Chain 7:  8% 44% 45% 10%



• Molecule 65: Viomycin

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	24010	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	0.175	Depositor
Minimum map value	-0.080	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.011	Depositor
Map size (\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 (\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: 5OH, MG, DPP, UAL, KBE

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	0.40	0/450	0.60	0/599
3	C	0.28	0/416	0.52	0/554
4	D	0.47	0/380	0.76	2/498 (0.4%)
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	0.30	0/1195	0.67	3/1602 (0.2%)
13	M	0.35	0/989	0.52	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	0.86	2/1300 (0.2%)
18	R	0.33	0/892	0.73	2/1193 (0.2%)
19	S	0.32	0/817	0.61	0/1088
20	T	0.49	0/722	0.64	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	0.66	0/550	1.01	2/728 (0.3%)
27	b	0.49	0/2121	0.65	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	0.74	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	0.41	0/1152	0.55	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	0.61	0/1242
41	q	0.52	0/960	0.62	1/1278 (0.1%)
42	r	0.43	0/829	0.69	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	0.53	0/605
51	1	0.51	0/69796	0.62	22/108888 (0.0%)
52	2	0.43	0/2872	0.46	0/4479
53	3	0.42	0/36963	0.43	0/57662
54	4	0.52	0/808	0.65	0/1251
55	8	0.56	0/599	0.70	1/919 (0.1%)
56	9	0.49	0/468	0.56	0/719
57	A1	0.55	0/2106	0.81	0/2868
57	A2	0.49	0/2048	0.75	0/2786
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	0.76	0/2431	1.22	1/3385 (0.0%)
62	NG	1.10	0/756	1.06	0/1048
63	5	0.57	0/1812	0.86	3/2823 (0.1%)
64	6	0.40	0/1832	0.48	0/2855
64	7	0.39	0/1832	0.57	1/2855 (0.0%)
65	h	3.16	2/11 (18.2%)	0.75	0/13
All	All	0.48	6/191576 (0.0%)	0.62	67/282857 (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	-6.71	1.38	1.52
65	h	4	SER	CA-C	-6.16	1.40	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	B1	1350	ASN	CG-ND2	-5.36	1.22	1.33
58	B1	424	ASN	CG-ND2	-5.17	1.22	1.33
58	B1	1108	GLN	CD-OE1	5.11	1.33	1.23
58	B1	1268	ASN	CG-OD1	5.04	1.33	1.23

All (67) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	P	73	VAL	N-CA-C	-9.03	104.53	113.20
41	q	33	VAL	N-CA-C	-8.80	104.72	112.12
12	L	64	ALA	N-CA-C	-7.70	105.05	114.75
51	1	1130	U	C2'-C3'-O3'	7.58	120.88	109.50
64	7	33	U	C2'-C3'-O3'	7.28	120.42	109.50
51	1	2326	C	C2'-C3'-O3'	7.22	120.33	109.50
58	B1	450	HIS	CB-CG-CD2	-6.59	122.63	131.20
51	1	761	A	C4'-C3'-O3'	-6.52	103.22	113.00
58	B1	777	HIS	CB-CG-CD2	-6.38	122.91	131.20
58	B1	61	ILE	CA-C-N	-6.37	114.00	121.64
58	B1	61	ILE	C-N-CA	-6.37	114.00	121.64
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'	5.86	119.49	110.70
58	B1	450	HIS	CB-CG-ND1	5.71	131.26	122.70
51	1	2060	A	C2'-C3'-O3'	5.68	118.03	109.50
26	Z	35	GLU	CA-C-N	5.64	132.32	121.54
26	Z	35	GLU	C-N-CA	5.64	132.32	121.54
51	1	1790	C	N1-C1'-C2'	5.63	120.44	112.00
15	O	57	VAL	CA-C-N	5.59	132.22	121.54
15	O	57	VAL	C-N-CA	5.59	132.22	121.54
38	n	47	VAL	N-CA-C	-5.55	107.46	112.12
10	J	155	LYS	N-CA-C	-5.50	107.82	114.75
51	1	1451	C	N1-C1'-C2'	5.46	120.19	112.00
51	1	1905	C	C4'-C3'-O3'	-5.45	104.83	113.00
58	B1	777	HIS	CB-CG-ND1	5.45	130.88	122.70
51	1	1696	G	N9-C1'-C2'	5.44	120.15	112.00
51	1	960	A	N9-C1'-C2'	5.41	120.11	112.00
4	D	3	ARG	CA-C-N	5.40	127.78	120.38
4	D	3	ARG	C-N-CA	5.40	127.78	120.38
51	1	1020	A	C2'-C3'-O3'	5.39	117.59	109.50
55	8	7	DC	C2'-C3'-O3'	-5.38	103.43	111.50
51	1	1782	U	N1-C1'-C2'	5.33	119.99	112.00
33	i	24	GLY	N-CA-C	5.30	123.15	112.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	1	2055	C	N1-C1'-C2'	5.28	119.92	112.00
51	1	2428	G	N9-C1'-C2'	5.28	119.91	112.00
30	e	141	ASP	CA-C-N	5.27	131.60	121.54
30	e	141	ASP	C-N-CA	5.27	131.60	121.54
12	L	5	VAL	CA-C-N	5.26	127.75	120.49
12	L	5	VAL	C-N-CA	5.26	127.75	120.49
51	1	980	A	N9-C1'-C2'	5.24	119.86	112.00
63	5	39	U	C4'-C3'-O3'	5.23	120.85	113.00
34	j	110	PRO	N-CA-C	5.23	120.73	113.98
51	1	2576	G	N9-C1'-C2'	5.21	119.82	112.00
58	B1	27	PRO	N-CA-C	-5.21	106.25	113.81
63	5	57	G	C4'-C3'-O3'	5.20	117.21	109.40
21	U	78	VAL	CA-C-N	5.17	129.62	121.56
21	U	78	VAL	C-N-CA	5.17	129.62	121.56
51	1	1565	C	N1-C1'-C2'	5.15	119.72	112.00
51	1	2430	A	N9-C1'-C2'	5.14	119.70	112.00
51	1	1328	A	N9-C1'-C2'	5.12	119.69	112.00
23	W	14	ALA	N-CA-C	-5.12	106.12	112.93
10	J	87	VAL	N-CA-C	5.12	116.00	109.30
61	NA	427	ASP	N-CA-C	-5.10	107.72	114.31
18	R	3	ILE	CA-C-N	5.09	131.26	121.54
18	R	3	ILE	C-N-CA	5.09	131.26	121.54
51	1	2777	G	N9-C1'-C2'	5.09	119.63	112.00
17	Q	42	LYS	CA-C-N	5.08	129.60	121.62
17	Q	42	LYS	C-N-CA	5.08	129.60	121.62
33	i	71	LYS	CA-C-N	5.08	134.19	121.80
33	i	71	LYS	C-N-CA	5.08	134.19	121.80
58	B1	61	ILE	CA-C-O	-5.07	115.67	120.95
51	1	1087	G	N9-C1'-C2'	5.05	119.58	112.00
48	x	25	LYS	N-CA-C	5.03	121.52	110.80
51	1	972	A	N9-C1'-C2'	5.01	119.52	112.00
51	1	1672	A	N9-C1'-C2'	5.00	119.51	112.00
59	B2	902	LEU	N-CA-C	-5.00	105.83	111.28

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	9	0
3	C	409	0	440	4	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	36	0
8	H	1624	0	1699	26	0
9	I	1643	0	1710	34	0
10	J	1156	0	1199	18	0
11	K	817	0	808	16	0
12	L	1181	0	1240	19	0
13	M	979	0	1034	8	0
14	N	1022	0	1070	23	0
15	O	786	0	828	15	0
16	P	869	0	878	21	0
17	Q	955	0	1019	30	0
18	R	883	0	944	20	0
19	S	805	0	847	10	0
20	T	714	0	737	6	0
21	U	649	0	666	15	0
22	V	648	0	691	8	0
23	W	535	0	552	8	0
24	X	637	0	665	7	0
25	Y	665	0	714	11	0
26	Z	544	0	579	12	0
27	b	2082	0	2157	46	0
28	c	1565	0	1616	28	0
29	d	1552	0	1619	27	0
30	e	1410	0	1447	23	0
31	f	1323	0	1374	31	0
32	g	400	0	423	7	0
33	i	1032	0	1088	41	0
34	j	1129	0	1162	22	0
35	k	938	0	1012	17	0
36	l	1045	0	1117	17	0
37	m	1074	0	1157	13	0
38	n	960	0	1000	19	0
39	o	892	0	923	16	0
40	p	917	0	965	17	0
41	q	947	0	1022	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	r	816	0	839	19	0
43	s	857	0	922	11	0
44	t	738	0	807	10	0
45	u	779	0	834	13	0
46	v	753	0	780	9	0
47	w	575	0	592	8	0
48	x	625	0	655	12	0
49	y	509	0	543	12	0
50	z	449	0	491	9	0
51	1	62317	0	31346	1462	0
52	2	2568	0	1303	15	0
53	3	33012	0	16618	188	0
54	4	729	0	364	5	0
55	8	539	0	305	29	0
56	9	417	0	224	0	0
57	A1	2088	0	1895	22	0
57	A2	2029	0	1864	17	0
58	B1	10353	0	10548	317	0
59	B2	10546	0	10550	167	0
60	W0	650	0	658	11	0
61	NA	2432	0	1171	10	0
62	NG	758	0	334	14	0
63	5	1622	0	821	26	0
64	6	1640	0	837	7	0
64	7	1640	0	837	21	0
65	h	48	0	40	9	0
66	B1	1	0	0	0	0
All	All	178130	0	126632	2811	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 9.

All (2811) 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	1.09
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
51:1:1807:G:H2'	51:1:1808:A:H5'	1.44	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:750:PRO:HB3	59:B2:549:ASP:OD2	1.60	0.99
51:1:1082:U:H3'	51:1:1083:U:H5''	1.41	0.99
58:B1:111:THR:HG23	58:B1:300:GLN:CD	1.86	0.99
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	1.06	0.97
58:B1:68:TYR:O	58:B1:75:TYR:CE2	2.20	0.94
51:1:2713:U:H3'	51:1:2714:G:C5'	1.98	0.94
51:1:644:A:H2'	51:1:645:C:H5''	1.50	0.94
51:1:2156:G:H2'	51:1:2157:G:H5'	1.47	0.93
54:4:56:G:H21	58:B1:427:PRO:HD3	1.34	0.93
51:1:655:A:H4'	51:1:656:G:H5'	1.50	0.93
30:e:84:ILE:HD13	51:1:2312:U:H5'	1.51	0.93
30:e:130:GLY:HA3	51:1:2305:U:H5''	1.51	0.91
51:1:1102:C:H2'	51:1:1103:A:H8	1.35	0.91
51:1:1702:G:H2'	51:1:1703:G:H5''	1.51	0.91
58:B1:202:ARG:HG2	58:B1:202:ARG:HH11	1.35	0.90
58:B1:68:TYR:C	58:B1:75:TYR:HE2	1.80	0.90
51:1:890:C:H2'	51:1:891:G:H5'	1.53	0.90
51:1:1668:A:H4'	51:1:1669:A:H5'	1.54	0.90
51:1:1019:U:H3	51:1:1142:A:H62	1.17	0.89
14:N:3:ASN:N	14:N:5:TYR:HH	1.70	0.88
51:1:2097:A:H2'	51:1:2098:U:C6	2.08	0.88
63:5:9:A:H2'	63:5:11:C:H41	1.38	0.88
51:1:1060:U:H4'	51:1:1061:U:H5''	1.55	0.88
51:1:11:C:H2'	51:1:12:U:H5''	1.54	0.87
31:f:174:LYS:HG3	51:1:2529:G:H4'	1.56	0.87
2:B:8:THR:HB	51:1:2020:A:H5'	1.56	0.86
58:B1:317:THR:HA	58:B1:323:PRO:HA	1.55	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
51:1:1869:G:H3'	51:1:1870:C:H5'	1.58	0.85
58:B1:633:ALA:HB2	59:B2:808:ASN:H	1.41	0.85
17:Q:40:THR:HG21	65:h:6:5OH:OS	1.77	0.85
40:p:52:ARG:HH21	51:1:2720:U:C5'	1.86	0.85
51:1:2792:A:H2'	51:1:2793:C:H5''	1.59	0.85
58:B1:68:TYR:HB3	58:B1:75:TYR:OH	1.76	0.85
51:1:1175:A:H3'	51:1:1176:U:H5'	1.59	0.84
17:Q:69:GLU:HG3	53:3:521:G:H4'	1.59	0.84
51:1:475:C:H4'	51:1:510:C:H5'	1.59	0.84
51:1:1666:G:C2'	51:1:1667:G:H5'	2.07	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:770:LEU:HD13	59:B2:618:GLN:HG3	1.61	0.83
51:1:2584:U:H2'	51:1:2585:U:H5'	1.58	0.82
51:1:849:A:H2'	51:1:850:U:C6	2.14	0.82
51:1:1141:U:H4'	51:1:1142:A:O4'	1.80	0.82
33:i:119:ALA:HB2	51:1:1082:U:H5'	1.60	0.82
51:1:757:G:H2'	51:1:758:C:H5'	1.61	0.81
58:B1:141:PHE:CE2	58:B1:296:LYS:HB2	2.16	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
51:1:2112:G:H2'	51:1:2113:U:H5'	1.63	0.81
3:C:40:PRO:HG3	51:1:2348:U:H4'	1.63	0.81
51:1:545:U:C2	51:1:546:U:H1'	2.16	0.80
51:1:2799:A:H2'	51:1:2800:A:H5'	1.63	0.80
38:n:36:THR:HG22	51:1:1278:C:OP1	1.80	0.80
58:B1:68:TYR:O	58:B1:75:TYR:HE2	1.58	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
55:8:1:DC:H5''	58:B1:210:SER:OG	1.80	0.80
58:B1:141:PHE:HE2	58:B1:296:LYS:HB2	1.45	0.80
58:B1:144:TYR:HE1	58:B1:162:GLU:OE2	1.64	0.80
51:1:1197:G:O2'	51:1:1198:U:H5'	1.81	0.80
51:1:1071:G:O2'	51:1:1089:A:H2'	1.82	0.79
58:B1:37:GLU:O	58:B1:61:ILE:HD11	1.81	0.79
7:G:18:GLN:HG3	7:G:189:ASN:HB3	1.65	0.79
51:1:784:G:H5'	51:1:785:G:OP1	1.81	0.79
51:1:1775:U:H2'	51:1:1776:G:H5'	1.64	0.79
51:1:1064:C:H41	51:1:1069:A:H5''	1.47	0.79
51:1:2130:U:H2'	51:1:2131:U:H5''	1.65	0.78
51:1:1536:C:H4'	51:1:1537:G:C2	2.18	0.78
58:B1:111:THR:HG23	58:B1:300:GLN:OE1	1.81	0.78
58:B1:186:GLN:HG3	58:B1:238:ILE:HG13	1.65	0.78
51:1:2286:G:H4'	51:1:2287:A:O4'	1.82	0.78
33:i:55:PRO:HG3	51:1:1060:U:OP2	1.83	0.78
28:c:114:LYS:HB2	51:1:2680:U:OP1	1.84	0.77
51:1:275:C:H2'	51:1:276:U:C4'	2.14	0.77
51:1:2792:A:C3'	51:1:2793:C:H5''	2.14	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'	1.82	0.77
51:1:1702:G:C2'	51:1:1703:G:H5''	2.13	0.77
35:k:6:THR:HG22	51:1:1666:G:O2'	1.83	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2215:C:H2'	51:1:2216:G:C8	2.18	0.77
51:1:1736:U:H2'	51:1:1737:G:O4'	1.85	0.77
51:1:1310:G:C2'	51:1:1311:G:H5'	2.14	0.77
51:1:368:A:H2'	51:1:369:U:H5'	1.66	0.77
51:1:2156:G:C2'	51:1:2157:G:H5'	2.14	0.76
51:1:310:A:O2'	51:1:311:A:H2'	1.85	0.76
51:1:1063:G:H1	51:1:1075:C:N4	1.84	0.76
55:8:13:DT:H72	58:B1:791:ALA:HB2	1.66	0.76
55:8:15:DC:H1'	58:B1:426:ALA:HB1	1.67	0.76
58:B1:202:ARG:HG2	58:B1:202:ARG:NH1	1.99	0.76
51:1:1394:U:H4'	51:1:1603:A:H4'	1.66	0.76
51:1:548:G:H2'	51:1:549:G:O4'	1.84	0.76
51:1:275:C:H3'	51:1:276:U:H5''	1.66	0.75
58:B1:68:TYR:C	58:B1:75:TYR:CE2	2.65	0.75
51:1:2792:A:C2'	51:1:2793:C:H5''	2.16	0.75
51:1:958:U:H2'	52:2:89:U:O2	1.87	0.75
51:1:1020:A:H5'	51:1:1021:A:C8	2.22	0.74
51:1:1773:A:H2'	51:1:1774:C:H5'	1.68	0.74
51:1:1425:G:H2'	51:1:1426:G:C8	2.23	0.74
51:1:1555:G:H5'	51:1:1555:G:H8	1.51	0.74
51:1:2611:C:O2	51:1:2611:C:H2'	1.86	0.74
51:1:1083:U:H2'	51:1:1085:A:OP2	1.87	0.74
51:1:1061:U:H3'	51:1:1062:G:C5'	2.18	0.74
51:1:2432:A:H1'	64:7:75:C:O4'	1.86	0.74
55:8:3:DC:H2'	55:8:4:DT:H72	1.69	0.74
51:1:2097:A:H2'	51:1:2098:U:H6	1.50	0.74
53:3:456:A:H61	53:3:476:U:H3	1.36	0.74
37:m:14:LYS:NZ	51:1:956:G:N7	2.35	0.74
51:1:543:G:H2'	51:1:544:C:H5''	1.68	0.73
51:1:1310:G:H2'	51:1:1311:G:H5'	1.69	0.73
58:B1:107:LEU:HD11	58:B1:242:LEU:HB2	1.70	0.73
51:1:545:U:H2'	51:1:546:U:O4'	1.88	0.73
51:1:322:A:H5'	51:1:340:A:C1'	2.19	0.73
51:1:1670:C:H2'	51:1:1671:U:H5'	1.70	0.73
51:1:481:G:H1'	51:1:506:G:N2	2.04	0.73
58:B1:110:PRO:HG2	58:B1:183:GLU:HG3	1.68	0.73
58:B1:210:SER:HB3	58:B1:213:LYS:HB2	1.71	0.73
51:1:404:A:H1'	51:1:406:G:C4	2.23	0.73
51:1:1433:A:H2'	51:1:1434:A:O4'	1.89	0.73
51:1:2834:G:H2'	51:1:2879:A:H61	1.54	0.73
58:B1:105:ILE:HD12	58:B1:242:LEU:HD22	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:282:LEU:HA	58:B1:286:ALA:HA	1.70	0.73
31:f:15:ASP:HB3	31:f:26:LYS:H	1.54	0.72
58:B1:142:GLU:HG3	58:B1:142:GLU:O	1.89	0.72
51:1:1942:C:H3'	51:1:1943:U:H2'	1.70	0.72
55:8:3:DC:C2'	55:8:4:DT:H72	2.19	0.72
58:B1:1143:ASP:OD1	58:B1:1148:ARG:NH1	2.21	0.72
64:7:50:U:H2'	64:7:51:C:C4	2.24	0.72
51:1:2036:C:H2'	51:1:2037:A:C8	2.23	0.72
58:B1:220:ARG:HG2	58:B1:220:ARG:HH11	1.54	0.72
51:1:864:G:O2'	51:1:865:C:H5'	1.89	0.72
51:1:2713:U:C3'	51:1:2714:G:C5'	2.67	0.72
51:1:1795:C:H2'	51:1:1796:U:O4'	1.90	0.72
51:1:2671:G:H2'	51:1:2672:U:C6	2.25	0.72
58:B1:211:GLU:HG2	58:B1:215:LYS:HE3	1.70	0.72
53:3:452:A:H61	53:3:480:U:H3	1.37	0.71
51:1:1872:A:H2'	51:1:1873:G:O4'	1.89	0.71
51:1:1858:A:H1'	51:1:1885:A:C2	2.26	0.71
17:Q:33:CYS:HA	17:Q:54:VAL:HG12	1.70	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
58:B1:93:THR:HB	58:B1:97:VAL:HG21	1.73	0.71
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE22	1.55	0.71
51:1:394:C:H2'	51:1:395:U:O4'	1.90	0.71
51:1:1386:C:H2'	51:1:1387:A:H8	1.56	0.71
53:3:1491:G:C6	65:h:2:DPP:HB3	2.25	0.71
58:B1:157:GLN:OE1	58:B1:157:GLN:HA	1.89	0.71
36:l:59:ARG:HD2	51:1:250:G:H4'	1.71	0.71
51:1:2151:U:H2'	51:1:2152:G:H8	1.56	0.71
53:3:663:A:H61	53:3:742:G:H1	1.39	0.71
58:B1:128:LEU:HD11	58:B1:189:LEU:HG	1.73	0.71
51:1:633:A:H2'	51:1:634:C:H5'	1.72	0.70
51:1:2297:A:N1	51:1:2321:U:H5	1.89	0.70
51:1:723:C:H2'	51:1:724:U:C6	2.27	0.70
51:1:1983:G:O2'	51:1:1984:G:H5'	1.91	0.70
51:1:1019:U:H3	51:1:1142:A:N6	1.89	0.70
51:1:368:A:C2'	51:1:369:U:H5'	2.20	0.70
65:h:6:5OH:N	65:h:6:5OH:HS	2.07	0.70
51:1:2267:A:H5''	51:1:2268:A:H5''	1.74	0.70
51:1:1292:G:H2'	51:1:1293:C:C6	2.27	0.70
34:j:7:LYS:HG2	51:1:538:A:H4'	1.73	0.70
51:1:2151:U:H2'	51:1:2152:G:C8	2.27	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:47:ARG:NH2	51:1:774:G:H5''	2.07	0.70
51:1:612:G:H2'	51:1:614:A:C8	2.26	0.70
51:1:1102:C:H2'	51:1:1103:A:C8	2.22	0.69
42:r:79:ARG:NH1	51:1:572:A:OP2	2.25	0.69
51:1:1670:C:C2'	51:1:1671:U:H5'	2.21	0.69
59:B2:65:ASN:HB3	59:B2:105:TYR:HB2	1.74	0.69
51:1:319:G:H1	51:1:323:C:H5	1.41	0.69
51:1:940:G:H2'	51:1:941:A:H5''	1.73	0.69
51:1:1555:G:H5'	51:1:1555:G:C8	2.27	0.69
51:1:1889:A:H2'	51:1:1890:A:H8	1.58	0.69
51:1:322:A:H5'	51:1:340:A:H1'	1.73	0.69
51:1:419:U:H2'	51:1:420:C:C6	2.27	0.69
51:1:1337:G:H2'	51:1:1338:G:H8	1.57	0.69
51:1:2092:U:H4'	51:1:2093:G:H5''	1.75	0.69
51:1:2114:A:H2	51:1:2167:U:H1'	1.58	0.69
36:l:30:THR:HG22	51:1:810:U:O4	1.93	0.69
51:1:282:A:H2'	51:1:283:G:H8	1.57	0.69
51:1:392:U:H2'	51:1:393:C:H6	1.58	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
51:1:849:A:H2'	51:1:850:U:H6	1.58	0.69
57:A1:297:LYS:CB	61:NA:79:ALA:HB1	2.22	0.69
51:1:644:A:H2'	51:1:645:C:C5'	2.21	0.69
51:1:2626:C:O2'	51:1:2627:G:H5'	1.91	0.69
58:B1:243:PRO:HG2	59:B2:1332:SER:O	1.93	0.69
58:B1:832:LYS:C	58:B1:1242:ARG:HH12	2.01	0.69
50:z:38:GLU:OE2	51:1:928:A:H5'	1.94	0.68
51:1:905:A:C2'	51:1:906:U:H5'	2.23	0.68
51:1:1137:G:O2'	51:1:1138:G:H5'	1.92	0.68
51:1:2869:G:H2'	51:1:2870:C:C6	2.28	0.68
58:B1:39:LYS:O	58:B1:273:ILE:CG2	2.41	0.68
51:1:528:A:C8	51:1:528:A:H3'	2.27	0.68
51:1:2510:C:N4	51:1:2511:U:O4	2.27	0.68
55:8:3:DC:C6	55:8:4:DT:H72	2.29	0.68
58:B1:141:PHE:CD2	58:B1:293:ARG:O	2.47	0.68
51:1:1999:C:H5''	51:1:2723:C:O2'	1.94	0.68
51:1:2403:C:O2'	51:1:2404:U:H5'	1.92	0.68
51:1:2747:G:O6	51:1:2755:C:H5''	1.93	0.68
51:1:419:U:H2'	51:1:420:C:H6	1.58	0.68
51:1:2758:A:H2'	51:1:2759:G:H5'	1.75	0.68
52:2:65:U:H3'	52:2:108:A:H61	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:x:16:ASN:ND2	48:x:26:ARG:HB3	2.09	0.68
51:1:402:A:H2'	51:1:403:U:H5'	1.74	0.68
51:1:1063:G:H1	51:1:1075:C:H41	1.42	0.68
51:1:1082:U:H3'	51:1:1083:U:C5'	2.22	0.68
51:1:1702:G:C3'	51:1:1703:G:H5''	2.24	0.68
51:1:894:U:H2'	51:1:895:U:O4'	1.93	0.68
51:1:1061:U:H3'	51:1:1062:G:H5'	1.76	0.67
51:1:1078:U:H2'	51:1:1088:A:OP1	1.94	0.67
58:B1:984:LEU:HB3	58:B1:993:GLU:HB2	1.77	0.67
51:1:226:A:H2'	51:1:227:A:O4'	1.93	0.67
55:8:23:DC:H2''	55:8:24:DC:C5	2.30	0.67
58:B1:161:THR:HG22	58:B1:164:GLN:HB2	1.75	0.67
9:I:73:ASN:HA	9:I:76:LYS:HB2	1.77	0.67
58:B1:117:LEU:HD12	58:B1:117:LEU:O	1.94	0.67
51:1:1484:U:H2'	51:1:1485:U:C6	2.30	0.67
51:1:1889:A:H2'	51:1:1890:A:C8	2.29	0.67
53:3:437:U:H3	53:3:495:A:H62	1.42	0.67
51:1:246:C:H2'	51:1:247:G:H5'	1.76	0.67
51:1:1432:G:O2'	51:1:1433:A:H5'	1.94	0.67
51:1:2157:G:H2'	51:1:2158:A:H2	1.59	0.67
51:1:1717:A:H2'	51:1:1718:G:H5'	1.77	0.67
51:1:2278:A:C3'	51:1:2279:G:H5''	2.25	0.67
63:5:47:U:H4'	63:5:48:C:H5'	1.75	0.67
51:1:2898:U:H2'	51:1:2899:A:C8	2.29	0.67
36:l:39:LYS:NZ	51:1:942:G:OP2	2.28	0.67
51:1:1270:C:H5''	51:1:1271:G:H5'	1.77	0.67
51:1:1438:U:O2'	51:1:1439:A:H5'	1.94	0.67
4:D:37:LYS:HD3	4:D:39:ARG:HD3	1.77	0.67
51:1:703:U:C2'	51:1:704:G:H5'	2.25	0.67
51:1:905:A:H2'	51:1:906:U:H5'	1.77	0.67
51:1:2555:U:H2'	51:1:2556:C:H5'	1.78	0.67
58:B1:108:ALA:CB	58:B1:279:LEU:HD22	2.25	0.67
51:1:466:A:H2'	51:1:467:G:H5'	1.76	0.66
51:1:2516:A:O2'	51:1:2517:C:H5'	1.95	0.66
51:1:2595:G:N2	51:1:2598:A:OP2	2.23	0.66
58:B1:978:ARG:HG2	58:B1:1197:ASN:HD21	1.61	0.66
51:1:707:G:O2'	51:1:708:G:H5'	1.94	0.66
51:1:1176:U:H2'	51:1:1177:G:C8	2.29	0.66
51:1:2233:U:H2'	51:1:2234:G:C8	2.30	0.66
58:B1:1037:PHE:HB3	58:B1:1040:MET:HB2	1.77	0.66
51:1:673:C:H2'	51:1:674:G:H5'	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:1355:ARG:NH1	58:B1:1369:ARG:HH12	1.92	0.66
45:u:25:LYS:HD3	45:u:36:GLU:HB3	1.75	0.66
51:1:1020:A:H1'	51:1:1021:A:OP2	1.95	0.66
51:1:1733:G:O2'	51:1:1734:G:H5'	1.95	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
51:1:2221:G:O2'	51:1:2222:C:H5'	1.95	0.66
51:1:2233:U:H2'	51:1:2234:G:H8	1.59	0.66
51:1:2278:A:H3'	51:1:2279:G:H5''	1.78	0.66
51:1:112:U:H2'	51:1:113:U:H5'	1.76	0.66
17:Q:109:ARG:HH21	17:Q:112:ALA:HB3	1.60	0.66
28:c:4:LEU:HD23	28:c:29:VAL:HG11	1.77	0.66
51:1:414:C:H2'	51:1:415:A:C8	2.30	0.66
51:1:521:U:H2'	51:1:522:A:C8	2.31	0.66
51:1:1064:C:N4	51:1:1069:A:H5''	2.09	0.66
51:1:2625:G:H2'	51:1:2626:C:C6	2.30	0.66
17:Q:47:ALA:HB3	17:Q:49:ARG:HE	1.60	0.66
51:1:1098:A:H2'	51:1:1099:G:H5'	1.77	0.66
51:1:2844:G:H2'	51:1:2845:U:C6	2.31	0.66
58:B1:285:LEU:HB2	62:NG:111:ILE:HA	1.78	0.66
33:i:27:LEU:HD22	33:i:32:VAL:HG21	1.78	0.66
51:1:2193:G:H2'	51:1:2194:U:C6	2.31	0.66
58:B1:193:ASP:HB3	58:B1:196:GLN:HB2	1.78	0.66
51:1:65:U:H2'	51:1:66:C:H6	1.59	0.66
51:1:528:A:H3'	51:1:528:A:H8	1.60	0.66
51:1:635:C:H2'	51:1:636:G:C8	2.31	0.66
51:1:644:A:C2'	51:1:645:C:H5''	2.22	0.66
51:1:870:U:C2'	51:1:871:U:H5'	2.26	0.66
51:1:1746:A:H2'	51:1:1747:U:C6	2.31	0.66
51:1:1788:C:O2'	51:1:1789:A:H5'	1.96	0.66
38:n:63:ARG:NE	51:1:1454:C:H5'	2.10	0.65
51:1:2760:C:O2'	51:1:2761:A:H5'	1.96	0.65
58:B1:395:LYS:HZ2	58:B1:399:LYS:CD	2.10	0.65
27:b:227:VAL:HG11	51:1:784:G:C2	2.31	0.65
51:1:1572:A:O2'	51:1:1573:G:H5'	1.97	0.65
7:G:67:LEU:HD12	7:G:153:MET:HE1	1.77	0.65
51:1:359:G:O2'	51:1:360:U:H5'	1.97	0.65
51:1:488:G:N2	51:1:491:G:H5''	2.11	0.65
51:1:536:G:H2'	51:1:537:G:H5'	1.79	0.65
51:1:1098:A:C2'	51:1:1099:G:H5'	2.27	0.65
51:1:1270:C:H5''	51:1:1271:G:C5'	2.25	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2052:A:O2'	51:1:2053:G:H5'	1.96	0.65
51:1:2170:A:H2'	51:1:2171:A:O4'	1.97	0.65
19:S:38:GLU:HA	19:S:41:TRP:HB3	1.79	0.65
51:1:613:A:H5''	51:1:614:A:C8	2.32	0.65
51:1:1796:U:H2'	51:1:1797:G:H8	1.61	0.65
51:1:2290:G:H2'	51:1:2291:U:C6	2.32	0.65
51:1:543:G:H2'	51:1:544:C:C5'	2.26	0.65
51:1:1666:G:H2'	51:1:1667:G:C5'	2.24	0.65
51:1:1853:A:H2'	51:1:1854:A:C8	2.32	0.65
58:B1:108:ALA:HB3	58:B1:279:LEU:HD22	1.77	0.65
58:B1:141:PHE:HD2	58:B1:293:ARG:O	1.79	0.65
43:s:6:LYS:HB2	51:1:494:G:H4'	1.78	0.65
53:3:85:U:H5''	53:3:86:G:H5'	1.78	0.65
55:8:3:DC:C2'	55:8:4:DT:C7	2.75	0.65
55:8:13:DT:OP2	58:B1:791:ALA:HB1	1.95	0.65
28:c:149:ASN:HB3	51:1:2572:A:OP2	1.97	0.64
51:1:2792:A:H3'	51:1:2793:C:H5''	1.80	0.64
59:B2:906:PHE:CE2	61:NA:102:PHE:CB	2.81	0.64
51:1:201:C:O2'	51:1:202:U:H5'	1.97	0.64
51:1:905:A:O2'	51:1:906:U:H5'	1.97	0.64
51:1:1766:G:O2'	51:1:1767:G:H5'	1.98	0.64
51:1:2834:G:O2'	51:1:2835:A:H5'	1.97	0.64
58:B1:111:THR:CG2	58:B1:300:GLN:CD	2.67	0.64
59:B2:314:ASN:HD21	59:B2:348:SER:HA	1.62	0.64
4:D:24:THR:HG23	4:D:27:GLY:H	1.61	0.64
16:P:19:VAL:HG22	16:P:82:GLU:HB2	1.79	0.64
51:1:870:U:H2'	51:1:871:U:H5'	1.79	0.64
51:1:2114:A:N7	51:1:2115:G:H1'	2.12	0.64
58:B1:162:GLU:HA	58:B1:162:GLU:OE1	1.97	0.64
58:B1:245:LEU:HG	58:B1:246:PRO:HD2	1.80	0.64
51:1:256:A:O2'	51:1:257:C:H5'	1.98	0.64
51:1:306:U:H2'	51:1:307:G:O4'	1.98	0.64
51:1:414:C:H2'	51:1:415:A:H8	1.63	0.64
51:1:622:G:O2'	51:1:623:C:H5'	1.98	0.64
51:1:2112:G:C2'	51:1:2113:U:H5'	2.27	0.64
12:L:59:GLU:HA	12:L:62:GLU:HB3	1.80	0.64
31:f:154:GLU:HG3	31:f:156:TYR:H	1.61	0.64
51:1:940:G:C3'	51:1:941:A:H5''	2.28	0.64
51:1:1857:G:H22	51:1:1884:G:H2'	1.62	0.64
11:K:38:ARG:HE	11:K:97:THR:HA	1.62	0.64
27:b:106:PRO:HD2	27:b:109:LEU:HD22	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:65:U:H2'	51:1:66:C:C6	2.33	0.64
58:B1:68:TYR:HB3	58:B1:75:TYR:CE2	2.32	0.64
51:1:703:U:H2'	51:1:704:G:H5'	1.77	0.64
58:B1:201:LEU:HB2	58:B1:221:ILE:HD13	1.80	0.64
58:B1:1357:ILE:HD11	59:B2:1287:LEU:HD13	1.80	0.64
51:1:1161:C:H2'	51:1:1162:G:H8	1.61	0.63
26:Z:32:ARG:HG2	26:Z:33:ARG:HG3	1.80	0.63
51:1:2404:U:O2'	51:1:2405:G:H5'	1.97	0.63
51:1:2811:G:O2'	51:1:2812:G:H5'	1.97	0.63
62:NG:128:PHE:CB	62:NG:158:LEU:CB	2.75	0.63
26:Z:65:ARG:NH2	53:3:1087:G:N3	2.47	0.63
51:1:2073:C:O2'	51:1:2074:U:H5'	1.98	0.63
58:B1:975:ILE:HG22	58:B1:977:SER:H	1.62	0.63
51:1:2469:A:H2'	51:1:2470:G:O4'	1.98	0.63
51:1:2799:A:C2'	51:1:2800:A:H5'	2.27	0.63
53:3:1490:U:H2'	53:3:1491:G:C8	2.33	0.63
16:P:87:GLY:H	16:P:113:THR:HG22	1.62	0.63
51:1:161:A:N7	51:1:162:U:H5	1.96	0.63
51:1:1280:G:O2'	51:1:1281:G:H5'	1.99	0.63
9:I:152:SER:H	9:I:155:LYS:HD3	1.63	0.63
51:1:212:G:O2'	51:1:213:A:H5'	1.99	0.63
51:1:815:C:C2	51:1:1193:G:N2	2.66	0.63
51:1:1164:C:O2'	51:1:1165:A:H5'	1.99	0.63
51:1:317:G:H2'	51:1:318:C:H6	1.64	0.63
51:1:2636:C:H2'	51:1:2637:U:H6	1.64	0.63
59:B2:120:GLN:NE2	59:B2:490:GLN:OE1	2.32	0.63
51:1:1909:C:H2'	51:1:1910:G:H8	1.64	0.63
51:1:1921:G:O2'	51:1:1922:G:H5'	1.98	0.63
53:3:373:A:H61	53:3:391:G:H1'	1.64	0.63
58:B1:128:LEU:HA	58:B1:192:MET:HE1	1.81	0.63
7:G:173:LYS:O	7:G:177:ASN:ND2	2.32	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
51:1:1038:G:H2'	51:1:1039:A:C8	2.32	0.62
51:1:1149:G:H2'	51:1:1150:C:C6	2.34	0.62
51:1:1524:G:H2'	51:1:1525:A:H8	1.63	0.62
51:1:2898:U:H2'	51:1:2899:A:H8	1.64	0.62
58:B1:1355:ARG:NH1	58:B1:1369:ARG:NH1	2.47	0.62
51:1:1181:U:H2'	51:1:1182:G:C8	2.33	0.62
58:B1:285:LEU:HD13	58:B1:285:LEU:H	1.63	0.62
51:1:37:C:O2'	51:1:38:A:H5'	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:445:C:H2'	51:1:446:G:O4'	1.98	0.62
51:1:554:U:H2'	51:1:555:G:O4'	1.99	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
51:1:2314:A:H2'	51:1:2315:G:C8	2.33	0.62
51:1:1448:G:H2'	51:1:1449:G:H8	1.64	0.62
51:1:2092:U:H5	51:1:2199:A:H2	1.48	0.62
55:8:3:DC:H2'	55:8:4:DT:C7	2.30	0.62
1:A:1:MET:HG2	52:2:43:C:H5''	1.82	0.62
16:P:45:THR:HG23	16:P:48:GLY:H	1.65	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
51:1:1086:A:H5'	51:1:1103:A:H2	1.65	0.62
51:1:2734:A:H2'	51:1:2735:G:H5'	1.82	0.62
58:B1:111:THR:CG2	58:B1:300:GLN:NE2	2.63	0.62
7:G:179:GLY:HA3	61:NA:243:LYS:CB	2.29	0.62
51:1:889:C:H2'	51:1:890:C:O4'	1.99	0.62
58:B1:918:ILE:HG22	59:B2:1280:ALA:HB1	1.79	0.62
51:1:941:A:H2'	51:1:942:G:O4'	2.00	0.62
64:7:46:G:C2'	64:7:47:U:H5'	2.29	0.62
51:1:590:A:O2'	51:1:591:U:H5'	2.00	0.62
51:1:1680:U:H2'	51:1:1681:G:O4'	2.00	0.62
58:B1:461:PHE:HD2	59:B2:813:GLU:HB2	1.61	0.62
22:V:30:HIS:HD2	22:V:33:TYR:H	1.48	0.61
28:c:181:ASP:HB3	28:c:186:LEU:HB2	1.82	0.61
34:j:3:THR:N	51:1:995:C:N3	2.48	0.61
45:u:87:GLU:HG2	45:u:92:VAL:HG21	1.82	0.61
51:1:161:A:H3'	51:1:162:U:H5''	1.81	0.61
51:1:236:C:H2'	51:1:237:C:H6	1.64	0.61
51:1:2097:A:H2'	51:1:2098:U:O4'	2.00	0.61
51:1:2637:U:H2'	51:1:2638:G:H5'	1.82	0.61
58:B1:144:TYR:CE1	58:B1:162:GLU:OE2	2.51	0.61
58:B1:223:LEU:HG	58:B1:223:LEU:O	2.00	0.61
59:B2:1282:GLY:HA3	60:W0:17:PHE:HE1	1.63	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'	2.00	0.61
30:e:9:ASP:OD1	30:e:9:ASP:N	2.33	0.61
57:A1:38:THR:HB	57:A2:45:ARG:HD3	1.82	0.61
31:f:174:LYS:HG3	51:1:2529:G:C4'	2.29	0.61
34:j:132:HIS:CD2	51:1:7:G:H5'	2.35	0.61
51:1:11:C:C2'	51:1:12:U:H5''	2.29	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1503:A:H3'	51:1:1504:A:H5''	1.81	0.61
58:B1:68:TYR:HB3	58:B1:75:TYR:CZ	2.35	0.61
51:1:322:A:H5'	51:1:340:A:O4'	2.00	0.61
51:1:1040:A:H2	51:1:1115:G:H22	1.48	0.61
58:B1:1161:GLY:HA3	58:B1:1179:PRO:HA	1.82	0.61
59:B2:528:ARG:NH2	59:B2:576:SER:O	2.30	0.61
7:G:15:PHE:HB2	7:G:39:ILE:HG23	1.82	0.61
51:1:1954:G:H1'	51:1:1956:U:O4	2.01	0.61
59:B2:55:SER:OG	59:B2:465:ARG:NH1	2.33	0.61
4:D:3:ARG:O	4:D:6:GLN:NE2	2.33	0.61
32:g:50:ARG:HH22	32:g:51:ARG:HH21	1.49	0.61
51:1:547:A:H3'	51:1:547:A:N3	2.16	0.61
51:1:940:G:C2'	51:1:941:A:H5''	2.30	0.61
55:8:1:DC:H2''	55:8:2:DC:C5	2.35	0.61
51:1:1553:A:HO2'	51:1:1554:U:H5	1.48	0.61
58:B1:395:LYS:HZ2	58:B1:399:LYS:HD3	1.65	0.61
63:5:39:U:H2'	63:5:40:C:C6	2.36	0.61
33:i:135:MET:HE2	51:1:1062:G:H21	1.65	0.61
34:j:39:LYS:HE3	51:1:1009:A:OP1	2.01	0.61
51:1:1948:G:H21	53:3:1418:A:H2	1.49	0.61
51:1:2188:U:H2'	51:1:2189:U:O4'	2.01	0.61
51:1:2852:G:O2'	51:1:2853:C:H5'	2.01	0.61
51:1:172:A:H2'	51:1:173:A:H8	1.66	0.61
53:3:1032:G:H21	53:3:1033:G:H4'	1.64	0.61
58:B1:395:LYS:NZ	58:B1:399:LYS:HD3	2.15	0.61
51:1:558:U:H6	51:1:558:U:O5'	1.84	0.60
51:1:1775:U:C2'	51:1:1776:G:H5'	2.30	0.60
55:8:13:DT:C7	58:B1:791:ALA:HB2	2.29	0.60
58:B1:100:GLU:HA	59:B2:1328:LYS:HE2	1.82	0.60
7:G:86:CYS:SG	7:G:87:ASP:N	2.74	0.60
29:d:149:ILE:HG23	29:d:188:MET:HB3	1.83	0.60
37:m:17:ASN:O	37:m:38:ARG:NH1	2.34	0.60
51:1:435:C:H2'	51:1:436:C:H5'	1.82	0.60
51:1:1508:A:H2'	51:1:1509:A:O4'	2.01	0.60
51:1:1775:U:H2'	51:1:1776:G:C5'	2.29	0.60
51:1:2812:G:H2'	51:1:2813:A:C8	2.36	0.60
47:w:38:GLY:HA2	51:1:2330:G:H21	1.66	0.60
51:1:198:C:H42	51:1:248:G:H1	1.49	0.60
51:1:1717:A:C2'	51:1:1718:G:H5'	2.31	0.60
51:1:2386:A:O2'	51:1:2387:U:H5'	2.01	0.60
17:Q:40:THR:OG1	65:h:6:5OH:HR	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:153:LEU:HD23	51:1:1799:G:C2	2.37	0.60
51:1:1287:A:C5	51:1:1288:G:C6	2.89	0.60
51:1:2327:A:H2'	51:1:2328:A:C8	2.35	0.60
53:3:1351:U:H3	53:3:1371:G:H1	1.49	0.60
51:1:2093:G:O2'	51:1:2094:A:H5'	2.01	0.60
51:1:2804:U:H2'	51:1:2805:C:C6	2.36	0.60
53:3:1133:G:H1	53:3:1141:C:H42	1.48	0.60
57:A1:211:ILE:HG12	57:A1:219:ARG:HH12	1.65	0.60
58:B1:342:LEU:HD23	58:B1:1352:ILE:HG23	1.83	0.60
58:B1:770:LEU:HD13	59:B2:618:GLN:CG	2.30	0.60
14:N:40:ARG:NH2	14:N:41:GLU:OE2	2.34	0.60
37:m:86:LYS:NZ	51:1:955:U:OP1	2.33	0.60
39:o:4:LYS:HD3	39:o:7:ARG:HH21	1.65	0.60
51:1:1857:G:N2	51:1:1884:G:H2'	2.17	0.60
58:B1:750:PRO:CB	59:B2:549:ASP:OD2	2.45	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
51:1:1437:C:H2'	51:1:1438:U:C6	2.36	0.60
51:1:2187:U:O2'	51:1:2188:U:H5'	2.02	0.60
58:B1:951:GLN:NE2	58:B1:1014:GLY:O	2.35	0.60
51:1:1071:G:H1'	51:1:1089:A:C8	2.37	0.60
51:1:1538:G:H2'	51:1:1539:U:C6	2.37	0.60
51:1:2137:U:H2'	51:1:2138:G:H8	1.67	0.60
53:3:1040:U:H2'	53:3:1041:G:H8	1.67	0.60
57:A1:112:ALA:HB3	57:A1:126:PRO:HA	1.83	0.60
58:B1:154:LEU:HD21	58:B1:160:LEU:HD21	1.83	0.60
18:R:102:LYS:HG2	18:R:103:THR:HG23	1.83	0.60
51:1:723:C:H2'	51:1:724:U:H6	1.64	0.60
51:1:851:C:H2'	51:1:852:U:C6	2.36	0.60
51:1:2749:A:OP2	51:1:2751:G:H5''	2.02	0.60
58:B1:926:PRO:HG2	58:B1:1248:ILE:HD11	1.84	0.60
29:d:68:ALA:HA	51:1:1255:U:C5	2.37	0.59
51:1:854:C:O2'	51:1:855:G:H5'	2.02	0.59
51:1:2091:C:H5	51:1:2092:U:HO2'	1.49	0.59
58:B1:633:ALA:HA	59:B2:806:PRO:O	2.01	0.59
6:F:14:CYS:SG	6:F:33:HIS:ND1	2.75	0.59
45:u:40:LEU:HD12	45:u:59:GLU:HG2	1.84	0.59
51:1:893:C:H2'	51:1:894:U:C6	2.36	0.59
51:1:1171:G:H2'	51:1:1172:C:O4'	2.02	0.59
51:1:2717:C:C4	51:1:2718:G:N7	2.70	0.59
55:8:7:DC:H2''	55:8:8:DT:H71	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:1072:ASN:ND2	59:B2:1111:GLN:OE1	2.35	0.59
21:U:70:ARG:HH22	53:3:451:A:H5'	1.66	0.59
51:1:1773:A:C2'	51:1:1774:C:H5'	2.31	0.59
9:I:69:ARG:NH1	53:3:401:C:OP2	2.36	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
51:1:841:G:O2'	51:1:842:U:H5'	2.02	0.59
51:1:1026:G:H2'	51:1:1027:A:H8	1.67	0.59
58:B1:99:ARG:NH1	58:B1:99:ARG:HG3	2.17	0.59
58:B1:725:MET:SD	59:B2:1101:LEU:HD23	2.42	0.59
51:1:1670:C:H2'	51:1:1671:U:C5'	2.31	0.59
51:1:2165:C:H2'	51:1:2166:U:C6	2.38	0.59
14:N:17:ARG:HB2	14:N:65:THR:HG23	1.83	0.59
29:d:77:ILE:CG2	51:1:1256:G:H21	2.15	0.59
51:1:215:G:H4'	51:1:216:A:H4'	1.84	0.59
58:B1:275:ARG:NH1	58:B1:278:ARG:NH1	2.51	0.59
30:e:51:ASN:OD1	30:e:149:ARG:NH1	2.34	0.59
42:r:4:VAL:HG22	42:r:40:MET:HG2	1.85	0.59
51:1:49:A:H5''	51:1:51:G:O4'	2.02	0.59
51:1:794:A:H2'	51:1:795:C:O4'	2.02	0.59
51:1:1725:U:H2'	51:1:1726:C:C6	2.38	0.59
51:1:2643:G:H2'	51:1:2644:G:H5'	1.84	0.59
59:B2:1142:ARG:NH1	59:B2:1161:LEU:O	2.36	0.59
22:V:11:VAL:HA	22:V:22:VAL:HA	1.83	0.59
58:B1:514:THR:HG21	58:B1:596:LEU:HD12	1.84	0.59
59:B2:69:GLN:HE21	59:B2:101:ARG:HD2	1.67	0.59
59:B2:887:VAL:HA	59:B2:917:SER:HA	1.85	0.59
47:w:40:LYS:HE3	51:1:2330:G:O2'	2.03	0.59
51:1:246:C:C2'	51:1:247:G:H5'	2.33	0.59
51:1:1077:A:C8	51:1:1078:U:H1'	2.37	0.59
51:1:1524:G:H2'	51:1:1525:A:C8	2.38	0.59
51:1:2743:U:H3'	51:1:2744:G:H5''	1.84	0.59
55:8:11:DC:H2'	55:8:12:DG:C8	2.37	0.59
51:1:1469:A:H2'	51:1:1470:A:C8	2.38	0.59
51:1:2360:G:C2'	51:1:2361:G:H5'	2.31	0.59
51:1:2533:U:H2'	51:1:2534:A:H5'	1.85	0.59
53:3:422:C:O2'	53:3:423:G:N2	2.36	0.59
37:m:66:ARG:NH1	37:m:104:GLU:OE2	2.36	0.58
51:1:1098:A:H2'	51:1:1099:G:C5'	2.33	0.58
51:1:2215:C:H2'	51:1:2216:G:H8	1.65	0.58
51:1:2789:C:H2'	51:1:2893:A:N7	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:161:THR:HG23	58:B1:164:GLN:H	1.68	0.58
58:B1:615:LYS:HG2	60:W0:5:THR:HG21	1.85	0.58
24:X:30:LEU:HB2	24:X:48:ILE:HG22	1.85	0.58
51:1:1042:G:H2'	51:1:1043:C:C6	2.37	0.58
51:1:1337:G:H2'	51:1:1338:G:C8	2.37	0.58
51:1:1511:G:H2'	51:1:1512:C:C6	2.38	0.58
51:1:1845:G:O2'	51:1:1846:G:H5'	2.02	0.58
53:3:148:G:H1'	53:3:1447:A:H1'	1.84	0.58
23:W:49:LYS:HA	23:W:52:ARG:HH21	1.68	0.58
27:b:34:GLU:HG3	27:b:63:ILE:HD11	1.84	0.58
51:1:2812:G:H2'	51:1:2813:A:H8	1.68	0.58
51:1:528:A:C8	51:1:528:A:C3'	2.86	0.58
51:1:1463:C:H2'	51:1:1464:G:H8	1.68	0.58
51:1:1893:C:H2'	51:1:1894:C:H5'	1.86	0.58
51:1:2183:A:H2'	51:1:2184:A:C4	2.38	0.58
58:B1:97:VAL:HG11	58:B1:101:ARG:NH2	2.18	0.58
58:B1:201:LEU:HD11	58:B1:220:ARG:HH11	1.67	0.58
33:i:25:PRO:HG2	51:1:1068:G:H21	1.68	0.58
51:1:834:G:H2'	51:1:835:C:O4'	2.04	0.58
55:8:9:DG:H4'	58:B1:120:LEU:HG	1.84	0.58
58:B1:1361:THR:HB	59:B2:1284:ALA:HB3	1.86	0.58
27:b:141:HIS:ND1	27:b:192:GLY:O	2.35	0.58
28:c:55:LYS:NZ	28:c:59:ARG:O	2.36	0.58
51:1:1565:C:O2'	51:1:1566:A:H8	1.87	0.58
51:1:2834:G:H2'	51:1:2879:A:N6	2.17	0.58
53:3:1125:U:H2'	53:3:1126:U:H2'	1.86	0.58
15:O:46:LYS:HG2	15:O:68:ARG:HG2	1.84	0.58
27:b:157:ALA:O	51:1:1820:U:C2	2.56	0.58
29:d:1:MET:HG2	29:d:16:GLU:HG2	1.86	0.58
33:i:22:PRO:HA	51:1:1067:A:O2'	2.04	0.58
51:1:1333:G:O2'	51:1:1334:G:H5'	2.03	0.58
51:1:1561:C:H2'	51:1:1562:U:C6	2.39	0.58
51:1:1579:A:H2'	51:1:1580:A:C8	2.38	0.58
51:1:2153:C:H2'	51:1:2154:A:H5'	1.85	0.58
1:A:26:SER:OG	1:A:27:THR:N	2.37	0.58
28:c:129:THR:OG1	28:c:140:HIS:O	2.22	0.58
51:1:673:C:C2'	51:1:674:G:H5'	2.34	0.58
58:B1:370:LYS:HG2	58:B1:441:LEU:HD23	1.84	0.58
58:B1:1167:LYS:HZ2	58:B1:1170:LYS:HB2	1.69	0.58
14:N:79:ARG:HH21	14:N:102:PHE:HA	1.67	0.58
30:e:47:LYS:O	30:e:51:ASN:ND2	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:z:4:ILE:HD11	50:z:58:GLU:HG2	1.86	0.58
51:1:621:A:H2'	51:1:622:G:H5'	1.86	0.58
51:1:640:C:O2'	51:1:641:U:H5'	2.04	0.58
51:1:2636:C:H2'	51:1:2637:U:C6	2.39	0.58
53:3:409:U:H3	53:3:433:G:H1	1.51	0.58
58:B1:99:ARG:CG	58:B1:99:ARG:HH11	2.17	0.58
58:B1:438:GLU:HG3	58:B1:485:MET:HE1	1.84	0.58
51:1:32:C:H2'	51:1:33:C:C6	2.39	0.57
51:1:2897:U:H2'	51:1:2898:U:C6	2.39	0.57
53:3:159:G:N2	53:3:162:A:OP2	2.34	0.57
27:b:220:ARG:NH1	51:1:1789:A:OP2	2.38	0.57
38:n:22:ARG:HG3	38:n:70:THR:HA	1.86	0.57
38:n:63:ARG:CZ	51:1:1454:C:H5'	2.34	0.57
51:1:327:G:O2'	51:1:328:U:H5'	2.04	0.57
51:1:2899:A:O2'	51:1:2900:A:H5'	2.04	0.57
58:B1:160:LEU:HD22	58:B1:164:GLN:HB3	1.86	0.57
58:B1:412:LEU:HD22	58:B1:441:LEU:HD21	1.84	0.57
51:1:146:A:H2'	51:1:147:C:C6	2.39	0.57
51:1:235:U:H2'	51:1:236:C:C6	2.39	0.57
51:1:323:C:H3'	51:1:323:C:OP2	2.05	0.57
51:1:2092:U:H4'	51:1:2093:G:C5'	2.34	0.57
51:1:2570:G:H2'	51:1:2571:U:H5'	1.85	0.57
51:1:2762:C:H2'	51:1:2763:G:H5'	1.86	0.57
9:I:10:LEU:HD23	9:I:62:ARG:HB3	1.86	0.57
9:I:201:GLU:O	53:3:8:A:N6	2.36	0.57
41:q:30:VAL:HG13	51:1:580:U:O3'	2.04	0.57
51:1:1173:U:C5	51:1:1174:U:H1'	2.40	0.57
51:1:1400:U:O2'	51:1:1401:G:H5'	2.04	0.57
51:1:2845:U:H2'	51:1:2846:G:H8	1.69	0.57
14:N:35:GLU:HA	14:N:39:GLY:HA3	1.85	0.57
39:o:56:LYS:NZ	52:2:117:G:OP1	2.36	0.57
51:1:1275:A:C6	51:1:1296:G:H4'	2.40	0.57
27:b:259:ASN:ND2	27:b:262:THR:OG1	2.38	0.57
28:c:63:PRO:HG3	51:1:2787:C:H1'	1.85	0.57
39:o:25:ARG:NH1	52:2:8:C:O3'	2.37	0.57
40:p:1:SER:OG	40:p:2:ASN:N	2.37	0.57
51:1:877:A:N1	51:1:899:A:H2'	2.20	0.57
59:B2:839:VAL:HG12	59:B2:1049:ILE:HG12	1.87	0.57
7:G:114:LYS:HE3	7:G:151:LYS:HB2	1.86	0.57
19:S:5:MET:HE1	53:3:981:U:H5''	1.86	0.57
51:1:2186:G:O2'	51:1:2187:U:H5'	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:42:GLU:HB3	58:B1:52:GLU:HG3	1.86	0.57
59:B2:707:ALA:O	59:B2:711:ASP:HB2	2.03	0.57
10:J:54:GLU:HG2	10:J:56:PRO:HD2	1.86	0.57
25:Y:59:ARG:NH1	53:3:177:G:OP1	2.37	0.57
31:f:44:HIS:HA	31:f:49:LEU:HG	1.87	0.57
34:j:116:ARG:NH2	51:1:529:A:OP2	2.32	0.57
51:1:163:C:H2'	51:1:164:C:O4'	2.05	0.57
51:1:503:A:H4'	51:1:505:A:H5''	1.87	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
51:1:1526:C:H2'	51:1:1527:G:O4'	2.04	0.57
57:A2:82:LEU:HD11	57:A2:171:LEU:HD23	1.86	0.57
58:B1:247:PRO:HA	58:B1:250:ARG:HG3	1.87	0.57
58:B1:741:ALA:O	58:B1:762:ASN:ND2	2.38	0.57
58:B1:1046:ILE:HD12	58:B1:1059:LEU:HB3	1.86	0.57
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
51:1:635:C:H2'	51:1:636:G:H8	1.70	0.57
59:B2:1142:ARG:NH2	59:B2:1166:ASP:OD1	2.38	0.57
31:f:151:ARG:HB3	31:f:161:VAL:HG23	1.86	0.57
51:1:287:G:H2'	51:1:288:U:C6	2.40	0.57
51:1:1520:U:O2'	51:1:1521:G:H5'	2.05	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
59:B2:13:LYS:HB2	59:B2:1180:MET:HE2	1.86	0.57
10:J:44:ARG:NH2	10:J:70:MET:SD	2.78	0.56
31:f:40:VAL:O	31:f:54:ARG:NH2	2.38	0.56
49:y:39:GLN:HG2	51:1:96:C:OP1	2.05	0.56
51:1:727:A:H2'	51:1:728:G:C8	2.40	0.56
57:A2:28:LEU:HB2	57:A2:201:LEU:HB3	1.86	0.56
58:B1:102:MET:HG2	58:B1:246:PRO:HG3	1.87	0.56
58:B1:241:VAL:O	58:B1:241:VAL:HG12	2.04	0.56
31:f:174:LYS:HE2	51:1:2529:G:H4'	1.86	0.56
51:1:1528:A:H2'	51:1:1529:G:H5'	1.87	0.56
51:1:2457:U:O2'	51:1:2458:G:H5'	2.04	0.56
58:B1:130:MET:HE2	58:B1:135:ILE:HG12	1.87	0.56
59:B2:1122:LYS:NZ	59:B2:1126:ASP:OD1	2.38	0.56
7:G:58:LYS:O	7:G:62:ARG:NH1	2.38	0.56
16:P:111:ASP:HB2	26:Z:16:ARG:HH22	1.68	0.56
39:o:52:SER:OG	39:o:53:THR:N	2.38	0.56
39:o:69:ASP:N	39:o:69:ASP:OD1	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:288:U:H2'	51:1:289:G:H8	1.71	0.56
51:1:655:A:H4'	51:1:656:G:C5'	2.30	0.56
51:1:885:C:N4	51:1:886:A:H62	2.03	0.56
2:B:43:THR:HG1	2:B:46:GLY:H	1.52	0.56
19:S:26:LEU:HA	19:S:30:ILE:HD12	1.87	0.56
21:U:55:ASP:OD1	21:U:55:ASP:N	2.38	0.56
51:1:69:C:H2'	51:1:70:G:H8	1.70	0.56
51:1:1485:U:H2'	51:1:1486:U:C6	2.41	0.56
51:1:1917:U:O2'	51:1:1918:A:H5'	2.06	0.56
51:1:2584:U:C2'	51:1:2585:U:H5'	2.34	0.56
53:3:202:G:H21	53:3:466:A:H61	1.53	0.56
58:B1:1166:GLY:HA3	58:B1:1174:ARG:HB2	1.88	0.56
59:B2:818:VAL:HG22	59:B2:1096:ILE:HG12	1.87	0.56
63:5:38:A:C8	63:5:39:U:H1'	2.40	0.56
45:u:36:GLU:HA	45:u:61:GLU:HG2	1.86	0.56
51:1:359:G:C2'	51:1:360:U:H5'	2.36	0.56
51:1:2395:C:H42	51:1:2421:G:H1	1.54	0.56
58:B1:510:LEU:HD22	58:B1:601:ILE:HD12	1.86	0.56
4:D:9:VAL:HG22	51:1:1309:G:OP1	2.06	0.56
46:v:57:TYR:OH	46:v:79:ARG:NH2	2.38	0.56
51:1:74:A:H4'	51:1:75:G:O5'	2.05	0.56
51:1:78:U:H2'	51:1:79:C:C6	2.40	0.56
51:1:358:U:H2'	51:1:359:G:C8	2.41	0.56
51:1:1130:U:O2'	51:1:1131:G:OP1	2.20	0.56
51:1:1182:G:H2'	51:1:1183:U:O4'	2.06	0.56
51:1:1597:A:H5''	51:1:1598:A:H5'	1.86	0.56
51:1:1678:A:H2'	51:1:1679:A:H5'	1.86	0.56
53:3:927:G:O2'	53:3:1503:A:N7	2.38	0.56
64:7:52:G:H2'	64:7:53:G:H8	1.69	0.56
19:S:52:ARG:O	19:S:58:ARG:NH1	2.39	0.56
49:y:49:ASP:OD1	49:y:52:ARG:NH2	2.39	0.56
51:1:366:C:O2'	51:1:367:G:H5'	2.04	0.56
51:1:780:G:H21	51:1:783:A:H62	1.54	0.56
51:1:1097:U:H2'	51:1:1098:A:O4'	2.06	0.56
51:1:1319:C:O2'	51:1:1320:C:H5'	2.05	0.56
51:1:2626:C:H2'	51:1:2627:G:O4'	2.06	0.56
12:L:113:LYS:O	53:3:1239:A:O2'	2.22	0.56
17:Q:8:ARG:NH2	53:3:880:C:OP1	2.36	0.56
28:c:134:HIS:CE1	51:1:1675:C:C4	2.94	0.56
38:n:2:ARG:HA	38:n:5:LYS:HD3	1.88	0.56
51:1:296:U:H2'	51:1:297:G:C8	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1120:G:O2'	51:1:1121:C:H5'	2.05	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
51:1:2662:A:H2'	51:1:2663:G:O4'	2.05	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
8:H:39:ARG:NH1	8:H:54:ILE:O	2.39	0.56
18:R:100:ARG:NH1	18:R:103:THR:OG1	2.38	0.56
26:Z:44:ARG:NH1	53:3:722:G:OP2	2.39	0.56
51:1:184:C:H2'	51:1:185:G:C8	2.41	0.56
51:1:543:G:H2'	51:1:544:C:O4'	2.05	0.56
51:1:155:A:H2'	51:1:156:A:C8	2.41	0.56
51:1:633:A:C2'	51:1:634:C:H5'	2.35	0.56
53:3:1036:A:H2'	53:3:1037:C:H5'	1.88	0.56
11:K:12:PRO:HB2	11:K:44:ARG:HH21	1.70	0.55
12:L:4:ARG:HB3	12:L:6:ILE:HG23	1.88	0.55
27:b:250:GLN:NE2	27:b:251:THR:O	2.38	0.55
49:y:28:LEU:HA	49:y:31:GLN:HB2	1.88	0.55
51:1:133:U:O2'	51:1:134:G:H5'	2.06	0.55
51:1:720:U:H2'	51:1:721:A:C8	2.41	0.55
51:1:2236:U:H2'	51:1:2237:G:H5'	1.88	0.55
53:3:49:U:H3	53:3:362:G:H1'	1.71	0.55
53:3:830:G:H1	53:3:856:C:H42	1.53	0.55
58:B1:39:LYS:O	58:B1:273:ILE:HG21	2.06	0.55
58:B1:144:TYR:HE1	58:B1:162:GLU:CD	2.14	0.55
16:P:63:GLN:HG3	16:P:98:ALA:HB2	1.88	0.55
27:b:216:ARG:NH2	51:1:781:A:OP1	2.38	0.55
28:c:18:ASP:N	28:c:18:ASP:OD1	2.36	0.55
33:i:5:GLN:O	33:i:30:GLN:NE2	2.40	0.55
35:k:76:VAL:H	40:p:72:VAL:HG22	1.71	0.55
51:1:184:C:H2'	51:1:185:G:H8	1.70	0.55
58:B1:1175:LEU:HD22	58:B1:1190:ILE:HD11	1.88	0.55
7:G:45:THR:O	7:G:49:PHE:N	2.35	0.55
8:H:76:ILE:HD11	54:4:20:U:H4'	1.87	0.55
35:k:65:THR:HG23	35:k:68:GLY:H	1.69	0.55
51:1:112:U:C2'	51:1:113:U:H5'	2.37	0.55
51:1:461:C:H2'	51:1:462:C:C6	2.41	0.55
51:1:613:A:H2'	51:1:613:A:N3	2.21	0.55
51:1:1410:G:H2'	51:1:1411:U:C6	2.41	0.55
51:1:1670:C:O5'	51:1:1670:C:H6	1.90	0.55
63:5:40:C:H2'	63:5:41:C:C6	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:91:VAL:HG22	7:G:150:ILE:HD11	1.88	0.55
11:K:2:ARG:NH1	53:3:738:C:OP1	2.39	0.55
30:e:23:SER:HB3	30:e:26:GLN:HB2	1.88	0.55
51:1:118:A:OP2	51:1:119:A:H5''	2.06	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''	1.88	0.55
51:1:2637:U:C2'	51:1:2638:G:H5'	2.36	0.55
51:1:2845:U:H2'	51:1:2846:G:C8	2.42	0.55
53:3:158:G:N2	53:3:163:C:O2	2.36	0.55
53:3:1040:U:H2'	53:3:1041:G:C8	2.42	0.55
25:Y:73:ARG:NH2	53:3:261:U:OP2	2.36	0.55
51:1:172:A:H2'	51:1:173:A:C8	2.40	0.55
51:1:317:G:H2'	51:1:318:C:C6	2.42	0.55
51:1:825:A:O2'	51:1:826:U:H5'	2.06	0.55
51:1:1048:A:H2'	51:1:1049:C:H5'	1.88	0.55
51:1:1772:A:H5'	51:1:1773:A:OP2	2.06	0.55
51:1:2488:G:O2'	51:1:2489:U:H5'	2.07	0.55
51:1:2510:C:C4	51:1:2511:U:C4	2.93	0.55
51:1:759:G:H2'	51:1:760:G:C8	2.41	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
51:1:1541:C:O2'	51:1:1542:U:H5'	2.06	0.55
51:1:1745:A:O2'	51:1:1746:A:H5'	2.07	0.55
51:1:1909:C:H2'	51:1:1910:G:C8	2.41	0.55
58:B1:833:GLU:HB2	58:B1:1242:ARG:NH1	2.22	0.55
29:d:84:THR:HG21	51:1:586:A:H5'	1.87	0.55
33:i:10:LEU:HA	51:1:1061:U:C2	2.42	0.55
50:z:15:ARG:HE	50:z:52:PHE:HE2	1.53	0.55
51:1:439:A:H2'	51:1:440:C:C6	2.42	0.55
51:1:2743:U:C3'	51:1:2744:G:H5''	2.37	0.55
54:4:4:U:H3	63:5:36:A:H61	1.55	0.55
58:B1:145:VAL:HG23	58:B1:159:ILE:HG22	1.89	0.55
36:l:89:VAL:HG23	36:l:121:THR:HG23	1.88	0.55
43:s:98:LYS:HD3	51:1:2012:G:OP1	2.06	0.55
51:1:543:G:H2'	51:1:544:C:C4'	2.37	0.55
51:1:757:G:H2'	51:1:758:C:C5'	2.35	0.55
58:B1:638:SER:OG	58:B1:639:VAL:N	2.36	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
51:1:359:G:H2'	51:1:360:U:O4'	2.07	0.55
51:1:1086:A:H5'	51:1:1103:A:C2	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1545:A:H2'	51:1:1546:G:O4'	2.07	0.55
51:1:2827:C:O2'	51:1:2828:G:H5'	2.07	0.55
57:A2:294:ASN:HA	61:NA:463:GLY:HA2	1.87	0.55
58:B1:508:LEU:HD22	59:B2:1101:LEU:HD21	1.88	0.55
59:B2:633:LEU:HD13	59:B2:644:LEU:HD23	1.89	0.55
7:G:138:ARG:NH1	7:G:141:GLU:OE2	2.40	0.55
51:1:2114:A:C2	51:1:2167:U:H1'	2.41	0.55
51:1:2545:G:O2'	51:1:2546:U:H5'	2.07	0.55
51:1:2850:A:N1	51:1:2869:G:H4'	2.21	0.55
57:A1:29:GLU:HB3	57:A1:200:LYS:HG3	1.88	0.55
35:k:70:ARG:HG2	35:k:76:VAL:HG12	1.88	0.54
51:1:392:U:H2'	51:1:393:C:C6	2.42	0.54
51:1:613:A:H5''	51:1:614:A:N7	2.22	0.54
53:3:505:G:H5''	53:3:534:U:H2'	1.89	0.54
58:B1:804:ALA:HA	58:B1:1259:GLN:HG3	1.88	0.54
58:B1:1155:ILE:HG13	58:B1:1210:ILE:HB	1.89	0.54
49:y:15:ASN:O	49:y:19:LEU:N	2.41	0.54
51:1:296:U:H2'	51:1:297:G:H8	1.71	0.54
51:1:1511:G:H2'	51:1:1512:C:H6	1.73	0.54
51:1:1601:G:C2'	51:1:1602:U:H5'	2.37	0.54
57:A2:100:LEU:HD23	57:A2:115:ILE:HG21	1.89	0.54
58:B1:58:CYS:SG	58:B1:59:ALA:N	2.80	0.54
58:B1:799:ARG:HG2	58:B1:1325:PHE:HZ	1.72	0.54
59:B2:29:SER:O	59:B2:33:ASP:HB2	2.07	0.54
49:y:19:LEU:O	49:y:23:ARG:N	2.35	0.54
51:1:128:C:H2'	51:1:129:C:H6	1.70	0.54
51:1:923:G:O2'	51:1:924:G:H5'	2.07	0.54
51:1:1091:G:H2'	51:1:1092:C:C6	2.42	0.54
51:1:2195:U:O2'	51:1:2196:C:H5'	2.06	0.54
51:1:2345:G:H5'	51:1:2347:C:H5'	1.89	0.54
58:B1:37:GLU:O	58:B1:61:ILE:CD1	2.52	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
37:m:27:SER:H	37:m:66:ARG:HH12	1.54	0.54
51:1:340:A:H2'	51:1:341:C:O4'	2.06	0.54
51:1:1083:U:H2'	51:1:1084:A:H3'	1.89	0.54
51:1:2114:A:C8	51:1:2115:G:H1'	2.42	0.54
51:1:2217:G:O2'	51:1:2218:G:H5'	2.06	0.54
8:H:71:ARG:HB3	8:H:74:ILE:HD13	1.89	0.54
10:J:23:THR:HA	10:J:28:ARG:HA	1.88	0.54
16:P:86:LYS:HG3	16:P:114:PRO:HD3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:84:ARG:NH2	53:3:1059:C:O3'	2.40	0.54
51:1:1297:C:H2'	51:1:1298:C:C6	2.43	0.54
51:1:2734:A:C2'	51:1:2735:G:H5'	2.38	0.54
52:2:40:U:N3	52:2:44:G:OP2	2.40	0.54
7:G:19:THR:HA	7:G:37:VAL:HA	1.88	0.54
31:f:103:ASN:ND2	31:f:113:ASP:OD1	2.41	0.54
51:1:472:A:H2'	51:1:473:G:H5'	1.90	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
57:A1:47:LEU:HD23	57:A1:51:MET:HG3	1.89	0.54
58:B1:770:LEU:CD1	59:B2:618:GLN:HG3	2.36	0.54
60:W0:3:ARG:NH1	60:W0:55:GLU:OE2	2.40	0.54
7:G:53:LEU:HD21	7:G:215:ALA:HB1	1.88	0.54
12:L:73:GLU:HG2	12:L:90:VAL:HG22	1.89	0.54
38:n:35:LYS:NZ	38:n:100:CYS:SG	2.81	0.54
51:1:53:A:H2'	51:1:54:G:H5'	1.89	0.54
51:1:1014:A:H2'	51:1:1015:U:C6	2.43	0.54
51:1:1389:G:O2'	51:1:1390:U:H5'	2.07	0.54
51:1:1748:C:H2'	51:1:1749:A:H8	1.73	0.54
51:1:2190:G:O2'	51:1:2191:A:H5'	2.08	0.54
53:3:923:A:N6	53:3:1392:G:O6	2.40	0.54
59:B2:904:ALA:O	61:NA:8:VAL:CB	2.56	0.54
64:7:11:A:H2'	64:7:12:G:H8	1.72	0.54
27:b:227:VAL:HG11	51:1:784:G:N1	2.23	0.54
51:1:8:C:H2'	51:1:9:G:H8	1.73	0.54
51:1:682:G:N2	51:1:796:C:O2	2.41	0.54
51:1:1601:G:O2'	51:1:1602:U:H5'	2.08	0.54
51:1:1856:U:H2'	51:1:1857:G:O4'	2.08	0.54
51:1:2297:A:N1	51:1:2321:U:C5	2.75	0.54
58:B1:111:THR:HG22	58:B1:300:GLN:NE2	2.23	0.54
59:B2:985:GLU:HB3	59:B2:988:LYS:HB2	1.89	0.54
36:l:80:SER:HB3	36:l:114:GLY:HA3	1.89	0.54
42:r:51:VAL:HG22	42:r:52:PRO:HD2	1.89	0.54
51:1:21:A:O2'	51:1:22:C:H5'	2.08	0.54
51:1:143:C:H2'	51:1:144:A:H8	1.73	0.54
51:1:268:C:H2'	51:1:269:C:H6	1.73	0.54
58:B1:759:ILE:HG23	58:B1:771:GLN:HB3	1.89	0.54
58:B1:800:LEU:HB3	58:B1:920:ALA:HB1	1.89	0.54
59:B2:684:ASN:OD1	59:B2:687:ARG:NH2	2.41	0.54
41:q:90:ASP:OD1	41:q:90:ASP:N	2.37	0.54
51:1:141:G:H3'	51:1:142:A:O4'	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:402:A:C2'	51:1:403:U:H5'	2.38	0.54
51:1:784:G:C5'	51:1:785:G:OP1	2.54	0.54
53:3:1023:U:H2'	53:3:1024:G:C8	2.43	0.54
57:A2:43:LEU:HD13	57:A2:217:ILE:HD11	1.90	0.54
59:B2:103:VAL:HB	59:B2:114:VAL:HG11	1.89	0.54
7:G:126:ASP:OD1	7:G:126:ASP:N	2.42	0.53
17:Q:64:SER:OG	17:Q:65:TYR:N	2.41	0.53
21:U:69:ASP:OD1	21:U:69:ASP:N	2.38	0.53
29:d:76:PRO:HD2	51:1:673:C:H5''	1.89	0.53
51:1:44:A:O2'	51:1:45:G:H5'	2.08	0.53
51:1:358:U:H2'	51:1:359:G:H8	1.72	0.53
51:1:2092:U:C5	51:1:2199:A:H2	2.26	0.53
58:B1:30:ILE:HG21	58:B1:241:VAL:O	2.08	0.53
3:C:20:TYR:OH	51:1:2348:U:H5'	2.08	0.53
7:G:102:ASN:ND2	53:3:1073:U:O2	2.39	0.53
44:t:54:GLU:HB3	44:t:88:LYS:HE3	1.90	0.53
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
51:1:1063:G:N1	51:1:1075:C:N4	2.52	0.53
51:1:1111:A:H2'	51:1:1112:G:H4'	1.90	0.53
51:1:1288:G:C6	51:1:1327:A:C2	2.96	0.53
51:1:1386:C:H2'	51:1:1387:A:C8	2.41	0.53
51:1:1528:A:C2'	51:1:1529:G:H5'	2.38	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
58:B1:209:ASN:HA	58:B1:214:ARG:HH21	1.73	0.53
58:B1:633:ALA:HB2	59:B2:808:ASN:N	2.19	0.53
59:B2:628:HIS:HB3	59:B2:647:ARG:HH21	1.74	0.53
59:B2:811:ASN:HA	59:B2:815:SER:HB2	1.90	0.53
64:7:25:C:H42	64:7:45:G:H22	1.56	0.53
25:Y:66:ILE:HG21	25:Y:70:LYS:HB3	1.91	0.53
30:e:21:TYR:OH	30:e:164:GLU:OE1	2.26	0.53
34:j:2:LYS:HA	51:1:995:C:N3	2.23	0.53
51:1:973:A:H5'	51:1:1188:U:H1'	1.90	0.53
51:1:2631:G:O2'	51:1:2632:A:H5'	2.08	0.53
1:A:35:ASP:OD1	18:R:2:ARG:NH1	2.42	0.53
16:P:15:VAL:HG12	16:P:76:TYR:HB3	1.90	0.53
25:Y:47:GLN:NE2	25:Y:51:ASN:OD1	2.40	0.53
37:m:64:TRP:HB2	37:m:104:GLU:HB2	1.89	0.53
39:o:40:ILE:HD12	39:o:44:GLY:HA2	1.90	0.53
40:p:105:LYS:O	40:p:108:ARG:NH2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1005:C:H6	51:1:1005:C:O5'	1.90	0.53
51:1:2092:U:C4'	51:1:2093:G:H5''	2.37	0.53
51:1:2644:G:O2'	51:1:2645:G:H5'	2.09	0.53
57:A1:205:MET:HE3	57:A1:213:PRO:HB3	1.91	0.53
58:B1:99:ARG:HG3	58:B1:99:ARG:HH11	1.73	0.53
58:B1:814:CYS:SG	58:B1:883:ARG:NH2	2.81	0.53
59:B2:360:LEU:HD13	59:B2:378:ARG:HH11	1.72	0.53
9:I:154:VAL:HA	9:I:157:ALA:HB3	1.91	0.53
12:L:77:ARG:NH2	53:3:1381:U:O2	2.41	0.53
13:M:92:PRO:O	13:M:116:ARG:NH2	2.42	0.53
42:r:75:VAL:HG23	42:r:86:GLN:HG2	1.90	0.53
51:1:268:C:H2'	51:1:269:C:C6	2.44	0.53
51:1:279:A:N6	51:1:361:G:H1'	2.21	0.53
51:1:1310:G:O2'	51:1:1311:G:H5'	2.06	0.53
51:1:2092:U:C5	51:1:2199:A:C2	2.97	0.53
34:j:38:GLY:HA3	34:j:50:THR:HG23	1.90	0.53
39:o:31:THR:HG23	39:o:34:HIS:H	1.73	0.53
51:1:876:C:H2'	51:1:877:A:O4'	2.08	0.53
51:1:894:U:O2'	51:1:895:U:H5'	2.09	0.53
51:1:1565:C:HO2'	51:1:1566:A:H8	1.53	0.53
51:1:2123:G:H2'	51:1:2124:G:H8	1.73	0.53
51:1:2328:A:H8	51:1:2328:A:O5'	1.90	0.53
51:1:2758:A:H2'	51:1:2759:G:C5'	2.39	0.53
53:3:959:A:HO2'	53:3:984:C:HO2'	1.53	0.53
58:B1:39:LYS:O	58:B1:273:ILE:HG23	2.08	0.53
51:1:53:A:C2'	51:1:54:G:H5'	2.39	0.53
51:1:57:C:H2'	51:1:58:G:O4'	2.08	0.53
58:B1:785:ASP:O	58:B1:789:LYS:HB2	2.08	0.53
58:B1:975:ILE:HD11	58:B1:1003:LEU:HD11	1.91	0.53
59:B2:1117:LEU:HD12	59:B2:1195:ILE:HG12	1.90	0.53
9:I:55:ARG:O	9:I:59:LYS:N	2.41	0.53
33:i:53:PRO:HD2	33:i:77:VAL:HG11	1.91	0.53
51:1:176:A:O2'	51:1:177:G:H5'	2.08	0.53
51:1:820:A:O2'	51:1:821:A:H5'	2.08	0.53
51:1:878:A:H2'	51:1:879:G:O4'	2.09	0.53
51:1:925:A:O2'	51:1:926:G:H5'	2.08	0.53
51:1:1171:G:H2'	51:1:1172:C:C4'	2.38	0.53
53:3:458:U:H3	53:3:474:G:H1	1.56	0.53
58:B1:111:THR:HG23	58:B1:300:GLN:NE2	2.24	0.53
63:5:38:A:H2'	63:5:39:U:H4'	1.91	0.53
14:N:115:VAL:HG23	53:3:1367:C:H5''	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:52:ARG:NH2	53:3:835:U:OP1	2.42	0.53
33:i:27:LEU:HD13	33:i:32:VAL:HG11	1.90	0.53
35:k:42:THR:HG22	35:k:57:VAL:HG12	1.91	0.53
51:1:140:C:H2'	51:1:141:G:H5'	1.90	0.53
51:1:441:U:O2'	51:1:442:G:H5'	2.08	0.53
51:1:1278:C:O2'	51:1:1279:G:H5'	2.09	0.53
51:1:1530:G:N2	51:1:1542:U:H1'	2.23	0.53
51:1:2762:C:C2'	51:1:2763:G:H5'	2.39	0.53
10:J:104:ILE:O	10:J:111:ARG:NH1	2.41	0.53
50:z:36:GLU:O	50:z:37:ARG:NH1	2.42	0.53
51:1:341:C:O2'	51:1:342:A:H5'	2.08	0.53
51:1:729:G:H5''	51:1:730:A:H5''	1.91	0.53
51:1:995:C:H6	51:1:995:C:H5'	1.73	0.53
51:1:1175:A:H3'	51:1:1176:U:C5'	2.37	0.53
51:1:1558:C:O4'	51:1:1560:G:C8	2.62	0.53
51:1:1599:U:H2'	51:1:1600:C:C6	2.43	0.53
51:1:1782:U:H2'	51:1:1783:A:H5''	1.90	0.53
51:1:2425:A:H4'	51:1:2426:A:H5''	1.91	0.53
51:1:2625:G:O2'	51:1:2626:C:H5'	2.09	0.53
53:3:1244:G:H1	53:3:1293:C:H42	1.57	0.53
17:Q:49:ARG:NH1	17:Q:88:ASP:OD2	2.42	0.52
42:r:4:VAL:HG12	42:r:13:ARG:HA	1.91	0.52
51:1:368:A:H2'	51:1:369:U:C5'	2.39	0.52
51:1:519:U:H2'	51:1:520:G:H8	1.74	0.52
51:1:2102:G:H2'	51:1:2103:C:O4'	2.09	0.52
51:1:2194:U:H2'	51:1:2195:U:C6	2.44	0.52
51:1:2290:G:H2'	51:1:2291:U:H6	1.74	0.52
53:3:1023:U:H2'	53:3:1024:G:H8	1.74	0.52
57:A2:28:LEU:HD22	57:A2:201:LEU:HD23	1.91	0.52
33:i:25:PRO:HG2	51:1:1068:G:N2	2.24	0.52
51:1:543:G:C2'	51:1:544:C:H5''	2.37	0.52
51:1:1161:C:H2'	51:1:1162:G:C8	2.44	0.52
51:1:1789:A:H2'	51:1:1790:C:O4'	2.09	0.52
51:1:1794:A:O2'	51:1:1795:C:H5'	2.10	0.52
51:1:1917:U:C2'	51:1:1918:A:H5'	2.39	0.52
58:B1:78:LEU:O	58:B1:78:LEU:HD13	2.08	0.52
58:B1:215:LYS:HA	58:B1:218:THR:HG22	1.91	0.52
58:B1:746:LEU:HG	58:B1:758:PRO:HG3	1.90	0.52
59:B2:243:PRO:HB2	59:B2:274:ILE:HG23	1.90	0.52
7:G:61:SER:OG	7:G:62:ARG:NH1	2.42	0.52
30:e:162:ASP:OD1	30:e:162:ASP:N	2.37	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:r:54:VAL:HG13	42:r:55:ASP:H	1.75	0.52
47:w:55:LEU:HD12	47:w:76:ILE:HD12	1.90	0.52
51:1:481:G:H1'	51:1:506:G:H21	1.71	0.52
51:1:1409:U:H2'	51:1:1410:G:C8	2.44	0.52
51:1:1560:G:H2'	51:1:1560:G:N3	2.24	0.52
51:1:1827:U:H2'	51:1:1828:G:H5'	1.90	0.52
51:1:2707:U:H2'	51:1:2708:G:C8	2.44	0.52
53:3:203:G:N2	53:3:204:G:O6	2.43	0.52
57:A1:100:LEU:HD21	57:A1:121:VAL:HG11	1.90	0.52
58:B1:832:LYS:HB3	58:B1:1242:ARG:NH1	2.24	0.52
11:K:23:GLU:HA	11:K:26:THR:HG22	1.90	0.52
28:c:23:PRO:HB3	51:1:2682:A:N3	2.24	0.52
51:1:40:U:H2'	51:1:41:C:C6	2.43	0.52
51:1:213:A:O2'	51:1:214:G:H5'	2.09	0.52
51:1:723:C:O2'	51:1:724:U:H5'	2.09	0.52
51:1:1678:A:H2'	51:1:1679:A:C5'	2.38	0.52
51:1:2470:G:O2'	51:1:2471:A:H5'	2.10	0.52
59:B2:524:ILE:HG21	59:B2:708:VAL:HG13	1.92	0.52
8:H:30:ASP:N	8:H:30:ASP:OD1	2.41	0.52
8:H:107:LYS:HB3	8:H:110:LEU:HD23	1.92	0.52
27:b:257:ARG:NH2	27:b:262:THR:OG1	2.42	0.52
31:f:7:PRO:O	31:f:68:ARG:NH2	2.38	0.52
51:1:2529:G:H5''	51:1:2530:A:H5''	1.91	0.52
26:Z:28:LEU:HA	26:Z:31:VAL:HG12	1.90	0.52
51:1:611:C:H2'	51:1:612:G:O4'	2.09	0.52
51:1:1503:A:C3'	51:1:1504:A:H5''	2.40	0.52
51:1:2617:U:H2'	51:1:2618:G:H5'	1.91	0.52
64:7:43:A:H2'	64:7:44:A:C8	2.44	0.52
8:H:133:MET:HE3	8:H:167:TYR:HB2	1.91	0.52
10:J:152:VAL:HG21	13:M:98:LEU:HD13	1.91	0.52
51:1:49:A:O5'	51:1:51:G:H5'	2.09	0.52
51:1:2204:G:H2'	51:1:2205:A:C8	2.44	0.52
51:1:2670:A:H2'	51:1:2671:G:H8	1.75	0.52
51:1:2731:G:H2'	51:1:2732:G:C8	2.45	0.52
51:1:2776:A:C6	51:1:2782:G:H1'	2.45	0.52
58:B1:99:ARG:HA	58:B1:248:ASP:HB2	1.92	0.52
58:B1:144:TYR:CE1	58:B1:162:GLU:CD	2.88	0.52
1:A:9:TYR:OH	30:e:101:ARG:NH2	2.41	0.52
40:p:28:LYS:HB3	40:p:39:LEU:HD21	1.91	0.52
51:1:215:G:C4'	51:1:216:A:H4'	2.39	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)
51:1:870:U:O2'	51:1:871:U:H5'	2.10	0.52
51:1:1507:C:H2'	51:1:1508:A:C4'	2.40	0.52
51:1:1878:G:O2'	51:1:1879:C:H5'	2.09	0.52
51:1:2216:G:H2'	51:1:2217:G:H8	1.74	0.52
57:A2:140:ILE:HD12	57:A2:142:MET:HE3	1.91	0.52
58:B1:375:GLU:HG2	59:B2:1245:ALA:O	2.10	0.52
33:i:56:VAL:HB	33:i:68:PHE:HB2	1.92	0.52
51:1:1047:G:N2	51:1:1110:G:H2'	2.25	0.52
51:1:1662:U:H2'	51:1:1663:G:O4'	2.09	0.52
51:1:2013:A:H5''	51:1:2013:A:C8	2.44	0.52
51:1:2236:U:C2'	51:1:2237:G:H5'	2.39	0.52
51:1:2747:G:O6	51:1:2754:U:H2'	2.09	0.52
59:B2:255:ILE:HB	59:B2:263:VAL:HB	1.92	0.52
27:b:92:LEU:HD11	27:b:100:ARG:HB3	1.91	0.52
31:f:174:LYS:CG	51:1:2529:G:H4'	2.34	0.52
46:v:77:VAL:HG23	46:v:89:ILE:HG12	1.92	0.52
51:1:69:C:H2'	51:1:70:G:C8	2.45	0.52
51:1:386:G:H3'	51:1:387:U:H5''	1.92	0.52
51:1:1338:G:H2'	51:1:1339:G:H8	1.74	0.52
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE21	1.68	0.52
58:B1:850:LYS:HB2	58:B1:857:LEU:HB2	1.91	0.52
59:B2:125:GLY:HA2	59:B2:499:SER:HB2	1.92	0.52
59:B2:1070:HIS:NE2	59:B2:1114:GLU:OE1	2.36	0.52
7:G:14:HIS:HB3	7:G:42:LEU:HD21	1.91	0.51
9:I:12:ARG:NH1	9:I:32:LYS:O	2.42	0.51
10:J:106:ALA:O	10:J:111:ARG:NH2	2.43	0.51
15:O:24:GLU:HA	15:O:27:GLU:HB2	1.93	0.51
51:1:1722:A:H62	51:1:1738:G:H1'	1.75	0.51
51:1:1930:G:C2'	51:1:1931:U:OP2	2.58	0.51
51:1:2463:C:O2'	51:1:2464:G:H5'	2.10	0.51
51:1:2651:C:O2'	51:1:2652:C:H5'	2.10	0.51
53:3:1077:G:N2	53:3:1080:A:OP2	2.40	0.51
57:A1:16:ILE:HG23	57:A1:26:VAL:HG22	1.91	0.51
58:B1:112:ALA:HA	58:B1:238:ILE:HA	1.91	0.51
9:I:150:LYS:O	9:I:155:LYS:NZ	2.42	0.51
43:s:109:ASP:OD1	43:s:109:ASP:N	2.42	0.51
51:1:8:C:H2'	51:1:9:G:C8	2.45	0.51
51:1:1534:U:H2'	51:1:1536:C:O4'	2.10	0.51
51:1:1574:C:H2'	51:1:1575:C:H6	1.74	0.51
51:1:1722:A:O2'	51:1:1723:G:H5'	2.10	0.51
51:1:1910:G:H1	51:1:1920:C:H42	1.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1923:U:H2'	51:1:1924:C:C6	2.46	0.51
51:1:2105:U:N3	51:1:2184:A:C2	2.78	0.51
53:3:816:A:OP1	53:3:1526:G:O2'	2.28	0.51
58:B1:205:LEU:HG	58:B1:217:LEU:HB3	1.91	0.51
59:B2:93:SER:HA	59:B2:128:PRO:HA	1.92	0.51
35:k:31:ARG:NH2	51:1:2676:C:OP2	2.43	0.51
51:1:282:A:H2'	51:1:283:G:C8	2.42	0.51
51:1:736:C:H42	51:1:760:G:H1	1.59	0.51
4:D:3:ARG:NH1	51:1:752:A:OP1	2.44	0.51
23:W:71:ASP:N	23:W:71:ASP:OD1	2.44	0.51
51:1:138:U:C5	51:1:139:U:H5	2.28	0.51
51:1:291:G:O2'	51:1:292:U:H5'	2.11	0.51
51:1:1542:U:O2'	51:1:1543:G:H5'	2.09	0.51
58:B1:68:TYR:CA	58:B1:75:TYR:HE2	2.22	0.51
10:J:123:LEU:HD12	53:3:7:A:H2'	1.92	0.51
15:O:5:ARG:N	15:O:76:ILE:O	2.43	0.51
43:s:67:ASP:OD1	43:s:67:ASP:N	2.39	0.51
51:1:286:U:H2'	51:1:287:G:H8	1.75	0.51
51:1:1403:A:H2'	51:1:1404:C:C6	2.45	0.51
51:1:2555:U:O2	51:1:2555:U:O4'	2.29	0.51
51:1:2611:C:O2	51:1:2611:C:C2'	2.58	0.51
53:3:460:A:H2'	53:3:461:A:H8	1.75	0.51
59:B2:786:GLY:N	59:B2:789:THR:OG1	2.41	0.51
2:B:2:VAL:HG23	51:1:2015:A:C6	2.46	0.51
21:U:6:LEU:HD22	21:U:17:TYR:HB3	1.91	0.51
30:e:69:ALA:O	30:e:80:GLN:NE2	2.43	0.51
36:l:42:SER:HB2	51:1:672:C:H5	1.76	0.51
51:1:439:A:H2'	51:1:440:C:H6	1.75	0.51
51:1:891:G:H2'	51:1:892:A:C8	2.46	0.51
51:1:1112:G:H2'	51:1:1113:U:O4'	2.10	0.51
51:1:1668:A:C4'	51:1:1669:A:H5'	2.36	0.51
51:1:1678:A:C2'	51:1:1679:A:H5'	2.40	0.51
51:1:2570:G:C2'	51:1:2571:U:H5'	2.40	0.51
58:B1:390:LEU:N	58:B1:390:LEU:CD1	2.73	0.51
64:6:1:C:H2'	64:6:2:G:H8	1.75	0.51
6:F:19:ARG:HB2	6:F:24:ARG:HD2	1.92	0.51
22:V:60:ILE:HA	22:V:74:LEU:HA	1.93	0.51
51:1:707:G:H2'	51:1:708:G:O4'	2.11	0.51
51:1:724:U:O2'	51:1:725:G:H5'	2.11	0.51
51:1:2670:A:H2'	51:1:2671:G:C8	2.45	0.51
58:B1:683:ILE:HD12	58:B1:754:ILE:HG21	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:1179:PRO:HD2	58:B1:1184:ASP:HA	1.93	0.51
59:B2:400:VAL:HG21	59:B2:452:ARG:HE	1.76	0.51
64:7:9:G:O4'	64:7:46:G:N3	2.43	0.51
8:H:175:HIS:ND1	53:3:1109:C:OP2	2.44	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
30:e:91:ARG:NH2	52:2:43:C:O2	2.36	0.51
45:u:73:ASN:ND2	45:u:80:ASP:OD2	2.43	0.51
51:1:251:A:H2'	51:1:252:G:O4'	2.10	0.51
51:1:355:U:H2'	51:1:356:G:C8	2.45	0.51
51:1:492:A:H2'	51:1:493:G:O4'	2.09	0.51
51:1:1415:U:H1'	51:1:1588:G:N2	2.26	0.51
51:1:2618:G:H2'	51:1:2619:C:O4'	2.11	0.51
58:B1:972:LYS:HD2	58:B1:1004:ALA:HA	1.93	0.51
3:C:7:LYS:HD3	51:1:2420:C:H5''	1.93	0.51
8:H:130:ARG:NH2	8:H:165:GLU:OE1	2.43	0.51
30:e:27:VAL:O	30:e:29:ARG:NH1	2.41	0.51
31:f:136:ASP:HB3	31:f:139:VAL:HG12	1.92	0.51
51:1:246:C:H2'	51:1:247:G:C5'	2.40	0.51
51:1:757:G:C2'	51:1:758:C:H5'	2.38	0.51
51:1:2687:U:H2'	51:1:2688:G:O4'	2.11	0.51
58:B1:201:LEU:HD12	58:B1:224:LEU:HD12	1.92	0.51
58:B1:275:ARG:HH12	58:B1:278:ARG:NH1	2.09	0.51
58:B1:412:LEU:HD23	58:B1:416:ILE:HG13	1.92	0.51
59:B2:714:VAL:HB	59:B2:787:PRO:HD2	1.92	0.51
4:D:14:ARG:NH1	51:1:1377:G:O3'	2.44	0.51
15:O:39:PRO:HD2	53:3:1123:U:H4'	1.92	0.51
39:o:40:ILE:HG22	39:o:47:VAL:HG12	1.91	0.51
44:t:65:GLY:N	44:t:79:ASP:OD1	2.43	0.51
48:x:64:ASP:N	48:x:64:ASP:OD1	2.43	0.51
51:1:145:C:H2'	51:1:146:A:C8	2.46	0.51
51:1:800:A:H4'	51:1:801:G:H3'	1.92	0.51
51:1:1717:A:H2'	51:1:1718:G:C5'	2.40	0.51
58:B1:1361:THR:OG1	59:B2:1282:GLY:O	2.28	0.51
59:B2:246:LEU:HB3	59:B2:269:ILE:HD13	1.91	0.51
27:b:50:THR:HG23	51:1:1813:G:H21	1.76	0.50
27:b:207:ALA:HB2	51:1:1790:C:O2'	2.11	0.50
51:1:580:U:O5'	51:1:580:U:H6	1.94	0.50
51:1:1468:U:H2'	51:1:1522:A:N6	2.26	0.50
51:1:2285:C:O2'	51:1:2286:G:H5'	2.11	0.50
53:3:928:G:O2'	53:3:1533:C:OP1	2.22	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:23:THR:HG22	10:J:28:ARG:HB3	1.91	0.50
15:O:29:ALA:O	15:O:33:GLY:N	2.42	0.50
28:c:161:MET:HE1	51:1:2050:C:O2	2.11	0.50
29:d:77:ILE:HG23	51:1:1256:G:N2	2.26	0.50
33:i:126:ARG:HD2	51:1:1080:A:H4'	1.93	0.50
37:m:38:ARG:HB3	37:m:98:PRO:HD3	1.92	0.50
51:1:2593:U:O2'	51:1:2594:C:H5'	2.11	0.50
51:1:2815:C:O2'	51:1:2816:G:H5'	2.11	0.50
53:3:202:G:H1	53:3:215:C:H42	1.57	0.50
58:B1:505:ASP:OD2	59:B2:812:PHE:HA	2.11	0.50
64:6:43:A:H2'	64:6:44:A:C8	2.45	0.50
29:d:191:ASP:O	29:d:195:GLN:NE2	2.44	0.50
33:i:25:PRO:HG3	51:1:1095:A:C2	2.46	0.50
35:k:75:SER:OG	40:p:72:VAL:O	2.26	0.50
51:1:208:C:O5'	51:1:208:C:H6	1.93	0.50
51:1:928:A:O2'	51:1:929:U:H5'	2.10	0.50
51:1:1270:C:H5''	51:1:1271:G:H5''	1.93	0.50
51:1:1310:G:H2'	51:1:1311:G:C5'	2.38	0.50
51:1:1416:G:H2'	51:1:1417:C:C6	2.45	0.50
51:1:1754:A:C6	51:1:1755:A:C6	2.98	0.50
62:NG:161:SER:HA	62:NG:170:PRO:HA	1.93	0.50
14:N:89:TYR:HB3	14:N:93:LEU:HD21	1.92	0.50
51:1:288:U:H2'	51:1:289:G:C8	2.47	0.50
51:1:438:G:H2'	51:1:439:A:H8	1.76	0.50
51:1:630:G:H4'	51:1:640:C:H4'	1.93	0.50
51:1:1528:A:H2'	51:1:1529:G:O4'	2.11	0.50
51:1:1539:U:H2'	51:1:1540:G:H8	1.76	0.50
51:1:1676:A:H8	51:1:1676:A:O5'	1.95	0.50
51:1:2052:A:C2'	51:1:2053:G:H5'	2.41	0.50
59:B2:9:LYS:HG2	59:B2:1171:ARG:HH12	1.77	0.50
59:B2:974:ARG:HD2	59:B2:1014:LEU:HD21	1.92	0.50
12:L:65:LEU:O	12:L:69:ARG:N	2.43	0.50
51:1:155:A:H2'	51:1:156:A:H8	1.76	0.50
51:1:386:G:H3'	51:1:387:U:C5'	2.41	0.50
51:1:673:C:H2'	51:1:674:G:C5'	2.41	0.50
51:1:1293:C:H2'	51:1:1294:U:C6	2.46	0.50
51:1:2248:C:H2'	51:1:2249:U:H5'	1.93	0.50
55:8:13:DT:OP2	58:B1:791:ALA:CB	2.59	0.50
64:7:9:G:C2	64:7:45:G:C6	3.00	0.50
19:S:68:ARG:NH2	53:3:974:A:OP1	2.45	0.50
20:T:23:SER:OG	20:T:25:GLU:OE1	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:v:51:GLN:OE1	46:v:79:ARG:NH2	2.40	0.50
51:1:539:G:O2'	51:1:540:C:H5'	2.11	0.50
51:1:1441:G:H2'	51:1:1442:U:H6	1.71	0.50
51:1:2302:U:O2'	51:1:2303:G:H5'	2.12	0.50
51:1:2888:C:H2'	51:1:2889:C:H6	1.77	0.50
57:A1:18:GLN:HA	57:A1:24:ALA:HA	1.94	0.50
7:G:103:TRP:HA	7:G:106:VAL:HG12	1.93	0.50
20:T:2:LEU:HD22	20:T:34:GLN:HB2	1.92	0.50
27:b:206:LYS:HD2	51:1:729:G:C8	2.46	0.50
51:1:1348:C:C5	51:1:1349:C:C5	3.00	0.50
51:1:2348:U:O2'	51:1:2349:G:H5'	2.12	0.50
53:3:494:G:H2'	53:3:496:A:H8	1.76	0.50
58:B1:102:MET:HG2	58:B1:246:PRO:HD3	1.94	0.50
58:B1:902:ASP:HB3	58:B1:905:ARG:HB2	1.93	0.50
58:B1:1371:ARG:HE	58:B1:1372:ARG:NH1	2.10	0.50
59:B2:232:ILE:HG12	59:B2:237:LEU:HG	1.94	0.50
59:B2:400:VAL:HG11	59:B2:452:ARG:HD2	1.94	0.50
17:Q:40:THR:CG2	65:h:6:5OH:OS	2.55	0.50
27:b:257:ARG:HH22	27:b:262:THR:HG1	1.57	0.50
33:i:134:SER:OG	51:1:1062:G:N2	2.45	0.50
34:j:2:LYS:HG2	51:1:995:C:N4	2.27	0.50
51:1:197:A:H2	51:1:2434:A:N6	2.10	0.50
51:1:1087:G:H2'	51:1:1089:A:H5'	1.94	0.50
51:1:1345:C:H6	51:1:1345:C:H5'	1.77	0.50
51:1:1593:A:H2'	51:1:1594:U:C6	2.47	0.50
51:1:2250:G:H8	51:1:2250:G:O5'	1.95	0.50
51:1:2525:G:N2	51:1:2539:C:C2	2.79	0.50
51:1:2670:A:O2'	51:1:2671:G:H5'	2.12	0.50
53:3:664:G:H22	53:3:741:G:H1	1.60	0.50
58:B1:145:VAL:HG12	58:B1:184:ALA:HB1	1.94	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
21:U:5:ARG:HB3	53:3:376:G:H5''	1.93	0.50
51:1:131:A:H2'	51:1:132:G:H8	1.77	0.50
51:1:262:A:H2'	51:1:263:G:O4'	2.12	0.50
64:7:9:G:O4'	64:7:46:G:C2	2.65	0.50
15:O:42:LEU:HB3	15:O:71:LEU:HB2	1.94	0.49
17:Q:120:ARG:HH12	53:3:500:G:H5'	1.77	0.49
27:b:137:GLY:O	27:b:162:GLN:NE2	2.45	0.49
27:b:146:LYS:HB2	27:b:149:LYS:HB2	1.93	0.49
38:n:49:GLU:O	38:n:53:THR:OG1	2.29	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:t:7:LEU:HD13	44:t:46:ALA:HA	1.94	0.49
51:1:30:G:H2'	51:1:31:C:C6	2.47	0.49
51:1:173:A:H2'	51:1:174:U:C6	2.47	0.49
51:1:521:U:H2'	51:1:522:A:H8	1.73	0.49
51:1:840:C:O2'	51:1:841:G:H5'	2.12	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
51:1:1144:A:H2'	51:1:1145:C:C6	2.47	0.49
51:1:1614:A:H2'	51:1:1615:C:H5'	1.94	0.49
51:1:2257:U:O2'	51:1:2258:C:H5'	2.13	0.49
53:3:1266:G:N2	53:3:1269:A:OP2	2.29	0.49
58:B1:437:PHE:HZ	58:B1:453:VAL:HG11	1.76	0.49
59:B2:902:LEU:HD21	59:B2:908:GLU:HB2	1.93	0.49
7:G:221:ARG:HG2	7:G:224:ARG:HH11	1.77	0.49
21:U:36:VAL:HG12	21:U:53:ASP:HB3	1.95	0.49
27:b:50:THR:HG23	51:1:1813:G:N2	2.27	0.49
27:b:92:LEU:HD21	27:b:100:ARG:HD3	1.93	0.49
28:c:81:GLU:HG3	51:1:2636:C:O5'	2.13	0.49
31:f:41:GLU:HG2	31:f:54:ARG:HH21	1.78	0.49
33:i:25:PRO:HB3	51:1:1095:A:N1	2.27	0.49
51:1:355:U:H2'	51:1:356:G:H8	1.77	0.49
51:1:644:A:H2'	51:1:645:C:C4'	2.42	0.49
51:1:1748:C:H2'	51:1:1749:A:C8	2.47	0.49
51:1:2533:U:H2'	51:1:2534:A:C5'	2.42	0.49
51:1:2634:A:O2'	51:1:2635:A:H5'	2.12	0.49
53:3:517:G:N2	53:3:533:A:OP2	2.34	0.49
53:3:1137:C:H4'	53:3:1138:G:H5'	1.94	0.49
11:K:42:TRP:HB2	11:K:59:TYR:HB2	1.93	0.49
27:b:147:PRO:HG3	27:b:184:GLU:HG2	1.92	0.49
51:1:1916:A:H2'	51:1:1917:U:O4'	2.12	0.49
51:1:2758:A:C2'	51:1:2759:G:H5'	2.40	0.49
55:8:3:DC:H2''	55:8:4:DT:C7	2.42	0.49
58:B1:220:ARG:HG2	58:B1:220:ARG:NH1	2.25	0.49
58:B1:421:VAL:O	58:B1:436:ALA:HA	2.12	0.49
59:B2:533:LEU:HD13	59:B2:540:ARG:HH21	1.77	0.49
11:K:46:GLN:HA	11:K:56:LYS:HB3	1.94	0.49
28:c:13:ARG:NH2	40:p:74:GLN:OE1	2.43	0.49
28:c:56:LYS:NZ	51:1:2830:C:H5''	2.28	0.49
51:1:16:C:H2'	51:1:17:G:H8	1.77	0.49
51:1:286:U:H2'	51:1:287:G:C8	2.47	0.49
51:1:519:U:H2'	51:1:520:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1084:A:O2'	51:1:1105:U:H4'	2.12	0.49
51:1:1388:G:O2'	51:1:1389:G:H5'	2.12	0.49
51:1:2241:A:O2'	51:1:2242:G:H5'	2.12	0.49
51:1:2298:A:O2'	51:1:2299:U:H5'	2.12	0.49
51:1:2734:A:H2'	51:1:2735:G:C5'	2.42	0.49
25:Y:53:MET:HE2	25:Y:57:VAL:HG21	1.94	0.49
25:Y:59:ARG:O	25:Y:63:LYS:N	2.46	0.49
27:b:70:LYS:O	27:b:117:SER:OG	2.30	0.49
30:e:135:ILE:HG23	30:e:140:ILE:HD11	1.93	0.49
31:f:87:GLN:NE2	31:f:129:GLU:OE2	2.45	0.49
33:i:110:GLN:HG2	33:i:121:ILE:HD13	1.93	0.49
51:1:178:U:H2'	51:1:179:C:H6	1.77	0.49
51:1:367:G:H2'	51:1:368:A:O4'	2.13	0.49
51:1:886:A:C5	51:1:887:U:H1'	2.47	0.49
51:1:905:A:H2'	51:1:906:U:C5'	2.40	0.49
51:1:2286:G:H21	51:1:2287:A:N6	2.09	0.49
51:1:2836:U:H2'	51:1:2837:A:C8	2.47	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
17:Q:97:VAL:HG12	17:Q:99:GLY:H	1.78	0.49
27:b:56:GLY:HA2	27:b:212:TRP:HA	1.94	0.49
51:1:69:C:O2'	51:1:70:G:H5'	2.13	0.49
51:1:187:G:C6	51:1:188:G:N7	2.80	0.49
51:1:236:C:H2'	51:1:237:C:C6	2.46	0.49
51:1:488:G:H22	51:1:491:G:H5''	1.77	0.49
51:1:898:C:C2'	51:1:899:A:H5'	2.43	0.49
51:1:900:A:H2'	51:1:901:C:H5'	1.94	0.49
51:1:1796:U:H2'	51:1:1797:G:C8	2.45	0.49
53:3:1178:G:N2	53:3:1181:G:OP2	2.43	0.49
58:B1:124:ILE:HG23	58:B1:128:LEU:HD12	1.94	0.49
7:G:101:THR:HG23	7:G:174:GLU:HG3	1.95	0.49
15:O:89:ARG:HH22	62:NG:165:PHE:H	1.60	0.49
30:e:57:ALA:HB2	30:e:64:PRO:HD3	1.95	0.49
38:n:8:ARG:HH21	38:n:43:GLU:HG3	1.77	0.49
42:r:71:LYS:HA	42:r:90:ARG:HG2	1.95	0.49
51:1:609:A:H2'	51:1:610:C:O4'	2.11	0.49
53:3:113:G:N3	53:3:353:A:O2'	2.42	0.49
53:3:890:G:O2'	53:3:906:A:N6	2.46	0.49
59:B2:732:ILE:HD11	59:B2:769:PRO:HB3	1.95	0.49
59:B2:857:VAL:HG13	59:B2:919:ARG:HH21	1.78	0.49
63:5:51:U:H2'	63:5:52:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:2:ARG:NH2	53:3:933:G:O6	2.46	0.49
30:e:84:ILE:HD11	51:1:2311:A:H1'	1.94	0.49
51:1:121:G:H4'	51:1:149:A:H5'	1.95	0.49
51:1:1119:U:O2'	51:1:1120:G:H5'	2.13	0.49
53:3:401:C:O2'	53:3:621:A:N3	2.45	0.49
53:3:481:G:O2'	53:3:483:C:N4	2.46	0.49
58:B1:201:LEU:HD11	58:B1:220:ARG:HG2	1.95	0.49
58:B1:749:LYS:HB3	58:B1:755:ILE:HD11	1.94	0.49
51:1:482:A:H1'	51:1:498:G:N2	2.27	0.49
51:1:1111:A:H2'	51:1:1111:A:N3	2.28	0.49
51:1:1785:A:O2'	51:1:1786:A:H8	1.96	0.49
51:1:2283:C:H2'	51:1:2284:A:O4'	2.11	0.49
51:1:2553:G:H22	63:5:75:C:H42	1.60	0.49
53:3:1064:G:O2'	53:3:1190:G:N2	2.46	0.49
58:B1:550:VAL:O	58:B1:569:LEU:HA	2.13	0.49
59:B2:565:GLU:HA	59:B2:569:ILE:HG12	1.95	0.49
13:M:29:SER:OG	13:M:30:LYS:N	2.43	0.49
17:Q:70:GLY:O	17:Q:107:LYS:NZ	2.44	0.49
35:k:5:GLN:HE21	51:1:1668:A:H5''	1.78	0.49
48:x:1:SER:O	48:x:49:ARG:NH1	2.46	0.49
51:1:67:U:H2'	51:1:68:G:H8	1.77	0.49
51:1:1668:A:N3	51:1:1670:C:N4	2.60	0.49
51:1:2180:U:O2'	51:1:2181:U:H5'	2.13	0.49
51:1:2281:A:O2'	51:1:2282:G:H5'	2.12	0.49
51:1:2510:C:N4	51:1:2511:U:C4	2.81	0.49
53:3:780:A:N6	53:3:801:U:OP2	2.42	0.49
55:8:14:DC:H2'	55:8:15:DC:C6	2.48	0.49
57:A2:294:ASN:HA	61:NA:463:GLY:CA	2.41	0.49
11:K:41:ASP:OD1	11:K:58:HIS:NE2	2.39	0.48
44:t:70:HIS:N	44:t:73:ARG:O	2.44	0.48
51:1:554:U:O2'	51:1:555:G:H5'	2.13	0.48
51:1:940:G:H2'	51:1:941:A:C5'	2.41	0.48
51:1:1077:A:H8	51:1:1078:U:H1'	1.77	0.48
51:1:1266:G:O2'	51:1:2012:G:O6	2.25	0.48
51:1:1400:U:H2'	51:1:1401:G:H8	1.78	0.48
51:1:1465:G:H2'	51:1:1466:U:O4'	2.13	0.48
51:1:1534:U:H4'	51:1:1535:A:N1	2.27	0.48
51:1:2329:U:H2'	51:1:2330:G:H8	1.78	0.48
51:1:2527:C:O2'	51:1:2528:U:H5'	2.13	0.48
57:A1:100:LEU:HB2	57:A1:144:ILE:HG23	1.94	0.48
40:p:2:ASN:HD21	51:1:2876:G:H4'	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:54:G:H2'	51:1:55:G:O4'	2.12	0.48
51:1:360:U:H2'	51:1:361:G:C1'	2.44	0.48
51:1:481:G:C2'	51:1:482:A:OP2	2.61	0.48
51:1:718:A:H2'	51:1:719:C:O4'	2.12	0.48
51:1:1387:A:C5'	51:1:1469:A:H1'	2.38	0.48
51:1:1409:U:H2'	51:1:1410:G:H8	1.76	0.48
51:1:1871:A:H2'	51:1:1872:A:O4'	2.13	0.48
51:1:1910:G:N2	51:1:1911:U:C2	2.81	0.48
51:1:2214:C:H2'	51:1:2215:C:O4'	2.14	0.48
51:1:2367:G:O2'	51:1:2368:C:H5'	2.13	0.48
9:I:153:ARG:NH2	53:3:435:A:N3	2.61	0.48
26:Z:55:HIS:HA	26:Z:58:LYS:HD2	1.95	0.48
31:f:163:TYR:HB2	31:f:166:GLU:HB2	1.95	0.48
33:i:85:ILE:HD12	33:i:97:VAL:HG12	1.95	0.48
37:m:74:THR:HG21	37:m:86:LYS:HG2	1.94	0.48
45:u:88:ASP:OD1	45:u:88:ASP:N	2.43	0.48
51:1:92:U:H2'	51:1:93:G:H5'	1.95	0.48
51:1:841:G:C2	51:1:938:G:C2	3.01	0.48
51:1:1117:C:H2'	51:1:1118:C:H6	1.78	0.48
51:1:2843:G:O2'	51:1:2844:G:H5'	2.13	0.48
65:h:6:5OH:N	65:h:6:5OH:CS	2.75	0.48
14:N:10:ARG:NH2	53:3:1119:C:OP2	2.47	0.48
40:p:59:THR:HG22	40:p:72:VAL:HG12	1.95	0.48
49:y:16:THR:O	49:y:20:ASN:ND2	2.46	0.48
51:1:214:G:H2'	51:1:215:G:C8	2.48	0.48
51:1:553:G:H2'	51:1:554:U:O4'	2.13	0.48
51:1:572:A:H8	51:1:572:A:O5'	1.97	0.48
51:1:898:C:O2'	51:1:899:A:H5'	2.13	0.48
51:1:1645:G:H5''	51:1:1646:C:H5'	1.94	0.48
51:1:1702:G:H2'	51:1:1703:G:C5'	2.35	0.48
53:3:768:A:N3	53:3:1512:U:O2'	2.46	0.48
53:3:898:G:N2	53:3:901:A:OP2	2.46	0.48
53:3:1223:C:H5'	53:3:1224:U:H5''	1.96	0.48
59:B2:318:SER:OG	59:B2:320:ASP:OD1	2.31	0.48
59:B2:411:ARG:NH2	59:B2:427:ASP:OD2	2.44	0.48
59:B2:836:LEU:HD13	59:B2:1054:LEU:HD13	1.95	0.48
14:N:91:GLU:HA	14:N:94:ARG:HB2	1.94	0.48
16:P:96:ILE:HD13	16:P:109:ILE:HD13	1.94	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
31:f:122:ALA:HB2	31:f:132:LEU:HD23	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:o:15:ARG:NH2	52:2:8:C:OP1	2.47	0.48
51:1:118:A:H2'	51:1:120:U:O4	2.13	0.48
51:1:706:A:H2'	51:1:707:G:H5'	1.95	0.48
51:1:1437:C:H2'	51:1:1438:U:H6	1.78	0.48
51:1:1536:C:H5''	51:1:1537:G:C4	2.48	0.48
51:1:1729:U:H5	51:1:1731:G:N2	2.12	0.48
51:1:2126:A:H5'	51:1:2127:G:O5'	2.13	0.48
53:3:776:G:N2	53:3:802:A:OP2	2.39	0.48
53:3:880:C:H2'	53:3:881:G:H8	1.78	0.48
58:B1:115:TRP:O	58:B1:1333:THR:HG21	2.13	0.48
42:r:68:ARG:O	42:r:90:ARG:NH2	2.46	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	2.49	0.48
51:1:1087:G:O6	51:1:1089:A:C2	2.67	0.48
51:1:1680:U:O2'	51:1:1681:G:H5'	2.13	0.48
58:B1:968:ASN:HA	58:B1:1117:SER:HB2	1.96	0.48
1:A:37:CYS:O	1:A:41:HIS:N	2.45	0.48
9:I:94:GLU:HG3	9:I:190:LEU:HD21	1.95	0.48
45:u:39:ASN:HB3	45:u:62:ALA:HB3	1.95	0.48
51:1:2393:U:H2'	51:1:2394:C:H5'	1.94	0.48
53:3:673:A:H2'	53:3:674:G:C8	2.49	0.48
58:B1:1347:LEU:HG	58:B1:1357:ILE:HG23	1.96	0.48
6:F:6:SER:O	6:F:6:SER:OG	2.31	0.48
13:M:83:ARG:NH2	53:3:587:G:OP1	2.44	0.48
15:O:58:ASN:ND2	53:3:1061:G:O2'	2.45	0.48
17:Q:82:ARG:O	17:Q:95:HIS:N	2.47	0.48
29:d:143:LEU:HD13	29:d:146:VAL:HG11	1.94	0.48
41:q:103:VAL:HA	41:q:106:THR:HG22	1.94	0.48
51:1:129:C:H2'	51:1:130:C:H6	1.79	0.48
51:1:217:A:H2'	51:1:218:A:O4'	2.13	0.48
51:1:2547:A:H61	51:1:2561:U:H3	1.62	0.48
59:B2:363:LEU:HB3	59:B2:381:ALA:HB1	1.96	0.48
14:N:44:ARG:HG2	14:N:45:MET:HE2	1.95	0.48
38:n:100:CYS:H	38:n:111:ALA:HA	1.79	0.48
51:1:820:A:H2'	51:1:821:A:O4'	2.14	0.48
51:1:1257:C:O5'	51:1:1257:C:H6	1.97	0.48
51:1:1537:G:H3'	51:1:1537:G:N3	2.28	0.48
51:1:1742:U:O2'	51:1:1743:G:H5'	2.14	0.48
51:1:2016:U:O5'	51:1:2016:U:H6	1.97	0.48
53:3:358:U:H2'	53:3:359:G:H8	1.78	0.48
58:B1:190:LYS:HB2	58:B1:190:LYS:HE3	1.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:554:HIS:HD2	59:B2:558:VAL:HB	1.77	0.48
12:L:41:ILE:HD11	53:3:1240:U:H5'	1.94	0.48
14:N:94:ARG:HG2	14:N:97:LEU:HD12	1.95	0.48
20:T:48:ASP:OD1	53:3:667:G:O2'	2.25	0.48
29:d:149:ILE:HD11	29:d:172:ALA:HA	1.96	0.48
42:r:7:SER:OG	42:r:8:GLY:N	2.47	0.48
46:v:79:ARG:HA	46:v:86:LEU:HA	1.95	0.48
51:1:473:G:O2'	51:1:474:G:H5'	2.14	0.48
51:1:2050:C:N4	51:1:2051:A:C6	2.81	0.48
51:1:2208:C:H2'	51:1:2209:G:C8	2.48	0.48
51:1:2649:C:O2'	51:1:2650:U:H5'	2.13	0.48
53:3:1531:A:O2'	53:3:1532:U:H5'	2.14	0.48
59:B2:562:GLU:OE1	59:B2:662:SER:OG	2.28	0.48
59:B2:1286:THR:O	59:B2:1290:MET:HB2	2.14	0.48
33:i:79:LEU:HD13	33:i:132:ALA:HB2	1.94	0.47
36:l:129:LYS:HG2	51:1:636:G:OP1	2.14	0.47
51:1:5:A:H2'	51:1:6:A:C8	2.49	0.47
51:1:275:C:C3'	51:1:276:U:H5''	2.40	0.47
51:1:596:U:C2	51:1:662:G:N2	2.82	0.47
57:A1:182:ARG:O	57:A1:205:MET:HA	2.14	0.47
58:B1:103:GLY:H	58:B1:244:VAL:HG22	1.79	0.47
58:B1:395:LYS:NZ	58:B1:399:LYS:CE	2.77	0.47
58:B1:1221:LEU:HD22	58:B1:1306:LEU:HB2	1.96	0.47
59:B2:529:ARG:HH11	59:B2:572:ILE:HG22	1.77	0.47
64:7:50:U:H2'	64:7:51:C:C5	2.49	0.47
29:d:48:THR:OG1	29:d:49:ARG:N	2.47	0.47
51:1:40:U:H2'	51:1:41:C:H6	1.78	0.47
51:1:476:G:H4'	51:1:502:A:N1	2.28	0.47
51:1:813:U:C2	51:1:1195:G:N2	2.83	0.47
51:1:2098:U:H2'	51:1:2099:U:O4'	2.14	0.47
51:1:2286:G:H21	51:1:2287:A:H61	1.62	0.47
51:1:2895:G:H2'	51:1:2896:C:C6	2.49	0.47
58:B1:1027:VAL:HB	58:B1:1121:LEU:HB2	1.95	0.47
14:N:86:LEU:HD12	14:N:97:LEU:HD11	1.95	0.47
27:b:152:GLN:HB3	51:1:1818:U:N3	2.29	0.47
28:c:190:LYS:HE2	51:1:2729:G:H4'	1.95	0.47
47:w:19:VAL:HA	47:w:34:VAL:HG22	1.96	0.47
51:1:214:G:O2'	51:1:215:G:H5'	2.14	0.47
51:1:852:U:H2'	51:1:853:C:C6	2.49	0.47
51:1:1026:G:OP2	51:1:1134:A:H1'	2.13	0.47
51:1:1324:G:O2'	51:1:1326:U:OP2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1807:G:C2'	51:1:1808:A:H5'	2.29	0.47
51:1:2047:C:O5'	51:1:2047:C:H6	1.98	0.47
51:1:2362:C:O5'	51:1:2362:C:H6	1.97	0.47
51:1:2828:G:O2'	51:1:2829:A:H5'	2.13	0.47
52:2:51:G:H22	52:2:53:A:H62	1.61	0.47
53:3:530:G:N1	53:3:1492:A:N1	2.59	0.47
57:A2:102:LEU:HD12	57:A2:115:ILE:HG12	1.96	0.47
58:B1:29:MET:HG2	59:B2:1336:ASN:ND2	2.29	0.47
58:B1:1261:LEU:HD12	58:B1:1304:ARG:HH21	1.78	0.47
63:5:37:A:H3'	63:5:38:A:C8	2.49	0.47
7:G:129:THR:HB	7:G:132:GLU:HB2	1.96	0.47
9:I:93:LEU:O	9:I:99:ASN:ND2	2.39	0.47
27:b:131:MET:HE2	27:b:187:CYS:HB2	1.96	0.47
51:1:1267:U:H2'	51:1:1267:U:O2	2.14	0.47
51:1:1509:A:H2'	51:1:1510:G:C8	2.49	0.47
51:1:2149:U:H2'	51:1:2150:C:C6	2.49	0.47
51:1:2298:A:C2'	51:1:2299:U:H5'	2.45	0.47
51:1:2554:U:H2'	51:1:2555:U:O2	2.15	0.47
55:8:14:DC:H2'	55:8:15:DC:H6	1.79	0.47
59:B2:1311:GLY:O	60:W0:31:GLN:NE2	2.47	0.47
62:NG:161:SER:CA	62:NG:170:PRO:HA	2.43	0.47
63:5:29:G:H3'	63:5:30:G:C8	2.50	0.47
9:I:171:GLU:HB3	9:I:180:THR:HG22	1.97	0.47
12:L:112:ASP:HB2	12:L:118:ARG:HG2	1.96	0.47
16:P:34:THR:OG1	16:P:35:ASP:N	2.47	0.47
33:i:8:VAL:HG21	33:i:26:ALA:HB1	1.96	0.47
34:j:65:THR:HG22	51:1:1141:U:OP2	2.15	0.47
47:w:29:ALA:N	47:w:60:ASP:OD1	2.48	0.47
51:1:1098:A:O2'	51:1:1099:G:H5'	2.15	0.47
51:1:1285:A:H2'	51:1:1286:A:H5'	1.96	0.47
51:1:1400:U:H2'	51:1:1401:G:C8	2.50	0.47
51:1:1463:C:H2'	51:1:1464:G:C8	2.49	0.47
51:1:1464:G:H2'	51:1:1465:G:C8	2.49	0.47
51:1:1491:G:H2'	51:1:1492:G:H8	1.80	0.47
51:1:1913:A:N7	53:3:1494:G:H4'	2.29	0.47
51:1:2156:G:C3'	51:1:2157:G:H5'	2.44	0.47
53:3:38:G:H22	53:3:397:A:H5'	1.78	0.47
58:B1:255:LEU:HD23	58:B1:261:ALA:HB2	1.95	0.47
58:B1:809:VAL:HG21	58:B1:909:ILE:HG12	1.95	0.47
12:L:79:VAL:HB	12:L:84:TYR:HD2	1.80	0.47
12:L:107:ALA:HA	12:L:122:GLU:HG3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:114:SER:O	53:3:35:G:O2'	2.30	0.47
18:R:15:VAL:HG11	18:R:30:LYS:HG2	1.97	0.47
28:c:136:ASN:OD1	51:1:2579:C:O2'	2.32	0.47
33:i:79:LEU:HD21	33:i:105:LEU:HD21	1.96	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
51:1:297:G:H2'	51:1:298:G:O4'	2.14	0.47
51:1:762:U:N3	51:1:1431:A:OP1	2.47	0.47
51:1:1464:G:H2'	51:1:1465:G:H8	1.78	0.47
53:3:1305:G:N2	53:3:1331:G:H2'	2.29	0.47
58:B1:128:LEU:HD21	58:B1:188:LEU:HB3	1.97	0.47
58:B1:352:ARG:HB2	59:B2:1268:GLN:NE2	2.30	0.47
58:B1:833:GLU:N	58:B1:1242:ARG:HH12	2.12	0.47
58:B1:1150:PRO:HG3	58:B1:1214:PRO:HB2	1.96	0.47
58:B1:1167:LYS:NZ	58:B1:1170:LYS:HB2	2.30	0.47
4:D:29:GLN:O	4:D:29:GLN:NE2	2.47	0.47
9:I:159:GLU:HA	9:I:162:GLU:HB2	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
17:Q:70:GLY:O	17:Q:98:ARG:NH2	2.47	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
26:Z:19:LYS:H	26:Z:19:LYS:HG3	1.53	0.47
31:f:16:VAL:HA	31:f:25:ILE:HG12	1.96	0.47
31:f:87:GLN:HB3	31:f:162:ARG:HG3	1.97	0.47
31:f:88:LEU:HD21	31:f:104:LEU:HD23	1.97	0.47
32:g:8:LYS:HD3	32:g:14:SER:HA	1.96	0.47
32:g:47:PHE:HA	32:g:51:ARG:HB2	1.96	0.47
33:i:20:SER:HA	33:i:24:GLY:HA3	1.95	0.47
51:1:156:A:H2'	51:1:157:C:C6	2.50	0.47
51:1:555:G:O2'	51:1:556:A:H8	1.96	0.47
51:1:555:G:HO2'	51:1:556:A:H8	1.61	0.47
51:1:1019:U:N3	51:1:1142:A:N6	2.57	0.47
51:1:1036:G:O2'	51:1:1037:G:H5'	2.15	0.47
51:1:1105:U:H2'	51:1:1106:G:H8	1.80	0.47
51:1:1141:U:H4'	51:1:1142:A:C1'	2.45	0.47
51:1:1219:U:O2'	51:1:1220:G:H5'	2.15	0.47
51:1:1297:C:H2'	51:1:1298:C:H6	1.79	0.47
51:1:1389:G:C2	51:1:1390:U:C2	3.02	0.47
51:1:1435:G:O2'	51:1:1436:G:H5'	2.15	0.47
51:1:1465:G:HO2'	51:1:1466:U:H5'	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1517:G:O2'	51:1:1518:C:H5'	2.15	0.47
51:1:1851:U:OP1	64:7:4:G:H4'	2.15	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'	2.15	0.47
51:1:2295:C:O2'	51:1:2296:U:H5'	2.15	0.47
51:1:2445:G:C6	51:1:2446:G:C6	3.02	0.47
51:1:2455:G:C6	51:1:2456:C:N4	2.83	0.47
51:1:2899:A:H2'	51:1:2900:A:O4'	2.15	0.47
53:3:410:G:H21	53:3:432:A:H62	1.62	0.47
53:3:617:G:H1	53:3:623:C:H42	1.62	0.47
58:B1:842:ARG:HH22	58:B1:1250:ASP:HB2	1.80	0.47
63:5:50:U:H2'	63:5:51:U:C6	2.49	0.47
64:7:48:C:H5''	64:7:50:U:OP1	2.15	0.47
27:b:156:SER:OG	27:b:157:ALA:N	2.44	0.47
36:l:39:LYS:HG2	51:1:832:U:OP1	2.15	0.47
51:1:435:C:C2'	51:1:436:C:H5'	2.44	0.47
51:1:551:G:O2'	51:1:552:U:H5'	2.15	0.47
51:1:708:G:H2'	51:1:709:U:C6	2.50	0.47
51:1:1020:A:C1'	51:1:1021:A:OP2	2.61	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
51:1:1090:A:C2	51:1:1102:C:H1'	2.50	0.47
51:1:1922:G:H2'	51:1:1923:U:C6	2.50	0.47
51:1:2259:U:H2'	51:1:2260:C:O4'	2.15	0.47
54:4:3:G:H1	64:6:34:C:H42	1.63	0.47
58:B1:87:LYS:HA	62:NG:140:PRO:HA	1.97	0.47
58:B1:772:TYR:HE2	59:B2:561:ILE:HG21	1.80	0.47
58:B1:1036:ARG:HE	58:B1:1081:VAL:HG11	1.79	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
5:E:5:THR:HG22	5:E:62:PRO:HD2	1.97	0.47
19:S:32:ASP:O	19:S:34:ASN:ND2	2.48	0.47
39:o:68:LYS:HE3	52:2:49:C:H5''	1.97	0.47
51:1:30:G:C5	51:1:31:C:C4	3.03	0.47
51:1:143:C:H2'	51:1:144:A:C8	2.49	0.47
51:1:466:A:H2'	51:1:467:G:C5'	2.44	0.47
51:1:712:G:H2'	51:1:713:G:H5'	1.96	0.47
51:1:854:C:H2'	51:1:855:G:H8	1.79	0.47
51:1:900:A:C2'	51:1:901:C:H5'	2.45	0.47
51:1:1873:G:O2'	51:1:1874:C:H5'	2.15	0.47
51:1:1874:C:H2'	51:1:1875:G:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1927:A:H2'	51:1:1928:A:C8	2.50	0.47
51:1:2241:A:H2'	51:1:2242:G:C8	2.50	0.47
51:1:2395:C:H2'	51:1:2396:G:O4'	2.15	0.47
51:1:2563:U:H2'	51:1:2565:A:OP2	2.15	0.47
51:1:2679:A:O2'	51:1:2680:U:H5'	2.15	0.47
6:F:27:CYS:HG	6:F:33:HIS:HD1	1.55	0.47
27:b:145:MET:HE1	51:1:1800:C:H2'	1.98	0.47
27:b:184:GLU:HG3	27:b:186:ASP:H	1.80	0.47
33:i:54:ILE:HD12	33:i:73:PRO:HD3	1.95	0.47
34:j:2:LYS:HA	51:1:995:C:C4	2.50	0.47
46:v:26:PHE:HE2	46:v:89:ILE:HG13	1.80	0.47
51:1:859:G:C2'	51:1:860:U:OP2	2.62	0.47
51:1:877:A:O2'	51:1:878:A:H5''	2.14	0.47
51:1:1067:A:H2'	51:1:1068:G:C8	2.49	0.47
51:1:1922:G:O2'	51:1:1923:U:H5'	2.15	0.47
53:3:512:U:H2'	53:3:513:C:C6	2.50	0.47
57:A1:35:PHE:HA	57:A1:38:THR:HG22	1.97	0.47
58:B1:891:ASP:OD2	58:B1:1290:ARG:NH2	2.47	0.47
58:B1:1060:VAL:HG13	58:B1:1106:ILE:HG12	1.97	0.47
9:I:1:ALA:N	53:3:405:U:O4	2.45	0.46
29:d:119:ILE:HB	29:d:187:VAL:HG12	1.96	0.46
31:f:29:ASN:ND2	31:f:80:GLU:O	2.48	0.46
35:k:47:ILE:HG22	35:k:49:ARG:H	1.80	0.46
46:v:83:LYS:HB3	46:v:85:LYS:HZ3	1.80	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
51:1:1536:C:H5''	51:1:1537:G:C5	2.50	0.46
53:3:1225:A:H2'	53:3:1225:A:N3	2.30	0.46
58:B1:108:ALA:HB1	58:B1:279:LEU:HD22	1.96	0.46
17:Q:45:ASN:ND2	17:Q:88:ASP:OD2	2.39	0.46
18:R:7:ASN:HD22	18:R:20:SER:HB2	1.80	0.46
26:Z:29:ALA:O	26:Z:32:ARG:NH1	2.49	0.46
51:1:338:G:O2'	51:1:339:U:H5'	2.14	0.46
51:1:554:U:C2'	51:1:555:G:H5'	2.46	0.46
51:1:570:G:H5'	51:1:983:A:C2	2.51	0.46
51:1:848:C:H2'	51:1:849:A:H8	1.81	0.46
51:1:2294:G:O2'	51:1:2295:C:H5'	2.15	0.46
51:1:2626:C:H2'	51:1:2627:G:H8	1.80	0.46
53:3:1035:A:H1'	53:3:1036:A:O5'	2.16	0.46
58:B1:385:LEU:HD23	58:B1:390:LEU:HB2	1.98	0.46
58:B1:526:VAL:HG12	58:B1:549:LYS:HB2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:1146:GLU:OE2	58:B1:1310:THR:HG22	2.14	0.46
58:B1:1219:ASP:O	58:B1:1223:LEU:HB2	2.15	0.46
58:B1:1357:ILE:HD13	59:B2:1279:GLU:HG2	1.97	0.46
59:B2:400:VAL:HG22	59:B2:584:TYR:HB3	1.96	0.46
59:B2:903:ARG:HA	59:B2:907:GLY:HA2	1.97	0.46
12:L:137:ARG:NH1	12:L:138:GLU:OE2	2.48	0.46
14:N:40:ARG:NH2	53:3:1291:U:O3'	2.38	0.46
31:f:90:GLY:HA2	31:f:159:LYS:HG2	1.98	0.46
48:x:38:TRP:NE1	48:x:40:GLU:OE1	2.41	0.46
51:1:93:G:O2'	51:1:94:A:H5'	2.16	0.46
51:1:438:G:O2'	51:1:439:A:H5'	2.16	0.46
51:1:1117:C:H2'	51:1:1118:C:C6	2.50	0.46
51:1:1146:C:O2'	51:1:1147:A:H5'	2.16	0.46
51:1:2858:C:H2'	51:1:2859:G:O4'	2.15	0.46
58:B1:211:GLU:CG	58:B1:215:LYS:HE3	2.44	0.46
59:B2:1314:GLN:HB2	60:W0:28:ARG:HH12	1.79	0.46
63:5:8:U:H2'	63:5:13:C:N4	2.30	0.46
14:N:11:ARG:NH2	53:3:1347:G:O6	2.49	0.46
20:T:37:HIS:HD2	20:T:38:LEU:HD12	1.80	0.46
45:u:6:ARG:HB2	51:1:85:G:P	2.55	0.46
51:1:538:A:O2'	51:1:539:G:H5'	2.14	0.46
51:1:686:U:H6	51:1:788:A:H61	1.61	0.46
51:1:1209:U:O3'	51:1:1212:G:H5'	2.16	0.46
52:2:39:A:O2'	52:2:46:A:N1	2.47	0.46
58:B1:375:GLU:HB3	59:B2:1245:ALA:HB3	1.97	0.46
58:B1:800:LEU:HD12	58:B1:800:LEU:HA	1.79	0.46
59:B2:1002:LEU:HD21	59:B2:1007:LYS:HB2	1.98	0.46
3:C:13:SER:OG	3:C:47:ILE:O	2.27	0.46
8:H:171:ARG:HG2	8:H:173:PRO:HD3	1.96	0.46
12:L:142:ARG:HA	12:L:145:GLU:HG3	1.97	0.46
17:Q:72:ASN:HD21	17:Q:103:CYS:HA	1.81	0.46
31:f:100:ASN:OD1	31:f:100:ASN:N	2.47	0.46
33:i:115:ASP:OD2	51:1:1059:G:H4'	2.14	0.46
48:x:14:GLY:HA3	48:x:28:PHE:HE1	1.81	0.46
51:1:848:C:H2'	51:1:849:A:C8	2.51	0.46
51:1:853:C:O2'	51:1:854:C:H5'	2.16	0.46
51:1:1367:A:H3'	51:1:1368:G:O4'	2.15	0.46
51:1:1572:A:H2'	51:1:1573:G:O4'	2.16	0.46
51:1:1768:C:H42	51:1:1984:G:H1	1.62	0.46
51:1:2247:A:H2'	51:1:2248:C:H6	1.81	0.46
58:B1:43:THR:HG22	58:B1:57:PHE:HE1	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:198:CYS:HA	58:B1:221:ILE:CD1	2.45	0.46
59:B2:517:GLN:HB3	59:B2:760:ASN:H	1.79	0.46
10:J:73:VAL:HG11	10:J:143:LEU:HB3	1.98	0.46
11:K:3:HIS:HA	11:K:65:GLU:HA	1.97	0.46
43:s:72:THR:OG1	43:s:73:LYS:N	2.48	0.46
51:1:569:U:H1'	51:1:947:A:O4'	2.16	0.46
51:1:1183:U:H2'	51:1:1184:U:H6	1.80	0.46
51:1:1381:G:H2'	51:1:1382:G:H5'	1.98	0.46
51:1:1528:A:H2'	51:1:1529:G:C5'	2.44	0.46
51:1:2290:G:O2'	51:1:2291:U:H5'	2.16	0.46
51:1:2496:C:H2'	51:1:2497:A:O4'	2.16	0.46
51:1:2528:U:O2'	51:1:2529:G:H3'	2.16	0.46
51:1:2743:U:H2'	51:1:2744:G:O4'	2.16	0.46
58:B1:420:PRO:HA	58:B1:437:PHE:O	2.15	0.46
64:6:21:A:H62	64:6:47:U:H1'	1.81	0.46
28:c:4:LEU:HD11	28:c:100:LEU:HD21	1.98	0.46
29:d:132:LYS:HG2	29:d:136:GLN:HE22	1.81	0.46
40:p:74:GLN:O	40:p:77:SER:OG	2.30	0.46
51:1:44:A:H2'	51:1:45:G:O4'	2.15	0.46
51:1:389:G:O2'	51:1:390:U:H5'	2.15	0.46
51:1:409:G:H2'	51:1:410:G:C8	2.51	0.46
51:1:1516:G:O2'	51:1:1517:G:H5'	2.15	0.46
51:1:1574:C:H2'	51:1:1575:C:C6	2.50	0.46
51:1:1726:C:H2'	51:1:1727:C:C6	2.50	0.46
51:1:1766:G:C2'	51:1:1767:G:H5'	2.45	0.46
51:1:1923:U:O2'	51:1:1924:C:H5'	2.16	0.46
51:1:2180:U:H2'	51:1:2181:U:O4'	2.14	0.46
53:3:1383:C:H4'	64:7:35:A:H2	1.81	0.46
57:A1:59:VAL:HG22	57:A1:144:ILE:HA	1.97	0.46
58:B1:175:GLU:H	58:B1:175:GLU:HG3	1.66	0.46
58:B1:343:LEU:HD11	58:B1:1324:SER:HB3	1.97	0.46
59:B2:712:SER:OG	59:B2:713:GLY:N	2.49	0.46
2:B:31:LYS:HG2	51:1:2885:G:N2	2.31	0.46
11:K:5:GLU:HB2	11:K:90:MET:HB2	1.98	0.46
33:i:109:ALA:HA	33:i:112:LYS:HB2	1.98	0.46
51:1:595:C:C2	51:1:596:U:C5	3.04	0.46
51:1:1173:U:C6	51:1:1174:U:H1'	2.51	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
51:1:2329:U:H2'	51:1:2330:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2581:G:H2'	51:1:2581:G:N3	2.30	0.46
51:1:2625:G:H2'	51:1:2626:C:H6	1.76	0.46
51:1:2836:U:H2'	51:1:2837:A:H8	1.81	0.46
59:B2:207:THR:OG1	59:B2:354:ASP:OD2	2.32	0.46
62:NG:135:ARG:O	62:NG:178:VAL:HA	2.16	0.46
6:F:33:HIS:O	6:F:34:LYS:C	2.59	0.46
16:P:127:ARG:HB2	26:Z:34:ARG:HH22	1.81	0.46
18:R:97:ARG:HB2	18:R:99:GLN:HE22	1.81	0.46
27:b:99:GLU:OE2	51:1:1491:G:O2'	2.33	0.46
28:c:170:VAL:HG21	51:1:2679:A:H5'	1.97	0.46
35:k:70:ARG:NH1	51:1:2684:U:O4'	2.49	0.46
51:1:688:U:H5'	51:1:1780:A:C2	2.51	0.46
51:1:1486:U:O2'	51:1:1487:U:H5'	2.14	0.46
51:1:1520:U:H2'	51:1:1521:G:O4'	2.16	0.46
51:1:2360:G:H2'	51:1:2361:G:C5'	2.40	0.46
51:1:2783:U:H2'	51:1:2784:U:C6	2.51	0.46
53:3:459:A:H2'	53:3:460:A:C8	2.50	0.46
53:3:618:C:N4	53:3:621:A:OP2	2.49	0.46
58:B1:109:SER:HB2	58:B1:296:LYS:HG2	1.98	0.46
58:B1:515:ARG:NH2	58:B1:718:SER:O	2.48	0.46
63:5:26:A:H61	63:5:44:G:H22	1.64	0.46
8:H:152:VAL:HG12	8:H:197:VAL:HG22	1.98	0.46
10:J:28:ARG:NH2	53:3:1397:C:OP2	2.38	0.46
10:J:110:MET:HE3	10:J:110:MET:HB2	1.79	0.46
17:Q:23:LEU:HD12	17:Q:29:LYS:HD2	1.97	0.46
30:e:71:LYS:HA	30:e:71:LYS:HD2	1.78	0.46
31:f:1:SER:HA	51:1:2749:A:OP1	2.15	0.46
43:s:82:MET:HE1	51:1:1322:A:H5''	1.98	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
51:1:1034:G:C5	51:1:1035:U:C4	3.04	0.46
51:1:2101:A:H2'	51:1:2102:G:H8	1.81	0.46
51:1:2813:A:O2'	51:1:2814:A:H5'	2.15	0.46
53:3:1200:C:H5''	53:3:1201:A:H3'	1.97	0.46
55:8:1:DC:H2''	55:8:2:DC:C6	2.51	0.46
58:B1:201:LEU:CD1	58:B1:224:LEU:HD12	2.47	0.46
59:B2:900:LYS:HB3	59:B2:900:LYS:HE3	1.62	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
15:O:100:ILE:O	62:NG:170:PRO:O	2.34	0.45
22:V:10:ARG:NE	22:V:55:GLY:O	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:33:THR:OG1	23:W:34:GLU:N	2.49	0.45
35:k:5:GLN:NE2	51:1:1668:A:H5''	2.31	0.45
35:k:121:GLU:HG2	35:k:122:VAL:HG23	1.97	0.45
39:o:29:HIS:HB3	39:o:36:TYR:HB2	1.98	0.45
51:1:540:C:O2'	51:1:541:A:H5'	2.16	0.45
51:1:1287:A:O2'	51:1:1288:G:H5'	2.16	0.45
51:1:1807:G:H2'	51:1:1808:A:C5'	2.30	0.45
51:1:1923:U:H5''	64:6:24:U:O2'	2.17	0.45
51:1:2642:G:O5'	51:1:2642:G:H8	1.98	0.45
51:1:2849:U:H4'	51:1:2868:A:C2	2.51	0.45
9:I:114:ARG:HA	9:I:117:VAL:HG22	1.98	0.45
36:l:69:ARG:NH1	51:1:2406:A:C2	2.84	0.45
37:m:34:LYS:N	37:m:129:THR:O	2.47	0.45
51:1:6:A:H2'	51:1:7:G:C8	2.52	0.45
51:1:290:U:O2'	51:1:291:G:H5'	2.16	0.45
51:1:342:A:H2'	51:1:343:C:O4'	2.16	0.45
51:1:367:G:O2'	51:1:368:A:H5'	2.17	0.45
51:1:438:G:H2'	51:1:439:A:C8	2.51	0.45
51:1:607:U:O4	51:1:620:G:H5'	2.17	0.45
51:1:637:A:C6	51:1:652:U:H4'	2.50	0.45
51:1:1550:C:O2'	51:1:1551:A:H5'	2.17	0.45
51:1:1710:G:H2'	51:1:1711:A:C8	2.51	0.45
51:1:2030:A:N3	51:1:2499:C:H5''	2.31	0.45
51:1:2085:U:O2'	51:1:2086:U:H5'	2.16	0.45
51:1:2350:C:H2'	51:1:2351:G:O4'	2.16	0.45
55:8:13:DT:C6	58:B1:791:ALA:HA	2.51	0.45
57:A1:231:PHE:O	57:A2:218:ARG:NH1	2.49	0.45
57:A2:64:VAL:HG11	57:A2:78:ILE:HG21	1.97	0.45
4:D:12:ARG:NH1	51:1:465:G:OP1	2.49	0.45
10:J:101:GLY:H	10:J:121:ASN:HB3	1.81	0.45
16:P:124:LYS:HB3	26:Z:34:ARG:HB3	1.98	0.45
22:V:11:VAL:HG13	22:V:58:VAL:HG21	1.98	0.45
28:c:151:THR:O	51:1:1130:U:C4	2.70	0.45
32:g:28:ASN:ND2	51:1:2092:U:OP2	2.36	0.45
51:1:2047:C:O2'	51:1:2048:G:H5'	2.16	0.45
51:1:2122:U:H2'	51:1:2123:G:O4'	2.16	0.45
51:1:2339:C:H2'	51:1:2340:A:H8	1.81	0.45
51:1:2651:C:H2'	51:1:2652:C:H6	1.81	0.45
51:1:2844:G:H2'	51:1:2845:U:O4'	2.16	0.45
59:B2:28:LEU:HD21	59:B2:524:ILE:HG13	1.98	0.45
63:5:22:G:H2'	63:5:23:A:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:18:GLN:HG3	7:G:189:ASN:CB	2.40	0.45
9:I:13:ARG:NH1	53:3:542:G:O3'	2.50	0.45
19:S:58:ARG:HH21	53:3:980:C:H4'	1.81	0.45
40:p:92:ARG:H	40:p:92:ARG:HG2	1.60	0.45
42:r:38:VAL:HG13	42:r:54:VAL:HG12	1.99	0.45
51:1:239:C:H2'	51:1:240:C:O4'	2.16	0.45
51:1:360:U:H2'	51:1:361:G:H1'	1.99	0.45
51:1:519:U:C2	51:1:520:G:C8	3.03	0.45
51:1:536:G:H2'	51:1:537:G:C5'	2.44	0.45
51:1:1049:C:C2'	51:1:1050:A:H5'	2.47	0.45
51:1:1140:C:C2'	51:1:1141:U:H5'	2.47	0.45
51:1:2661:G:O2'	51:1:2662:A:H5'	2.16	0.45
60:W0:25:ARG:NH1	60:W0:61:ASN:OD1	2.49	0.45
63:5:49:C:H2'	63:5:50:U:C6	2.52	0.45
64:7:7:G:H3'	64:7:49:G:OP2	2.16	0.45
7:G:65:LYS:HG2	7:G:153:MET:HG3	1.98	0.45
7:G:172:ILE:O	7:G:176:ASN:ND2	2.50	0.45
23:W:47:ARG:HA	23:W:47:ARG:HD3	1.80	0.45
29:d:136:GLN:HA	29:d:139:LYS:HE2	1.99	0.45
33:i:10:LEU:HD21	33:i:27:LEU:HD21	1.99	0.45
34:j:108:MET:CE	51:1:1138:G:H21	2.29	0.45
51:1:654:A:N3	51:1:654:A:H5''	2.31	0.45
51:1:707:G:C2'	51:1:708:G:H5'	2.47	0.45
51:1:1210:G:P	51:1:1212:G:H5'	2.56	0.45
51:1:1239:G:O2'	51:1:1240:U:H5'	2.17	0.45
51:1:1412:U:H2'	51:1:1413:A:H8	1.81	0.45
51:1:1930:G:HO2'	51:1:1931:U:P	2.38	0.45
51:1:2648:G:C2	51:1:2649:C:C2	3.04	0.45
53:3:647:C:H2'	53:3:648:A:H8	1.81	0.45
53:3:1253:G:H2'	53:3:1254:A:C8	2.52	0.45
58:B1:67:ASP:OD1	58:B1:67:ASP:O	2.35	0.45
58:B1:75:TYR:CD2	58:B1:75:TYR:O	2.70	0.45
58:B1:1158:GLU:HA	58:B1:1223:LEU:HD21	1.99	0.45
59:B2:735:LYS:HA	59:B2:748:ILE:HG22	1.97	0.45
64:6:46:G:H5''	64:6:47:U:OP2	2.17	0.45
2:B:8:THR:OG1	2:B:9:ARG:N	2.49	0.45
31:f:133:LYS:NZ	31:f:134:GLY:O	2.44	0.45
34:j:85:LYS:NZ	51:1:2768:U:OP1	2.49	0.45
51:1:111:A:O2'	51:1:112:U:H5'	2.17	0.45
51:1:639:U:H2'	51:1:640:C:C6	2.52	0.45
51:1:1500:G:O2'	51:1:1501:G:H5'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
51:1:2141:G:H1	51:1:2151:U:H3	1.63	0.45
51:1:2364:C:O2'	51:1:2365:G:H5'	2.17	0.45
51:1:2889:C:O2'	51:1:2890:G:H5'	2.17	0.45
53:3:112:G:N2	53:3:354:G:O5'	2.48	0.45
53:3:1376:U:H2'	53:3:1377:A:C8	2.52	0.45
58:B1:213:LYS:HA	58:B1:213:LYS:HE3	1.99	0.45
59:B2:230:PHE:HB2	59:B2:333:ILE:HB	1.98	0.45
7:G:166:ASP:HB3	7:G:190:SER:HB2	1.99	0.45
8:H:5:HIS:CE1	8:H:7:ASN:HB3	2.51	0.45
12:L:142:ARG:HH21	64:7:42:G:H4'	1.81	0.45
16:P:35:ASP:OD1	16:P:39:ASN:N	2.50	0.45
29:d:32:VAL:HG21	36:l:6:LEU:HD13	1.99	0.45
51:1:355:U:H6	51:1:355:U:O5'	1.99	0.45
51:1:1863:G:H2'	51:1:1864:U:C6	2.51	0.45
51:1:2658:C:H2'	51:1:2659:G:O4'	2.16	0.45
58:B1:395:LYS:NZ	58:B1:399:LYS:HE2	2.32	0.45
11:K:75:GLU:O	11:K:79:ARG:N	2.47	0.45
33:i:112:LYS:HD2	33:i:128:ILE:HD12	1.97	0.45
48:x:30:PRO:HG2	48:x:32:LEU:HD11	1.98	0.45
51:1:195:A:H3'	51:1:196:A:H4'	1.98	0.45
51:1:1140:C:H2'	51:1:1141:U:H5'	1.97	0.45
51:1:1170:C:H2'	51:1:1171:G:C8	2.51	0.45
51:1:2636:C:O2'	51:1:2637:U:H5'	2.16	0.45
51:1:2869:G:H2'	51:1:2870:C:O4'	2.17	0.45
55:8:20:DA:H4'	59:B2:143:ARG:NH1	2.31	0.45
58:B1:375:GLU:O	59:B2:1247:SER:HB3	2.16	0.45
59:B2:674:ASP:OD2	59:B2:1070:HIS:ND1	2.50	0.45
59:B2:800:MET:HB2	59:B2:800:MET:HE3	1.69	0.45
59:B2:1314:GLN:HA	60:W0:28:ARG:HH22	1.80	0.45
5:E:48:MET:HE3	5:E:48:MET:HB3	1.86	0.45
7:G:142:LYS:NZ	53:3:1098:C:OP1	2.49	0.45
24:X:27:LYS:HE2	24:X:27:LYS:HB3	1.77	0.45
33:i:135:MET:CE	51:1:1062:G:H21	2.30	0.45
44:t:34:VAL:HG21	44:t:43:ILE:HD11	1.99	0.45
51:1:198:C:N4	51:1:248:G:H1	2.14	0.45
51:1:854:C:H2'	51:1:855:G:C8	2.52	0.45
51:1:2201:G:H2'	51:1:2202:U:O4'	2.17	0.45
51:1:2717:C:N3	51:1:2718:G:N7	2.65	0.45
53:3:959:A:O2'	53:3:984:C:O2'	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1498:U:H4'	53:3:1519:A:H2	1.82	0.45
58:B1:388:ARG:HG2	58:B1:388:ARG:NH1	2.32	0.45
8:H:5:HIS:HE1	8:H:7:ASN:HB3	1.82	0.45
45:u:12:VAL:HA	45:u:69:VAL:HG12	1.99	0.45
49:y:19:LEU:HD23	49:y:19:LEU:HA	1.86	0.45
51:1:1020:A:C2	51:1:1141:U:C2	3.05	0.45
51:1:1280:G:C2'	51:1:1281:G:H5'	2.46	0.45
51:1:1672:A:N3	51:1:2582:G:H5'	2.27	0.45
51:1:1680:U:C2'	51:1:1681:G:H5'	2.47	0.45
51:1:1749:A:H2'	51:1:1750:G:H8	1.82	0.45
51:1:1866:A:H2'	51:1:1867:G:O4'	2.16	0.45
51:1:2204:G:H2'	51:1:2205:A:H8	1.81	0.45
51:1:2241:A:H2'	51:1:2242:G:H8	1.82	0.45
58:B1:770:LEU:HD13	59:B2:618:GLN:CD	2.42	0.45
58:B1:1357:ILE:HG22	58:B1:1359:ALA:H	1.82	0.45
59:B2:557:ARG:NH2	59:B2:607:SER:O	2.49	0.45
59:B2:746:ALA:O	59:B2:974:ARG:NH2	2.45	0.45
7:G:26:MET:HE1	7:G:186:VAL:HB	1.99	0.44
9:I:120:LYS:HG2	9:I:130:ASN:HB3	1.99	0.44
15:O:29:ALA:HB2	15:O:87:LEU:HD11	1.99	0.44
25:Y:4:LYS:HA	25:Y:4:LYS:HD3	1.86	0.44
40:p:88:ARG:HH11	40:p:114:ASN:HD21	1.66	0.44
45:u:32:LYS:HG2	45:u:65:GLN:HA	1.99	0.44
51:1:432:A:O2'	51:1:433:C:H5'	2.17	0.44
51:1:500:G:N2	51:1:502:A:H3'	2.32	0.44
51:1:940:G:H3'	51:1:941:A:H5''	1.97	0.44
51:1:1173:U:H5	51:1:1174:U:H1'	1.81	0.44
51:1:1507:C:H2'	51:1:1508:A:H4'	1.99	0.44
51:1:1868:C:H2'	51:1:1869:G:C8	2.52	0.44
51:1:2880:C:O2	51:1:2880:C:H2'	2.17	0.44
58:B1:128:LEU:CD2	58:B1:188:LEU:HB3	2.47	0.44
58:B1:213:LYS:HE3	58:B1:213:LYS:CA	2.47	0.44
58:B1:352:ARG:CD	59:B2:1268:GLN:NE2	2.67	0.44
58:B1:484:MET:CE	59:B2:1278:LEU:HD21	2.47	0.44
58:B1:1227:HIS:HA	58:B1:1230:THR:HG22	1.99	0.44
62:NG:133:MET:HA	62:NG:147:VAL:HA	1.98	0.44
63:5:8:U:H2'	63:5:13:C:H41	1.81	0.44
11:K:62:MET:HB3	11:K:64:VAL:HG13	1.98	0.44
12:L:70:PRO:HG3	12:L:98:LEU:HD23	1.97	0.44
14:N:84:ARG:NH2	53:3:1119:C:OP1	2.48	0.44
19:S:44:VAL:O	19:S:48:GLN:NE2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:107:LYS:HE2	27:b:107:LYS:HB2	1.87	0.44
28:c:59:ARG:HA	28:c:59:ARG:HD3	1.83	0.44
30:e:122:ASP:OD2	30:e:126:ASN:ND2	2.42	0.44
31:f:132:LEU:HB3	31:f:140:ILE:HD11	1.99	0.44
40:p:52:ARG:NH2	51:1:2720:U:OP1	2.50	0.44
45:u:17:ASP:HA	45:u:20:LYS:HE2	2.00	0.44
51:1:167:A:H2'	51:1:168:G:O4'	2.16	0.44
51:1:395:U:H2'	51:1:396:G:C8	2.52	0.44
51:1:974:G:H1'	51:1:975:A:C8	2.52	0.44
51:1:1488:C:H2'	51:1:1489:C:C6	2.51	0.44
51:1:2312:U:O2'	51:1:2313:C:H5'	2.17	0.44
53:3:765:G:H1	53:3:812:G:HO2'	1.63	0.44
58:B1:115:TRP:HB3	58:B1:1333:THR:CG2	2.46	0.44
65:h:2:DPP:NG	65:h:3:SER:N	2.65	0.44
2:B:4:GLN:HG3	51:1:2054:A:C2	2.52	0.44
21:U:70:ARG:O	21:U:74:LEU:N	2.47	0.44
27:b:1:ALA:N	27:b:19:VAL:O	2.41	0.44
31:f:175:LYS:HD3	31:f:175:LYS:HA	1.70	0.44
32:g:1:MET:N	32:g:20:ASN:OD1	2.39	0.44
33:i:9:LYS:HD2	51:1:1061:U:OP1	2.18	0.44
51:1:354:A:H2'	51:1:355:U:O4'	2.17	0.44
51:1:893:C:H2'	51:1:894:U:O4'	2.17	0.44
51:1:1710:G:O2'	51:1:1711:A:H5'	2.17	0.44
51:1:1800:C:O2	51:1:1802:A:C8	2.70	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
51:1:2402:U:O2'	51:1:2403:C:H3'	2.17	0.44
51:1:2411:A:H2'	51:1:2412:A:C8	2.53	0.44
53:3:142:G:O2'	53:3:196:A:N1	2.45	0.44
58:B1:478:LEU:HD21	60:W0:47:THR:HG23	1.99	0.44
58:B1:804:ALA:HB2	58:B1:1256:ILE:CD1	2.48	0.44
59:B2:909:LYS:HD3	59:B2:909:LYS:HA	1.36	0.44
63:5:70:G:H2'	63:5:71:G:C8	2.51	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
8:H:134:LYS:HB3	8:H:134:LYS:HE2	1.84	0.44
10:J:24:VAL:HG23	10:J:26:GLY:H	1.82	0.44
17:Q:72:ASN:OD1	17:Q:72:ASN:N	2.50	0.44
41:q:82:LEU:HD22	41:q:87:VAL:HB	1.98	0.44
42:r:48:LYS:HA	42:r:48:LYS:HD2	1.77	0.44
47:w:12:SER:OG	47:w:13:GLU:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:z:30:ARG:HG2	50:z:33:HIS:HB2	1.99	0.44
51:1:30:G:H2'	51:1:31:C:O4'	2.16	0.44
51:1:208:C:O2'	51:1:209:C:H5'	2.18	0.44
51:1:336:C:O2'	51:1:337:C:H5'	2.18	0.44
51:1:1232:G:H2'	51:1:1233:C:C6	2.53	0.44
51:1:1539:U:H2'	51:1:1540:G:C8	2.53	0.44
51:1:1717:A:C2	51:1:1718:G:H1'	2.53	0.44
51:1:2137:U:H2'	51:1:2138:G:C8	2.50	0.44
51:1:2626:C:H2'	51:1:2627:G:C8	2.51	0.44
51:1:2741:A:H2'	51:1:2742:G:H5'	1.98	0.44
53:3:477:C:H2'	53:3:478:A:C8	2.52	0.44
57:A1:192:VAL:HG12	57:A1:193:GLU:H	1.82	0.44
57:A1:212:ASP:OD1	57:A1:212:ASP:N	2.48	0.44
58:B1:76:LYS:NZ	58:B1:76:LYS:HB3	2.32	0.44
58:B1:472:LEU:CD1	59:B2:1294:LYS:HG2	2.47	0.44
58:B1:850:LYS:HB3	58:B1:855:ASP:HB2	2.00	0.44
59:B2:176:ILE:HD11	59:B2:428:VAL:HG21	1.98	0.44
14:N:104:THR:HG23	53:3:1180:A:H5'	1.99	0.44
38:n:103:ARG:HH11	51:1:1287:A:H5'	1.83	0.44
47:w:37:ARG:HA	47:w:37:ARG:HD3	1.70	0.44
48:x:51:SER:OG	48:x:54:GLY:N	2.48	0.44
49:y:6:LEU:HD13	49:y:56:LEU:HD22	1.98	0.44
49:y:20:ASN:HA	49:y:23:ARG:HB2	1.99	0.44
51:1:169:G:O2'	51:1:170:U:H5'	2.18	0.44
51:1:402:A:H2'	51:1:403:U:C5'	2.44	0.44
51:1:704:G:H1'	51:1:727:A:H62	1.83	0.44
51:1:720:U:H2'	51:1:721:A:H8	1.82	0.44
51:1:1452:G:H2'	51:1:1453:A:OP2	2.17	0.44
51:1:1869:G:H3'	51:1:1870:C:C5'	2.38	0.44
51:1:1882:U:O2'	51:1:1883:U:H5'	2.17	0.44
51:1:2805:C:O2'	51:1:2806:C:H5'	2.18	0.44
53:3:75:G:H2'	53:3:76:G:C8	2.53	0.44
57:A2:48:LEU:HA	57:A2:48:LEU:HD23	1.86	0.44
57:A2:80:GLU:HG3	59:B2:694:ARG:HH22	1.81	0.44
58:B1:62:PHE:N	58:B1:62:PHE:CD1	2.86	0.44
58:B1:209:ASN:HA	58:B1:214:ARG:NH2	2.30	0.44
58:B1:434:ILE:HD11	59:B2:1274:GLU:HG3	1.99	0.44
58:B1:506:VAL:HG23	58:B1:628:GLY:HA3	1.99	0.44
58:B1:926:PRO:HB2	58:B1:1241:TYR:HE1	1.82	0.44
59:B2:444:ASP:OD1	59:B2:444:ASP:N	2.51	0.44
12:L:113:LYS:HB3	53:3:1297:G:H21	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:28:ARG:NH1	53:3:390:U:O2'	2.46	0.44
28:c:106:LYS:HA	28:c:176:ASP:HA	1.99	0.44
28:c:150:GLN:HE22	51:1:2032:G:H1'	1.82	0.44
31:f:106:LEU:O	31:f:151:ARG:NH2	2.38	0.44
33:i:131:THR:HB	51:1:1060:U:O4	2.18	0.44
34:j:34:ARG:NH2	34:j:39:LYS:O	2.51	0.44
51:1:107:G:H2'	51:1:108:G:H8	1.82	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
51:1:545:U:O2	51:1:546:U:H1'	2.17	0.44
51:1:696:G:H2'	51:1:697:G:O4'	2.18	0.44
51:1:1288:G:C5	51:1:1327:A:C2	3.04	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
53:3:146:G:N2	53:3:177:G:N7	2.66	0.44
53:3:490:C:H2'	53:3:491:G:C8	2.53	0.44
58:B1:68:TYR:O	58:B1:75:TYR:CD2	2.70	0.44
58:B1:161:THR:H	58:B1:164:GLN:HB2	1.82	0.44
58:B1:1033:GLY:HA3	58:B1:1081:VAL:O	2.18	0.44
63:5:69:G:H2'	63:5:70:G:C8	2.52	0.44
18:R:43:LYS:HB2	18:R:46:GLU:HG2	1.99	0.44
18:R:107:THR:OG1	53:3:947:G:O3'	2.35	0.44
27:b:97:ASP:N	27:b:97:ASP:OD1	2.45	0.44
29:d:147:LEU:HD11	29:d:170:ARG:HG2	1.98	0.44
33:i:91:LYS:HB2	33:i:91:LYS:HE3	1.72	0.44
33:i:106:GLN:OE1	33:i:125:THR:OG1	2.31	0.44
42:r:19:THR:OG1	42:r:95:ASP:OD1	2.35	0.44
45:u:76:THR:HB	45:u:78:LYS:HE3	1.99	0.44
51:1:68:G:H2'	51:1:69:C:O4'	2.18	0.44
51:1:163:C:O2'	51:1:164:C:H5'	2.17	0.44
51:1:473:G:C2'	51:1:474:G:H5'	2.48	0.44
51:1:819:A:H5'	51:1:973:A:N1	2.33	0.44
51:1:1087:G:H22	51:1:1103:A:H1'	1.76	0.44
51:1:1605:C:H2'	51:1:1606:C:H5'	1.98	0.44
51:1:1625:C:H2'	51:1:1626:A:O4'	2.18	0.44
51:1:2700:A:O2'	51:1:2701:U:H5'	2.17	0.44
53:3:1200:C:O2'	53:3:1205:U:O4	2.34	0.44
55:8:16:DT:H2'	55:8:17:DC:C6	2.52	0.44
58:B1:1046:ILE:HG22	58:B1:1061:VAL:HA	2.00	0.44
59:B2:24:VAL:HG11	59:B2:704:MET:HE1	1.98	0.44
59:B2:1246:ARG:HH11	59:B2:1266:GLY:HA2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:88:MET:HE3	15:O:88:MET:HB3	1.70	0.44
36:l:95:LEU:HD22	36:l:100:ILE:HD11	2.00	0.44
51:1:131:A:H2'	51:1:132:G:C8	2.53	0.44
51:1:255:A:H2'	51:1:256:A:O4'	2.18	0.44
51:1:388:G:N7	51:1:390:U:H2'	2.33	0.44
51:1:1199:U:H2'	51:1:1200:C:C6	2.52	0.44
51:1:1338:G:H2'	51:1:1339:G:C8	2.51	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
58:B1:287:ALA:HB1	58:B1:288:PRO:HD2	1.99	0.44
58:B1:978:ARG:HD3	58:B1:999:TYR:H	1.83	0.44
59:B2:829:THR:HG23	59:B2:1059:ARG:HG2	2.00	0.44
63:5:63:G:H2'	63:5:64:A:C8	2.53	0.44
8:H:37:LYS:HD3	8:H:37:LYS:HA	1.81	0.44
9:I:85:THR:HA	9:I:88:ASN:HB2	2.00	0.44
14:N:74:GLN:OE1	53:3:1249:C:O2'	2.35	0.44
14:N:119:LYS:NZ	53:3:1350:A:N7	2.64	0.44
18:R:1:ALA:HB3	18:R:56:ARG:HH22	1.82	0.44
24:X:76:THR:OG1	24:X:77:ARG:N	2.51	0.44
29:d:68:ALA:HA	51:1:1255:U:C6	2.52	0.44
42:r:1:MET:HE3	42:r:101:ILE:HB	1.99	0.44
51:1:29:U:O5'	51:1:29:U:H6	2.01	0.44
51:1:518:G:O2'	51:1:519:U:H5'	2.18	0.44
51:1:1536:C:H4'	51:1:1537:G:N1	2.32	0.44
51:1:1565:C:C5	51:1:1567:G:C6	3.06	0.44
51:1:1747:U:H2'	51:1:1748:C:C6	2.53	0.44
51:1:2671:G:C2	51:1:2672:U:C2	3.06	0.44
52:2:66:A:H4'	52:2:67:G:C8	2.53	0.44
53:3:560:A:H5''	53:3:561:U:H5'	2.00	0.44
53:3:908:A:H2'	53:3:909:A:H8	1.83	0.44
59:B2:906:PHE:HE2	61:NA:102:PHE:CB	2.28	0.44
7:G:122:ASP:N	7:G:122:ASP:OD1	2.51	0.43
8:H:76:ILE:HB	8:H:80:GLY:HA2	2.00	0.43
17:Q:3:VAL:HA	17:Q:6:LEU:HD12	2.00	0.43
25:Y:67:HIS:O	25:Y:69:ASN:ND2	2.51	0.43
42:r:80:ARG:HD3	51:1:566:U:O4	2.17	0.43
51:1:150:U:H2'	51:1:151:C:C6	2.52	0.43
51:1:350:G:H2'	51:1:351:C:O4'	2.18	0.43
51:1:1010:A:H1'	51:1:1153:C:H1'	2.00	0.43
51:1:1670:C:O2'	51:1:1671:U:H5'	2.16	0.43
51:1:2236:U:H2'	51:1:2237:G:C5'	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:162:A:C5	53:3:163:C:H1'	2.53	0.43
53:3:1053:G:H4'	53:3:1054:C:H3'	2.00	0.43
58:B1:139:LEU:HD23	58:B1:139:LEU:HA	1.89	0.43
59:B2:300:ASP:OD1	59:B2:313:ALA:N	2.51	0.43
59:B2:538:LEU:HD13	59:B2:543:ALA:HB2	2.00	0.43
62:NG:161:SER:CB	62:NG:170:PRO:HA	2.48	0.43
63:5:13:C:H42	63:5:46:G:N2	2.16	0.43
2:B:4:GLN:NE2	51:1:2056:G:O2'	2.52	0.43
2:B:8:THR:HG23	2:B:11:LYS:H	1.81	0.43
7:G:67:LEU:HD21	7:G:91:VAL:HG23	2.00	0.43
9:I:125:ASN:HB2	9:I:127:ARG:HD3	2.01	0.43
10:J:104:ILE:HD11	10:J:114:LEU:HD13	1.99	0.43
22:V:44:HIS:HB3	22:V:70:LYS:HG2	1.99	0.43
27:b:153:LEU:HD23	51:1:1799:G:N2	2.33	0.43
34:j:109:LEU:HA	34:j:109:LEU:HD23	1.85	0.43
38:n:65:LEU:HD11	51:1:2870:C:H5''	1.99	0.43
41:q:47:ARG:NH2	41:q:51:GLN:OE1	2.51	0.43
51:1:150:U:O2'	51:1:151:C:H5'	2.18	0.43
51:1:161:A:C5	51:1:162:U:H5	2.36	0.43
51:1:1095:A:H3'	51:1:1096:A:H8	1.83	0.43
51:1:1571:A:H2'	51:1:1572:A:C8	2.54	0.43
51:1:1761:C:H2'	51:1:1762:A:O4'	2.18	0.43
51:1:2285:C:C2'	51:1:2286:G:H5'	2.48	0.43
57:A1:185:TYR:HA	57:A1:202:VAL:O	2.16	0.43
58:B1:33:TRP:HZ2	59:B2:1336:ASN:OD1	2.00	0.43
58:B1:141:PHE:HE2	58:B1:296:LYS:CB	2.23	0.43
58:B1:1024:THR:HG23	58:B1:1123:ARG:HA	2.00	0.43
8:H:134:LYS:HG2	8:H:138:GLN:HE21	1.82	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
21:U:79:ASN:HB2	21:U:82:ALA:HB3	1.99	0.43
27:b:20:ASN:HB3	27:b:23:LEU:HD13	2.01	0.43
35:k:38:ILE:HG22	35:k:61:VAL:HB	2.01	0.43
48:x:1:SER:OG	51:1:1365:A:OP2	2.35	0.43
48:x:36:ARG:NH2	51:1:2200:C:OP2	2.52	0.43
51:1:648:G:H2'	51:1:649:G:H8	1.83	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
51:1:2643:G:C2'	51:1:2644:G:H5'	2.49	0.43
58:B1:58:CYS:SG	58:B1:60:ARG:HG2	2.59	0.43
58:B1:515:ARG:HH12	58:B1:724:MET:HG2	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:1079:LYS:HD3	58:B1:1098:GLN:HB3	2.00	0.43
59:B2:895:LEU:HD13	59:B2:895:LEU:HA	1.71	0.43
59:B2:1072:ASN:OD1	59:B2:1072:ASN:N	2.52	0.43
63:5:27:G:H1	63:5:43:C:H42	1.64	0.43
8:H:51:VAL:HA	8:H:69:THR:HG22	2.00	0.43
14:N:98:ARG:HG2	14:N:103:VAL:HG21	2.01	0.43
16:P:17:ASP:OD1	16:P:17:ASP:N	2.44	0.43
21:U:31:ARG:HB2	53:3:310:G:H5''	2.00	0.43
23:W:33:THR:HG22	23:W:37:LYS:H	1.83	0.43
24:X:6:LYS:NZ	53:3:1314:C:OP1	2.52	0.43
27:b:140:VAL:HG12	27:b:191:LEU:HD23	2.01	0.43
31:f:84:LYS:HD2	31:f:84:LYS:HA	1.87	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
51:1:721:A:H2'	51:1:722:A:C8	2.53	0.43
51:1:1741:C:O2'	51:1:1742:U:H5'	2.19	0.43
53:3:680:C:H2'	53:3:681:A:H8	1.84	0.43
53:3:1513:A:H2'	53:3:1514:G:H8	1.83	0.43
55:8:3:DC:N1	55:8:4:DT:H72	2.34	0.43
55:8:15:DC:H5'	59:B2:1269:ARG:HD3	2.00	0.43
58:B1:45:ASN:HD22	58:B1:48:THR:H	1.65	0.43
58:B1:111:THR:CG2	58:B1:300:GLN:HA	2.48	0.43
58:B1:201:LEU:CB	58:B1:221:ILE:HD13	2.47	0.43
58:B1:362:ARG:HB2	58:B1:364:HIS:HD2	1.83	0.43
14:N:105:ARG:NH1	14:N:109:GLN:OE1	2.49	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
18:R:28:ARG:HH21	18:R:62:PHE:HB2	1.84	0.43
25:Y:14:GLU:OE1	25:Y:17:ARG:NH2	2.52	0.43
25:Y:49:ALA:HA	25:Y:52:GLU:HG3	2.00	0.43
28:c:62:LYS:NZ	51:1:2810:A:H5''	2.34	0.43
38:n:39:PRO:HG2	51:1:1651:G:H4'	2.00	0.43
51:1:30:G:O2'	51:1:31:C:H5'	2.17	0.43
51:1:648:G:H5''	51:1:2352:A:H5''	2.00	0.43
51:1:684:G:C2	51:1:794:A:C2	3.06	0.43
51:1:1087:G:H5''	51:1:1088:A:OP2	2.18	0.43
51:1:1306:C:N4	51:1:1606:C:H2'	2.34	0.43
53:3:422:C:H4'	53:3:423:G:C2	2.54	0.43
53:3:490:C:H2'	53:3:491:G:H8	1.84	0.43
53:3:501:C:H2'	53:3:502:A:C8	2.53	0.43
53:3:1442:G:H1	53:3:1460:C:H42	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:646:SER:OG	59:B2:647:ARG:N	2.51	0.43
59:B2:998:LEU:HG	59:B2:1011:LEU:HB3	1.99	0.43
60:W0:58:LEU:HD12	60:W0:59:ILE:HG12	2.00	0.43
11:K:47:LEU:HG	11:K:56:LYS:HA	2.01	0.43
30:e:171:ALA:C	30:e:173:ASP:H	2.26	0.43
33:i:123:ALA:HB1	51:1:1081:U:H4'	2.00	0.43
33:i:129:GLU:HG3	33:i:139:VAL:HG21	2.00	0.43
34:j:47:HIS:CG	51:1:536:G:H21	2.37	0.43
36:l:69:ARG:CZ	51:1:2406:A:N3	2.82	0.43
43:s:74:ILE:HB	43:s:105:VAL:HG23	1.99	0.43
51:1:43:G:H2'	51:1:44:A:C8	2.53	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
51:1:541:A:H2'	51:1:542:C:O4'	2.19	0.43
51:1:1258:U:H2'	51:1:1259:G:C8	2.54	0.43
51:1:1751:U:H2'	51:1:1752:C:C6	2.54	0.43
51:1:2305:U:O2'	51:1:2306:C:H5'	2.19	0.43
51:1:2371:G:O2'	51:1:2372:U:H5'	2.19	0.43
51:1:2562:U:C2'	51:1:2563:U:H5'	2.49	0.43
51:1:2736:A:O2'	51:1:2737:G:H5'	2.19	0.43
53:3:944:G:N1	53:3:1338:G:OP2	2.34	0.43
58:B1:105:ILE:HD12	58:B1:242:LEU:CD2	2.44	0.43
58:B1:120:LEU:HD22	58:B1:120:LEU:HA	1.77	0.43
59:B2:11:ILE:HG22	59:B2:1172:LEU:HD11	1.99	0.43
59:B2:811:ASN:ND2	59:B2:1098:LEU:O	2.51	0.43
62:NG:125:LYS:O	62:NG:127:LEU:N	2.52	0.43
13:M:52:GLY:HA3	13:M:56:PRO:HA	2.01	0.43
27:b:48:ILE:HG12	51:1:779:U:OP2	2.18	0.43
29:d:3:LEU:HD23	29:d:3:LEU:HA	1.88	0.43
51:1:841:G:C2'	51:1:842:U:H5'	2.49	0.43
51:1:870:U:H2'	51:1:871:U:C5'	2.48	0.43
51:1:1287:A:H3'	51:1:1288:G:N2	2.33	0.43
51:1:1426:G:C6	51:1:1427:A:C6	3.06	0.43
51:1:1915:U:O2	51:1:1915:U:O4'	2.34	0.43
51:1:2660:A:H2'	51:1:2661:G:O4'	2.18	0.43
51:1:2834:G:C2'	51:1:2835:A:H5'	2.49	0.43
51:1:2839:G:O2'	51:1:2840:C:H5'	2.18	0.43
53:3:28:A:O2'	53:3:296:U:OP1	2.33	0.43
53:3:1253:G:H2'	53:3:1254:A:H8	1.83	0.43
55:8:12:DG:OP1	58:B1:795:TYR:CE1	2.71	0.43
58:B1:797:THR:HG22	58:B1:924:GLY:HA3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:115:ILE:HD12	16:P:116:PRO:HD2	1.99	0.43
17:Q:31:GLY:HA2	17:Q:56:LEU:HA	2.01	0.43
27:b:7:PRO:HB3	27:b:13:ARG:HG3	2.00	0.43
27:b:131:MET:H	27:b:131:MET:HG2	1.57	0.43
27:b:244:VAL:HG12	27:b:250:GLN:HA	2.01	0.43
29:d:188:MET:HB2	29:d:192:ALA:HB3	1.99	0.43
31:f:151:ARG:HD3	31:f:151:ARG:HA	1.88	0.43
34:j:51:GLY:HA3	34:j:121:LYS:HE2	2.00	0.43
37:m:17:ASN:OD1	37:m:97:GLN:NE2	2.51	0.43
51:1:156:A:O2'	51:1:157:C:H5'	2.18	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
51:1:623:C:O2'	51:1:624:C:H5'	2.18	0.43
51:1:1172:C:H2'	51:1:1173:U:O4'	2.19	0.43
51:1:1601:G:H2'	51:1:1602:U:H5'	2.01	0.43
51:1:1864:U:O5'	51:1:1864:U:H6	2.02	0.43
51:1:2102:G:H1	51:1:2187:U:H3	1.66	0.43
51:1:2584:U:O5'	51:1:2584:U:H6	2.02	0.43
57:A1:78:ILE:HA	57:A1:81:ILE:HG22	2.00	0.43
58:B1:96:LYS:NZ	59:B2:1298:VAL:HG11	2.34	0.43
58:B1:111:THR:HG21	58:B1:303:VAL:HB	1.99	0.43
58:B1:820:ILE:HG12	58:B1:884:SER:HB2	2.01	0.43
58:B1:847:ASP:N	58:B1:847:ASP:OD1	2.49	0.43
58:B1:1108:GLN:HG3	58:B1:1109:LEU:HD12	2.00	0.43
59:B2:125:GLY:H	59:B2:495:ALA:HB1	1.84	0.43
64:7:11:A:H2'	64:7:12:G:C8	2.52	0.43
17:Q:113:ARG:NH1	53:3:36:C:O2'	2.51	0.43
30:e:77:LYS:HE2	30:e:77:LYS:HB2	1.89	0.43
32:g:1:MET:HE3	32:g:1:MET:HB3	1.77	0.43
36:l:109:LYS:HE2	51:1:636:G:N7	2.34	0.43
37:m:96:ILE:HD13	37:m:96:ILE:HA	1.82	0.43
51:1:108:G:O2'	51:1:109:C:H5'	2.19	0.43
51:1:864:G:C2'	51:1:865:C:H5'	2.48	0.43
51:1:1092:C:H2'	51:1:1093:G:O4'	2.18	0.43
51:1:1306:C:H41	51:1:1606:C:H2'	1.84	0.43
51:1:2152:G:N3	51:1:2152:G:H2'	2.33	0.43
51:1:2870:C:H2'	51:1:2871:U:H5'	2.01	0.43
53:3:1005:A:OP2	53:3:1024:G:N2	2.48	0.43
58:B1:141:PHE:CD2	58:B1:297:ARG:HB2	2.54	0.43
58:B1:568:SER:HB3	58:B1:570:LYS:NZ	2.34	0.43
59:B2:1313:HIS:CD2	60:W0:31:GLN:HE22	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:j:47:HIS:CG	51:1:536:G:N2	2.87	0.43
42:r:24:LYS:HE2	42:r:24:LYS:HB3	1.89	0.43
51:1:12:U:O2	51:1:12:U:H2'	2.18	0.43
51:1:528:A:C2	51:1:2043:C:H4'	2.53	0.43
51:1:595:C:H2'	51:1:596:U:C6	2.54	0.43
51:1:629:G:H2'	51:1:630:G:O4'	2.19	0.43
51:1:783:A:C8	51:1:783:A:H3'	2.54	0.43
51:1:918:A:H2'	51:1:919:U:O4'	2.19	0.43
51:1:1487:U:H2'	51:1:1488:C:C6	2.54	0.43
51:1:2462:C:H2'	51:1:2463:C:C6	2.53	0.43
51:1:2713:U:C3'	51:1:2714:G:H5'	2.27	0.43
53:3:1209:C:O2'	53:3:1214:C:N4	2.52	0.43
55:8:2:DC:H6	55:8:2:DC:H2'	1.73	0.43
58:B1:141:PHE:CE2	58:B1:296:LYS:CB	2.94	0.43
58:B1:282:LEU:CA	58:B1:286:ALA:HA	2.45	0.43
58:B1:395:LYS:NZ	58:B1:399:LYS:CD	2.74	0.43
58:B1:894:VAL:HG22	58:B1:1258:ARG:HH11	1.83	0.43
27:b:206:LYS:HB2	51:1:729:G:C5	2.54	0.42
39:o:40:ILE:HA	39:o:47:VAL:HA	2.00	0.42
49:y:11:VAL:HA	49:y:14:LEU:HB2	2.00	0.42
51:1:128:C:H2'	51:1:129:C:C6	2.53	0.42
51:1:705:A:C2	51:1:727:A:H1'	2.54	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
51:1:1049:C:H2'	51:1:1050:A:H5'	2.00	0.42
51:1:1054:A:H2'	51:1:1055:G:C8	2.54	0.42
51:1:1230:A:H2'	51:1:1231:U:O4'	2.19	0.42
51:1:1520:U:C2'	51:1:1521:G:H5'	2.49	0.42
51:1:1739:A:H2'	51:1:1740:G:O4'	2.19	0.42
51:1:1993:U:O2	51:1:1993:U:H2'	2.18	0.42
51:1:2073:C:C2'	51:1:2074:U:H5'	2.49	0.42
51:1:2144:G:H1'	51:1:2147:A:N6	2.34	0.42
53:3:958:A:N3	53:3:985:C:O2'	2.48	0.42
58:B1:242:LEU:C	58:B1:242:LEU:HD23	2.44	0.42
58:B1:244:VAL:HA	58:B1:269:TYR:OH	2.19	0.42
58:B1:731:ARG:HB3	59:B2:1105:SER:HB2	2.00	0.42
58:B1:950:ILE:HB	58:B1:1018:ALA:HB3	2.01	0.42
59:B2:557:ARG:HB3	59:B2:587:LEU:HD13	2.00	0.42
64:6:69:C:H2'	64:6:70:G:H8	1.83	0.42
8:H:106:ARG:HG2	8:H:107:LYS:HG3	2.01	0.42
9:I:53:GLN:HA	9:I:198:LEU:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:119:HIS:O	9:I:145:ARG:NH2	2.52	0.42
11:K:38:ARG:HH11	11:K:61:LEU:HD21	1.83	0.42
18:R:91:ARG:HD2	51:1:888:C:OP1	2.18	0.42
27:b:86:ARG:HD3	27:b:86:ARG:HA	1.84	0.42
29:d:127:GLU:O	29:d:156:ASN:ND2	2.51	0.42
33:i:127:SER:OG	51:1:1059:G:N2	2.51	0.42
42:r:62:GLU:HG3	42:r:97:LYS:HB3	2.01	0.42
50:z:38:GLU:CD	51:1:928:A:H5'	2.43	0.42
51:1:1433:A:H2'	51:1:1434:A:C1'	2.49	0.42
51:1:1907:G:C5	51:1:1908:C:C4	3.07	0.42
51:1:2106:U:H2'	51:1:2107:G:O4'	2.18	0.42
51:1:2216:G:H2'	51:1:2217:G:C8	2.54	0.42
53:3:460:A:H2'	53:3:461:A:C8	2.54	0.42
53:3:987:G:H2'	53:3:988:G:H8	1.84	0.42
53:3:1348:U:H2'	53:3:1349:A:H8	1.84	0.42
58:B1:56:LEU:HD12	58:B1:56:LEU:HA	1.84	0.42
58:B1:107:LEU:HA	58:B1:276:ASN:ND2	2.33	0.42
58:B1:395:LYS:HE3	58:B1:395:LYS:HB3	1.45	0.42
58:B1:513:MET:HG3	58:B1:544:LEU:HD11	2.01	0.42
8:H:61:LYS:HE2	8:H:96:VAL:HG12	2.01	0.42
29:d:47:LYS:HE2	51:1:451:U:H4'	2.00	0.42
51:1:8:C:C2	51:1:9:G:C8	3.07	0.42
51:1:481:G:H2'	51:1:482:A:OP2	2.18	0.42
51:1:644:A:C3'	51:1:645:C:H5''	2.49	0.42
51:1:955:U:H2'	51:1:956:G:H5'	2.02	0.42
51:1:1246:A:H2'	51:1:1247:A:O4'	2.19	0.42
51:1:2314:A:H2'	51:1:2315:G:H8	1.78	0.42
51:1:2812:G:O2'	51:1:2813:A:H5'	2.19	0.42
58:B1:59:ALA:HB1	58:B1:90:VAL:HG23	2.01	0.42
58:B1:68:TYR:HB3	58:B1:75:TYR:HE2	1.81	0.42
58:B1:385:LEU:CD2	58:B1:390:LEU:HB2	2.50	0.42
58:B1:824:PRO:HD3	58:B1:835:LEU:HD12	2.00	0.42
58:B1:839:VAL:HG12	58:B1:864:LEU:HD12	2.02	0.42
59:B2:741:MET:HE3	59:B2:974:ARG:HH12	1.84	0.42
16:P:126:ARG:O	53:3:796:C:H5''	2.19	0.42
24:X:51:HIS:HB2	24:X:56:HIS:CE1	2.55	0.42
29:d:53:THR:HB	51:1:452:G:H8	1.85	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
37:m:69:PRO:HA	37:m:94:ALA:HB2	2.01	0.42
51:1:1197:G:C2'	51:1:1198:U:H5'	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2024:G:H2'	51:1:2025:C:C6	2.54	0.42
57:A1:68:TYR:HE1	57:A1:79:LEU:HD13	1.83	0.42
58:B1:220:ARG:HH11	58:B1:220:ARG:CG	2.26	0.42
58:B1:243:PRO:HG2	59:B2:1332:SER:C	2.44	0.42
58:B1:375:GLU:HB3	59:B2:1245:ALA:CB	2.48	0.42
9:I:101:VAL:HG22	9:I:106:PHE:HB2	2.01	0.42
14:N:30:ASN:HD21	14:N:66:VAL:H	1.66	0.42
14:N:113:LYS:HA	14:N:120:ALA:HB2	2.01	0.42
18:R:16:ILE:O	18:R:19:THR:OG1	2.26	0.42
18:R:87:GLY:O	18:R:91:ARG:N	2.52	0.42
18:R:89:ARG:HB2	18:R:96:VAL:HG22	2.01	0.42
21:U:4:ILE:HG12	21:U:21:VAL:HG22	2.00	0.42
24:X:36:ARG:HB3	53:3:1320:C:N4	2.34	0.42
36:l:108:ALA:HB3	36:l:125:LEU:HG	2.01	0.42
40:p:63:ILE:HA	40:p:68:GLY:HA2	2.01	0.42
47:w:14:ALA:HB1	51:1:2271:G:OP1	2.19	0.42
51:1:90:U:H2'	51:1:91:A:C8	2.55	0.42
51:1:1335:C:H2'	51:1:1336:A:H8	1.84	0.42
51:1:1914:C:O2	51:1:1914:C:O4'	2.38	0.42
51:1:1983:G:HO2'	51:1:1984:G:H5'	1.83	0.42
51:1:2482:A:H2'	51:1:2483:C:C6	2.54	0.42
51:1:2741:A:N6	51:1:2742:G:C2	2.88	0.42
53:3:1531:A:C2'	53:3:1532:U:H5'	2.50	0.42
58:B1:24:LEU:HD21	58:B1:116:PHE:CE2	2.54	0.42
58:B1:388:ARG:HG2	58:B1:388:ARG:HH11	1.84	0.42
58:B1:586:GLY:HA3	58:B1:612:LEU:HD11	2.01	0.42
58:B1:616:PRO:HA	58:B1:619:ILE:HG22	2.02	0.42
59:B2:1157:GLN:HG3	59:B2:1159:VAL:HG13	2.00	0.42
62:NG:135:ARG:O	62:NG:178:VAL:CA	2.68	0.42
18:R:11:HIS:HA	18:R:43:LYS:HD2	2.01	0.42
34:j:138:GLN:H	34:j:138:GLN:HG2	1.63	0.42
51:1:94:A:H2'	51:1:95:A:C8	2.54	0.42
51:1:623:C:H2'	51:1:624:C:H6	1.85	0.42
51:1:809:G:C6	51:1:810:U:C4	3.08	0.42
51:1:892:A:O2'	51:1:893:C:H5'	2.19	0.42
51:1:2091:C:H5	51:1:2092:U:O2'	2.02	0.42
51:1:2292:U:H2'	51:1:2293:G:C8	2.55	0.42
51:1:2852:G:H2'	51:1:2853:C:O4'	2.20	0.42
58:B1:137:ARG:HA	58:B1:142:GLU:HG2	2.02	0.42
58:B1:434:ILE:HD11	59:B2:1274:GLU:CG	2.49	0.42
8:H:1:GLY:HA2	53:3:1060:U:C5	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:152:SER:HB3	53:3:436:C:H4'	2.00	0.42
16:P:124:LYS:H	16:P:124:LYS:HG3	1.58	0.42
26:Z:39:LYS:HA	26:Z:42:THR:HB	2.02	0.42
28:c:134:HIS:HE1	51:1:1675:C:C4	2.38	0.42
36:l:39:LYS:HZ3	51:1:942:G:P	2.41	0.42
38:n:16:HIS:CD2	51:1:1275:A:C2	3.07	0.42
41:q:111:LYS:HD2	41:q:111:LYS:HA	1.80	0.42
43:s:87:PRO:HG3	51:1:1615:C:C6	2.54	0.42
51:1:4:U:O2'	51:1:5:A:H5'	2.20	0.42
51:1:510:C:OP1	51:1:510:C:H3'	2.20	0.42
51:1:758:C:H2'	51:1:759:G:H8	1.84	0.42
51:1:908:C:O2'	51:1:909:A:H5'	2.20	0.42
51:1:1020:A:O5'	51:1:1020:A:H8	2.02	0.42
51:1:1204:A:H4'	51:1:1205:A:H5''	2.02	0.42
51:1:1327:A:H2'	51:1:1328:A:H5'	2.01	0.42
51:1:1642:G:H2'	51:1:1643:G:O4'	2.19	0.42
51:1:1710:G:H2'	51:1:1711:A:H8	1.85	0.42
51:1:1901:A:C2	51:1:1902:C:C5	3.08	0.42
51:1:1931:U:C5	51:1:1968:G:N2	2.88	0.42
51:1:2098:U:C2'	51:1:2099:U:H5'	2.49	0.42
51:1:2583:G:H8	51:1:2583:G:O5'	2.03	0.42
51:1:2701:U:H3'	51:1:2702:G:H5''	2.01	0.42
51:1:2741:A:H2'	51:1:2742:G:C5'	2.50	0.42
53:3:75:G:H1	53:3:95:C:H42	1.67	0.42
53:3:1243:C:H2'	53:3:1244:G:H8	1.84	0.42
58:B1:848:VAL:HB	58:B1:858:VAL:HG22	2.02	0.42
59:B2:524:ILE:HD12	59:B2:712:SER:HB2	2.02	0.42
59:B2:590:PRO:HB2	59:B2:655:VAL:HG21	2.01	0.42
20:T:66:LEU:HB3	20:T:77:TYR:HE1	1.84	0.42
39:o:33:ARG:O	39:o:65:THR:OG1	2.28	0.42
46:v:62:THR:O	46:v:62:THR:OG1	2.35	0.42
51:1:115:C:O2'	51:1:116:C:H5'	2.20	0.42
51:1:191:A:C2	51:1:192:C:C4	3.08	0.42
51:1:532:A:H2'	51:1:532:A:N3	2.34	0.42
51:1:837:C:O5'	51:1:837:C:H6	2.02	0.42
51:1:1034:G:C6	51:1:1035:U:N3	2.88	0.42
51:1:1917:U:H2'	51:1:1918:A:H5'	2.01	0.42
53:3:322:C:O2	53:3:332:G:N2	2.52	0.42
53:3:1013:G:N2	53:3:1016:A:OP2	2.35	0.42
53:3:1492:A:H5'	65:h:6:5OH:NP	2.35	0.42
58:B1:506:VAL:H	58:B1:506:VAL:HG12	1.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:8:LYS:NZ	51:1:2467:C:OP1	2.37	0.42
11:K:40:GLU:HB3	11:K:61:LEU:HB3	2.02	0.42
33:i:25:PRO:HG3	51:1:1095:A:N1	2.34	0.42
33:i:109:ALA:O	33:i:113:ALA:N	2.53	0.42
35:k:7:MET:HE2	35:k:18:ARG:HD3	2.01	0.42
41:q:54:ARG:HD3	51:1:1155:A:H5''	2.01	0.42
44:t:40:LYS:HE3	44:t:60:THR:HG22	2.01	0.42
50:z:57:GLU:OE1	50:z:57:GLU:N	2.53	0.42
51:1:552:U:O2'	51:1:553:G:H5'	2.20	0.42
51:1:673:C:O2'	51:1:674:G:H5'	2.19	0.42
51:1:1316:U:O2'	51:1:1317:G:H5'	2.20	0.42
51:1:1381:G:C2'	51:1:1382:G:H5'	2.49	0.42
51:1:1500:G:H2'	51:1:1501:G:H8	1.83	0.42
51:1:1589:U:H2'	51:1:1590:A:C8	2.55	0.42
51:1:2092:U:H5	51:1:2199:A:C2	2.30	0.42
51:1:2193:G:H2'	51:1:2194:U:H6	1.83	0.42
51:1:2848:G:C2	51:1:2867:G:C4	3.08	0.42
53:3:1410:A:C2	53:3:1491:G:N1	2.88	0.42
58:B1:201:LEU:HD11	58:B1:220:ARG:NH1	2.32	0.42
58:B1:279:LEU:HD13	58:B1:299:LEU:HD13	2.02	0.42
58:B1:1026:PRO:HB2	58:B1:1028:ILE:HG23	2.00	0.42
59:B2:50:GLU:HG2	59:B2:73:TYR:HE1	1.85	0.42
59:B2:861:ALA:HB1	59:B2:882:ILE:HD13	2.01	0.42
59:B2:1275:VAL:HG13	59:B2:1287:LEU:HD11	2.01	0.42
15:O:46:LYS:HE3	15:O:46:LYS:HB2	1.88	0.42
18:R:32:ILE:HG23	18:R:58:GLU:HB3	2.02	0.42
28:c:176:ASP:N	28:c:176:ASP:OD1	2.44	0.42
43:s:9:HIS:H	43:s:102:HIS:CE1	2.38	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
51:1:397:U:O5'	51:1:397:U:H6	2.03	0.42
51:1:422:A:H2'	51:1:423:A:O4'	2.20	0.42
51:1:431:U:O5'	51:1:431:U:H6	2.03	0.42
51:1:598:U:H2'	51:1:599:A:C8	2.54	0.42
51:1:903:C:H2'	51:1:904:G:H8	1.85	0.42
51:1:1336:A:H2'	51:1:1337:G:H8	1.85	0.42
51:1:1600:C:H2'	51:1:1601:G:C8	2.55	0.42
51:1:1812:U:H5''	51:1:1812:U:H6	1.85	0.42
51:1:1886:U:O2'	51:1:1887:C:H5'	2.20	0.42
51:1:2628:C:H3'	51:1:2629:U:H5'	2.01	0.42
53:3:73:C:H2'	53:3:74:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1238:A:OP1	53:3:1335:U:O2'	2.35	0.42
53:3:1513:A:H2'	53:3:1514:G:C8	2.55	0.42
58:B1:559:ALA:HB3	58:B1:562:GLU:HB3	2.01	0.42
58:B1:820:ILE:HD11	58:B1:822:MET:HE2	2.02	0.42
63:5:4:C:H2'	63:5:5:G:C8	2.55	0.42
8:H:110:LEU:HD21	8:H:143:LEU:HB3	2.02	0.41
12:L:68:VAL:HG23	12:L:99:ALA:HB1	2.02	0.41
13:M:42:GLU:HG2	13:M:100:ILE:HG21	2.02	0.41
21:U:68:SER:OG	21:U:69:ASP:N	2.53	0.41
40:p:113:LEU:HD13	40:p:113:LEU:HA	1.86	0.41
46:v:14:LYS:HB2	52:2:98:G:H1	1.84	0.41
48:x:71:ARG:NH2	48:x:77:TYR:OH	2.42	0.41
49:y:30:MET:HE3	49:y:30:MET:HB3	1.83	0.41
51:1:281:C:H2'	51:1:282:A:C8	2.54	0.41
51:1:535:G:O2'	51:1:536:G:H5'	2.20	0.41
51:1:1070:A:H5'	51:1:1072:C:OP1	2.20	0.41
51:1:1314:C:H42	51:1:1338:G:H1	1.68	0.41
51:1:1719:G:O2'	51:1:1720:U:H5'	2.20	0.41
51:1:2389:G:H5''	51:1:2390:U:H5'	2.01	0.41
51:1:2612:C:O5'	51:1:2612:C:H6	2.04	0.41
51:1:2895:G:H2'	51:1:2896:C:H6	1.84	0.41
53:3:440:C:H2'	53:3:441:A:H8	1.85	0.41
58:B1:245:LEU:CG	58:B1:246:PRO:HD2	2.47	0.41
58:B1:390:LEU:H	58:B1:390:LEU:HD13	1.85	0.41
59:B2:478:ARG:HD2	59:B2:492:MET:HA	2.02	0.41
59:B2:542:ARG:H	59:B2:542:ARG:HG2	1.69	0.41
59:B2:699:LEU:HG	59:B2:799:ASN:HD22	1.85	0.41
59:B2:998:LEU:HD21	59:B2:1015:ALA:HB2	2.02	0.41
7:G:162:VAL:N	7:G:183:PHE:O	2.38	0.41
8:H:19:SER:HB2	8:H:39:ARG:HH21	1.85	0.41
17:Q:29:LYS:HA	17:Q:29:LYS:HD3	1.65	0.41
17:Q:98:ARG:HA	17:Q:103:CYS:HB2	2.02	0.41
18:R:7:ASN:CG	18:R:9:PRO:HD2	2.45	0.41
29:d:145:ASP:HA	29:d:166:LYS:HB3	2.02	0.41
32:g:11:ASN:ND2	51:1:2095:A:OP1	2.53	0.41
33:i:78:LEU:HA	33:i:81:LYS:HB3	2.02	0.41
35:k:53:LYS:HA	35:k:53:LYS:HD3	1.96	0.41
46:v:58:SER:OG	46:v:59:GLU:OE1	2.36	0.41
51:1:439:A:H2'	51:1:440:C:O4'	2.19	0.41
51:1:1727:C:O2'	51:1:1728:C:H5'	2.20	0.41
51:1:2160:C:H2'	51:1:2161:C:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:842:U:H5''	53:3:846:G:C6	2.55	0.41
53:3:1382:C:H2'	53:3:1383:C:H6	1.84	0.41
58:B1:390:LEU:N	58:B1:390:LEU:HD13	2.35	0.41
15:O:12:ALA:HB2	15:O:96:VAL:HG13	2.03	0.41
22:V:7:LEU:N	22:V:59:GLU:OE2	2.53	0.41
37:m:123:LYS:HE2	51:1:2467:C:O2	2.20	0.41
50:z:37:ARG:HD3	50:z:37:ARG:HA	1.83	0.41
51:1:191:A:H2'	51:1:192:C:C6	2.56	0.41
51:1:573:U:O2'	51:1:574:A:H3'	2.20	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
51:1:1176:U:H2'	51:1:1177:G:N9	2.35	0.41
51:1:1343:G:N3	51:1:1343:G:H2'	2.35	0.41
51:1:1488:C:H2'	51:1:1489:C:H6	1.84	0.41
51:1:1594:U:O2'	51:1:1595:C:H5'	2.20	0.41
51:1:1964:G:H4'	51:1:1965:C:OP2	2.19	0.41
51:1:2287:A:C4	51:1:2289:G:N7	2.87	0.41
53:3:497:G:H2'	53:3:498:A:C8	2.55	0.41
53:3:1124:G:H1	53:3:1149:C:H42	1.68	0.41
54:4:55:G:H5'	59:B2:688:GLN:HE22	1.85	0.41
55:8:14:DC:C2	55:8:15:DC:C5	3.09	0.41
58:B1:144:TYR:CE1	58:B1:162:GLU:OE1	2.73	0.41
58:B1:201:LEU:HD23	58:B1:201:LEU:HA	1.92	0.41
58:B1:450:HIS:HA	58:B1:451:PRO:HD3	1.91	0.41
58:B1:515:ARG:HG2	58:B1:516:ASP:H	1.85	0.41
58:B1:930:LEU:HA	58:B1:1244:GLN:HG3	2.02	0.41
59:B2:741:MET:SD	59:B2:974:ARG:NH2	2.93	0.41
7:G:190:SER:OG	7:G:191:ASP:N	2.54	0.41
15:O:57:VAL:HG22	15:O:58:ASN:H	1.85	0.41
18:R:104:ASN:HB3	18:R:105:ALA:H	1.69	0.41
22:V:11:VAL:HG23	22:V:55:GLY:H	1.85	0.41
34:j:13:ARG:NH1	34:j:49:ASP:O	2.41	0.41
41:q:23:TYR:HB3	41:q:27:ARG:HB2	2.02	0.41
42:r:49:ILE:HA	42:r:54:VAL:HG23	2.02	0.41
51:1:127:A:H5''	51:1:128:C:O4'	2.21	0.41
51:1:170:U:H2'	51:1:171:U:C6	2.55	0.41
51:1:638:G:H2'	51:1:639:U:C6	2.55	0.41
51:1:1213:A:C1'	51:1:1237:A:C2	3.03	0.41
51:1:1416:G:H2'	51:1:1417:C:H6	1.82	0.41
51:1:1721:G:H1'	51:1:1739:A:N6	2.35	0.41
51:1:2379:G:H2'	51:1:2380:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:A1:76:GLU:HB3	57:A1:80:GLU:HB3	2.01	0.41
58:B1:109:SER:CB	58:B1:296:LYS:HG2	2.51	0.41
59:B2:897:PRO:O	59:B2:900:LYS:N	2.53	0.41
62:NG:175:PHE:O	62:NG:178:VAL:O	2.38	0.41
8:H:178:ARG:NH1	53:3:1112:C:O2'	2.54	0.41
9:I:24:VAL:HG22	53:3:409:U:H4'	2.02	0.41
26:Z:9:GLU:HB3	26:Z:10:PRO:HD3	2.03	0.41
28:c:90:PHE:HD1	28:c:94:GLN:HG2	1.83	0.41
30:e:124:ARG:NH2	51:1:2315:G:N3	2.68	0.41
43:s:70:LYS:N	43:s:108:SER:O	2.45	0.41
50:z:31:ILE:HD11	51:1:989:G:P	2.61	0.41
51:1:137:U:H3	51:1:142:A:H61	1.69	0.41
51:1:197:A:H2	51:1:2434:A:H62	1.69	0.41
51:1:543:G:C3'	51:1:544:C:H5''	2.51	0.41
51:1:722:A:H2'	51:1:723:C:C6	2.56	0.41
51:1:724:U:H2'	51:1:725:G:C8	2.56	0.41
51:1:759:G:H2'	51:1:760:G:H8	1.83	0.41
51:1:1045:C:H1'	51:1:1047:G:C2	2.56	0.41
51:1:1107:G:H2'	51:1:1108:U:O4'	2.20	0.41
51:1:1767:G:N2	51:1:1986:C:C2	2.89	0.41
51:1:2224:G:H4'	51:1:2226:C:N3	2.35	0.41
51:1:2248:C:C2'	51:1:2249:U:H5'	2.49	0.41
51:1:2335:A:N7	51:1:2337:G:C5	2.88	0.41
51:1:2411:A:O2'	51:1:2412:A:H5'	2.20	0.41
51:1:2467:C:N4	51:1:2468:A:C6	2.89	0.41
51:1:2743:U:H2'	51:1:2744:G:C4'	2.50	0.41
58:B1:102:MET:HG2	58:B1:246:PRO:CG	2.49	0.41
59:B2:22:LEU:HB3	59:B2:655:VAL:HG11	2.01	0.41
59:B2:22:LEU:HD22	59:B2:603:ILE:HG21	2.02	0.41
59:B2:870:ILE:HB	59:B2:944:ARG:HD3	2.02	0.41
59:B2:979:LEU:HD11	59:B2:1011:LEU:HD11	2.03	0.41
63:5:9:A:H1'	63:5:45:U:H2'	2.01	0.41
9:I:44:LYS:HA	9:I:44:LYS:HD2	1.55	0.41
15:O:89:ARG:NH2	62:NG:165:PHE:H	2.18	0.41
33:i:100:ILE:HB	33:i:139:VAL:HG12	2.03	0.41
36:l:39:LYS:HE3	36:l:39:LYS:HB2	1.84	0.41
39:o:16:ARG:HD3	39:o:16:ARG:HA	1.84	0.41
41:q:57:ARG:NH1	51:1:1154:G:OP2	2.52	0.41
42:r:81:LYS:NZ	51:1:568:U:O4	2.54	0.41
51:1:49:A:P	51:1:51:G:H5'	2.60	0.41
51:1:56:A:H1'	51:1:127:A:C2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:481:G:H1'	51:1:506:G:H22	1.84	0.41
51:1:940:G:H2'	51:1:941:A:C4'	2.51	0.41
51:1:1024:G:H21	51:1:1144:A:C4'	2.33	0.41
51:1:1092:C:O2'	51:1:1093:G:H5'	2.21	0.41
51:1:1239:G:H2'	51:1:1240:U:O4'	2.21	0.41
51:1:1412:U:H2'	51:1:1413:A:C8	2.56	0.41
51:1:1782:U:C2'	51:1:1783:A:H5''	2.51	0.41
51:1:1936:A:N6	51:1:1963:U:H3	2.17	0.41
53:3:146:G:H2'	53:3:147:G:C8	2.56	0.41
53:3:370:C:H2'	53:3:371:A:H8	1.86	0.41
53:3:1228:C:H2'	53:3:1229:A:C8	2.56	0.41
57:A2:57:THR:HG23	57:A2:158:ARG:HH21	1.86	0.41
58:B1:144:TYR:N	58:B1:144:TYR:CD1	2.88	0.41
58:B1:224:LEU:HD23	58:B1:224:LEU:HA	1.89	0.41
58:B1:609:TYR:HD2	58:B1:610:ARG:NH1	2.17	0.41
58:B1:647:PRO:HG3	58:B1:697:MET:HB3	2.01	0.41
58:B1:1350:ASN:HA	58:B1:1353:VAL:HG12	2.02	0.41
59:B2:657:THR:HG21	59:B2:1188:ASP:HB2	2.03	0.41
7:G:17:HIS:C	7:G:19:THR:H	2.28	0.41
7:G:173:LYS:HE3	7:G:173:LYS:HB2	1.76	0.41
23:W:24:ASP:OD1	23:W:24:ASP:N	2.53	0.41
30:e:39:VAL:HG12	30:e:85:GLY:HA2	2.03	0.41
39:o:8:ILE:O	39:o:12:THR:OG1	2.33	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
51:1:259:G:O2'	51:1:260:G:H5'	2.20	0.41
51:1:284:U:H2'	51:1:285:G:C8	2.55	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
51:1:1150:C:C2	51:1:1151:A:C8	3.09	0.41
51:1:1418:G:H1'	51:1:1581:G:N2	2.36	0.41
51:1:1505:A:O2'	51:1:1506:U:H5'	2.19	0.41
51:1:1614:A:O5'	51:1:1614:A:C8	2.73	0.41
51:1:2646:C:H2'	51:1:2647:U:O4'	2.21	0.41
51:1:2697:G:C2	51:1:2711:A:C2	3.08	0.41
58:B1:239:LEU:HD23	58:B1:239:LEU:N	2.36	0.41
59:B2:310:ILE:HG21	59:B2:325:LEU:HB3	2.02	0.41
59:B2:487:LEU:HD22	59:B2:487:LEU:HA	1.77	0.41
59:B2:616:ILE:HG13	59:B2:652:TYR:HB2	2.01	0.41
59:B2:678:ARG:HA	59:B2:678:ARG:HD3	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:146:MET:HE2	10:J:146:MET:HB3	1.76	0.41
27:b:57:HIS:ND1	51:1:1567:G:H5'	2.35	0.41
27:b:209:ALA:HA	27:b:212:TRP:CE2	2.55	0.41
33:i:41:PHE:O	33:i:45:THR:N	2.54	0.41
51:1:79:C:O2	51:1:346:A:H2	2.03	0.41
51:1:490:C:O2'	51:1:491:G:P	2.79	0.41
51:1:724:U:H2'	51:1:725:G:O4'	2.21	0.41
51:1:877:A:H2'	51:1:878:A:H5''	2.02	0.41
51:1:1063:G:N2	51:1:1075:C:H41	2.18	0.41
51:1:1283:G:N2	51:1:1285:A:H3'	2.35	0.41
51:1:1328:A:H2'	51:1:1330:C:C4	2.56	0.41
51:1:1334:G:C6	51:1:1335:C:C4	3.09	0.41
51:1:1467:U:C4	51:1:1468:U:C4	3.08	0.41
51:1:1553:A:O2'	51:1:1554:U:H5	2.02	0.41
51:1:1750:G:H2'	51:1:1751:U:C6	2.56	0.41
51:1:1991:U:H2'	51:1:1992:G:H5'	2.02	0.41
51:1:2600:A:H8	51:1:2600:A:O5'	2.03	0.41
51:1:2660:A:H2'	51:1:2661:G:C8	2.56	0.41
51:1:2757:A:H2'	51:1:2758:A:H5''	2.02	0.41
57:A1:205:MET:HE1	57:A1:217:ILE:HG13	2.02	0.41
58:B1:71:LEU:HB2	58:B1:90:VAL:HG11	2.03	0.41
60:W0:26:ARG:HA	60:W0:26:ARG:HD2	1.92	0.41
2:B:39:ARG:HA	2:B:39:ARG:HD2	1.91	0.41
5:E:7:ARG:NH2	51:1:245:G:N7	2.59	0.41
7:G:178:LEU:HD22	61:NA:244:ARG:CB	2.50	0.41
10:J:90:GLY:O	10:J:129:SER:OG	2.36	0.41
27:b:70:LYS:HD2	27:b:73:ILE:HD12	2.02	0.41
28:c:4:LEU:HD21	28:c:98:VAL:HA	2.03	0.41
28:c:169:ARG:O	51:1:2773:C:H4'	2.21	0.41
30:e:36:ASN:HB3	30:e:152:ASP:HB3	2.03	0.41
33:i:77:VAL:HA	33:i:80:LYS:HE2	2.02	0.41
38:n:28:LEU:O	38:n:32:GLU:N	2.38	0.41
39:o:24:THR:HB	39:o:42:PRO:HG3	2.03	0.41
43:s:29:VAL:HG21	43:s:55:ILE:HG21	2.03	0.41
51:1:211:C:O2'	51:1:212:G:H5'	2.21	0.41
51:1:511:U:H2'	51:1:512:G:H5'	2.03	0.41
51:1:679:C:H2'	51:1:680:C:C6	2.56	0.41
51:1:724:U:C4	51:1:725:G:C6	3.08	0.41
51:1:924:G:O2'	51:1:925:A:H5'	2.21	0.41
51:1:1020:A:H5'	51:1:1021:A:N7	2.35	0.41
51:1:1107:G:H2'	51:1:1108:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1160:G:C6	51:1:1161:C:C4	3.09	0.41
51:1:1283:G:H22	51:1:1286:A:P	2.44	0.41
51:1:1410:G:H2'	51:1:1411:U:H6	1.85	0.41
51:1:1591:A:H2'	51:1:1592:C:C6	2.56	0.41
51:1:1822:C:H2'	51:1:1823:G:H8	1.85	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
51:1:2437:G:O4'	51:1:2598:A:C2	2.73	0.41
58:B1:1361:THR:N	59:B2:1282:GLY:O	2.53	0.41
59:B2:738:GLU:HA	59:B2:741:MET:HE2	2.03	0.41
59:B2:888:THR:HB	59:B2:889:PRO:HD3	2.02	0.41
7:G:18:GLN:HB3	7:G:21:TYR:HB2	2.03	0.41
9:I:10:LEU:HG	9:I:62:ARG:HD2	2.03	0.41
9:I:101:VAL:HG13	9:I:113:ALA:HB1	2.03	0.41
18:R:10:ASP:HB3	18:R:45:SER:HB3	2.03	0.41
24:X:49:ALA:HA	24:X:58:PRO:HA	2.03	0.41
31:f:157:LYS:HD3	51:1:2658:C:H5''	2.02	0.41
51:1:426:C:O2'	51:1:427:U:H5'	2.21	0.41
51:1:706:A:H2'	51:1:707:G:C5'	2.51	0.41
51:1:1048:A:N6	51:1:1111:A:C8	2.89	0.41
51:1:1077:A:H3'	51:1:1078:U:H4'	2.02	0.41
51:1:1165:A:O2'	51:1:1166:G:H5'	2.21	0.41
51:1:1452:G:C2'	51:1:1453:A:OP2	2.68	0.41
51:1:1482:G:H2'	51:1:1483:G:H8	1.85	0.41
51:1:1868:C:H2'	51:1:1869:G:H8	1.86	0.41
51:1:2105:U:C2	51:1:2184:A:H2	2.39	0.41
51:1:2221:G:H2'	51:1:2222:C:C6	2.56	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
51:1:2575:C:H2'	51:1:2578:G:O6	2.21	0.41
51:1:2776:A:C6	51:1:2778:A:C6	3.09	0.41
52:2:65:U:H3'	52:2:108:A:N6	2.30	0.41
53:3:297:G:N2	53:3:300:A:OP2	2.39	0.41
53:3:373:A:N1	53:3:391:G:O2'	2.49	0.41
57:A2:42:ALA:HB1	57:A2:224:LEU:HD11	2.03	0.41
58:B1:26:SER:HB3	58:B1:29:MET:H	1.86	0.41
58:B1:1289:ASN:O	58:B1:1293:GLU:HB2	2.20	0.41
59:B2:469:VAL:HA	59:B2:472:GLU:HG2	2.01	0.41
9:I:87:GLU:N	9:I:87:GLU:OE2	2.53	0.40
31:f:21:GLN:NE2	31:f:37:ASN:O	2.54	0.40
34:j:17:VAL:HG13	34:j:137:PRO:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:n:22:ARG:HH22	51:1:2709:G:H5'	1.86	0.40
38:n:71:ARG:HE	38:n:71:ARG:HB3	1.68	0.40
42:r:4:VAL:HG23	42:r:39:LEU:HB2	2.03	0.40
44:t:17:SER:OG	44:t:20:ALA:N	2.48	0.40
44:t:68:LYS:HD3	44:t:68:LYS:HA	1.83	0.40
51:1:244:A:H2'	51:1:245:G:O4'	2.20	0.40
51:1:518:G:H2'	51:1:519:U:C6	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
51:1:914:G:H5'	51:1:915:C:OP2	2.21	0.40
51:1:1116:G:O2'	51:1:1117:C:H5'	2.22	0.40
51:1:1279:G:H2'	51:1:1280:G:C8	2.56	0.40
51:1:1430:G:O2'	51:1:1431:A:H5'	2.21	0.40
51:1:2098:U:H2'	51:1:2099:U:H5'	2.03	0.40
51:1:2106:U:H3'	51:1:2107:G:H8	1.86	0.40
51:1:2210:U:H6	51:1:2210:U:OP1	2.04	0.40
51:1:2680:U:O2'	51:1:2681:C:H5'	2.21	0.40
53:3:202:G:H2'	53:3:203:G:C8	2.55	0.40
53:3:1304:G:N1	53:3:1332:A:OP2	2.54	0.40
59:B2:176:ILE:HD12	59:B2:184:LEU:HD23	2.03	0.40
1:A:62:LYS:HE3	1:A:62:LYS:HB3	1.89	0.40
6:F:30:GLU:HA	6:F:31:PRO:HD3	1.91	0.40
10:J:156:ARG:HE	13:M:42:GLU:HG3	1.87	0.40
19:S:15:LEU:HB3	19:S:54:SER:HB3	2.02	0.40
30:e:64:PRO:HA	30:e:88:VAL:HG22	2.03	0.40
38:n:114:GLU:OE1	38:n:118:ARG:NH1	2.50	0.40
44:t:28:ASN:HD21	44:t:91:GLN:HB3	1.85	0.40
51:1:55:G:N2	51:1:116:C:C2	2.90	0.40
51:1:224:U:O4	51:1:420:C:H5'	2.21	0.40
51:1:309:A:N3	51:1:329:G:O2'	2.53	0.40
51:1:466:A:C2'	51:1:467:G:H5'	2.46	0.40
51:1:1152:C:H2'	51:1:1153:C:C6	2.55	0.40
51:1:1599:U:H2'	51:1:1600:C:H6	1.85	0.40
51:1:1722:A:N6	51:1:1738:G:H1'	2.36	0.40
51:1:2098:U:H2'	51:1:2099:U:C5'	2.51	0.40
51:1:2649:C:N3	51:1:2650:U:C4	2.89	0.40
59:B2:859:GLU:CB	61:NA:38:LYS:O	2.69	0.40
59:B2:1247:SER:OG	59:B2:1248:THR:N	2.55	0.40
14:N:22:PRO:HA	14:N:60:LEU:HA	2.03	0.40
16:P:30:ILE:HG23	16:P:45:THR:HB	2.02	0.40
23:W:52:ARG:HE	23:W:52:ARG:HB2	1.66	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:d:163:ASN:HD21	51:1:322:A:P	2.45	0.40
51:1:120:U:C2	51:1:149:A:C6	3.10	0.40
51:1:194:G:O6	51:1:195:A:C6	2.75	0.40
51:1:955:U:H2'	51:1:956:G:C5'	2.52	0.40
51:1:1605:C:H2'	51:1:1606:C:C5'	2.52	0.40
51:1:1715:G:O2'	51:1:1716:U:C6	2.75	0.40
51:1:1722:A:H2'	51:1:1723:G:O4'	2.21	0.40
51:1:2038:G:H2'	51:1:2039:U:O4'	2.21	0.40
51:1:2828:G:N1	51:1:2829:A:C5	2.90	0.40
53:3:146:G:H2'	53:3:147:G:H8	1.86	0.40
53:3:987:G:H2'	53:3:988:G:C8	2.56	0.40
58:B1:807:LEU:HD21	58:B1:894:VAL:HG21	2.04	0.40
63:5:17:C:H2'	63:5:18:G:C8	2.56	0.40
64:7:10:G:OP1	64:7:46:G:H4'	2.21	0.40
9:I:55:ARG:HA	9:I:55:ARG:HD3	1.88	0.40
9:I:123:MET:HB2	9:I:143:SER:HB3	2.04	0.40
9:I:150:LYS:HD2	9:I:155:LYS:HD2	2.04	0.40
11:K:22:ILE:H	11:K:22:ILE:HG13	1.70	0.40
12:L:125:ASP:HB2	12:L:130:LYS:HG3	2.03	0.40
17:Q:110:LYS:HB2	17:Q:110:LYS:HE2	1.89	0.40
48:x:55:MET:HE2	48:x:55:MET:HB3	1.91	0.40
51:1:10:A:C6	51:1:2800:A:C2	3.09	0.40
51:1:1346:G:O2'	51:1:1347:A:H5'	2.22	0.40
51:1:1695:G:H2'	51:1:1696:G:O5'	2.22	0.40
51:1:2568:U:O5'	51:1:2568:U:H6	2.04	0.40
53:3:304:U:H2'	53:3:305:G:C8	2.56	0.40
53:3:685:G:N1	53:3:704:A:OP2	2.52	0.40
55:8:2:DC:C6	55:8:2:DC:H5'	2.56	0.40
64:7:69:C:H2'	64:7:70:G:C8	2.56	0.40
8:H:14:VAL:HG11	8:H:180:ASP:HB3	2.03	0.40
9:I:146:GLU:HA	9:I:149:LYS:HZ3	1.85	0.40
16:P:17:ASP:HB3	16:P:80:ASN:HD21	1.87	0.40
18:R:53:ASP:OD1	18:R:53:ASP:N	2.55	0.40
34:j:78:THR:HB	51:1:2641:G:H5''	2.04	0.40
35:k:13:ASN:HB3	35:k:100:PHE:CZ	2.57	0.40
51:1:379:G:N1	51:1:396:G:C6	2.89	0.40
51:1:467:G:H8	51:1:467:G:O5'	2.04	0.40
51:1:485:C:O2'	51:1:486:C:H5'	2.22	0.40
51:1:1123:C:H2'	51:1:1124:G:C8	2.57	0.40
51:1:1317:G:H2'	51:1:1318:U:C6	2.56	0.40
51:1:1749:A:C4	51:1:1750:G:C8	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1783:A:N1	51:1:2587:A:H2'	2.37	0.40
51:1:1827:U:C2'	51:1:1828:G:H5'	2.51	0.40
51:1:1975:G:H2'	51:1:1976:U:H5'	2.04	0.40
51:1:2093:G:N7	51:1:2225:A:H2'	2.37	0.40
51:1:2585:U:O2	51:1:2585:U:O4'	2.39	0.40
51:1:2615:U:O2	51:1:2615:U:H2'	2.20	0.40
51:1:2648:G:O2'	51:1:2649:C:H5'	2.21	0.40
51:1:2788:C:H2'	51:1:2789:C:C6	2.56	0.40
51:1:2833:U:O2'	51:1:2834:G:H5'	2.22	0.40
52:2:31:C:H2'	52:2:53:A:H61	1.86	0.40
53:3:202:G:H2'	53:3:203:G:H8	1.85	0.40
58:B1:472:LEU:HD11	59:B2:1294:LYS:HG2	2.02	0.40
58:B1:734:ALA:O	58:B1:738:ARG:HB2	2.22	0.40
58:B1:1050:THR:HG23	58:B1:1057:SER:HB3	2.02	0.40
58:B1:1064:SER:OG	58:B1:1168:GLU:OE1	2.31	0.40
59:B2:859:GLU:HB3	61:NA:38:LYS:O	2.21	0.40
59:B2:890:LYS:HB3	59:B2:891:GLY:H	1.72	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	204/233 (88%)	194 (95%)	10 (5%)	0	100	100
9	I	203/206 (98%)	173 (85%)	29 (14%)	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%)	99 (88%)	12 (11%)	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	37
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%)	159 (91%)	15 (9%)	0	100	100
32	g	50/149 (34%)	44 (88%)	5 (10%)	1 (2%)	6	31
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	35
42	r	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	13	49
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	295/329 (90%)	273 (92%)	21 (7%)	1 (0%)	37	72
57	A2	282/329 (86%)	271 (96%)	11 (4%)	0	100	100
58	B1	1329/1407 (94%)	1202 (90%)	123 (9%)	4 (0%)	37	72
59	B2	1338/1342 (100%)	1201 (90%)	131 (10%)	6 (0%)	30	68
60	W0	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
61	NA	490/495 (99%)	472 (96%)	15 (3%)	3 (1%)	22	60
62	NG	150/181 (83%)	132 (88%)	12 (8%)	6 (4%)	2	18
65	h	2/6 (33%)	1 (50%)	1 (50%)	0	100	100
All	All	9586/10235 (94%)	8662 (90%)	885 (9%)	39 (0%)	32	68

All (39) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
42	r	54	VAL
48	x	25	LYS
58	B1	121	PRO
59	B2	897	PRO
61	NA	187	ARG
61	NA	188	PRO
62	NG	102	PRO
6	F	34	LYS
57	A1	250	ASP
59	B2	43	PRO

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Mol	Chain	Res	Type
62	NG	126	THR
62	NG	163	SER
59	B2	888	THR
2	B	23	ALA
7	G	19	THR
18	R	5	GLY
22	V	50	ASN
32	g	12	LEU
41	q	23	TYR
58	B1	43	THR
58	B1	193	ASP
7	G	17	HIS
15	O	58	ASN
23	W	13	THR
45	u	97	SER
58	B1	1325	PHE
59	B2	896	THR
59	B2	909	LYS
9	I	45	PRO
23	W	17	VAL
61	NA	137	ILE
62	NG	169	THR
62	NG	170	PRO
26	Z	10	PRO
41	q	6	GLY
62	NG	122	PRO
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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	48
6	F	34/34 (100%)	30 (88%)	4 (12%)	4	16
7	G	180/199 (90%)	174 (97%)	6 (3%)	33	53
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	82
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	52
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	48
21	U	65/65 (100%)	64 (98%)	1 (2%)	60	75
22	V	74/78 (95%)	72 (97%)	2 (3%)	40	59
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	12
27	b	216/218 (99%)	212 (98%)	4 (2%)	52	70
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
33	i	109/110 (99%)	108 (99%)	1 (1%)	75	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	j	116/116 (100%)	116 (100%)	0	100	100
35	k	103/104 (99%)	103 (100%)	0	100	100
36	l	102/103 (99%)	101 (99%)	1 (1%)	73	82
37	m	109/109 (100%)	103 (94%)	6 (6%)	18	40
38	n	100/103 (97%)	99 (99%)	1 (1%)	73	82
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	52
42	r	84/84 (100%)	82 (98%)	2 (2%)	44	63
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%)	185 (100%)	1 (0%)	86	89
58	B1	1110/1168 (95%)	1017 (92%)	93 (8%)	9	28
59	B2	1150/1157 (99%)	1117 (97%)	33 (3%)	37	57
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%)	7132 (97%)	249 (3%)	34	52

All (249) 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
6	F	34	LYS

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Mol	Chain	Res	Type
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
16	P	124	LYS

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Mol	Chain	Res	Type
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
36	l	85	VAL

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Mol	Chain	Res	Type
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	53	PHE
42	r	55	ASP
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
58	B1	24	LEU
58	B1	40	LYS
58	B1	42	GLU
58	B1	44	ILE
58	B1	47	ARG
58	B1	49	PHE
58	B1	50	LYS
58	B1	60	ARG
58	B1	66	LYS
58	B1	69	GLU

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Mol	Chain	Res	Type
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
58	B1	212	THR
58	B1	216	LYS
58	B1	222	LYS
58	B1	223	LEU
58	B1	227	PHE

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Mol	Chain	Res	Type
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
58	B1	1327	GLU
58	B1	1328	THR
58	B1	1331	VAL
58	B1	1332	LEU
59	B2	44	GLU

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Mol	Chain	Res	Type
59	B2	49	LEU
59	B2	56	VAL
59	B2	146	VAL
59	B2	483	ASP
59	B2	487	LEU
59	B2	516	ASP
59	B2	538	LEU
59	B2	540	ARG
59	B2	545	PHE
59	B2	546	GLU
59	B2	615	VAL
59	B2	857	VAL
59	B2	859	GLU
59	B2	887	VAL
59	B2	890	LYS
59	B2	892	GLU
59	B2	894	GLN
59	B2	895	LEU
59	B2	900	LYS
59	B2	901	LEU
59	B2	902	LEU
59	B2	903	ARG
59	B2	905	ILE
59	B2	906	PHE
59	B2	909	LYS
59	B2	913	VAL
59	B2	916	SER
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	61	ASN
2	B	4	GLN
3	C	25	ASN
3	C	44	GLN

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Mol	Chain	Res	Type
4	D	16	HIS
6	F	35	GLN
7	G	14	HIS
7	G	108	GLN
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	197	HIS
10	J	76	ASN
10	J	121	ASN
12	L	85	GLN
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	56	HIS
24	X	68	HIS
25	Y	2	ASN
25	Y	77	ASN
26	Z	8	ASN
27	b	24	HIS
27	b	69	ASN

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Mol	Chain	Res	Type
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	62	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	104	GLN
37	m	13	HIS
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	75	GLN
46	v	87	GLN
47	w	53	HIS
48	x	16	ASN
48	x	33	HIS

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Mol	Chain	Res	Type
49	y	31	GLN
49	y	38	GLN
49	y	41	HIS
49	y	45	GLN
50	z	8	GLN
57	A1	37	HIS
57	A1	66	HIS
57	A1	84	ASN
57	A1	117	HIS
57	A1	128	HIS
57	A1	227	GLN
57	A2	227	GLN
58	B1	45	ASN
58	B1	196	GLN
58	B1	364	HIS
58	B1	424	ASN
58	B1	450	HIS
58	B1	469	HIS
58	B1	805	GLN
58	B1	865	HIS
58	B1	1195	GLN
58	B1	1238	GLN
58	B1	1259	GLN
59	B2	69	GLN
59	B2	314	ASN
59	B2	330	HIS
59	B2	343	HIS
59	B2	518	ASN
59	B2	554	HIS
59	B2	688	GLN
59	B2	808	ASN
59	B2	1080	ASN
59	B2	1237	HIS
59	B2	1268	GLN
59	B2	1313	HIS
60	W0	7	GLN
60	W0	31	GLN
60	W0	62	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	1	2902/2904 (99%)	399 (13%)	16 (0%)
52	2	119/120 (99%)	17 (14%)	1 (0%)
53	3	1538/1542 (99%)	253 (16%)	4 (0%)
54	4	33/56 (58%)	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	4819/4852 (99%)	765 (15%)	32 (0%)

All (765) 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
51	1	255	A
51	1	265	A

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Mol	Chain	Res	Type
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
51	1	575	A
51	1	603	A

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Mol	Chain	Res	Type
51	1	614	A
51	1	616	A
51	1	627	A
51	1	628	G
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
51	1	896	A

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Mol	Chain	Res	Type
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
51	1	1104	C

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Mol	Chain	Res	Type
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
51	1	1490	A

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Mol	Chain	Res	Type
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
51	1	1816	C

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Mol	Chain	Res	Type
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
51	1	2096	C

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Mol	Chain	Res	Type
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
51	1	2327	A

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Mol	Chain	Res	Type
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
51	1	2609	U

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Mol	Chain	Res	Type
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
52	2	67	G

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Mol	Chain	Res	Type
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
53	3	210	C

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Mol	Chain	Res	Type
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
53	3	429	U

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Mol	Chain	Res	Type
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
53	3	655	A

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Mol	Chain	Res	Type
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
53	3	975	A

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Mol	Chain	Res	Type
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
53	3	1227	A

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Mol	Chain	Res	Type
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	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	1492	A
53	3	1497	G
53	3	1499	A

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Mol	Chain	Res	Type
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
63	5	30	G
63	5	32	U
63	5	33	U

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Mol	Chain	Res	Type
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
64	7	19	G
64	7	20	U
64	7	21	A

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Mol	Chain	Res	Type
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
51	1	2732	G
52	2	88	C
53	3	4	U

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Mol	Chain	Res	Type
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	KBE	h	1	65	8,8,9	0.61	0	7,8,10	1.21	1 (14%)
65	5OH	h	6	65	8,12,13	0.76	0	3,16,18	1.52	1 (33%)
65	UAL	h	5	65	7,8,9	2.31	3 (42%)	5,9,11	2.91	2 (40%)

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	KBE	h	1	65	-	0/7/7/8	-

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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	h	5	UAL	C1-N1	-4.88	1.32	1.40
65	h	5	UAL	C-CA	-2.90	1.40	1.45
65	h	5	UAL	CA-N	2.03	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	115.63	125.60
65	h	5	UAL	O-C-CA	-3.23	121.28	125.39
65	h	6	5OH	CR-CB-CA	-2.38	110.04	112.61
65	h	1	KBE	CB-CA-C	-2.07	109.22	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 9 short contacts:

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

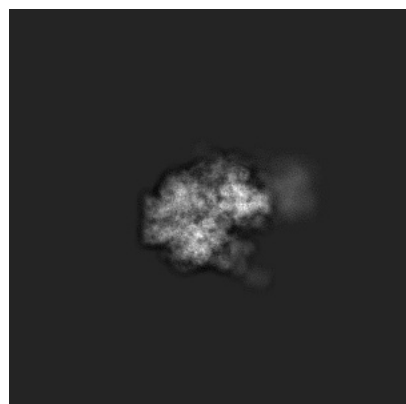
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39168. These allow visual inspection of the internal detail of the map and identification of artifacts.

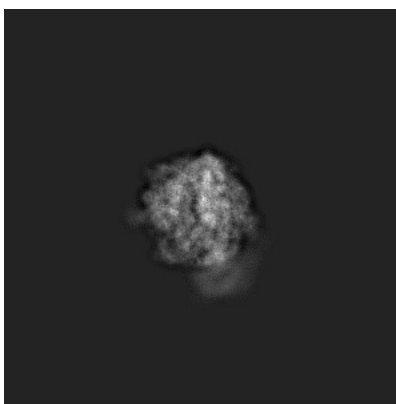
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

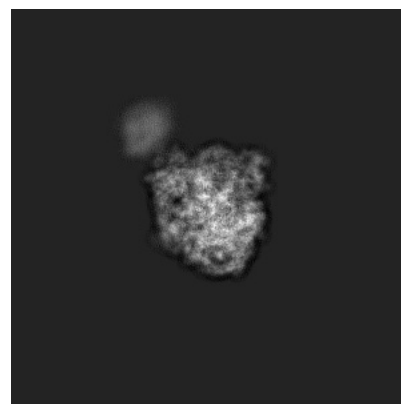
6.1.1 Primary map



X

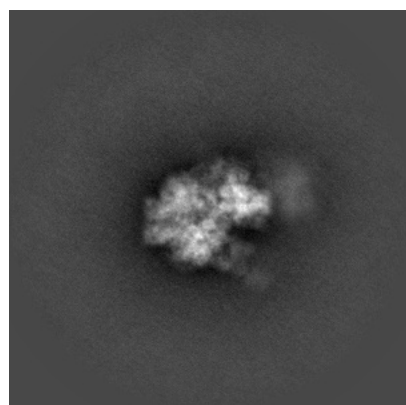


Y

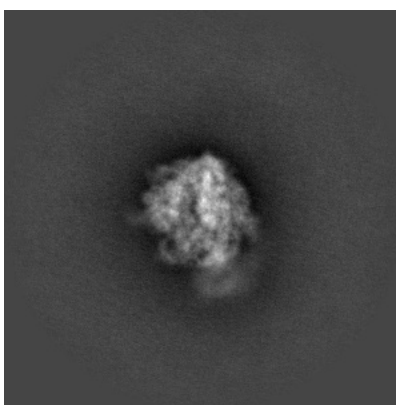


Z

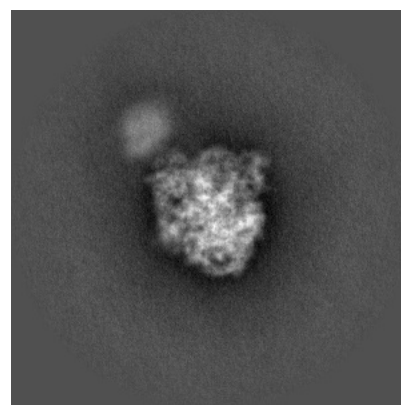
6.1.2 Raw map



X



Y

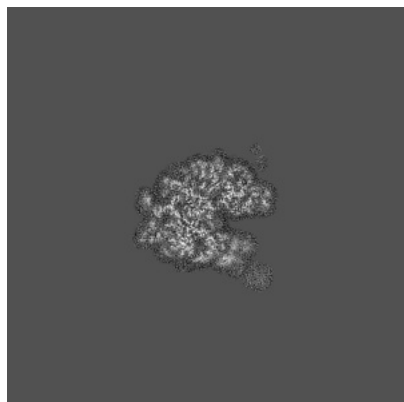


Z

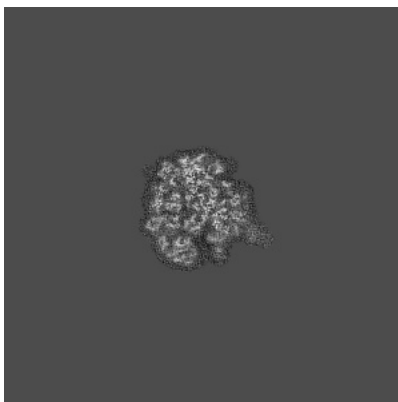
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

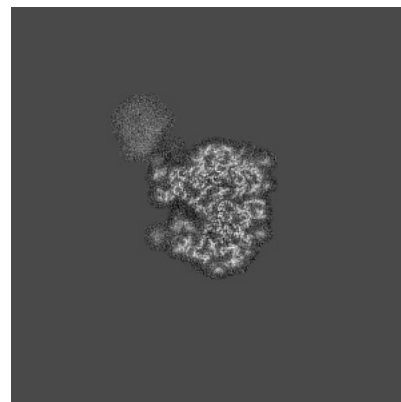
6.2.1 Primary map



X Index: 240

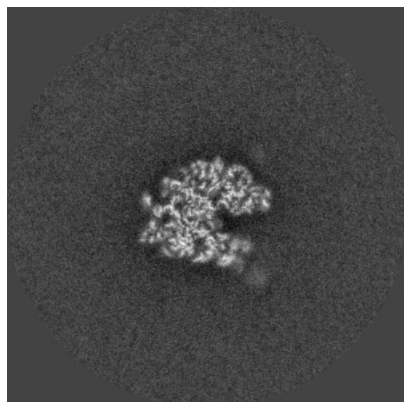


Y Index: 240

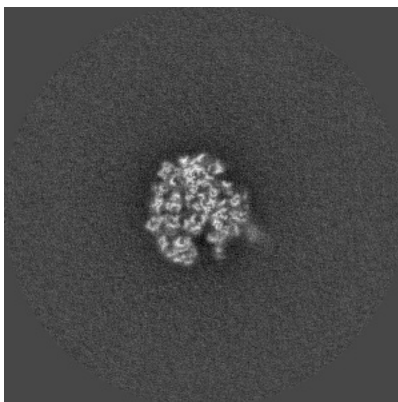


Z Index: 240

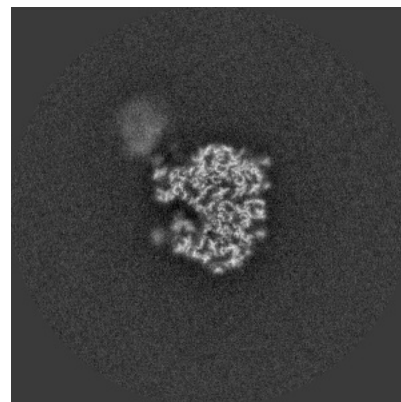
6.2.2 Raw map



X Index: 240



Y Index: 240

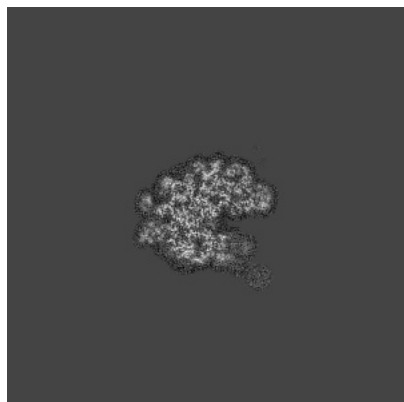


Z Index: 240

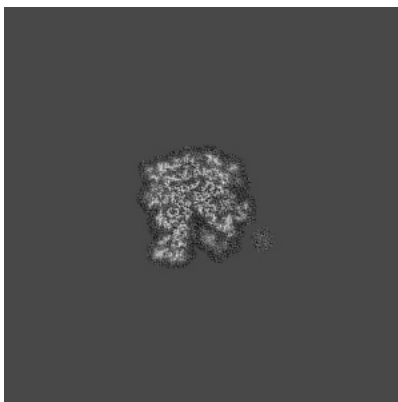
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

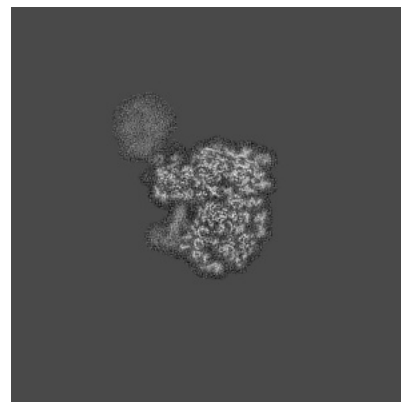
6.3.1 Primary map



X Index: 243

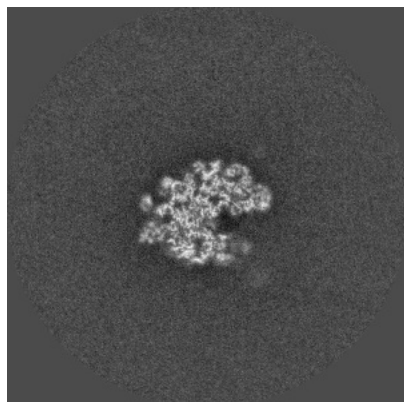


Y Index: 224

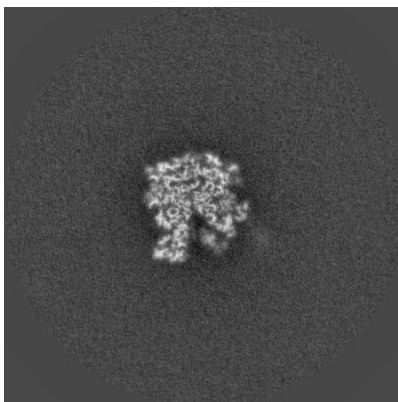


Z Index: 245

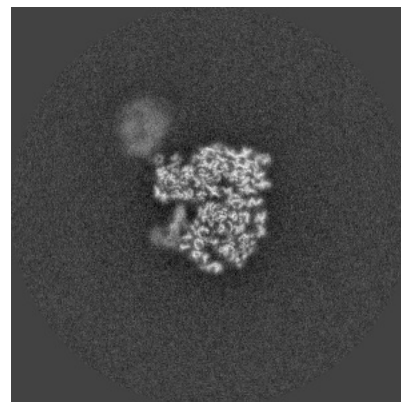
6.3.2 Raw map



X Index: 243



Y Index: 224

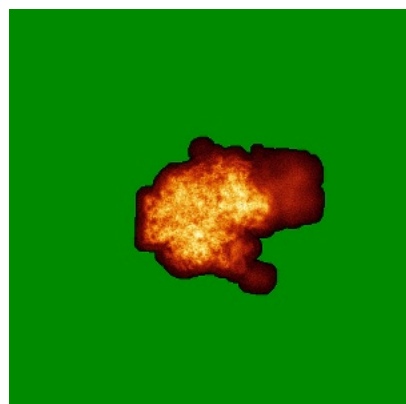


Z Index: 245

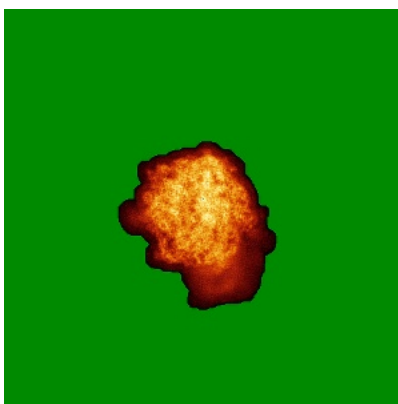
The images above show the largest variance slices of the map in three orthogonal directions.

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

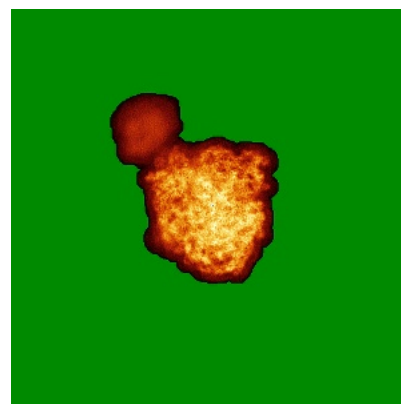
6.4.1 Primary map



X

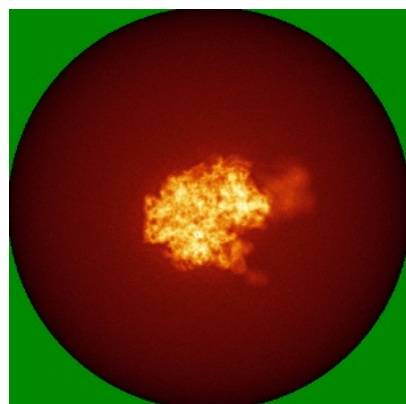


Y

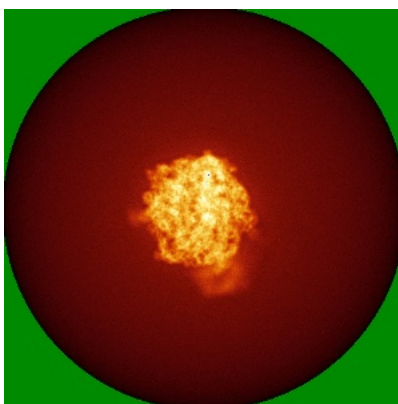


Z

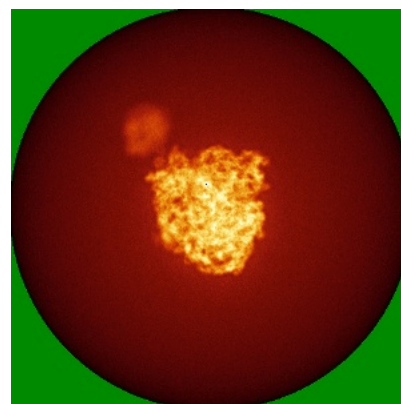
6.4.2 Raw map



X



Y

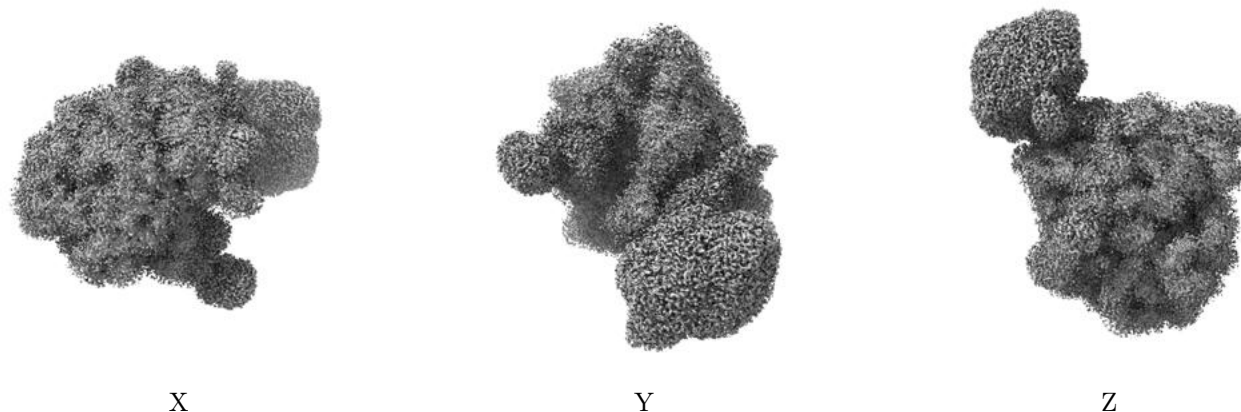


Z

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.

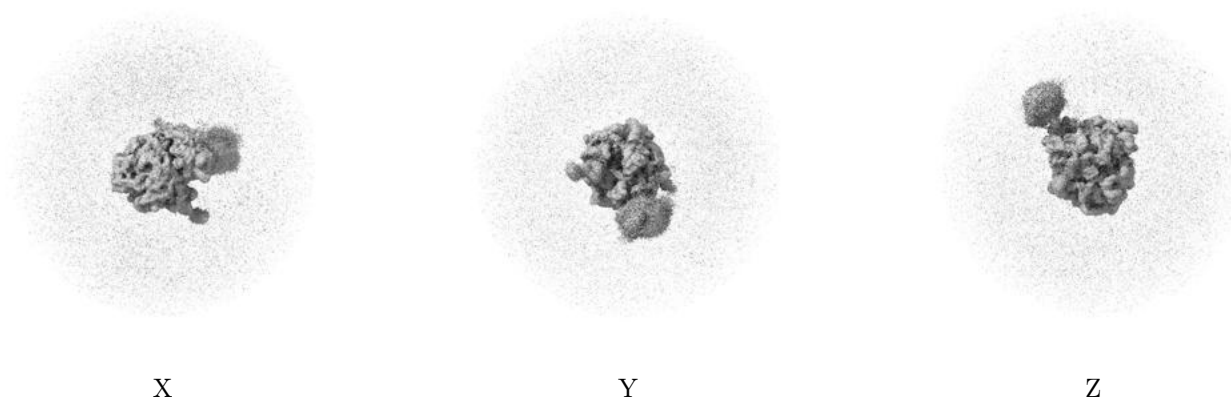
6.5 Orthogonal surface views [i](#)

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.

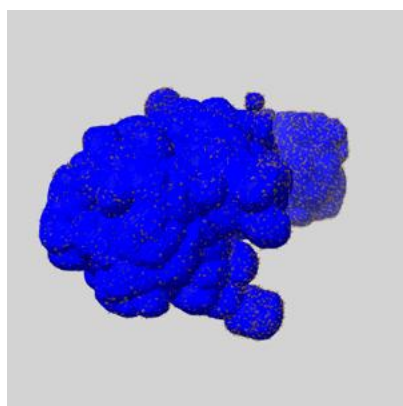
6.6 Mask visualisation [i](#)

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

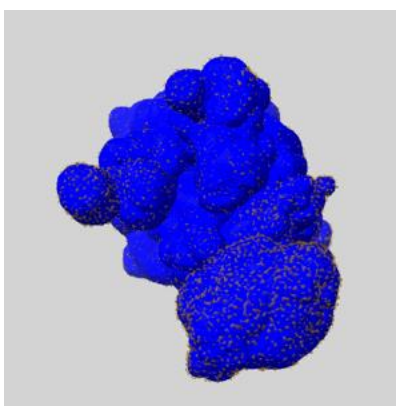
A mask typically either:

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

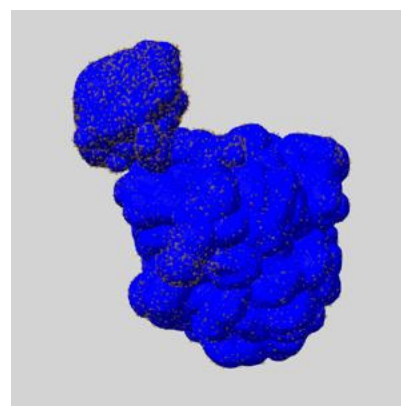
6.6.1 emd_39168_msk_1.map [i](#)



X



Y

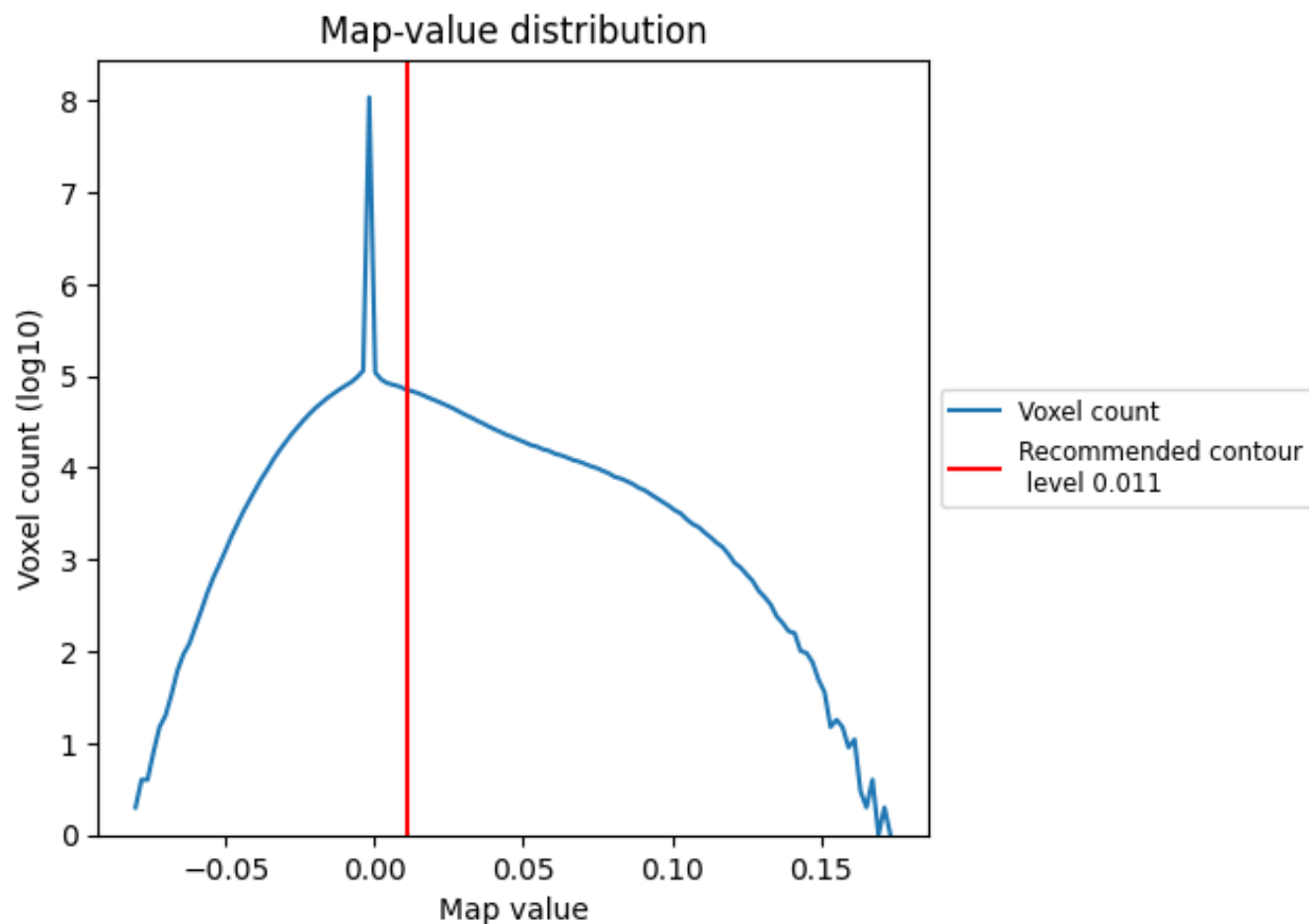


Z

7 Map analysis [i](#)

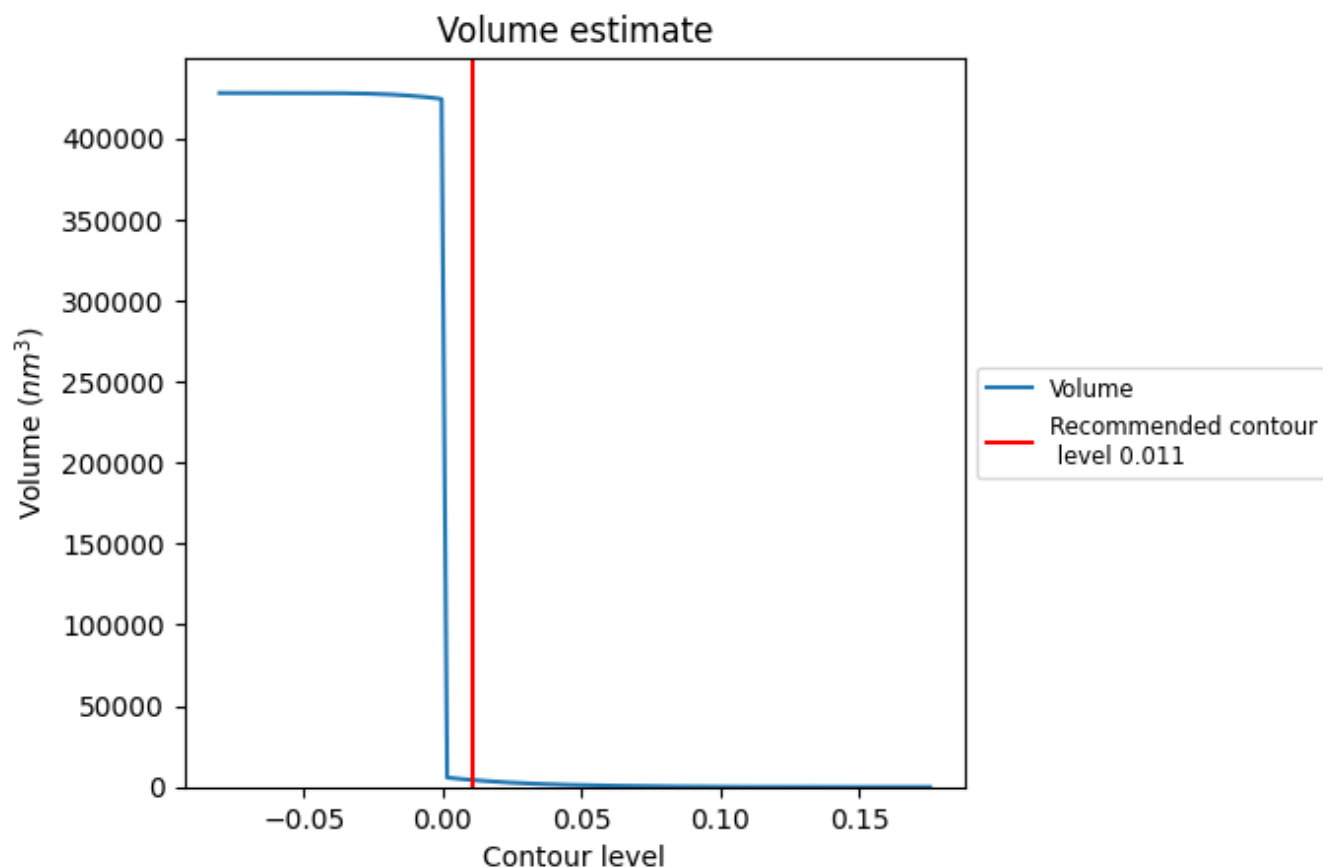
This section contains the results of statistical analysis of the map.

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.

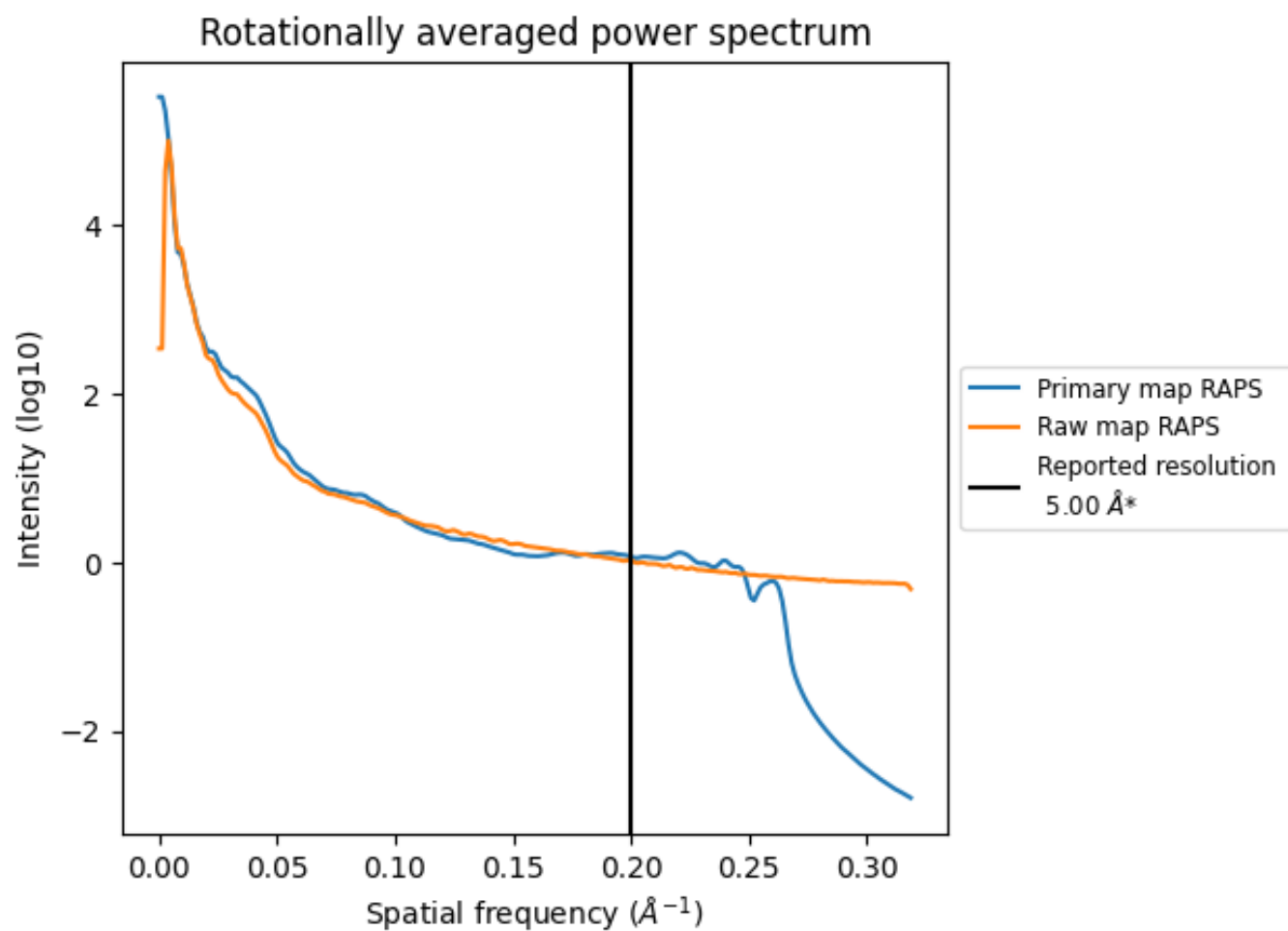
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4264 nm³; this corresponds to an approximate mass of 3852 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 ⓘ

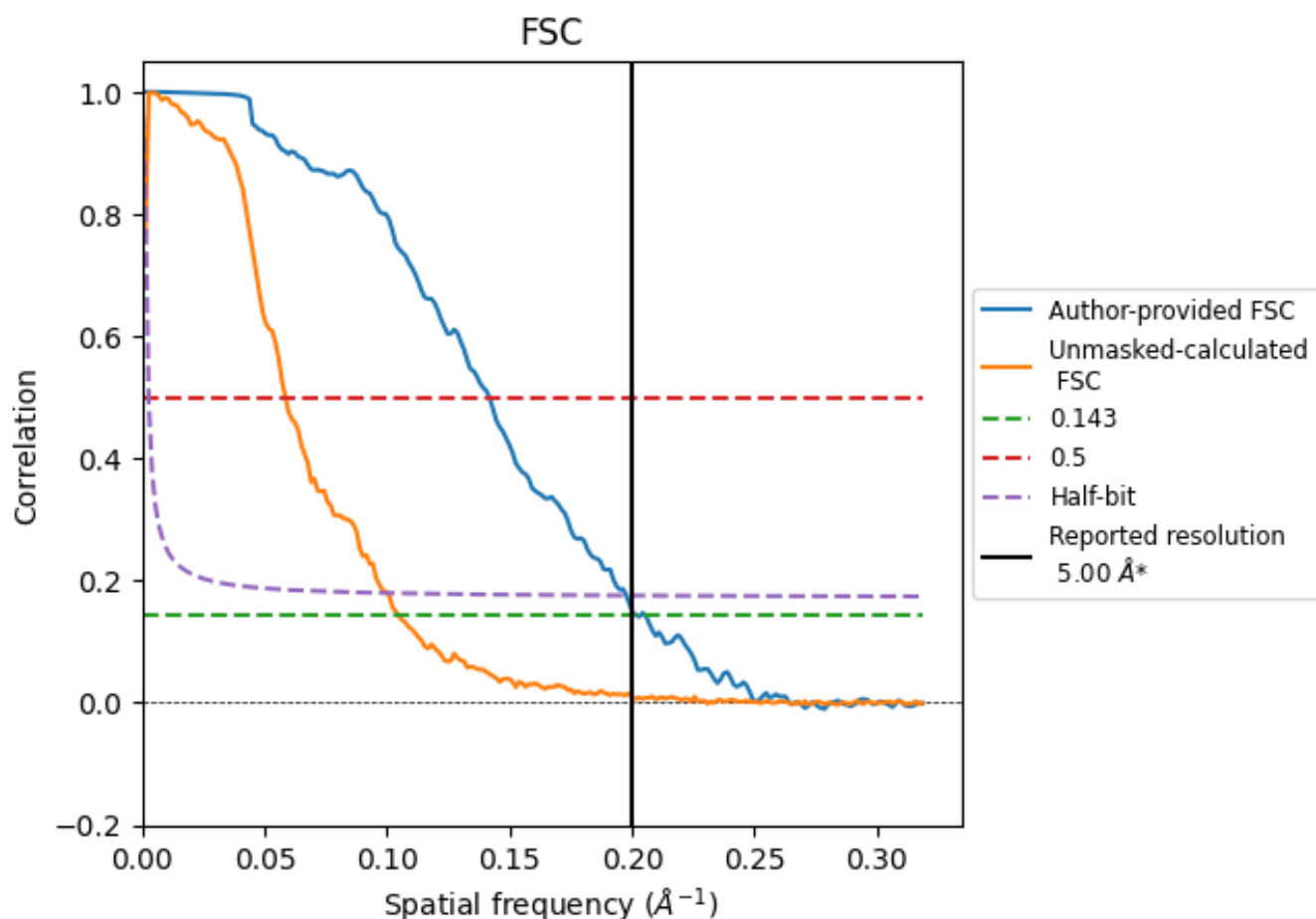


*Reported resolution corresponds to spatial frequency of 0.200 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.200 Å⁻¹

8.2 Resolution estimates [i](#)

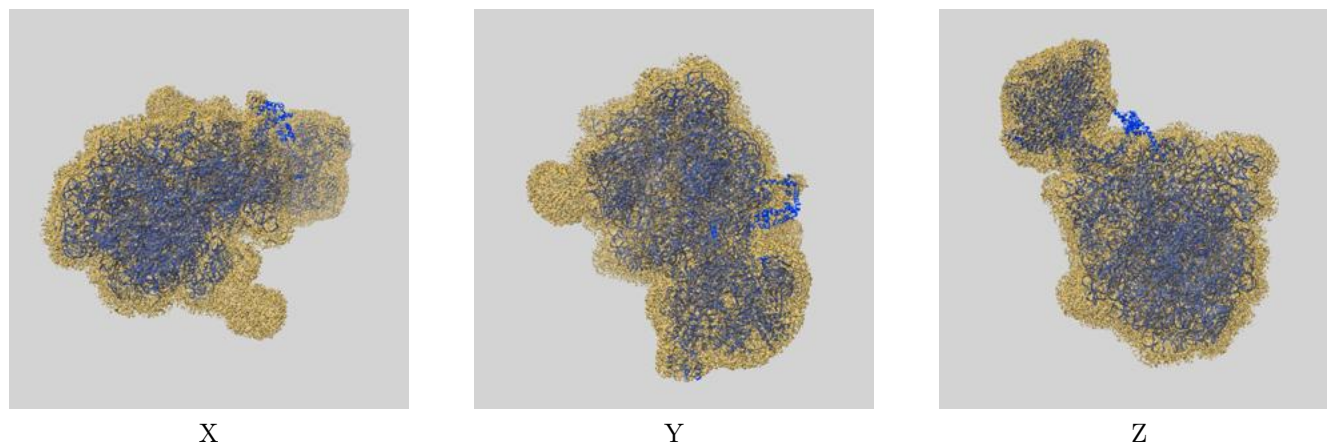
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.00	-	-
Author-provided FSC curve	4.95	7.06	5.06
Unmasked-calculated*	9.57	17.09	666.67

*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 9.57 differs from the reported value 5.0 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-39168 and PDB model 8YDE. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



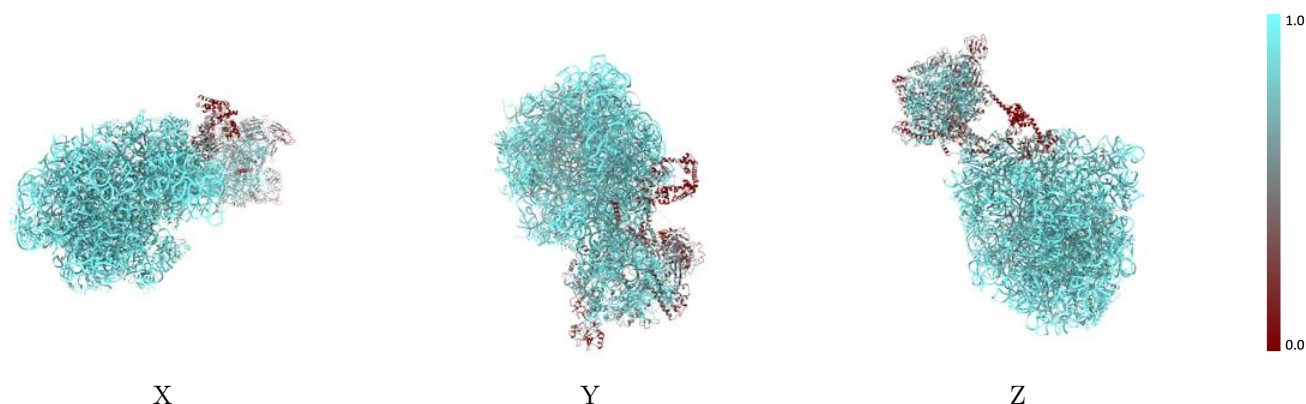
The images above show the 3D surface view of the map at the recommended contour level 0.011 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



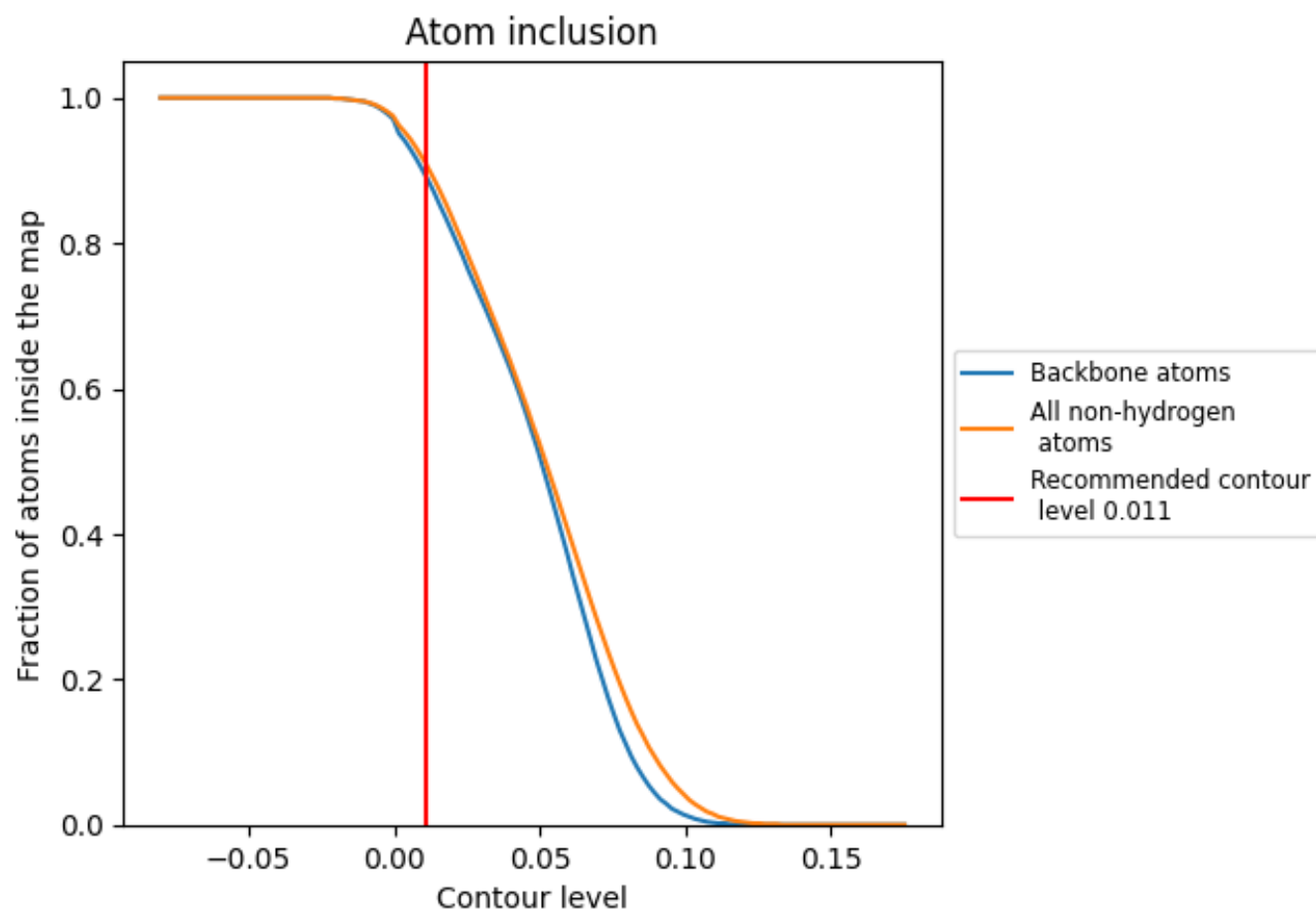
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



At the recommended contour level, 89% of all backbone atoms, 91% 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	 0.9090	 0.2050
1	 0.9900	 0.2870
2	 0.9940	 0.2410
3	 0.9850	 0.2310
4	 0.7830	 0.0350
5	 0.9180	 0.0970
6	 0.9840	 0.2870
7	 0.7850	 0.0720
8	 0.8050	 0.0210
9	 0.7840	 0.0180
A	 0.8920	 0.1370
A1	 0.3580	 0.0100
A2	 0.3940	 0.0010
B	 0.9490	 0.2720
B1	 0.7120	 0.0000
B2	 0.6820	 -0.0070
C	 0.9350	 0.2470
D	 0.9410	 0.3120
E	 0.9450	 0.3080
F	 0.9490	 0.2430
G	 0.9190	 0.1650
H	 0.9080	 0.2190
I	 0.8090	 0.0590
J	 0.9300	 0.2570
K	 0.9350	 0.1620
L	 0.9340	 0.1930
M	 0.9450	 0.2460
N	 0.9640	 0.1760
NA	 0.3260	 0.0200
NG	 0.7490	 0.0140
O	 0.8940	 0.1390
P	 0.9390	 0.2150
Q	 0.8870	 0.1910
R	 0.9360	 0.1580
S	 0.9350	 0.2000



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Chain	Atom inclusion	Q-score
T	 0.9380	 0.2080
U	 0.8260	 0.0950
V	 0.8960	 0.1270
W	 0.9420	 0.1980
W0	 0.4180	 -0.0170
X	 0.9320	 0.1540
Y	 0.9030	 0.1380
Z	 0.8470	 0.1280
b	 0.9520	 0.3240
c	 0.9510	 0.2750
d	 0.9590	 0.2500
e	 0.9510	 0.2170
f	 0.9450	 0.1520
g	 0.9470	 0.1660
h	 0.9580	 0.2930
i	 0.8450	 0.0000
j	 0.9490	 0.2820
k	 0.8920	 0.2490
l	 0.9580	 0.2790
m	 0.9320	 0.2880
n	 0.9490	 0.2520
o	 0.9710	 0.2180
p	 0.9110	 0.1910
q	 0.9580	 0.2990
r	 0.9690	 0.2980
s	 0.9320	 0.2810
t	 0.9210	 0.1940
u	 0.9670	 0.2250
v	 0.9500	 0.2270
w	 0.9460	 0.2820
x	 0.9500	 0.3090
y	 0.9520	 0.1600
z	 0.9660	 0.2910