



Full wwPDB EM Validation Report ⓘ

Aug 18, 2025 – 02:52 PM JST

PDB ID : 8YDF / pdb_00008ydf
EMDB ID : EMD-39169
Title : E.coli transcription translation coupling complex in TTC-B state 1 (subclass 2) containing mRNA with 39-mer spacer, NusG, NusA, fMet-tRNA(iMet), Phe-tRNA(Phe), and viomycin
Authors : Zhang, J.; Lu, G.; Wang, C.; Lin, J.
Deposited on : 2024-02-20
Resolution : 4.60 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

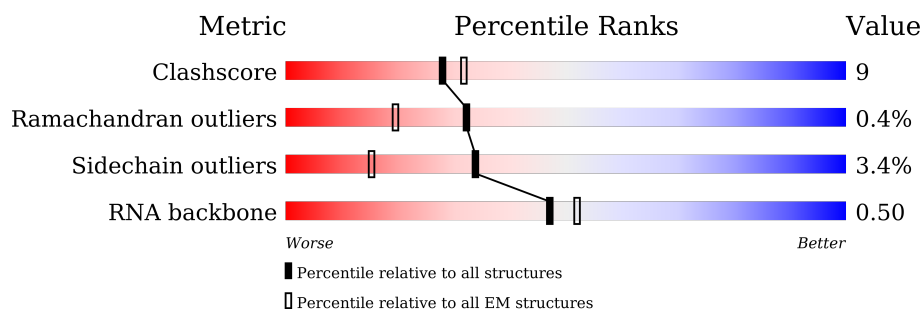
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 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>80%14%6%</div> </div>
2	B	57	<div> <div>79%18%..</div> </div>
3	C	55	<div> <div>80%11%9%</div> </div>
4	D	46	<div> <div>76%22%. .</div> </div>
5	E	65	<div> <div>88%11%. .</div> </div>
6	F	38	<div> <div>68%29%. .</div> </div>
7	G	241	<div> <div>67%22%. 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	

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 178150 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	36	Total	C	N	O	P	0	0
			749	335	107	271	36		

- 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		

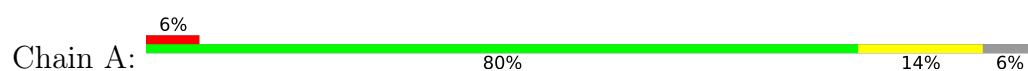
- Molecule 66 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

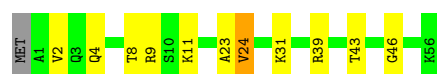
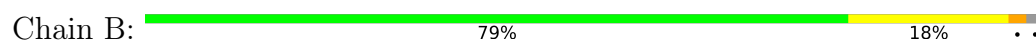
3 Residue-property plots [i](#)

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.

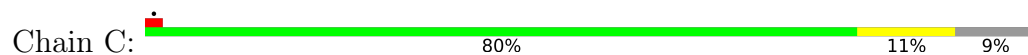
• Molecule 1: 50S ribosomal protein L31



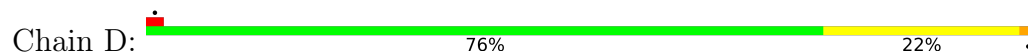
• Molecule 2: 50S ribosomal protein L32



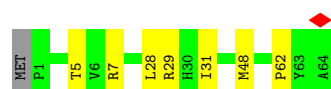
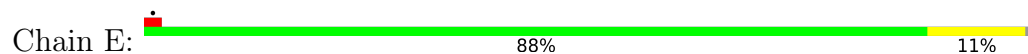
• Molecule 3: 50S ribosomal protein L33



• Molecule 4: 50S ribosomal protein L34

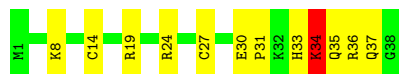


• Molecule 5: 50S ribosomal protein L35



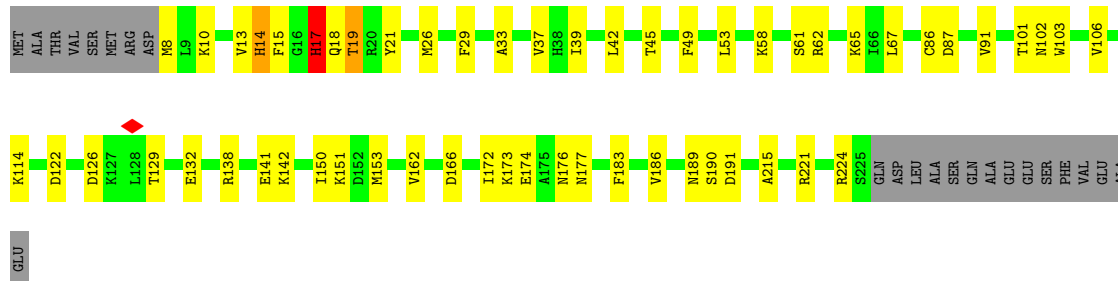
- Molecule 6: 50S ribosomal protein L36

Chain F:  68% 29%



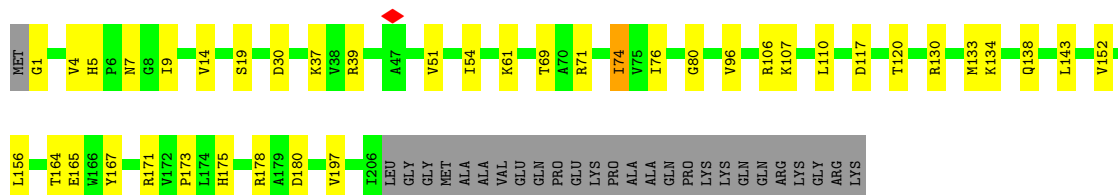
- Molecule 7: 30S ribosomal protein S2

Chain G:  67% 22% 10%



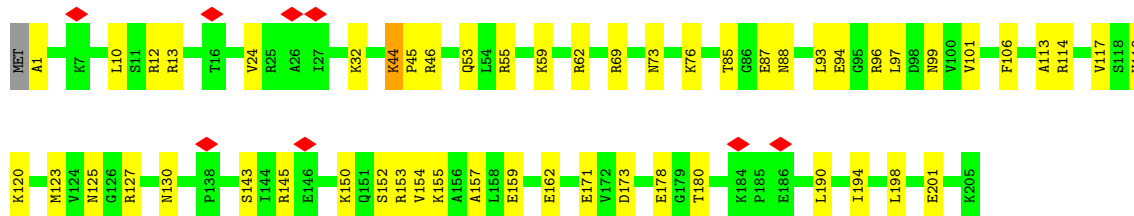
- Molecule 8: 30S ribosomal protein S3

Chain H:  71% 17% 12%




- Molecule 9: 30S ribosomal protein S4

Chain I:  74% 25%



- Molecule 10: 30S ribosomal protein S5

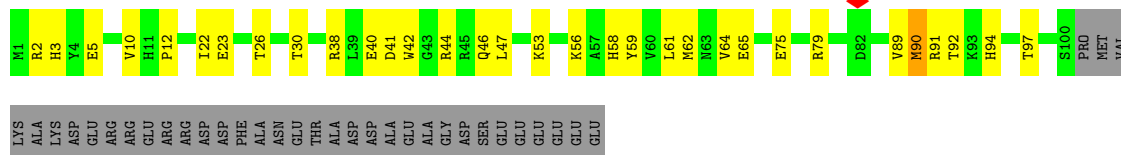
Chain J:  77% 17% 6%



Q165
LYS

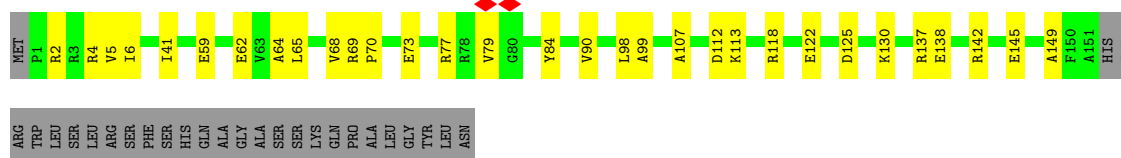
- Molecule 11: 30S ribosomal protein S6, fully modified isoform

Chain K:  50% 23% 26%




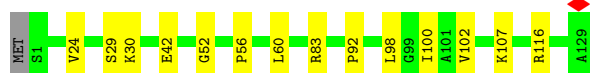
- Molecule 12: 30S ribosomal protein S7

Chain L:  67% 17% 16%



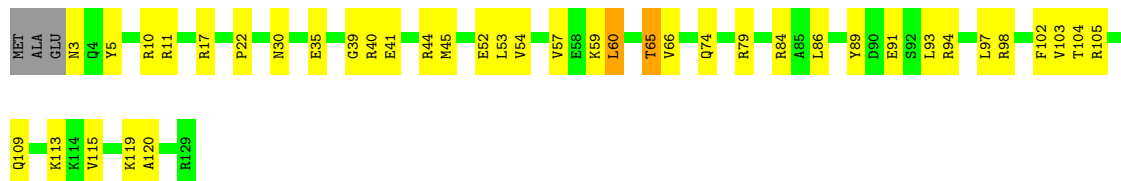
- Molecule 13: 30S ribosomal protein S8

Chain M:  88% 11%



- Molecule 14: 30S ribosomal protein S9

Chain N:  67% 29%



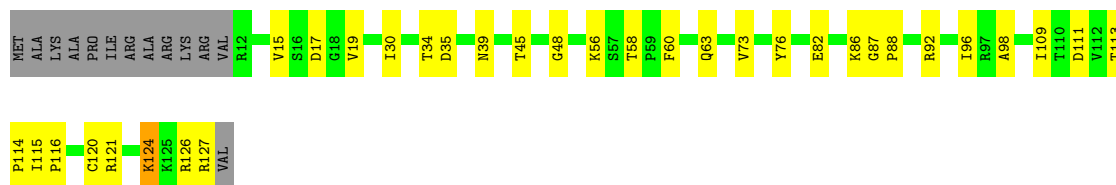
- Molecule 15: 30S ribosomal protein S10

Chain O:  72% 18% 5% 5%



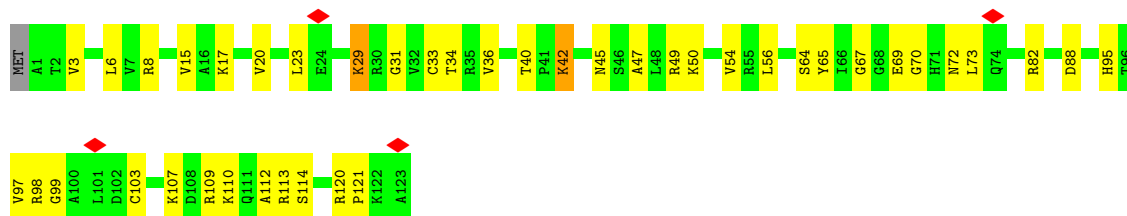
- Molecule 16: 30S ribosomal protein S11

Chain P:  64% 25% 10%



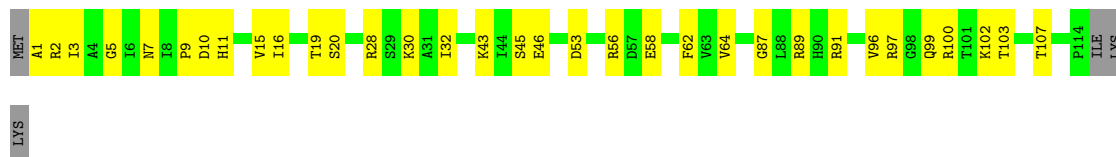
- Molecule 17: 30S ribosomal protein S12

Chain Q:  65% 32% 2%




- Molecule 18: 30S ribosomal protein S13

Chain R:  69% 28% 2%




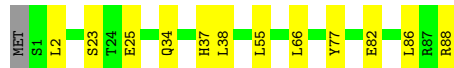
- Molecule 19: 30S ribosomal protein S14

Chain S:  84% 15% 1%




- Molecule 20: 30S ribosomal protein S15

Chain T:  85% 13% 2%




- Molecule 21: 30S ribosomal protein S16

Chain U:  6% 76% 18%



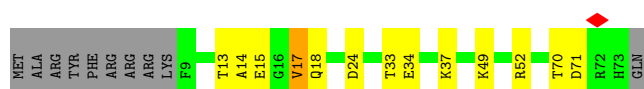
- Molecule 22: 30S ribosomal protein S17

Chain V: 



- Molecule 23: 30S ribosomal protein S18

Chain W: 




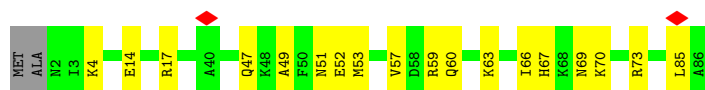
- Molecule 24: 30S ribosomal protein S19

Chain X: 



- Molecule 25: 30S ribosomal protein S20

Chain Y: 




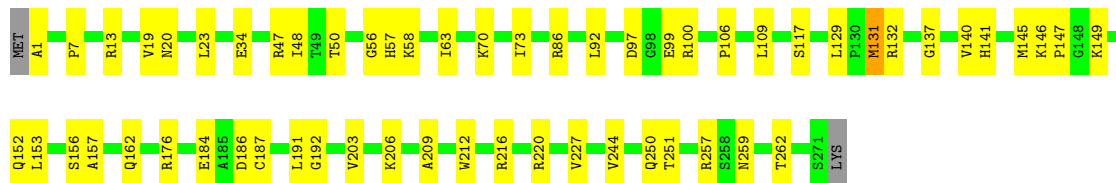
- Molecule 26: 30S ribosomal protein S21

Chain Z: 




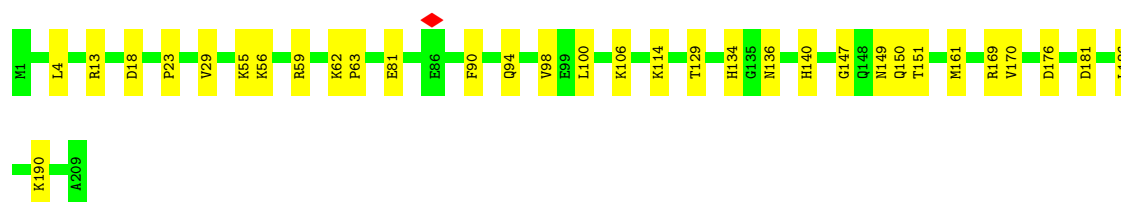
- Molecule 27: 50S ribosomal protein L2

Chain b: 



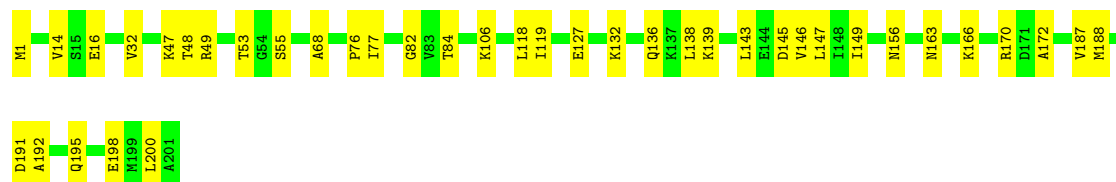
- Molecule 28: 50S ribosomal protein L3

Chain c: 



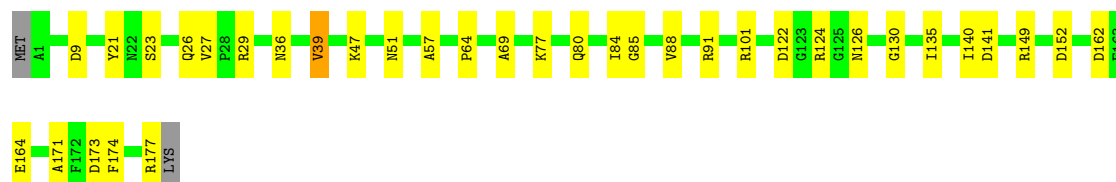
- Molecule 29: 50S ribosomal protein L4

Chain d: 81% 19%



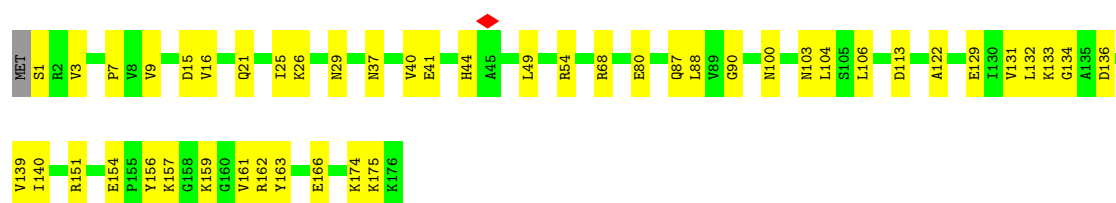
- Molecule 30: 50S ribosomal protein L5

Chain e: 79% 19% ..



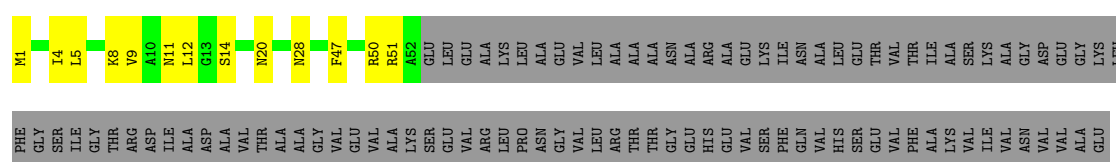
- Molecule 31: 50S ribosomal protein L6

Chain f: 73% 26% .

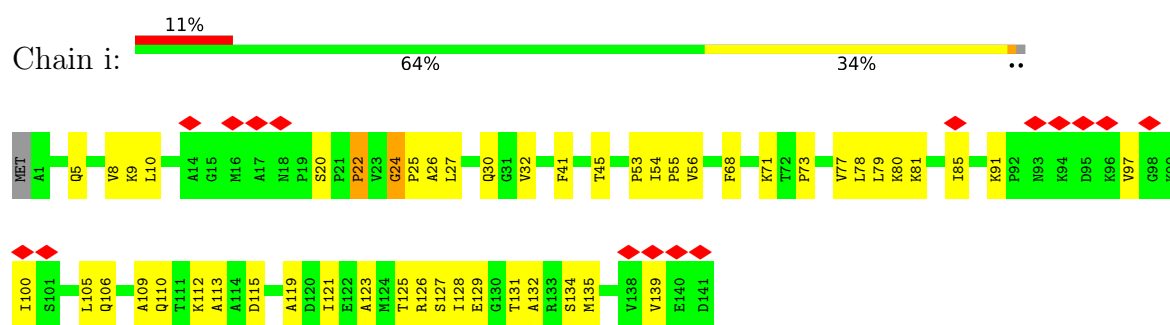


- Molecule 32: 50S ribosomal protein L9

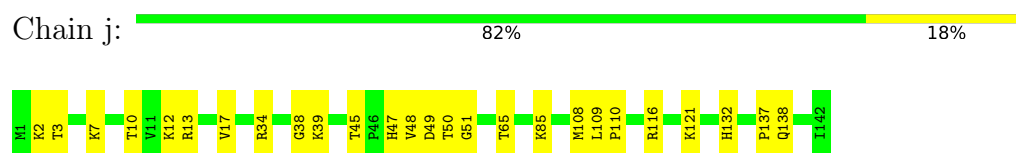
Chain g: 26% 9% 65%



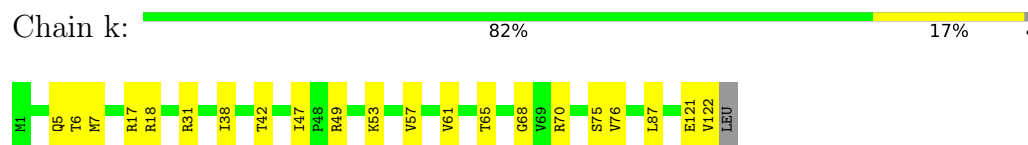
- Molecule 33: 50S ribosomal protein L11



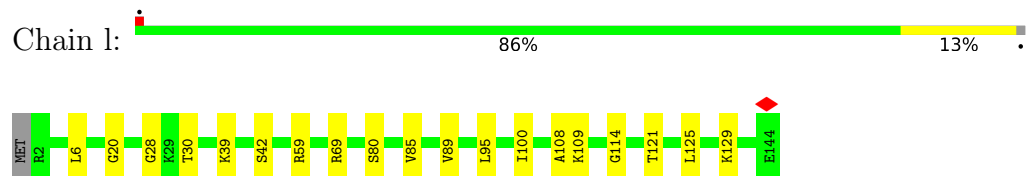
- Molecule 34: 50S ribosomal protein L13



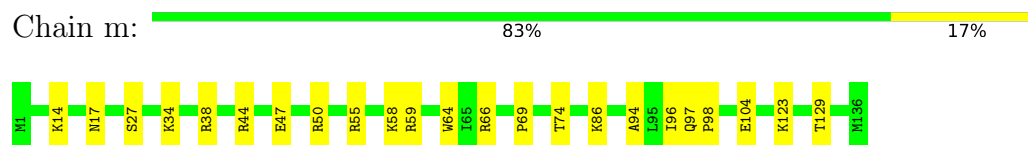
- Molecule 35: 50S ribosomal protein L14



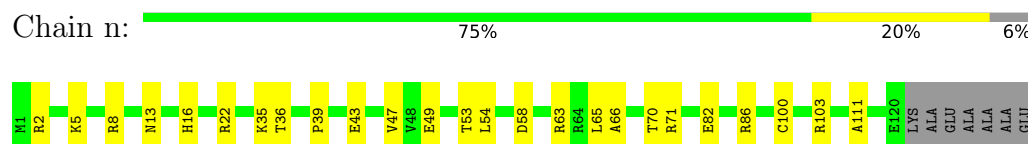
- Molecule 36: 50S ribosomal protein L15



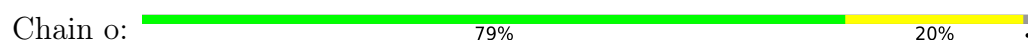
- Molecule 37: 50S ribosomal protein L16



- Molecule 38: 50S ribosomal protein L17



- Molecule 39: 50S ribosomal protein L18





- Molecule 40: 50S ribosomal protein L19

Chain p: 83% 16%



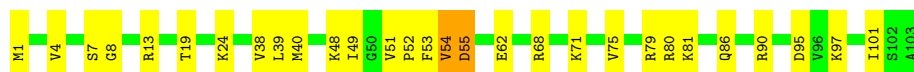
- Molecule 41: 50S ribosomal protein L20

Chain q: 84% 14%



- Molecule 42: 50S ribosomal protein L21

Chain r: 72% 26%



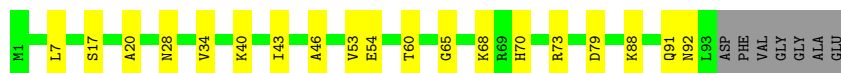
- Molecule 43: 50S ribosomal protein L22

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%



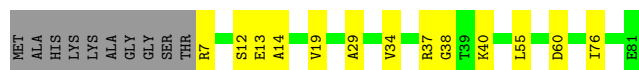
- Molecule 46: 50S ribosomal protein L25

Chain v: 85% 15%



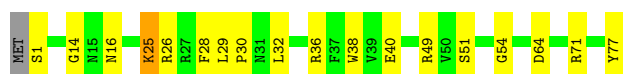
- Molecule 47: 50S ribosomal protein L27

Chain w: 73% 15% 12%



- Molecule 48: 50S ribosomal protein L28

Chain x: 76% 22% ..



- Molecule 49: 50S ribosomal protein L29

Chain y: 76% 24%



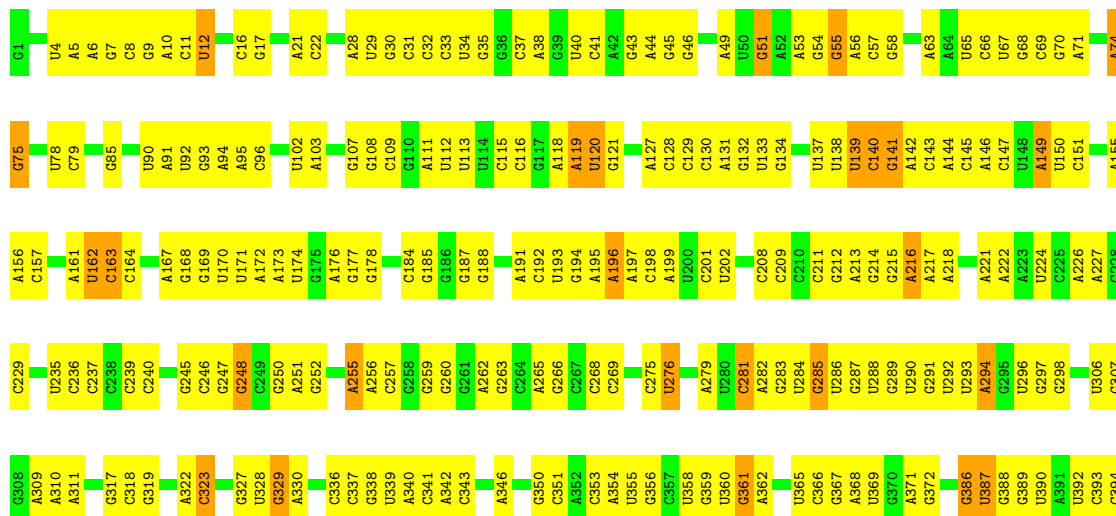
- Molecule 50: 50S ribosomal protein L30

Chain z: 76% 22% .



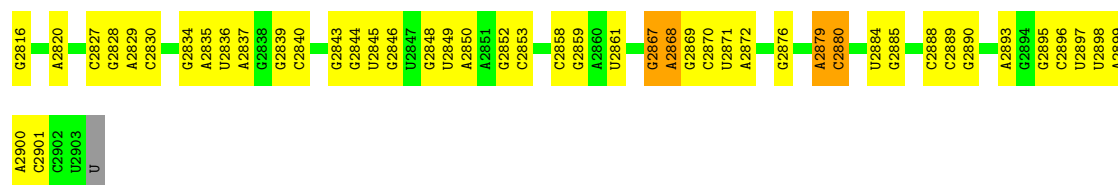
- Molecule 51: 23S rRNA

Chain 1: 43% 51% 6%



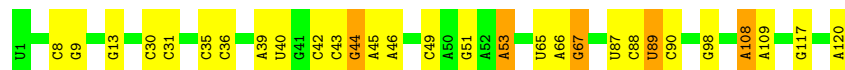


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G2742	A2577	G2490	U2403	G2316	G2238	A2171	C2103	A2014	A1918	G1846	A1762	U1680	A1583
U2743	G2578	U2491	C2402	U2321	G2239	A2172	C2104	U2016	A1919	A1847	G1763	G1681	G1588
G2744	G2579	U2492	U2404	U2322	G2240	C2174	U2106	G2020	G1921	A1848	U1765	G1695	U1589
G2747	G2581	C2496	G2405	G2325	A2241	U2180	G2107	A2020	G1922	U1851	G1766	G1696	A1590
U2748	G2582	A2497	U2406	C2326	U2243	U2181	G2110	C2021	U1923	U1852	U1772	G1697	A1591
G2749	G2583	C2498	A2407	A2327	A2247	U2182	G2111	U2022	C1924	A1853	G1767	A1698	C1592
U2750	U2584	U2499	U2411	A2328	C2248	A2183	G2112	G2024	A1927	A1854	U1773	G1699	U1593
G2751	U2585	G2502	A2412	G2330	U2249	U2184	G2113	G2025	A1928	U1855	G1702	G1702	U1594
U2752	G2593	G2505	C2420	A2333	G2250	A2185	G2114	U2026	G1929	U1856	C1774	G1703	A1596
U2754	U2594	U2506	G2421	U2334	U2257	G2186	G2115	G2027	U1931	G1857	U1775	G1710	A1597
C2755	G2595	C2507	C2422	A2335	U2258	U2187	U2118	A2030	G1935	A1858	G1776	A1711	A1598
U2756	A2598	C2507	U2423	A2336	U2259	U2188	A2119	A2031	G1936	G1863	A1780	G1711	A1599
A2758	G2599	G2510	C2424	G2337	C2260	U2189	U2122	G2032	A1937	U1864	U1781	G1715	C1600
G2759	A2600	U2511	A2425	C2338	A2267	G2190	G2123	A2033	U1938	U1865	U1782	U1716	U1602
C2760	C2601	G2511	U2426	C2339	A2268	A2191	G2124	U2034	U1939	A1866	A1783	A1717	A1603
A2761	A2602	A2516	G2427	A2340	A2269	U2192	G2125	G2035	G1942	G1867	A1784	G1718	C1604
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G2763	C2610	A2518	U2430	A2346	G2272	U2194	G2127	A2037	U1943	G1869	A1786	U1720	C1606
A2765	G2611	G2525	U2431	U2347	C2275	U2195	G2128	G2038	G1948	C1870	U1787	G1721	C1607
U2768	U2612	G2526	C2432	G2348	A2278	U2197	C2129	U2039	G1948	A1871	C1788	A1722	A1608
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C2771	U2615	G2529	A2435	G2351	G2280	C2200	U2132	G2048	A1953	A1794	U1726	A1616	C1616
A2772	C2616	A2530	G2436	A2352	G2281	U2201	G2133	G2049	G1954	C1795	C1727	C1625	C1625
U2773	U2617	G2533	G2437	G2360	G2282	U2202	A2134	C2050	U1955	U1796	C1728	U1729	C1626
U2774	G2618	U2534	C2440	G2361	C2283	U2203	U2137	A2051	U1963	U1797	C1730	U1730	A1634
U2775	C2619	A2534	U2441	G2362	A2284	G2204	G2138	A2052	U1963	G1799	G1731	G1731	A1634
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U2777	C2621	G2545	U2446	C2364	A2286	C2208	G2144	A2054	U1965	U1883	G1733	G1733	C1643
A2778	G2622	U2546	G2447	G2365	G2287	U2210	G2145	C2055	A1966	A1884	G1734	G1734	C1643
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U2785	C2636	G2557	C2462	G2379	A2297	G2217	U2151	U2074	A1978	C1894	U1741	U1741	G1651
U2786	U2637	U2561	G2463	C2380	A2298	G2218	G2152	U2085	G1983	C1816	G1742	G1742	U1662
U2787	G2638	U2562	G2464	A2381	U2299	G2219	C2153	U2086	G1984	G1817	G1743	G1743	G1663
U2788	G2639	U2563	C2467	G2382	U2300	G2220	U2155	C2091	G1985	U1818	A1744	A1744	G1666
U2789	A2642	A2564	U2468	G2383	U2301	G2221	G2156	G2092	C1986	A1819	A1745	A1745	G1667
U2790	G2643	A2565	A2469	C2384	G2302	G2222	G2157	U2093	G1987	U1820	A1746	U1747	G1667
U2791	G2644	A2566	U2470	A2385	G2303	G2223	G2158	C2094	G1988	A1821	C1748	C1748	A1668
U2792	G2645	G2567	G2471	A2386	G2304	A2225	G2159	U2095	U1991	C1822	A1749	A1749	C1669
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U2794	G2647	G2569	U2472	G2388	C2306	A2227	C2161	U2097	U1993	U1827	U1751	U1751	U1671
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U2796	G2649	U2571	U2474	G2390	A2309	G2231	A2163	A2097	C1987	U1829	A1754	A1754	G1673
U2797	A2650	A2572	A2482	G2391	A2310	U2233	C2164	U2098	A1998	A1912	G1674	G1674	C1675
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U2799	G2652	G2574	G2484	U2393	U2312	G2235	U2166	G2100	G1999	C1832	U1758	U1758	A1677
U2800	C2653	C2575	G2485	C2394	U2313	G2236	U2167	A2101	G2012	C1833	U1678	U1678	A1678
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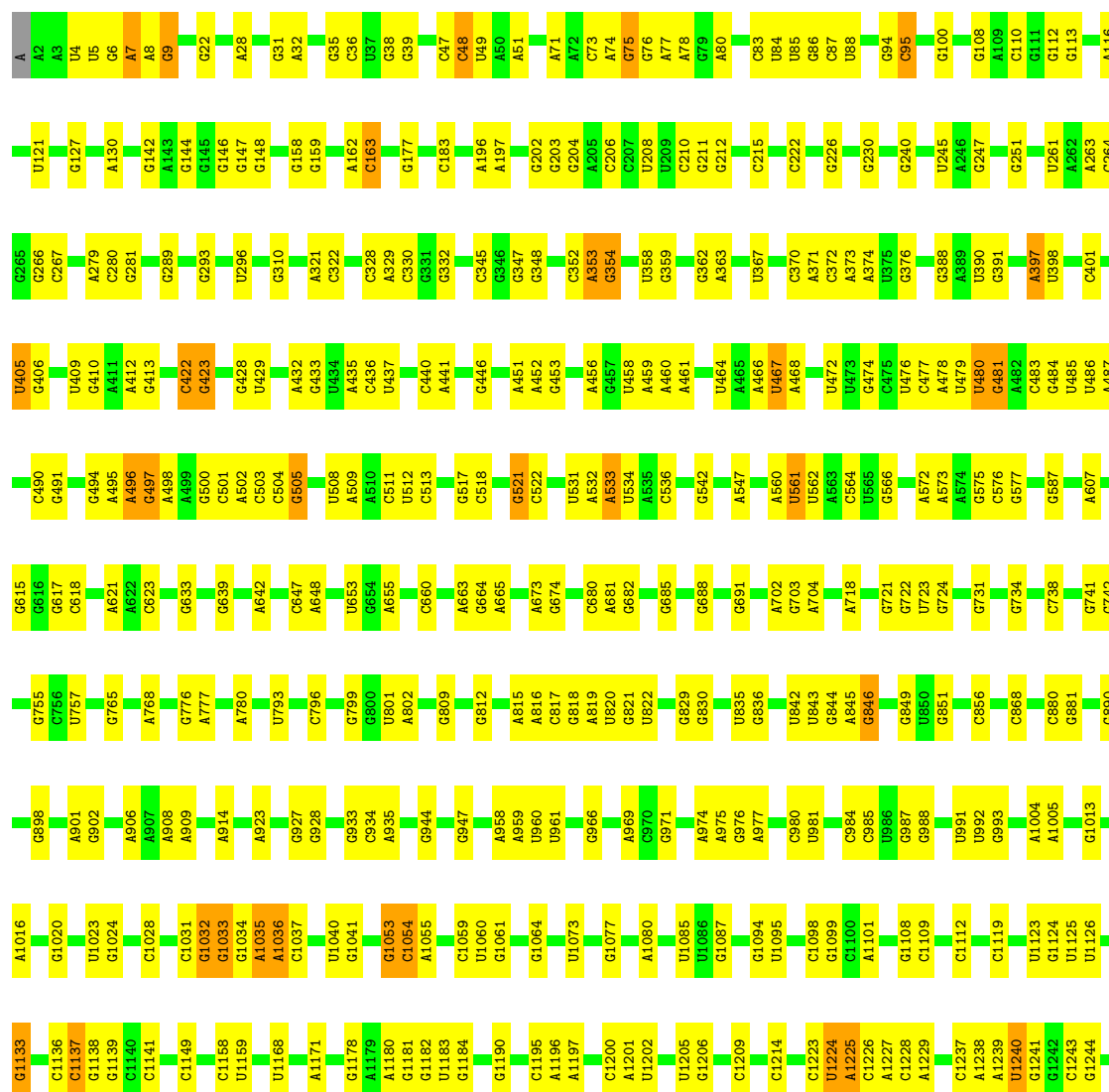
• Molecule 52: 5S rRNA

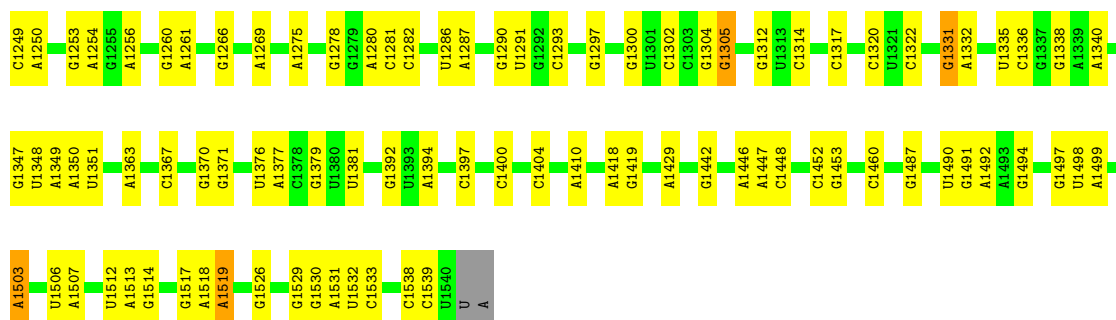
Chain 2: 76% 20%



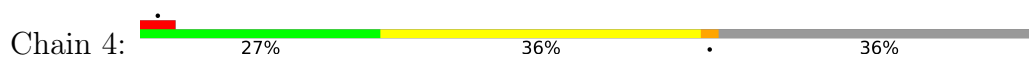
• Molecule 53: 16S rRNA

Chain 3: 69% 29%





• Molecule 54: mRNA



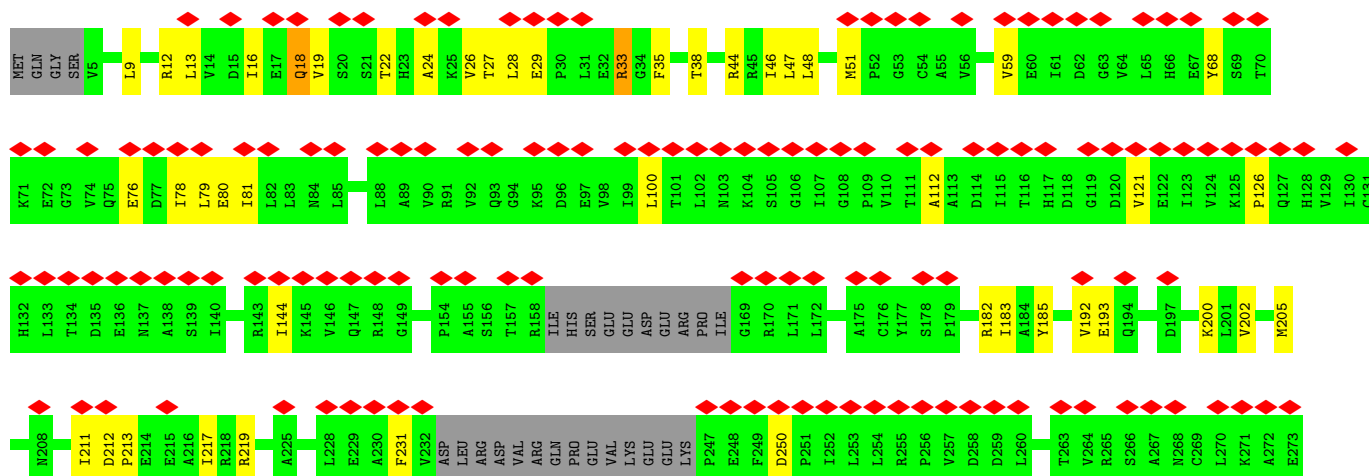
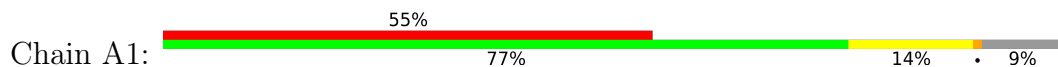
• Molecule 55: template DNA strand

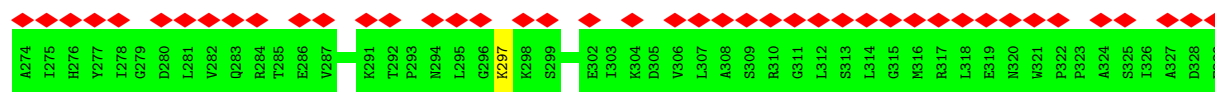


• Molecule 56: non-template DNA strand

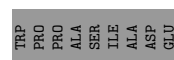
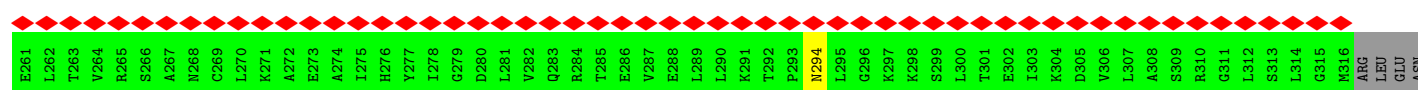
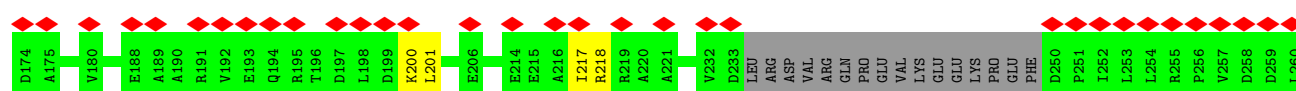
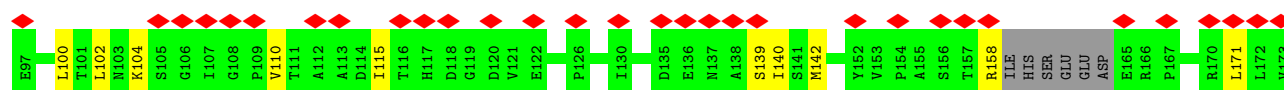
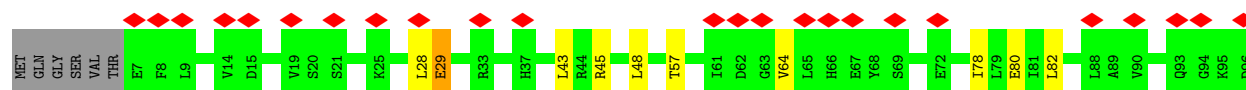
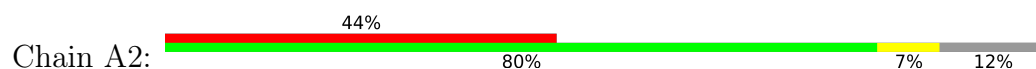


• Molecule 57: DNA-directed RNA polymerase subunit alpha

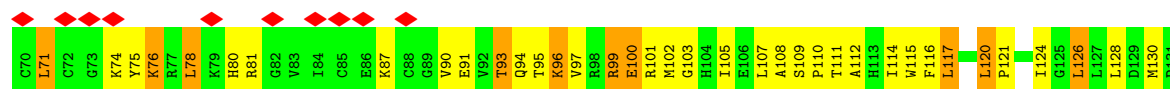
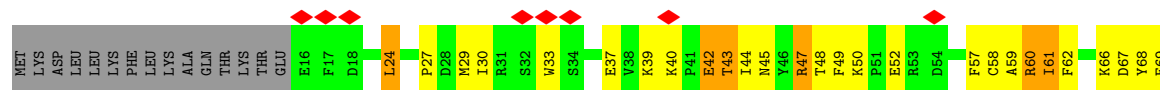


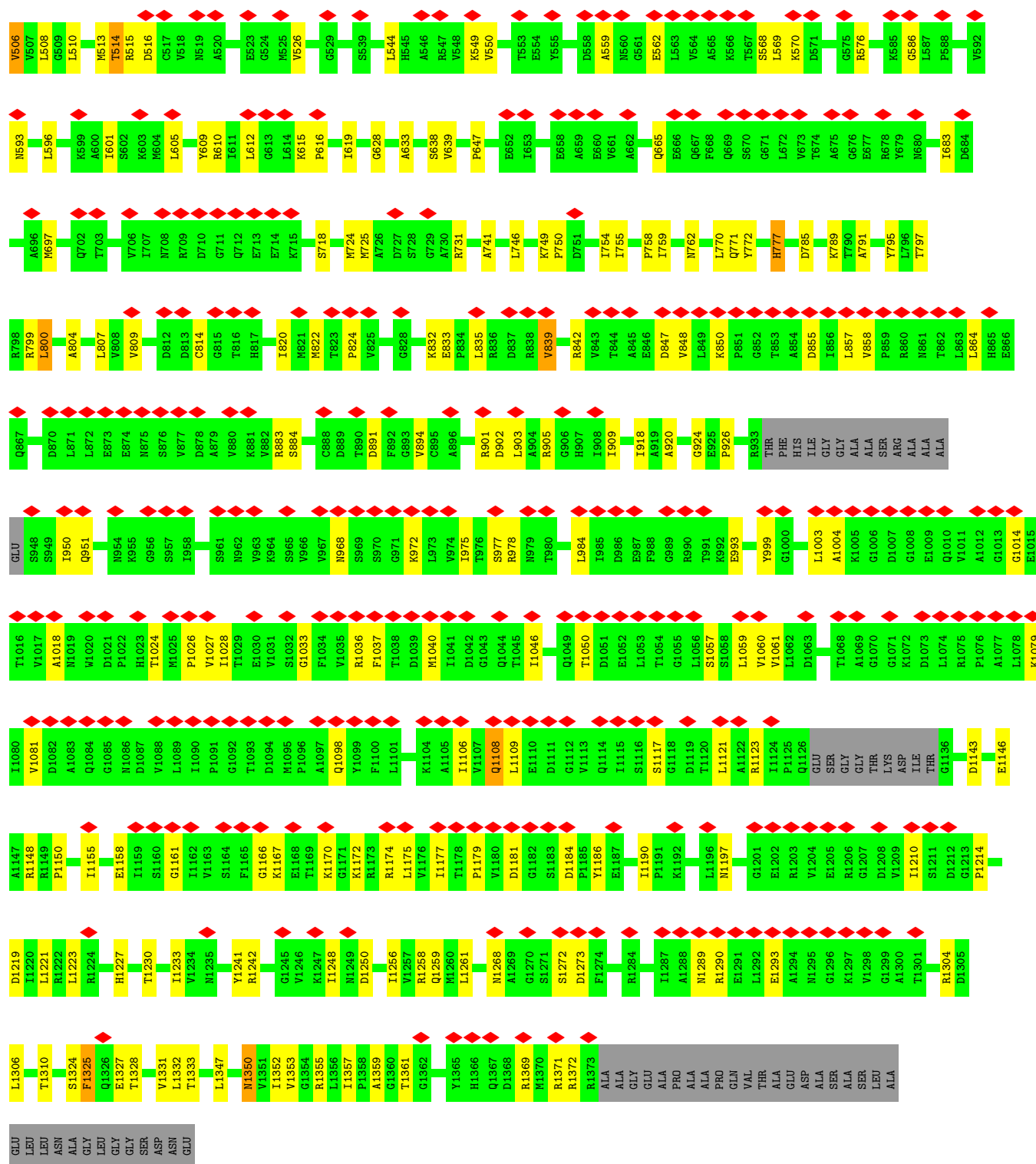


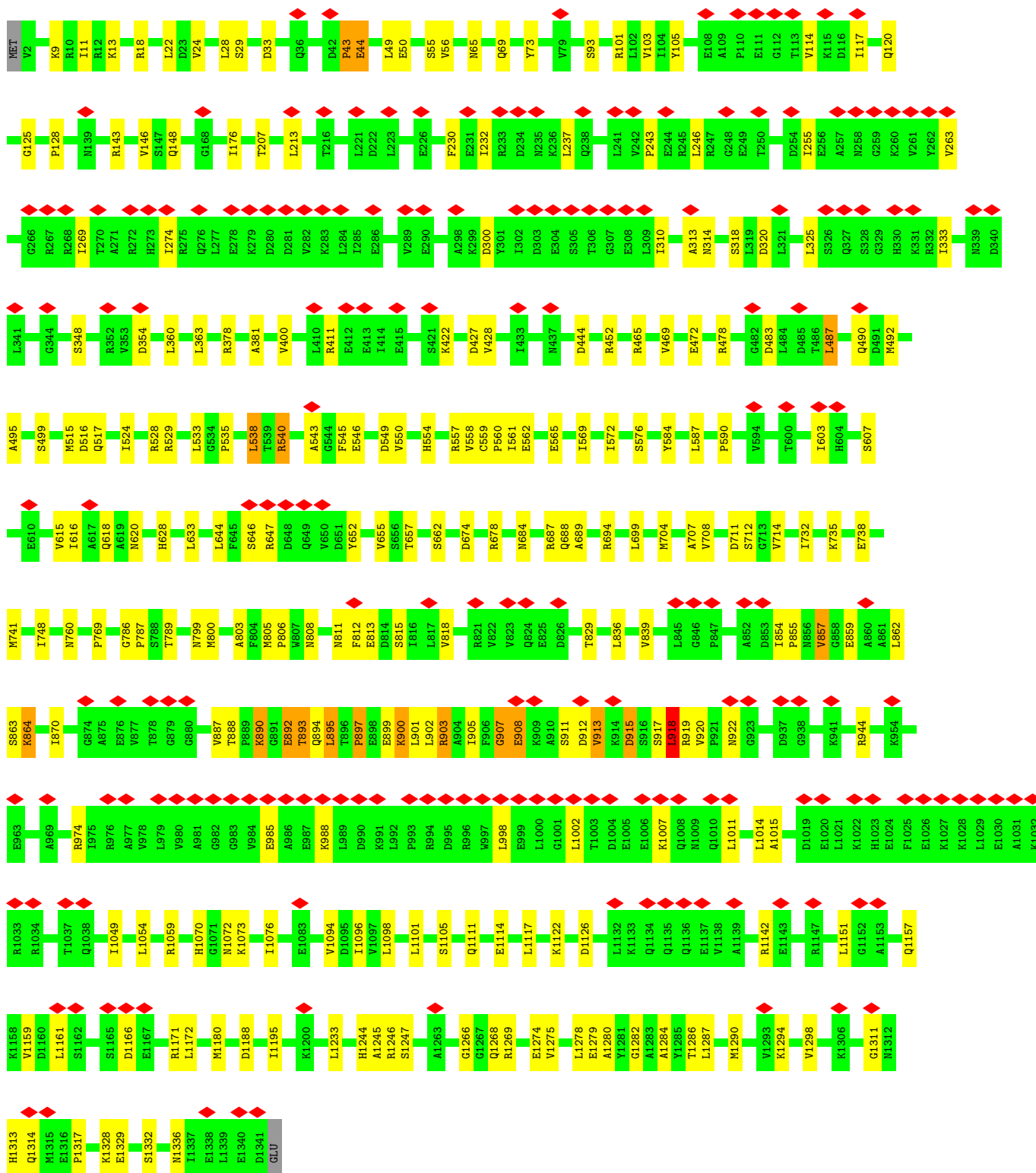
• Molecule 57: DNA-directed RNA polymerase subunit alpha

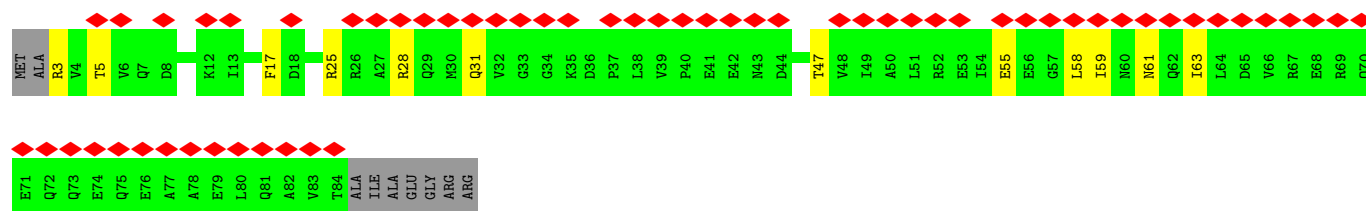


• Molecule 58: DNA-directed RNA polymerase subunit beta'





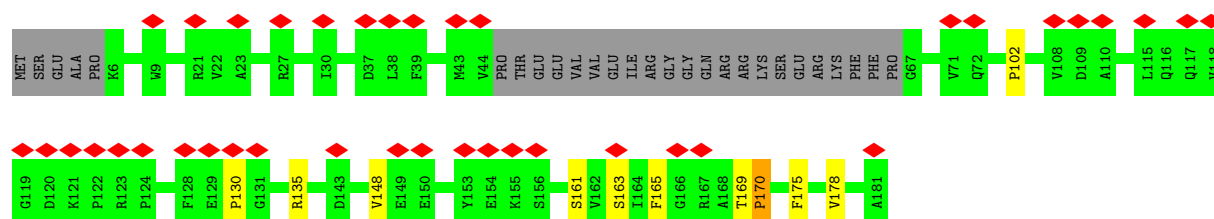
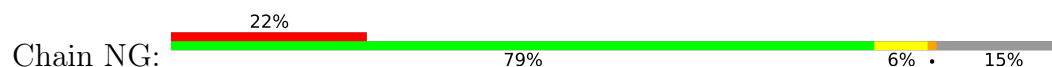




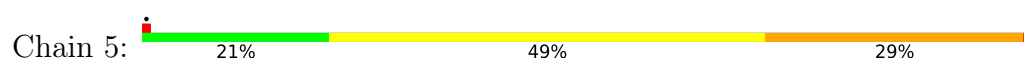
• Molecule 61: Transcription termination/antitermination protein NusA

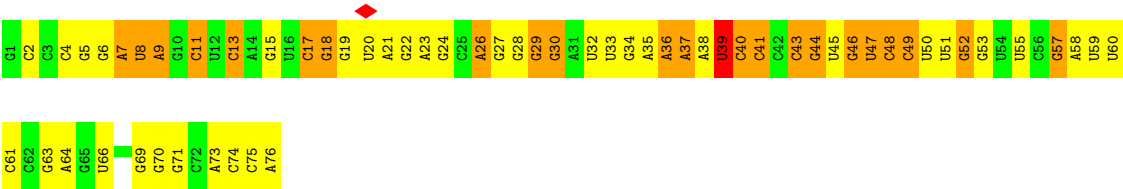


• Molecule 62: Transcription termination/antitermination protein NusG

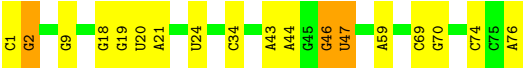


• Molecule 63: tRNA(Phe)

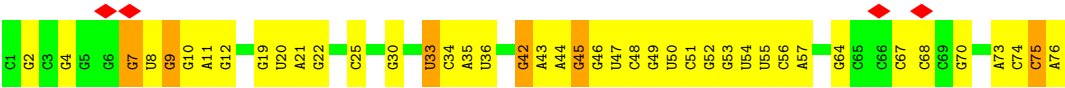




• Molecule 64: tRNA(fMet)



• Molecule 64: tRNA(fMet)



• Molecule 65: Viomycin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32000	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	0.179	Depositor
Minimum map value	-0.082	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.012	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: DPP, UAL, MG, 5OH, 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	0.41	0/450	0.60	2/599 (0.3%)
3	C	0.28	0/416	0.52	0/554
4	D	0.47	0/380	0.76	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	0.31	0/1195	0.66	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	0.85	2/1300 (0.2%)
18	R	0.33	0/892	0.72	2/1193 (0.2%)
19	S	0.33	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	0.54	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	0.42	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	0.63	1/1278 (0.1%)
42	r	0.44	0/829	0.69	0/1107
43	s	0.43	0/864	0.58	0/1156
44	t	0.33	0/744	0.52	0/994
45	u	0.46	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	0.63	0/677
50	z	0.41	0/453	0.53	0/605
51	1	0.51	0/69796	0.62	21/108888 (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	0/830	0.65	0/1285
55	8	0.56	0/599	0.71	1/919 (0.1%)
56	9	0.49	0/468	0.53	0/719
57	A1	0.55	0/2106	0.82	0/2868
57	A2	0.49	0/2048	0.76	0/2786
58	B1	0.57	5/10510 (0.0%)	0.75	8/14196 (0.1%)
59	B2	0.47	0/10714	0.68	2/14459 (0.0%)
60	W0	0.30	0/652	0.61	0/879
61	NA	0.78	0/2431	1.21	0/3385
62	NG	1.12	0/756	1.07	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	3.17	2/11 (18.2%)	0.75	0/13
All	All	0.48	7/191598 (0.0%)	0.62	68/282891 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

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

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	h	3	SER	CA-C	-6.73	1.38	1.52
65	h	4	SER	CA-C	-6.14	1.40	1.52
58	B1	1350	ASN	CG-ND2	-5.25	1.22	1.33
58	B1	1108	GLN	CD-OE1	5.17	1.33	1.23
58	B1	424	ASN	CG-ND2	-5.09	1.22	1.33
58	B1	665	GLN	CD-OE1	5.05	1.33	1.23
58	B1	1268	ASN	CG-OD1	5.02	1.33	1.23

All (68) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	P	73	VAL	N-CA-C	-9.06	104.50	113.20
41	q	33	VAL	N-CA-C	-8.80	104.73	112.12
12	L	64	ALA	N-CA-C	-7.67	105.09	114.75
51	1	1130	U	C2'-C3'-O3'	7.58	120.86	109.50
64	7	33	U	C2'-C3'-O3'	7.22	120.33	109.50
51	1	2326	C	C2'-C3'-O3'	7.22	120.33	109.50
58	B1	450	HIS	CB-CG-CD2	-6.57	122.65	131.20
51	1	761	A	C4'-C3'-O3'	-6.53	103.21	113.00
58	B1	777	HIS	CB-CG-CD2	-6.37	122.92	131.20
58	B1	61	ILE	CA-C-N	-6.37	113.99	121.64
58	B1	61	ILE	C-N-CA	-6.37	113.99	121.64
28	c	147	GLY	CA-C-N	-6.09	115.19	122.44
28	c	147	GLY	C-N-CA	-6.09	115.19	122.44
59	B2	907	GLY	CA-C-O	-5.95	115.81	121.87
63	5	39	U	C3'-C2'-O2'	5.88	119.51	110.70
58	B1	450	HIS	CB-CG-ND1	5.71	131.26	122.70
51	1	2060	A	C2'-C3'-O3'	5.69	118.03	109.50
26	Z	35	GLU	CA-C-N	5.65	132.34	121.54
26	Z	35	GLU	C-N-CA	5.65	132.34	121.54
38	n	47	VAL	N-CA-C	-5.65	107.37	112.12
15	O	57	VAL	CA-C-N	5.58	132.20	121.54
15	O	57	VAL	C-N-CA	5.58	132.20	121.54
10	J	155	LYS	N-CA-C	-5.54	107.77	114.75
58	B1	777	HIS	CB-CG-ND1	5.48	130.92	122.70
51	1	1451	C	N1-C1'-C2'	5.48	120.22	112.00
51	1	960	A	N9-C1'-C2'	5.46	120.18	112.00
51	1	1905	C	C4'-C3'-O3'	-5.45	104.83	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	1	1020	A	C2'-C3'-O3'	5.43	117.64	109.50
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	1696	G	N9-C1'-C2'	5.40	120.10	112.00
55	8	7	DC	C2'-C3'-O3'	-5.35	103.48	111.50
33	i	24	GLY	N-CA-C	5.34	123.23	112.34
51	1	1782	U	N1-C1'-C2'	5.32	119.98	112.00
51	1	2428	G	N9-C1'-C2'	5.32	119.98	112.00
30	e	141	ASP	CA-C-N	5.29	131.65	121.54
30	e	141	ASP	C-N-CA	5.29	131.65	121.54
51	1	2055	C	N1-C1'-C2'	5.26	119.90	112.00
12	L	5	VAL	CA-C-N	5.25	127.73	120.49
12	L	5	VAL	C-N-CA	5.25	127.73	120.49
51	1	2576	G	N9-C1'-C2'	5.24	119.86	112.00
63	5	57	G	C4'-C3'-O3'	5.24	117.26	109.40
34	j	110	PRO	N-CA-C	5.24	120.73	113.98
58	B1	27	PRO	N-CA-C	-5.23	106.23	113.81
63	5	39	U	C4'-C3'-O3'	5.22	120.83	113.00
51	1	1565	C	N1-C1'-C2'	5.21	119.81	112.00
51	1	1328	A	N9-C1'-C2'	5.20	119.81	112.00
51	1	980	A	N9-C1'-C2'	5.18	119.78	112.00
21	U	78	VAL	CA-C-N	5.16	129.60	121.56
21	U	78	VAL	C-N-CA	5.16	129.60	121.56
59	B2	897	PRO	N-CA-C	-5.15	106.07	113.75
51	1	2430	A	N9-C1'-C2'	5.15	119.73	112.00
58	B1	61	ILE	CA-C-O	-5.10	115.65	120.95
10	J	87	VAL	N-CA-C	5.09	115.97	109.30
23	W	14	ALA	N-CA-C	-5.09	106.17	112.93
51	1	2777	G	N9-C1'-C2'	5.07	119.60	112.00
51	1	1087	G	N9-C1'-C2'	5.06	119.60	112.00
33	i	71	LYS	CA-C-N	5.05	134.13	121.80
33	i	71	LYS	C-N-CA	5.05	134.13	121.80
18	R	3	ILE	CA-C-N	5.05	131.19	121.54
18	R	3	ILE	C-N-CA	5.05	131.19	121.54
48	x	25	LYS	N-CA-C	5.04	121.54	110.80
17	Q	42	LYS	CA-C-N	5.04	129.53	121.62
17	Q	42	LYS	C-N-CA	5.04	129.53	121.62
51	1	1672	A	N9-C1'-C2'	5.03	119.55	112.00
51	1	972	A	N9-C1'-C2'	5.01	119.52	112.00
2	B	24	VAL	CA-C-N	5.00	131.09	121.54
2	B	24	VAL	C-N-CA	5.00	131.09	121.54

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
59	B2	903	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	522	0	524	8	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	4	0
6	F	302	0	343	6	0
7	G	1704	0	1732	34	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	18	0
12	L	1181	0	1240	19	0
13	M	979	0	1034	9	0
14	N	1022	0	1070	23	0
15	O	786	0	828	15	0
16	P	869	0	878	22	0
17	Q	955	0	1019	30	0
18	R	883	0	944	19	0
19	S	805	0	847	10	0
20	T	714	0	737	5	0
21	U	649	0	666	15	0
22	V	648	0	691	8	0
23	W	535	0	552	7	0
24	X	637	0	665	7	0
25	Y	665	0	714	11	0
26	Z	544	0	579	13	0
27	b	2082	0	2157	46	0
28	c	1565	0	1616	28	0
29	d	1552	0	1619	28	0
30	e	1410	0	1447	22	0
31	f	1323	0	1374	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	16	0
37	m	1074	0	1157	13	0
38	n	960	0	1000	18	0
39	o	892	0	923	16	0
40	p	917	0	965	17	0
41	q	947	0	1022	9	0
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	9	0
48	x	625	0	655	11	0
49	y	509	0	543	12	0
50	z	449	0	491	9	0
51	1	62317	0	31346	1456	0
52	2	2568	0	1303	15	0
53	3	33012	0	16618	185	0
54	4	749	0	374	6	0
55	8	539	0	305	29	0
56	9	417	0	224	1	0
57	A1	2088	0	1895	25	0
57	A2	2029	0	1864	18	0
58	B1	10353	0	10548	321	0
59	B2	10546	0	10550	172	0
60	W0	650	0	658	10	0
61	NA	2432	0	1171	6	0
62	NG	758	0	334	10	0
63	5	1622	0	821	27	0
64	6	1640	0	837	7	0
64	7	1640	0	837	19	0
65	h	48	0	40	8	0
66	B1	1	0	0	0	0
All	All	178150	0	126642	2807	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 (2807) 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	1.06
51:1:1666:G:H2'	51:1:1667:G:H5'	1.41	1.03
51:1:2713:U:H3'	51:1:2714:G:H5'	1.41	1.03
51:1:1672:A:C2	51:1:2582:G:H5'	1.95	1.02
58:B1:750:PRO:HB3	59:B2:549:ASP:OD2	1.60	1.01
58:B1:111:THR:HG23	58:B1:300:GLN:CD	1.86	1.01
51:1:1082:U:H3'	51:1:1083:U:H5''	1.41	0.99
51:1:1807:G:H2'	51:1:1808:A:H5'	1.44	0.99
40:p:52:ARG:NH2	51:1:2720:U:H5''	1.78	0.99
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	0.96
51:1:644:A:H2'	51:1:645:C:H5''	1.50	0.94
51:1:2713:U:H3'	51:1:2714:G:C5'	1.98	0.94
58:B1:68:TYR:O	58:B1:75:TYR:CE2	2.20	0.94
30:e:84:ILE:HD13	51:1:2312:U:H5'	1.51	0.93
51:1:655:A:H4'	51:1:656:G:H5'	1.50	0.92
51:1:2156:G:H2'	51:1:2157:G:H5'	1.47	0.92
30:e:130:GLY:HA3	51:1:2305:U:H5''	1.51	0.92
58:B1:202:ARG:HG2	58:B1:202:ARG:HH11	1.35	0.91
51:1:1702:G:H2'	51:1:1703:G:H5''	1.51	0.91
51:1:1102:C:H2'	51:1:1103:A:H8	1.35	0.91
54:4:56:G:H21	58:B1:427:PRO:HD3	1.34	0.91
51:1:890:C:H2'	51:1:891:G:H5'	1.53	0.90
51:1:1019:U:H3	51:1:1142:A:H62	1.17	0.90
51:1:1668:A:H4'	51:1:1669:A:H5'	1.54	0.90
59:B2:895:LEU:HD21	59:B2:911:SER:HB3	1.54	0.90
58:B1:68:TYR:C	58:B1:75:TYR:HE2	1.80	0.90
14:N:3:ASN:N	14:N:5:TYR:HH	1.70	0.89
58:B1:317:THR:HA	58:B1:323:PRO:HA	1.55	0.89
59:B2:854:ILE:HG21	59:B2:917:SER:HB3	1.54	0.89
51:1:2097:A:H2'	51:1:2098:U:C6	2.08	0.88
51:1:1060:U:H4'	51:1:1061:U:H5''	1.55	0.88
63:5:9:A:H2'	63:5:11:C:H41	1.38	0.88
51:1:11:C:H2'	51:1:12:U:H5''	1.54	0.87
31:f:174:LYS:HG3	51:1:2529:G:H4'	1.56	0.87
51:1:1869:G:H3'	51:1:1870:C:H5'	1.57	0.86
51:1:2333:A:H5'	51:1:2334:U:H2'	1.57	0.86
2:B:8:THR:HB	51:1:2020:A:H5'	1.56	0.86
17:Q:40:THR:HG21	65:h:6:5OH:OS	1.76	0.86
51:1:1387:A:H5'	51:1:1469:A:H1'	1.58	0.86
51:1:2792:A:H2'	51:1:2793:C:H5''	1.59	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:p:52:ARG:HH21	51:1:2720:U:C5'	1.86	0.85
51:1:1175:A:H3'	51:1:1176:U:H5'	1.59	0.85
58:B1:68:TYR:HB3	58:B1:75:TYR:OH	1.76	0.84
51:1:475:C:H4'	51:1:510:C:H5'	1.59	0.84
17:Q:69:GLU:HG3	53:3:521:G:H4'	1.59	0.84
59:B2:895:LEU:HG	59:B2:912:ASP:HB2	1.56	0.84
51:1:1666:G:C2'	51:1:1667:G:H5'	2.07	0.83
58:B1:633:ALA:HB2	59:B2:808:ASN:H	1.41	0.83
51:1:2584:U:H2'	51:1:2585:U:H5'	1.58	0.83
59:B2:855:PRO:HB3	61:NA:103:ASP:CB	2.08	0.83
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
58:B1:141:PHE:HE2	58:B1:296:LYS:HB2	1.45	0.82
51:1:279:A:H61	51:1:361:G:H1'	1.46	0.81
55:8:1:DC:H5''	58:B1:210:SER:OG	1.80	0.81
58:B1:770:LEU:HD13	59:B2:618:GLN:HG3	1.61	0.81
51:1:2224:G:H4'	51:1:2226:C:C2	2.16	0.81
51:1:757:G:H2'	51:1:758:C:H5'	1.61	0.81
3:C:40:PRO:HG3	51:1:2348:U:H4'	1.63	0.81
51:1:2112:G:H2'	51:1:2113:U:H5'	1.63	0.81
51:1:2360:G:H2'	51:1:2361:G:H5'	1.62	0.81
51:1:2799:A:H2'	51:1:2800:A:H5'	1.63	0.80
58:B1:37:GLU:O	58:B1:61:ILE:HD11	1.81	0.80
51:1:545:U:C2	51:1:546:U:H1'	2.16	0.80
58:B1:68:TYR:O	58:B1:75:TYR:HE2	1.58	0.80
38:n:36:THR:HG22	51:1:1278:C:OP1	1.80	0.80
58:B1:111:THR:HG23	58:B1:300:GLN:OE1	1.81	0.80
51:1:1087:G:N2	51:1:1103:A:H1'	1.96	0.80
51:1:1071:G:O2'	51:1:1089:A:H2'	1.82	0.80
64:7:46:G:H2'	64:7:47:U:H5'	1.64	0.80
58:B1:141:PHE:CE2	58:B1:296:LYS:HB2	2.16	0.80
51:1:784:G:H5'	51:1:785:G:OP1	1.81	0.79
51:1:1197:G:O2'	51:1:1198:U:H5'	1.81	0.79
58:B1:144:TYR:HE1	58:B1:162:GLU:OE2	1.64	0.79
51:1:1775:U:H2'	51:1:1776:G:H5'	1.64	0.79
7:G:18:GLN:HG3	7:G:189:ASN:HB3	1.65	0.79
58:B1:186:GLN:HG3	58:B1:238:ILE:HG13	1.65	0.79
51:1:1064:C:H41	51:1:1069:A:H5''	1.47	0.79
51:1:1536:C:H4'	51:1:1537:G:C2	2.18	0.78
51:1:2130:U:H2'	51:1:2131:U:H5''	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1490:U:H2'	53:3:1491:G:C8	2.17	0.78
33:i:55:PRO:HG3	51:1:1060:U:OP2	1.83	0.78
51:1:275:C:H2'	51:1:276:U:C4'	2.14	0.78
51:1:2286:G:H4'	51:1:2287:A:O4'	1.83	0.78
28:c:114:LYS:HB2	51:1:2680:U:OP1	1.84	0.77
51:1:1275:A:N6	51:1:1296:G:H4'	2.00	0.77
51:1:1702:G:C2'	51:1:1703:G:H5''	2.13	0.77
51:1:2792:A:C3'	51:1:2793:C:H5''	2.14	0.77
51:1:368:A:H2'	51:1:369:U:H5'	1.66	0.77
51:1:2215:C:H2'	51:1:2216:G:C8	2.18	0.77
51:1:1297:C:OP1	51:1:2710:C:H4'	1.82	0.77
51:1:2156:G:C2'	51:1:2157:G:H5'	2.14	0.77
55:8:13:DT:H72	58:B1:791:ALA:HB2	1.66	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
35:k:6:THR:HG22	51:1:1666:G:O2'	1.83	0.76
55:8:15:DC:H1'	58:B1:426:ALA:HB1	1.67	0.76
51:1:1063:G:H1	51:1:1075:C:N4	1.83	0.76
51:1:275:C:H3'	51:1:276:U:H5''	1.66	0.76
51:1:1394:U:H4'	51:1:1603:A:H4'	1.66	0.76
51:1:310:A:O2'	51:1:311:A:H2'	1.85	0.76
58:B1:202:ARG:HG2	58:B1:202:ARG:NH1	1.99	0.75
51:1:548:G:H2'	51:1:549:G:O4'	1.84	0.75
51:1:2792:A:C2'	51:1:2793:C:H5''	2.15	0.75
51:1:1020:A:H5'	51:1:1021:A:C8	2.22	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	1.86	0.74
51:1:958:U:H2'	52:2:89:U:O2	1.87	0.74
59:B2:890:LYS:HG2	59:B2:913:VAL:HG22	1.69	0.74
51:1:543:G:H2'	51:1:544:C:H5''	1.67	0.74
51:1:1425:G:H2'	51:1:1426:G:C8	2.23	0.74
51:1:1670:C:H2'	51:1:1671:U:H5'	1.70	0.74
51:1:2432:A:H1'	64:7:75:C:O4'	1.86	0.74
51:1:1061:U:H3'	51:1:1062:G:C5'	2.18	0.74
51:1:545:U:H2'	51:1:546:U:O4'	1.88	0.74
51:1:1555:G:H5'	51:1:1555:G:H8	1.51	0.74
51:1:1310:G:H2'	51:1:1311:G:H5'	1.68	0.74
51:1:1773:A:H2'	51:1:1774:C:H5'	1.68	0.73
53:3:456:A:H61	53:3:476:U:H3	1.36	0.73
55:8:3:DC:H2'	55:8:4:DT:H72	1.69	0.73
51:1:481:G:H1'	51:1:506:G:N2	2.04	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:322:A:H5'	51:1:340:A:C1'	2.19	0.73
51:1:2036:C:H2'	51:1:2037:A:C8	2.23	0.73
58:B1:110:PRO:HG2	58:B1:183:GLU:HG3	1.68	0.73
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
51:1:404:A:H1'	51:1:406:G:C4	2.23	0.72
51:1:2097:A:H2'	51:1:2098:U:H6	1.50	0.72
55:8:3:DC:C2'	55:8:4:DT:H72	2.19	0.72
58:B1:220:ARG:HG2	58:B1:220:ARG:HH11	1.55	0.72
51:1:1433:A:H2'	51:1:1434:A:O4'	1.89	0.72
51:1:2834:G:H2'	51:1:2879:A:H61	1.54	0.72
51:1:1942:C:H3'	51:1:1943:U:H2'	1.70	0.72
64:7:50:U:H2'	64:7:51:C:C4	2.24	0.72
51:1:2713:U:C3'	51:1:2714:G:C5'	2.67	0.72
58:B1:107:LEU:HD11	58:B1:242:LEU:HB2	1.70	0.72
58:B1:211:GLU:HG2	58:B1:215:LYS:HE3	1.70	0.72
51:1:864:G:O2'	51:1:865:C:H5'	1.89	0.72
51:1:2671:G:H2'	51:1:2672:U:C6	2.25	0.72
58:B1:157:GLN:OE1	58:B1:157:GLN:HA	1.89	0.72
58:B1:105:ILE:HD12	58:B1:242:LEU:HD22	1.71	0.72
53:3:452:A:H61	53:3:480:U:H3	1.37	0.72
58:B1:142:GLU:HG3	58:B1:142:GLU:O	1.89	0.72
58:B1:1143:ASP:OD1	58:B1:1148:ARG:NH1	2.21	0.72
51:1:1441:G:H2'	51:1:1442:U:C6	2.25	0.71
51:1:1795:C:H2'	51:1:1796:U:O4'	1.90	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
51:1:394:C:H2'	51:1:395:U:O4'	1.90	0.71
51:1:890:C:C2'	51:1:891:G:H5'	2.21	0.71
51:1:1386:C:H2'	51:1:1387:A:H8	1.56	0.71
53:3:663:A:H61	53:3:742:G:H1	1.39	0.71
51:1:633:A:H2'	51:1:634:C:H5'	1.72	0.71
51:1:2151:U:H2'	51:1:2152:G:H8	1.56	0.71
58:B1:128:LEU:HD11	58:B1:189:LEU:HG	1.73	0.71
51:1:2297:A:N1	51:1:2321:U:H5	1.89	0.71
53:3:1491:G:C6	65:h:2:DPP:HB3	2.25	0.71
51:1:368:A:C2'	51:1:369:U:H5'	2.20	0.70
58:B1:210:SER:HB3	58:B1:213:LYS:HB2	1.71	0.70
36:l:59:ARG:HD2	51:1:250:G:H4'	1.71	0.70
51:1:723:C:H2'	51:1:724:U:C6	2.27	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1019:U:H3	51:1:1142:A:N6	1.89	0.70
51:1:1983:G:O2'	51:1:1984:G:H5'	1.91	0.70
58:B1:93:THR:HB	58:B1:97:VAL:HG21	1.73	0.70
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE22	1.55	0.70
34:j:7:LYS:HG2	51:1:538:A:H4'	1.72	0.70
42:r:79:ARG:NH1	51:1:572:A:OP2	2.24	0.70
51:1:2267:A:H5''	51:1:2268:A:H5''	1.74	0.70
65:h:6:5OH:N	65:h:6:5OH:HS	2.07	0.70
51:1:612:G:H2'	51:1:614:A:C8	2.26	0.70
51:1:1292:G:H2'	51:1:1293:C:C6	2.27	0.70
51:1:1670:C:C2'	51:1:1671:U:H5'	2.21	0.70
51:1:2151:U:H2'	51:1:2152:G:C8	2.27	0.70
57:A1:297:LYS:CB	61:NA:79:ALA:HB1	2.22	0.70
51:1:1555:G:H5'	51:1:1555:G:C8	2.27	0.69
27:b:47:ARG:NH2	51:1:774:G:H5''	2.07	0.69
57:A2:294:ASN:HA	61:NA:464:ILE:H	1.57	0.69
51:1:1102:C:H2'	51:1:1103:A:C8	2.22	0.69
51:1:1889:A:H2'	51:1:1890:A:H8	1.58	0.69
51:1:2114:A:H2	51:1:2167:U:H1'	1.57	0.69
51:1:419:U:H2'	51:1:420:C:C6	2.27	0.69
51:1:2092:U:H4'	51:1:2093:G:H5''	1.74	0.69
36:l:30:THR:HG22	51:1:810:U:O4	1.93	0.69
51:1:849:A:H2'	51:1:850:U:H6	1.58	0.69
59:B2:65:ASN:HB3	59:B2:105:TYR:HB2	1.73	0.69
65:h:4:SER:O	65:h:5:UAL:N1	2.26	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
51:1:528:A:C8	51:1:528:A:H3'	2.27	0.69
51:1:1137:G:O2'	51:1:1138:G:H5'	1.92	0.69
58:B1:161:THR:HG22	58:B1:164:GLN:HB2	1.75	0.69
58:B1:243:PRO:HG2	59:B2:1332:SER:O	1.93	0.69
51:1:319:G:H1	51:1:323:C:H5	1.41	0.69
51:1:905:A:C2'	51:1:906:U:H5'	2.23	0.69
51:1:940:G:H2'	51:1:941:A:H5''	1.73	0.69
51:1:2403:C:O2'	51:1:2404:U:H5'	1.92	0.69
8:H:117:ASP:HA	8:H:120:THR:HG22	1.75	0.68
51:1:2869:G:H2'	51:1:2870:C:C6	2.28	0.68
51:1:322:A:H5'	51:1:340:A:H1'	1.74	0.68
51:1:644:A:H2'	51:1:645:C:C5'	2.22	0.68
51:1:1337:G:H2'	51:1:1338:G:H8	1.58	0.68
51:1:2510:C:N4	51:1:2511:U:O4	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2626:C:O2'	51:1:2627:G:H5'	1.91	0.68
58:B1:39:LYS:O	58:B1:273:ILE:CG2	2.41	0.68
50:z:38:GLU:OE2	51:1:928:A:H5'	1.94	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
48:x:16:ASN:ND2	48:x:26:ARG:HB3	2.09	0.68
51:1:226:A:H2'	51:1:227:A:O4'	1.93	0.68
51:1:402:A:H2'	51:1:403:U:H5'	1.74	0.68
51:1:1999:C:H5''	51:1:2723:C:O2'	1.94	0.68
51:1:2747:G:O6	51:1:2755:C:H5''	1.93	0.68
51:1:2758:A:H2'	51:1:2759:G:H5'	1.75	0.68
51:1:419:U:H2'	51:1:420:C:H6	1.58	0.68
52:2:65:U:H3'	52:2:108:A:H61	1.58	0.68
58:B1:68:TYR:C	58:B1:75:TYR:CE2	2.65	0.68
58:B1:832:LYS:C	58:B1:1242:ARG:HH12	2.01	0.68
51:1:894:U:H2'	51:1:895:U:O4'	1.93	0.68
51:1:1702:G:C3'	51:1:1703:G:H5''	2.24	0.68
51:1:1078:U:H2'	51:1:1088:A:OP1	1.94	0.68
58:B1:141:PHE:CD2	58:B1:293:ARG:O	2.47	0.68
51:1:1061:U:H3'	51:1:1062:G:H5'	1.76	0.67
51:1:1484:U:H2'	51:1:1485:U:C6	2.30	0.67
9:I:73:ASN:HA	9:I:76:LYS:HB2	1.77	0.67
51:1:246:C:H2'	51:1:247:G:H5'	1.76	0.67
58:B1:117:LEU:HD12	58:B1:117:LEU:O	1.94	0.67
51:1:1717:A:H2'	51:1:1718:G:H5'	1.77	0.67
51:1:1889:A:H2'	51:1:1890:A:C8	2.29	0.67
51:1:2157:G:H2'	51:1:2158:A:H2	1.59	0.67
55:8:23:DC:H2''	55:8:24:DC:C5	2.30	0.67
63:5:47:U:H4'	63:5:48:C:H5'	1.75	0.67
51:1:466:A:H2'	51:1:467:G:H5'	1.76	0.67
51:1:1176:U:H2'	51:1:1177:G:C8	2.29	0.67
58:B1:108:ALA:CB	58:B1:279:LEU:HD22	2.25	0.67
51:1:707:G:O2'	51:1:708:G:H5'	1.94	0.67
51:1:1438:U:O2'	51:1:1439:A:H5'	1.94	0.67
53:3:437:U:H3	53:3:495:A:H62	1.42	0.67
55:8:13:DT:OP2	58:B1:791:ALA:HB1	1.95	0.67
4:D:37:LYS:HD3	4:D:39:ARG:HD3	1.77	0.67
36:l:39:LYS:NZ	51:1:942:G:OP2	2.28	0.67
51:1:1432:G:O2'	51:1:1433:A:H5'	1.94	0.67
51:1:2278:A:C3'	51:1:2279:G:H5''	2.25	0.67
51:1:2516:A:O2'	51:1:2517:C:H5'	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2898:U:H2'	51:1:2899:A:C8	2.29	0.67
51:1:2013:A:H5''	51:1:2013:A:H8	1.59	0.66
51:1:2555:U:H2'	51:1:2556:C:H5'	1.78	0.66
51:1:2595:G:N2	51:1:2598:A:OP2	2.23	0.66
58:B1:984:LEU:HB3	58:B1:993:GLU:HB2	1.77	0.66
59:B2:897:PRO:HA	59:B2:900:LYS:HD2	1.76	0.66
51:1:1270:C:H5''	51:1:1271:G:H5'	1.77	0.66
51:1:703:U:C2'	51:1:704:G:H5'	2.25	0.66
51:1:905:A:H2'	51:1:906:U:H5'	1.78	0.66
51:1:1733:G:O2'	51:1:1734:G:H5'	1.95	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
28:c:4:LEU:HD23	28:c:29:VAL:HG11	1.77	0.66
55:8:3:DC:C6	55:8:4:DT:H72	2.29	0.66
51:1:2625:G:H2'	51:1:2626:C:C6	2.30	0.66
51:1:2733:A:O2'	51:1:2734:A:H5'	1.96	0.66
58:B1:1355:ARG:NH1	58:B1:1369:ARG:HH12	1.93	0.66
51:1:521:U:H2'	51:1:522:A:C8	2.30	0.66
51:1:1020:A:H1'	51:1:1021:A:OP2	1.95	0.66
58:B1:108:ALA:HB3	58:B1:279:LEU:HD22	1.77	0.66
58:B1:978:ARG:HG2	58:B1:1197:ASN:HD21	1.61	0.66
51:1:2221:G:O2'	51:1:2222:C:H5'	1.95	0.66
17:Q:47:ALA:HB3	17:Q:49:ARG:HE	1.60	0.66
45:u:25:LYS:HD3	45:u:36:GLU:HB3	1.75	0.66
51:1:644:A:C2'	51:1:645:C:H5''	2.22	0.66
51:1:673:C:H2'	51:1:674:G:H5'	1.77	0.66
51:1:1064:C:N4	51:1:1069:A:H5''	2.10	0.66
51:1:2844:G:H2'	51:1:2845:U:C6	2.31	0.66
58:B1:193:ASP:HB3	58:B1:196:GLN:HB2	1.78	0.66
51:1:635:C:H2'	51:1:636:G:C8	2.31	0.66
51:1:2193:G:H2'	51:1:2194:U:C6	2.31	0.66
51:1:2233:U:H2'	51:1:2234:G:H8	1.59	0.66
17:Q:109:ARG:HH21	17:Q:112:ALA:HB3	1.60	0.66
37:m:14:LYS:NZ	51:1:956:G:N7	2.35	0.66
51:1:414:C:H2'	51:1:415:A:C8	2.31	0.66
51:1:1098:A:H2'	51:1:1099:G:H5'	1.77	0.66
51:1:1746:A:H2'	51:1:1747:U:C6	2.31	0.66
51:1:2278:A:H3'	51:1:2279:G:H5''	1.78	0.66
27:b:227:VAL:HG11	51:1:784:G:C2	2.31	0.65
33:i:27:LEU:HD22	33:i:32:VAL:HG21	1.78	0.65
51:1:870:U:C2'	51:1:871:U:H5'	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2760:C:O2'	51:1:2761:A:H5'	1.96	0.65
51:1:1788:C:O2'	51:1:1789:A:H5'	1.96	0.65
38:n:63:ARG:NE	51:1:1454:C:H5'	2.10	0.65
51:1:536:G:H2'	51:1:537:G:H5'	1.79	0.65
51:1:2290:G:H2'	51:1:2291:U:C6	2.31	0.65
51:1:112:U:H2'	51:1:113:U:H5'	1.76	0.65
51:1:528:A:H3'	51:1:528:A:H8	1.59	0.65
51:1:1098:A:C2'	51:1:1099:G:H5'	2.27	0.65
51:1:488:G:N2	51:1:491:G:H5''	2.11	0.65
51:1:1572:A:O2'	51:1:1573:G:H5'	1.97	0.65
51:1:2052:A:O2'	51:1:2053:G:H5'	1.96	0.65
59:B2:903:ARG:HH21	59:B2:908:GLU:H	1.44	0.65
7:G:67:LEU:HD12	7:G:153:MET:HE1	1.77	0.65
51:1:65:U:H2'	51:1:66:C:H6	1.60	0.65
51:1:359:G:O2'	51:1:360:U:H5'	1.97	0.65
51:1:543:G:H2'	51:1:544:C:C5'	2.26	0.65
51:1:1270:C:H5''	51:1:1271:G:C5'	2.25	0.65
51:1:2170:A:H2'	51:1:2171:A:O4'	1.97	0.65
53:3:959:A:HO2'	53:3:984:C:HO2'	1.44	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
59:B2:314:ASN:HD21	59:B2:348:SER:HA	1.62	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
51:1:201:C:O2'	51:1:202:U:H5'	1.97	0.64
51:1:1796:U:H2'	51:1:1797:G:H8	1.61	0.64
51:1:2114:A:N7	51:1:2115:G:H1'	2.12	0.64
59:B2:528:ARG:NH2	59:B2:576:SER:O	2.30	0.64
28:c:149:ASN:HB3	51:1:2572:A:OP2	1.97	0.64
58:B1:141:PHE:HD2	58:B1:293:ARG:O	1.79	0.64
43:s:6:LYS:HB2	51:1:494:G:H4'	1.78	0.64
51:1:905:A:O2'	51:1:906:U:H5'	1.97	0.64
51:1:622:G:O2'	51:1:623:C:H5'	1.98	0.64
51:1:1766:G:O2'	51:1:1767:G:H5'	1.98	0.64
51:1:2112:G:C2'	51:1:2113:U:H5'	2.27	0.64
53:3:85:U:H5''	53:3:86:G:H5'	1.78	0.64
51:1:870:U:H2'	51:1:871:U:H5'	1.79	0.64
51:1:2792:A:H3'	51:1:2793:C:H5''	1.80	0.64
51:1:2834:G:O2'	51:1:2835:A:H5'	1.97	0.64
4:D:24:THR:HG23	4:D:27:GLY:H	1.61	0.64
17:Q:42:LYS:HB3	53:3:1491:G:H5''	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
55:8:3:DC:C2'	55:8:4:DT:C7	2.75	0.64
58:B1:285:LEU:HD13	58:B1:285:LEU:H	1.62	0.64
58:B1:975:ILE:HG22	58:B1:977:SER:H	1.62	0.64
12:L:59:GLU:HA	12:L:62:GLU:HB3	1.80	0.64
16:P:19:VAL:HG22	16:P:82:GLU:HB2	1.79	0.64
51:1:2811:G:O2'	51:1:2812:G:H5'	1.97	0.64
58:B1:68:TYR:HB3	58:B1:75:TYR:CE2	2.32	0.64
58:B1:461:PHE:HD2	59:B2:813:GLU:HB2	1.61	0.64
31:f:154:GLU:HG3	31:f:156:TYR:H	1.61	0.64
51:1:703:U:H2'	51:1:704:G:H5'	1.77	0.64
58:B1:245:LEU:HG	58:B1:246:PRO:HD2	1.79	0.64
51:1:256:A:O2'	51:1:257:C:H5'	1.98	0.64
51:1:940:G:C3'	51:1:941:A:H5''	2.28	0.64
51:1:2799:A:C2'	51:1:2800:A:H5'	2.27	0.64
11:K:38:ARG:HE	11:K:97:THR:HA	1.62	0.63
51:1:65:U:H2'	51:1:66:C:C6	2.33	0.63
27:b:106:PRO:HD2	27:b:109:LEU:HD22	1.79	0.63
51:1:1161:C:H2'	51:1:1162:G:H8	1.61	0.63
51:1:1857:G:H22	51:1:1884:G:H2'	1.62	0.63
59:B2:1282:GLY:HA3	60:W0:17:PHE:HE1	1.63	0.63
9:I:152:SER:H	9:I:155:LYS:HD3	1.64	0.63
58:B1:918:ILE:HG22	59:B2:1280:ALA:HB1	1.79	0.63
26:Z:65:ARG:NH2	53:3:1087:G:N3	2.47	0.63
51:1:2404:U:O2'	51:1:2405:G:H5'	1.97	0.63
51:1:2636:C:H2'	51:1:2637:U:H6	1.64	0.63
58:B1:1357:ILE:HD11	59:B2:1287:LEU:HD13	1.80	0.63
26:Z:32:ARG:HG2	26:Z:33:ARG:HG3	1.80	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
58:B1:162:GLU:HA	58:B1:162:GLU:OE1	1.97	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
51:1:1038:G:H2'	51:1:1039:A:C8	2.32	0.63
51:1:1149:G:H2'	51:1:1150:C:C6	2.33	0.63
58:B1:128:LEU:HA	58:B1:192:MET:HE1	1.81	0.63
58:B1:144:TYR:CE1	58:B1:162:GLU:OE2	2.51	0.63
51:1:2073:C:O2'	51:1:2074:U:H5'	1.98	0.63
51:1:2469:A:H2'	51:1:2470:G:O4'	1.98	0.63
51:1:317:G:H2'	51:1:318:C:H6	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1524:G:H2'	51:1:1525:A:H8	1.63	0.63
59:B2:120:GLN:NE2	59:B2:490:GLN:OE1	2.32	0.63
51:1:37:C:O2'	51:1:38:A:H5'	1.99	0.63
53:3:373:A:H61	53:3:391:G:H1'	1.64	0.63
55:8:13:DT:C7	58:B1:791:ALA:HB2	2.29	0.63
51:1:1181:U:H2'	51:1:1182:G:C8	2.33	0.62
51:1:1280:G:O2'	51:1:1281:G:H5'	1.99	0.62
51:1:1909:C:H2'	51:1:1910:G:H8	1.64	0.62
51:1:2298:A:H2'	51:1:2299:U:O4'	1.99	0.62
7:G:173:LYS:O	7:G:177:ASN:ND2	2.32	0.62
51:1:872:U:O2'	51:1:873:C:H5'	1.99	0.62
51:1:1164:C:O2'	51:1:1165:A:H5'	1.99	0.62
51:1:2314:A:H2'	51:1:2315:G:C8	2.33	0.62
51:1:1921:G:O2'	51:1:1922:G:H5'	1.98	0.62
51:1:1935:G:H1'	51:1:1964:G:N2	2.15	0.62
51:1:2898:U:H2'	51:1:2899:A:H8	1.64	0.62
34:j:45:THR:HB	34:j:48:VAL:HG22	1.81	0.62
51:1:1448:G:H2'	51:1:1449:G:H8	1.64	0.62
58:B1:111:THR:CG2	58:B1:300:GLN:NE2	2.63	0.62
58:B1:201:LEU:HB2	58:B1:221:ILE:HD13	1.80	0.62
16:P:58:THR:HG22	16:P:60:PHE:H	1.65	0.62
51:1:1086:A:H5'	51:1:1103:A:H2	1.65	0.62
16:P:45:THR:HG23	16:P:48:GLY:H	1.65	0.62
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
51:1:590:A:O2'	51:1:591:U:H5'	2.00	0.62
51:1:2734:A:H2'	51:1:2735:G:H5'	1.82	0.62
58:B1:100:GLU:HA	59:B2:1328:LYS:HE2	1.82	0.62
1:A:1:MET:HG2	52:2:43:C:H5''	1.82	0.62
22:V:30:HIS:HD2	22:V:33:TYR:H	1.48	0.62
34:j:3:THR:N	51:1:995:C:N3	2.48	0.62
44:t:53:VAL:HG12	44:t:92:ASN:HD22	1.65	0.62
51:1:161:A:H3'	51:1:162:U:H5''	1.81	0.62
51:1:1680:U:H2'	51:1:1681:G:O4'	2.00	0.62
51:1:2092:U:H5	51:1:2199:A:H2	1.48	0.62
28:c:181:ASP:HB3	28:c:186:LEU:HB2	1.82	0.62
51:1:940:G:C2'	51:1:941:A:H5''	2.30	0.62
51:1:941:A:H2'	51:1:942:G:O4'	2.00	0.62
51:1:2345:G:N3	51:1:2381:A:H2'	2.15	0.62
55:8:3:DC:H2'	55:8:4:DT:C7	2.30	0.62
58:B1:395:LYS:NZ	58:B1:399:LYS:HD3	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:55:SER:OG	59:B2:465:ARG:NH1	2.33	0.62
58:B1:111:THR:CG2	58:B1:300:GLN:CD	2.66	0.61
51:1:236:C:H2'	51:1:237:C:H6	1.64	0.61
51:1:1040:A:H2	51:1:1115:G:H22	1.48	0.61
51:1:2097:A:H2'	51:1:2098:U:O4'	2.00	0.61
51:1:2404:U:H2'	51:1:2405:G:O4'	2.00	0.61
55:8:1:DC:H2''	55:8:2:DC:C5	2.35	0.61
57:A1:211:ILE:HG12	57:A1:219:ARG:HH12	1.65	0.61
58:B1:770:LEU:HD13	59:B2:618:GLN:CG	2.30	0.61
7:G:15:PHE:HB2	7:G:39:ILE:HG23	1.82	0.61
17:Q:40:THR:OG1	65:h:6:5OH:HR	2.00	0.61
30:e:9:ASP:OD1	30:e:9:ASP:N	2.34	0.61
45:u:87:GLU:HG2	45:u:92:VAL:HG21	1.82	0.61
51:1:889:C:H2'	51:1:890:C:O4'	1.99	0.61
64:7:46:G:C2'	64:7:47:U:H5'	2.29	0.61
34:j:132:HIS:CD2	51:1:7:G:H5'	2.36	0.61
51:1:11:C:C2'	51:1:12:U:H5''	2.29	0.61
51:1:2637:U:H2'	51:1:2638:G:H5'	1.82	0.61
57:A1:38:THR:HB	57:A2:45:ARG:HD3	1.82	0.61
58:B1:1355:ARG:NH1	58:B1:1369:ARG:NH1	2.47	0.61
51:1:1954:G:H1'	51:1:1956:U:O4	2.01	0.61
4:D:3:ARG:O	4:D:6:GLN:NE2	2.33	0.61
51:1:1503:A:H3'	51:1:1504:A:H5''	1.82	0.61
51:1:1508:A:H2'	51:1:1509:A:O4'	2.00	0.61
53:3:1032:G:H21	53:3:1033:G:H4'	1.65	0.61
57:A1:112:ALA:HB3	57:A1:126:PRO:HA	1.83	0.61
63:5:39:U:H2'	63:5:40:C:C6	2.36	0.61
31:f:174:LYS:HG3	51:1:2529:G:C4'	2.29	0.61
32:g:50:ARG:HH22	32:g:51:ARG:HH21	1.49	0.61
51:1:2852:G:O2'	51:1:2853:C:H5'	2.01	0.61
58:B1:342:LEU:HD23	58:B1:1352:ILE:HG23	1.83	0.61
58:B1:1161:GLY:HA3	58:B1:1179:PRO:HA	1.82	0.61
51:1:435:C:H2'	51:1:436:C:H5'	1.82	0.61
51:1:547:A:H3'	51:1:547:A:N3	2.16	0.61
51:1:1775:U:H2'	51:1:1776:G:C5'	2.29	0.61
51:1:2188:U:H2'	51:1:2189:U:O4'	2.01	0.61
53:3:1133:G:H1	53:3:1141:C:H42	1.48	0.61
34:j:39:LYS:HE3	51:1:1009:A:OP1	2.01	0.61
51:1:2327:A:H2'	51:1:2328:A:C8	2.35	0.61
58:B1:223:LEU:HG	58:B1:223:LEU:O	2.00	0.61
29:d:149:ILE:HG23	29:d:188:MET:HB3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:o:4:LYS:HD3	39:o:7:ARG:HH21	1.65	0.60
51:1:198:C:H42	51:1:248:G:H1	1.49	0.60
51:1:322:A:H5'	51:1:340:A:O4'	2.00	0.60
51:1:723:C:H2'	51:1:724:U:H6	1.64	0.60
58:B1:633:ALA:HA	59:B2:806:PRO:O	2.01	0.60
14:N:40:ARG:NH2	14:N:41:GLU:OE2	2.34	0.60
33:i:135:MET:HE2	51:1:1062:G:H21	1.65	0.60
37:m:17:ASN:O	37:m:38:ARG:NH1	2.34	0.60
47:w:38:GLY:HA2	51:1:2330:G:H21	1.66	0.60
51:1:172:A:H2'	51:1:173:A:H8	1.66	0.60
51:1:2386:A:O2'	51:1:2387:U:H5'	2.01	0.60
51:1:2812:G:H2'	51:1:2813:A:C8	2.36	0.60
51:1:558:U:H6	51:1:558:U:O5'	1.84	0.60
51:1:1717:A:C2'	51:1:1718:G:H5'	2.30	0.60
51:1:2804:U:H2'	51:1:2805:C:C6	2.36	0.60
27:b:153:LEU:HD23	51:1:1799:G:C2	2.37	0.60
58:B1:68:TYR:HB3	58:B1:75:TYR:CZ	2.35	0.60
7:G:86:CYS:SG	7:G:87:ASP:N	2.74	0.60
51:1:1437:C:H2'	51:1:1438:U:C6	2.36	0.60
53:3:1351:U:H3	53:3:1371:G:H1	1.49	0.60
51:1:1775:U:C2'	51:1:1776:G:H5'	2.30	0.60
51:1:1857:G:N2	51:1:1884:G:H2'	2.17	0.60
51:1:2093:G:O2'	51:1:2094:A:H5'	2.01	0.60
51:1:893:C:H2'	51:1:894:U:C6	2.36	0.60
51:1:1287:A:C5	51:1:1288:G:C6	2.89	0.60
53:3:1040:U:H2'	53:3:1041:G:H8	1.67	0.60
51:1:851:C:H2'	51:1:852:U:C6	2.36	0.60
55:8:7:DC:H2''	55:8:8:DT:H71	1.84	0.60
58:B1:201:LEU:HD11	58:B1:220:ARG:HH11	1.67	0.60
51:1:1198:U:H2'	51:1:1199:U:C6	2.37	0.60
51:1:2187:U:O2'	51:1:2188:U:H5'	2.02	0.60
58:B1:395:LYS:HZ2	58:B1:399:LYS:CD	2.15	0.60
37:m:86:LYS:NZ	51:1:955:U:OP1	2.33	0.60
51:1:283:G:H2'	51:1:284:U:H5'	1.83	0.60
51:1:1071:G:H1'	51:1:1089:A:C8	2.37	0.60
51:1:1183:U:H2'	51:1:1184:U:C6	2.37	0.60
51:1:1538:G:H2'	51:1:1539:U:C6	2.37	0.60
51:1:2749:A:OP2	51:1:2751:G:H5''	2.02	0.60
58:B1:99:ARG:NH1	58:B1:99:ARG:HG3	2.17	0.60
29:d:68:ALA:HA	51:1:1255:U:C5	2.37	0.59
29:d:77:ILE:CG2	51:1:1256:G:H21	2.15	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2137:U:H2'	51:1:2138:G:H8	1.67	0.59
51:1:2717:C:C4	51:1:2718:G:N7	2.70	0.59
58:B1:161:THR:HG23	58:B1:164:GLN:H	1.67	0.59
58:B1:412:LEU:HD22	58:B1:441:LEU:HD21	1.84	0.59
58:B1:725:MET:SD	59:B2:1101:LEU:HD23	2.42	0.59
58:B1:951:GLN:NE2	58:B1:1014:GLY:O	2.35	0.59
6:F:14:CYS:SG	6:F:33:HIS:ND1	2.75	0.59
18:R:102:LYS:HG2	18:R:103:THR:HG23	1.83	0.59
51:1:1773:A:C2'	51:1:1774:C:H5'	2.31	0.59
58:B1:154:LEU:HD21	58:B1:160:LEU:HD21	1.83	0.59
51:1:1171:G:H2'	51:1:1172:C:O4'	2.02	0.59
59:B2:1072:ASN:ND2	59:B2:1111:GLN:OE1	2.35	0.59
51:1:49:A:H5''	51:1:51:G:O4'	2.02	0.59
51:1:2643:G:H2'	51:1:2644:G:H5'	1.83	0.59
58:B1:514:THR:HG21	58:B1:596:LEU:HD12	1.85	0.59
58:B1:750:PRO:CB	59:B2:549:ASP:OD2	2.45	0.59
29:d:77:ILE:HG23	51:1:1256:G:H21	1.68	0.59
42:r:4:VAL:HG22	42:r:40:MET:HG2	1.84	0.59
45:u:40:LEU:HD12	45:u:59:GLU:HG2	1.84	0.59
51:1:841:G:O2'	51:1:842:U:H5'	2.02	0.59
51:1:854:C:O2'	51:1:855:G:H5'	2.02	0.59
51:1:1026:G:H2'	51:1:1027:A:H8	1.67	0.59
55:8:9:DG:H4'	58:B1:120:LEU:HG	1.84	0.59
55:8:11:DC:H2'	55:8:12:DG:C8	2.37	0.59
9:I:69:ARG:NH1	53:3:401:C:OP2	2.36	0.59
14:N:17:ARG:HB2	14:N:65:THR:HG23	1.83	0.59
51:1:215:G:H4'	51:1:216:A:H4'	1.84	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
59:B2:69:GLN:HE21	59:B2:101:ARG:HD2	1.67	0.59
51:1:246:C:C2'	51:1:247:G:H5'	2.33	0.59
51:1:2215:C:H2'	51:1:2216:G:H8	1.65	0.59
59:B2:918:LEU:O	59:B2:918:LEU:HD23	2.02	0.59
22:V:11:VAL:HA	22:V:22:VAL:HA	1.83	0.59
51:1:2091:C:H5	51:1:2092:U:HO2'	1.50	0.59
51:1:2789:C:H2'	51:1:2893:A:N7	2.17	0.59
58:B1:370:LYS:HG2	58:B1:441:LEU:HD23	1.84	0.59
37:m:66:ARG:NH1	37:m:104:GLU:OE2	2.36	0.59
47:w:40:LYS:HE3	51:1:2330:G:O2'	2.03	0.59
51:1:1077:A:C8	51:1:1078:U:H1'	2.38	0.59
51:1:1469:A:H2'	51:1:1470:A:C8	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1725:U:H2'	51:1:1726:C:C6	2.38	0.59
51:1:2533:U:H2'	51:1:2534:A:H5'	1.85	0.59
51:1:2743:U:H3'	51:1:2744:G:H5''	1.84	0.59
58:B1:926:PRO:HG2	58:B1:1248:ILE:HD11	1.84	0.59
21:U:70:ARG:HH22	53:3:451:A:H5'	1.66	0.59
27:b:34:GLU:HG3	27:b:63:ILE:HD11	1.84	0.59
30:e:51:ASN:OD1	30:e:149:ARG:NH1	2.34	0.59
58:B1:275:ARG:NH1	58:B1:278:ARG:NH1	2.51	0.59
23:W:49:LYS:HA	23:W:52:ARG:HH21	1.68	0.58
51:1:528:A:C8	51:1:528:A:C3'	2.86	0.58
51:1:794:A:H2'	51:1:795:C:O4'	2.02	0.58
51:1:1098:A:H2'	51:1:1099:G:C5'	2.33	0.58
51:1:1524:G:H2'	51:1:1525:A:C8	2.38	0.58
51:1:1845:G:O2'	51:1:1846:G:H5'	2.03	0.58
51:1:1893:C:H2'	51:1:1894:C:H5'	1.85	0.58
53:3:422:C:O2'	53:3:423:G:N2	2.36	0.58
57:A2:28:LEU:HB2	57:A2:201:LEU:HB3	1.85	0.58
58:B1:438:GLU:HG3	58:B1:485:MET:HE1	1.85	0.58
51:1:1511:G:H2'	51:1:1512:C:C6	2.38	0.58
51:1:1579:A:H2'	51:1:1580:A:C8	2.38	0.58
24:X:30:LEU:HB2	24:X:48:ILE:HG22	1.85	0.58
51:1:2183:A:H2'	51:1:2184:A:C4	2.37	0.58
51:1:2360:G:C2'	51:1:2361:G:H5'	2.31	0.58
27:b:141:HIS:ND1	27:b:192:GLY:O	2.35	0.58
51:1:1042:G:H2'	51:1:1043:C:C6	2.37	0.58
51:1:1463:C:H2'	51:1:1464:G:H8	1.68	0.58
51:1:1553:A:HO2'	51:1:1554:U:H5	1.51	0.58
58:B1:241:VAL:O	58:B1:241:VAL:HG12	2.04	0.58
27:b:157:ALA:O	51:1:1820:U:C2	2.56	0.58
28:c:55:LYS:NZ	28:c:59:ARG:O	2.36	0.58
51:1:1333:G:O2'	51:1:1334:G:H5'	2.03	0.58
53:3:148:G:H1'	53:3:1447:A:H1'	1.84	0.58
59:B2:707:ALA:O	59:B2:711:ASP:HB2	2.04	0.58
15:O:46:LYS:HG2	15:O:68:ARG:HG2	1.84	0.58
51:1:834:G:H2'	51:1:835:C:O4'	2.04	0.58
51:1:1565:C:O2'	51:1:1566:A:H8	1.87	0.58
53:3:1490:U:H2'	53:3:1491:G:H8	1.64	0.58
29:d:1:MET:HG2	29:d:16:GLU:HG2	1.86	0.58
51:1:1561:C:H2'	51:1:1562:U:C6	2.38	0.58
51:1:2812:G:H2'	51:1:2813:A:H8	1.68	0.58
57:A2:82:LEU:HD11	57:A2:171:LEU:HD23	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:SER:OG	1:A:27:THR:N	2.37	0.58
30:e:162:ASP:OD1	30:e:162:ASP:N	2.37	0.58
33:i:25:PRO:HG2	51:1:1068:G:H21	1.67	0.58
38:n:22:ARG:HG3	38:n:70:THR:HA	1.86	0.58
50:z:4:ILE:HD11	50:z:58:GLU:HG2	1.85	0.58
51:1:2570:G:H2'	51:1:2571:U:H5'	1.85	0.58
51:1:621:A:H2'	51:1:622:G:H5'	1.86	0.58
51:1:1110:G:HO2'	51:1:1111:A:H8	1.51	0.58
51:1:1337:G:H2'	51:1:1338:G:C8	2.38	0.58
51:1:2153:C:H2'	51:1:2154:A:H5'	1.85	0.58
51:1:2834:G:H2'	51:1:2879:A:N6	2.17	0.58
51:1:2897:U:H2'	51:1:2898:U:C6	2.39	0.58
53:3:1125:U:H2'	53:3:1126:U:H2'	1.86	0.58
58:B1:638:SER:OG	58:B1:639:VAL:N	2.36	0.58
9:I:201:GLU:O	53:3:8:A:N6	2.36	0.58
14:N:79:ARG:HH21	14:N:102:PHE:HA	1.67	0.58
28:c:129:THR:OG1	28:c:140:HIS:O	2.22	0.58
33:i:22:PRO:HA	51:1:1067:A:O2'	2.04	0.58
38:n:63:ARG:CZ	51:1:1454:C:H5'	2.34	0.58
39:o:56:LYS:NZ	52:2:117:G:OP1	2.36	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
59:B2:1142:ARG:NH1	59:B2:1161:LEU:O	2.36	0.58
30:e:47:LYS:O	30:e:51:ASN:ND2	2.37	0.57
51:1:327:G:O2'	51:1:328:U:H5'	2.04	0.57
51:1:1400:U:O2'	51:1:1401:G:H5'	2.04	0.57
51:1:2092:U:H4'	51:1:2093:G:C5'	2.34	0.57
58:B1:42:GLU:HB3	58:B1:52:GLU:HG3	1.86	0.57
58:B1:1046:ILE:HD12	58:B1:1059:LEU:HB3	1.86	0.57
7:G:114:LYS:HE3	7:G:151:LYS:HB2	1.85	0.57
51:1:32:C:H2'	51:1:33:C:C6	2.40	0.57
51:1:235:U:H2'	51:1:236:C:C6	2.39	0.57
51:1:673:C:C2'	51:1:674:G:H5'	2.34	0.57
9:I:10:LEU:HD23	9:I:62:ARG:HB3	1.86	0.57
27:b:220:ARG:NH1	51:1:1789:A:OP2	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
51:1:146:A:H2'	51:1:147:C:C6	2.39	0.57
51:1:323:C:H3'	51:1:323:C:OP2	2.05	0.57
51:1:640:C:O2'	51:1:641:U:H5'	2.04	0.57
51:1:2899:A:O2'	51:1:2900:A:H5'	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:97:VAL:HG11	58:B1:101:ARG:NH2	2.18	0.57
41:q:30:VAL:HG13	51:1:580:U:O3'	2.04	0.57
51:1:1275:A:C6	51:1:1296:G:H4'	2.40	0.57
51:1:2762:C:H2'	51:1:2763:G:H5'	1.86	0.57
14:N:35:GLU:HA	14:N:39:GLY:HA3	1.85	0.57
16:P:111:ASP:HB2	26:Z:16:ARG:HH22	1.68	0.57
51:1:163:C:H2'	51:1:164:C:O4'	2.04	0.57
58:B1:160:LEU:HD22	58:B1:164:GLN:HB3	1.87	0.57
58:B1:615:LYS:HG2	60:W0:5:THR:HG21	1.86	0.57
59:B2:1122:LYS:NZ	59:B2:1126:ASP:OD1	2.38	0.57
10:J:44:ARG:NH2	10:J:70:MET:SD	2.78	0.57
19:S:5:MET:HE1	53:3:981:U:H5''	1.86	0.57
51:1:1173:U:C5	51:1:1174:U:H1'	2.40	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: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
31:f:151:ARG:HB3	31:f:161:VAL:HG23	1.86	0.57
51:1:877:A:N1	51:1:899:A:H2'	2.20	0.57
53:3:159:G:N2	53:3:162:A:OP2	2.34	0.57
58:B1:37:GLU:O	58:B1:61:ILE:CD1	2.52	0.57
27:b:259:ASN:ND2	27:b:262:THR:OG1	2.38	0.57
38:n:54:LEU:HD23	38:n:66:ALA:HB2	1.86	0.57
40:p:1:SER:OG	40:p:2:ASN:N	2.37	0.57
51:1:503:A:H4'	51:1:505:A:H5''	1.87	0.57
51:1:2845:U:H2'	51:1:2846:G:H8	1.69	0.57
58:B1:510:LEU:HD22	58:B1:601:ILE:HD12	1.86	0.57
58:B1:741:ALA:O	58:B1:762:ASN:ND2	2.38	0.57
16:P:92:ARG:NH2	16:P:111:ASP:OD1	2.38	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
58:B1:1361:THR:HB	59:B2:1284:ALA:HB3	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
51:1:2186:G:O2'	51:1:2187:U:H5'	2.04	0.57
51:1:2584:U:C2'	51:1:2585:U:H5'	2.34	0.57
7:G:58:LYS:O	7:G:62:ARG:NH1	2.38	0.56
51:1:1130:U:O2'	51:1:1131:G:OP1	2.20	0.56
51:1:1526:C:H2'	51:1:1527:G:O4'	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2457:U:O2'	51:1:2458:G:H5'	2.05	0.56
58:B1:247:PRO:HA	58:B1:250:ARG:HG3	1.87	0.56
63:5:38:A:C8	63:5:39:U:H1'	2.40	0.56
31:f:40:VAL:O	31:f:54:ARG:NH2	2.38	0.56
34:j:116:ARG:NH2	51:1:529:A:OP2	2.32	0.56
51:1:288:U:H2'	51:1:289:G:H8	1.71	0.56
51:1:635:C:H2'	51:1:636:G:H8	1.70	0.56
58:B1:102:MET:HG2	58:B1:246:PRO:HG3	1.87	0.56
4:D:9:VAL:HG22	51:1:1309:G:OP1	2.06	0.56
31:f:174:LYS:HE2	51:1:2529:G:H4'	1.86	0.56
49:y:39:GLN:HG2	51:1:96:C:OP1	2.05	0.56
51:1:358:U:H2'	51:1:359:G:C8	2.40	0.56
51:1:727:A:H2'	51:1:728:G:C8	2.40	0.56
51:1:885:C:N4	51:1:886:A:H62	2.03	0.56
51:1:1485:U:H2'	51:1:1486:U:C6	2.41	0.56
51:1:1528:A:H2'	51:1:1529:G:H5'	1.87	0.56
51:1:1917:U:O2'	51:1:1918:A:H5'	2.05	0.56
51:1:2662:A:H2'	51:1:2663:G:O4'	2.05	0.56
53:3:202:G:H21	53:3:466:A:H61	1.53	0.56
58:B1:99:ARG:CG	58:B1:99:ARG:HH11	2.17	0.56
58:B1:130:MET:HE2	58:B1:135:ILE:HG12	1.87	0.56
58:B1:144:TYR:HE1	58:B1:162:GLU:CD	2.14	0.56
2:B:43:THR:HG1	2:B:46:GLY:H	1.53	0.56
45:u:36:GLU:HA	45:u:61:GLU:HG2	1.86	0.56
51:1:543:G:H2'	51:1:544:C:O4'	2.05	0.56
51:1:1097:U:H2'	51:1:1098:A:O4'	2.06	0.56
51:1:1485:U:H2'	51:1:1486:U:H6	1.70	0.56
18:R:100:ARG:NH1	18:R:103:THR:OG1	2.38	0.56
51:1:78:U:H2'	51:1:79:C:C6	2.40	0.56
51:1:359:G:C2'	51:1:360:U:H5'	2.36	0.56
51:1:1182:G:H2'	51:1:1183:U:O4'	2.06	0.56
58:B1:395:LYS:HZ2	58:B1:399:LYS:HD3	1.69	0.56
58:B1:508:LEU:HD22	59:B2:1101:LEU:HD21	1.88	0.56
8:H:76:ILE:HD11	54:4:20:U:H4'	1.87	0.56
27:b:250:GLN:NE2	27:b:251:THR:O	2.37	0.56
38:n:2:ARG:HA	38:n:5:LYS:HD3	1.88	0.56
51:1:74:A:H4'	51:1:75:G:O5'	2.05	0.56
51:1:633:A:C2'	51:1:634:C:H5'	2.35	0.56
51:1:1319:C:O2'	51:1:1320:C:H5'	2.05	0.56
51:1:1597:A:H5''	51:1:1598:A:H5'	1.87	0.56
53:3:830:G:H1	53:3:856:C:H42	1.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:818:VAL:HG22	59:B2:1096:ILE:HG12	1.87	0.56
64:7:52:G:H2'	64:7:53:G:H8	1.69	0.56
17:Q:8:ARG:NH2	53:3:880:C:OP1	2.36	0.56
19:S:26:LEU:HA	19:S:30:ILE:HD12	1.87	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
51:1:69:C:H2'	51:1:70:G:H8	1.69	0.56
51:1:296:U:H2'	51:1:297:G:C8	2.41	0.56
51:1:780:G:H21	51:1:783:A:H62	1.54	0.56
51:1:1120:G:O2'	51:1:1121:C:H5'	2.05	0.56
51:1:2626:C:H2'	51:1:2627:G:O4'	2.06	0.56
11:K:2:ARG:NH1	53:3:738:C:OP1	2.39	0.56
26:Z:44:ARG:NH1	53:3:722:G:OP2	2.39	0.56
28:c:134:HIS:CE1	51:1:1675:C:C4	2.94	0.56
51:1:655:A:H4'	51:1:656:G:C5'	2.30	0.56
51:1:2533:U:C2'	51:1:2534:A:H5'	2.36	0.56
11:K:12:PRO:HB2	11:K:44:ARG:HH21	1.70	0.56
16:P:63:GLN:HG3	16:P:98:ALA:HB2	1.88	0.56
21:U:55:ASP:OD1	21:U:55:ASP:N	2.38	0.56
51:1:155:A:H2'	51:1:156:A:C8	2.41	0.56
51:1:366:C:O2'	51:1:367:G:H5'	2.04	0.56
51:1:1410:G:H2'	51:1:1411:U:C6	2.41	0.56
51:1:1678:A:H2'	51:1:1679:A:H5'	1.86	0.56
8:H:39:ARG:NH1	8:H:54:ILE:O	2.39	0.56
30:e:23:SER:HB3	30:e:26:GLN:HB2	1.88	0.56
39:o:52:SER:OG	39:o:53:THR:N	2.38	0.56
46:v:57:TYR:OH	46:v:79:ARG:NH2	2.38	0.56
51:1:2236:U:H2'	51:1:2237:G:H5'	1.88	0.56
51:1:2395:C:H42	51:1:2421:G:H1	1.54	0.56
53:3:503:C:H2'	53:3:504:C:C6	2.41	0.56
57:A1:29:GLU:HB3	57:A1:200:LYS:HG3	1.88	0.56
59:B2:839:VAL:HG12	59:B2:1049:ILE:HG12	1.87	0.56
27:b:216:ARG:NH2	51:1:781:A:OP1	2.38	0.55
33:i:5:GLN:O	33:i:30:GLN:NE2	2.40	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
51:1:461:C:H2'	51:1:462:C:C6	2.41	0.55
51:1:720:U:H2'	51:1:721:A:C8	2.41	0.55
53:3:1036:A:H2'	53:3:1037:C:H5'	1.88	0.55
51:1:184:C:H2'	51:1:185:G:C8	2.41	0.55
51:1:2510:C:C4	51:1:2511:U:C4	2.93	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:985:GLU:HB3	59:B2:988:LYS:HB2	1.89	0.55
63:5:40:C:H2'	63:5:41:C:C6	2.41	0.55
29:d:84:THR:HG21	51:1:586:A:H5'	1.87	0.55
51:1:184:C:H2'	51:1:185:G:H8	1.70	0.55
51:1:877:A:C2'	51:1:878:A:H5''	2.37	0.55
51:1:2637:U:C2'	51:1:2638:G:H5'	2.36	0.55
12:L:4:ARG:HB3	12:L:6:ILE:HG23	1.88	0.55
36:l:89:VAL:HG23	36:l:121:THR:HG23	1.88	0.55
50:z:15:ARG:HE	50:z:52:PHE:HE2	1.53	0.55
51:1:317:G:H2'	51:1:318:C:C6	2.42	0.55
51:1:543:G:H2'	51:1:544:C:C4'	2.37	0.55
51:1:613:A:H2'	51:1:613:A:N3	2.21	0.55
51:1:1048:A:H2'	51:1:1049:C:H5'	1.88	0.55
51:1:1670:C:O5'	51:1:1670:C:H6	1.90	0.55
51:1:1697:G:H4'	51:1:1978:A:H5''	1.89	0.55
51:1:2845:U:H2'	51:1:2846:G:C8	2.42	0.55
53:3:49:U:H3	53:3:362:G:H1'	1.71	0.55
58:B1:833:GLU:HB2	58:B1:1242:ARG:NH1	2.22	0.55
59:B2:103:VAL:HB	59:B2:114:VAL:HG11	1.89	0.55
7:G:91:VAL:HG22	7:G:150:ILE:HD11	1.88	0.55
51:1:112:U:C2'	51:1:113:U:H5'	2.37	0.55
51:1:439:A:H2'	51:1:440:C:C6	2.42	0.55
51:1:1506:U:H2'	51:1:1507:C:C6	2.41	0.55
51:1:1545:A:H2'	51:1:1546:G:O4'	2.06	0.55
51:1:1772:A:H5'	51:1:1773:A:OP2	2.06	0.55
51:1:1909:C:H2'	51:1:1910:G:C8	2.41	0.55
51:1:2488:G:O2'	51:1:2489:U:H5'	2.07	0.55
51:1:2827:C:O2'	51:1:2828:G:H5'	2.07	0.55
33:i:10:LEU:HA	51:1:1061:U:C2	2.42	0.55
51:1:172:A:H2'	51:1:173:A:C8	2.40	0.55
51:1:759:G:H2'	51:1:760:G:C8	2.41	0.55
51:1:825:A:O2'	51:1:826:U:H5'	2.07	0.55
53:3:1040:U:H2'	53:3:1041:G:C8	2.42	0.55
7:G:45:THR:O	7:G:49:PHE:N	2.35	0.55
25:Y:60:GLN:HA	25:Y:63:LYS:HB3	1.89	0.55
25:Y:73:ARG:NH2	53:3:261:U:OP2	2.36	0.55
35:k:76:VAL:H	40:p:72:VAL:HG22	1.71	0.55
43:s:98:LYS:HD3	51:1:2012:G:OP1	2.06	0.55
51:1:1448:G:H2'	51:1:1449:G:C8	2.42	0.55
51:1:2743:U:C3'	51:1:2744:G:H5''	2.37	0.55
59:B2:1142:ARG:NH2	59:B2:1166:ASP:OD1	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:7:9:G:C2	64:7:45:G:O6	2.60	0.55
7:G:138:ARG:NH1	7:G:141:GLU:OE2	2.40	0.55
35:k:65:THR:HG23	35:k:68:GLY:H	1.69	0.55
51:1:118:A:OP2	51:1:119:A:H5''	2.06	0.55
51:1:359:G:H2'	51:1:360:U:O4'	2.07	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
28:c:18:ASP:N	28:c:18:ASP:OD1	2.36	0.55
51:1:757:G:H2'	51:1:758:C:C5'	2.35	0.55
51:1:2114:A:C2	51:1:2167:U:H1'	2.41	0.55
51:1:2195:U:O2'	51:1:2196:C:H5'	2.06	0.55
53:3:505:G:H5''	53:3:534:U:H2'	1.89	0.55
54:4:4:U:H3	63:5:36:A:H61	1.55	0.55
49:y:15:ASN:O	49:y:19:LEU:N	2.40	0.55
51:1:296:U:H2'	51:1:297:G:H8	1.71	0.55
51:1:392:U:H2'	51:1:393:C:C6	2.42	0.55
51:1:613:A:H5''	51:1:614:A:N7	2.22	0.55
51:1:2217:G:O2'	51:1:2218:G:H5'	2.06	0.55
58:B1:633:ALA:HB2	59:B2:808:ASN:N	2.19	0.55
58:B1:1166:GLY:HA3	58:B1:1174:ARG:HB2	1.87	0.55
35:k:70:ARG:HG2	35:k:76:VAL:HG12	1.89	0.54
39:o:69:ASP:N	39:o:69:ASP:OD1	2.36	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
51:1:2345:G:H5'	51:1:2347:C:H5'	1.89	0.54
51:1:2545:G:O2'	51:1:2546:U:H5'	2.07	0.54
58:B1:39:LYS:O	58:B1:273:ILE:HG21	2.06	0.54
8:H:71:ARG:HB3	8:H:74:ILE:HD13	1.89	0.54
37:m:27:SER:H	37:m:66:ARG:HH12	1.54	0.54
51:1:2114:A:C8	51:1:2115:G:H1'	2.42	0.54
57:A2:100:LEU:HD23	57:A2:115:ILE:HG21	1.89	0.54
29:d:76:PRO:HA	29:d:82:GLY:HA3	1.90	0.54
51:1:1086:A:H5'	51:1:1103:A:C2	2.41	0.54
51:1:1565:C:HO2'	51:1:1566:A:H8	1.53	0.54
51:1:2850:A:N1	51:1:2869:G:H4'	2.21	0.54
52:2:40:U:N3	52:2:44:G:OP2	2.40	0.54
58:B1:1175:LEU:HD22	58:B1:1190:ILE:HD11	1.88	0.54
10:J:23:THR:HA	10:J:28:ARG:HA	1.88	0.54
12:L:113:LYS:O	53:3:1239:A:O2'	2.22	0.54
51:1:128:C:H2'	51:1:129:C:H6	1.70	0.54
51:1:472:A:H2'	51:1:473:G:H5'	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1511:G:H2'	51:1:1512:C:H6	1.73	0.54
51:1:1530:G:H22	51:1:1542:U:H1'	1.73	0.54
51:1:1601:G:C2'	51:1:1602:U:H5'	2.37	0.54
51:1:2297:A:N1	51:1:2321:U:C5	2.75	0.54
53:3:158:G:N2	53:3:163:C:O2	2.36	0.54
58:B1:759:ILE:HG23	58:B1:771:GLN:HB3	1.89	0.54
7:G:19:THR:HA	7:G:37:VAL:HA	1.88	0.54
19:S:84:ARG:NH2	53:3:1059:C:O3'	2.40	0.54
51:1:784:G:C5'	51:1:785:G:OP1	2.54	0.54
51:1:1068:G:N2	51:1:1096:A:H1'	2.23	0.54
51:1:2734:A:C2'	51:1:2735:G:H5'	2.38	0.54
58:B1:145:VAL:HG23	58:B1:159:ILE:HG22	1.89	0.54
58:B1:799:ARG:HG2	58:B1:1325:PHE:HZ	1.72	0.54
7:G:53:LEU:HD21	7:G:215:ALA:HB1	1.88	0.54
36:l:20:GLY:HA2	36:l:28:GLY:HA2	1.90	0.54
51:1:682:G:N2	51:1:796:C:O2	2.41	0.54
51:1:1297:C:H2'	51:1:1298:C:C6	2.43	0.54
59:B2:917:SER:O	59:B2:919:ARG:HG3	2.07	0.54
17:Q:64:SER:OG	17:Q:65:TYR:N	2.41	0.54
21:U:69:ASP:OD1	21:U:69:ASP:N	2.38	0.54
51:1:21:A:O2'	51:1:22:C:H5'	2.08	0.54
51:1:268:C:H2'	51:1:269:C:H6	1.73	0.54
51:1:1083:U:H2'	51:1:1084:A:H3'	1.89	0.54
51:1:1856:U:H2'	51:1:1857:G:O4'	2.08	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	2.41	0.54
59:B2:29:SER:O	59:B2:33:ASP:HB2	2.08	0.54
64:7:11:A:H2'	64:7:12:G:H8	1.72	0.54
12:L:73:GLU:HG2	12:L:90:VAL:HG22	1.89	0.54
29:d:76:PRO:HD2	51:1:673:C:H5''	1.89	0.54
51:1:1601:G:O2'	51:1:1602:U:H5'	2.08	0.54
51:1:2092:U:C4'	51:1:2093:G:H5''	2.37	0.54
58:B1:746:LEU:HG	58:B1:758:PRO:HG3	1.90	0.54
30:e:21:TYR:OH	30:e:164:GLU:OE1	2.26	0.54
42:r:51:VAL:HG22	42:r:52:PRO:HD2	1.89	0.54
48:x:29:LEU:HD12	51:1:2230:G:H5''	1.90	0.54
49:y:19:LEU:O	49:y:23:ARG:N	2.35	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
57:A2:29:GLU:HG3	57:A2:200:LYS:HG3	1.88	0.54
59:B2:684:ASN:OD1	59:B2:687:ARG:NH2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:102:ASN:ND2	53:3:1073:U:O2	2.39	0.54
16:P:86:LYS:HG3	16:P:114:PRO:HD3	1.89	0.54
51:1:8:C:H2'	51:1:9:G:H8	1.73	0.54
51:1:340:A:H2'	51:1:341:C:O4'	2.06	0.54
51:1:402:A:C2'	51:1:403:U:H5'	2.38	0.54
51:1:752:A:H62	51:1:2609:U:H3	1.56	0.54
51:1:1389:G:O2'	51:1:1390:U:H5'	2.07	0.54
51:1:2092:U:C5	51:1:2199:A:H2	2.26	0.54
53:3:1023:U:H2'	53:3:1024:G:C8	2.43	0.54
58:B1:58:CYS:SG	58:B1:59:ALA:N	2.80	0.54
58:B1:99:ARG:HG3	58:B1:99:ARG:HH11	1.73	0.54
58:B1:814:CYS:SG	58:B1:883:ARG:NH2	2.81	0.54
27:b:227:VAL:HG11	51:1:784:G:N1	2.23	0.53
34:j:2:LYS:HA	51:1:995:C:N3	2.23	0.53
38:n:35:LYS:NZ	38:n:100:CYS:SG	2.81	0.53
51:1:1528:A:C2'	51:1:1529:G:H5'	2.38	0.53
51:1:1748:C:H2'	51:1:1749:A:H8	1.73	0.53
57:A1:100:LEU:HD21	57:A1:121:VAL:HG11	1.90	0.53
58:B1:804:ALA:HA	58:B1:1259:GLN:HG3	1.88	0.53
58:B1:1155:ILE:HG13	58:B1:1210:ILE:HB	1.89	0.53
25:Y:66:ILE:HG21	25:Y:70:LYS:HB3	1.91	0.53
31:f:103:ASN:ND2	31:f:113:ASP:OD1	2.41	0.53
36:l:80:SER:HB3	36:l:114:GLY:HA3	1.89	0.53
37:m:64:TRP:HB2	37:m:104:GLU:HB2	1.89	0.53
44:t:54:GLU:HB3	44:t:88:LYS:HE3	1.90	0.53
51:1:44:A:O2'	51:1:45:G:H5'	2.08	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
51:1:1310:G:O2'	51:1:1311:G:H5'	2.06	0.53
51:1:2850:A:C2	51:1:2869:G:H4'	2.43	0.53
59:B2:1117:LEU:HD12	59:B2:1195:ILE:HG12	1.90	0.53
1:A:35:ASP:OD1	18:R:2:ARG:NH1	2.42	0.53
39:o:40:ILE:HD12	39:o:44:GLY:HA2	1.91	0.53
41:q:90:ASP:OD1	41:q:90:ASP:N	2.37	0.53
51:1:143:C:H2'	51:1:144:A:H8	1.73	0.53
51:1:358:U:H2'	51:1:359:G:H8	1.72	0.53
51:1:2644:G:O2'	51:1:2645:G:H5'	2.09	0.53
58:B1:205:LEU:HG	58:B1:217:LEU:HB3	1.91	0.53
9:I:55:ARG:O	9:I:59:LYS:N	2.40	0.53
12:L:77:ARG:NH2	53:3:1381:U:O2	2.41	0.53
16:P:15:VAL:HG12	16:P:76:TYR:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:r:75:VAL:HG23	42:r:86:GLN:HG2	1.90	0.53
51:1:141:G:H3'	51:1:142:A:O4'	2.07	0.53
51:1:973:A:H5'	51:1:1188:U:H1'	1.90	0.53
51:1:1005:C:H6	51:1:1005:C:O5'	1.90	0.53
51:1:1175:A:H3'	51:1:1176:U:C5'	2.37	0.53
51:1:2123:G:H2'	51:1:2124:G:H8	1.73	0.53
51:1:2631:G:O2'	51:1:2632:A:H5'	2.08	0.53
58:B1:111:THR:HG22	58:B1:300:GLN:NE2	2.23	0.53
58:B1:209:ASN:HA	58:B1:214:ARG:HH21	1.74	0.53
58:B1:975:ILE:HD11	58:B1:1003:LEU:HD11	1.91	0.53
59:B2:633:LEU:HD13	59:B2:644:LEU:HD23	1.89	0.53
64:7:25:C:H42	64:7:45:G:H22	1.56	0.53
9:I:154:VAL:HA	9:I:157:ALA:HB3	1.91	0.53
13:M:92:PRO:O	13:M:116:ARG:NH2	2.42	0.53
34:j:38:GLY:HA3	34:j:50:THR:HG23	1.90	0.53
51:1:268:C:H2'	51:1:269:C:C6	2.44	0.53
51:1:820:A:O2'	51:1:821:A:H5'	2.08	0.53
51:1:1063:G:N1	51:1:1075:C:N4	2.52	0.53
51:1:1171:G:H2'	51:1:1172:C:C4'	2.38	0.53
51:1:1386:C:H2'	51:1:1387:A:C8	2.41	0.53
51:1:2092:U:C5	51:1:2199:A:C2	2.97	0.53
51:1:2742:G:O2'	51:1:2743:U:H5'	2.08	0.53
57:A1:47:LEU:HD23	57:A1:51:MET:HG3	1.90	0.53
58:B1:785:ASP:O	58:B1:789:LYS:HB2	2.08	0.53
59:B2:628:HIS:HB3	59:B2:647:ARG:HH21	1.74	0.53
3:C:20:TYR:OH	51:1:2348:U:H5'	2.08	0.53
39:o:31:THR:HG23	39:o:34:HIS:H	1.73	0.53
40:p:105:LYS:O	40:p:108:ARG:NH2	2.42	0.53
51:1:876:C:H2'	51:1:877:A:O4'	2.08	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
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
51:1:53:A:C2'	51:1:54:G:H5'	2.39	0.53
51:1:140:C:H2'	51:1:141:G:H5'	1.90	0.53
51:1:176:A:O2'	51:1:177:G:H5'	2.08	0.53
51:1:279:A:N6	51:1:361:G:H1'	2.20	0.53
51:1:521:U:H2'	51:1:522:A:H8	1.73	0.53
51:1:925:A:O2'	51:1:926:G:H5'	2.08	0.53
51:1:1530:G:N2	51:1:1542:U:H1'	2.23	0.53
51:1:1558:C:O4'	51:1:1560:G:C8	2.62	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
51:1:1948:G:H21	53:3:1418:A:H2	1.49	0.53
53:3:458:U:H3	53:3:474:G:H1	1.56	0.53
57:A1:205:MET:HE3	57:A1:213:PRO:HB3	1.91	0.53
63:5:38:A:H2'	63:5:39:U:H4'	1.91	0.53
10:J:104:ILE:O	10:J:111:ARG:NH1	2.41	0.53
25:Y:47:GLN:NE2	25:Y:51:ASN:OD1	2.40	0.53
47:w:55:LEU:HD12	47:w:76:ILE:HD12	1.90	0.53
51:1:368:A:H2'	51:1:369:U:C5'	2.39	0.53
51:1:1278:C:O2'	51:1:1279:G:H5'	2.09	0.53
51:1:2762:C:C2'	51:1:2763:G:H5'	2.39	0.53
58:B1:832:LYS:HB3	58:B1:1242:ARG:NH1	2.24	0.53
14:N:115:VAL:HG23	53:3:1367:C:H5''	1.91	0.53
35:k:42:THR:HG22	35:k:57:VAL:HG12	1.91	0.53
50:z:36:GLU:O	50:z:37:ARG:NH1	2.42	0.53
51:1:894:U:O2'	51:1:895:U:H5'	2.09	0.53
51:1:1827:U:H2'	51:1:1828:G:H5'	1.90	0.53
51:1:2102:G:H2'	51:1:2103:C:O4'	2.09	0.53
57:A2:43:LEU:HD13	57:A2:217:ILE:HD11	1.90	0.53
58:B1:770:LEU:CD1	59:B2:618:GLN:HG3	2.36	0.53
58:B1:800:LEU:HB3	58:B1:920:ALA:HB1	1.90	0.53
17:Q:49:ARG:NH1	17:Q:88:ASP:OD2	2.42	0.53
26:Z:28:LEU:HA	26:Z:31:VAL:HG12	1.90	0.53
33:i:25:PRO:HG2	51:1:1068:G:N2	2.24	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
57:A1:16:ILE:HG23	57:A1:26:VAL:HG22	1.91	0.53
59:B2:243:PRO:HB2	59:B2:274:ILE:HG23	1.90	0.53
59:B2:360:LEU:HD13	59:B2:378:ARG:HH11	1.72	0.53
59:B2:1070:HIS:NE2	59:B2:1114:GLU:OE1	2.36	0.53
33:i:53:PRO:HD2	33:i:77:VAL:HG11	1.91	0.52
42:r:4:VAL:HG12	42:r:13:ARG:HA	1.91	0.52
51:1:40:U:H2'	51:1:41:C:C6	2.43	0.52
51:1:341:C:O2'	51:1:342:A:H5'	2.08	0.52
51:1:441:U:O2'	51:1:442:G:H5'	2.08	0.52
51:1:519:U:H2'	51:1:520:G:H8	1.75	0.52
51:1:729:G:H5''	51:1:730:A:H5''	1.91	0.52
51:1:2425:A:H4'	51:1:2426:A:H5''	1.91	0.52
51:1:2707:U:H2'	51:1:2708:G:C8	2.44	0.52
58:B1:39:LYS:O	58:B1:273:ILE:HG23	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:215:LYS:HA	58:B1:218:THR:HG22	1.92	0.52
7:G:61:SER:OG	7:G:62:ARG:NH1	2.42	0.52
51:1:57:C:H2'	51:1:58:G:O4'	2.09	0.52
51:1:878:A:H2'	51:1:879:G:O4'	2.09	0.52
51:1:1161:C:H2'	51:1:1162:G:C8	2.44	0.52
51:1:1409:U:H2'	51:1:1410:G:C8	2.44	0.52
51:1:1678:A:H2'	51:1:1679:A:C5'	2.38	0.52
51:1:1917:U:C2'	51:1:1918:A:H5'	2.39	0.52
51:1:2194:U:H2'	51:1:2195:U:C6	2.44	0.52
53:3:1023:U:H2'	53:3:1024:G:H8	1.74	0.52
64:7:43:A:H2'	64:7:44:A:C8	2.44	0.52
27:b:257:ARG:NH2	27:b:262:THR:OG1	2.42	0.52
42:r:54:VAL:HG13	42:r:55:ASP:H	1.74	0.52
51:1:1794:A:O2'	51:1:1795:C:H5'	2.10	0.52
51:1:2747:G:O6	51:1:2754:U:H2'	2.09	0.52
59:B2:246:LEU:HB3	59:B2:269:ILE:HD13	1.91	0.52
10:J:152:VAL:HG21	13:M:98:LEU:HD13	1.91	0.52
51:1:481:G:H1'	51:1:506:G:H21	1.71	0.52
51:1:543:G:C2'	51:1:544:C:H5''	2.37	0.52
51:1:611:C:H2'	51:1:612:G:O4'	2.09	0.52
51:1:1560:G:H2'	51:1:1560:G:N3	2.24	0.52
51:1:2204:G:H2'	51:1:2205:A:C8	2.44	0.52
51:1:2290:G:H2'	51:1:2291:U:H6	1.74	0.52
53:3:203:G:N2	53:3:204:G:O6	2.43	0.52
58:B1:99:ARG:HA	58:B1:248:ASP:HB2	1.92	0.52
59:B2:524:ILE:HG21	59:B2:708:VAL:HG13	1.92	0.52
51:1:49:A:O5'	51:1:51:G:H5'	2.09	0.52
51:1:2470:G:O2'	51:1:2471:A:H5'	2.10	0.52
59:B2:811:ASN:HA	59:B2:815:SER:HB2	1.90	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
51:1:723:C:O2'	51:1:724:U:H5'	2.09	0.52
58:B1:68:TYR:CA	58:B1:75:TYR:HE2	2.22	0.52
58:B1:78:LEU:O	58:B1:78:LEU:HD13	2.08	0.52
51:1:213:A:O2'	51:1:214:G:H5'	2.09	0.52
51:1:995:C:H6	51:1:995:C:H5'	1.74	0.52
51:1:1507:C:H2'	51:1:1508:A:C4'	2.40	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
51:1:2617:U:H2'	51:1:2618:G:H5'	1.91	0.52
58:B1:30:ILE:HG21	58:B1:241:VAL:O	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:107:LYS:HB3	8:H:110:LEU:HD23	1.92	0.52
9:I:150:LYS:O	9:I:155:LYS:NZ	2.43	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
51:1:2776:A:C6	51:1:2782:G:H1'	2.45	0.52
10:J:106:ALA:O	10:J:111:ARG:NH2	2.43	0.52
51:1:138:U:C5	51:1:139:U:H5	2.28	0.52
51:1:215:G:C4'	51:1:216:A:H4'	2.39	0.52
51:1:1878:G:O2'	51:1:1879:C:H5'	2.09	0.52
51:1:1930:G:C2'	51:1:1931:U:OP2	2.58	0.52
51:1:2105:U:N3	51:1:2184:A:C2	2.78	0.52
51:1:2651:C:O2'	51:1:2652:C:H5'	2.10	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
53:3:113:G:N3	53:3:353:A:O2'	2.42	0.52
57:A2:28:LEU:HD22	57:A2:201:LEU:HD23	1.91	0.52
58:B1:390:LEU:N	58:B1:390:LEU:CD1	2.73	0.52
8:H:30:ASP:N	8:H:30:ASP:OD1	2.41	0.52
27:b:92:LEU:HD11	27:b:100:ARG:HB3	1.91	0.52
35:k:75:SER:OG	40:p:72:VAL:O	2.26	0.52
40:p:28:LYS:HB3	40:p:39:LEU:HD21	1.91	0.52
43:s:109:ASP:OD1	43:s:109:ASP:N	2.42	0.52
46:v:83:LYS:HD3	46:v:85:LYS:HZ1	1.75	0.52
51:1:597:G:H2'	51:1:598:U:C6	2.45	0.52
51:1:870:U:O2'	51:1:871:U:H5'	2.10	0.52
51:1:1338:G:H2'	51:1:1339:G:H8	1.74	0.52
51:1:1503:A:C3'	51:1:1504:A:H5''	2.40	0.52
51:1:2216:G:H2'	51:1:2217:G:H8	1.74	0.52
51:1:2463:C:O2'	51:1:2464:G:H5'	2.10	0.52
53:3:816:A:OP1	53:3:1526:G:O2'	2.28	0.52
8:H:133:MET:HE3	8:H:167:TYR:HB2	1.91	0.51
35:k:31:ARG:NH2	51:1:2676:C:OP2	2.43	0.51
51:1:8:C:H2'	51:1:9:G:C8	2.45	0.51
51:1:386:G:H3'	51:1:387:U:H5''	1.93	0.51
51:1:1534:U:H2'	51:1:1536:C:O4'	2.10	0.51
51:1:2529:G:H5''	51:1:2530:A:H5''	1.91	0.51
53:3:1077:G:N2	53:3:1080:A:OP2	2.40	0.51
23:W:71:ASP:N	23:W:71:ASP:OD1	2.44	0.51
27:b:257:ARG:HH22	27:b:262:THR:HG1	1.56	0.51
30:e:27:VAL:O	30:e:29:ARG:NH1	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:v:77:VAL:HG23	46:v:89:ILE:HG12	1.92	0.51
51:1:69:C:H2'	51:1:70:G:C8	2.46	0.51
51:1:282:A:H2'	51:1:283:G:C8	2.42	0.51
51:1:439:A:H2'	51:1:440:C:H6	1.75	0.51
51:1:1403:A:H2'	51:1:1404:C:C6	2.45	0.51
51:1:1722:A:O2'	51:1:1723:G:H5'	2.10	0.51
51:1:2611:C:O2	51:1:2611:C:C2'	2.58	0.51
58:B1:144:TYR:CE1	58:B1:162:GLU:CD	2.88	0.51
15:O:5:ARG:N	15:O:76:ILE:O	2.43	0.51
15:O:24:GLU:HA	15:O:27:GLU:HB2	1.93	0.51
51:1:757:G:C2'	51:1:758:C:H5'	2.38	0.51
51:1:891:G:H2'	51:1:892:A:C8	2.46	0.51
51:1:1668:A:C4'	51:1:1669:A:H5'	2.36	0.51
51:1:1923:U:H2'	51:1:1924:C:C6	2.46	0.51
57:A2:140:ILE:HD12	57:A2:142:MET:HE3	1.92	0.51
58:B1:201:LEU:HD12	58:B1:224:LEU:HD12	1.92	0.51
58:B1:375:GLU:HG2	59:B2:1245:ALA:O	2.10	0.51
58:B1:683:ILE:HD12	58:B1:754:ILE:HG21	1.92	0.51
58:B1:1167:LYS:HZ2	58:B1:1170:LYS:HB2	1.76	0.51
59:B2:974:ARG:HD2	59:B2:1014:LEU:HD21	1.92	0.51
4:D:3:ARG:NH1	51:1:752:A:OP1	2.44	0.51
7:G:14:HIS:HB3	7:G:42:LEU:HD21	1.90	0.51
21:U:6:LEU:HD22	21:U:17:TYR:HB3	1.91	0.51
31:f:7:PRO:O	31:f:68:ARG:NH2	2.38	0.51
51:1:246:C:H2'	51:1:247:G:C5'	2.40	0.51
51:1:492:A:H2'	51:1:493:G:O4'	2.09	0.51
51:1:736:C:H42	51:1:760:G:H1	1.58	0.51
51:1:1574:C:H2'	51:1:1575:C:H6	1.74	0.51
51:1:1910:G:H1	51:1:1920:C:H42	1.58	0.51
51:1:2555:U:O2	51:1:2555:U:O4'	2.29	0.51
58:B1:112:ALA:HA	58:B1:238:ILE:HA	1.91	0.51
58:B1:850:LYS:HB2	58:B1:857:LEU:HB2	1.91	0.51
59:B2:93:SER:HA	59:B2:128:PRO:HA	1.93	0.51
59:B2:714:VAL:HB	59:B2:787:PRO:HD2	1.92	0.51
60:W0:3:ARG:NH1	60:W0:55:GLU:OE2	2.40	0.51
22:V:60:ILE:HA	22:V:74:LEU:HA	1.93	0.51
51:1:291:G:O2'	51:1:292:U:H5'	2.11	0.51
51:1:1112:G:H2'	51:1:1113:U:O4'	2.10	0.51
64:6:1:C:H2'	64:6:2:G:H8	1.75	0.51
2:B:2:VAL:HG23	51:1:2015:A:C6	2.46	0.51
6:F:19:ARG:HB2	6:F:24:ARG:HD2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:12:ARG:NH1	9:I:32:LYS:O	2.42	0.51
17:Q:36:VAL:HG21	17:Q:73:LEU:HB3	1.91	0.51
45:u:73:ASN:ND2	45:u:80:ASP:OD2	2.43	0.51
51:1:1717:A:H2'	51:1:1718:G:C5'	2.40	0.51
51:1:1722:A:H62	51:1:1738:G:H1'	1.75	0.51
58:B1:220:ARG:HG2	58:B1:220:ARG:NH1	2.25	0.51
64:7:9:G:O4'	64:7:46:G:N3	2.42	0.51
1:A:9:TYR:OH	30:e:101:ARG:NH2	2.41	0.51
8:H:130:ARG:NH2	8:H:165:GLU:OE1	2.43	0.51
15:O:29:ALA:O	15:O:33:GLY:N	2.42	0.51
17:Q:40:THR:CG2	65:h:6:5OH:OS	2.55	0.51
21:U:25:ARG:O	53:3:110:C:O2'	2.28	0.51
28:c:13:ARG:NH2	40:p:74:GLN:OE1	2.43	0.51
31:f:174:LYS:CG	51:1:2529:G:H4'	2.34	0.51
51:1:286:U:H2'	51:1:287:G:H8	1.76	0.51
51:1:355:U:H2'	51:1:356:G:C8	2.45	0.51
51:1:707:G:H2'	51:1:708:G:O4'	2.11	0.51
51:1:724:U:O2'	51:1:725:G:H5'	2.11	0.51
51:1:1542:U:O2'	51:1:1543:G:H5'	2.09	0.51
51:1:2670:A:H2'	51:1:2671:G:C8	2.45	0.51
58:B1:275:ARG:HH12	58:B1:278:ARG:NH1	2.09	0.51
8:H:175:HIS:ND1	53:3:1109:C:OP2	2.44	0.51
10:J:23:THR:HG22	10:J:28:ARG:HB3	1.91	0.51
15:O:39:PRO:HD2	53:3:1123:U:H4'	1.92	0.51
30:e:69:ALA:O	30:e:80:GLN:NE2	2.43	0.51
30:e:91:ARG:NH2	52:2:43:C:O2	2.36	0.51
37:m:38:ARG:HB3	37:m:98:PRO:HD3	1.92	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
51:1:1678:A:C2'	51:1:1679:A:H5'	2.40	0.51
51:1:2687:U:H2'	51:1:2688:G:O4'	2.11	0.51
53:3:460:A:H2'	53:3:461:A:H8	1.75	0.51
10:J:123:LEU:HD12	53:3:7:A:H2'	1.92	0.51
27:b:50:THR:HG23	51:1:1813:G:H21	1.76	0.51
36:l:42:SER:HB2	51:1:672:C:H5	1.76	0.51
51:1:800:A:H4'	51:1:801:G:H3'	1.92	0.51
51:1:1415:U:H1'	51:1:1588:G:N2	2.26	0.51
51:1:2570:G:C2'	51:1:2571:U:H5'	2.40	0.51
53:3:202:G:H1	53:3:215:C:H42	1.57	0.51
58:B1:902:ASP:HB3	58:B1:905:ARG:HB2	1.93	0.51
59:B2:125:GLY:HA2	59:B2:499:SER:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:NA:137:ILE:O	61:NA:138:ILE:C	2.53	0.51
31:f:136:ASP:HB3	31:f:139:VAL:HG12	1.92	0.51
33:i:25:PRO:HG3	51:1:1095:A:C2	2.46	0.51
51:1:251:A:H2'	51:1:252:G:O4'	2.10	0.51
51:1:580:U:O5'	51:1:580:U:H6	1.94	0.51
51:1:2618:G:H2'	51:1:2619:C:O4'	2.11	0.51
33:i:126:ARG:HD2	51:1:1080:A:H4'	1.93	0.50
39:o:40:ILE:HG22	39:o:47:VAL:HG12	1.91	0.50
51:1:438:G:H2'	51:1:439:A:H8	1.76	0.50
51:1:928:A:O2'	51:1:929:U:H5'	2.10	0.50
51:1:1468:U:H2'	51:1:1522:A:N6	2.26	0.50
58:B1:437:PHE:HZ	58:B1:453:VAL:HG11	1.76	0.50
58:B1:505:ASP:OD2	59:B2:812:PHE:HA	2.11	0.50
4:D:14:ARG:NH1	51:1:1377:G:O3'	2.44	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
51:1:673:C:H2'	51:1:674:G:C5'	2.41	0.50
58:B1:1179:PRO:HD2	58:B1:1184:ASP:HA	1.93	0.50
64:6:43:A:H2'	64:6:44:A:C8	2.45	0.50
12:L:65:LEU:O	12:L:69:ARG:N	2.43	0.50
20:T:23:SER:OG	20:T:25:GLU:OE1	2.30	0.50
44:t:65:GLY:N	44:t:79:ASP:OD1	2.43	0.50
46:v:51:GLN:OE1	46:v:79:ARG:NH2	2.40	0.50
51:1:1310:G:H2'	51:1:1311:G:C5'	2.38	0.50
51:1:1754:A:C6	51:1:1755:A:C6	2.98	0.50
51:1:2285:C:O2'	51:1:2286:G:H5'	2.11	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
53:3:1013:G:N2	53:3:1016:A:OP2	2.35	0.50
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE21	1.67	0.50
59:B2:400:VAL:HG21	59:B2:452:ARG:HE	1.76	0.50
3:C:7:LYS:HD3	51:1:2420:C:H5''	1.93	0.50
51:1:1539:U:H2'	51:1:1540:G:H8	1.76	0.50
53:3:664:G:H22	53:3:741:G:H1	1.60	0.50
55:8:13:DT:OP2	58:B1:791:ALA:CB	2.59	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:156:SER:OG	27:b:157:ALA:N	2.44	0.50
27:b:206:LYS:HD2	51:1:729:G:C8	2.46	0.50
28:c:161:MET:HE1	51:1:2050:C:O2	2.11	0.50
29:d:191:ASP:O	29:d:195:GLN:NE2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
51:1:1270:C:H5''	51:1:1271:G:H5''	1.93	0.50
51:1:2248:C:H2'	51:1:2249:U:H5'	1.93	0.50
51:1:2348:U:O2'	51:1:2349:G:H5'	2.12	0.50
59:B2:411:ARG:NH2	59:B2:427:ASP:OD2	2.44	0.50
59:B2:529:ARG:HH11	59:B2:572:ILE:HG22	1.77	0.50
19:S:68:ARG:NH2	53:3:974:A:OP1	2.45	0.50
51:1:131:A:H2'	51:1:132:G:H8	1.77	0.50
51:1:386:G:H3'	51:1:387:U:C5'	2.41	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
51:1:2250:G:H8	51:1:2250:G:O5'	1.95	0.50
51:1:2888:C:H2'	51:1:2889:C:H6	1.77	0.50
53:3:1266:G:N2	53:3:1269:A:OP2	2.29	0.50
64:7:9:G:C2	64:7:45:G:C6	3.00	0.50
7:G:126:ASP:OD1	7:G:126:ASP:N	2.42	0.50
8:H:4:VAL:HG21	8:H:9:ILE:HD13	1.93	0.50
15:O:42:LEU:HB3	15:O:71:LEU:HB2	1.94	0.50
21:U:5:ARG:HB3	53:3:376:G:H5''	1.93	0.50
51:1:630:G:H4'	51:1:640:C:H4'	1.93	0.50
51:1:1087:G:H2'	51:1:1089:A:H5'	1.94	0.50
51:1:1348:C:C5	51:1:1349:C:C5	3.00	0.50
51:1:1528:A:H2'	51:1:1529:G:O4'	2.11	0.50
51:1:1593:A:H2'	51:1:1594:U:C6	2.47	0.50
51:1:2302:U:O2'	51:1:2303:G:H5'	2.12	0.50
58:B1:972:LYS:HD2	58:B1:1004:ALA:HA	1.93	0.50
59:B2:255:ILE:HB	59:B2:263:VAL:HB	1.92	0.50
59:B2:533:LEU:HD13	59:B2:540:ARG:HH21	1.77	0.50
62:NG:161:SER:HA	62:NG:170:PRO:HA	1.93	0.50
51:1:208:C:O5'	51:1:208:C:H6	1.93	0.50
51:1:1061:U:H4'	51:1:1070:A:H1'	1.93	0.50
51:1:1416:G:H2'	51:1:1417:C:C6	2.46	0.50
51:1:1748:C:H2'	51:1:1749:A:C8	2.47	0.50
51:1:2670:A:O2'	51:1:2671:G:H5'	2.12	0.50
51:1:2758:A:C2'	51:1:2759:G:H5'	2.40	0.50
53:3:494:G:H2'	53:3:496:A:H8	1.76	0.50
58:B1:412:LEU:HD23	58:B1:416:ILE:HG13	1.92	0.50
58:B1:421:VAL:O	58:B1:436:ALA:HA	2.12	0.50
58:B1:1371:ARG:HE	58:B1:1372:ARG:NH1	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:36:VAL:HG12	21:U:53:ASP:HB3	1.94	0.50
27:b:50:THR:HG23	51:1:1813:G:N2	2.27	0.50
27:b:147:PRO:HG3	27:b:184:GLU:HG2	1.92	0.50
44:t:7:LEU:HD13	44:t:46:ALA:HA	1.94	0.50
51:1:262:A:H2'	51:1:263:G:O4'	2.12	0.50
51:1:898:C:H2'	51:1:899:A:O4'	2.12	0.50
51:1:2525:G:N2	51:1:2539:C:C2	2.79	0.50
57:A1:100:LEU:HB2	57:A1:144:ILE:HG23	1.94	0.50
58:B1:145:VAL:HG12	58:B1:184:ALA:HB1	1.94	0.50
7:G:221:ARG:HG2	7:G:224:ARG:HH11	1.77	0.49
17:Q:120:ARG:HH12	53:3:500:G:H5'	1.77	0.49
27:b:92:LEU:HD21	27:b:100:ARG:HD3	1.93	0.49
33:i:25:PRO:HB3	51:1:1095:A:N1	2.27	0.49
51:1:30:G:H2'	51:1:31:C:C6	2.47	0.49
51:1:155:A:H2'	51:1:156:A:H8	1.76	0.49
51:1:355:U:H2'	51:1:356:G:H8	1.77	0.49
51:1:539:G:O2'	51:1:540:C:H5'	2.12	0.49
51:1:1345:C:H6	51:1:1345:C:H5'	1.77	0.49
53:3:1178:G:N2	53:3:1181:G:OP2	2.43	0.49
58:B1:395:LYS:NZ	58:B1:399:LYS:CD	2.74	0.49
59:B2:232:ILE:HG12	59:B2:237:LEU:HG	1.94	0.49
64:7:9:G:O4'	64:7:46:G:C2	2.65	0.49
1:A:35:ASP:OD1	1:A:35:ASP:N	2.42	0.49
27:b:137:GLY:O	27:b:162:GLN:NE2	2.45	0.49
31:f:41:GLU:HG2	31:f:54:ARG:HH21	1.77	0.49
51:1:173:A:H2'	51:1:174:U:C6	2.47	0.49
51:1:840:C:O2'	51:1:841:G:H5'	2.12	0.49
51:1:1293:C:H2'	51:1:1294:U:C6	2.46	0.49
51:1:1388:G:O2'	51:1:1389:G:H5'	2.12	0.49
51:1:1614:A:H2'	51:1:1615:C:H5'	1.94	0.49
51:1:1789:A:H2'	51:1:1790:C:O4'	2.13	0.49
51:1:1916:A:H2'	51:1:1917:U:O4'	2.12	0.49
51:1:2257:U:O2'	51:1:2258:C:H5'	2.13	0.49
51:1:2634:A:O2'	51:1:2635:A:H5'	2.12	0.49
51:1:2734:A:H2'	51:1:2735:G:C5'	2.42	0.49
53:3:1538:C:O2'	53:3:1539:C:H5'	2.11	0.49
58:B1:749:LYS:HB3	58:B1:755:ILE:HD11	1.94	0.49
59:B2:18:ARG:HE	59:B2:620:ASN:HA	1.77	0.49
27:b:146:LYS:HB2	27:b:149:LYS:HB2	1.94	0.49
28:c:81:GLU:HG3	51:1:2636:C:O5'	2.13	0.49
31:f:87:GLN:NE2	31:f:129:GLU:OE2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:187:G:C6	51:1:188:G:N7	2.80	0.49
51:1:1441:G:H2'	51:1:1442:U:H6	1.71	0.49
51:1:1702:G:H2'	51:1:1703:G:C5'	2.35	0.49
51:1:2241:A:O2'	51:1:2242:G:H5'	2.12	0.49
51:1:2286:G:H21	51:1:2287:A:N6	2.09	0.49
51:1:2533:U:H2'	51:1:2534:A:C5'	2.42	0.49
51:1:2836:U:H2'	51:1:2837:A:C8	2.47	0.49
53:3:401:C:O2'	53:3:621:A:N3	2.45	0.49
53:3:928:G:O2'	53:3:1533:C:OP1	2.22	0.49
57:A1:18:GLN:HA	57:A1:24:ALA:HA	1.94	0.49
59:B2:554:HIS:HD2	59:B2:558:VAL:HB	1.77	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
51:1:519:U:H2'	51:1:520:G:C8	2.48	0.49
51:1:609:A:H2'	51:1:610:C:O4'	2.11	0.49
51:1:644:A:H2'	51:1:645:C:C4'	2.42	0.49
51:1:1144:A:H2'	51:1:1145:C:C6	2.48	0.49
51:1:2283:C:H2'	51:1:2284:A:O4'	2.11	0.49
53:3:1137:C:H4'	53:3:1138:G:H5'	1.94	0.49
58:B1:1361:THR:OG1	59:B2:1282:GLY:O	2.28	0.49
11:K:46:GLN:HA	11:K:56:LYS:HB3	1.93	0.49
28:c:56:LYS:NZ	51:1:2830:C:H5''	2.28	0.49
33:i:110:GLN:HG2	33:i:121:ILE:HD13	1.93	0.49
51:1:482:A:H1'	51:1:498:G:N2	2.27	0.49
51:1:1796:U:H2'	51:1:1797:G:C8	2.45	0.49
51:1:2298:A:O2'	51:1:2299:U:H5'	2.12	0.49
53:3:1064:G:O2'	53:3:1190:G:N2	2.46	0.49
59:B2:400:VAL:HG11	59:B2:452:ARG:HD2	1.93	0.49
11:K:42:TRP:HB2	11:K:59:TYR:HB2	1.93	0.49
15:O:89:ARG:HH22	62:NG:165:PHE:H	1.60	0.49
17:Q:70:GLY:O	17:Q:107:LYS:NZ	2.44	0.49
30:e:57:ALA:HB2	30:e:64:PRO:HD3	1.95	0.49
42:r:71:LYS:HA	42:r:90:ARG:HG2	1.95	0.49
51:1:16:C:H2'	51:1:17:G:H8	1.77	0.49
51:1:236:C:H2'	51:1:237:C:C6	2.46	0.49
51:1:900:A:H2'	51:1:901:C:H5'	1.94	0.49
53:3:780:A:N6	53:3:801:U:OP2	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:56:GLY:HA2	27:b:212:TRP:HA	1.94	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)
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
51:1:286:U:H2'	51:1:287:G:C8	2.47	0.49
51:1:367:G:H2'	51:1:368:A:O4'	2.13	0.49
51:1:898:C:C2'	51:1:899:A:H5'	2.43	0.49
51:1:1084:A:O2'	51:1:1105:U:H4'	2.12	0.49
51:1:1387:A:C5'	51:1:1469:A:H1'	2.38	0.49
51:1:1785:A:O2'	51:1:1786:A:H8	1.96	0.49
51:1:2329:U:H2'	51:1:2330:G:H8	1.78	0.49
53:3:890:G:O2'	53:3:906:A:N6	2.46	0.49
58:B1:102:MET:HG2	58:B1:246:PRO:HD3	1.94	0.49
59:B2:9:LYS:HG2	59:B2:1171:ARG:HH12	1.77	0.49
63:5:51:U:H2'	63:5:52:G:C8	2.48	0.49
35:k:5:GLN:HE21	51:1:1668:A:H5''	1.78	0.49
51:1:69:C:O2'	51:1:70:G:H5'	2.13	0.49
51:1:78:U:H2'	51:1:79:C:H6	1.77	0.49
51:1:1111:A:H2'	51:1:1111:A:N3	2.28	0.49
51:1:1119:U:O2'	51:1:1120:G:H5'	2.13	0.49
55:8:3:DC:H2''	55:8:4:DT:C7	2.43	0.49
58:B1:255:LEU:HD23	58:B1:261:ALA:HB2	1.95	0.49
65:h:6:5OH:N	65:h:6:5OH:CS	2.75	0.49
7:G:101:THR:HG23	7:G:174:GLU:HG3	1.95	0.49
12:L:2:ARG:NH2	53:3:933:G:O6	2.46	0.49
17:Q:97:VAL:HG12	17:Q:99:GLY:H	1.78	0.49
29:d:77:ILE:HG23	51:1:1256:G:N2	2.26	0.49
30:e:84:ILE:HD11	51:1:2311:A:H1'	1.94	0.49
51:1:554:U:O2'	51:1:555:G:H5'	2.13	0.49
51:1:718:A:H2'	51:1:719:C:O4'	2.12	0.49
51:1:121:G:H4'	51:1:149:A:H5'	1.95	0.49
51:1:488:G:H22	51:1:491:G:H5''	1.77	0.49
51:1:886:A:C5	51:1:887:U:H1'	2.47	0.49
51:1:898:C:O2'	51:1:899:A:H5'	2.13	0.49
51:1:905:A:H2'	51:1:906:U:C5'	2.41	0.49
51:1:1465:G:H2'	51:1:1466:U:O4'	2.13	0.49
58:B1:550:VAL:O	58:B1:569:LEU:HA	2.13	0.49
59:B2:855:PRO:CG	59:B2:915:ASP:HB2	2.42	0.49
38:n:8:ARG:HH21	38:n:43:GLU:HG3	1.77	0.48
44:t:70:HIS:N	44:t:73:ARG:O	2.44	0.48
51:1:1534:U:H4'	51:1:1535:A:N1	2.27	0.48
51:1:2281:A:O2'	51:1:2282:G:H5'	2.12	0.48
51:1:2510:C:N4	51:1:2511:U:C4	2.81	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2527:C:O2'	51:1:2528:U:H5'	2.13	0.48
53:3:481:G:O2'	53:3:483:C:N4	2.46	0.48
1:A:37:CYS:O	1:A:41:HIS:N	2.45	0.48
51:1:1117:C:H2'	51:1:1118:C:H6	1.78	0.48
51:1:1409:U:H2'	51:1:1410:G:H8	1.76	0.48
51:1:1645:G:H5''	51:1:1646:C:H5'	1.94	0.48
51:1:1668:A:N3	51:1:1670:C:N4	2.60	0.48
51:1:2553:G:H22	63:5:75:C:H42	1.60	0.48
55:8:14:DC:H2'	55:8:15:DC:C6	2.48	0.48
16:P:96:ILE:HD13	16:P:109:ILE:HD13	1.94	0.48
21:U:18:GLN:HA	21:U:38:PHE:HA	1.95	0.48
26:Z:55:HIS:HA	26:Z:58:LYS:HD2	1.95	0.48
37:m:74:THR:HG21	37:m:86:LYS:HG2	1.94	0.48
40:p:2:ASN:HD21	51:1:2876:G:H4'	1.79	0.48
45:u:88:ASP:OD1	45:u:88:ASP:N	2.43	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
51:1:553:G:H2'	51:1:554: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	1.77	0.48
51:1:1871:A:H2'	51:1:1872:A:O4'	2.13	0.48
51:1:2180:U:O2'	51:1:2181:U:H5'	2.13	0.48
51:1:2214:C:H2'	51:1:2215:C:O4'	2.14	0.48
17:Q:110:LYS:HG3	17:Q:121:PRO:HG3	1.94	0.48
28:c:176:ASP:OD2	28:c:176:ASP:N	2.44	0.48
29:d:143:LEU:HD13	29:d:146:VAL:HG11	1.94	0.48
39:o:15:ARG:NH2	52:2:8:C:OP1	2.47	0.48
45:u:39:ASN:HB3	45:u:62:ALA:HB3	1.95	0.48
49:y:16:THR:O	49:y:20:ASN:ND2	2.46	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
51:1:1536: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
51:1:2367:G:O2'	51:1:2368:C:H5'	2.13	0.48
51:1:2843:G:O2'	51:1:2844:G:H5'	2.13	0.48
53:3:1223:C:H5'	53:3:1224:U:H5''	1.96	0.48
59:B2:786:GLY:N	59:B2:789:THR:OG1	2.41	0.48
13:M:29:SER:OG	13:M:30:LYS:N	2.44	0.48
14:N:10:ARG:NH2	53:3:1119:C:OP2	2.46	0.48
33:i:85:ILE:HD12	33:i:97:VAL:HG12	1.95	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
51:1:92:U:H2'	51:1:93:G:H5'	1.95	0.48
51:1:118:A:H2'	51:1:120:U:O4	2.13	0.48
51:1:214:G:H2'	51:1:215:G:C8	2.48	0.48
51:1:217:A:H2'	51:1:218:A:O4'	2.13	0.48
51:1:2126:A:H5'	51:1:2127:G:O5'	2.13	0.48
53:3:673:A:H2'	53:3:674:G:C8	2.49	0.48
53:3:776:G:N2	53:3:802:A:OP2	2.39	0.48
58:B1:968:ASN:HA	58:B1:1117:SER:HB2	1.96	0.48
11:K:41:ASP:OD2	11:K:58:HIS:NE2	2.39	0.48
12:L:41:ILE:HD11	53:3:1240:U:H5'	1.94	0.48
41:q:103:VAL:HA	41:q:106:THR:HG22	1.94	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
51:1:1910:G:N2	51:1:1911:U:C2	2.81	0.48
53:3:358:U:H2'	53:3:359:G:H8	1.78	0.48
53:3:517:G:N2	53:3:533:A:OP2	2.34	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
55:8:14:DC:H2'	55:8:15:DC:H6	1.79	0.48
58:B1:103:GLY:H	58:B1:244:VAL:HG22	1.79	0.48
58:B1:111:THR:HG23	58:B1:300:GLN:NE2	2.24	0.48
58:B1:201:LEU:HD11	58:B1:220:ARG:HG2	1.95	0.48
59:B2:562:GLU:OE1	59:B2:662:SER:OG	2.28	0.48
59:B2:800:MET:HE3	59:B2:800:MET:HB2	1.69	0.48
9:I:93:LEU:O	9:I:99:ASN:ND2	2.39	0.48
9:I:153:ARG:NH2	53:3:435:A:N3	2.61	0.48
29:d:149:ILE:HD11	29:d:172:ALA:HA	1.96	0.48
38:n:100:CYS:H	38:n:111:ALA:HA	1.79	0.48
51:1:275:C:C3'	51:1:276:U:H5''	2.40	0.48
51:1:572:A:H8	51:1:572:A:O5'	1.97	0.48
51:1:820:A:H2'	51:1:821:A:O4'	2.14	0.48
51:1:2547:A:H61	51:1:2561:U:H3	1.62	0.48
58:B1:1027:VAL:HB	58:B1:1121:LEU:HB2	1.95	0.48
9:I:94:GLU:HG3	9:I:190:LEU:HD21	1.95	0.48
13:M:83:ARG:NH2	53:3:587:G:OP1	2.43	0.48
14:N:91:GLU:HA	14:N:94:ARG:HB2	1.94	0.48
31:f:163:TYR:HB2	31:f:166:GLU:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:p:59:THR:HG22	40:p:72:VAL:HG12	1.95	0.48
51:1:596:U:C2	51:1:662:G:N2	2.82	0.48
51:1:841:G:C2	51:1:938:G:C2	3.01	0.48
51:1:940:G:H2'	51:1:941:A:C5'	2.41	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
58:B1:124:ILE:HG23	58:B1:128:LEU:HD12	1.94	0.48
58:B1:809:VAL:HG21	58:B1:909:ILE:HG12	1.95	0.48
58:B1:1261:LEU:HD12	58:B1:1304:ARG:HH21	1.79	0.48
31:f:122:ALA:HB2	31:f:132:LEU:HD23	1.94	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
51:1:2393:U:H2'	51:1:2394:C:H5'	1.94	0.48
51:1:2649:C:O2'	51:1:2650:U:H5'	2.13	0.48
58:B1:1036:ARG:HE	58:B1:1081:VAL:HG11	1.79	0.48
58:B1:1146:GLU:OE2	58:B1:1310:THR:HG22	2.14	0.48
17:Q:82:ARG:O	17:Q:95:HIS:N	2.47	0.48
29:d:48:THR:OG1	29:d:49:ARG:N	2.47	0.48
36:l:129:LYS:HG2	51:1:636:G:OP1	2.14	0.48
42:r:7:SER:OG	42:r:8:GLY:N	2.47	0.48
51:1:40:U:H2'	51:1:41:C:H6	1.78	0.48
51:1:129:C:H2'	51:1:130:C:H6	1.79	0.48
53:3:927:G:O2'	53:3:1503:A:N7	2.38	0.48
57:A1:182:ARG:O	57:A1:205:MET:HA	2.14	0.48
59:B2:363:LEU:HB3	59:B2:381:ALA:HB1	1.96	0.48
59:B2:732:ILE:HD11	59:B2:769:PRO:HB3	1.95	0.48
14:N:44:ARG:HG2	14:N:45:MET:HE2	1.95	0.47
15:O:58:ASN:ND2	53:3:1061:G:O2'	2.45	0.47
17:Q:45:ASN:ND2	17:Q:88:ASP:OD2	2.39	0.47
46:v:79:ARG:HA	46:v:86:LEU:HA	1.95	0.47
51:1:5:A:H2'	51:1:6:A:C8	2.49	0.47
51:1:1257:C:O5'	51:1:1257:C:H6	1.97	0.47
51:1:1267:U:H2'	51:1:1267:U:O2	2.14	0.47
51:1:2050:C:N4	51:1:2051:A:C6	2.81	0.47
51:1:2208:C:H2'	51:1:2209:G:C8	2.48	0.47
53:3:1531:A:O2'	53:3:1532:U:H5'	2.13	0.47
59:B2:517:GLN:HB3	59:B2:760:ASN:H	1.79	0.47
27:b:131:MET:HE2	27:b:187:CYS:HB2	1.96	0.47
28:c:136:ASN:OD1	51:1:2579:C:O2'	2.32	0.47
51:1:473:G:O2'	51:1:474:G:H5'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
51:1:852:U:H2'	51:1:853:C:C6	2.49	0.47
51:1:1464:G:H2'	51:1:1465:G:H8	1.78	0.47
51:1:2286:G:H21	51:1:2287:A:H61	1.62	0.47
51:1:2362:C:O5'	51:1:2362:C:H6	1.97	0.47
52:2:51:G:H22	52:2:53:A:H62	1.61	0.47
58:B1:891:ASP:OD2	58:B1:1290:ARG:NH2	2.47	0.47
59:B2:207:THR:OG1	59:B2:354:ASP:OD2	2.32	0.47
59:B2:400:VAL:HG22	59:B2:584:TYR:HB3	1.96	0.47
63:5:37:A:H3'	63:5:38:A:C8	2.49	0.47
14:N:94:ARG:HG2	14:N:97:LEU:HD12	1.95	0.47
33:i:79:LEU:HD21	33:i:105:LEU:HD21	1.96	0.47
47:w:19:VAL:HA	47:w:34:VAL:HG22	1.97	0.47
51:1:214:G:O2'	51:1:215:G:H5'	2.14	0.47
51:1:1026:G:OP2	51:1:1134:A:H1'	2.13	0.47
51:1:2047:C:O5'	51:1:2047:C:H6	1.98	0.47
51:1:2098:U:H2'	51:1:2099:U:O4'	2.14	0.47
51:1:2156:G:C3'	51:1:2157:G:H5'	2.44	0.47
51:1:2895:G:H2'	51:1:2896:C:C6	2.49	0.47
57:A2:102:LEU:HD12	57:A2:115:ILE:HG12	1.96	0.47
58:B1:108:ALA:HB1	58:B1:279:LEU:HD22	1.96	0.47
58:B1:395:LYS:NZ	58:B1:399:LYS:CE	2.77	0.47
59:B2:1286:THR:O	59:B2:1290:MET:HB2	2.14	0.47
59:B2:1314:GLN:HB2	60:W0:28:ARG:HH12	1.79	0.47
62:NG:161:SER:CA	62:NG:170:PRO:HA	2.44	0.47
64:7:50:U:H2'	64:7:51:C:C5	2.49	0.47
4:D:29:GLN:O	4:D:29:GLN:NE2	2.47	0.47
9:I:171:GLU:HB3	9:I:180:THR:HG22	1.97	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
31:f:87:GLN:HB3	31:f:162:ARG:HG3	1.96	0.47
32:g:8:LYS:HD3	32:g:14:SER:HA	1.95	0.47
33:i:8:VAL:HG21	33:i:26:ALA:HB1	1.97	0.47
33:i:79:LEU:HD13	33:i:132:ALA:HB2	1.94	0.47
34:j:65:THR:HG22	51:1:1141:U:OP2	2.15	0.47
51:1:555:G:HO2'	51:1:556:A:H8	1.61	0.47
51:1:1463:C:H2'	51:1:1464: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2445:G:C6	51:1:2446:G:C6	3.02	0.47
51:1:2554:U:H2'	51:1:2555:U:O2	2.15	0.47
58:B1:141:PHE:CE2	58:B1:296:LYS:CB	2.94	0.47
58:B1:833:GLU:N	58:B1:1242:ARG:HH12	2.12	0.47
63:5:29:G:H3'	63:5:30:G:C8	2.50	0.47
1:A:2:LYS:NZ	52:2:42:C:OP2	2.38	0.47
17:Q:70:GLY:O	17:Q:98:ARG:NH2	2.47	0.47
51:1:297:G:H2'	51:1:298:G:O4'	2.14	0.47
51:1:466:A:H2'	51:1:467:G:C5'	2.44	0.47
51:1:555:G:O2'	51:1:556:A:H8	1.96	0.47
51:1:1491:G:H2'	51:1:1492:G:H8	1.80	0.47
51:1:1509:A:H2'	51:1:1510:G:C8	2.49	0.47
59:B2:565:GLU:HA	59:B2:569:ILE:HG12	1.95	0.47
63:5:50:U:H2'	63:5:51:U:C6	2.49	0.47
7:G:129:THR:HB	7:G:132:GLU:HB2	1.96	0.47
16:P:34:THR:OG1	16:P:35:ASP:N	2.47	0.47
17:Q:114:SER:O	53:3:35:G:O2'	2.30	0.47
18:R:15:VAL:HG11	18:R:30:LYS:HG2	1.97	0.47
32:g:47:PHE:HA	32:g:51:ARG:HB2	1.96	0.47
47:w:29:ALA:N	47:w:60:ASP:OD2	2.48	0.47
51:1:712:G:H2'	51:1:713:G:H5'	1.96	0.47
51:1:1105:U:H2'	51:1:1106:G:H8	1.80	0.47
51:1:1285:A:H2'	51:1:1286:A:H5'	1.96	0.47
51:1:1324:G:O2'	51:1:1326:U:OP2	2.29	0.47
51:1:1517:G:O2'	51:1:1518:C:H5'	2.15	0.47
51:1:2194:U:O2'	51:1:2195:U:H5'	2.15	0.47
53:3:617:G:H1	53:3:623:C:H42	1.63	0.47
57:A1:59:VAL:HG22	57:A1:144:ILE:HA	1.97	0.47
58:B1:1347:LEU:HG	58:B1:1357:ILE:HG23	1.96	0.47
59:B2:689:ALA:HB2	59:B2:1233:LEU:HD23	1.97	0.47
11:K:10:VAL:HG23	11:K:58:HIS:HB3	1.97	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
12:L:112:ASP:HB2	12:L:118:ARG:HG2	1.96	0.47
12:L:149:ALA:HB1	16:P:58:THR:HG21	1.97	0.47
19:S:32:ASP:O	19:S:34:ASN:ND2	2.48	0.47
26:Z:19:LYS:H	26:Z:19:LYS:HG3	1.53	0.47
31:f:88:LEU:HD21	31:f:104:LEU:HD23	1.97	0.47
49:y:15:ASN:OD1	49:y:16:THR:N	2.48	0.47
51:1:30:G:C5	51:1:31:C:C4	3.03	0.47
51:1:156:A:H2'	51:1:157:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:708:G:H2'	51:1:709:U:C6	2.50	0.47
51:1:762:U:N3	51:1:1431:A:OP1	2.47	0.47
51:1:1020:A:C1'	51:1:1021:A:OP2	2.61	0.47
51:1:1067:A:H2'	51:1:1068:G:C8	2.49	0.47
51:1:1068:G:H2'	51:1:1069:A:H4'	1.96	0.47
51:1:1098:A:O2'	51:1:1099:G:H5'	2.15	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
51:1:1389:G:C2	51:1:1390:U:C2	3.02	0.47
51:1:1400:U:H2'	51:1:1401:G:C8	2.50	0.47
51:1:1464:G:H2'	51:1:1465:G:C8	2.49	0.47
51:1:1807:G:C2'	51:1:1808:A:H5'	2.29	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
51:1:2455:G:C6	51:1:2456:C:N4	2.83	0.47
51:1:2563:U:H2'	51:1:2565:A:OP2	2.15	0.47
51:1:2828:G:O2'	51:1:2829:A:H5'	2.14	0.47
53:3:38:G:H22	53:3:397:A:H5'	1.78	0.47
53:3:410:G:H21	53:3:432:A:H62	1.62	0.47
58:B1:190:LYS:HE3	58:B1:190:LYS:HB2	1.41	0.47
58:B1:352:ARG:HB2	59:B2:1268:GLN:NE2	2.30	0.47
58:B1:842:ARG:HH22	58:B1:1250:ASP:HB2	1.80	0.47
59:B2:836:LEU:HD13	59:B2:1054:LEU:HD13	1.95	0.47
59:B2:1311:GLY:O	60:W0:31:GLN:NE2	2.47	0.47
64:7:48:C:H5''	64:7:50:U:OP1	2.15	0.47
5:E:5:THR:HG22	5:E:62:PRO:HD2	1.97	0.47
9:I:159:GLU:HA	9:I:162:GLU:HB2	1.97	0.47
31:f:16:VAL:HA	31:f:25:ILE:HG12	1.96	0.47
34:j:2:LYS:HA	51:1:995:C:C4	2.50	0.47
36:l:39:LYS:HG2	51:1:832:U:OP1	2.15	0.47
39:o:68:LYS:HE3	52:2:49:C:H5''	1.97	0.47
51:1:859:G:C2'	51:1:860:U:OP2	2.62	0.47
51:1:1019:U:N3	51:1:1142:A:N6	2.57	0.47
51:1:1435:G:O2'	51:1:1436:G:H5'	2.15	0.47
57:A2:64:VAL:HG11	57:A2:78:ILE:HG21	1.97	0.47
58:B1:128:LEU:HD21	58:B1:188:LEU:HB3	1.97	0.47
58:B1:375:GLU:HB3	59:B2:1245:ALA:HB3	1.97	0.47
58:B1:1150:PRO:HG3	58:B1:1214:PRO:HB2	1.97	0.47
58:B1:1167:LYS:NZ	58:B1:1170:LYS:HB2	2.30	0.47
59:B2:318:SER:OG	59:B2:320:ASP:OD1	2.31	0.47
9:I:44:LYS:HA	9:I:44:LYS:HD2	1.55	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:7:ASN:HD22	18:R:20:SER:HB2	1.80	0.47
21:U:25:ARG:NH1	53:3:230:G:O2'	2.48	0.47
27:b:145:MET:HE1	51:1:1800:C:H2'	1.97	0.47
33:i:20:SER:HA	33:i:24:GLY:HA3	1.95	0.47
35:k:47:ILE:HG22	35:k:49:ARG:H	1.80	0.47
51:1:149:A:H2'	51:1:150:U:C6	2.49	0.47
51:1:551:G:O2'	51:1:552:U:H5'	2.15	0.47
51:1:854:C:H2'	51:1:855:G:H8	1.79	0.47
51:1:979:A:H2'	51:1:982:C:H42	1.80	0.47
51:1:1036:G:O2'	51:1:1037:G:H5'	2.15	0.47
51:1:1090:A:C2	51:1:1102:C:H1'	2.50	0.47
51:1:2241:A:H2'	51:1:2242:G:C8	2.50	0.47
51:1:2294:G:O2'	51:1:2295:C:H5'	2.15	0.47
51:1:2858:C:H2'	51:1:2859:G:O4'	2.15	0.47
53:3:1305:G:N2	53:3:1331:G:H2'	2.30	0.47
54:4:3:G:H1	64:6:34:C:H42	1.63	0.47
57:A1:212:ASP:OD1	57:A1:212:ASP:N	2.48	0.47
58:B1:29:MET:HG2	59:B2:1336:ASN:ND2	2.29	0.47
59:B2:1314:GLN:HA	60:W0:28:ARG:HH22	1.80	0.47
29:d:55:SER:OG	51:1:797:G:OP1	2.28	0.47
33:i:115:ASP:OD2	51:1:1059:G:H4'	2.14	0.47
51:1:338:G:O2'	51:1:339:U:H5'	2.14	0.47
51:1:900:A:C2'	51:1:901:C:H5'	2.45	0.47
51:1:1117:C:H2'	51:1:1118:C:C6	2.50	0.47
51:1:1874:C:H2'	51:1:1875:G:O4'	2.15	0.47
51:1:1927:A:H2'	51:1:1928:A:C8	2.50	0.47
51:1:2259:U:H2'	51:1:2260:C:O4'	2.15	0.47
51:1:2295:C:O2'	51:1:2296:U:H5'	2.15	0.47
51:1:2395:C:H2'	51:1:2396:G:O4'	2.15	0.47
51:1:2679:A:O2'	51:1:2680:U:H5'	2.15	0.47
51:1:2899:A:H2'	51:1:2900:A:O4'	2.15	0.47
53:3:512:U:H2'	53:3:513:C:C6	2.50	0.47
54:4:56:G:OP1	59:B2:1073:LYS:NZ	2.35	0.47
14:N:40:ARG:NH2	53:3:1291:U:O3'	2.38	0.46
20:T:38:LEU:HD22	20:T:55:LEU:HD13	1.96	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
51:1:435:C:C2'	51:1:436:C:H5'	2.44	0.46
51:1:848:C:H2'	51:1:849:A:H8	1.80	0.46
51:1:1090:A:H61	51:1:1101:U:H3	1.62	0.46
51:1:1297:C:H2'	51:1:1298:C:H6	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1807:G:H2'	51:1:1808:A:C5'	2.30	0.46
51:1:1873:G:O2'	51:1:1874:C:H5'	2.15	0.46
51:1:1922:G:H2'	51:1:1923:U:C6	2.50	0.46
52:2:39:A:O2'	52:2:46:A:N1	2.47	0.46
58:B1:43:THR:HG22	58:B1:57:PHE:HE1	1.80	0.46
58:B1:420:PRO:HA	58:B1:437:PHE:O	2.15	0.46
59:B2:857:VAL:HG13	59:B2:919:ARG:HH21	1.79	0.46
63:5:8:U:H2'	63:5:13:C:N4	2.30	0.46
10:J:28:ARG:NH2	53:3:1397:C:OP2	2.38	0.46
46:v:26:PHE:HE2	46:v:89:ILE:HG13	1.80	0.46
51:1:44:A:H2'	51:1:45:G:O4'	2.15	0.46
51:1:283:G:C2'	51:1:284:U:H5'	2.45	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
51:1:686:U:H6	51:1:788:A:H61	1.61	0.46
51:1:1536:C:H5''	51:1:1537:G:C5	2.50	0.46
51:1:1922:G:O2'	51:1:1923:U:H5'	2.15	0.46
53:3:1035:A:H1'	53:3:1036:A:O5'	2.16	0.46
53:3:1225:A:H2'	53:3:1225:A:N3	2.30	0.46
58:B1:198:CYS:HA	58:B1:221:ILE:CD1	2.45	0.46
9:I:1:ALA:N	53:3:405:U:O4	2.45	0.46
10:J:125:LYS:NZ	53:3:9:G:OP2	2.38	0.46
11:K:3:HIS:HA	11:K:65:GLU:HA	1.97	0.46
12:L:137:ARG:NH1	12:L:138:GLU:OE2	2.48	0.46
26:Z:29:ALA:O	26:Z:32:ARG:NH1	2.49	0.46
27:b:184:GLU:HG3	27:b:186:ASP:H	1.80	0.46
31:f:90:GLY:HA2	31:f:159:LYS:HG2	1.98	0.46
51:1:538:A:O2'	51:1:539:G:H5'	2.14	0.46
51:1:877:A:O2'	51:1:878:A:H5''	2.14	0.46
51:1:1209:U:O3'	51:1:1212:G:H5'	2.16	0.46
51:1:1516:G:O2'	51:1:1517:G:H5'	2.15	0.46
51:1:2180:U:H2'	51:1:2181:U:O4'	2.14	0.46
51:1:2247:A:H2'	51:1:2248:C:H6	1.81	0.46
57:A1:35:PHE:HA	57:A1:38:THR:HG22	1.98	0.46
28:c:4:LEU:HD11	28:c:100:LEU:HD21	1.97	0.46
33:i:54:ILE:HD12	33:i:73:PRO:HD3	1.95	0.46
45:u:6:ARG:HB2	51:1:85:G:P	2.55	0.46
51:1:93:G:O2'	51:1:94:A:H5'	2.16	0.46
51:1:143:C:H2'	51:1:144:A:C8	2.49	0.46
51:1:389:G:O2'	51:1:390:U:H5'	2.15	0.46
51:1:853:C:O2'	51:1:854:C:H5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1183:U:H2'	51:1:1184:U:H6	1.80	0.46
51:1:1572:A:H2'	51:1:1573:G:O4'	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
58:B1:343:LEU:HD11	58:B1:1324:SER:HB3	1.98	0.46
58:B1:1221:LEU:HD22	58:B1:1306:LEU:HB2	1.96	0.46
8:H:171:ARG:HG2	8:H:173:PRO:HD3	1.96	0.46
14:N:11:ARG:NH2	53:3:1347:G:O6	2.49	0.46
17:Q:72:ASN:HD21	17:Q:103:CYS:HA	1.81	0.46
20:T:37:HIS:HD2	20:T:38:LEU:HD12	1.80	0.46
27:b:99:GLU:OE2	51:1:1491:G:O2'	2.33	0.46
51:1:438:G:O2'	51:1:439:A:H5'	2.16	0.46
51:1:848:C:H2'	51:1:849:A:C8	2.51	0.46
51:1:1146:C:O2'	51:1:1147:A:H5'	2.16	0.46
51:1:1367:A:H3'	51:1:1368:G:O4'	2.15	0.46
51:1:1480:C:H2'	51:1:1481:U:C6	2.49	0.46
51:1:1486:U:O2'	51:1:1487:U:H5'	2.14	0.46
51:1:2625:G:H2'	51:1:2626:C:H6	1.76	0.46
51:1:2743:U:H2'	51:1:2744:G:O4'	2.16	0.46
55:8:13:DT:C6	58:B1:791:ALA:HA	2.51	0.46
58:B1:515:ARG:NH2	58:B1:718:SER:O	2.48	0.46
58:B1:526:VAL:HG12	58:B1:549:LYS:HB2	1.96	0.46
59:B2:907:GLY:O	59:B2:908:GLU:HB2	2.16	0.46
12:L:142:ARG:HA	12:L:145:GLU:HG3	1.97	0.46
51:1:1344:U:H3'	51:1:1345:C:H5'	1.97	0.46
51:1:1381:G:H2'	51:1:1382:G:H5'	1.98	0.46
51:1:1574:C:H2'	51:1:1575:C:C6	2.50	0.46
51:1:1766:G:C2'	51:1:1767:G:H5'	2.45	0.46
51:1:1913:A:N7	53:3:1494:G:H4'	2.29	0.46
51:1:2626:C:H2'	51:1:2627:G:H8	1.80	0.46
51:1:2813:A:O2'	51:1:2814:A:H5'	2.15	0.46
53:3:459:A:H2'	53:3:460:A:C8	2.50	0.46
59:B2:176:ILE:HD11	59:B2:428:VAL:HG21	1.98	0.46
2:B:31:LYS:HG2	51:1:2885:G:N2	2.31	0.46
6:F:33:HIS:O	6:F:34:LYS:C	2.59	0.46
10:J:110:MET:HE3	10:J:110:MET:HB2	1.79	0.46
22:V:10:ARG:NE	22:V:55:GLY:O	2.48	0.46
29:d:132:LYS:HG2	29:d:136:GLN:HE22	1.81	0.46
43:s:72:THR:OG1	43:s:73:LYS:N	2.48	0.46
48:x:14:GLY:HA3	48:x:28:PHE:HE2	1.81	0.46
51:1:409:G:H2'	51:1:410:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:595:C:C2	51:1:596:U:C5	3.04	0.46
51:1:1726:C:H2'	51:1:1727:C:C6	2.50	0.46
51:1:1768:C:H42	51:1:1984:G:H1	1.62	0.46
51:1:2290:G:O2'	51:1:2291:U:H5'	2.16	0.46
51:1:2581:G:H2'	51:1:2581:G:N3	2.30	0.46
51:1:2783:U:H2'	51:1:2784:U:C6	2.51	0.46
55:8:20:DA:H4'	59:B2:143:ARG:NH1	2.31	0.46
63:5:26:A:H61	63:5:44:G:H22	1.64	0.46
64:6:21:A:H62	64:6:47:U:H1'	1.81	0.46
8:H:152:VAL:HG12	8:H:197:VAL:HG22	1.98	0.46
10:J:73:VAL:HG11	10:J:143:LEU:HB3	1.98	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
51:1:688:U:H5'	51:1:1780:A:C2	2.51	0.46
51:1:1923:U:O2'	51:1:1924:C:H5'	2.16	0.46
51:1:2085:U:O2'	51:1:2086:U:H5'	2.16	0.46
53:3:618:C:N4	53:3:621:A:OP2	2.49	0.46
58:B1:209:ASN:HA	58:B1:214:ARG:NH2	2.30	0.46
58:B1:385:LEU:HD23	58:B1:390:LEU:HB2	1.98	0.46
59:B2:735:LYS:HA	59:B2:748:ILE:HG22	1.98	0.46
16:P:127:ARG:HB2	26:Z:34:ARG:HH22	1.81	0.46
35:k:121:GLU:HG2	35:k:122:VAL:HG23	1.97	0.46
43:s:82:MET:HE1	51:1:1322:A:H5''	1.98	0.46
51:1:569:U:H1'	51:1:947:A:O4'	2.16	0.46
51:1:1528:A:H2'	51:1:1529:G:C5'	2.44	0.46
51:1:2047:C:O2'	51:1:2048:G:H5'	2.16	0.46
51:1:2836:U:H2'	51:1:2837:A:H8	1.81	0.46
51:1:2849:U:H4'	51:1:2868:A:C2	2.51	0.46
57:A2:80:GLU:HG3	59:B2:694:ARG:HH22	1.81	0.46
58:B1:375:GLU:O	59:B2:1247:SER:HB3	2.16	0.46
58:B1:772:TYR:HE2	59:B2:561:ILE:HG21	1.80	0.46
58:B1:1219:ASP:O	58:B1:1223:LEU:HB2	2.15	0.46
59:B2:855:PRO:CB	61:NA:103:ASP:CB	2.87	0.46
59:B2:890:LYS:HE3	59:B2:915:ASP:HA	1.98	0.46
15:O:100:ILE:O	62:NG:170:PRO:O	2.34	0.46
18:R:97:ARG:HB2	18:R:99:GLN:HE22	1.81	0.46
28:c:170:VAL:HG21	51:1:2679:A:H5'	1.97	0.46
31:f:100:ASN:OD1	31:f:100:ASN:N	2.47	0.46
35:k:5:GLN:NE2	51:1:1668:A:H5''	2.31	0.46
35:k:70:ARG:NH1	51:1:2684:U:O4'	2.49	0.46
51:1:290:U:O2'	51:1:291:G:H5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:342:A:H2'	51:1:343:C:O4'	2.16	0.46
51:1:519:U:C2	51:1:520:G:C8	3.03	0.46
51:1:1034:G:C5	51:1:1035:U:C4	3.04	0.46
51:1:1287:A:O2'	51:1:1288:G:H5'	2.16	0.46
51:1:1520:U:H2'	51:1:1521:G:O4'	2.16	0.46
51:1:1923:U:H5''	64:6:24:U:O2'	2.16	0.46
51:1:2329:U:H2'	51:1:2330:G:C8	2.51	0.46
58:B1:115:TRP:HB3	58:B1:1333:THR:CG2	2.46	0.46
4:D:12:ARG:NH1	51:1:465:G:OP1	2.49	0.45
7:G:18:GLN:HG3	7:G:189:ASN:CB	2.41	0.45
23:W:33:THR:OG1	23:W:34:GLU:N	2.49	0.45
28:c:59:ARG:HA	28:c:59:ARG:HD3	1.83	0.45
37:m:34:LYS:N	37:m:129:THR:O	2.47	0.45
48:x:38:TRP:NE1	48:x:40:GLU:OE1	2.41	0.45
51:1:1550:C:O2'	51:1:1551:A:H5'	2.17	0.45
51:1:2101:A:H2'	51:1:2102:G:H8	1.81	0.45
53:3:647:C:H2'	53:3:648:A:H8	1.81	0.45
58:B1:847:ASP:N	58:B1:847:ASP:OD1	2.49	0.45
59:B2:24:VAL:HG11	59:B2:704:MET:HE1	1.99	0.45
60:W0:25:ARG:NH1	60:W0:61:ASN:OD1	2.49	0.45
62:NG:135:ARG:O	62:NG:178:VAL:HA	2.16	0.45
63:5:6:G:H2'	63:5:7:A:C8	2.51	0.45
7:G:65:LYS:HG2	7:G:153:MET:HG3	1.98	0.45
16:P:19:VAL:O	16:P:34:THR:N	2.45	0.45
17:Q:23:LEU:HD12	17:Q:29:LYS:HD2	1.97	0.45
22:V:11:VAL:HG13	22:V:58:VAL:HG21	1.98	0.45
33:i:91:LYS:HB2	33:i:91:LYS:HE3	1.72	0.45
51:1:239:C:H2'	51:1:240:C:O4'	2.16	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
51:1:2122:U:H2'	51:1:2123:G:O4'	2.16	0.45
53:3:1200:C:H5''	53:3:1201:A:H3'	1.97	0.45
58:B1:1357:ILE:HD13	59:B2:1279:GLU:HG2	1.97	0.45
3:C:13:SER:OG	3:C:47:ILE:O	2.27	0.45
9:I:173:ASP:HB3	9:I:178:GLU:HB3	1.98	0.45
16:P:124:LYS:HB3	26:Z:34:ARG:HB3	1.98	0.45
28:c:151:THR:O	51:1:1130:U:C4	2.70	0.45
31:f:1:SER:HA	51:1:2749:A:OP1	2.15	0.45
33:i:10:LEU:HD21	33:i:27:LEU:HD21	1.99	0.45
39:o:29:HIS:HB3	39:o:36:TYR:HB2	1.98	0.45
48:x:30:PRO:HG2	48:x:32:LEU:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:6:A:H2'	51:1:7:G:C8	2.52	0.45
51:1:28:A:O2'	51:1:29:U:H5'	2.16	0.45
51:1:111:A:O2'	51:1:112:U:H5'	2.17	0.45
51:1:289:G:H2'	51:1:290:U:C6	2.50	0.45
51:1:367:G:O2'	51:1:368:A:H5'	2.17	0.45
51:1:540:C:O2'	51:1:541:A:H5'	2.16	0.45
51:1:637:A:C6	51:1:652:U:H4'	2.51	0.45
51:1:2315:G:H2'	51:1:2316:G:H8	1.80	0.45
51:1:2350:C:H2'	51:1:2351:G:O4'	2.16	0.45
51:1:2844:G:H2'	51:1:2845:U:O4'	2.16	0.45
57:A1:231:PHE:O	57:A2:218:ARG:NH1	2.50	0.45
58:B1:1158:GLU:HA	58:B1:1223:LEU:HD21	1.99	0.45
59:B2:103:VAL:HG12	59:B2:117:ILE:HG22	1.97	0.45
8:H:5:HIS:CE1	8:H:7:ASN:HB3	2.51	0.45
9:I:114:ARG:HA	9:I:117:VAL:HG22	1.98	0.45
16:P:56:LYS:NZ	53:3:691:G:O6	2.38	0.45
42:r:38:VAL:HG13	42:r:54:VAL:HG12	1.99	0.45
47:w:7:ARG:HA	47:w:7:ARG:HD3	1.77	0.45
51:1:654:A:N3	51:1:654:A:H5''	2.31	0.45
51:1:1140:C:C2'	51:1:1141:U:H5'	2.47	0.45
51:1:1239:G:O2'	51:1:1240:U:H5'	2.17	0.45
51:1:1500:G:O2'	51:1:1501:G:H5'	2.17	0.45
51:1:1930:G:HO2'	51:1:1931:U:P	2.38	0.45
51:1:2030:A:N3	51:1:2499:C:H5''	2.31	0.45
51:1:2642:G:O5'	51:1:2642:G:H8	1.98	0.45
58:B1:1060:VAL:HG13	58:B1:1106:ILE:HG12	1.97	0.45
58:B1:1227:HIS:HA	58:B1:1230:THR:HG22	1.98	0.45
59:B2:1002:LEU:HD21	59:B2:1007:LYS:HB2	1.98	0.45
63:5:22:G:H2'	63:5:23:A:C8	2.51	0.45
64:6:46:G:H5''	64:6:47:U:OP2	2.17	0.45
7:G:166:ASP:HB3	7:G:190:SER:HB2	1.99	0.45
9:I:13:ARG:NH1	53:3:542:G:O3'	2.50	0.45
10:J:101:GLY:H	10:J:121:ASN:HB3	1.82	0.45
19:S:58:ARG:HH21	53:3:980:C:H4'	1.81	0.45
30:e:122:ASP:OD2	30:e:126:ASN:ND2	2.42	0.45
34:j:85:LYS:NZ	51:1:2768:U:OP1	2.49	0.45
36:l:69:ARG:NH1	51:1:2406:A:C2	2.84	0.45
51:1:1049:C:C2'	51:1:1050:A:H5'	2.47	0.45
51:1:1210:G:P	51:1:1212:G:H5'	2.56	0.45
51:1:1863:G:H2'	51:1:1864:U:C6	2.51	0.45
51:1:1952:A:H2'	51:1:1953:A:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2339:C:H2'	51:1:2340:A:H8	1.82	0.45
51:1:2648:G:C2	51:1:2649:C:C2	3.04	0.45
51:1:2658:C:H2'	51:1:2659:G:O4'	2.16	0.45
51:1:2661:G:O2'	51:1:2662:A:H5'	2.16	0.45
58:B1:109:SER:HB2	58:B1:296:LYS:HG2	1.98	0.45
58:B1:388:ARG:HG2	58:B1:388:ARG:NH1	2.32	0.45
58:B1:506:VAL:HG23	58:B1:628:GLY:HA3	1.99	0.45
59:B2:230:PHE:HB2	59:B2:333:ILE:HB	1.98	0.45
59:B2:674:ASP:OD2	59:B2:1070:HIS:ND1	2.50	0.45
63:5:49:C:H2'	63:5:50:U:C6	2.52	0.45
7:G:142:LYS:NZ	53:3:1098:C:OP1	2.49	0.45
7:G:172:ILE:O	7:G:176:ASN:ND2	2.50	0.45
29:d:136:GLN:HA	29:d:139:LYS:HE2	1.99	0.45
40:p:92:ARG:H	40:p:92:ARG:HG2	1.60	0.45
51:1:355:U:H6	51:1:355:U:O5'	1.99	0.45
51:1:707:G:C2'	51:1:708:G:H5'	2.47	0.45
51:1:1672:A:N3	51:1:2582:G:H5'	2.28	0.45
51:1:1710:G:H2'	51:1:1711:A:C8	2.51	0.45
51:1:1832:C:O5'	51:1:1832:C:H6	2.00	0.45
51:1:2360:G:H2'	51:1:2361:G:C5'	2.40	0.45
55:8:1:DC:H2''	55:8:2:DC:C6	2.51	0.45
58:B1:395:LYS:NZ	58:B1:399:LYS:HE2	2.32	0.45
29:d:32:VAL:HG21	36:l:6:LEU:HD13	1.99	0.45
31:f:133:LYS:NZ	31:f:134:GLY:O	2.43	0.45
34:j:108:MET:CE	51:1:1138:G:H21	2.29	0.45
51:1:854:C:H2'	51:1:855:G:C8	2.52	0.45
51:1:1170:C:H2'	51:1:1171:G:C8	2.51	0.45
51:1:2236:U:H2'	51:1:2237:G:C5'	2.46	0.45
51:1:2651:C:H2'	51:1:2652:C:H6	1.82	0.45
51:1:2869:G:H2'	51:1:2870:C:O4'	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'	2.49	0.45
53:3:1376:U:H2'	53:3:1377:A:C8	2.52	0.45
58:B1:75:TYR:CD2	58:B1:75:TYR:O	2.70	0.45
58:B1:352:ARG:CD	59:B2:1268:GLN:NE2	2.67	0.45
64:7:7:G:H3'	64:7:49:G:OP2	2.16	0.45
2:B:8:THR:OG1	2:B:9:ARG:N	2.49	0.45
8:H:5:HIS:HE1	8:H:7:ASN:HB3	1.82	0.45
11:K:62:MET:HB3	11:K:64:VAL:HG13	1.98	0.45
25:Y:4:LYS:HA	25:Y:4:LYS:HD3	1.86	0.45
27:b:97:ASP:N	27:b:97:ASP:OD1	2.44	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:g:28:ASN:ND2	51:1:2092:U:OP2	2.36	0.45
51:1:360:U:H2'	51:1:361:G:H1'	1.99	0.45
51:1:1173:U:C6	51:1:1174:U:H1'	2.51	0.45
51:1:1488:C:H2'	51:1:1489:C:C6	2.51	0.45
51:1:1866:A:H2'	51:1:1867:G:O4'	2.16	0.45
51:1:2364:C:O2'	51:1:2365:G:H5'	2.17	0.45
51:1:2717:C:N3	51:1:2718:G:N7	2.65	0.45
58:B1:201:LEU:CD1	58:B1:224:LEU:HD12	2.47	0.45
58:B1:202:ARG:NH1	58:B1:202:ARG:CG	2.73	0.45
58:B1:213:LYS:CA	58:B1:213:LYS:HE3	2.47	0.45
58:B1:770:LEU:HD13	59:B2:618:GLN:CD	2.42	0.45
59:B2:28:LEU:HD21	59:B2:524:ILE:HG13	1.97	0.45
6:F:27:CYS:HG	6:F:33:HIS:HD1	1.56	0.45
7:G:26:MET:HE1	7:G:186:VAL:HB	1.99	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
44:t:34:VAL:HG21	44:t:43:ILE:HD11	1.99	0.45
45:u:12:VAL:HA	45:u:69:VAL:HG12	1.99	0.45
51:1:167:A:H2'	51:1:168:G:O4'	2.16	0.45
51:1:195:A:H3'	51:1:196:A:H4'	1.98	0.45
51:1:500:G:N2	51:1:502:A:H3'	2.32	0.45
51:1:536:G:H2'	51:1:537:G:C5'	2.43	0.45
51:1:639:U:H2'	51:1:640:C:C6	2.52	0.45
51:1:940:G:H3'	51:1:941:A:H5''	1.97	0.45
51:1:1020:A:C2	51:1:1141:U:C2	3.05	0.45
51:1:1140:C:H2'	51:1:1141:U:H5'	1.98	0.45
51:1:1338:G:H2'	51:1:1339:G:C8	2.51	0.45
51:1:1749:A:H2'	51:1:1750:G:H8	1.82	0.45
53:3:1253:G:H2'	53:3:1254:A:C8	2.52	0.45
53:3:1498:U:H4'	53:3:1519:A:H2	1.82	0.45
8:H:134:LYS:HB3	8:H:134:LYS:HE2	1.84	0.45
15:O:29:ALA:HB2	15:O:87:LEU:HD11	1.99	0.45
21:U:70:ARG:O	21:U:74:LEU:N	2.47	0.45
33:i:112:LYS:HD2	33:i:128:ILE:HD12	1.97	0.45
33:i:135:MET:CE	51:1:1062:G:H21	2.30	0.45
34:j:109:LEU:HD23	34:j:109:LEU:HA	1.85	0.45
40:p:52:ARG:NH2	51:1:2720:U:OP1	2.50	0.45
42:r:48:LYS:HA	42:r:48:LYS:HD2	1.78	0.45
51:1:1280:G:C2'	51:1:1281:G:H5'	2.46	0.45
51:1:1868:C:H2'	51:1:1869:G:C8	2.51	0.45
51:1:1893:C:C2'	51:1:1894:C:H5'	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2201:G:H2'	51:1:2202:U:O4'	2.17	0.45
51:1:2204:G:H2'	51:1:2205:A:H8	1.81	0.45
51:1:2626:C:H2'	51:1:2627:G:C8	2.51	0.45
51:1:2636:C:O2'	51:1:2637:U:H5'	2.16	0.45
51:1:2880:C:O2	51:1:2880:C:H2'	2.17	0.45
55:8:16:DT:H2'	55:8:17:DC:C6	2.52	0.45
57:A1:185:TYR:HA	57:A1:202:VAL:O	2.16	0.45
58:B1:484:MET:CE	59:B2:1278:LEU:HD21	2.47	0.45
58:B1:1108:GLN:HG3	58:B1:1109:LEU:HD12	1.99	0.45
12:L:70:PRO:HG3	12:L:98:LEU:HD23	1.97	0.44
17:Q:72:ASN:OD1	17:Q:72:ASN:N	2.50	0.44
21:U:28:ARG:NH1	53:3:390:U:O2'	2.46	0.44
31:f:132:LEU:HB3	31:f:140:ILE:HD11	2.00	0.44
45:u:17:ASP:HA	45:u:20:LYS:HE2	1.99	0.44
45:u:32:LYS:HG2	45:u:65:GLN:HA	1.99	0.44
51:1:327:G:H2'	51:1:328:U:O4'	2.17	0.44
51:1:2141:G:H1	51:1:2151:U:H3	1.63	0.44
51:1:2241:A:H2'	51:1:2242:G:H8	1.82	0.44
53:3:765:G:H1	53:3:812:G:HO2'	1.63	0.44
59:B2:1246:ARG:HH11	59:B2:1266:GLY:HA2	1.82	0.44
63:5:8:U:H2'	63:5:13:C:H41	1.81	0.44
33:i:106:GLN:OE1	33:i:125:THR:OG1	2.31	0.44
38:n:103:ARG:HH11	51:1:1287:A:H5'	1.82	0.44
48:x:51:SER:OG	48:x:54:GLY:N	2.48	0.44
51:1:30:G:H2'	51:1:31:C:O4'	2.17	0.44
51:1:354:A:H2'	51:1:355:U:O4'	2.17	0.44
51:1:432:A:O2'	51:1:433:C:H5'	2.17	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
51:1:1800:C:O2	51:1:1802:A:C8	2.70	0.44
51:1:1922:G:H2'	51:1:1923:U:O4'	2.17	0.44
51:1:2700:A:O2'	51:1:2701:U:H5'	2.16	0.44
58:B1:76:LYS:NZ	58:B1:76:LYS:HB3	2.32	0.44
58:B1:105:ILE:HD12	58:B1:242:LEU:CD2	2.44	0.44
58:B1:434:ILE:HD11	59:B2:1274:GLU:HG3	2.00	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	2.47	0.44
58:B1:926:PRO:HB2	58:B1:1241:TYR:HE1	1.82	0.44
59:B2:557:ARG:NH2	59:B2:607:SER:O	2.50	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)
14:N:84:ARG:NH2	53:3:1119:C:OP1	2.48	0.44
27:b:1:ALA:N	27:b:19:VAL:O	2.41	0.44
34:j:10:THR:O	34:j:12:LYS:NZ	2.36	0.44
51:1:163:C:O2'	51:1:164:C:H5'	2.17	0.44
51:1:169:G:O2'	51:1:170:U:H5'	2.18	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
51:1:1173:U:H5	51:1:1174:U:H1'	1.81	0.44
51:1:1452:G:H2'	51:1:1453:A:OP2	2.17	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:H4'	1.99	0.44
51:1:1680:U:C2'	51:1:1681:G:H5'	2.47	0.44
51:1:1710:G:O2'	51:1:1711:A:H5'	2.17	0.44
51:1:2741:A:H2'	51:1:2742:G:H5'	1.98	0.44
53:3:142:G:O2'	53:3:196:A:N1	2.45	0.44
53:3:1200:C:O2'	53:3:1205:U:O4	2.34	0.44
59:B2:998:LEU:HG	59:B2:1011:LEU:HB3	1.99	0.44
63:5:70:G:H2'	63:5:71:G:C8	2.51	0.44
2:B:4:GLN:HG3	51:1:2054:A:C2	2.52	0.44
7:G:33:ALA:HB3	7:G:37:VAL:HG12	1.99	0.44
9:I:120:LYS:HG2	9:I:130:ASN:HB3	1.99	0.44
40:p:88:ARG:HH11	40:p:114:ASN:HD21	1.66	0.44
41:q:82:LEU:HD22	41:q:87:VAL:HB	1.98	0.44
51:1:395:U:H2'	51:1:396:G:C8	2.52	0.44
51:1:704:G:H1'	51:1:727:A:H62	1.83	0.44
51:1:819:A:H5'	51:1:973:A:N1	2.33	0.44
51:1:1412:U:H2'	51:1:1413:A:H8	1.81	0.44
51:1:1882:U:O2'	51:1:1883:U:H5'	2.17	0.44
51:1:2312:U:O2'	51:1:2313:C:H5'	2.17	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
51:1:2805:C:O2'	51:1:2806:C:H5'	2.18	0.44
58:B1:161:THR:H	58:B1:164:GLN:HB2	1.82	0.44
58:B1:213:LYS:HE3	58:B1:213:LYS:HA	1.99	0.44
58:B1:1357:ILE:HG22	58:B1:1359:ALA:H	1.82	0.44
4:D:12:ARG:HH12	51:1:465:G:P	2.41	0.44
10:J:24:VAL:HG23	10:J:26:GLY:H	1.82	0.44
18:R:43:LYS:HB2	18:R:46:GLU:HG2	1.99	0.44
22:V:44:HIS:HB3	22:V:70:LYS:HG2	1.99	0.44
29:d:147:LEU:HD11	29:d:170:ARG:HG2	1.98	0.44
33:i:9:LYS:HD2	51:1:1061:U:OP1	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
49:y:20:ASN:HA	49:y:23:ARG:HB2	1.99	0.44
51:1:68:G:H2'	51:1:69:C:O4'	2.18	0.44
51:1:255:A:H2'	51:1:256:A:O4'	2.18	0.44
51:1:545:U:O2	51:1:546:U:H1'	2.17	0.44
51:1:974:G:H1'	51:1:975:A:C8	2.53	0.44
53:3:75:G:H2'	53:3:76:G:C8	2.53	0.44
57:A2:48:LEU:HD23	57:A2:48:LEU:HA	1.86	0.44
58:B1:67:ASP:OD1	58:B1:67:ASP:O	2.35	0.44
58:B1:128:LEU:CD2	58:B1:188:LEU:HB3	2.47	0.44
58:B1:141:PHE:HE2	58:B1:296:LYS:CB	2.23	0.44
63:5:69:G:H2'	63:5:70:G:C8	2.52	0.44
32:g:1:MET:N	32:g:20:ASN:OD1	2.39	0.44
42:r:19:THR:OG1	42:r:95:ASP:OD2	2.35	0.44
47:w:37:ARG:HA	47:w:37:ARG:HD3	1.70	0.44
51:1:29:U:O5'	51:1:29:U:H6	2.00	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
51:1:473:G:C2'	51:1:474:G:H5'	2.48	0.44
51:1:1625:C:H2'	51:1:1626:A:O4'	2.18	0.44
53:3:146:G:N2	53:3:177:G:N7	2.66	0.44
53:3:477:C:H2'	53:3:478:A:C8	2.52	0.44
53:3:490:C:H2'	53:3:491:G:C8	2.53	0.44
56:9:12:DC:H3'	58:B1:47:ARG:HH12	1.83	0.44
57:A1:192:VAL:HG12	57:A1:193:GLU:H	1.83	0.44
58:B1:472:LEU:CD1	59:B2:1294:LYS:HG2	2.47	0.44
58:B1:978:ARG:HD3	58:B1:999:TYR:H	1.82	0.44
65:h:2:DPP:NG	65:h:3:SER:N	2.65	0.44
11:K:75:GLU:O	11:K:79:ARG:N	2.47	0.44
28:c:150:GLN:HE22	51:1:2032:G:H1'	1.82	0.44
38:n:58:ASP:OD1	38:n:63:ARG:NH2	2.44	0.44
42:r:80:ARG:HD3	51:1:566:U:O4	2.17	0.44
47:w:12:SER:OG	47:w:13:GLU:N	2.51	0.44
51:1:131:A:H2'	51:1:132:G:C8	2.53	0.44
51:1:388:G:N7	51:1:390:U:H2'	2.33	0.44
51:1:893:C:H2'	51:1:894:U:O4'	2.17	0.44
51:1:1288:G:C5	51:1:1327:A:C2	3.04	0.44
51:1:1507:C:H2'	51:1:1508:A:O4'	2.18	0.44
51:1:1869:G:H3'	51:1:1870:C:C5'	2.38	0.44
51:1:1998:A:O2'	51:1:1999:C:H5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:A1:78:ILE:HA	57:A1:81:ILE:HG22	2.00	0.44
58:B1:222:LYS:HA	58:B1:222:LYS:HD2	1.33	0.44
58:B1:1079:LYS:HD3	58:B1:1098:GLN:HB3	2.00	0.44
63:5:13:C:H42	63:5:46:G:N2	2.16	0.44
7:G:122:ASP:OD2	7:G:122:ASP:N	2.51	0.44
14:N:119:LYS:NZ	53:3:1350:A:N7	2.64	0.44
29:d:68:ALA:HA	51:1:1255:U:C6	2.52	0.44
31:f:175:LYS:HD3	31:f:175:LYS:HA	1.70	0.44
36:l:95:LEU:HD22	36:l:100:ILE:HD11	2.00	0.44
42:r:1:MET:HE3	42:r:101:ILE:HB	1.99	0.44
45:u:76:THR:HB	45:u:78:LYS:HE3	1.99	0.44
49:y:6:LEU:HD13	49:y:56:LEU:HD22	1.98	0.44
50:z:30:ARG:HG2	50:z:33:HIS:HB2	1.99	0.44
51:1:150:U:O2'	51:1:151:C:H5'	2.18	0.44
51:1:696:G:H2'	51:1:697:G:O4'	2.18	0.44
51:1:1199:U:H2'	51:1:1200:C:C6	2.52	0.44
51:1:1670:C:O2'	51:1:1671:U:H5'	2.16	0.44
58:B1:33:TRP:HZ2	59:B2:1336:ASN:OD1	2.00	0.44
59:B2:11:ILE:HG22	59:B2:1172:LEU:HD11	1.99	0.44
7:G:67:LEU:HD21	7:G:91:VAL:HG23	2.00	0.44
9:I:85:THR:HA	9:I:88:ASN:HB2	2.00	0.44
14:N:104:THR:HG23	53:3:1180:A:H5'	1.99	0.44
24:X:27:LYS:HE2	24:X:27:LYS:HB3	1.77	0.44
24:X:76:THR:OG1	24:X:77:ARG:N	2.51	0.44
42:r:24:LYS:HE2	42:r:24:LYS:HB3	1.89	0.44
51:1:150:U:H2'	51:1:151:C:C6	2.53	0.44
51:1:1536:C:H4'	51:1:1537:G:N1	2.33	0.44
51:1:2226:C:C5	51:1:2227:A:N7	2.86	0.44
51:1:2671:G:C2	51:1:2672:U:C2	3.06	0.44
63:5:63:G:H2'	63:5:64:A:C8	2.53	0.44
2:B:4:GLN:NE2	51:1:2056:G:O2'	2.51	0.43
5:E:48:MET:HE3	5:E:48:MET:HB3	1.86	0.43
10:J:104:ILE:HD11	10:J:114:LEU:HD13	1.99	0.43
13:M:24:VAL:HG23	13:M:60:LEU:HB2	2.00	0.43
14:N:74:GLN:OE1	53:3:1249:C:O2'	2.35	0.43
18:R:1:ALA:HB3	18:R:56:ARG:HH22	1.82	0.43
25:Y:67:HIS:O	25:Y:69:ASN:ND2	2.51	0.43
28:c:106:LYS:HA	28:c:176:ASP:HA	1.99	0.43
51:1:30:G:O2'	51:1:31:C:H5'	2.17	0.43
51:1:1010:A:H1'	51:1:1153:C:H1'	1.99	0.43
51:1:1087:G:H5''	51:1:1088:A:OP2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1565:C:C5	51:1:1567:G:C6	3.07	0.43
51:1:1605:C:H2'	51:1:1606:C:H5'	1.98	0.43
51:1:2643:G:C2'	51:1:2644:G:H5'	2.48	0.43
53:3:162:A:C5	53:3:163:C:H1'	2.53	0.43
58:B1:731:ARG:HB3	59:B2:1105:SER:HB2	2.00	0.43
62:NG:161:SER:CB	62:NG:170:PRO:HA	2.48	0.43
8:H:76:ILE:HB	8:H:80:GLY:HA2	2.00	0.43
9:I:125:ASN:HB2	9:I:127:ARG:HD3	2.01	0.43
14:N:98:ARG:HG2	14:N:103:VAL:HG21	2.00	0.43
17:Q:3:VAL:HA	17:Q:6:LEU:HD12	2.01	0.43
18:R:107:THR:OG1	53:3:947:G:O3'	2.35	0.43
27:b:7:PRO:HB3	27:b:13:ARG:HG3	2.00	0.43
27:b:153:LEU:HD23	51:1:1799:G:N2	2.33	0.43
35:k:38:ILE:HG22	35:k:61:VAL:HB	2.00	0.43
38:n:65:LEU:HD11	51:1:2870:C:H5''	2.00	0.43
51:1:28:A:H2'	51:1:29:U:C6	2.53	0.43
51:1:402:A:H2'	51:1:403:U:C5'	2.44	0.43
51:1:518:G:O2'	51:1:519:U:H5'	2.18	0.43
51:1:648:G:H2'	51:1:649:G:H8	1.83	0.43
51:1:720:U:H2'	51:1:721:A:H8	1.82	0.43
51:1:993:G:O2'	51:1:994:C:H5'	2.19	0.43
51:1:1095:A:H3'	51:1:1096:A:H8	1.83	0.43
51:1:1306:C:N4	51:1:1606:C:H2'	2.34	0.43
51:1:1383:A:H2	51:1:1406:U:H1'	1.83	0.43
51:1:1741:C:O2'	51:1:1742:U:H5'	2.18	0.43
51:1:1761:C:H2'	51:1:1762:A:O4'	2.18	0.43
51:1:2137:U:H2'	51:1:2138:G:C8	2.50	0.43
51:1:2285:C:C2'	51:1:2286:G:H5'	2.48	0.43
52:2:66:A:H4'	52:2:67:G:C8	2.53	0.43
53:3:908:A:H2'	53:3:909:A:H8	1.83	0.43
58:B1:515:ARG:HH12	58:B1:724:MET:HG2	1.84	0.43
58:B1:824:PRO:HD3	58:B1:835:LEU:HD12	2.00	0.43
59:B2:300:ASP:OD1	59:B2:313:ALA:N	2.51	0.43
59:B2:487:LEU:HD22	59:B2:487:LEU:HA	1.77	0.43
63:5:27:G:H1	63:5:43:C:H42	1.64	0.43
21:U:79:ASN:HB2	21:U:82:ALA:HB3	1.99	0.43
49:y:19:LEU:HD23	49:y:19:LEU:HA	1.87	0.43
51:1:161:A:C5	51:1:162:U:H5	2.35	0.43
51:1:684:G:C2	51:1:794:A:C2	3.06	0.43
51:1:1747:U:H2'	51:1:1748:C:C6	2.53	0.43
53:3:560:A:H5''	53:3:561:U:H5'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1053:G:H4'	53:3:1054:C:H3'	2.00	0.43
58:B1:62:PHE:CD1	58:B1:62:PHE:N	2.86	0.43
58:B1:201:LEU:CB	58:B1:221:ILE:HD13	2.47	0.43
58:B1:1024:THR:HG23	58:B1:1123:ARG:HA	2.00	0.43
60:W0:58:LEU:HD12	60:W0:59:ILE:HG12	2.00	0.43
10:J:110:MET:HA	10:J:113:VAL:HG12	2.01	0.43
18:R:28:ARG:HH21	18:R:62:PHE:HB2	1.84	0.43
24:X:6:LYS:NZ	53:3:1314:C:OP1	2.52	0.43
25:Y:14:GLU:OE1	25:Y:17:ARG:NH2	2.52	0.43
27:b:20:ASN:HB3	27:b:23:LEU:HD13	2.01	0.43
34:j:138:GLN:H	34:j:138:GLN:HG2	1.62	0.43
36:l:69:ARG:CZ	51:1:2406:A:N3	2.82	0.43
48:x:36:ARG:NH2	51:1:2200:C:OP2	2.52	0.43
51:1:648:G:H5''	51:1:2352:A:H5''	2.00	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
51:1:1087:G:H22	51:1:1103:A:H1'	1.75	0.43
51:1:1092:C:H2'	51:1:1093:G:O4'	2.18	0.43
51:1:2371:G:O2'	51:1:2372:U:H5'	2.19	0.43
53:3:680:C:H2'	53:3:681:A:H8	1.84	0.43
53:3:1005:A:OP2	53:3:1024:G:N2	2.48	0.43
58:B1:45:ASN:HD22	58:B1:48:THR:H	1.65	0.43
58:B1:375:GLU:HB3	59:B2:1245:ALA:CB	2.48	0.43
58:B1:1046:ILE:HG22	58:B1:1061:VAL:HA	2.00	0.43
59:B2:444:ASP:OD1	59:B2:444:ASP:N	2.51	0.43
2:B:8:THR:HG23	2:B:11:LYS:H	1.81	0.43
8:H:134:LYS:HG2	8:H:138:GLN:HE21	1.82	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
21:U:31:ARG:HB2	53:3:310:G:H5''	2.00	0.43
27:b:140:VAL:HG12	27:b:191:LEU:HD23	2.01	0.43
30:e:171:ALA:C	30:e:173:ASP:H	2.26	0.43
41:q:47:ARG:NH2	41:q:51:GLN:OE1	2.51	0.43
51:1:350:G:H2'	51:1:351:C:O4'	2.18	0.43
51:1:721:A:H2'	51:1:722:A:C8	2.53	0.43
51:1:1571:A:H2'	51:1:1572:A:C8	2.54	0.43
51:1:2562:U:C2'	51:1:2563:U:H5'	2.49	0.43
53:3:1513:A:H2'	53:3:1514:G:H8	1.83	0.43
58:B1:287:ALA:HB1	58:B1:288:PRO:HD2	2.00	0.43
58:B1:362:ARG:HB2	58:B1:364:HIS:HD2	1.83	0.43
8:H:51:VAL:HA	8:H:69:THR:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:38:ARG:HH11	11:K:61:LEU:HD21	1.83	0.43
25:Y:49:ALA:HA	25:Y:52:GLU:HG3	2.00	0.43
27:b:131:MET:H	27:b:131:MET:HG2	1.57	0.43
28:c:62:LYS:NZ	51:1:2810:A:H5''	2.34	0.43
31:f:106:LEU:O	31:f:151:ARG:NH2	2.37	0.43
34:j:47:HIS:CG	51:1:536:G:H21	2.37	0.43
43:s:74:ILE:HB	43:s:105:VAL:HG23	1.99	0.43
51:1:2102:G:H1	51:1:2187:U:H3	1.66	0.43
51:1:2152:G:N3	51:1:2152:G:H2'	2.33	0.43
51:1:2305:U:O2'	51:1:2306:C:H5'	2.19	0.43
51:1:2584:U:O5'	51:1:2584:U:H6	2.02	0.43
51:1:2736:A:O2'	51:1:2737:G:H5'	2.19	0.43
53:3:1442:G:H1	53:3:1460:C:H42	1.66	0.43
58:B1:559:ALA:HB3	58:B1:562:GLU:HB3	2.01	0.43
58:B1:797:THR:HG22	58:B1:924:GLY:HA3	2.01	0.43
58:B1:1026:PRO:HB2	58:B1:1028:ILE:HG23	2.00	0.43
59:B2:1157:GLN:HG3	59:B2:1159:VAL:HG13	2.01	0.43
11:K:47:LEU:HG	11:K:56:LYS:HA	2.01	0.43
13:M:52:GLY:HA3	13:M:56:PRO:HA	2.01	0.43
16:P:17:ASP:OD1	16:P:17:ASP:N	2.44	0.43
16:P:115:ILE:HD12	16:P:116:PRO:HD2	1.99	0.43
17:Q:113:ARG:NH1	53:3:36:C:O2'	2.51	0.43
18:R:91:ARG:HD2	51:1:888:C:OP1	2.18	0.43
23:W:33:THR:HG22	23:W:37:LYS:H	1.83	0.43
27:b:48:ILE:HG12	51:1:779:U:OP2	2.18	0.43
27:b:244:VAL:HG12	27:b:250:GLN:HA	2.01	0.43
33:i:123:ALA:HB1	51:1:1081:U:H4'	2.00	0.43
36:l:39:LYS:HZ3	51:1:942:G:P	2.40	0.43
51:1:143:G:H2'	51:1:44:A:C8	2.53	0.43
51:1:467:G:O2'	51:1:468:G:H5'	2.19	0.43
51:1:541:A:H2'	51:1:542:C:O4'	2.19	0.43
51:1:1054:A:H2'	51:1:1055:G:C8	2.53	0.43
51:1:1287:A:H3'	51:1:1288:G:N2	2.33	0.43
51:1:2834:G:C2'	51:1:2835:A:H5'	2.49	0.43
51:1:2870:C:H2'	51:1:2871:U:H5'	2.01	0.43
53:3:422:C:H4'	53:3:423:G:C2	2.54	0.43
58:B1:59:ALA:HB1	58:B1:90:VAL:HG23	2.01	0.43
58:B1:111:THR:HG21	58:B1:303:VAL:HB	2.00	0.43
59:B2:811:ASN:ND2	59:B2:1098:LEU:O	2.51	0.43
17:Q:31:GLY:HA2	17:Q:56:LEU:HA	2.01	0.43
29:d:188:MET:HB2	29:d:192:ALA:HB3	1.99	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
36:l:109:LYS:HE2	51:1:636:G:N7	2.34	0.43
39:o:8:ILE:O	39:o:12:THR:OG1	2.33	0.43
48:x:1:SER:OG	51:1:1365:A:OP2	2.35	0.43
49:y:30:MET:HE3	49:y:30:MET:HB3	1.83	0.43
51:1:156:A:O2'	51:1:157:C:H5'	2.18	0.43
51:1:365:U:H2'	51:1:366:C:C6	2.53	0.43
51:1:864:G:C2'	51:1:865:C:H5'	2.48	0.43
51:1:1258:U:H2'	51:1:1259:G:C8	2.54	0.43
51:1:1306:C:H41	51:1:1606:C:H2'	1.84	0.43
51:1:1915:U:O2	51:1:1915:U:O4'	2.34	0.43
51:1:2144:G:H1'	51:1:2147:A:N6	2.34	0.43
51:1:2713:U:C3'	51:1:2714:G:H5'	2.27	0.43
53:3:944:G:N1	53:3:1338:G:OP2	2.34	0.43
58:B1:141:PHE:CD2	58:B1:297:ARG:HB2	2.54	0.43
59:B2:646:SER:OG	59:B2:647:ARG:N	2.51	0.43
59:B2:678:ARG:HD3	59:B2:678:ARG:HA	1.84	0.43
64:6:69:C:H2'	64:6:70:G:H8	1.83	0.43
29:d:127:GLU:O	29:d:156:ASN:ND2	2.51	0.43
49:y:11:VAL:HA	49:y:14:LEU:HB2	2.00	0.43
51:1:108:G:O2'	51:1:109:C:H5'	2.19	0.43
51:1:128:C:H2'	51:1:129:C:C6	2.53	0.43
51:1:192:C:H2'	51:1:193:U:H5'	1.99	0.43
51:1:572:A:O5'	51:1:572:A:C8	2.72	0.43
51:1:1049:C:H2'	51:1:1050:A:H5'	2.00	0.43
51:1:1739:A:H2'	51:1:1740:G:O4'	2.19	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	2.54	0.43
58:B1:58:CYS:SG	58:B1:60:ARG:HG2	2.59	0.43
58:B1:201:LEU:HD11	58:B1:220:ARG:NH1	2.32	0.43
59:B2:538:LEU:HD13	59:B2:543:ALA:HB2	2.01	0.43
59:B2:892:GLU:HB3	59:B2:893:THR:H	1.67	0.43
64:7:11:A:H2'	64:7:12:G:C8	2.52	0.43
9:I:119:HIS:O	9:I:145:ARG:NH2	2.52	0.43
31:f:151:ARG:HD3	31:f:151:ARG:HA	1.88	0.43
33:i:127:SER:OG	51:1:1059:G:N2	2.51	0.43
33:i:129:GLU:HG3	33:i:139:VAL:HG21	2.00	0.43
38:n:39:PRO:HG2	51:1:1651:G:H4'	2.01	0.43
43:s:67:ASP:OD1	43:s:67:ASP:N	2.39	0.43
51:1:1172:C:H2'	51:1:1173:U:O4'	2.19	0.43
51:1:1426:G:C6	51:1:1427:A:C6	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1601:G:H2'	51:1:1602:U:H5'	2.01	0.43
51:1:1907:G:C5	51:1:1908:C:C4	3.07	0.43
51:1:2216:G:H2'	51:1:2217:G:C8	2.54	0.43
51:1:2660:A:H2'	51:1:2661:G:O4'	2.18	0.43
51:1:2812:G:O2'	51:1:2813:A:H5'	2.19	0.43
53:3:1209:C:O2'	53:3:1214:C:N4	2.52	0.43
57:A1:68:TYR:HE1	57:A1:79:LEU:HD13	1.83	0.43
58:B1:388:ARG:HG2	58:B1:388:ARG:HH11	1.84	0.43
58:B1:434:ILE:HD11	59:B2:1274:GLU:CG	2.49	0.43
59:B2:590:PRO:HB2	59:B2:655:VAL:HG21	2.01	0.43
59:B2:829:THR:HG23	59:B2:1059:ARG:HG2	2.00	0.43
9:I:53:GLN:HA	9:I:198:LEU:HD12	2.01	0.42
14:N:105:ARG:NH1	14:N:109:GLN:OE1	2.49	0.42
27:b:206:LYS:HB2	51:1:729:G:C5	2.54	0.42
51:1:12:U:O2	51:1:12:U:H2'	2.18	0.42
51:1:528:A:C2	51:1:2043:C:H4'	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
51:1:783:A:C8	51:1:783:A:H3'	2.54	0.42
51:1:871:U:H2'	51:1:872:U:C6	2.54	0.42
51:1:918:A:H2'	51:1:919:U:O4'	2.19	0.42
51:1:1230:A:H2'	51:1:1231:U:O4'	2.19	0.42
51:1:1751:U:H2'	51:1:1752:C:C6	2.54	0.42
51:1:1864:U:O5'	51:1:1864:U:H6	2.02	0.42
51:1:2024:G:H2'	51:1:2025:C:C6	2.54	0.42
51:1:2462:C:H2'	51:1:2463:C:C6	2.53	0.42
51:1:2839:G:O2'	51:1:2840:C:H5'	2.18	0.42
53:3:1531:A:C2'	53:3:1532:U:H5'	2.49	0.42
57:A1:76:GLU:HB3	57:A1:80:GLU:HB3	2.01	0.42
57:A2:104:LYS:O	57:A2:139:SER:OG	2.36	0.42
58:B1:111:THR:CG2	58:B1:300:GLN:HA	2.48	0.42
58:B1:568:SER:HB3	58:B1:570:LYS:NZ	2.34	0.42
59:B2:125:GLY:H	59:B2:495:ALA:HB1	1.84	0.42
59:B2:515:MET:HE2	59:B2:515:MET:HB3	1.82	0.42
59:B2:1313:HIS:CD2	60:W0:31:GLN:HE22	2.37	0.42
15:O:88:MET:HE3	15:O:88:MET:HB3	1.70	0.42
16:P:126:ARG:O	53:3:796:C:H5''	2.19	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
29:d:47:LYS:HE2	51:1:451:U:H4'	2.00	0.42
34:j:51:GLY:HA3	34:j:121:LYS:HE2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:w:14:ALA:HB1	51:1:2271:G:OP1	2.19	0.42
51:1:94:A:H2'	51:1:95:A:C8	2.54	0.42
51:1:623:C:O2'	51:1:624:C:H5'	2.18	0.42
51:1:629:G:H2'	51:1:630:G:O4'	2.19	0.42
51:1:1246:A:H2'	51:1:1247:A:O4'	2.19	0.42
51:1:1335:C:H2'	51:1:1336:A:H8	1.84	0.42
51:1:1433:A:H2'	51:1:1434:A:C1'	2.49	0.42
55:8:3:DC:N1	55:8:4:DT:H72	2.34	0.42
55:8:12:DG:OP1	58:B1:795:TYR:CE1	2.71	0.42
58:B1:107:LEU:HA	58:B1:276:ASN:ND2	2.33	0.42
58:B1:244:VAL:HA	58:B1:269:TYR:OH	2.19	0.42
58:B1:1033:GLY:HA3	58:B1:1081:VAL:O	2.18	0.42
8:H:1:GLY:HA2	53:3:1060:U:C5	2.54	0.42
8:H:61:LYS:HE2	8:H:96:VAL:HG12	2.01	0.42
8:H:106:ARG:HG2	8:H:107:LYS:HG3	2.01	0.42
14:N:113:LYS:HA	14:N:120:ALA:HB2	2.01	0.42
17:Q:29:LYS:HA	17:Q:29:LYS:HD3	1.65	0.42
18:R:89:ARG:HB2	18:R:96:VAL:HG22	2.01	0.42
20:T:66:LEU:HB3	20:T:77:TYR:HE1	1.84	0.42
27:b:86:ARG:HD3	27:b:86:ARG:HA	1.84	0.42
40:p:63:ILE:HA	40:p:68:GLY:HA2	2.01	0.42
41:q:54:ARG:HD3	51:1:1155:A:H5''	2.01	0.42
42:r:62:GLU:HG3	42:r:97:LYS:HB3	2.01	0.42
51:1:595:C:H2'	51:1:596:U:C6	2.54	0.42
51:1:1914:C:O2	51:1:1914:C:O4'	2.37	0.42
51:1:2073:C:C2'	51:1:2074:U:H5'	2.50	0.42
53:3:1348:U:H2'	53:3:1349:A:H8	1.84	0.42
57:A1:211:ILE:HD12	57:A1:211:ILE:HA	1.92	0.42
58:B1:24:LEU:HD21	58:B1:116:PHE:CE2	2.54	0.42
58:B1:850:LYS:HB3	58:B1:855:ASP:HB2	2.00	0.42
8:H:37:LYS:HD3	8:H:37:LYS:HA	1.81	0.42
24:X:51:HIS:HB2	24:X:56:HIS:CE1	2.55	0.42
36:l:108:ALA:HB3	36:l:125:LEU:HG	2.01	0.42
37:m:17:ASN:OD1	37:m:97:GLN:NE2	2.51	0.42
39:o:40:ILE:HA	39:o:47:VAL:HA	2.00	0.42
43:s:87:PRO:HG3	51:1:1615:C:C6	2.54	0.42
50:z:38:GLU:CD	51:1:928:A:H5'	2.43	0.42
51:1:8:C:C2	51:1:9:G:C8	3.07	0.42
51:1:644:A:C3'	51:1:645:C:H5''	2.49	0.42
51:1:1487:U:H2'	51:1:1488:C:C6	2.54	0.42
51:1:1993:U:O2	51:1:1993:U:H2'	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2106:U:H2'	51:1:2107:G:O4'	2.18	0.42
51:1:2292:U:H2'	51:1:2293:G:C8	2.55	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
53:3:460:A:H2'	53:3:461:A:C8	2.54	0.42
58:B1:242:LEU:C	58:B1:242:LEU:HD23	2.44	0.42
58:B1:385:LEU:CD2	58:B1:390:LEU:HB2	2.50	0.42
58:B1:950:ILE:HB	58:B1:1018:ALA:HB3	2.01	0.42
58:B1:1350:ASN:HA	58:B1:1353:VAL:HG12	2.02	0.42
59:B2:469:VAL:HA	59:B2:472:GLU:HG2	2.02	0.42
26:Z:39:LYS:HA	26:Z:42:THR:HB	2.02	0.42
29:d:53:THR:HB	51:1:452:G:H8	1.85	0.42
35:k:17:ARG:HD3	35:k:47:ILE:HD11	2.02	0.42
48:x:71:ARG:NH2	48:x:77:TYR:OH	2.42	0.42
51:1:90:U:H2'	51:1:91:A:C8	2.55	0.42
51:1:623:C:H2'	51:1:624:C:H6	1.85	0.42
51:1:1197:G:C2'	51:1:1198:U:H5'	2.50	0.42
51:1:1520:U:C2'	51:1:1521:G:H5'	2.49	0.42
51:1:1901:A:C2	51:1:1902:C:C5	3.07	0.42
51:1:1931:U:C5	51:1:1968:G:N2	2.88	0.42
51:1:2314:A:H2'	51:1:2315:G:H8	1.77	0.42
58:B1:96:LYS:NZ	59:B2:1298:VAL:HG11	2.34	0.42
59:B2:741:MET:SD	59:B2:974:ARG:NH2	2.93	0.42
9:I:152:SER:HB3	53:3:436:C:H4'	2.00	0.42
29:d:106:LYS:HG3	29:d:200:LEU:HD13	2.01	0.42
37:m:69:PRO:HA	37:m:94:ALA:HB2	2.01	0.42
51:1:115:C:O2'	51:1:116:C:H5'	2.20	0.42
51:1:481:G:H2'	51:1:482:A:OP2	2.19	0.42
51:1:892:A:O2'	51:1:893:C:H5'	2.20	0.42
51:1:955:U:H2'	51:1:956:G:H5'	2.02	0.42
51:1:1327:A:H2'	51:1:1328:A:H5'	2.01	0.42
51:1:2852:G:H2'	51:1:2853:C:O4'	2.20	0.42
58:B1:279:LEU:HD13	58:B1:299:LEU:HD13	2.02	0.42
58:B1:647:PRO:HG3	58:B1:697:MET:HB3	2.01	0.42
59:B2:524:ILE:HD12	59:B2:712:SER:HB2	2.02	0.42
62:NG:130:PRO:HA	62:NG:148:VAL:O	2.20	0.42
11:K:26:THR:O	11:K:30:THR:OG1	2.29	0.42
28:c:134:HIS:HE1	51:1:1675:C:C4	2.38	0.42
35:k:7:MET:HE2	35:k:18:ARG:HD3	2.01	0.42
38:n:16:HIS:CD2	51:1:1275:A:C2	3.07	0.42
51:1:4:U:O2'	51:1:5:A:H5'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:256:A:C2'	51:1:257:C:H5'	2.50	0.42
51:1:1204:A:H4'	51:1:1205:A:H5''	2.02	0.42
51:1:1316:U:O2'	51:1:1317:G:H5'	2.20	0.42
51:1:1710:G:H2'	51:1:1711:A:H8	1.85	0.42
51:1:2091:C:H5	51:1:2092:U:O2'	2.02	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
53:3:987:G:H2'	53:3:988:G:H8	1.84	0.42
53:3:1243:C:H2'	53:3:1244:G:H8	1.84	0.42
58:B1:211:GLU:CG	58:B1:215:LYS:HE3	2.44	0.42
58:B1:390:LEU:N	58:B1:390:LEU:HD13	2.35	0.42
58:B1:848:VAL:HB	58:B1:858:VAL:HG22	2.02	0.42
62:NG:135:ARG:O	62:NG:178:VAL:CA	2.68	0.42
9:I:101:VAL:HG22	9:I:106:PHE:HB2	2.01	0.42
18:R:11:HIS:HA	18:R:43:LYS:HD2	2.01	0.42
18:R:87:GLY:O	18:R:91:ARG:N	2.52	0.42
19:S:44:VAL:O	19:S:48:GLN:NE2	2.50	0.42
51:1:191:A:C2	51:1:192:C:C4	3.08	0.42
51:1:837:C:O5'	51:1:837:C:H6	2.02	0.42
51:1:1336:A:H2'	51:1:1337:G:H8	1.85	0.42
51:1:1642:G:H2'	51:1:1643:G:O4'	2.20	0.42
51:1:1917:U:H2'	51:1:1918:A:H5'	2.01	0.42
51:1:2098:U:C2'	51:1:2099:U:H5'	2.49	0.42
51:1:2193:G:H2'	51:1:2194:U:H6	1.83	0.42
53:3:28:A:O2'	53:3:296:U:OP1	2.33	0.42
53:3:73:C:H2'	53:3:74:A:C8	2.55	0.42
53:3:958:A:N3	53:3:985:C:O2'	2.48	0.42
53:3:1410:A:C2	53:3:1491:G:N1	2.88	0.42
55:8:15:DC:H5'	59:B2:1269:ARG:HD3	2.01	0.42
58:B1:506:VAL:H	58:B1:506:VAL:HG12	1.59	0.42
58:B1:513:MET:HG3	58:B1:544:LEU:HD11	2.01	0.42
58:B1:894:VAL:HG22	58:B1:1258:ARG:HH11	1.83	0.42
8:H:19:SER:HB2	8:H:39:ARG:HH21	1.85	0.42
8:H:110:LEU:HD21	8:H:143:LEU:HB3	2.02	0.42
11:K:40:GLU:HB3	11:K:61:LEU:HB3	2.02	0.42
41:q:111:LYS:HD2	41:q:111:LYS:HA	1.81	0.42
50:z:57:GLU:OE1	50:z:57:GLU:N	2.53	0.42
51:1:598:U:H2'	51:1:599:A:C8	2.54	0.42
51:1:673:C:O2'	51:1:674:G:H5'	2.19	0.42
51:1:758:C:H2'	51:1:759:G:H8	1.84	0.42
51:1:809:G:C6	51:1:810:U:C4	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1020:A:O5'	51:1:1020:A:H8	2.02	0.42
51:1:1034:G:C6	51:1:1035:U:N3	2.88	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	1.84	0.42
51:1:2583:G:H8	51:1:2583:G:O5'	2.03	0.42
51:1:2848:G:C2	51:1:2867:G:C4	3.08	0.42
54:4:55:G:H5'	59:B2:688:GLN:HE22	1.85	0.42
57:A2:294:ASN:HA	61:NA:464:ILE:N	2.28	0.42
58:B1:175:GLU:H	58:B1:175:GLU:HG3	1.65	0.42
58:B1:586:GLY:HA3	58:B1:612:LEU:HD11	2.01	0.42
58:B1:1289:ASN:O	58:B1:1293:GLU:HB2	2.20	0.42
59:B2:557:ARG:HB3	59:B2:587:LEU:HD13	2.00	0.42
59:B2:741:MET:HE3	59:B2:974:ARG:HH12	1.85	0.42
7:G:173:LYS:HE3	7:G:173:LYS:HB2	1.76	0.42
13:M:107:LYS:HA	13:M:107:LYS:HD2	1.85	0.42
14:N:30:ASN:HD21	14:N:66:VAL:H	1.66	0.42
21:U:68:SER:OG	21:U:69:ASP:N	2.53	0.42
30:e:77:LYS:HE2	30:e:77:LYS:HB2	1.89	0.42
32:g:1:MET:HE3	32:g:1:MET:HB3	1.77	0.42
37:m:123:LYS:HE2	51:1:2467:C:O2	2.20	0.42
43:s:9:HIS:H	43:s:102:HIS:CE1	2.38	0.42
44:t:40:LYS:HE3	44:t:60:THR:HG22	2.01	0.42
46:v:14:LYS:HB2	52:2:98:G:H1	1.85	0.42
50:z:37:ARG:HD3	50:z:37:ARG:HA	1.83	0.42
51:1:397:U:O5'	51:1:397:U:H6	2.03	0.42
51:1:908:C:O2'	51:1:909:A:H5'	2.20	0.42
51:1:1589:U:H2'	51:1:1590:A:C8	2.55	0.42
53:3:1513:A:H2'	53:3:1514:G:C8	2.55	0.42
57:A1:205:MET:HE1	57:A1:217:ILE:HG13	2.02	0.42
58:B1:144:TYR:N	58:B1:144:TYR:CD1	2.88	0.42
58:B1:820:ILE:HG12	58:B1:884:SER:HB2	2.01	0.42
59:B2:22:LEU:HD22	59:B2:603:ILE:HG21	2.02	0.42
59:B2:1275:VAL:HG13	59:B2:1287:LEU:HD11	2.01	0.42
13:M:42:GLU:HG2	13:M:100:ILE:HG21	2.02	0.41
18:R:32:ILE:HG23	18:R:58:GLU:HB3	2.02	0.41
32:g:11:ASN:ND2	51:1:2095:A:OP1	2.53	0.41
33:i:109:ALA:O	33:i:113:ALA:N	2.53	0.41
43:s:70:LYS:N	43:s:108:SER:O	2.45	0.41
51:1:196:A:N3	51:1:196:A:H2'	2.36	0.41
51:1:422:A:H2'	51:1:423:A:O4'	2.20	0.41
51:1:439:A:H2'	51:1:440:C:O4'	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:510:C:OP1	51:1:510:C:H3'	2.20	0.41
51:1:552:U:O2'	51:1:553:G:H5'	2.20	0.41
51:1:1176:U:H2'	51:1:1177:G:N9	2.35	0.41
51:1:2160:C:H2'	51:1:2161:C:O4'	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	2.03	0.41
53:3:75:G:H1	53:3:95:C:H42	1.67	0.41
53:3:1253:G:H2'	53:3:1254:A:H8	1.83	0.41
59:B2:616:ILE:HG13	59:B2:652:TYR:HB2	2.01	0.41
63:5:4:C:H2'	63:5:5:G:C8	2.55	0.41
11:K:22:ILE:H	11:K:22:ILE:HG13	1.70	0.41
12:L:68:VAL:HG23	12:L:99:ALA:HB1	2.02	0.41
15:O:12:ALA:HB2	15:O:96:VAL:HG13	2.02	0.41
15:O:57:VAL:HG22	15:O:58:ASN:H	1.85	0.41
22:V:7:LEU:N	22:V:59:GLU:OE2	2.53	0.41
22:V:11:VAL:HG23	22:V:55:GLY:H	1.85	0.41
33:i:25:PRO:HG3	51:1:1095:A:N1	2.34	0.41
33:i:78:LEU:HA	33:i:81:LYS:HB3	2.02	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
46:v:62:THR:O	46:v:62:THR:OG1	2.35	0.41
51:1:535:G:O2'	51:1:536:G:H5'	2.19	0.41
51:1:638:G:H2'	51:1:639:U:C6	2.55	0.41
51:1:903:C:H2'	51:1:904:G:H8	1.85	0.41
51:1:1314:C:H42	51:1:1338:G:H1	1.68	0.41
51:1:1505:A:O2'	51:1:1506:U:H5'	2.19	0.41
51:1:1600:C:H2'	51:1:1601:G:C8	2.55	0.41
51:1:1719:G:O2'	51:1:1720:U:H5'	2.20	0.41
51:1:1812:U:H5''	51:1:1812:U:H6	1.85	0.41
51:1:1964:G:H4'	51:1:1965:C:OP2	2.19	0.41
51:1:2092:U:H5	51:1:2199:A:C2	2.30	0.41
51:1:2287:A:C4	51:1:2289:G:N7	2.88	0.41
51:1:2628:C:H3'	51:1:2629:U:H5'	2.01	0.41
53:3:322:C:O2	53:3:332:G:N2	2.52	0.41
53:3:440:C:H2'	53:3:441:A:H8	1.85	0.41
53:3:497:G:H2'	53:3:498:A:C8	2.55	0.41
58:B1:144:TYR:CE1	58:B1:162:GLU:OE1	2.73	0.41
58:B1:395:LYS:HE3	58:B1:395:LYS:HB3	1.45	0.41
58:B1:1177:ILE:HD12	58:B1:1186:TYR:HE2	1.85	0.41
59:B2:870:ILE:HB	59:B2:944:ARG:HD3	2.02	0.41
62:NG:175:PHE:O	62:NG:178:VAL:O	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
28:c:90:PHE:HD1	28:c:94:GLN:HG2	1.83	0.41
40:p:113:LEU:HD13	40:p:113:LEU:HA	1.86	0.41
51:1:281:C:H2'	51:1:282:A:C8	2.54	0.41
51:1:532:A:H2'	51:1:532:A:N3	2.34	0.41
51:1:573:U:O2'	51:1:574:A:H3'	2.21	0.41
51:1:849:A:H2'	51:1:850:U:C5	2.54	0.41
51:1:1024:G:H21	51:1:1144:A:C4'	2.33	0.41
51:1:1045:C:H1'	51:1:1047:G:C2	2.56	0.41
51:1:1343:G:N3	51:1:1343:G:H2'	2.35	0.41
51:1:1416:G:H2'	51:1:1417:C:H6	1.82	0.41
51:1:1594:U:O2'	51:1:1595:C:H5'	2.20	0.41
51:1:1721:G:H1'	51:1:1739:A:N6	2.35	0.41
51:1:1727:C:O2'	51:1:1728:C:H5'	2.20	0.41
51:1:1936:A:N6	51:1:1963:U:H3	2.18	0.41
51:1:2895:G:H2'	51:1:2896:C:H6	1.85	0.41
53:3:842:U:H5''	53:3:846:G:C6	2.55	0.41
58:B1:71:LEU:HD23	58:B1:71:LEU:HA	1.75	0.41
58:B1:137:ARG:HA	58:B1:142:GLU:HG2	2.02	0.41
59:B2:310:ILE:HG21	59:B2:325:LEU:HB3	2.03	0.41
59:B2:859:GLU:O	59:B2:863:SER:N	2.52	0.41
59:B2:998:LEU:HD21	59:B2:1015:ALA:HB2	2.02	0.41
29:d:145:ASP:HA	29:d:166:LYS:HB3	2.02	0.41
41:q:23:TYR:HB3	41:q:27:ARG:HB2	2.02	0.41
51:1:127:A:H5''	51:1:128:C:O4'	2.21	0.41
51:1:137:U:H3	51:1:142:A:H61	1.69	0.41
51:1:191:A:H2'	51:1:192:C:C6	2.56	0.41
51:1:197:A:H2	51:1:2434:A:H62	1.69	0.41
51:1:431:U:O5'	51:1:431:U:H6	2.03	0.41
51:1:759:G:H2'	51:1:760:G:H8	1.83	0.41
51:1:1070:A:H5'	51:1:1072:C:OP1	2.20	0.41
51:1:1239:G:H2'	51:1:1240:U:O4'	2.21	0.41
51:1:1553:A:O2'	51:1:1554:U:H5	2.02	0.41
51:1:1614:A:O5'	51:1:1614:A:C8	2.73	0.41
51:1:1886:U:O2'	51:1:1887:C:H5'	2.20	0.41
51:1:2248:C:C2'	51:1:2249:U:H5'	2.49	0.41
51:1:2411:A:O2'	51:1:2412:A:H5'	2.20	0.41
51:1:2697:G:C2	51:1:2711:A:C2	3.08	0.41
53:3:1124:G:H1	53:3:1149:C:H42	1.68	0.41
55:8:2:DC:H6	55:8:2:DC:H2'	1.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:243:PRO:HG2	59:B2:1332:SER:C	2.44	0.41
58:B1:245:LEU:CG	58:B1:246:PRO:HD2	2.47	0.41
58:B1:515:ARG:HG2	58:B1:516:ASP:H	1.85	0.41
58:B1:616:PRO:HA	58:B1:619:ILE:HG22	2.02	0.41
59:B2:22:LEU:HB3	59:B2:655:VAL:HG11	2.01	0.41
59:B2:699:LEU:HG	59:B2:799:ASN:HD22	1.85	0.41
63:5:9:A:H1'	63:5:45:U:H2'	2.01	0.41
7:G:162:VAL:N	7:G:183:PHE:O	2.38	0.41
7:G:190:SER:OG	7:G:191:ASP:N	2.53	0.41
8:H:178:ARG:NH1	53:3:1112:C:O2'	2.54	0.41
9:I:55:ARG:HA	9:I:55:ARG:HD3	1.88	0.41
15:O:46:LYS:HB2	15:O:46:LYS:HE3	1.88	0.41
16:P:124:LYS:H	16:P:124:LYS:HG3	1.58	0.41
26:Z:9:GLU:HB3	26:Z:10:PRO:HD3	2.03	0.41
30:e:124:ARG:NH2	51:1:2315:G:N3	2.68	0.41
42:r:49:ILE:HA	42:r:54:VAL:HG23	2.02	0.41
46:v:58:SER:OG	46:v:59:GLU:OE1	2.36	0.41
51:1:170:U:H2'	51:1:171:U:C6	2.55	0.41
51:1:284:U:H2'	51:1:285:G:C8	2.55	0.41
51:1:543:G:C3'	51:1:544:C:H5''	2.51	0.41
51:1:630:G:N2	51:1:634:C:C4	2.88	0.41
51:1:724:U:H2'	51:1:725:G:C8	2.56	0.41
51:1:1063:G:N2	51:1:1075:C:H41	2.18	0.41
51:1:1213:A:C1'	51:1:1237:A:C2	3.03	0.41
51:1:1750:G:H2'	51:1:1751:U:C6	2.56	0.41
51:1:1767:G:N2	51:1:1986:C:C2	2.89	0.41
51:1:2335:A:N7	51:1:2337:G:C5	2.88	0.41
51:1:2379:G:H2'	51:1:2380:C:C6	2.56	0.41
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
53:3:370:C:H2'	53:3:371:A:H8	1.86	0.41
53:3:1228:C:H2'	53:3:1229:A:C8	2.55	0.41
58:B1:126:LEU:H	58:B1:126:LEU:HG	1.67	0.41
58:B1:390:LEU:HD13	58:B1:390:LEU:H	1.85	0.41
58:B1:839:VAL:HG12	58:B1:864:LEU:HD12	2.02	0.41
2:B:39:ARG:HA	2:B:39:ARG:HD2	1.91	0.41
18:R:16:ILE:O	18:R:19:THR:OG1	2.26	0.41
27:b:176:ARG:HA	27:b:176:ARG:HD2	1.94	0.41
33:i:100:ILE:HB	33:i:139:VAL:HG12	2.03	0.41
34:j:13:ARG:NH1	34:j:49:ASP:O	2.41	0.41
37:m:96:ILE:HD13	37:m:96:ILE:HA	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:4:ILE:HD13	45:u:69:VAL:HG23	2.03	0.41
50:z:31:ILE:HD11	51:1:989:G:P	2.61	0.41
51:1:79:C:O2	51:1:346:A:H2	2.03	0.41
51:1:481:G:H1'	51:1:506:G:H22	1.84	0.41
51:1:1048:A:C2'	51:1:1049:C:H5'	2.49	0.41
51:1:1092:C:O2'	51:1:1093:G:H5'	2.21	0.41
51:1:1283:G:N2	51:1:1285:A:H3'	2.35	0.41
53:3:31:G:N2	53:3:48:C:OP1	2.41	0.41
55:8:14:DC:C2	55:8:15:DC:C5	3.09	0.41
58:B1:1050:THR:HG23	58:B1:1057:SER:HB3	2.03	0.41
58:B1:1272:SER:OG	58:B1:1273:ASP:N	2.53	0.41
59:B2:805:MET:HE3	59:B2:805:MET:HB2	1.86	0.41
59:B2:1244:HIS:NE2	59:B2:1266:GLY:O	2.44	0.41
6:F:8:LYS:NZ	51:1:2467:C:OP1	2.37	0.41
9:I:24:VAL:HG22	53:3:409:U:H4'	2.02	0.41
24:X:49:ALA:HA	24:X:58:PRO:HA	2.03	0.41
27:b:58:LYS:HB2	27:b:58:LYS:HE3	1.87	0.41
30:e:39:VAL:HG12	30:e:85:GLY:HA2	2.03	0.41
43:s:29:VAL:HG21	43:s:55:ILE:HG21	2.03	0.41
51:1:191:A:C6	51:1:192:C:N4	2.88	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
51:1:877:A:H2'	51:1:878:A:H5''	2.02	0.41
51:1:1077:A:H3'	51:1:1078:U:H4'	2.02	0.41
51:1:1418:G:H1'	51:1:1581:G:N2	2.36	0.41
51:1:1488:C:H2'	51:1:1489:C:H6	1.84	0.41
51:1:1822:C:H2'	51:1:1823:G:H8	1.85	0.41
51:1:1868:C:H2'	51:1:1869:G:H8	1.86	0.41
51:1:2600:A:H8	51:1:2600:A:O5'	2.03	0.41
53:3:146:G:H2'	53:3:147:G:C8	2.56	0.41
53:3:757:U:OP1	53:3:822:U:O2'	2.36	0.41
58:B1:394:ILE:O	58:B1:394:ILE:HG13	2.19	0.41
9:I:87:GLU:N	9:I:87:GLU:OE2	2.53	0.41
15:O:89:ARG:NH2	62:NG:165:PHE:H	2.18	0.41
23:W:24:ASP:OD1	23:W:24:ASP:N	2.53	0.41
23:W:52:ARG:HE	23:W:52:ARG:HB2	1.66	0.41
33:i:41:PHE:O	33:i:45:THR:N	2.54	0.41
33:i:77:VAL:HA	33:i:80:LYS:HE2	2.02	0.41
39:o:24:THR:HB	39:o:42:PRO:HG3	2.02	0.41
44:t:17:SER:OG	44:t:20:ALA:N	2.48	0.41
51:1:198:C:N4	51:1:248:G:H1	2.14	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:597:G:H2'	51:1:598:U:H6	1.85	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:O4'	2.21	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
51:1:940:G:H2'	51:1:941:A:C4'	2.51	0.41
51:1:1150:C:C2	51:1:1151:A:C8	3.09	0.41
51:1:1452:G:C2'	51:1:1453:A:OP2	2.68	0.41
51:1:1467:U:C4	51:1:1468:U:C4	3.08	0.41
51:1:2098:U:H2'	51:1:2099:U:H5'	2.03	0.41
51:1:2437:G:O4'	51:1:2598:A:C2	2.73	0.41
51:1:2646:C:H2'	51:1:2647:U:O4'	2.21	0.41
58:B1:102:MET:HG2	58:B1:246:PRO:CG	2.49	0.41
58:B1:820:ILE:HD11	58:B1:822:MET:HE2	2.02	0.41
59:B2:213:LEU:HD13	59:B2:422:LYS:HG2	2.03	0.41
59:B2:559:CYS:HA	59:B2:560:PRO:HD3	1.91	0.41
5:E:29:ARG:HD3	5:E:29:ARG:HA	1.91	0.41
7:G:18:GLN:HB3	7:G:21:TYR:HB2	2.03	0.41
9:I:101:VAL:HG13	9:I:113:ALA:HB1	2.03	0.41
10:J:90:GLY:O	10:J:129:SER:OG	2.36	0.41
18:R:10:ASP:HB3	18:R:45:SER:HB3	2.03	0.41
27:b:57:HIS:ND1	51:1:1567:G:H5'	2.35	0.41
28:c:4:LEU:HD21	28:c:98:VAL:HA	2.02	0.41
35:k:53:LYS:HA	35:k:53:LYS:HD3	1.96	0.41
38:n:82:GLU:O	38:n:86:ARG:N	2.48	0.41
39:o:33:ARG:O	39:o:65:THR:OG1	2.28	0.41
42:r:81:LYS:NZ	51:1:568:U:O4	2.54	0.41
44:t:28:ASN:HD21	44:t:91:GLN:HB3	1.85	0.41
44:t:68:LYS:HA	44:t:68:LYS:HD3	1.83	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
51:1:259:G:O2'	51:1:260:G:H5'	2.20	0.41
51:1:490:C:O2'	51:1:491:G:P	2.79	0.41
51:1:511:U:H2'	51:1:512:G:H5'	2.02	0.41
51:1:688:U:H6	51:1:688:U:O5'	2.03	0.41
51:1:706:A:H2'	51:1:707:G:C5'	2.51	0.41
51:1:1020:A:H5'	51:1:1021:A:N7	2.35	0.41
51:1:1048:A:N6	51:1:1111:A:C8	2.89	0.41
51:1:1107:G:H2'	51:1:1108:U:O4'	2.20	0.41
51:1:1160:G:C6	51:1:1161:C:C4	3.09	0.41
51:1:1165:A:O2'	51:1:1166:G:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1283:G:H22	51:1:1286:A:P	2.44	0.41
51:1:1328:A:H2'	51:1:1330:C:C4	2.56	0.41
51:1:1412:U:H2'	51:1:1413:A:C8	2.56	0.41
51:1:1722:A:N6	51:1:1738:G:H1'	2.36	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
51:1:2038:G:H2'	51:1:2039:U:O4'	2.21	0.41
51:1:2106:U:H3'	51:1:2107:G:H8	1.86	0.41
51:1:2293:G:O2'	51:1:2294:G:H5'	2.21	0.41
51:1:2575:C:H2'	51:1:2578:G:O6	2.21	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:A1:44:ARG:HA	57:A1:183:ILE:HD12	2.03	0.41
57:A2:104:LYS:HG2	57:A2:110:VAL:HG22	2.03	0.41
58:B1:71:LEU:HB2	58:B1:90:VAL:HG11	2.03	0.41
58:B1:109:SER:CB	58:B1:296:LYS:HG2	2.51	0.41
58:B1:111:THR:HG23	58:B1:300:GLN:HA	2.03	0.41
58:B1:239:LEU:N	58:B1:239:LEU:HD23	2.36	0.41
58:B1:282:LEU:HA	58:B1:282:LEU:HD12	1.79	0.41
58:B1:351:GLY:O	58:B1:467:ALA:HA	2.21	0.41
58:B1:605:LEU:HD23	58:B1:605:LEU:HA	1.93	0.41
58:B1:609:TYR:HD2	58:B1:610:ARG:NH1	2.18	0.41
58:B1:800:LEU:HD12	58:B1:800:LEU:HA	1.79	0.41
58:B1:1361:THR:N	59:B2:1282:GLY:O	2.53	0.41
59:B2:50:GLU:HG2	59:B2:73:TYR:HE1	1.85	0.41
7:G:17:HIS:C	7:G:19:THR:H	2.28	0.41
9:I:10:LEU:HG	9:I:62:ARG:HD2	2.03	0.41
16:P:30:ILE:HG23	16:P:45:THR:HB	2.02	0.41
27:b:70:LYS:HD2	27:b:73:ILE:HD12	2.02	0.41
27:b:209:ALA:HA	27:b:212:TRP:CE2	2.55	0.41
30:e:36:ASN:HB3	30:e:152:ASP:HB3	2.03	0.41
31:f:21:GLN:NE2	31:f:37:ASN:O	2.54	0.41
34:j:17:VAL:HG13	34:j:137:PRO:HB2	2.03	0.41
42:r:4:VAL:HG23	42:r:39:LEU:HB2	2.03	0.41
51:1:914:G:H5'	51:1:915:C:OP2	2.21	0.41
51:1:1107:G:H2'	51:1:1108:U:C6	2.56	0.41
51:1:1334:G:C6	51:1:1335:C:C4	3.09	0.41
51:1:1482:G:H2'	51:1:1483:G:H8	1.85	0.41
51:1:1591:A:H2'	51:1:1592:C:C6	2.56	0.41
51:1:1991:U:H2'	51:1:1992:G:H5'	2.02	0.41
51:1:2105:U:C2	51:1:2184:A:H2	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2194:U:H2'	51:1:2195:U:H6	1.84	0.41
51:1:2615:U:O2	51:1:2615:U:H2'	2.20	0.41
53:3:987:G:H2'	53:3:988:G:C8	2.56	0.41
57:A2:57:THR:HG23	57:A2:158:ARG:HH21	1.86	0.41
58:B1:68:TYR:O	58:B1:75:TYR:CD2	2.70	0.41
58:B1:576:ARG:HD3	58:B1:593:ASN:HA	2.03	0.41
59:B2:657:THR:HG21	59:B2:1188:ASP:HB2	2.03	0.41
59:B2:738:GLU:HA	59:B2:741:MET:HE2	2.03	0.41
63:5:17:C:H2'	63:5:18:G:C8	2.56	0.41
19:S:15:LEU:HB3	19:S:54:SER:HB3	2.03	0.40
35:k:87:LEU:HD23	35:k:87:LEU:HA	1.97	0.40
51:1:224:U:O4	51:1:420:C:H5'	2.21	0.40
51:1:426:C:O2'	51:1:427:U:H5'	2.21	0.40
51:1:679:C:H2'	51:1:680:C:C6	2.56	0.40
51:1:1430:G:O2'	51:1:1431:A:H5'	2.21	0.40
51:1:1715:G:O2'	51:1:1716:U:C6	2.74	0.40
51:1:2210:U:H6	51:1:2210:U:OP1	2.04	0.40
51:1:2221:G:H2'	51:1:2222:C:C6	2.56	0.40
51:1:2393:U:C2'	51:1:2394:C:H5'	2.51	0.40
51:1:2568:U:O5'	51:1:2568:U:H6	2.04	0.40
51:1:2667:C:O5'	51:1:2667:C:H6	2.03	0.40
51:1:2680:U:O2'	51:1:2681:C:H5'	2.21	0.40
53:3:146:G:H2'	53:3:147:G:H8	1.86	0.40
53:3:202:G:H2'	53:3:203:G:C8	2.55	0.40
53:3:685:G:N1	53:3:704:A:OP2	2.52	0.40
58:B1:777:HIS:CD2	59:B2:550:VAL:HG13	2.56	0.40
9:I:150:LYS:HD2	9:I:155:LYS:HD2	2.04	0.40
10:J:156:ARG:HE	13:M:42:GLU:HG3	1.87	0.40
38:n:71:ARG:HE	38:n:71:ARG:HB3	1.68	0.40
51:1:211:C:O2'	51:1:212:G:H5'	2.21	0.40
51:1:309:A:N3	51:1:329:G:O2'	2.53	0.40
51:1:1279:G:H2'	51:1:1280:G:C8	2.56	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
53:3:1304:G:N1	53:3:1332:A:OP2	2.54	0.40
58:B1:108:ALA:HB2	58:B1:276:ASN:OD1	2.21	0.40
58:B1:282:LEU:CA	58:B1:286:ALA:HA	2.45	0.40
59:B2:803:ALA:HB2	59:B2:1094:VAL:HG21	2.03	0.40
11:K:53:LYS:HE2	11:K:53:LYS:HB2	1.95	0.40
18:R:53:ASP:OD1	18:R:53:ASP:N	2.55	0.40
28:c:169:ARG:O	51:1:2773:C:H4'	2.21	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	2.44	0.40
31:f:157:LYS:HD3	51:1:2658:C:H5''	2.02	0.40
51:1:55:G:N2	51:1:116:C:C2	2.90	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
51:1:359:G:H2'	51:1:360:U:C5'	2.51	0.40
51:1:674:G:C8	51:1:674:G:H3'	2.56	0.40
51:1:1152:C:H2'	51:1:1153:C:C6	2.55	0.40
51:1:1346:G:O2'	51:1:1347:A:H5'	2.22	0.40
51:1:1410:G:H2'	51:1:1411:U:H6	1.85	0.40
51:1:2049:G:O2'	51:1:2050:C:H5'	2.21	0.40
51:1:2647:U:O2'	51:1:2648:G:H5'	2.21	0.40
51:1:2776:A:C6	51:1:2778:A:C6	3.09	0.40
52:2:31:C:H2'	52:2:53:A:H61	1.87	0.40
53:3:202:G:H2'	53:3:203:G:H8	1.85	0.40
55:8:2:DC:C6	55:8:2:DC:H5'	2.56	0.40
58:B1:245:LEU:HD13	59:B2:1329:GLU:HA	2.03	0.40
59:B2:148:GLN:NE2	59:B2:535:PRO:O	2.40	0.40
59:B2:864:LYS:HB2	59:B2:864:LYS:HE3	1.81	0.40
64:7:10:G:OP1	64:7:46:G:H4'	2.21	0.40
6:F:30:GLU:HA	6:F:31:PRO:HD3	1.91	0.40
8:H:14:VAL:HG11	8:H:180:ASP:HB3	2.03	0.40
9:I:59:LYS:HE2	9:I:194:ILE:HG22	2.04	0.40
9:I:123:MET:HB2	9:I:143:SER:HB3	2.04	0.40
12:L:125:ASP:HB2	12:L:130:LYS:HG3	2.03	0.40
14:N:22:PRO:HA	14:N:60:LEU:HA	2.03	0.40
26:Z:15:LEU:HD23	26:Z:15:LEU:HA	1.80	0.40
29:d:138:LEU:HG	29:d:143:LEU:HD12	2.03	0.40
30:e:64:PRO:HA	30:e:88:VAL:HG22	2.03	0.40
38:n:22:ARG:HH22	51:1:2709:G:H5'	1.86	0.40
40:p:25:VAL:HG23	40:p:85:VAL:HA	2.04	0.40
51:1:1038:G:H2'	51:1:1039:A:H8	1.83	0.40
51:1:1042:G:H2'	51:1:1043:C:H6	1.85	0.40
51:1:1116:G:O2'	51:1:1117:C:H5'	2.22	0.40
51:1:1317:G:H2'	51:1:1318:U:C6	2.56	0.40
51:1:1695:G:H2'	51:1:1696:G:O5'	2.22	0.40
51:1:2828:G:N1	51:1:2829:A:C5	2.90	0.40
53:3:464:U:N3	53:3:467:U:OP2	2.42	0.40
57:A1:33:ARG:HE	57:A1:33:ARG:HB3	1.56	0.40
58:B1:68:TYR:CB	58:B1:75:TYR:HE2	2.34	0.40
58:B1:120:LEU:HD22	58:B1:120:LEU:HA	1.77	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:472:LEU:HD11	59:B2:1294:LYS:HG2	2.02	0.40
59:B2:478:ARG:HD2	59:B2:492:MET:HA	2.02	0.40
63:5:23:A:H2'	63:5:24:G:C8	2.56	0.40
1:A:62:LYS:HE3	1:A:62:LYS:HB3	1.89	0.40
5:E:7:ARG:NH2	51:1:245:G:N7	2.59	0.40
31:f:3:VAL:HG13	51:1:2751:G:H4'	2.02	0.40
51:1:467:G:H8	51:1:467:G:O5'	2.04	0.40
51:1:518:G:H2'	51:1:519:U:C6	2.55	0.40
51:1:1160:G:C2	51:1:1161:C:C2	3.10	0.40
51:1:1430:G:H2'	51:1:1431:A:O4'	2.21	0.40
51:1:1469:A:H2'	51:1:1470:A:H8	1.83	0.40
51:1:1599:U:H2'	51:1:1600:C:H6	1.85	0.40
51:1:1722:A:H2'	51:1:1723:G:O4'	2.21	0.40
51:1:1783:A:C8	51:1:1783:A:H5'	2.57	0.40
51:1:1827:U:C2'	51:1:1828:G:H5'	2.51	0.40
51:1:2093:G:N7	51:1:2225:A:H2'	2.37	0.40
58:B1:244:VAL:HA	58:B1:269:TYR:CZ	2.57	0.40
59:B2:43:PRO:HB2	59:B2:44:GLU:H	1.71	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	64/70 (91%)	59 (92%)	5 (8%)	0	100	100
2	B	54/57 (95%)	48 (89%)	4 (7%)	2 (4%)	2	20
3	C	48/55 (87%)	41 (85%)	7 (15%)	0	100	100
4	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
5	E	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
6	F	36/38 (95%)	32 (89%)	3 (8%)	1 (3%)	4	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	G	216/241 (90%)	187 (87%)	27 (12%)	2 (1%)	14	51
8	H	204/233 (88%)	194 (95%)	10 (5%)	0	100	100
9	I	203/206 (98%)	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%)	84 (86%)	14 (14%)	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	48
16	P	114/129 (88%)	100 (88%)	13 (11%)	1 (1%)	14	51
17	Q	121/124 (98%)	94 (78%)	27 (22%)	0	100	100
18	R	112/118 (95%)	98 (88%)	13 (12%)	1 (1%)	14	51
19	S	98/101 (97%)	83 (85%)	15 (15%)	0	100	100
20	T	86/89 (97%)	75 (87%)	11 (13%)	0	100	100
21	U	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
22	V	78/84 (93%)	69 (88%)	8 (10%)	1 (1%)	10	42
23	W	63/75 (84%)	56 (89%)	5 (8%)	2 (3%)	3	21
24	X	77/92 (84%)	71 (92%)	6 (8%)	0	100	100
25	Y	83/87 (95%)	78 (94%)	5 (6%)	0	100	100
26	Z	63/71 (89%)	44 (70%)	18 (29%)	1 (2%)	8	37
27	b	269/273 (98%)	244 (91%)	25 (9%)	0	100	100
28	c	207/209 (99%)	190 (92%)	17 (8%)	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	32
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	n	118/127 (93%)	103 (87%)	15 (13%)	0	100	100
39	o	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
40	p	112/115 (97%)	103 (92%)	9 (8%)	0	100	100
41	q	115/118 (98%)	110 (96%)	3 (3%)	2 (2%)	7	36
42	r	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	13	48
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	48
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%)	1204 (90%)	129 (10%)	5 (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	59
62	NG	150/181 (83%)	136 (91%)	10 (7%)	4 (3%)	4	26
65	h	2/6 (33%)	1 (50%)	1 (50%)	0	100	100
All	All	9586/10235 (94%)	8668 (90%)	882 (9%)	36 (0%)	32	68

All (36) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
42	r	54	VAL
48	x	25	LYS
58	B1	121	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
59	B2	918	LEU
61	NA	138	ILE
62	NG	163	SER
59	B2	888	THR
59	B2	908	GLU
2	B	23	ALA
7	G	19	THR
18	R	5	GLY
32	g	12	LEU
41	q	23	TYR
58	B1	43	THR
58	B1	193	ASP
7	G	17	HIS
15	O	58	ASN
22	V	50	ASN
23	W	13	THR
45	u	97	SER
58	B1	1325	PHE
9	I	45	PRO
23	W	17	VAL
62	NG	169	THR
62	NG	170	PRO
26	Z	10	PRO
41	q	6	GLY
59	B2	1317	PRO
2	B	24	VAL
16	P	88	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	59/62 (95%)	58 (98%)	1 (2%)	56	72
2	B	47/48 (98%)	47 (100%)	0	100	100
3	C	45/49 (92%)	44 (98%)	1 (2%)	47	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	38/38 (100%)	37 (97%)	1 (3%)	41	60
5	E	51/52 (98%)	49 (96%)	2 (4%)	27	49
6	F	34/34 (100%)	30 (88%)	4 (12%)	4	17
7	G	180/199 (90%)	174 (97%)	6 (3%)	33	54
8	H	170/190 (90%)	167 (98%)	3 (2%)	54	71
9	I	172/173 (99%)	168 (98%)	4 (2%)	45	64
10	J	119/126 (94%)	117 (98%)	2 (2%)	56	72
11	K	87/116 (75%)	82 (94%)	5 (6%)	17	39
12	L	124/147 (84%)	124 (100%)	0	100	100
13	M	104/105 (99%)	103 (99%)	1 (1%)	73	81
14	N	105/107 (98%)	98 (93%)	7 (7%)	13	34
15	O	86/90 (96%)	78 (91%)	8 (9%)	7	23
16	P	89/99 (90%)	86 (97%)	3 (3%)	32	53
17	Q	103/104 (99%)	98 (95%)	5 (5%)	21	42
18	R	92/96 (96%)	91 (99%)	1 (1%)	70	80
19	S	83/84 (99%)	83 (100%)	0	100	100
20	T	76/77 (99%)	73 (96%)	3 (4%)	27	49
21	U	65/65 (100%)	64 (98%)	1 (2%)	60	75
22	V	74/78 (95%)	72 (97%)	2 (3%)	40	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	13
27	b	216/218 (99%)	212 (98%)	4 (2%)	52	69
28	c	164/164 (100%)	164 (100%)	0	100	100
29	d	165/165 (100%)	162 (98%)	3 (2%)	54	71
30	e	148/150 (99%)	145 (98%)	3 (2%)	50	68
31	f	137/138 (99%)	135 (98%)	2 (2%)	60	75
32	g	41/114 (36%)	38 (93%)	3 (7%)	11	31
33	i	109/110 (99%)	108 (99%)	1 (1%)	75	83
34	j	116/116 (100%)	116 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	k	103/104 (99%)	103 (100%)	0	100	100
36	l	102/103 (99%)	101 (99%)	1 (1%)	73	81
37	m	109/109 (100%)	103 (94%)	6 (6%)	18	40
38	n	100/103 (97%)	99 (99%)	1 (1%)	73	81
39	o	86/87 (99%)	86 (100%)	0	100	100
40	p	99/100 (99%)	99 (100%)	0	100	100
41	q	89/90 (99%)	86 (97%)	3 (3%)	32	53
42	r	84/84 (100%)	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	75
65	h	2/2 (100%)	2 (100%)	0	100	100
All	All	7381/7914 (93%)	7132 (97%)	249 (3%)	34	53

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
6	F	35	GLN

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Mol	Chain	Res	Type
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
17	Q	15	VAL

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Mol	Chain	Res	Type
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
37	m	44	ARG

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Mol	Chain	Res	Type
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
58	B1	71	LEU

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Mol	Chain	Res	Type
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
58	B1	233	LYS

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Mol	Chain	Res	Type
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
59	B2	49	LEU

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Mol	Chain	Res	Type
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	862	LEU
59	B2	864	LYS
59	B2	887	VAL
59	B2	890	LYS
59	B2	892	GLU
59	B2	893	THR
59	B2	894	GLN
59	B2	895	LEU
59	B2	899	GLU
59	B2	900	LYS
59	B2	901	LEU
59	B2	902	LEU
59	B2	905	ILE
59	B2	913	VAL
59	B2	915	ASP
59	B2	918	LEU
59	B2	920	VAL
59	B2	922	ASN
59	B2	1076	ILE
59	B2	1151	LEU
60	W0	63	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (129) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	33	ASN
1	A	61	ASN
2	B	4	GLN
3	C	44	GLN
4	D	16	HIS

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Mol	Chain	Res	Type
6	F	37	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	151	GLN
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	68	HIS
25	Y	2	ASN
25	Y	77	ASN
26	Z	8	ASN
27	b	24	HIS
27	b	69	ASN
27	b	89	ASN

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Mol	Chain	Res	Type
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
38	n	13	ASN
40	p	2	ASN
40	p	114	ASN
41	q	55	GLN
41	q	58	GLN
42	r	18	GLN
42	r	82	HIS
43	s	7	HIS
44	t	28	ASN
44	t	59	ASN
44	t	92	ASN
45	u	52	ASN
45	u	68	ASN
46	v	75	GLN
46	v	87	GLN
47	w	53	HIS
48	x	16	ASN

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Mol	Chain	Res	Type
48	x	33	HIS
49	y	31	GLN
49	y	38	GLN
49	y	41	HIS
49	y	45	GLN
50	z	8	GLN
57	A1	37	HIS
57	A1	66	HIS
57	A1	84	ASN
57	A1	117	HIS
57	A1	128	HIS
57	A1	227	GLN
57	A2	23	HIS
57	A2	227	GLN
58	B1	45	ASN
58	B1	364	HIS
58	B1	424	ASN
58	B1	469	HIS
58	B1	805	GLN
58	B1	865	HIS
58	B1	1195	GLN
58	B1	1238	GLN
58	B1	1259	GLN
59	B2	69	GLN
59	B2	314	ASN
59	B2	330	HIS
59	B2	343	HIS
59	B2	518	ASN
59	B2	554	HIS
59	B2	580	GLN
59	B2	688	GLN
59	B2	762	ASN
59	B2	808	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%)	398 (13%)	16 (0%)
52	2	119/120 (99%)	16 (13%)	1 (0%)
53	3	1538/1542 (99%)	253 (16%)	4 (0%)
54	4	34/56 (60%)	17 (50%)	2 (5%)
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	4820/4852 (99%)	764 (15%)	32 (0%)

All (764) 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	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
51	1	910	A

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Mol	Chain	Res	Type
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
51	1	1111	A

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Mol	Chain	Res	Type
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
51	1	1491	G

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Mol	Chain	Res	Type
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
51	1	1829	A

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Mol	Chain	Res	Type
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
51	1	2100	G

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Mol	Chain	Res	Type
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
51	1	2333	A

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Mol	Chain	Res	Type
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
51	1	2613	U

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Mol	Chain	Res	Type
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	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
52	2	87	U
52	2	88	C

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Mol	Chain	Res	Type
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
53	3	211	G
53	3	212	G

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Mol	Chain	Res	Type
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
53	3	446	G
53	3	453	G

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Mol	Chain	Res	Type
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
53	3	660	C
53	3	665	A

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Mol	Chain	Res	Type
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
53	3	976	G
53	3	977	A

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Mol	Chain	Res	Type
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
53	3	1237	C
53	3	1238	A

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Mol	Chain	Res	Type
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
53	3	1503	A
53	3	1506	U

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Mol	Chain	Res	Type
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	23	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
63	5	34	G

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Mol	Chain	Res	Type
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
64	7	22	G

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Mol	Chain	Res	Type
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
53	3	1035	A

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Mol	Chain	Res	Type
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	0.08	0
65	5OH	h	6	65	8,12,13	0.76	0	3,16,18	1.52	1 (33%)
65	KBE	h	1	65	8,8,9	0.60	0	7,8,10	1.20	1 (14%)
65	UAL	h	5	65	7,8,9	2.29	3 (42%)	5,9,11	2.92	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	5OH	h	6	65	-	0/2/18/20	0/1/1/1
65	KBE	h	1	65	-	0/7/7/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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	-4.85	1.32	1.40
65	h	5	UAL	C-CA	-2.88	1.40	1.45
65	h	5	UAL	CA-N	2.01	1.40	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	h	5	UAL	CA-CB-N1	-5.30	115.59	125.60
65	h	5	UAL	O-C-CA	-3.24	121.27	125.39
65	h	6	5OH	CR-CB-CA	-2.37	110.06	112.61
65	h	1	KBE	CB-CA-C	-2.07	109.20	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 8 short contacts:

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

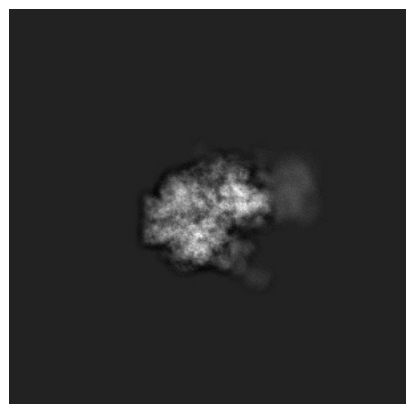
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39169. These allow visual inspection of the internal detail of the map and identification of artifacts.

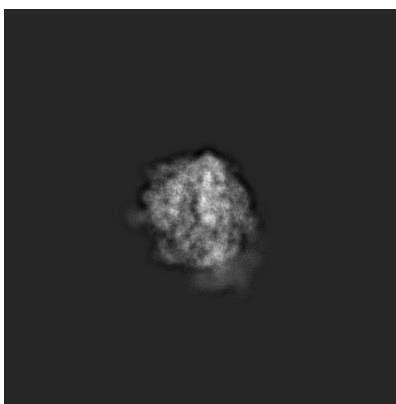
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

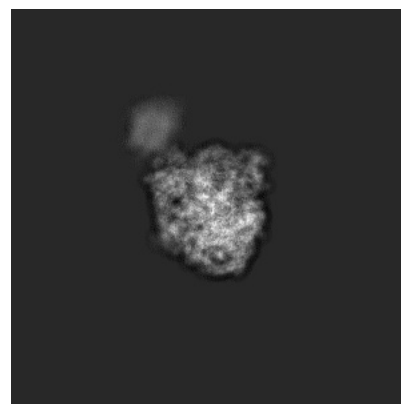
6.1.1 Primary map



X

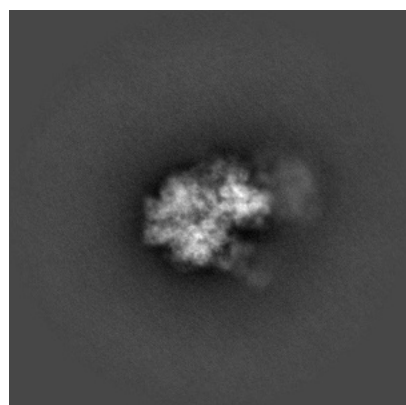


Y

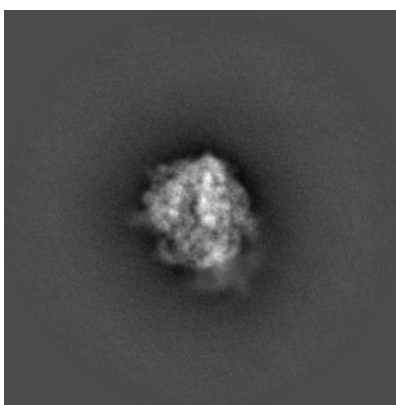


Z

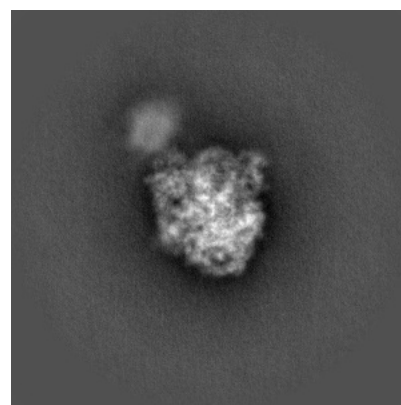
6.1.2 Raw map



X



Y

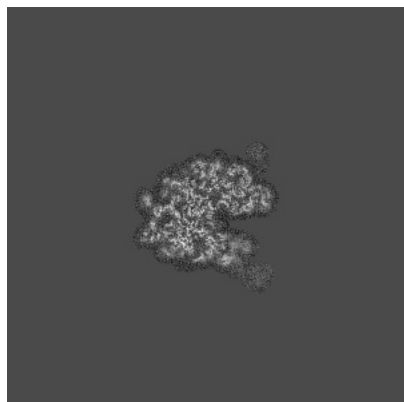


Z

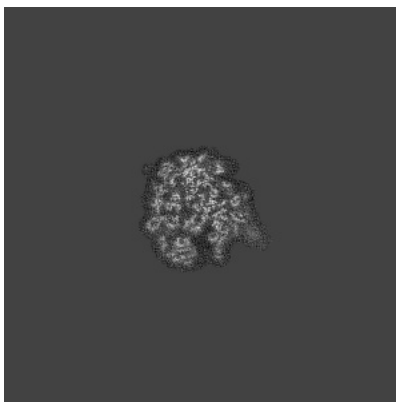
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

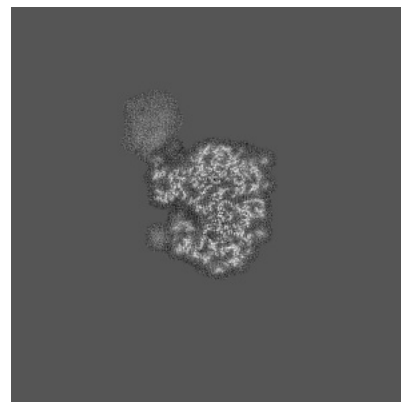
6.2.1 Primary map



X Index: 240

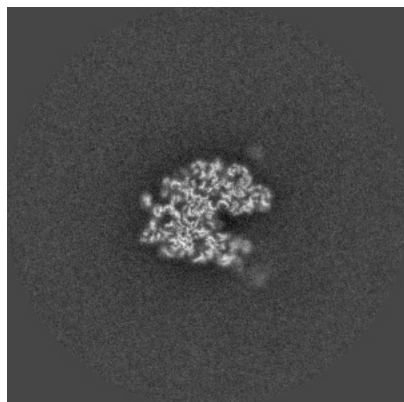


Y Index: 240

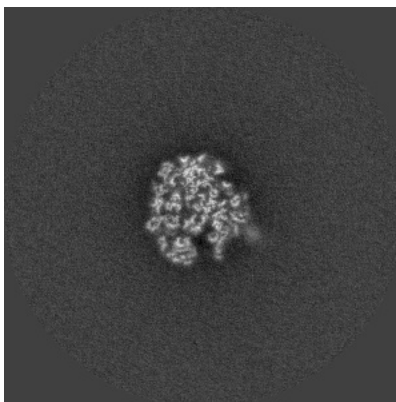


Z Index: 240

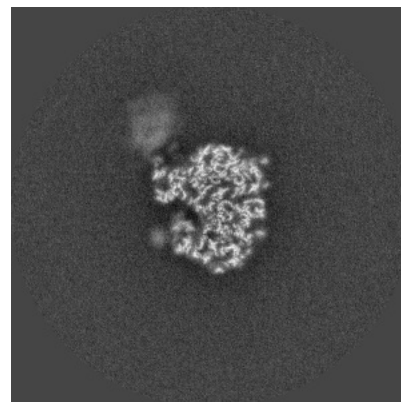
6.2.2 Raw map



X Index: 240



Y Index: 240

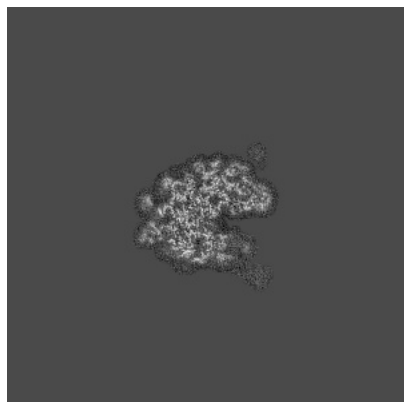


Z Index: 240

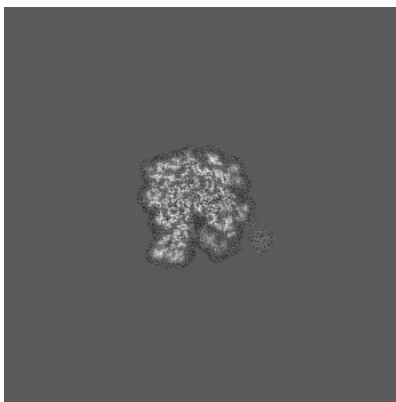
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

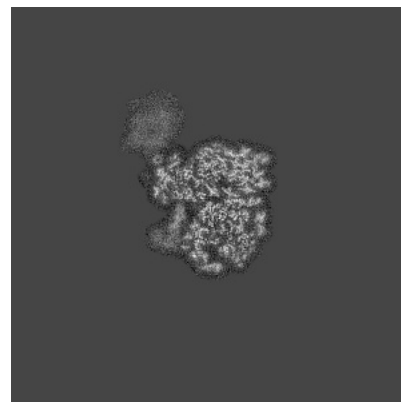
6.3.1 Primary map



X Index: 243

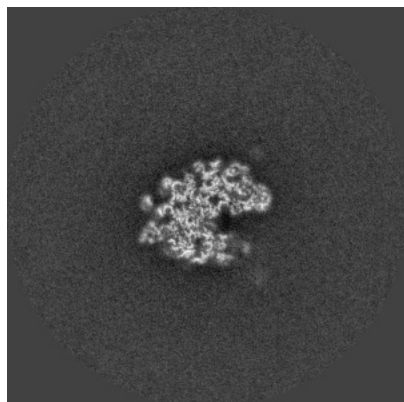


Y Index: 223

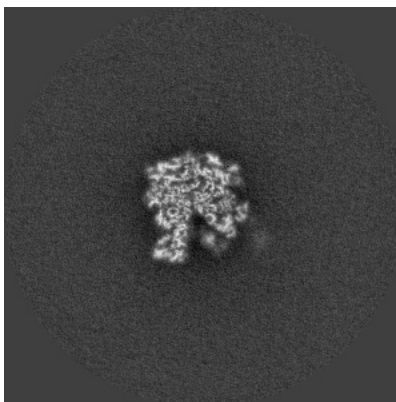


Z Index: 246

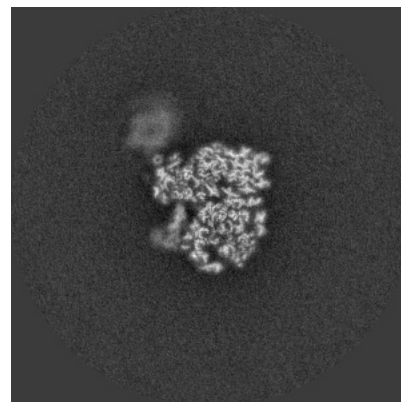
6.3.2 Raw map



X Index: 243



Y Index: 224

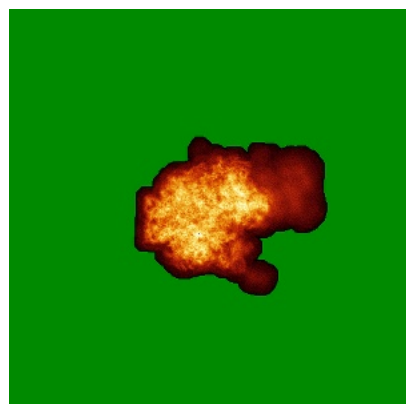


Z Index: 246

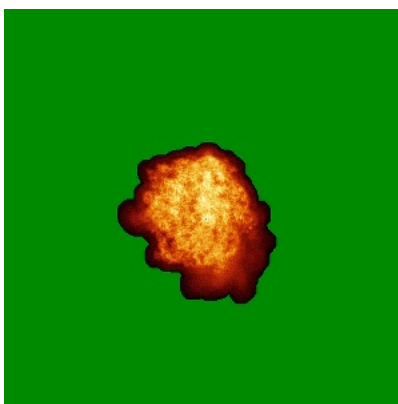
The images above show the largest variance slices of the map in three orthogonal directions.

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

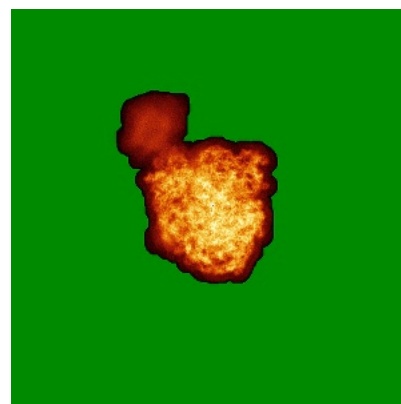
6.4.1 Primary map



X

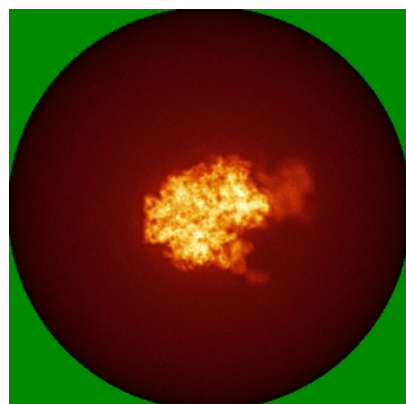


Y

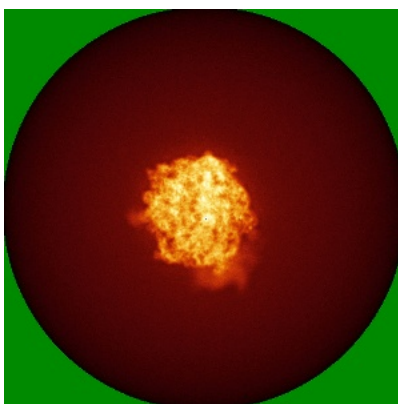


Z

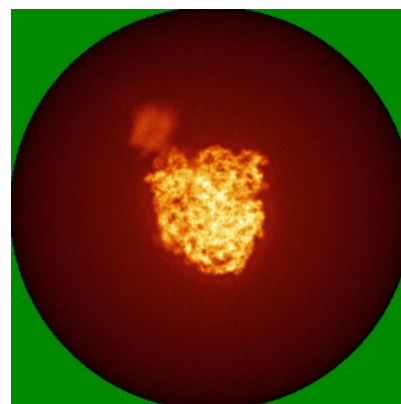
6.4.2 Raw map



X



Y

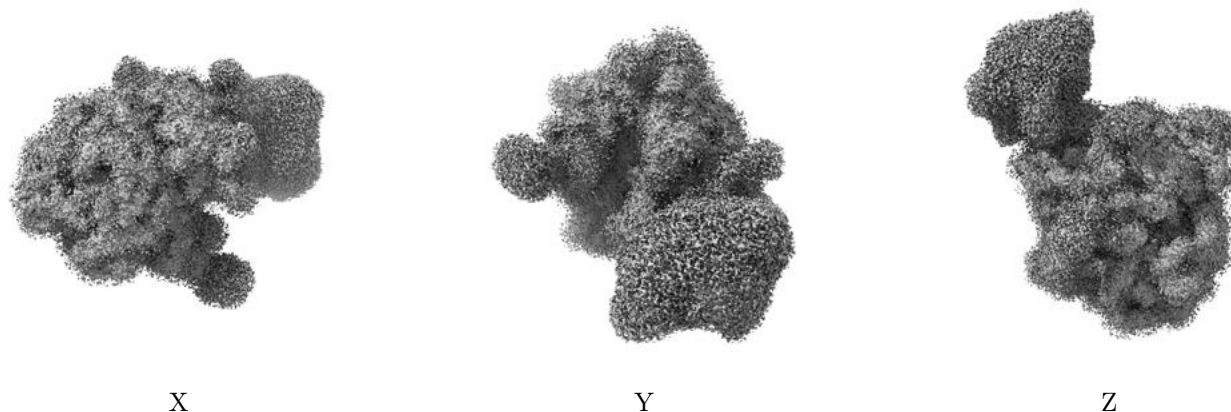


Z

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

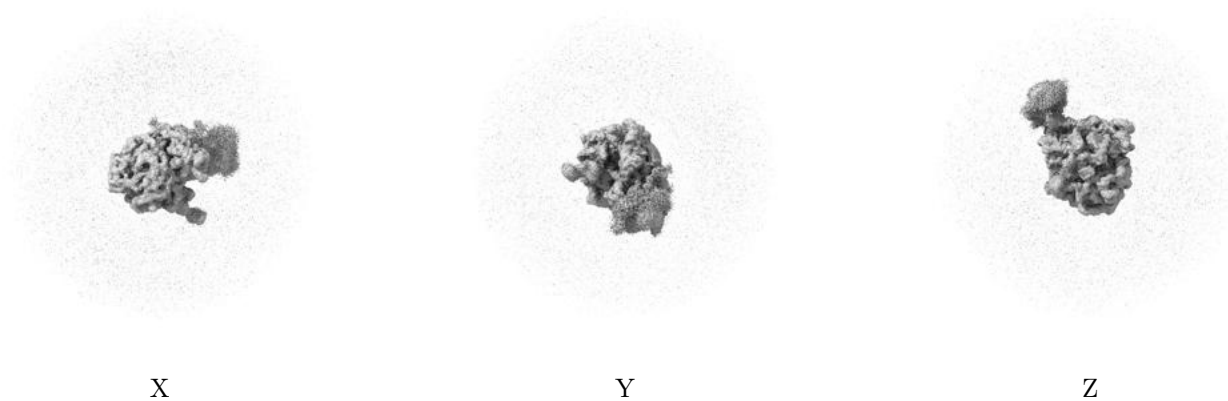
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.012. 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.

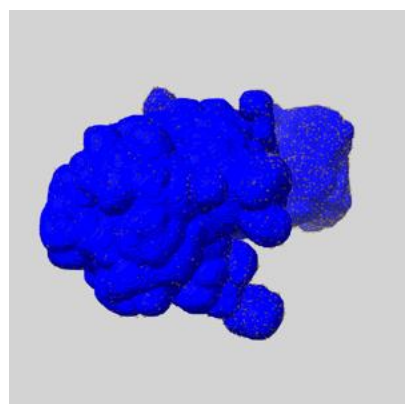
6.6 Mask visualisation [i](#)

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

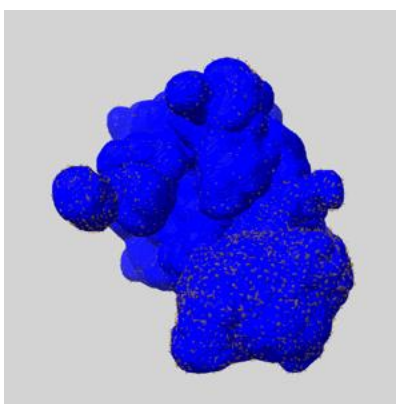
A mask typically either:

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

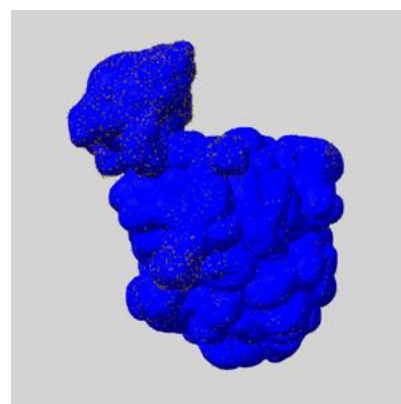
6.6.1 emd_39169_msk_1.map [i](#)



X



Y

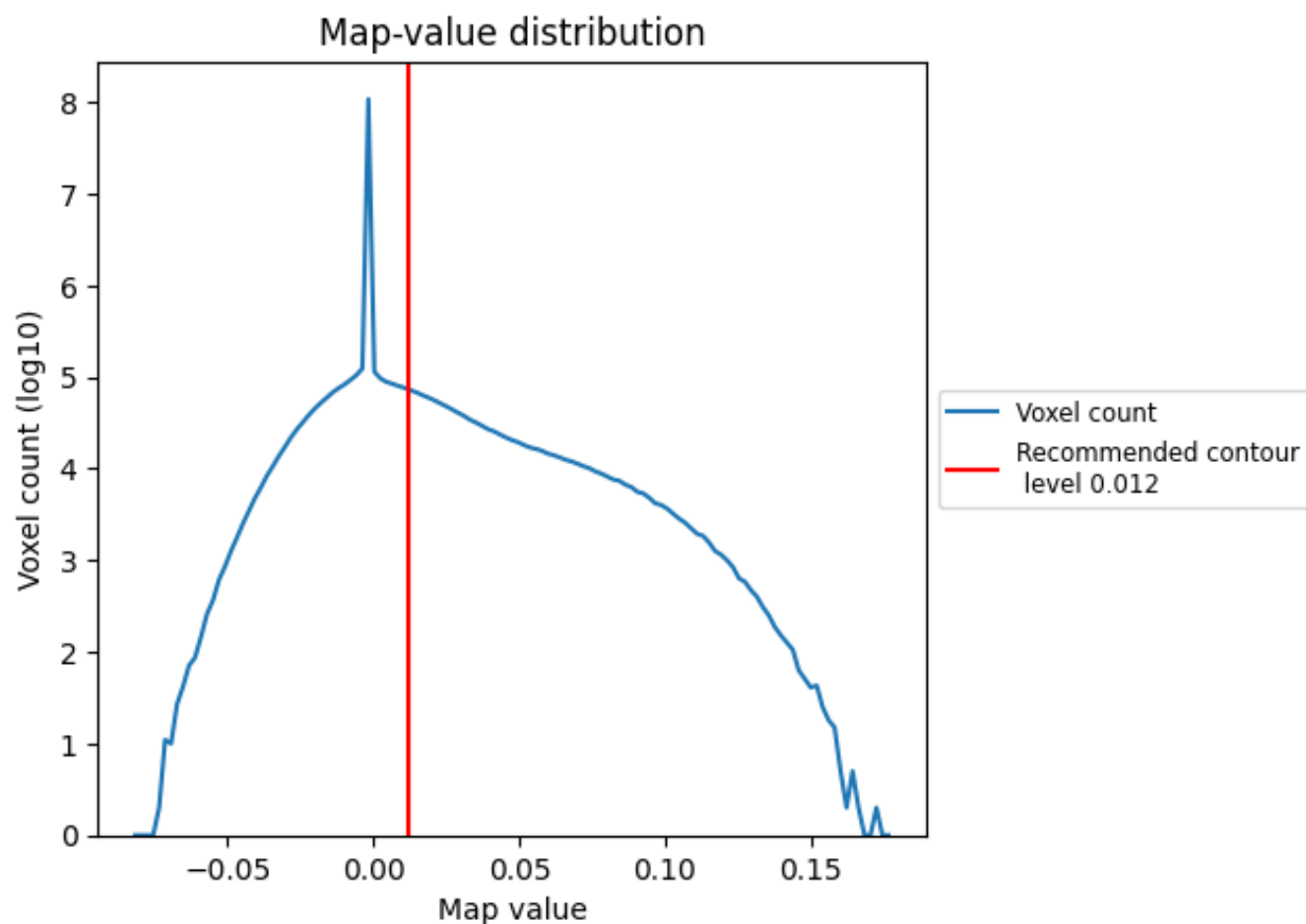


Z

7 Map analysis [i](#)

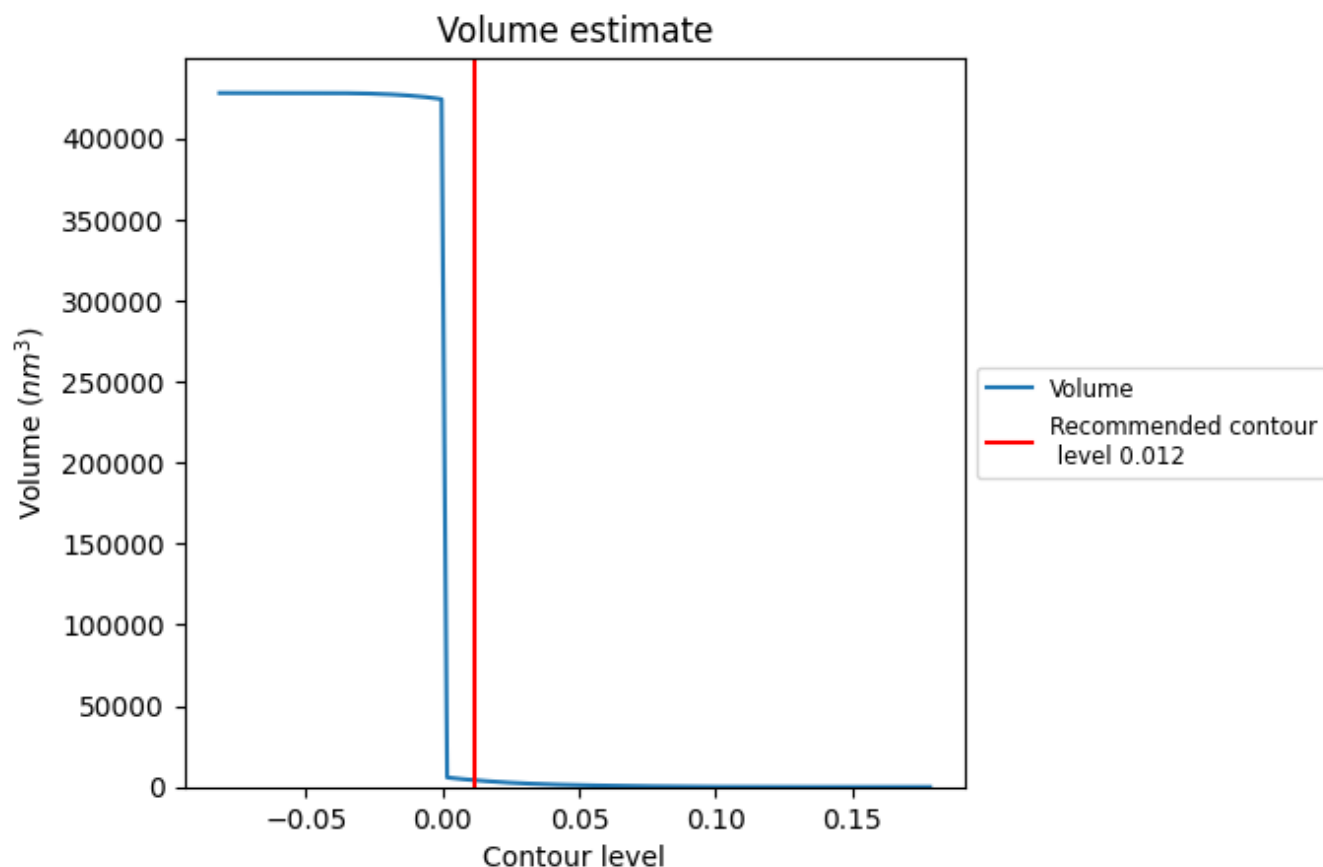
This section contains the results of statistical analysis of the map.

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.

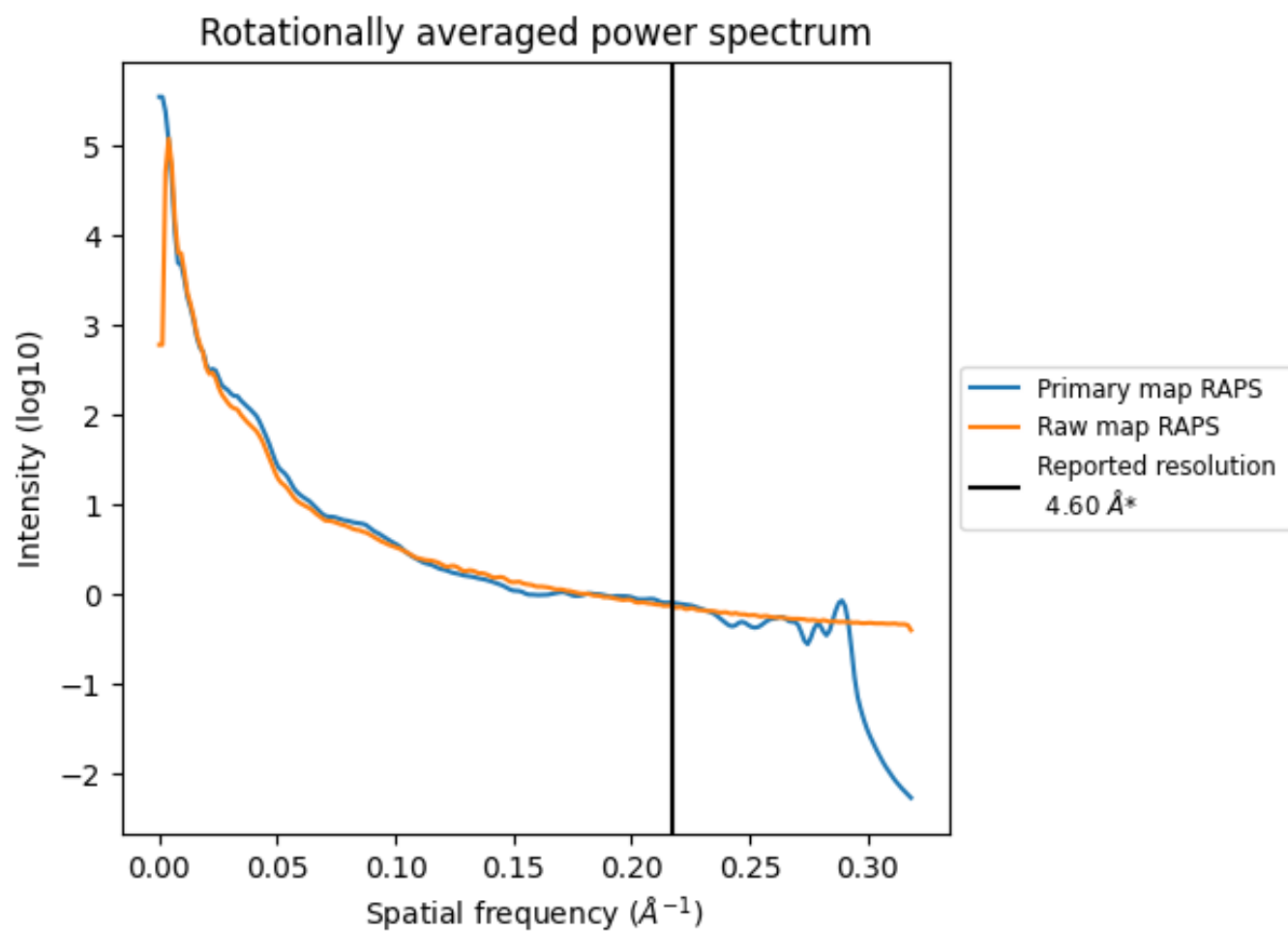
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4147 nm³; this corresponds to an approximate mass of 3746 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 ⓘ

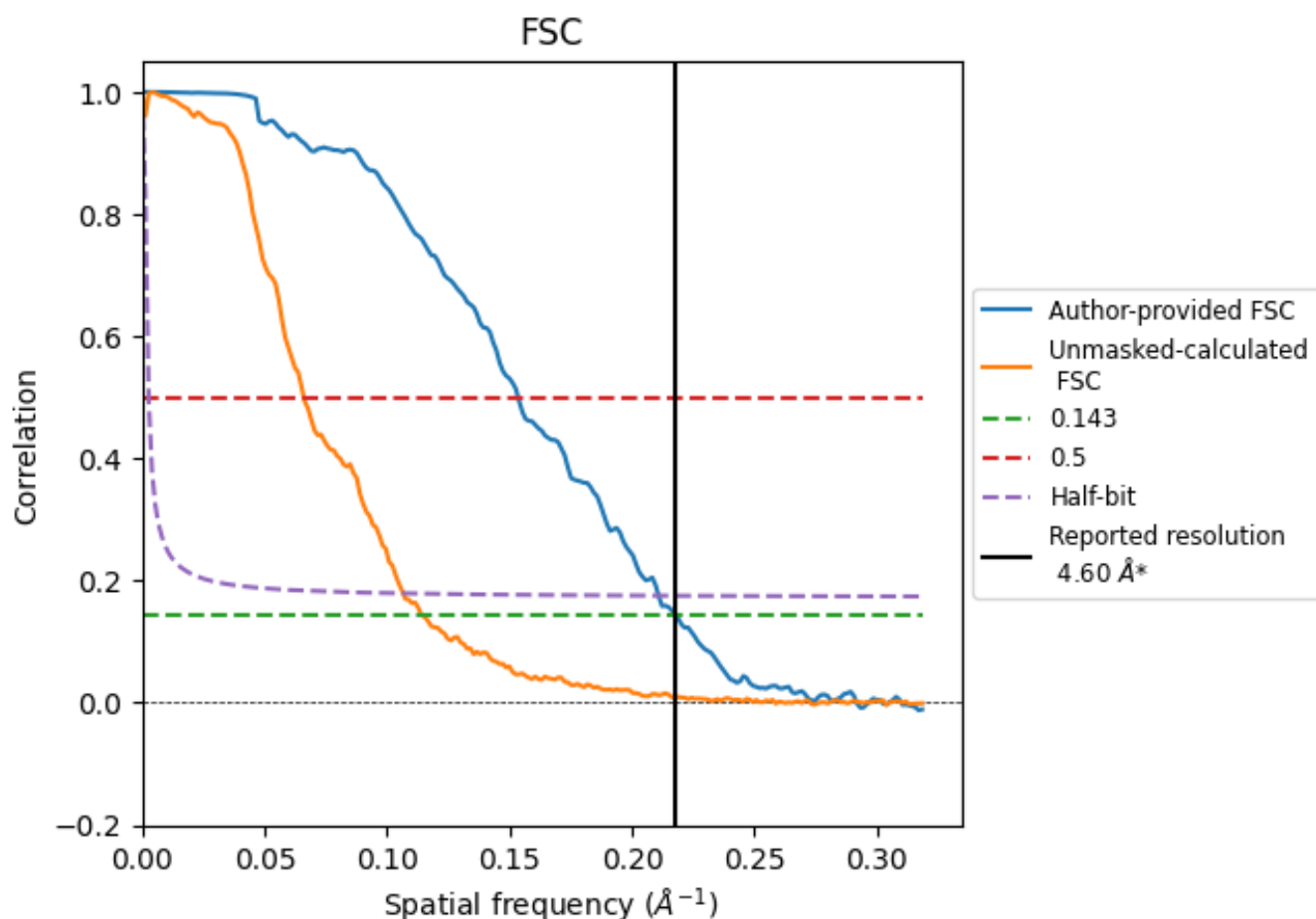


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

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 0.217 \AA^{-1}

8.2 Resolution estimates [i](#)

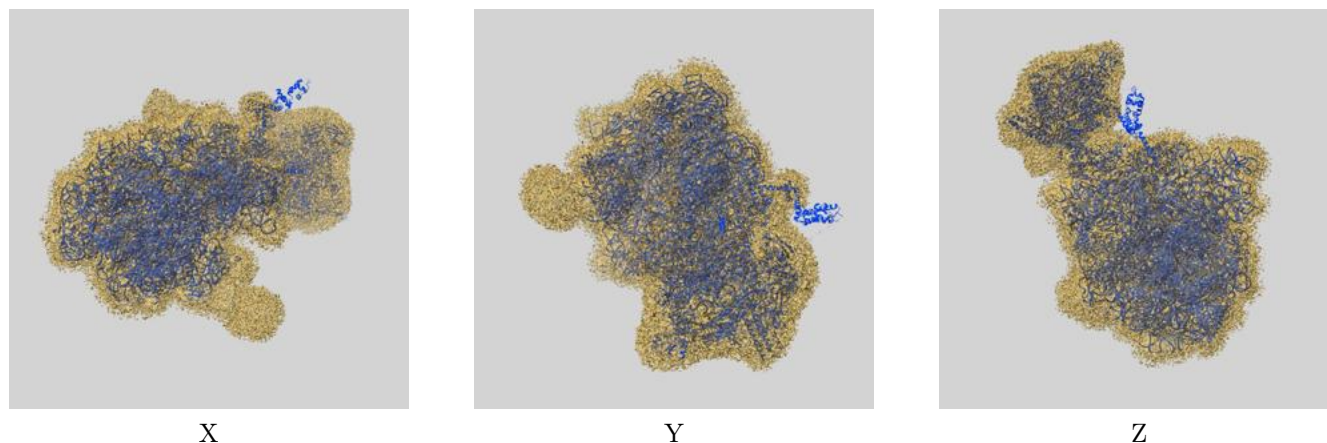
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.60	6.51	4.74
Unmasked-calculated*	8.76	15.15	9.39

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.76 differs from the reported value 4.6 by more than 10 %

9 Map-model fit [i](#)

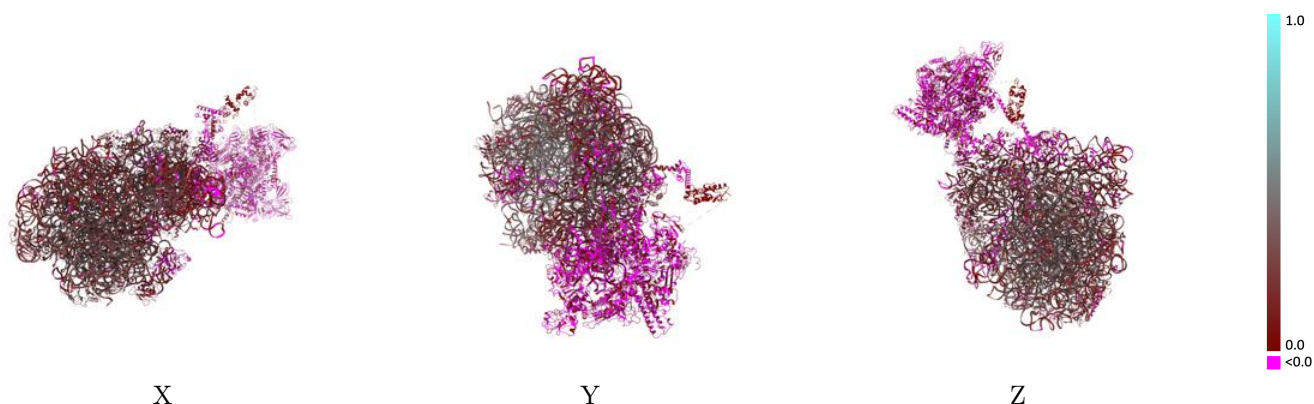
This section contains information regarding the fit between EMDB map EMD-39169 and PDB model 8YDF. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



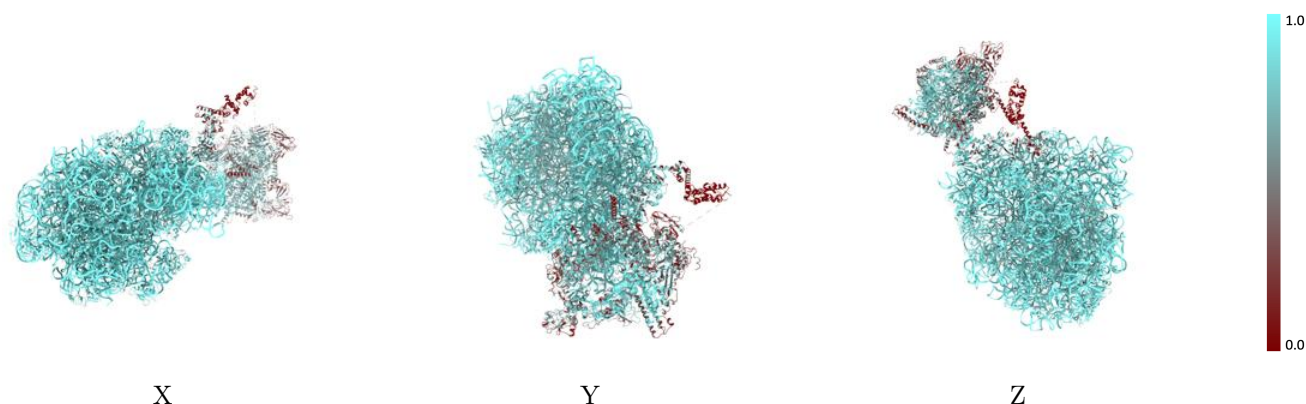
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



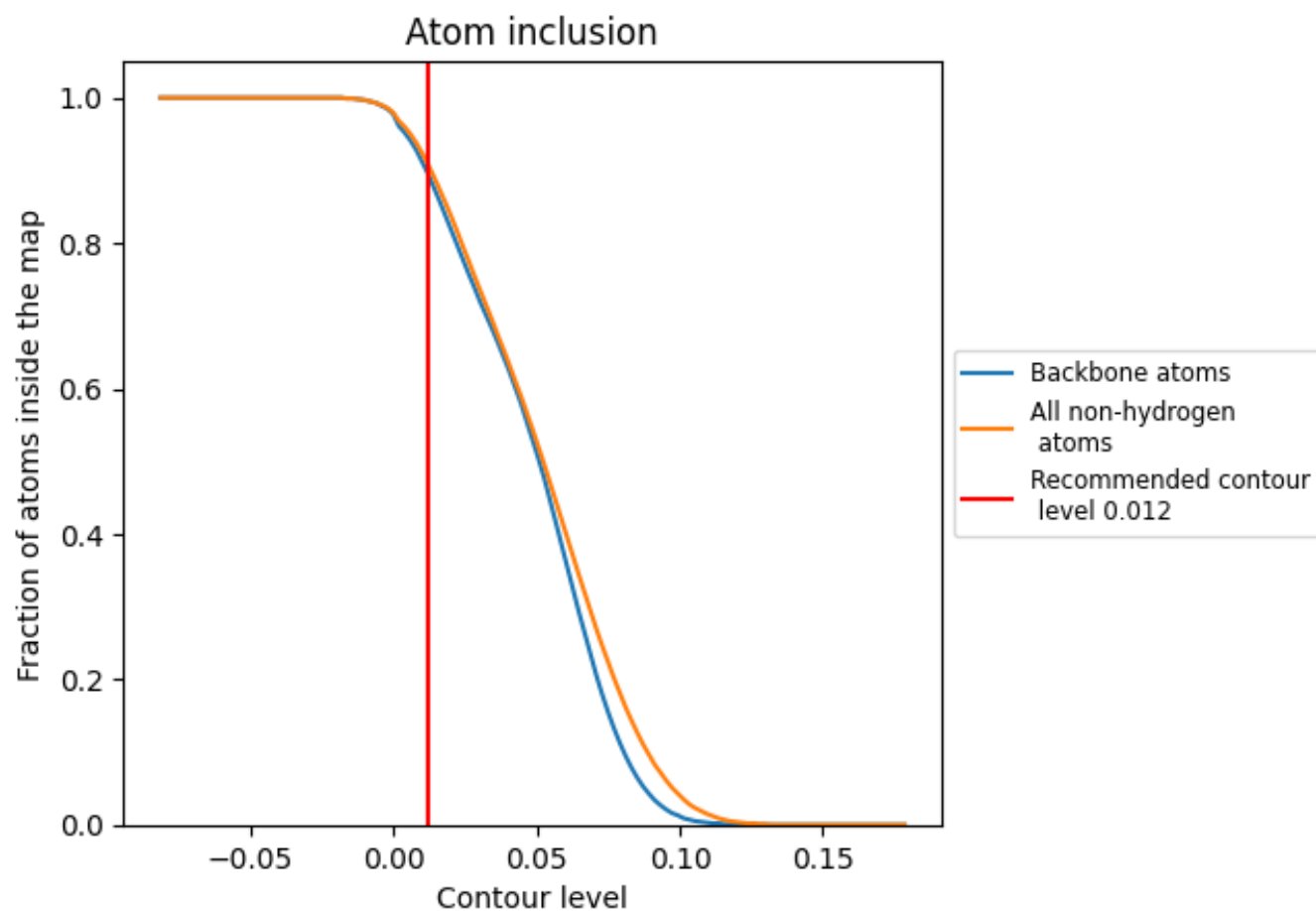
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.012).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9080	 0.2110
1	 0.9890	 0.2930
2	 0.9930	 0.2710
3	 0.9840	 0.2400
4	 0.7740	 0.0340
5	 0.9130	 0.1040
6	 0.9880	 0.3000
7	 0.7790	 0.0520
8	 0.8130	 -0.0050
9	 0.8300	 0.0090
A	 0.8920	 0.1740
A1	 0.3840	 0.0040
A2	 0.4300	 -0.0030
B	 0.9510	 0.2980
B1	 0.6240	 0.0030
B2	 0.7360	 0.0050
C	 0.9150	 0.2680
D	 0.9240	 0.3050
E	 0.9590	 0.3610
F	 0.9350	 0.2540
G	 0.9190	 0.1720
H	 0.9130	 0.2450
I	 0.8410	 0.0670
J	 0.9300	 0.2740
K	 0.9090	 0.1550
L	 0.9080	 0.1780
M	 0.9280	 0.2450
N	 0.9550	 0.1830
NA	 0.4790	 0.0200
NG	 0.7110	 0.0220
O	 0.9110	 0.1580
P	 0.9370	 0.1970
Q	 0.8900	 0.1870
R	 0.9310	 0.1930
S	 0.9520	 0.1930



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Chain	Atom inclusion	Q-score
T	 0.9490	 0.2410
U	 0.8600	 0.1250
V	 0.8810	 0.1110
W	 0.9380	 0.2100
W0	 0.2620	 -0.0060
X	 0.9420	 0.1920
Y	 0.9110	 0.1620
Z	 0.8320	 0.1350
b	 0.9290	 0.3070
c	 0.9430	 0.2610
d	 0.9580	 0.2550
e	 0.9480	 0.2340
f	 0.9550	 0.1790
g	 0.9360	 0.1830
h	 0.8540	 0.2030
i	 0.8420	 0.0110
j	 0.9490	 0.2870
k	 0.8840	 0.2450
l	 0.9560	 0.2830
m	 0.9430	 0.3280
n	 0.9590	 0.2430
o	 0.9780	 0.2200
p	 0.9010	 0.1870
q	 0.9670	 0.3360
r	 0.9660	 0.3010
s	 0.9220	 0.2510
t	 0.9060	 0.1790
u	 0.9540	 0.2000
v	 0.9570	 0.2360
w	 0.9540	 0.3110
x	 0.9320	 0.2850
y	 0.9170	 0.1220
z	 0.9570	 0.3170