



## Full wwPDB EM Validation Report ⓘ

Aug 4, 2025 – 10:51 PM JST

PDB ID : 8Y5R / pdb\_00008y5r  
EMDB ID : EMD-38947  
Title : E.coli Transcription translation coupling complex in TTC-B state 5 (subclass 1) containing mRNA with 27-mer spacer, NusG, NusA, fMet-tRNA(iMet), Phe-tRNA(Phe), and fusidic acid  
Authors : Zhang, J.; Lu, G.; Wang, C.; Lin, J.  
Deposited on : 2024-01-31  
Resolution : 4.50 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev126  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4-5-2 with Phenix2.0rc1  
buster-report : 1.1.7 (2018)  
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

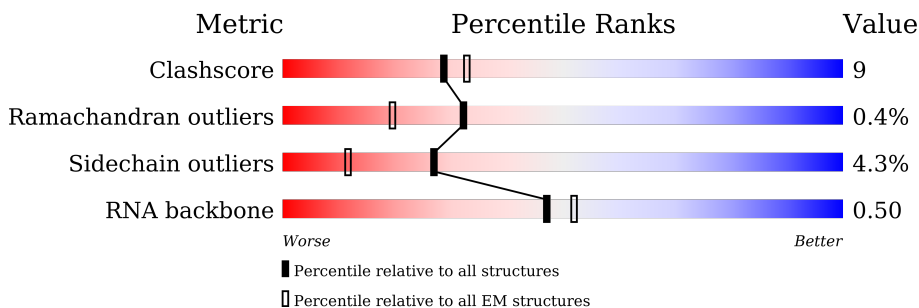
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*





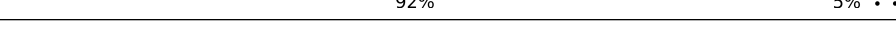


The reported resolution of this entry is 4.50 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	70	 80% 14% 6%
2	B	57	 77% 21% 2%
3	C	55	 84% 7% 9%
4	D	46	 76% 22% 2% 2%
5	E	65	 92% 5% 3% 2%
6	F	38	 74% 24% 2% 2%
7	G	241	 66% 23% 10%




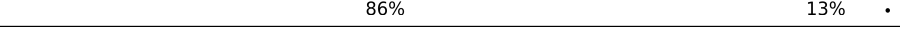
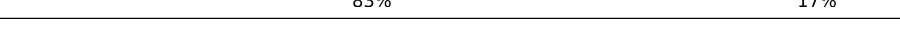
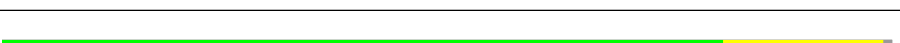
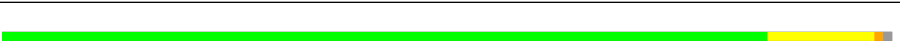




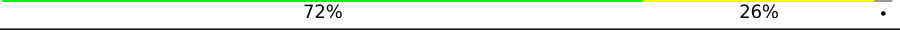
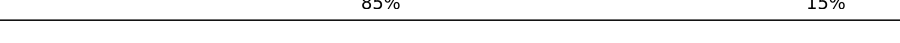





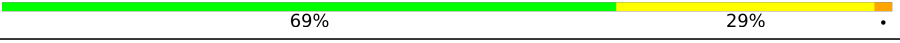

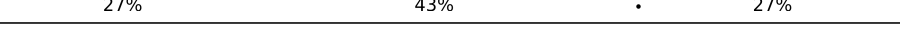
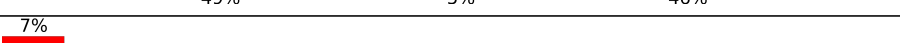



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Mol	Chain	Length	Quality of chain
8	H	233	
9	I	206	
10	J	167	
11	K	135	
12	L	179	
13	M	130	
14	N	130	
15	O	103	
16	P	129	
17	Q	124	
18	R	118	
19	S	101	
20	T	89	
21	U	82	
22	V	84	
23	W	75	
24	X	92	
25	Y	87	
26	Z	71	
27	b	273	
28	c	209	
29	d	201	
30	e	179	
31	f	177	
32	g	149	

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Mol	Chain	Length	Quality of chain
33	i	142	
34	j	142	
35	k	123	
36	l	144	
37	m	136	
38	n	127	
39	o	117	
40	p	115	
41	q	118	
42	r	103	
43	s	110	
44	t	100	
45	u	104	
46	v	94	
47	w	85	
48	x	78	
49	y	63	
50	z	59	
51	1	2904	
52	2	120	
53	3	1542	
54	4	44	
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	
65	0	716	

## 2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 181797 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
			521	323	98	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	39	Total	C	N	O	P	0	0
			809	362	113	295	39		

- 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		

- Molecule 65 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	0	673	Total	C	N	O	S	0	0
			5211	3289	900	999	23		

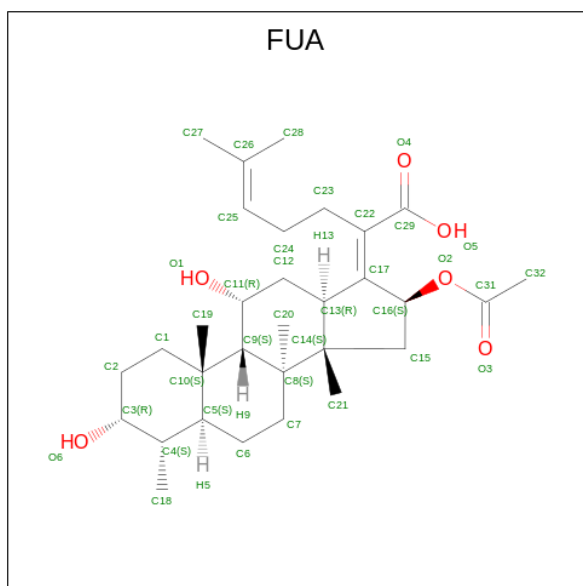
There are 12 discrepancies between the modelled and reference sequences:

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

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

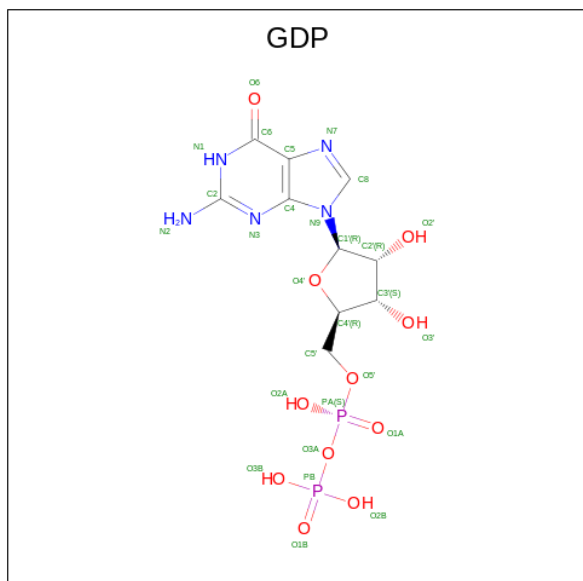
Mol	Chain	Residues	Atoms		AltConf
66	B1	1	Total	Mg	0
			1	1	

- Molecule 67 is FUSIDIC ACID (CCD ID: FUA) (formula:  $C_{31}H_{48}O_6$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
67	0	1	Total	C	O	0
			37	31	6	

- Molecule 68 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula:  $C_{10}H_{15}N_5O_{11}P_2$ ) (labeled as "Ligand of Interest" by depositor).




Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
68	0	1	28	10	5	11	2	0

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


These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 50S ribosomal protein L31

Chain A: 




- Molecule 2: 50S ribosomal protein L32

Chain B: 




- Molecule 3: 50S ribosomal protein L33

Chain C: 



- Molecule 4: 50S ribosomal protein L34

Chain D: 



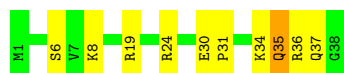
- Molecule 5: 50S ribosomal protein L35

Chain E: 



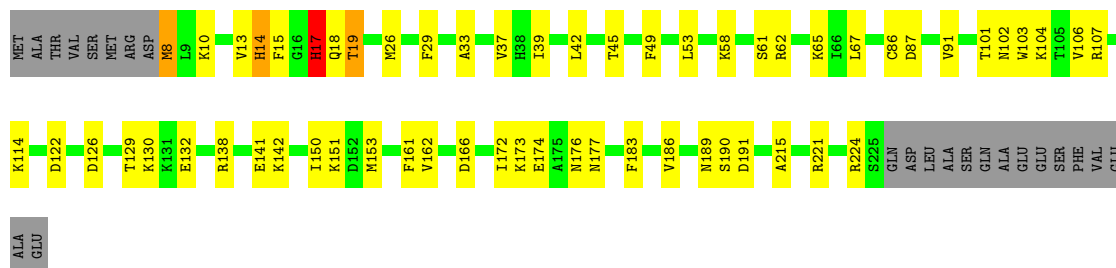
- Molecule 6: 50S ribosomal protein L36

Chain F:  74% 24% .



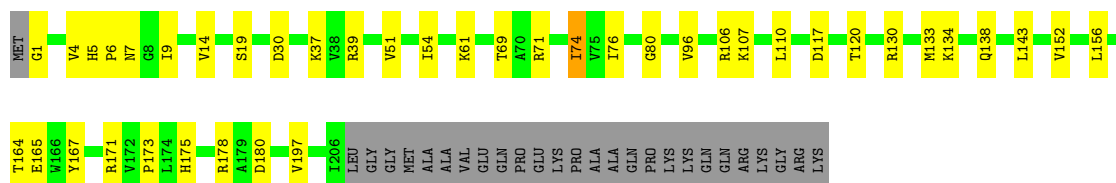
- Molecule 7: 30S ribosomal protein S2

Chain G:  66% 23% . 10%



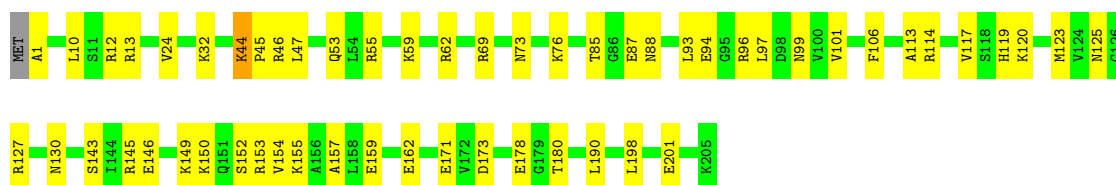
- Molecule 8: 30S ribosomal protein S3

Chain H:  71% 17% 12%




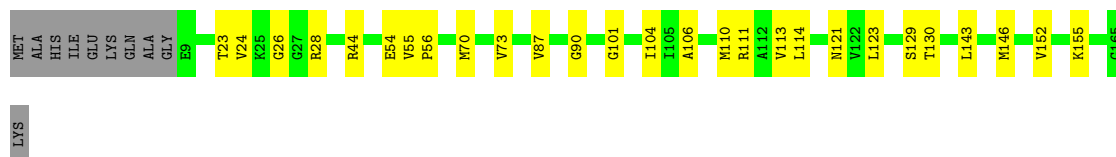
- Molecule 9: 30S ribosomal protein S4

Chain I:  73% 26%



- Molecule 10: 30S ribosomal protein S5

Chain J:  78% 16% 6%



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

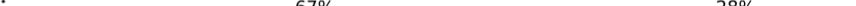
- Molecule 12: 30S ribosomal protein S7

[illegible]

- Molecule 13: 30S ribosomal protein S8

Chain M:  88% 12%

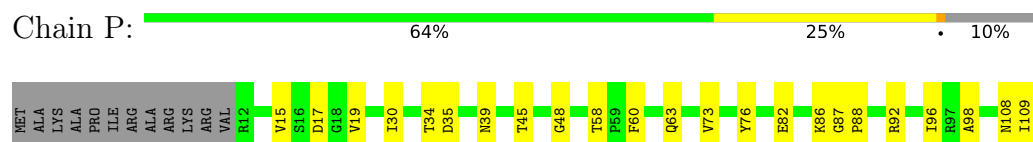
Residue	Category
Met	Green
S1	Green
V24	Green
T25	Green
M26	Green
S29	Green
K30	Yellow
E42	Yellow
G52	Yellow
P56	Yellow
L60	Yellow
R83	Yellow
L91	Yellow
P92	Yellow
L98	Yellow
G99	Green
I100	Green
A101	Green
V102	Green
R116	Yellow
A129	Green

Chain N:  67% 28% ..

NET  
ALA  
GLU  
N3  
Q4  
Y5  
R10  
R11  
R17  
P22  
N30  
E35  
G39  
R40  
R44  
M45  
V46  
V47  
E52  
L53  
V54  
V57  
E58  
K59  
L60  
T65  
V66  
Q74  
R79  
R84  
A85  
L86  
Y89  
D90  
E91  
S92  
L93  
R94  
L97  
R98  
F102  
V103  
T104  
P105  
Q109  
K113  
K114  
V115  
K119  
A120  
E129

Chain O:  71% 19% 5% 5%

Amino Acid	Category
MET	Green
GLN	Green
ASN	Green
GLN	Green
R5	Yellow
R9	Yellow
A12	Yellow
R16	Yellow
E24	Yellow
E27	Yellow
T28	Yellow
A29	Yellow
G33	Yellow
P39	Yellow
L42	Yellow
K46	Yellow
V57	Orange
N58	Orange
R68	Orange
L71	Orange
I76	Orange
K82	Orange
T83	Orange
L87	Grey
M88	Grey
R89	Grey
L90	Grey
D91	Grey
L92	Grey
V96	Grey
I100	Grey
S101	Grey
L102	Grey
GLY	Grey





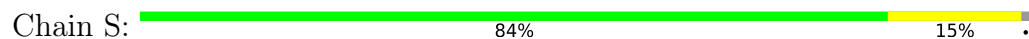
- Molecule 17: 30S ribosomal protein S12



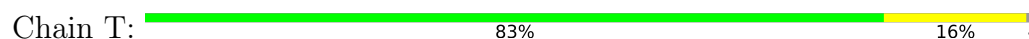
- Molecule 18: 30S ribosomal protein S13



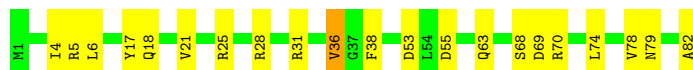
- Molecule 19: 30S ribosomal protein S14



- Molecule 20: 30S ribosomal protein S15

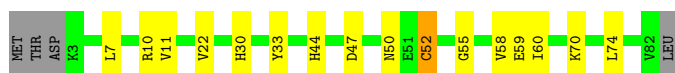


- Molecule 21: 30S ribosomal protein S16



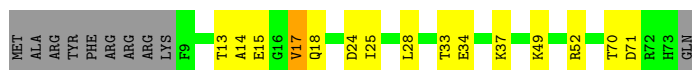
- Molecule 22: 30S ribosomal protein S17





- Molecule 23: 30S ribosomal protein S18

Chain W: 67% 19% 13%



- Molecule 24: 30S ribosomal protein S19

Chain X: 73% 13% 14%



- Molecule 25: 30S ribosomal protein S20

Chain Y: 76% 22%



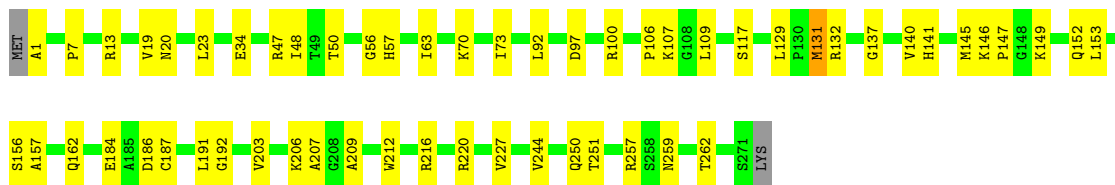
- Molecule 26: 30S ribosomal protein S21

Chain Z: 56% 34% 8%



- Molecule 27: 50S ribosomal protein L2

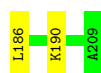
Chain b: 79% 20%



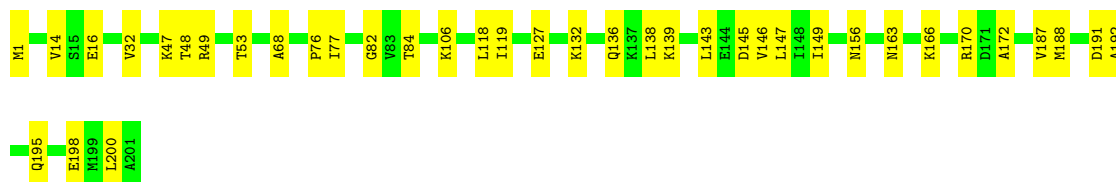
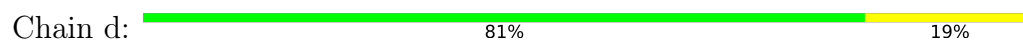
- Molecule 28: 50S ribosomal protein L3

Chain c: 83% 17%

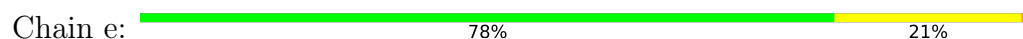




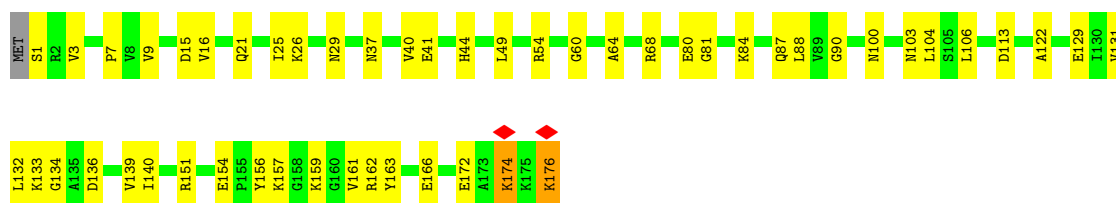
- Molecule 29: 50S ribosomal protein L4



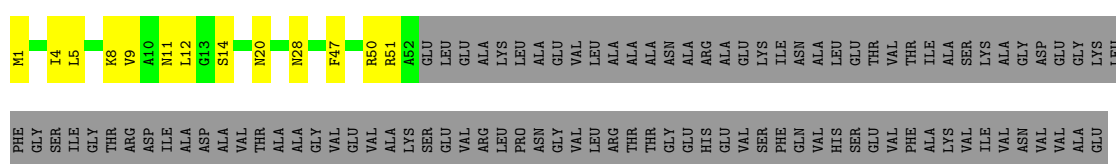
- Molecule 30: 50S ribosomal protein L5



- Molecule 31: 50S ribosomal protein L6



- Molecule 32: 50S ribosomal protein L9



- Molecule 33: 50S ribosomal protein L11





- Molecule 34: 50S ribosomal protein L13

Chain j: 85% 15%



- Molecule 35: 50S ribosomal protein L14

Chain k: 79% 20%



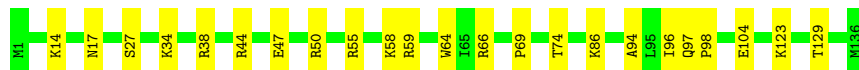
- Molecule 36: 50S ribosomal protein L15

Chain l: 86% 13%



- Molecule 37: 50S ribosomal protein L16

Chain m: 83% 17%



- Molecule 38: 50S ribosomal protein L17

Chain n: 75% 20% 6%




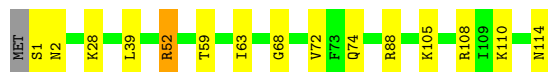
- Molecule 39: 50S ribosomal protein L18

Chain o: 81% 18%




- Molecule 40: 50S ribosomal protein L19

Chain p:  86% 12% ..



- Molecule 41: 50S ribosomal protein L20

Chain q:  83% 15% ..




- Molecule 42: 50S ribosomal protein L21

Chain r:  77% 23%



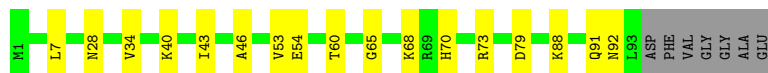
- Molecule 43: 50S ribosomal protein L22

Chain s:  85% 15%



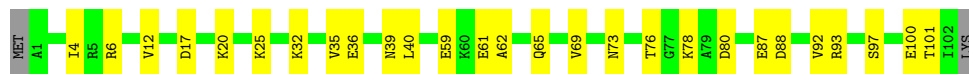
- Molecule 44: 50S ribosomal protein L23

Chain t:  76% 17% 7%




- Molecule 45: 50S ribosomal protein L24

Chain u:  72% 26% .



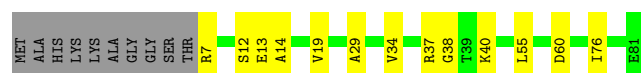
- Molecule 46: 50S ribosomal protein L25

Chain v:  85% 15%



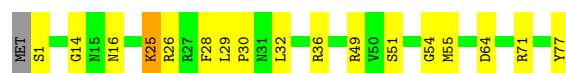
- Molecule 47: 50S ribosomal protein L27

Chain w:  73% 15% 12%




- Molecule 48: 50S ribosomal protein L28

Chain x:  77% 21% ..




- Molecule 49: 50S ribosomal protein L29

Chain y:  78% 22%



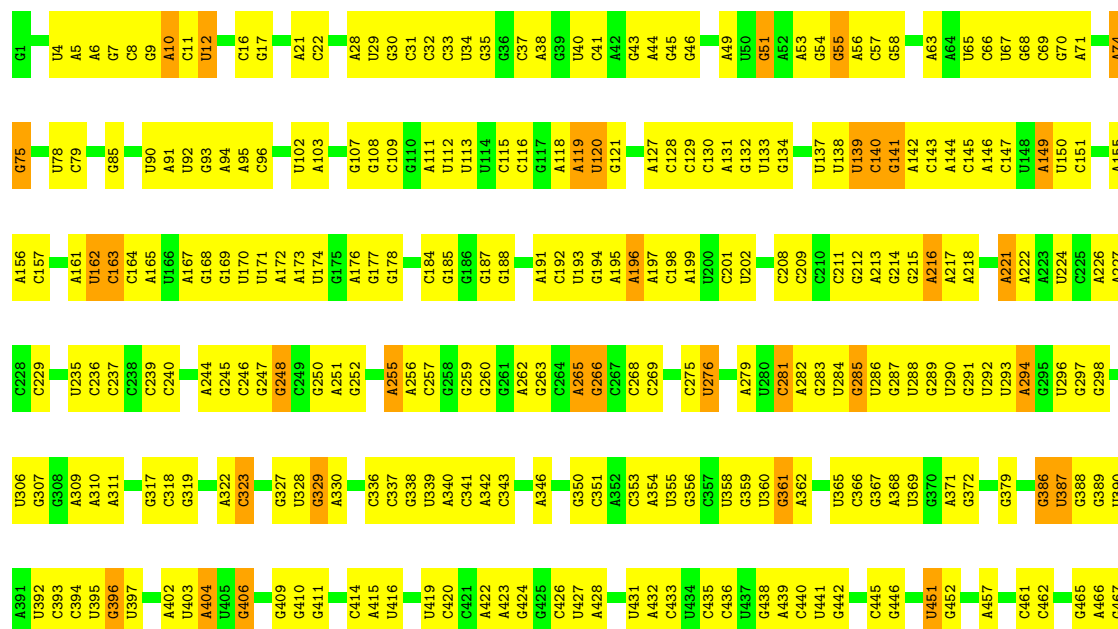
- Molecule 50: 50S ribosomal protein L30

Chain z:  76% 22% .



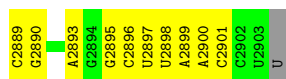
- Molecule 51: 23S rRNA

Chain 1:  43% 51% 7%



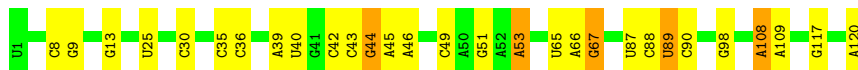
A1572	G1573	C1574	C1575	U1578	A1579	A1580	G1581	C1582	A1583	G1588	U1589	A1590	A1591	C1592	A1593	U1594	C1595	A1596	A1597	A1598	U1599	C1600	G1601	U1602	A1603	C1604	C1605	C1606	C1607	A1608	A1614	C1615	A1616	C1625	A1626	A1634	G1642	G1643	C1644	G1645	G1646	U1647	U1648	G1651	U1662	G1663	G1666	G1667	A1668	A1669								
A1336	G1337	G1338	G1339	G1343	U1344	C1345	G1346	A1347	C1348	C1349	U1352	A1365	A1366	A1367	G1368	G1377	A1378	U1379	C1380	G1381	C1382	A1383	C1386	A1387	G1388	U1389	U1390	U1394	U1400	G1401	U1402	A1403	C1404	U1405	U1406	U1409	U1410	U1411	U1412	A1413	U1414	U1415	A1416	C1417	A1418	A1419	A1420	G1425	G1426	A1427								
C1270	G1271	A1272	U1273	A1274	A1275	C1278	G1279	G1280	U1281	U1282	G1283	A1284	A1285	A1286	A1287	G1288	C1289	G1292	U1294	C1295	G1296	C1297	C1298	G1299	G1300	A1301	A1302	C1306	G1309	G1310	G1311	C1314	C1315	U1316	G1317	C1318	C1319	C1320	A1321	C1322	C1323	G1324	U1325	A1326	A1327	A1328	U1329	C1330	G1333	G1334	C1335							
U1176	G1177	C1178	G1179	U1180	U1181	U1182	U1183	U1184	G1185	G1186	U1187	U1188	G1193	A1194	G1195	C1196	G1197	U1198	U1199	C1200	A1204	A1205	U1209	G1210	G1211	G1212	A1213	U1219	G1220	G1225	A1230	U1231	G1232	C1233	A1237	G1238	G1239	U1240	A1246	A1247	A1253	A1254	U1255	G1256	C1257	U1258	G1259	G1266	U1267									
U1105	G1106	G1107	U1108	C1109	G1110	A1111	G1112	U1113	C1114	G1115	G1116	C1117	C1118	U1119	G1120	C1121	U1130	G1131	U1132	A1133	A1134	C1135	G1136	G1137	G1138	G1139	C1140	U1141	A1142	A1143	A1144	C1145	C1146	A1147	U1148	G1149	C1150	A1151	C1152	C1153	G1154	A1155	A1156	G1157	G1160	G1161	G1162	G1163	C1164	A1165	G1170	C1171	C1172	U1173	U1174	A1175		
C1043	G1044	C1045	A1046	G1047	A1048	C1049	A1050	A1054	G1055	G1056	A1057	U1058	U1059	A1060	U1061	G1062	G1063	C1064	U1065	U1066	A1067	G1068	A1069	A1070	G1071	C1072	A1073	G1074	C1075	C1076	A1077	U1078	C1079	A1080	U1081	U1082	U1083	A1084	A1085	A1086	G1087	A1088	A1089	A1090	G1091	C1092	G1093	U1094	A1095	A1096	U1097	A1098	G1099	C1100	U1101	C1102	A1103	C1104
C957	U958	A959	A960	C961	C968	A972	A973	G974	A975	A979	A980	A981	C982	A983	A984	C985	G989	C993	C994	C995	A996	C1005	A1009	A1010	G1011	U1012	C1013	A1014	U1015	U1019	A1020	A1021	G1022	U1023	G1024	G1025	A1026	A1027	G1031	A1032	U1033	G1034	U1035	A1036	G1037	U1038	A1039	U1040	G1041	C1042								
G879	C885	A886	U887	U888	C889	C890	C891	C892	C893	U894	U895	A896	C897	C898	A899	A900	C901	C902	A903	U904	U905	U906	G907	C908	A909	A910	C911	C840	G841	U842	A845	U846	U847	C848	A849	U850	C851	U852	C853	C854	G855	G858	G859	U860	G864	C865	U870	U871	U872	C873	C876	A877	A878					
U709	G712	G713	A718	C719	U720	A721	C722	G723	U724	G725	A727	A728	C729	A730	C736	G745	U746	C747	A752	G757	C758	G759	A760	U761	C671	C672	C673	C674	A677	C678	C679	C680	G681	G682	U683	G684	A685	C687	U688	G689	U690	C791	A792	A793	A794	C795	C796	A800	G801									
G548	G549	C550	A473	U551	G552	C475	C476	C481	A482	C488	C489	C490	A491	A492	C493	G498	U499	G500	A501	A502	A503	A504	A505	G506	C510	U511	G518	U519	U520	U521	A522	A526	C527	A528	A529	G530	C531	A532	G533	U534	G535	G536	G537	A538	G539	C540	A541	C542	G543	C544	U545	U546	A547					

U2804	G2729	G2642	A2566	A2468	C2385	U2305	C2226	G2159	G2093	C1990	C1908	G1823	G1750	C1670
C2805	G2730	G2643	G2567	A2469	A2386	C2306	A2227	C2160	A2094	U1991	C1909	U1827	U1751	U1671
C2806	G2731	G2644	G2568	G2470	A2387	A2309	G2230	C2161	A2095	U1992	U1911	U1828	G1752	A1672
A2810	G2732	G2645	G2569	A2471	A2388	C2310	U2233	A2163	C2096	G1993	A1912	A1829	G1753	G1673
G2811	G2733	G2646	G2570	A2476	U2390	A2311	U2234	C2164	A2097	U1993	A1913	C1832	C1674	C1675
G2812	G2734	G2647	A2572	A2482	G2391	U2312	G2236	C2165	U2098	C1997	C1914	C1833	A1676	A1677
G2813	G2735	G2648	G2573	C2483	A2392	C2313	G2237	C2166	U2099	C1998	U1915	C1834	A1678	A1679
A2814	G2736	U2650	G2574	G2493	U2393	A2314	G2238	U2167	A2101	U1999	A1916	G1763	U1758	A1680
C2815	G2737	C2395	G2575	G2488	C2394	G2315	G2238	U2168	G2102	C1999	U1917	G1764	A1762	U1680
G2816	G2738	C2396	G2576	U2489	G2395	G2316	G2239	U2169	G2103	C2002	A1918	G1765	G1766	G1681
A2820	A2741	G2658	A2577	G2490	G2396	U2321	U2240	A2170	G2104	A2013	A1919	G1845	G1767	G1695
C2827	G2742	G2659	U2491	U2492	U2402	G2325	A2241	A2171	C2105	A2014	C1920	G1846	U1768	G1696
G2828	U2743	A2660	G2580	G2492	C2403	G2326	G2242	U2172	U2106	A2015	G1921	G1847	G1769	G1697
G2829	G2744	G2661	U2581	U2492	U2404	C2327	U2243	A2173	G2107	U2016	U1922	G1764	A1698	G1699
C2830	G2745	G2662	G2582	A2496	G2405	A2328	A2247	U2180	G2110	A2020	C1924	G1765	U1772	G1702
G2831	G2746	G2663	G2583	C2497	G2406	A2329	U2248	U2181	G2111	C2021	A1927	G1773	A1773	G1703
G2832	A2747	G2664	G2584	C2498	A2407	U2329	U2249	U2182	G2112	U2022	A1928	C1774	U1775	G1704
G2833	A2748	G2665	U2584	C2499	A2407	G2330	G2250	A2183	U2113	C2023	G1929	G1776	G1776	G1710
A2834	A2749	A2670	G2585	C2502	A2411	U2333	U2257	U2184	G2114	C2024	U1931	G1777	A1711	A1711
A2835	G2750	G2671	U2586	G2502	A2412	A2334	U2257	U2185	G2115	U2025	U1931	G1777	A1711	A1711
U2837	U2751	U2672	A2587	G2502	A2412	A2334	U2257	U2186	G2116	U2026	U1931	G1777	A1711	A1711
G2838	C2755	C2676	U2593	G2505	C2420	A2335	U2257	U2187	G2117	G2027	G1935	G1863	A1780	G1715
G2839	U2756	A2679	C2594	U2506	G2421	A2336	U2259	U2188	G2118	A2030	A1936	U1864	U1781	G1716
C2840	A2757	U2680	G2595	C2507	G2422	G2337	C2260	U2189	U2122	A2031	A1937	U1865	U1782	U1716
G2843	A2758	C2681	A2598	C2510	C2423	C2338	A2267	G2190	G2123	G2032	A1938	U1866	U1783	A1717
G2844	G2759	G2682	G2599	U2511	G2424	C2339	A2268	A2191	G2124	G2033	U1939	G1867	A1784	G1718
U2845	G2760	C2683	A2600	G2512	A2425	A2340	G2271	G2192	G2125	U2034	A1785	G1868	A1785	G1719
G2846	G2761	U2684	G2601	A2516	A2426	G2345	G2271	G2193	G2126	C2035	C1942	G1869	A1786	U1720
U2847	G2762	U2684	C2602	C2517	C2427	A2346	G2271	U2194	G2127	C2036	U1943	G1870	A1787	G1721
G2848	G2763	U2687	A2602	C2518	G2428	A2346	G2271	U2195	G2128	C2037	U1944	A1871	C1788	A1722
U2849	A2764	G2688	U2610	A2518	G2429	U2347	G2271	C2196	G2129	A2037	G1945	G1872	A1789	G1723
A2850	A2765	G2689	C2611	G2525	A2430	U2348	G2271	U2197	U2130	C2043	G1948	G1873	C1790	G1724
G2851	U2768	U2690	G2612	C2526	A2431	C2349	A2278	A2198	U2131	C2044	A1952	G1874	U1794	U1725
C2852	G2773	G2697	U2613	C2527	A2432	C2350	G2279	A2199	U2132	G2048	A1953	G1875	C1796	C1726
G2853	G2773	G2697	U2614	U2528	A2433	G2351	A2281	C2200	G2133	G2049	G1954	G1878	C1797	C1727
C2858	A2776	U2700	G2615	G2529	A2434	A2352	G2282	G2201	A2134	C2050	U1955	G1879	U1798	C1728
G2859	G2777	G2701	U2616	U2530	A2435	G2357	C2283	U2202	U2137	A2051	C1965	G1799	G1799	U1729
A2860	A2778	G2702	G2617	U2533	G2436	G2357	A2284	G2204	U2137	A2052	U1956	U1882	C1730	C1730
U2861	U2779	U2703	G2618	A2534	G2437	G2360	C2285	A2205	G2138	G2053	U1963	U1883	G1731	C1731
G2867	G2782	G2707	C2619	C2539	U2441	C2361	A2286	G2208	G2141	A2054	U1964	U1884	A1801	G1732
A2868	U2783	G2708	G2625	G2545	G2445	G2362	A2286	G2209	G2144	C2055	G1964	A1885	A1802	G1733
G2869	U2784	G2709	C2626	G2546	G2446	C2363	G2289	U2210	C2145	G2056	C1965	U1886	G1807	A1735
C2870	A2785	G2710	G2627	U2546	G2447	G2365	G2290	A2211	C2146	G2060	U1966	C1887	G1807	U1736
G2871	G2787	G2711	C2628	A2547	A2448	A2366	U2291	U2212	C2147	G2061	C1967	G1888	A1808	G1737
A2872	C2788	U2713	U2629	U2554	A2448	C2367	U2292	U2213	G2148	G2061	G1968	G1889	A1809	G1738
G2876	C2789	G2714	G2630	U2555	G2455	C2368	G2293	C2214	U2149	G2069	A1969	A1890	A1739	A1739
A2879	A2792	G2717	G2631	U2556	C2456	G2371	G2294	C2215	C2150	G2089	U1970	C1893	U1812	G1740
C2880	C2793	G2718	A2632	C2565	U2457	U2372	U2296	G2216	U2151	C2073	U1971	C1894	G1813	U1741
U2884	U2798	U2720	A2634	U2561	G2462	G2379	A2298	G2217	G2152	U2074	A1978	C1816	G1816	U1742
G2885	A2799	U2723	A2635	U2562	C2463	A2381	U2299	G2218	C2153	U2085	U1978	U1817	G1817	A1745
G2886	U2800	G2723	C2636	U2563	G2464	G2382	U2302	G2222	U2155	U2086	G1983	U1818	A1819	A1746
C2888	G2801	U2726	G2638	U2564	G2464	G2383	U2303	G2223	G2156	U2086	G1984	U1820	A1821	U1747
					G2467	U2384	G2304	A2225	A2158	C2091	C1986	U1907	A1822	A1749



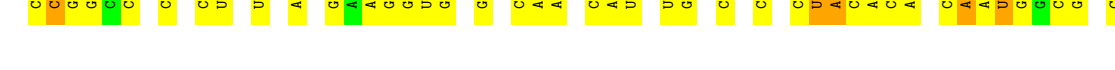
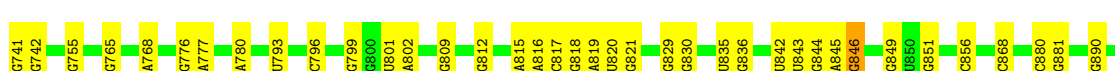
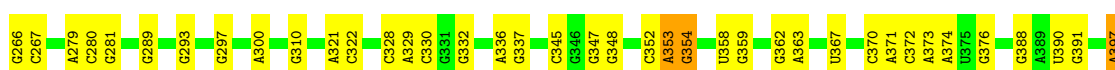
• Molecule 52: 5S rRNA

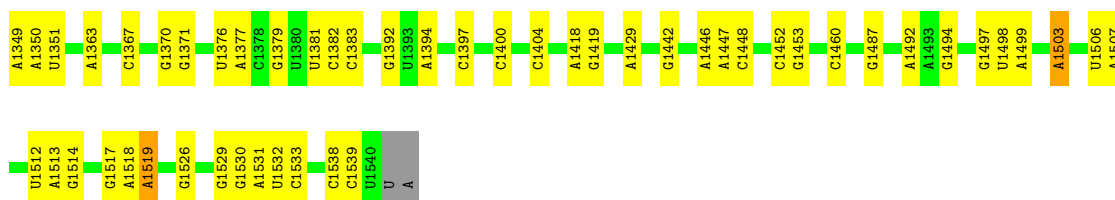
Chain 2: 76% 20% .



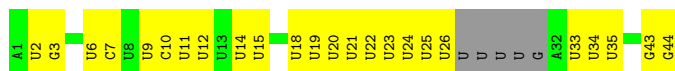
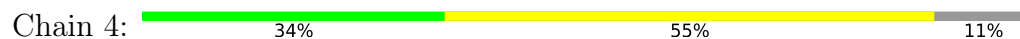
• Molecule 53: 16S rRNA

Chain 3: 69% 29% .

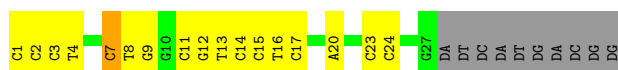




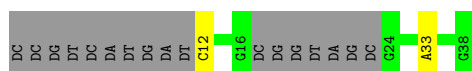
- Molecule 54: mRNA



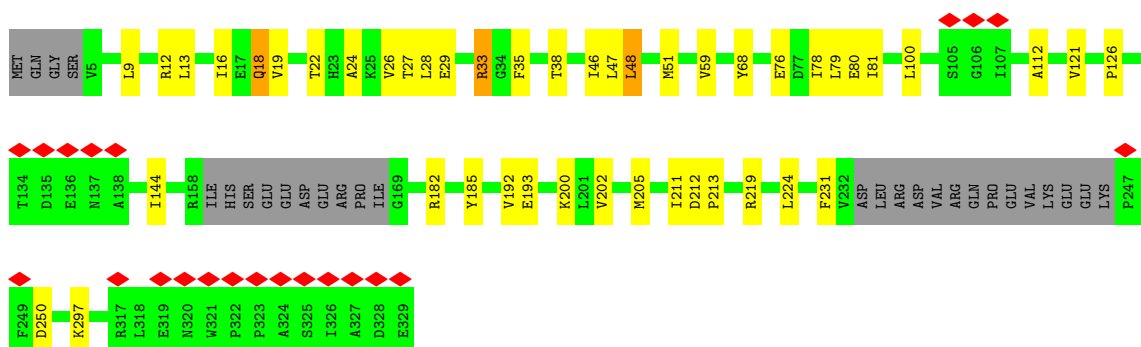
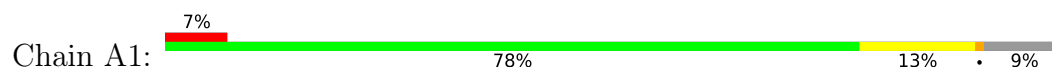
- Molecule 55: template DNA strand



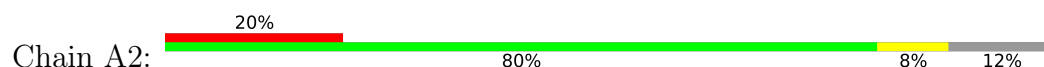
- Molecule 56: non-template DNA strand



- Molecule 57: DNA-directed RNA polymerase subunit alpha

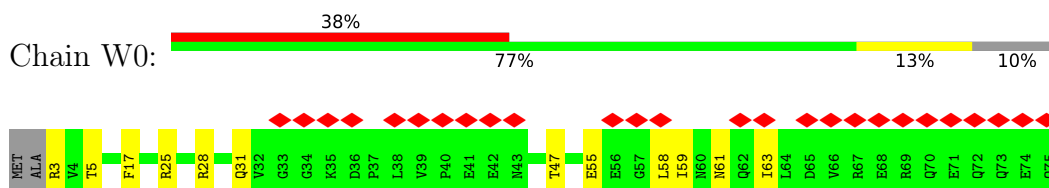
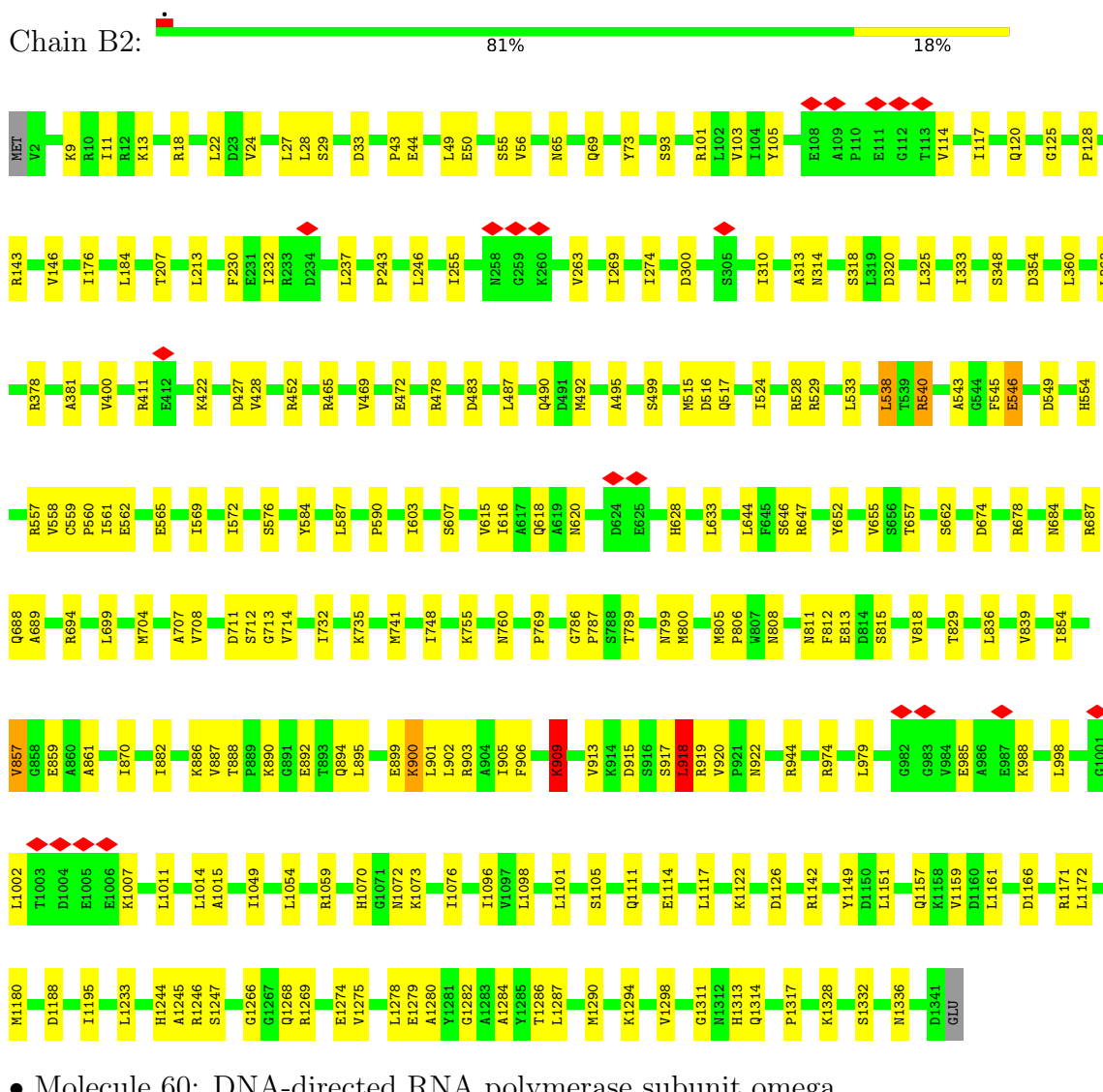


- Molecule 57: DNA-directed RNA polymerase subunit alpha

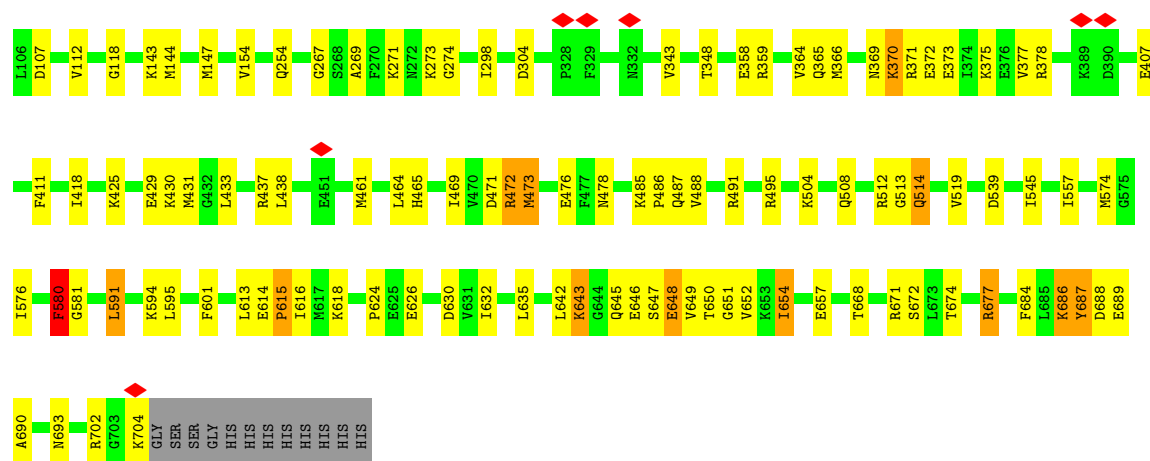




- Molecule 59: DNA-directed RNA polymerase subunit beta







## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	609587	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	47	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.087	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.007	Depositor
Map size ( $\text{\AA}$ )	753.60004, 753.60004, 753.60004	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.57, 1.57, 1.57	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.26	0/530	0.54	0/707
2	B	0.40	0/450	0.60	0/599
3	C	0.27	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	0.58	0/303	0.66	0/397
7	G	0.37	0/1735	0.64	0/2338
8	H	0.34	0/1651	0.55	0/2225
9	I	0.35	0/1665	0.71	0/2227
10	J	0.38	0/1169	0.68	2/1573 (0.1%)
11	K	0.46	0/835	0.77	0/1128
12	L	0.30	0/1195	0.66	3/1602 (0.2%)
13	M	0.35	0/989	0.52	0/1326
14	N	0.47	0/1034	0.77	0/1375
15	O	0.50	0/796	0.78	2/1077 (0.2%)
16	P	0.45	0/885	0.64	1/1195 (0.1%)
17	Q	0.50	0/969	0.86	2/1300 (0.2%)
18	R	0.33	0/892	0.73	2/1193 (0.2%)
19	S	0.33	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	0.64	0/2852
28	c	0.42	0/1586	0.59	2/2134 (0.1%)
29	d	0.43	0/1571	0.62	0/2113
30	e	0.43	0/1434	0.65	2/1926 (0.1%)
31	f	0.35	0/1343	0.55	0/1816
32	g	0.32	0/405	0.75	0/544

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	i	0.51	0/1046	0.87	3/1410 (0.2%)
34	j	0.41	0/1152	0.55	1/1551 (0.1%)
35	k	0.45	0/947	0.66	0/1268
36	l	0.40	0/1054	0.63	0/1403
37	m	0.56	0/1093	0.74	0/1460
38	n	0.46	0/973	0.72	1/1301 (0.1%)
39	o	0.32	0/902	0.51	0/1209
40	p	0.42	0/929	0.63	0/1242
41	q	0.52	0/960	0.62	1/1278 (0.1%)
42	r	0.45	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	0.64	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	0/896	0.68	0/1387
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	0.81	0/2868
57	A2	0.49	0/2048	0.76	0/2786
58	B1	0.57	4/10510 (0.0%)	0.75	8/14196 (0.1%)
59	B2	0.46	0/10714	0.67	0/14459
60	W0	0.30	0/652	0.60	0/879
61	NA	0.78	0/2431	1.22	0/3385
62	NG	1.12	0/756	1.07	0/1048
63	5	0.57	0/1812	0.85	1/2823 (0.0%)
64	6	0.39	0/1832	0.57	1/2855 (0.0%)
65	0	0.84	0/5308	1.17	6/7181 (0.1%)
All	All	0.49	4/195128 (0.0%)	0.64	68/287304 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	B1	1350	ASN	CG-ND2	-5.28	1.22	1.33
58	B1	1108	GLN	CD-OE1	5.18	1.33	1.23
58	B1	424	ASN	CG-ND2	-5.13	1.22	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	B1	665	GLN	CD-OE1	5.04	1.33	1.23

All (68) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	0	580	PHE	CA-CB-CG	9.59	123.39	113.80
16	P	73	VAL	N-CA-C	-9.05	104.52	113.20
41	q	33	VAL	N-CA-C	-8.73	104.78	112.12
12	L	64	ALA	N-CA-C	-7.68	105.07	114.75
51	1	1130	U	C2'-C3'-O3'	7.63	120.94	109.50
64	6	33	U	C2'-C3'-O3'	7.28	120.41	109.50
51	1	2326	C	C2'-C3'-O3'	7.18	120.27	109.50
58	B1	450	HIS	CB-CG-CD2	-6.58	122.65	131.20
51	1	761	A	C4'-C3'-O3'	-6.49	103.26	113.00
65	0	615	PRO	CB-CA-C	-6.47	102.50	110.98
58	B1	777	HIS	CB-CG-CD2	-6.41	122.87	131.20
58	B1	61	ILE	CA-C-N	-6.36	114.01	121.64
58	B1	61	ILE	C-N-CA	-6.36	114.01	121.64
28	c	147	GLY	CA-C-N	-6.02	115.28	122.44
28	c	147	GLY	C-N-CA	-6.02	115.28	122.44
58	B1	450	HIS	CB-CG-ND1	5.69	131.23	122.70
51	1	2060	A	C2'-C3'-O3'	5.68	118.03	109.50
65	0	657	GLU	CA-C-N	-5.63	118.43	123.33
65	0	657	GLU	C-N-CA	-5.63	118.43	123.33
26	Z	35	GLU	CA-C-N	5.60	132.23	121.54
26	Z	35	GLU	C-N-CA	5.60	132.23	121.54
51	1	1790	C	N1-C1'-C2'	5.60	120.39	112.00
15	O	57	VAL	CA-C-N	5.59	132.22	121.54
15	O	57	VAL	C-N-CA	5.59	132.22	121.54
38	n	47	VAL	N-CA-C	-5.56	107.45	112.12
10	J	155	LYS	N-CA-C	-5.53	107.79	114.75
51	1	960	A	N9-C1'-C2'	5.47	120.21	112.00
51	1	1451	C	N1-C1'-C2'	5.47	120.21	112.00
51	1	1905	C	C4'-C3'-O3'	-5.47	104.79	113.00
58	B1	777	HIS	CB-CG-ND1	5.47	130.90	122.70
51	1	1020	A	C2'-C3'-O3'	5.43	117.64	109.50
51	1	1696	G	N9-C1'-C2'	5.42	120.14	112.00
4	D	3	ARG	CA-C-N	5.40	127.78	120.38
4	D	3	ARG	C-N-CA	5.40	127.78	120.38
55	8	7	DC	C2'-C3'-O3'	-5.40	103.40	111.50
65	0	271	LYS	N-CA-C	-5.32	106.30	112.89
51	1	1782	U	N1-C1'-C2'	5.31	119.97	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	1	2428	G	N9-C1'-C2'	5.29	119.93	112.00
30	e	141	ASP	CA-C-N	5.24	131.56	121.54
30	e	141	ASP	C-N-CA	5.24	131.56	121.54
51	1	2055	C	N1-C1'-C2'	5.23	119.85	112.00
51	1	980	A	N9-C1'-C2'	5.23	119.84	112.00
12	L	5	VAL	CA-C-N	5.22	127.70	120.49
12	L	5	VAL	C-N-CA	5.22	127.70	120.49
34	j	110	PRO	N-CA-C	5.22	120.72	113.98
51	1	2576	G	N9-C1'-C2'	5.21	119.82	112.00
58	B1	27	PRO	N-CA-C	-5.21	106.26	113.81
21	U	78	VAL	CA-C-N	5.19	129.65	121.56
21	U	78	VAL	C-N-CA	5.19	129.65	121.56
51	1	2430	A	N9-C1'-C2'	5.16	119.74	112.00
51	1	1565	C	N1-C1'-C2'	5.15	119.72	112.00
23	W	14	ALA	N-CA-C	-5.14	106.09	112.93
51	1	1328	A	N9-C1'-C2'	5.14	119.71	112.00
18	R	3	ILE	CA-C-N	5.11	131.30	121.54
18	R	3	ILE	C-N-CA	5.11	131.30	121.54
63	5	57	G	C4'-C3'-O3'	5.11	117.06	109.40
33	i	71	LYS	CA-C-N	5.10	134.24	121.80
33	i	71	LYS	C-N-CA	5.10	134.24	121.80
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
65	0	375	LYS	N-CA-C	-5.09	106.92	112.72
33	i	22	PRO	N-CA-CB	-5.08	97.91	103.25
51	1	2777	G	N9-C1'-C2'	5.08	119.62	112.00
17	Q	42	LYS	CA-C-N	5.08	129.59	121.62
17	Q	42	LYS	C-N-CA	5.08	129.59	121.62
51	1	1087	G	N9-C1'-C2'	5.05	119.57	112.00
48	x	25	LYS	N-CA-C	5.04	121.54	110.80
51	1	972	A	N9-C1'-C2'	5.03	119.55	112.00

There are no chirality outliers.

There are no planarity outliers.

## 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	521	0	520	8	0
2	B	444	0	461	10	0
3	C	409	0	440	3	0
4	D	377	0	418	9	0
5	E	504	0	574	2	0
6	F	302	0	343	5	0
7	G	1704	0	1732	39	0
8	H	1624	0	1699	27	0
9	I	1643	0	1710	34	0
10	J	1156	0	1199	17	0
11	K	817	0	808	16	0
12	L	1181	0	1240	19	0
13	M	979	0	1034	9	0
14	N	1022	0	1070	21	0
15	O	786	0	828	15	0
16	P	869	0	878	20	0
17	Q	955	0	1019	24	0
18	R	883	0	944	20	0
19	S	805	0	847	10	0
20	T	714	0	737	7	0
21	U	649	0	666	16	0
22	V	648	0	691	9	0
23	W	535	0	552	7	0
24	X	637	0	665	8	0
25	Y	665	0	714	12	0
26	Z	544	0	579	12	0
27	b	2082	0	2157	45	0
28	c	1565	0	1616	32	0
29	d	1552	0	1619	27	0
30	e	1410	0	1447	22	0
31	f	1323	0	1374	30	0
32	g	400	0	423	7	0
33	i	1032	0	1088	36	0
34	j	1129	0	1162	20	0
35	k	938	0	1012	19	0
36	l	1045	0	1117	15	0
37	m	1074	0	1157	13	0
38	n	960	0	1000	18	0
39	o	892	0	923	15	0
40	p	917	0	965	12	0
41	q	947	0	1022	10	0
42	r	816	0	839	14	0
43	s	857	0	922	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	t	738	0	807	9	0
45	u	779	0	834	14	0
46	v	753	0	780	9	0
47	w	575	0	592	9	0
48	x	625	0	655	11	0
49	y	509	0	543	11	0
50	z	449	0	491	9	0
51	1	62317	0	31346	1455	0
52	2	2568	0	1303	15	0
53	3	33012	0	16618	185	0
54	4	809	0	404	4	0
55	8	539	0	305	27	0
56	9	417	0	224	2	0
57	A1	2088	0	1895	24	0
57	A2	2029	0	1864	18	0
58	B1	10353	0	10548	322	0
59	B2	10546	0	10550	164	0
60	W0	650	0	658	10	0
61	NA	2432	0	1171	3	0
62	NG	758	0	334	10	0
63	5	1622	0	821	28	0
64	6	1640	0	837	20	0
65	0	5211	0	5200	46	0
66	B1	1	0	0	0	0
67	0	37	0	47	0	0
68	0	28	0	12	0	0
All	All	181797	0	131050	2821	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 (2821) 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)
51:1:275:C:H2'	51:1:276:U:H4'	1.37	1.07
51:1:1672:A:C2	51:1:2582:G:H5'	1.95	1.02
51:1:1666:G:H2'	51:1:1667:G:H5'	1.41	1.01
58:B1:750:PRO:HB3	59:B2:549:ASP:OD2	1.60	1.01
51:1:1082:U:H3'	51:1:1083:U:H5''	1.41	1.00
51:1:2713:U:H3'	51:1:2714:G:H5'	1.41	1.00
51:1:1807:G:H2'	51:1:1808:A:H5'	1.44	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:111:THR:HG23	58:B1:300:GLN:CD	1.86	0.99
58:B1:352:ARG:HD2	59:B2:1268:GLN:NE2	1.79	0.98
51:1:2156:G:H2'	51:1:2157:G:H5'	1.47	0.95
58:B1:68:TYR:O	58:B1:75:TYR:CE2	2.20	0.95
51:1:1847:A:HO2'	51:1:1848:A:H8	1.06	0.94
51:1:644:A:H2'	51:1:645:C:H5''	1.50	0.93
51:1:2713:U:H3'	51:1:2714:G:C5'	1.98	0.93
51:1:655:A:H4'	51:1:656:G:H5'	1.50	0.92
51:1:1102:C:H2'	51:1:1103:A:H8	1.35	0.92
51:1:1702:G:H2'	51:1:1703:G:H5''	1.51	0.92
54:4:44:G:H21	58:B1:427:PRO:HD3	1.34	0.91
30:e:84:ILE:HD13	51:1:2312:U:H5'	1.51	0.91
30:e:130:GLY:HA3	51:1:2305:U:H5''	1.51	0.91
51:1:1019:U:H3	51:1:1142:A:H62	1.17	0.91
51:1:1668:A:H4'	51:1:1669:A:H5'	1.54	0.90
51:1:890:C:H2'	51:1:891:G:H5'	1.53	0.90
58:B1:68:TYR:C	58:B1:75:TYR:HE2	1.80	0.89
58:B1:202:ARG:HG2	58:B1:202:ARG:HH11	1.34	0.89
14:N:3:ASN:N	14:N:5:TYR:HH	1.70	0.89
63:5:9:A:H2'	63:5:11:C:H41	1.38	0.89
51:1:1060:U:H4'	51:1:1061:U:H5''	1.55	0.88
51:1:2097:A:H2'	51:1:2098:U:C6	2.08	0.88
58:B1:317:THR:HA	58:B1:323:PRO:HA	1.55	0.88
59:B2:854:ILE:HG21	59:B2:917:SER:HB3	1.54	0.88
65:0:348:THR:HA	65:0:359:ARG:HA	1.55	0.88
51:1:11:C:H2'	51:1:12:U:H5''	1.55	0.87
51:1:1869:G:H3'	51:1:1870:C:H5'	1.57	0.86
2:B:8:THR:HB	51:1:2020:A:H5'	1.56	0.86
58:B1:68:TYR:HB3	58:B1:75:TYR:OH	1.76	0.85
51:1:2792:A:H2'	51:1:2793:C:H5''	1.59	0.85
17:Q:69:GLU:HG3	53:3:521:G:H4'	1.59	0.85
51:1:1387:A:H5'	51:1:1469:A:H1'	1.58	0.84
51:1:2333:A:H5'	51:1:2334:U:H2'	1.57	0.84
51:1:1175:A:H3'	51:1:1176:U:H5'	1.59	0.83
51:1:2584:U:H2'	51:1:2585:U:H5'	1.58	0.83
58:B1:633:ALA:HB2	59:B2:808:ASN:H	1.41	0.83
58:B1:68:TYR:O	58:B1:75:TYR:HE2	1.58	0.83
33:i:119:ALA:HB2	51:1:1082:U:H5'	1.60	0.82
51:1:475:C:H4'	51:1:510:C:H5'	1.59	0.82
51:1:1666:G:C2'	51:1:1667:G:H5'	2.07	0.82
55:8:1:DC:H5''	58:B1:210:SER:OG	1.80	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:757:G:H2'	51:1:758:C:H5'	1.61	0.82
58:B1:770:LEU:HD13	59:B2:618:GLN:HG3	1.61	0.82
51:1:1141:U:H4'	51:1:1142:A:O4'	1.80	0.82
51:1:279:A:H61	51:1:361:G:H1'	1.46	0.81
51:1:849:A:H2'	51:1:850:U:C6	2.14	0.81
51:1:2799:A:H2'	51:1:2800:A:H5'	1.63	0.81
51:1:545:U:C2	51:1:546:U:H1'	2.16	0.81
51:1:2360:G:H2'	51:1:2361:G:H5'	1.62	0.81
58:B1:141:PHE:CE2	58:B1:296:LYS:HB2	2.16	0.81
38:n:36:THR:HG22	51:1:1278:C:OP1	1.80	0.81
58:B1:37:GLU:O	58:B1:61:ILE:HD11	1.81	0.81
51:1:1197:G:O2'	51:1:1198:U:H5'	1.81	0.80
51:1:2112:G:H2'	51:1:2113:U:H5'	1.63	0.80
51:1:1087:G:N2	51:1:1103:A:H1'	1.97	0.80
51:1:2224:G:H4'	51:1:2226:C:C2	2.16	0.80
58:B1:144:TYR:HE1	58:B1:162:GLU:OE2	1.64	0.80
51:1:1775:U:H2'	51:1:1776:G:H5'	1.64	0.80
51:1:784:G:H5'	51:1:785:G:OP1	1.81	0.80
58:B1:111:THR:HG23	58:B1:300:GLN:OE1	1.81	0.80
58:B1:141:PHE:HE2	58:B1:296:LYS:HB2	1.45	0.79
64:6:46:G:H2'	64:6:47:U:H5'	1.64	0.79
51:1:1064:C:H41	51:1:1069:A:H5''	1.47	0.79
7:G:18:GLN:HG3	7:G:189:ASN:HB3	1.65	0.79
51:1:1071:G:O2'	51:1:1089:A:H2'	1.82	0.79
3:C:40:PRO:HG3	51:1:2348:U:H4'	1.63	0.79
51:1:1297:C:OP1	51:1:2710:C:H4'	1.82	0.78
51:1:2286:G:H4'	51:1:2287:A:O4'	1.83	0.78
35:k:6:THR:HG22	51:1:1666:G:O2'	1.83	0.78
51:1:2130:U:H2'	51:1:2131:U:H5''	1.65	0.78
58:B1:186:GLN:HG3	58:B1:238:ILE:HG13	1.65	0.78
51:1:275:C:H2'	51:1:276:U:C4'	2.14	0.78
51:1:2215:C:H2'	51:1:2216:G:C8	2.18	0.78
51:1:2792:A:C3'	51:1:2793:C:H5''	2.14	0.78
65:0:508:GLN:HA	65:0:513:GLY:CA	2.12	0.78
51:1:1275:A:N6	51:1:1296:G:H4'	1.99	0.77
51:1:1310:G:C2'	51:1:1311:G:H5'	2.14	0.77
51:1:1536:C:H4'	51:1:1537:G:C2	2.18	0.77
65:0:624:PRO:HG2	65:0:677:ARG:HD2	1.66	0.77
51:1:1702:G:C2'	51:1:1703:G:H5''	2.13	0.77
33:i:55:PRO:HG3	51:1:1060:U:OP2	1.83	0.77
55:8:15:DC:H1'	58:B1:426:ALA:HB1	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:202:ARG:HG2	58:B1:202:ARG:NH1	1.99	0.77
51:1:2156:G:C2'	51:1:2157:G:H5'	2.14	0.77
51:1:310:A:O2'	51:1:311:A:H2'	1.85	0.76
51:1:1736:U:H2'	51:1:1737:G:O4'	1.85	0.76
28:c:114:LYS:HB2	51:1:2680:U:OP1	1.84	0.76
55:8:13:DT:H72	58:B1:791:ALA:HB2	1.66	0.76
51:1:1394:U:H4'	51:1:1603:A:H4'	1.66	0.76
51:1:548:G:H2'	51:1:549:G:O4'	1.84	0.76
51:1:368:A:H2'	51:1:369:U:H5'	1.66	0.76
51:1:1773:A:H2'	51:1:1774:C:H5'	1.68	0.76
51:1:2792:A:C2'	51:1:2793:C:H5''	2.16	0.75
51:1:275:C:H3'	51:1:276:U:H5''	1.66	0.75
51:1:958:U:H2'	52:2:89:U:O2	1.87	0.75
51:1:1063:G:H1	51:1:1075:C:N4	1.84	0.75
51:1:1083:U:H2'	51:1:1085:A:OP2	1.86	0.75
51:1:1310:G:H2'	51:1:1311:G:H5'	1.69	0.75
51:1:2611:C:O2	51:1:2611:C:H2'	1.86	0.75
51:1:2432:A:H1'	64:6:75:C:O4'	1.86	0.75
58:B1:110:PRO:HG2	58:B1:183:GLU:HG3	1.69	0.75
51:1:1020:A:H5'	51:1:1021:A:C8	2.22	0.74
51:1:1555:G:H5'	51:1:1555:G:H8	1.51	0.74
55:8:3:DC:H2'	55:8:4:DT:H72	1.69	0.74
51:1:1061:U:H3'	51:1:1062:G:C5'	2.18	0.74
51:1:1425:G:H2'	51:1:1426:G:C8	2.23	0.74
51:1:2097:A:H2'	51:1:2098:U:H6	1.50	0.74
58:B1:211:GLU:HG2	58:B1:215:LYS:HE3	1.70	0.73
51:1:404:A:H1'	51:1:406:G:C4	2.23	0.73
58:B1:1143:ASP:OD1	58:B1:1148:ARG:NH1	2.21	0.73
51:1:543:G:H2'	51:1:544:C:H5''	1.68	0.73
55:8:3:DC:C2'	55:8:4:DT:H72	2.19	0.73
31:f:15:ASP:HB3	31:f:26:LYS:H	1.54	0.73
51:1:322:A:H5'	51:1:340:A:C1'	2.19	0.73
51:1:1433:A:H2'	51:1:1434:A:O4'	1.89	0.73
51:1:1670:C:H2'	51:1:1671:U:H5'	1.70	0.73
63:5:30:G:H2'	63:5:31:A:C8	2.24	0.73
17:Q:33:CYS:HA	17:Q:54:VAL:HG12	1.70	0.73
58:B1:105:ILE:HD12	58:B1:242:LEU:HD22	1.71	0.73
64:6:50:U:H2'	64:6:51:C:C4	2.24	0.73
53:3:456:A:H61	53:3:476:U:H3	1.36	0.73
51:1:545:U:H2'	51:1:546:U:O4'	1.88	0.72
51:1:481:G:H1'	51:1:506:G:N2	2.04	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:157:GLN:OE1	58:B1:157:GLN:HA	1.89	0.72
65:0:508:GLN:HA	65:0:513:GLY:HA2	1.69	0.72
51:1:2713:U:C3'	51:1:2714:G:C5'	2.67	0.72
58:B1:210:SER:HB3	58:B1:213:LYS:HB2	1.71	0.72
58:B1:220:ARG:HG2	58:B1:220:ARG:HH11	1.55	0.72
51:1:633:A:H2'	51:1:634:C:H5'	1.72	0.72
51:1:1942:C:H3'	51:1:1943:U:H2'	1.70	0.72
51:1:1795:C:H2'	51:1:1796:U:O4'	1.90	0.72
51:1:2834:G:H2'	51:1:2879:A:H61	1.54	0.72
51:1:394:C:H2'	51:1:395:U:O4'	1.90	0.72
51:1:2036:C:H2'	51:1:2037:A:C8	2.23	0.72
51:1:2671:G:H2'	51:1:2672:U:C6	2.25	0.71
58:B1:107:LEU:HD11	58:B1:242:LEU:HB2	1.70	0.71
58:B1:282:LEU:HA	58:B1:286:ALA:HA	1.70	0.71
36:l:59:ARG:HD2	51:1:250:G:H4'	1.71	0.71
51:1:1858:A:H1'	51:1:1885:A:C2	2.26	0.71
58:B1:395:LYS:HZ2	58:B1:399:LYS:CD	2.03	0.71
51:1:1441:G:H2'	51:1:1442:U:C6	2.25	0.71
53:3:452:A:H61	53:3:480:U:H3	1.37	0.71
58:B1:68:TYR:C	58:B1:75:TYR:CE2	2.65	0.71
58:B1:93:THR:HB	58:B1:97:VAL:HG21	1.73	0.71
51:1:1670:C:C2'	51:1:1671:U:H5'	2.21	0.71
51:1:2151:U:H2'	51:1:2152:G:H8	1.56	0.71
51:1:368:A:C2'	51:1:369:U:H5'	2.20	0.71
51:1:612:G:H2'	51:1:614:A:C8	2.26	0.71
51:1:890:C:C2'	51:1:891:G:H5'	2.21	0.71
51:1:940:G:H2'	51:1:941:A:H5''	1.73	0.71
51:1:1019:U:H3	51:1:1142:A:N6	1.89	0.71
53:3:663:A:H61	53:3:742:G:H1	1.39	0.70
58:B1:142:GLU:HG3	58:B1:142:GLU:O	1.89	0.70
51:1:864:G:O2'	51:1:865:C:H5'	1.89	0.70
27:b:47:ARG:NH2	51:1:774:G:H5''	2.07	0.70
51:1:723:C:H2'	51:1:724:U:C6	2.27	0.70
42:r:79:ARG:NH1	51:1:572:A:OP2	2.25	0.70
33:i:22:PRO:HB3	51:1:1067:A:H4'	1.72	0.70
51:1:1983:G:O2'	51:1:1984:G:H5'	1.92	0.70
51:1:2626:C:O2'	51:1:2627:G:H5'	1.91	0.70
51:1:1386:C:H2'	51:1:1387:A:H8	1.56	0.70
51:1:1872:A:H2'	51:1:1873:G:O4'	1.89	0.70
51:1:2297:A:N1	51:1:2321:U:H5	1.89	0.70
57:A2:294:ASN:HA	61:NA:464:ILE:H	1.57	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2267:A:H5''	51:1:2268:A:H5''	1.74	0.70
57:A1:297:LYS:CB	61:NA:79:ALA:HB1	2.22	0.70
51:1:644:A:C2'	51:1:645:C:H5''	2.22	0.70
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE22	1.55	0.70
65:0:618:LYS:HG3	65:0:643:LYS:HZ3	1.55	0.70
51:1:322:A:H5'	51:1:340:A:H1'	1.73	0.69
34:j:7:LYS:HG2	51:1:538:A:H4'	1.73	0.69
51:1:1337:G:H2'	51:1:1338:G:H8	1.57	0.69
51:1:2092:U:H4'	51:1:2093:G:H5''	1.75	0.69
59:B2:65:ASN:HB3	59:B2:105:TYR:HB2	1.74	0.69
51:1:402:A:H2'	51:1:403:U:H5'	1.74	0.69
51:1:1102:C:H2'	51:1:1103:A:C8	2.22	0.69
51:1:1555:G:H5'	51:1:1555:G:C8	2.27	0.69
51:1:1565:C:HO2'	51:1:1566:A:H8	1.41	0.69
58:B1:128:LEU:HD11	58:B1:189:LEU:HG	1.73	0.69
51:1:1292:G:H2'	51:1:1293:C:C6	2.27	0.69
51:1:1889:A:H2'	51:1:1890:A:H8	1.58	0.69
51:1:2151:U:H2'	51:1:2152:G:C8	2.27	0.69
51:1:849:A:H2'	51:1:850:U:H6	1.58	0.69
51:1:1137:G:O2'	51:1:1138:G:H5'	1.92	0.69
51:1:2403:C:O2'	51:1:2404:U:H5'	1.92	0.69
58:B1:243:PRO:HG2	59:B2:1332:SER:O	1.93	0.69
36:l:30:THR:HG22	51:1:810:U:O4	1.93	0.69
51:1:644:A:H2'	51:1:645:C:C5'	2.21	0.69
51:1:2758:A:H2'	51:1:2759:G:H5'	1.75	0.69
51:1:2869:G:H2'	51:1:2870:C:C6	2.28	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
63:5:47:U:H4'	63:5:48:C:H5'	1.75	0.69
51:1:2114:A:H2	51:1:2167:U:H1'	1.58	0.68
51:1:2747:G:O6	51:1:2755:C:H5''	1.93	0.68
58:B1:832:LYS:C	58:B1:1242:ARG:HH12	2.01	0.68
51:1:319:G:H1	51:1:323:C:H5	1.41	0.68
51:1:1078:U:H2'	51:1:1088:A:OP1	1.94	0.68
53:3:437:U:H3	53:3:495:A:H62	1.41	0.68
58:B1:39:LYS:O	58:B1:273:ILE:CG2	2.41	0.68
58:B1:161:THR:HG22	58:B1:164:GLN:HB2	1.75	0.68
50:z:38:GLU:OE2	51:1:928:A:H5'	1.94	0.68
51:1:1999:C:H5''	51:1:2723:C:O2'	1.94	0.68
51:1:419:U:H2'	51:1:420:C:C6	2.27	0.68
51:1:905:A:C2'	51:1:906:U:H5'	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2510:C:N4	51:1:2511:U:O4	2.27	0.68
58:B1:111:THR:CG2	58:B1:300:GLN:CD	2.67	0.68
51:1:282:A:H2'	51:1:283:G:H8	1.57	0.68
51:1:419:U:H2'	51:1:420:C:H6	1.58	0.68
53:3:1338:G:H22	63:5:29:G:H22	1.42	0.68
51:1:1438:U:O2'	51:1:1439:A:H5'	1.94	0.68
51:1:1889:A:H2'	51:1:1890:A:C8	2.29	0.68
51:1:1702:G:C3'	51:1:1703:G:H5''	2.24	0.68
51:1:246:C:H2'	51:1:247:G:H5'	1.76	0.67
51:1:1432:G:O2'	51:1:1433:A:H5'	1.94	0.67
8:H:117:ASP:HA	8:H:120:THR:HG22	1.75	0.67
52:2:65:U:H3'	52:2:108:A:H61	1.58	0.67
58:B1:141:PHE:CD2	58:B1:293:ARG:O	2.47	0.67
51:1:466:A:H2'	51:1:467:G:H5'	1.76	0.67
51:1:1061:U:H3'	51:1:1062:G:H5'	1.76	0.67
58:B1:984:LEU:HB3	58:B1:993:GLU:HB2	1.76	0.67
51:1:112:U:H2'	51:1:113:U:H5'	1.76	0.67
51:1:226:A:H2'	51:1:227:A:O4'	1.94	0.67
51:1:703:U:C2'	51:1:704:G:H5'	2.25	0.67
51:1:2898:U:H2'	51:1:2899:A:C8	2.29	0.67
55:8:3:DC:C6	55:8:4:DT:H72	2.29	0.67
51:1:65:U:H2'	51:1:66:C:H6	1.59	0.67
51:1:1717:A:H2'	51:1:1718:G:H5'	1.77	0.67
51:1:2233:U:H2'	51:1:2234:G:C8	2.30	0.67
9:I:73:ASN:HA	9:I:76:LYS:HB2	1.77	0.67
48:x:16:ASN:ND2	48:x:26:ARG:HB3	2.09	0.67
58:B1:108:ALA:CB	58:B1:279:LEU:HD22	2.25	0.67
58:B1:1355:ARG:NH1	58:B1:1369:ARG:HH12	1.93	0.67
37:m:14:LYS:NZ	51:1:956:G:N7	2.35	0.67
51:1:2516:A:O2'	51:1:2517:C:H5'	1.95	0.67
65:0:104:ARG:HH22	65:0:407:GLU:HB3	1.57	0.67
58:B1:108:ALA:HB3	58:B1:279:LEU:HD22	1.77	0.67
4:D:37:LYS:HD3	4:D:39:ARG:HD3	1.77	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
51:1:521:U:H2'	51:1:522:A:C8	2.30	0.66
51:1:905:A:H2'	51:1:906:U:H5'	1.77	0.66
51:1:1270:C:H5''	51:1:1271:G:H5'	1.77	0.66
51:1:1484:U:H2'	51:1:1485:U:C6	2.30	0.66
58:B1:117:LEU:HD12	58:B1:117:LEU:O	1.94	0.66
65:0:364:VAL:HA	65:0:373:GLU:HA	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1063:G:H1	51:1:1075:C:H41	1.42	0.66
51:1:1176:U:H2'	51:1:1177:G:C8	2.29	0.66
55:8:13:DT:OP2	58:B1:791:ALA:HB1	1.95	0.66
51:1:707:G:O2'	51:1:708:G:H5'	1.94	0.66
51:1:894:U:H2'	51:1:895:U:O4'	1.93	0.66
51:1:2278:A:C3'	51:1:2279:G:H5''	2.25	0.66
51:1:528:A:H3'	51:1:528:A:H8	1.59	0.66
51:1:2278:A:H3'	51:1:2279:G:H5''	1.78	0.66
58:B1:1037:PHE:HB3	58:B1:1040:MET:HB2	1.78	0.66
51:1:2555:U:H2'	51:1:2556:C:H5'	1.77	0.66
51:1:2733:A:O2'	51:1:2734:A:H5'	1.96	0.66
45:u:25:LYS:HD3	45:u:36:GLU:HB3	1.75	0.66
51:1:673:C:H2'	51:1:674:G:H5'	1.77	0.66
17:Q:47:ALA:HB3	17:Q:49:ARG:HE	1.60	0.66
51:1:870:U:C2'	51:1:871:U:H5'	2.26	0.66
51:1:1082:U:H3'	51:1:1083:U:C5'	2.22	0.66
51:1:1733:G:O2'	51:1:1734:G:H5'	1.95	0.66
51:1:1020:A:H1'	51:1:1021:A:OP2	1.95	0.66
51:1:2233:U:H2'	51:1:2234:G:H8	1.59	0.66
51:1:2625:G:H2'	51:1:2626:C:C6	2.30	0.66
51:1:2760:C:O2'	51:1:2761:A:H5'	1.96	0.66
51:1:1064:C:N4	51:1:1069:A:H5''	2.10	0.66
51:1:2595:G:N2	51:1:2598:A:OP2	2.23	0.66
28:c:4:LEU:HD23	28:c:29:VAL:HG11	1.77	0.65
36:l:39:LYS:NZ	51:1:942:G:OP2	2.28	0.65
51:1:703:U:H2'	51:1:704:G:H5'	1.77	0.65
51:1:1746:A:H2'	51:1:1747:U:C6	2.31	0.65
51:1:2844:G:H2'	51:1:2845:U:C6	2.31	0.65
53:3:85:U:H5''	53:3:86:G:H5'	1.78	0.65
51:1:635:C:H2'	51:1:636:G:C8	2.31	0.65
51:1:1098:A:H2'	51:1:1099:G:H5'	1.77	0.65
51:1:2052:A:O2'	51:1:2053:G:H5'	1.96	0.65
58:B1:141:PHE:HD2	58:B1:293:ARG:O	1.80	0.65
58:B1:193:ASP:HB3	58:B1:196:GLN:HB2	1.78	0.65
7:G:67:LEU:HD12	7:G:153:MET:HE1	1.77	0.65
38:n:63:ARG:NE	51:1:1454:C:H5'	2.10	0.65
51:1:1270:C:H5''	51:1:1271:G:C5'	2.25	0.65
51:1:359:G:O2'	51:1:360:U:H5'	1.97	0.65
51:1:414:C:H2'	51:1:415:A:C8	2.31	0.65
65:0:508:GLN:HA	65:0:513:GLY:HA3	1.77	0.65
17:Q:109:ARG:HH21	17:Q:112:ALA:HB3	1.60	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:227:VAL:HG11	51:1:784:G:C2	2.31	0.65
51:1:543:G:H2'	51:1:544:C:C5'	2.26	0.65
51:1:2221:G:O2'	51:1:2222:C:H5'	1.95	0.65
51:1:2834:G:O2'	51:1:2835:A:H5'	1.97	0.65
19:S:38:GLU:HA	19:S:41:TRP:HB3	1.79	0.65
51:1:2013:A:H5''	51:1:2013:A:H8	1.59	0.65
51:1:536:G:H2'	51:1:537:G:H5'	1.79	0.65
51:1:1098:A:C2'	51:1:1099:G:H5'	2.27	0.65
51:1:1572:A:O2'	51:1:1573:G:H5'	1.97	0.65
51:1:1796:U:H2'	51:1:1797:G:H8	1.61	0.65
51:1:2193:G:H2'	51:1:2194:U:C6	2.32	0.65
58:B1:975:ILE:HG22	58:B1:977:SER:H	1.62	0.65
58:B1:978:ARG:HG2	58:B1:1197:ASN:HD21	1.61	0.65
51:1:905:A:O2'	51:1:906:U:H5'	1.97	0.65
31:f:154:GLU:HG3	31:f:156:TYR:H	1.61	0.65
51:1:613:A:H5''	51:1:614:A:C8	2.32	0.65
58:B1:68:TYR:HB3	58:B1:75:TYR:CE2	2.32	0.65
51:1:1161:C:H2'	51:1:1162:G:H8	1.61	0.64
51:1:1853:A:H2'	51:1:1854:A:C8	2.32	0.64
51:1:2290:G:H2'	51:1:2291:U:C6	2.32	0.64
51:1:2799:A:C2'	51:1:2800:A:H5'	2.27	0.64
4:D:24:THR:HG23	4:D:27:GLY:H	1.61	0.64
16:P:87:GLY:H	16:P:113:THR:HG22	1.62	0.64
28:c:149:ASN:HB3	51:1:2572:A:OP2	1.97	0.64
51:1:488:G:N2	51:1:491:G:H5''	2.11	0.64
51:1:1788:C:O2'	51:1:1789:A:H5'	1.96	0.64
51:1:256:A:O2'	51:1:257:C:H5'	1.98	0.64
51:1:306:U:H2'	51:1:307:G:O4'	1.98	0.64
51:1:2792:A:H3'	51:1:2793:C:H5''	1.80	0.64
26:Z:32:ARG:HG2	26:Z:33:ARG:HG3	1.80	0.64
51:1:2404:U:O2'	51:1:2405:G:H5'	1.97	0.64
58:B1:395:LYS:HZ2	58:B1:399:LYS:HD3	1.61	0.64
58:B1:918:ILE:HG22	59:B2:1280:ALA:HB1	1.79	0.64
51:1:414:C:H2'	51:1:415:A:H8	1.63	0.64
51:1:2112:G:C2'	51:1:2113:U:H5'	2.27	0.64
43:s:6:LYS:HB2	51:1:494:G:H4'	1.78	0.64
51:1:815:C:C2	51:1:1193:G:N2	2.66	0.64
51:1:2170:A:H2'	51:1:2171:A:O4'	1.97	0.64
55:8:3:DC:C2'	55:8:4:DT:C7	2.75	0.64
12:L:59:GLU:HA	12:L:62:GLU:HB3	1.80	0.64
51:1:1857:G:H22	51:1:1884:G:H2'	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1921:G:O2'	51:1:1922:G:H5'	1.98	0.64
51:1:2469:A:H2'	51:1:2470:G:O4'	1.98	0.64
59:B2:314:ASN:HD21	59:B2:348:SER:HA	1.62	0.64
59:B2:1282:GLY:HA3	60:W0:17:PHE:HE1	1.63	0.64
51:1:622:G:O2'	51:1:623:C:H5'	1.98	0.64
51:1:1038:G:H2'	51:1:1039:A:C8	2.32	0.64
51:1:1181:U:H2'	51:1:1182:G:C8	2.33	0.64
51:1:2073:C:O2'	51:1:2074:U:H5'	1.98	0.64
51:1:2114:A:N7	51:1:2115:G:H1'	2.12	0.64
16:P:19:VAL:HG22	16:P:82:GLU:HB2	1.79	0.64
27:b:106:PRO:HD2	27:b:109:LEU:HD22	1.79	0.64
51:1:1666:G:H2'	51:1:1667:G:C5'	2.24	0.64
58:B1:162:GLU:HA	58:B1:162:GLU:OE1	1.97	0.64
58:B1:461:PHE:HD2	59:B2:813:GLU:HB2	1.62	0.64
51:1:1164:C:O2'	51:1:1165:A:H5'	1.99	0.63
51:1:1766:G:O2'	51:1:1767:G:H5'	1.98	0.63
51:1:870:U:H2'	51:1:871:U:H5'	1.80	0.63
51:1:940:G:C3'	51:1:941:A:H5''	2.28	0.63
51:1:2811:G:O2'	51:1:2812:G:H5'	1.97	0.63
65:0:614:GLU:HB3	65:0:690:ALA:HB2	1.79	0.63
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
51:1:2314:A:H2'	51:1:2315:G:C8	2.33	0.63
51:1:1149:G:H2'	51:1:1150:C:C6	2.33	0.63
51:1:201:C:O2'	51:1:202:U:H5'	1.97	0.63
51:1:445:C:H2'	51:1:446:G:O4'	1.98	0.63
51:1:1280:G:O2'	51:1:1281:G:H5'	1.99	0.63
58:B1:245:LEU:HG	58:B1:246:PRO:HD2	1.80	0.63
7:G:173:LYS:O	7:G:177:ASN:ND2	2.32	0.63
26:Z:65:ARG:NH2	53:3:1087:G:N3	2.47	0.63
34:j:45:THR:HB	34:j:48:VAL:HG22	1.81	0.63
51:1:2636:C:H2'	51:1:2637:U:H6	1.64	0.63
51:1:2898:U:H2'	51:1:2899:A:H8	1.64	0.63
9:I:152:SER:H	9:I:155:LYS:HD3	1.63	0.63
51:1:212:G:O2'	51:1:213:A:H5'	1.99	0.63
51:1:1909:C:H2'	51:1:1910:G:H8	1.64	0.63
51:1:554:U:H2'	51:1:555:G:O4'	1.99	0.62
53:3:373:A:H61	53:3:391:G:H1'	1.64	0.62
58:B1:128:LEU:HA	58:B1:192:MET:HE1	1.81	0.62
1:A:1:MET:HG2	52:2:43:C:H5''	1.82	0.62
51:1:317:G:H2'	51:1:318:C:H6	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:u:87:GLU:HG2	45:u:92:VAL:HG21	1.82	0.62
51:1:1448:G:H2'	51:1:1449:G:H8	1.64	0.62
51:1:161:A:N7	51:1:162:U:H5	1.96	0.62
51:1:1524:G:H2'	51:1:1525:A:H8	1.63	0.62
51:1:2298:A:H2'	51:1:2299:U:O4'	1.99	0.62
55:8:13:DT:C7	58:B1:791:ALA:HB2	2.29	0.62
51:1:37:C:O2'	51:1:38:A:H5'	1.99	0.62
51:1:1680:U:H2'	51:1:1681:G:O4'	2.00	0.62
58:B1:285:LEU:HD13	58:B1:285:LEU:H	1.62	0.62
58:B1:1355:ARG:NH1	58:B1:1369:ARG:NH1	2.47	0.62
64:6:46:G:C2'	64:6:47:U:H5'	2.29	0.62
22:V:30:HIS:HD2	22:V:33:TYR:H	1.48	0.62
44:t:53:VAL:HG12	44:t:92:ASN:HD22	1.65	0.62
51:1:2092:U:H5	51:1:2199:A:H2	1.48	0.62
58:B1:100:GLU:HA	59:B2:1328:LYS:HE2	1.82	0.62
51:1:872:U:O2'	51:1:873:C:H5'	1.99	0.62
51:1:889:C:H2'	51:1:890:C:O4'	1.99	0.62
51:1:941:A:H2'	51:1:942:G:O4'	2.00	0.62
16:P:45:THR:HG23	16:P:48:GLY:H	1.65	0.62
51:1:1935:G:H1'	51:1:1964:G:N2	2.15	0.62
58:B1:111:THR:CG2	58:B1:300:GLN:NE2	2.63	0.62
51:1:161:A:H3'	51:1:162:U:H5''	1.81	0.61
51:1:2345:G:N3	51:1:2381:A:H2'	2.15	0.61
51:1:2734:A:H2'	51:1:2735:G:H5'	1.82	0.61
55:8:3:DC:H2'	55:8:4:DT:C7	2.30	0.61
59:B2:55:SER:OG	59:B2:465:ARG:NH1	2.33	0.61
4:D:3:ARG:O	4:D:6:GLN:NE2	2.34	0.61
16:P:58:THR:HG22	16:P:60:PHE:H	1.65	0.61
32:g:50:ARG:HH22	32:g:51:ARG:HH21	1.48	0.61
37:m:86:LYS:NZ	51:1:955:U:OP1	2.32	0.61
7:G:15:PHE:HB2	7:G:39:ILE:HG23	1.82	0.61
51:1:172:A:H2'	51:1:173:A:H8	1.66	0.61
55:8:1:DC:H2''	55:8:2:DC:C5	2.35	0.61
58:B1:633:ALA:HA	59:B2:806:PRO:O	2.01	0.61
58:B1:1357:ILE:HD11	59:B2:1287:LEU:HD13	1.80	0.61
2:B:43:THR:HG1	2:B:46:GLY:H	1.48	0.61
51:1:322:A:H5'	51:1:340:A:O4'	2.00	0.61
51:1:940:G:C2'	51:1:941:A:H5''	2.30	0.61
51:1:2404:U:H2'	51:1:2405:G:O4'	2.01	0.61
51:1:590:A:O2'	51:1:591:U:H5'	2.00	0.61
51:1:1040:A:H2	51:1:1115:G:H22	1.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1086:A:H5'	51:1:1103:A:H2	1.65	0.61
51:1:1503:A:H3'	51:1:1504:A:H5''	1.81	0.61
57:A1:211:ILE:HG12	57:A1:219:ARG:HH12	1.65	0.61
58:B1:68:TYR:HB3	58:B1:75:TYR:CZ	2.35	0.61
51:1:236:C:H2'	51:1:237:C:H6	1.64	0.61
51:1:547:A:H3'	51:1:547:A:N3	2.16	0.61
51:1:558:U:H6	51:1:558:U:O5'	1.84	0.61
51:1:723:C:H2'	51:1:724:U:H6	1.64	0.61
51:1:1717:A:C2'	51:1:1718:G:H5'	2.30	0.61
51:1:2188:U:H2'	51:1:2189:U:O4'	2.01	0.61
58:B1:395:LYS:NZ	58:B1:399:LYS:HD3	2.15	0.61
51:1:435:C:H2'	51:1:436:C:H5'	1.82	0.61
51:1:2097:A:H2'	51:1:2098:U:O4'	2.00	0.61
28:c:181:ASP:HB3	28:c:186:LEU:HB2	1.82	0.61
51:1:1775:U:C2'	51:1:1776:G:H5'	2.30	0.61
51:1:2804:U:H2'	51:1:2805:C:C6	2.36	0.61
58:B1:201:LEU:HB2	58:B1:221:ILE:HD13	1.80	0.61
18:R:102:LYS:HG2	18:R:103:THR:HG23	1.83	0.60
34:j:132:HIS:CD2	51:1:7:G:H5'	2.35	0.60
51:1:198:C:H42	51:1:248:G:H1	1.49	0.60
51:1:2637:U:H2'	51:1:2638:G:H5'	1.82	0.60
51:1:2852:G:O2'	51:1:2853:C:H5'	2.01	0.60
51:1:854:C:O2'	51:1:855:G:H5'	2.01	0.60
51:1:1954:G:H1'	51:1:1956:U:O4	2.01	0.60
51:1:2327:A:H2'	51:1:2328:A:C8	2.35	0.60
34:j:39:LYS:HE3	51:1:1009:A:OP1	2.01	0.60
37:m:17:ASN:O	37:m:38:ARG:NH1	2.34	0.60
51:1:1198:U:H2'	51:1:1199:U:C6	2.37	0.60
51:1:2812:G:H2'	51:1:2813:A:C8	2.36	0.60
58:B1:154:LEU:HD21	58:B1:160:LEU:HD21	1.83	0.60
58:B1:223:LEU:HG	58:B1:223:LEU:O	2.00	0.60
58:B1:770:LEU:HD13	59:B2:618:GLN:CG	2.30	0.60
57:A1:38:THR:HB	57:A2:45:ARG:HD3	1.82	0.60
58:B1:951:GLN:NE2	58:B1:1014:GLY:O	2.35	0.60
51:1:1437:C:H2'	51:1:1438:U:C6	2.36	0.60
53:3:1032:G:H21	53:3:1033:G:H4'	1.65	0.60
29:d:149:ILE:HG23	29:d:188:MET:HB3	1.83	0.60
33:i:135:MET:HE2	51:1:1062:G:H21	1.65	0.60
51:1:2093:G:O2'	51:1:2094:A:H5'	2.01	0.60
53:3:1133:G:H1	53:3:1141:C:H42	1.48	0.60
58:B1:1161:GLY:HA3	58:B1:1179:PRO:HA	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1026:G:H2'	51:1:1027:A:H8	1.67	0.60
51:1:1508:A:H2'	51:1:1509:A:O4'	2.01	0.60
51:1:1553:A:HO2'	51:1:1554:U:H5	1.48	0.60
51:1:1775:U:H2'	51:1:1776:G:C5'	2.29	0.60
55:8:7:DC:H2''	55:8:8:DT:H71	1.84	0.60
22:V:11:VAL:HA	22:V:22:VAL:HA	1.83	0.60
47:w:38:GLY:HA2	51:1:2330:G:H21	1.66	0.60
51:1:2137:U:H2'	51:1:2138:G:H8	1.67	0.60
53:3:1040:U:H2'	53:3:1041:G:H8	1.67	0.60
57:A1:112:ALA:HB3	57:A1:126:PRO:HA	1.83	0.60
58:B1:370:LYS:HG2	58:B1:441:LEU:HD23	1.84	0.60
58:B1:926:PRO:HG2	58:B1:1248:ILE:HD11	1.84	0.60
51:1:794:A:H2'	51:1:795:C:O4'	2.02	0.60
51:1:893:C:H2'	51:1:894:U:C6	2.36	0.60
51:1:1183:U:H2'	51:1:1184:U:C6	2.37	0.60
51:1:1287:A:C5	51:1:1288:G:C6	2.89	0.60
51:1:2187:U:O2'	51:1:2188:U:H5'	2.02	0.60
53:3:148:G:H1'	53:3:1447:A:H1'	1.84	0.60
53:3:1351:U:H3	53:3:1371:G:H1	1.49	0.60
55:8:11:DC:H2'	55:8:12:DG:C8	2.37	0.60
58:B1:342:LEU:HD23	58:B1:1352:ILE:HG23	1.83	0.60
59:B2:120:GLN:NE2	59:B2:490:GLN:OE1	2.32	0.60
51:1:2360:G:C2'	51:1:2361:G:H5'	2.31	0.60
58:B1:412:LEU:HD22	58:B1:441:LEU:HD21	1.84	0.60
59:B2:528:ARG:NH2	59:B2:576:SER:O	2.30	0.60
59:B2:1072:ASN:ND2	59:B2:1111:GLN:OE1	2.35	0.60
51:1:1670:C:H2'	51:1:1671:U:C5'	2.31	0.59
51:1:1773:A:C2'	51:1:1774:C:H5'	2.31	0.59
58:B1:99:ARG:NH1	58:B1:99:ARG:HG3	2.17	0.59
51:1:283:G:H2'	51:1:284:U:H5'	1.83	0.59
14:N:79:ARG:HH21	14:N:102:PHE:HA	1.67	0.59
33:i:19:PRO:HA	33:i:24:GLY:HA3	1.85	0.59
51:1:1071:G:H1'	51:1:1089:A:C8	2.37	0.59
51:1:1538:G:H2'	51:1:1539:U:C6	2.37	0.59
51:1:1857:G:N2	51:1:1884:G:H2'	2.17	0.59
51:1:2661:G:H5'	65:0:19:ILE:HD13	1.85	0.59
55:8:9:DG:H4'	58:B1:120:LEU:HG	1.84	0.59
51:1:11:C:C2'	51:1:12:U:H5''	2.29	0.59
51:1:851:C:H2'	51:1:852:U:C6	2.36	0.59
51:1:2386:A:O2'	51:1:2387:U:H5'	2.01	0.59
24:X:30:LEU:HB2	24:X:48:ILE:HG22	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:153:LEU:HD23	51:1:1799:G:C2	2.37	0.59
51:1:2643:G:H2'	51:1:2644:G:H5'	1.84	0.59
51:1:2743:U:H3'	51:1:2744:G:H5''	1.84	0.59
51:1:2789:C:H2'	51:1:2893:A:N7	2.18	0.59
59:B2:918:LEU:O	59:B2:918:LEU:HD23	2.02	0.59
30:e:51:ASN:OD1	30:e:149:ARG:NH1	2.34	0.59
39:o:4:LYS:HD3	39:o:7:ARG:HH21	1.65	0.59
51:1:841:G:O2'	51:1:842:U:H5'	2.02	0.59
51:1:1130:U:O2'	51:1:1131:G:OP1	2.20	0.59
51:1:2717:C:C4	51:1:2718:G:N7	2.70	0.59
29:d:77:ILE:HG23	51:1:1256:G:H21	1.68	0.59
51:1:2165:C:H2'	51:1:2166:U:C6	2.38	0.59
29:d:68:ALA:HA	51:1:1255:U:C5	2.37	0.59
45:u:40:LEU:HD12	45:u:59:GLU:HG2	1.84	0.59
51:1:2153:C:H2'	51:1:2154:A:H5'	1.85	0.59
51:1:2749:A:OP2	51:1:2751:G:H5''	2.02	0.59
58:B1:201:LEU:HD11	58:B1:220:ARG:HH11	1.67	0.59
58:B1:725:MET:SD	59:B2:1101:LEU:HD23	2.42	0.59
58:B1:750:PRO:CB	59:B2:549:ASP:OD2	2.45	0.59
65:0:557:ILE:HG21	65:0:576:ILE:HD12	1.85	0.59
9:I:69:ARG:NH1	53:3:401:C:OP2	2.36	0.59
9:I:201:GLU:O	53:3:8:A:N6	2.36	0.59
30:e:9:ASP:N	30:e:9:ASP:OD1	2.33	0.59
51:1:1042:G:H2'	51:1:1043:C:C6	2.37	0.59
59:B2:1142:ARG:NH1	59:B2:1161:LEU:O	2.36	0.59
14:N:17:ARG:HB2	14:N:65:THR:HG23	1.83	0.59
27:b:34:GLU:HG3	27:b:63:ILE:HD11	1.84	0.59
34:j:116:ARG:NH2	51:1:529:A:OP2	2.32	0.59
51:1:528:A:C8	51:1:528:A:C3'	2.86	0.59
51:1:1171:G:H2'	51:1:1172:C:O4'	2.02	0.59
58:B1:161:THR:HG23	58:B1:164:GLN:H	1.68	0.59
58:B1:438:GLU:HG3	58:B1:485:MET:HE1	1.85	0.59
28:c:55:LYS:NZ	28:c:59:ARG:O	2.36	0.58
29:d:77:ILE:CG2	51:1:1256:G:H21	2.15	0.58
34:j:3:THR:N	51:1:995:C:N3	2.48	0.58
51:1:246:C:C2'	51:1:247:G:H5'	2.33	0.58
51:1:1077:A:C8	51:1:1078:U:H1'	2.38	0.58
51:1:1337:G:H2'	51:1:1338:G:C8	2.38	0.58
51:1:1524:G:H2'	51:1:1525:A:C8	2.38	0.58
51:1:2533:U:H2'	51:1:2534:A:H5'	1.85	0.58
47:w:40:LYS:HE3	51:1:2330:G:O2'	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1333:G:O2'	51:1:1334:G:H5'	2.03	0.58
51:1:1725:U:H2'	51:1:1726:C:C6	2.38	0.58
51:1:2183:A:H2'	51:1:2184:A:C4	2.37	0.58
51:1:49:A:H5''	51:1:51:G:O4'	2.02	0.58
51:1:1469:A:H2'	51:1:1470:A:C8	2.38	0.58
51:1:2834:G:H2'	51:1:2879:A:N6	2.17	0.58
53:3:422:C:O2'	53:3:423:G:N2	2.36	0.58
15:O:46:LYS:HG2	15:O:68:ARG:HG2	1.84	0.58
42:r:4:VAL:HG22	42:r:40:MET:HG2	1.84	0.58
51:1:834:G:H2'	51:1:835:C:O4'	2.04	0.58
51:1:1098:A:H2'	51:1:1099:G:C5'	2.33	0.58
51:1:2215:C:H2'	51:1:2216:G:H8	1.65	0.58
59:B2:707:ALA:O	59:B2:711:ASP:HB2	2.04	0.58
65:O:618:LYS:HG3	65:O:643:LYS:NZ	2.19	0.58
21:U:70:ARG:HH22	53:3:451:A:H5'	1.66	0.58
51:1:1511:G:H2'	51:1:1512:C:C6	2.38	0.58
51:1:1561:C:H2'	51:1:1562:U:C6	2.39	0.58
51:1:2812:G:H2'	51:1:2813:A:H8	1.68	0.58
58:B1:514:THR:HG21	58:B1:596:LEU:HD12	1.84	0.58
51:1:146:A:H2'	51:1:147:C:C6	2.39	0.58
51:1:215:G:H4'	51:1:216:A:H4'	1.84	0.58
51:1:1400:U:O2'	51:1:1401:G:H5'	2.04	0.58
58:B1:275:ARG:NH1	58:B1:278:ARG:NH1	2.51	0.58
51:1:1845:G:O2'	51:1:1846:G:H5'	2.02	0.58
58:B1:144:TYR:CE1	58:B1:162:GLU:OE2	2.51	0.58
23:W:49:LYS:HA	23:W:52:ARG:HH21	1.69	0.58
30:e:47:LYS:O	30:e:51:ASN:ND2	2.37	0.58
51:1:640:C:O2'	51:1:641:U:H5'	2.04	0.58
51:1:1579:A:H2'	51:1:1580:A:C8	2.38	0.58
51:1:1893:C:H2'	51:1:1894:C:H5'	1.86	0.58
51:1:2636:C:H2'	51:1:2637:U:C6	2.39	0.58
53:3:409:U:H3	53:3:433:G:H1	1.51	0.58
58:B1:97:VAL:HG11	58:B1:101:ARG:NH2	2.18	0.58
58:B1:198:CYS:HA	58:B1:221:ILE:HD11	1.86	0.58
58:B1:1361:THR:HB	59:B2:1284:ALA:HB3	1.86	0.58
9:I:10:LEU:HD23	9:I:62:ARG:HB3	1.86	0.58
19:S:5:MET:HE1	53:3:981:U:H5''	1.86	0.58
29:d:1:MET:HG2	29:d:16:GLU:HG2	1.86	0.58
51:1:673:C:C2'	51:1:674:G:H5'	2.34	0.58
51:1:1565:C:O2'	51:1:1566:A:H8	1.87	0.58
51:1:2762:C:H2'	51:1:2763:G:H5'	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:45:THR:O	7:G:49:PHE:N	2.35	0.57
27:b:141:HIS:ND1	27:b:192:GLY:O	2.35	0.57
39:o:56:LYS:NZ	52:2:117:G:OP1	2.36	0.57
51:1:1275:A:C6	51:1:1296:G:H4'	2.39	0.57
51:1:1526:C:H2'	51:1:1527:G:O4'	2.04	0.57
51:1:2899:A:O2'	51:1:2900:A:H5'	2.04	0.57
58:B1:99:ARG:CG	58:B1:99:ARG:HH11	2.17	0.57
65:0:94:ASP:HB3	65:0:465:HIS:HB2	1.85	0.57
27:b:157:ALA:O	51:1:1820:U:C2	2.56	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
37:m:66:ARG:NH1	37:m:104:GLU:OE2	2.36	0.57
38:n:63:ARG:CZ	51:1:1454:C:H5'	2.34	0.57
49:y:39:GLN:HG2	51:1:96:C:OP1	2.05	0.57
51:1:32:C:H2'	51:1:33:C:C6	2.39	0.57
51:1:163:C:H2'	51:1:164:C:O4'	2.05	0.57
51:1:1463:C:H2'	51:1:1464:G:H8	1.68	0.57
58:B1:42:GLU:HB3	58:B1:52:GLU:HG3	1.86	0.57
45:u:36:GLU:HA	45:u:61:GLU:HG2	1.86	0.57
51:1:1108:U:H2'	51:1:1109:C:C2	2.40	0.57
58:B1:615:LYS:HG2	60:W0:5:THR:HG21	1.85	0.57
1:A:26:SER:OG	1:A:27:THR:N	2.37	0.57
16:P:111:ASP:HB2	26:Z:16:ARG:HH22	1.68	0.57
25:Y:59:ARG:NH1	53:3:177:G:OP1	2.37	0.57
38:n:22:ARG:HG3	38:n:70:THR:HA	1.86	0.57
57:A2:28:LEU:HB2	57:A2:201:LEU:HB3	1.85	0.57
59:B2:69:GLN:HE21	59:B2:101:ARG:HD2	1.67	0.57
51:1:621:A:H2'	51:1:622:G:H5'	1.86	0.57
51:1:1173:U:C5	51:1:1174:U:H1'	2.40	0.57
51:1:1528:A:H2'	51:1:1529:G:H5'	1.87	0.57
39:o:25:ARG:NH1	52:2:8:C:O3'	2.37	0.57
51:1:593:U:H2'	51:1:594:U:C6	2.40	0.57
51:1:1319:C:O2'	51:1:1320:C:H5'	2.05	0.57
51:1:2186:G:O2'	51:1:2187:U:H5'	2.04	0.57
58:B1:37:GLU:O	58:B1:61:ILE:CD1	2.52	0.57
58:B1:638:SER:OG	58:B1:639:VAL:N	2.36	0.57
25:Y:73:ARG:NH2	53:3:261:U:OP2	2.36	0.57
28:c:129:THR:OG1	28:c:140:HIS:O	2.22	0.57
51:1:74:A:H4'	51:1:75:G:O5'	2.05	0.57
51:1:235:U:H2'	51:1:236:C:C6	2.39	0.57
51:1:635:C:H2'	51:1:636:G:H8	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1520:U:O2'	51:1:1521:G:H5'	2.05	0.57
51:1:2897:U:H2'	51:1:2898:U:C6	2.39	0.57
58:B1:241:VAL:O	58:B1:241:VAL:HG12	2.04	0.57
58:B1:510:LEU:HD22	58:B1:601:ILE:HD12	1.86	0.57
21:U:55:ASP:OD1	21:U:55:ASP:N	2.38	0.57
38:n:54:LEU:HD23	38:n:66:ALA:HB2	1.86	0.57
41:q:30:VAL:HG13	51:1:580:U:O3'	2.04	0.57
51:1:287:G:H2'	51:1:288:U:C6	2.40	0.57
51:1:366:C:O2'	51:1:367:G:H5'	2.04	0.57
51:1:2092:U:H4'	51:1:2093:G:C5'	2.34	0.57
8:H:76:ILE:HD11	54:4:23:U:H4'	1.87	0.57
27:b:259:ASN:ND2	27:b:262:THR:OG1	2.38	0.57
51:1:323:C:H3'	51:1:323:C:OP2	2.05	0.57
51:1:327:G:O2'	51:1:328:U:H5'	2.04	0.57
53:3:1125:U:H2'	53:3:1126:U:H2'	1.85	0.57
57:A2:82:LEU:HD11	57:A2:171:LEU:HD23	1.86	0.57
58:B1:741:ALA:O	58:B1:762:ASN:ND2	2.38	0.57
59:B2:1122:LYS:NZ	59:B2:1126:ASP:OD1	2.38	0.57
51:1:69:C:H2'	51:1:70:G:H8	1.70	0.56
51:1:503:A:H4'	51:1:505:A:H5'	1.87	0.56
59:B2:1142:ARG:NH2	59:B2:1166:ASP:OD1	2.38	0.56
40:p:1:SER:OG	40:p:2:ASN:N	2.37	0.56
51:1:2570:G:H2'	51:1:2571:U:H5'	1.85	0.56
51:1:2662:A:H2'	51:1:2663:G:O4'	2.05	0.56
59:B2:818:VAL:HG22	59:B2:1096:ILE:HG12	1.87	0.56
7:G:114:LYS:HE3	7:G:151:LYS:HB2	1.86	0.56
10:J:54:GLU:HG2	10:J:56:PRO:HD2	1.86	0.56
18:R:100:ARG:NH1	18:R:103:THR:OG1	2.38	0.56
35:k:65:THR:HG23	35:k:68:GLY:H	1.69	0.56
46:v:57:TYR:OH	46:v:79:ARG:NH2	2.38	0.56
50:z:4:ILE:HD11	50:z:58:GLU:HG2	1.86	0.56
51:1:184:C:H2'	51:1:185:G:H8	1.70	0.56
51:1:358:U:H2'	51:1:359:G:C8	2.41	0.56
51:1:543:G:H2'	51:1:544:C:O4'	2.05	0.56
51:1:727:A:H2'	51:1:728:G:C8	2.40	0.56
51:1:2845:U:H2'	51:1:2846:G:H8	1.69	0.56
58:B1:247:PRO:HA	58:B1:250:ARG:HG3	1.87	0.56
31:f:44:HIS:HA	31:f:49:LEU:HG	1.87	0.56
39:o:52:SER:OG	39:o:53:THR:N	2.39	0.56
51:1:359:G:C2'	51:1:360:U:H5'	2.36	0.56
51:1:877:A:N1	51:1:899:A:H2'	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1485:U:H2'	51:1:1486:U:C6	2.41	0.56
51:1:1678:A:H2'	51:1:1679:A:H5'	1.86	0.56
58:B1:160:LEU:HD22	58:B1:164:GLN:HB3	1.86	0.56
58:B1:1167:LYS:HZ2	58:B1:1170:LYS:HB2	1.71	0.56
64:6:52:G:H2'	64:6:53:G:H8	1.69	0.56
27:b:250:GLN:NE2	27:b:251:THR:O	2.38	0.56
51:1:780:G:H21	51:1:783:A:H62	1.54	0.56
51:1:1590:A:O2'	51:1:1591:A:H5'	2.05	0.56
59:B2:13:LYS:HB2	59:B2:1180:MET:HE2	1.86	0.56
7:G:91:VAL:HG22	7:G:150:ILE:HD11	1.88	0.56
11:K:2:ARG:NH1	53:3:738:C:OP1	2.39	0.56
11:K:12:PRO:HB2	11:K:44:ARG:HH21	1.70	0.56
14:N:35:GLU:HA	14:N:39:GLY:HA3	1.86	0.56
16:P:92:ARG:NH2	16:P:111:ASP:OD1	2.38	0.56
38:n:2:ARG:HA	38:n:5:LYS:HD3	1.88	0.56
50:z:15:ARG:HE	50:z:52:PHE:HE2	1.53	0.56
51:1:296:U:H2'	51:1:297:G:C8	2.41	0.56
51:1:1120:G:O2'	51:1:1121:C:H5'	2.05	0.56
51:1:1410:G:H2'	51:1:1411:U:C6	2.41	0.56
51:1:2395:C:H42	51:1:2421:G:H1	1.54	0.56
53:3:159:G:N2	53:3:162:A:OP2	2.34	0.56
58:B1:1046:ILE:HD12	58:B1:1059:LEU:HB3	1.86	0.56
59:B2:1070:HIS:NE2	59:B2:1114:GLU:OE1	2.36	0.56
31:f:40:VAL:O	31:f:54:ARG:NH2	2.38	0.56
31:f:151:ARG:HB3	31:f:161:VAL:HG23	1.86	0.56
49:y:49:ASP:OD1	49:y:52:ARG:NH2	2.39	0.56
51:1:118:A:OP2	51:1:119:A:H5''	2.06	0.56
51:1:720:U:H2'	51:1:721:A:C8	2.41	0.56
51:1:1541:C:O2'	51:1:1542:U:H5'	2.06	0.56
51:1:2457:U:O2'	51:1:2458:G:H5'	2.05	0.56
51:1:2510:C:C4	51:1:2511:U:C4	2.93	0.56
58:B1:39:LYS:O	58:B1:273:ILE:HG21	2.06	0.56
58:B1:1166:GLY:HA3	58:B1:1174:ARG:HB2	1.88	0.56
63:5:37:A:H3'	63:5:38:A:H8	1.71	0.56
7:G:58:LYS:O	7:G:62:ARG:NH1	2.38	0.56
51:1:1182:G:H2'	51:1:1183:U:O4'	2.06	0.56
51:1:1485:U:H2'	51:1:1486:U:H6	1.70	0.56
51:1:1597:A:H5''	51:1:1598:A:H5'	1.87	0.56
51:1:2637:U:C2'	51:1:2638:G:H5'	2.36	0.56
58:B1:130:MET:HE2	58:B1:135:ILE:HG12	1.87	0.56
58:B1:804:ALA:HA	58:B1:1259:GLN:HG3	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:78:U:H2'	51:1:79:C:C6	2.40	0.56
51:1:133:U:O2'	51:1:134:G:H5'	2.06	0.56
51:1:288:U:H2'	51:1:289:G:H8	1.71	0.56
51:1:1097:U:H2'	51:1:1098:A:O4'	2.06	0.56
51:1:1772:A:H5'	51:1:1773:A:OP2	2.06	0.56
51:1:1917:U:O2'	51:1:1918:A:H5'	2.05	0.56
51:1:2626:C:H2'	51:1:2627:G:O4'	2.06	0.56
65:0:29:ARG:HE	65:0:269:ALA:HB1	1.70	0.56
10:J:44:ARG:NH2	10:J:70:MET:SD	2.78	0.56
51:1:2114:A:C2	51:1:2167:U:H1'	2.41	0.56
57:A1:29:GLU:HB3	57:A1:200:LYS:HG3	1.88	0.56
49:y:28:LEU:HA	49:y:31:GLN:HB2	1.88	0.55
51:1:340:A:H2'	51:1:341:C:O4'	2.06	0.55
51:1:759:G:H2'	51:1:760:G:C8	2.41	0.55
51:1:2584:U:C2'	51:1:2585:U:H5'	2.34	0.55
53:3:158:G:N2	53:3:163:C:O2	2.36	0.55
53:3:830:G:H1	53:3:856:C:H42	1.53	0.55
4:D:9:VAL:HG22	51:1:1309:G:OP1	2.06	0.55
19:S:26:LEU:HA	19:S:30:ILE:HD12	1.87	0.55
51:1:155:A:H2'	51:1:156:A:C8	2.41	0.55
51:1:172:A:H2'	51:1:173:A:C8	2.40	0.55
51:1:825:A:O2'	51:1:826:U:H5'	2.06	0.55
51:1:1086:A:H5'	51:1:1103:A:C2	2.41	0.55
51:1:1697:G:H4'	51:1:1978:A:H5''	1.88	0.55
53:3:503:C:H2'	53:3:504:C:C6	2.41	0.55
41:q:90:ASP:N	41:q:90:ASP:OD1	2.37	0.55
51:1:439:A:H2'	51:1:440:C:C6	2.42	0.55
51:1:633:A:C2'	51:1:634:C:H5'	2.35	0.55
51:1:655:A:H4'	51:1:656:G:C5'	2.30	0.55
51:1:885:C:N4	51:1:886:A:H62	2.03	0.55
51:1:1506:U:H2'	51:1:1507:C:C6	2.41	0.55
53:3:49:U:H3	53:3:362:G:H1'	1.71	0.55
58:B1:102:MET:HG2	58:B1:246:PRO:HG3	1.87	0.55
65:0:514:GLN:HE22	65:0:591:LEU:HD23	1.72	0.55
12:L:4:ARG:HB3	12:L:6:ILE:HG23	1.88	0.55
19:S:52:ARG:O	19:S:58:ARG:NH1	2.39	0.55
28:c:134:HIS:CE1	51:1:1675:C:C4	2.94	0.55
37:m:27:SER:H	37:m:66:ARG:HH12	1.54	0.55
51:1:613:A:H2'	51:1:613:A:N3	2.21	0.55
59:B2:985:GLU:HB3	59:B2:988:LYS:HB2	1.89	0.55
51:1:184:C:H2'	51:1:185:G:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:543:G:H2'	51:1:544:C:C4'	2.37	0.55
51:1:877:A:C2'	51:1:878:A:H5''	2.37	0.55
51:1:1448:G:H2'	51:1:1449:G:C8	2.42	0.55
51:1:2236:U:H2'	51:1:2237:G:H5'	1.88	0.55
58:B1:799:ARG:HG2	58:B1:1325:PHE:HZ	1.72	0.55
59:B2:103:VAL:HB	59:B2:114:VAL:HG11	1.89	0.55
59:B2:839:VAL:HG12	59:B2:1049:ILE:HG12	1.87	0.55
26:Z:44:ARG:NH1	53:3:722:G:OP2	2.39	0.55
27:b:216:ARG:NH2	51:1:781:A:OP1	2.38	0.55
28:c:18:ASP:OD1	28:c:18:ASP:N	2.36	0.55
51:1:296:U:H2'	51:1:297:G:H8	1.71	0.55
51:1:1389:G:O2'	51:1:1390:U:H5'	2.07	0.55
51:1:2488:G:O2'	51:1:2489:U:H5'	2.07	0.55
51:1:2743:U:C3'	51:1:2744:G:H5''	2.37	0.55
51:1:2845:U:H2'	51:1:2846:G:C8	2.42	0.55
58:B1:833:GLU:HB2	58:B1:1242:ARG:NH1	2.22	0.55
51:1:112:U:C2'	51:1:113:U:H5'	2.37	0.55
51:1:359:G:H2'	51:1:360:U:O4'	2.07	0.55
51:1:392:U:H2'	51:1:393:C:C6	2.42	0.55
51:1:461:C:H2'	51:1:462:C:C6	2.41	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
49:y:19:LEU:O	49:y:23:ARG:N	2.35	0.55
51:1:1048:A:H2'	51:1:1049:C:H5'	1.88	0.55
51:1:1601:G:C2'	51:1:1602:U:H5'	2.37	0.55
51:1:1909:C:H2'	51:1:1910:G:C8	2.41	0.55
51:1:1948:G:H21	53:3:1418:A:H2	1.49	0.55
51:1:2114:A:C8	51:1:2115:G:H1'	2.42	0.55
53:3:202:G:H21	53:3:466:A:H61	1.53	0.55
53:3:1040:U:H2'	53:3:1041:G:C8	2.42	0.55
7:G:19:THR:HA	7:G:37:VAL:HA	1.88	0.55
16:P:63:GLN:HG3	16:P:98:ALA:HB2	1.88	0.55
51:1:279:A:N6	51:1:361:G:H1'	2.21	0.55
51:1:1386:C:H2'	51:1:1387:A:C8	2.41	0.55
51:1:2195:U:O2'	51:1:2196:C:H5'	2.06	0.55
51:1:2217:G:O2'	51:1:2218:G:H5'	2.06	0.55
51:1:2533:U:C2'	51:1:2534:A:H5'	2.36	0.55
59:B2:917:SER:O	59:B2:919:ARG:HG3	2.07	0.55
57:A1:47:LEU:HD23	57:A1:51:MET:HG3	1.89	0.55
58:B1:58:CYS:SG	58:B1:59:ALA:N	2.80	0.55
36:l:89:VAL:HG23	36:l:121:THR:HG23	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1745:A:O2'	51:1:1746:A:H5'	2.07	0.54
51:1:2345:G:H5'	51:1:2347:C:H5'	1.89	0.54
51:1:2827:C:O2'	51:1:2828:G:H5'	2.07	0.54
53:3:923:A:N6	53:3:1392:G:O6	2.40	0.54
64:6:11:A:H2'	64:6:12:G:H8	1.72	0.54
8:H:39:ARG:NH1	8:H:54:ILE:O	2.39	0.54
12:L:73:GLU:HG2	12:L:90:VAL:HG22	1.89	0.54
30:e:23:SER:HB3	30:e:26:GLN:HB2	1.88	0.54
33:i:10:LEU:HA	51:1:1061:U:C2	2.42	0.54
51:1:317:G:H2'	51:1:318:C:C6	2.42	0.54
51:1:1005:C:H6	51:1:1005:C:O5'	1.90	0.54
51:1:1545:A:H2'	51:1:1546:G:O4'	2.06	0.54
53:3:927:G:O2'	53:3:1503:A:N7	2.38	0.54
58:B1:144:TYR:HE1	58:B1:162:GLU:CD	2.14	0.54
58:B1:145:VAL:HG23	58:B1:159:ILE:HG22	1.89	0.54
58:B1:508:LEU:HD22	59:B2:1101:LEU:HD21	1.88	0.54
58:B1:759:ILE:HG23	58:B1:771:GLN:HB3	1.89	0.54
7:G:138:ARG:NH1	7:G:141:GLU:OE2	2.40	0.54
51:1:622:G:HO2'	51:1:623:C:H5'	1.72	0.54
51:1:1288:G:C6	51:1:1327:A:C2	2.96	0.54
51:1:1310:G:O2'	51:1:1311:G:H5'	2.06	0.54
53:3:1036:A:H2'	53:3:1037:C:H5'	1.88	0.54
59:B2:29:SER:O	59:B2:33:ASP:HB2	2.07	0.54
59:B2:684:ASN:OD1	59:B2:687:ARG:NH2	2.41	0.54
64:6:9:G:C2	64:6:45:G:O6	2.60	0.54
7:G:53:LEU:HD21	7:G:215:ALA:HB1	1.88	0.54
12:L:113:LYS:O	53:3:1239:A:O2'	2.23	0.54
16:P:86:LYS:HG3	16:P:114:PRO:HD3	1.89	0.54
25:Y:47:GLN:NE2	25:Y:51:ASN:OD1	2.40	0.54
29:d:84:THR:HG21	51:1:586:A:H5'	1.87	0.54
37:m:64:TRP:HB2	37:m:104:GLU:HB2	1.89	0.54
51:1:1297:C:H2'	51:1:1298:C:C6	2.43	0.54
51:1:1670:C:O5'	51:1:1670:C:H6	1.90	0.54
51:1:1748:C:H2'	51:1:1749:A:H8	1.73	0.54
51:1:2091:C:H5	51:1:2092:U:HO2'	1.53	0.54
51:1:2734:A:C2'	51:1:2735:G:H5'	2.38	0.54
51:1:2850:A:N1	51:1:2869:G:H4'	2.21	0.54
59:B2:360:LEU:HD13	59:B2:378:ARG:HH11	1.72	0.54
51:1:128:C:H2'	51:1:129:C:H6	1.70	0.54
51:1:268:C:H2'	51:1:269:C:H6	1.73	0.54
51:1:1014:A:H2'	51:1:1015:U:C6	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:2:40:U:N3	52:2:44:G:OP2	2.40	0.54
57:A2:29:GLU:HG3	57:A2:200:LYS:HG3	1.88	0.54
58:B1:1155:ILE:HG13	58:B1:1210:ILE:HB	1.89	0.54
35:k:70:ARG:HG2	35:k:76:VAL:HG12	1.88	0.54
38:n:35:LYS:NZ	38:n:100:CYS:SG	2.81	0.54
51:1:472:A:H2'	51:1:473:G:H5'	1.90	0.54
51:1:1091:G:H2'	51:1:1092:C:C6	2.43	0.54
51:1:2545:G:O2'	51:1:2546:U:H5'	2.07	0.54
59:B2:633:LEU:HD13	59:B2:644:LEU:HD23	1.89	0.54
10:J:23:THR:HA	10:J:28:ARG:HA	1.88	0.54
21:U:69:ASP:OD1	21:U:69:ASP:N	2.38	0.54
29:d:76:PRO:HD2	51:1:673:C:H5''	1.89	0.54
44:t:54:GLU:HB3	44:t:88:LYS:HE3	1.90	0.54
51:1:682:G:N2	51:1:796:C:O2	2.41	0.54
51:1:876:C:H2'	51:1:877:A:O4'	2.08	0.54
51:1:1530:G:H22	51:1:1542:U:H1'	1.73	0.54
58:B1:800:LEU:HB3	58:B1:920:ALA:HB1	1.89	0.54
58:B1:1175:LEU:HD22	58:B1:1190:ILE:HD11	1.88	0.54
59:B2:243:PRO:HB2	59:B2:274:ILE:HG23	1.90	0.54
9:I:55:ARG:O	9:I:59:LYS:N	2.41	0.54
34:j:38:GLY:HA3	34:j:50:THR:HG23	1.90	0.54
51:1:143:C:H2'	51:1:144:A:H8	1.72	0.54
51:1:923:G:O2'	51:1:924:G:H5'	2.07	0.54
51:1:1856:U:H2'	51:1:1857:G:O4'	2.08	0.54
51:1:2092:U:C5	51:1:2199:A:H2	2.25	0.54
51:1:2328:A:H8	51:1:2328:A:O5'	1.90	0.54
51:1:2742:G:O2'	51:1:2743:U:H5'	2.08	0.54
58:B1:746:LEU:HG	58:B1:758:PRO:HG3	1.90	0.54
58:B1:814:CYS:SG	58:B1:883:ARG:NH2	2.81	0.54
59:B2:811:ASN:HA	59:B2:815:SER:HB2	1.90	0.54
7:G:86:CYS:SG	7:G:87:ASP:N	2.74	0.54
19:S:84:ARG:NH2	53:3:1059:C:O3'	2.40	0.54
20:T:48:ASP:OD1	53:3:667:G:O2'	2.25	0.54
25:Y:60:GLN:HA	25:Y:63:LYS:HB3	1.89	0.54
29:d:76:PRO:HA	29:d:82:GLY:HA3	1.90	0.54
49:y:15:ASN:O	49:y:19:LEU:N	2.41	0.54
51:1:141:G:H3'	51:1:142:A:O4'	2.07	0.54
51:1:1511:G:H2'	51:1:1512:C:H6	1.73	0.54
51:1:2123:G:H2'	51:1:2124:G:H8	1.73	0.54
51:1:2190:G:O2'	51:1:2191:A:H5'	2.08	0.54
58:B1:30:ILE:HG21	58:B1:241:VAL:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:15:VAL:HG12	16:P:76:TYR:HB3	1.90	0.54
27:b:227:VAL:HG11	51:1:784:G:N1	2.23	0.54
31:f:103:ASN:ND2	31:f:113:ASP:OD1	2.41	0.54
47:w:55:LEU:HD12	47:w:76:ILE:HD12	1.90	0.54
51:1:2631:G:O2'	51:1:2632:A:H5'	2.08	0.54
53:3:505:G:H5''	53:3:534:U:H2'	1.89	0.54
58:B1:39:LYS:O	58:B1:273:ILE:HG23	2.08	0.54
65:0:17:ALA:HB2	65:0:112:VAL:HB	1.89	0.54
7:G:126:ASP:OD1	7:G:126:ASP:N	2.41	0.53
51:1:8:C:H2'	51:1:9:G:H8	1.73	0.53
51:1:341:C:O2'	51:1:342:A:H5'	2.08	0.53
51:1:358:U:H2'	51:1:359:G:H8	1.72	0.53
51:1:757:G:H2'	51:1:758:C:C5'	2.35	0.53
51:1:1599:U:H2'	51:1:1600:C:C6	2.43	0.53
53:3:458:U:H3	53:3:474:G:H1	1.56	0.53
57:A2:28:LEU:HD22	57:A2:201:LEU:HD23	1.90	0.53
58:B1:785:ASP:O	58:B1:789:LYS:HB2	2.08	0.53
17:Q:8:ARG:NH2	53:3:880:C:OP1	2.36	0.53
51:1:176:A:O2'	51:1:177:G:H5'	2.08	0.53
51:1:441:U:O2'	51:1:442:G:H5'	2.08	0.53
51:1:543:G:C2'	51:1:544:C:H5''	2.37	0.53
51:1:1601:G:O2'	51:1:1602:U:H5'	2.08	0.53
51:1:2850:A:C2	51:1:2869:G:H4'	2.44	0.53
53:3:1023:U:H2'	53:3:1024:G:C8	2.43	0.53
58:B1:111:THR:HG22	58:B1:300:GLN:NE2	2.23	0.53
64:6:25:C:H42	64:6:45:G:H22	1.56	0.53
1:A:35:ASP:OD1	18:R:2:ARG:NH1	2.42	0.53
3:C:20:TYR:OH	51:1:2348:U:H5'	2.08	0.53
12:L:77:ARG:NH2	53:3:1381:U:O2	2.41	0.53
51:1:613:A:H5''	51:1:614:A:N7	2.22	0.53
58:B1:78:LEU:O	58:B1:78:LEU:HD13	2.08	0.53
8:H:71:ARG:HB3	8:H:74:ILE:HD13	1.89	0.53
10:J:104:ILE:O	10:J:111:ARG:NH1	2.41	0.53
11:K:23:GLU:HA	11:K:26:THR:HG22	1.90	0.53
30:e:21:TYR:OH	30:e:164:GLU:OE1	2.26	0.53
51:1:53:A:H2'	51:1:54:G:H5'	1.89	0.53
51:1:1083:U:H2'	51:1:1084:A:H3'	1.89	0.53
51:1:1913:A:N7	53:3:1494:G:H4'	2.22	0.53
51:1:2092:U:C5	51:1:2199:A:C2	2.97	0.53
51:1:2644:G:O2'	51:1:2645:G:H5'	2.09	0.53
57:A1:16:ILE:HG23	57:A1:26:VAL:HG22	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:1117:LEU:HD12	59:B2:1195:ILE:HG12	1.90	0.53
36:l:80:SER:HB3	36:l:114:GLY:HA3	1.90	0.53
51:1:40:U:H2'	51:1:41:C:C6	2.43	0.53
51:1:44:A:O2'	51:1:45:G:H5'	2.08	0.53
51:1:402:A:C2'	51:1:403:U:H5'	2.38	0.53
51:1:1560:G:H2'	51:1:1560:G:N3	2.24	0.53
51:1:2617:U:H2'	51:1:2618:G:H5'	1.91	0.53
53:3:1077:G:N2	53:3:1080:A:OP2	2.40	0.53
13:M:92:PRO:O	13:M:116:ARG:NH2	2.42	0.53
33:i:53:PRO:HD2	33:i:77:VAL:HG11	1.91	0.53
36:l:20:GLY:HA2	36:l:28:GLY:HA2	1.90	0.53
39:o:31:THR:HG23	39:o:34:HIS:H	1.73	0.53
39:o:69:ASP:N	39:o:69:ASP:OD1	2.36	0.53
51:1:481:G:H1'	51:1:506:G:H21	1.71	0.53
51:1:925:A:O2'	51:1:926:G:H5'	2.08	0.53
51:1:995:C:H6	51:1:995:C:H5'	1.74	0.53
51:1:1662:U:H2'	51:1:1663:G:O4'	2.09	0.53
17:Q:64:SER:OG	17:Q:65:TYR:N	2.41	0.53
48:x:29:LEU:HD12	51:1:2230:G:H5''	1.90	0.53
51:1:53:A:C2'	51:1:54:G:H5'	2.39	0.53
51:1:611:C:H2'	51:1:612:G:O4'	2.09	0.53
51:1:820:A:O2'	51:1:821:A:H5'	2.08	0.53
51:1:878:A:H2'	51:1:879:G:O4'	2.09	0.53
51:1:973:A:H5'	51:1:1188:U:H1'	1.90	0.53
51:1:1068:G:N2	51:1:1096:A:H1'	2.23	0.53
51:1:1528:A:C2'	51:1:1529:G:H5'	2.38	0.53
57:A1:100:LEU:HD21	57:A1:121:VAL:HG11	1.90	0.53
8:H:30:ASP:N	8:H:30:ASP:OD1	2.41	0.53
40:p:105:LYS:O	40:p:108:ARG:NH2	2.42	0.53
51:1:282:A:H2'	51:1:283:G:C8	2.42	0.53
51:1:1171:G:H2'	51:1:1172:C:C4'	2.38	0.53
51:1:1409:U:H2'	51:1:1410:G:C8	2.44	0.53
51:1:1678:A:H2'	51:1:1679:A:C5'	2.38	0.53
51:1:1917:U:C2'	51:1:1918:A:H5'	2.39	0.53
53:3:1023:U:H2'	53:3:1024:G:H8	1.74	0.53
9:I:154:VAL:HA	9:I:157:ALA:HB3	1.91	0.53
14:N:115:VAL:HG23	53:3:1367:C:H5''	1.91	0.53
40:p:28:LYS:HB3	40:p:39:LEU:HD21	1.91	0.53
51:1:21:A:O2'	51:1:22:C:H5'	2.08	0.53
51:1:140:C:H2'	51:1:141:G:H5'	1.90	0.53
51:1:268:C:H2'	51:1:269:C:C6	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:894:U:O2'	51:1:895:U:H5'	2.09	0.53
51:1:1063:G:N1	51:1:1075:C:N4	2.53	0.53
51:1:2425:A:H4'	51:1:2426:A:H5''	1.91	0.53
51:1:2758:A:H2'	51:1:2759:G:C5'	2.39	0.53
57:A2:100:LEU:HD23	57:A2:115:ILE:HG21	1.89	0.53
58:B1:770:LEU:CD1	59:B2:618:GLN:HG3	2.37	0.53
58:B1:975:ILE:HD11	58:B1:1003:LEU:HD11	1.91	0.53
59:B2:628:HIS:HB3	59:B2:647:ARG:HH21	1.74	0.53
7:G:61:SER:OG	7:G:62:ARG:NH1	2.42	0.53
31:f:7:PRO:O	31:f:68:ARG:NH2	2.38	0.53
34:j:2:LYS:HA	51:1:995:C:N3	2.23	0.53
51:1:1530:G:N2	51:1:1542:U:H1'	2.23	0.53
51:1:1782:U:H2'	51:1:1783:A:H5''	1.90	0.53
51:1:2092:U:C4'	51:1:2093:G:H5''	2.37	0.53
51:1:2297:A:N1	51:1:2321:U:C5	2.75	0.53
51:1:2747:G:O6	51:1:2754:U:H2'	2.09	0.53
53:3:1244:G:H1	53:3:1293:C:H42	1.57	0.53
8:H:133:MET:HE3	8:H:167:TYR:HB2	1.91	0.52
25:Y:66:ILE:HG21	25:Y:70:LYS:HB3	1.91	0.52
39:o:40:ILE:HD12	39:o:44:GLY:HA2	1.91	0.52
42:r:4:VAL:HG12	42:r:13:ARG:HA	1.91	0.52
50:z:36:GLU:O	50:z:37:ARG:NH1	2.42	0.52
51:1:57:C:H2'	51:1:58:G:O4'	2.08	0.52
51:1:1574:C:H2'	51:1:1575:C:H6	1.74	0.52
51:1:1827:U:H2'	51:1:1828:G:H5'	1.90	0.52
51:1:2194:U:H2'	51:1:2195:U:C6	2.44	0.52
51:1:2204:G:H2'	51:1:2205:A:C8	2.44	0.52
58:B1:68:TYR:CA	58:B1:75:TYR:HE2	2.22	0.52
27:b:92:LEU:HD11	27:b:100:ARG:HB3	1.91	0.52
51:1:1278:C:O2'	51:1:1279:G:H5'	2.09	0.52
53:3:1266:G:N2	53:3:1269:A:OP2	2.29	0.52
57:A2:43:LEU:HD13	57:A2:217:ILE:HD11	1.90	0.52
64:6:43:A:H2'	64:6:44:A:C8	2.44	0.52
30:e:91:ARG:NH2	52:2:43:C:O2	2.36	0.52
51:1:519:U:H2'	51:1:520:G:H8	1.75	0.52
51:1:752:A:H62	51:1:2609:U:H3	1.56	0.52
51:1:1111:A:H2'	51:1:1112:G:H4'	1.90	0.52
53:3:203:G:N2	53:3:204:G:O6	2.43	0.52
58:B1:633:ALA:HB2	59:B2:808:ASN:N	2.19	0.52
51:1:1794:A:O2'	51:1:1795:C:H5'	2.10	0.52
51:1:2463:C:O2'	51:1:2464:G:H5'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2758:A:C2'	51:1:2759:G:H5'	2.40	0.52
51:1:2762:C:C2'	51:1:2763:G:H5'	2.39	0.52
58:B1:390:LEU:N	58:B1:390:LEU:CD1	2.73	0.52
1:A:9:TYR:OH	30:e:101:ARG:NH2	2.41	0.52
17:Q:36:VAL:HG21	17:Q:73:LEU:HB3	1.91	0.52
51:1:870:U:O2'	51:1:871:U:H5'	2.10	0.52
51:1:1310:G:H2'	51:1:1311:G:C5'	2.38	0.52
51:1:2670:A:H2'	51:1:2671:G:H8	1.75	0.52
57:A1:205:MET:HE3	57:A1:213:PRO:HB3	1.90	0.52
58:B1:112:ALA:HA	58:B1:238:ILE:HA	1.91	0.52
17:Q:49:ARG:NH1	17:Q:88:ASP:OD2	2.42	0.52
51:1:251:A:H2'	51:1:252:G:O4'	2.10	0.52
51:1:597:G:H2'	51:1:598:U:C6	2.45	0.52
51:1:2102:G:H2'	51:1:2103:C:O4'	2.09	0.52
51:1:2707:U:H2'	51:1:2708:G:C8	2.44	0.52
59:B2:125:GLY:HA2	59:B2:499:SER:HB2	1.92	0.52
26:Z:28:LEU:HA	26:Z:31:VAL:HG12	1.90	0.52
27:b:257:ARG:NH2	27:b:262:THR:OG1	2.42	0.52
42:r:51:VAL:HG22	42:r:52:PRO:HD2	1.92	0.52
42:r:75:VAL:HG23	42:r:86:GLN:HG2	1.90	0.52
46:v:77:VAL:HG23	46:v:89:ILE:HG12	1.92	0.52
51:1:213:A:O2'	51:1:214:G:H5'	2.09	0.52
51:1:2236:U:C2'	51:1:2237:G:H5'	2.39	0.52
51:1:2611:C:O2	51:1:2611:C:C2'	2.58	0.52
51:1:2670:A:H2'	51:1:2671:G:C8	2.45	0.52
58:B1:832:LYS:HB3	58:B1:1242:ARG:NH1	2.24	0.52
7:G:14:HIS:HB3	7:G:42:LEU:HD21	1.91	0.52
7:G:102:ASN:ND2	53:3:1073:U:O2	2.39	0.52
8:H:107:LYS:HB3	8:H:110:LEU:HD23	1.92	0.52
23:W:52:ARG:NH2	53:3:835:U:OP1	2.42	0.52
28:c:23:PRO:HB3	51:1:2682:A:N3	2.24	0.52
51:1:215:G:C4'	51:1:216:A:H4'	2.39	0.52
51:1:729:G:H5''	51:1:730:A:H5''	1.92	0.52
51:1:784:G:C5'	51:1:785:G:OP1	2.54	0.52
51:1:1503:A:C3'	51:1:1504:A:H5''	2.40	0.52
51:1:1507:C:H2'	51:1:1508:A:C4'	2.40	0.52
51:1:1534:U:H2'	51:1:1536:C:O4'	2.10	0.52
51:1:1542:U:O2'	51:1:1543:G:H5'	2.09	0.52
51:1:1558:C:O4'	51:1:1560:G:C8	2.62	0.52
51:1:2216:G:H2'	51:1:2217:G:H8	1.74	0.52
51:1:2625:G:O2'	51:1:2626:C:H5'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:6:9:G:O4'	64:6:46:G:N3	2.42	0.52
9:I:150:LYS:O	9:I:155:LYS:NZ	2.43	0.52
10:J:152:VAL:HG21	13:M:98:LEU:HD13	1.91	0.52
33:i:56:VAL:HB	33:i:68:PHE:HB2	1.92	0.52
51:1:8:C:H2'	51:1:9:G:C8	2.45	0.52
51:1:1403:A:H2'	51:1:1404:C:C6	2.45	0.52
51:1:2570:G:C2'	51:1:2571:U:H5'	2.40	0.52
51:1:2731:G:H2'	51:1:2732:G:C8	2.45	0.52
58:B1:144:TYR:CE1	58:B1:162:GLU:CD	2.88	0.52
35:k:42:THR:HG22	35:k:57:VAL:HG12	1.91	0.52
51:1:1789:A:H2'	51:1:1790:C:O4'	2.09	0.52
51:1:1878:G:O2'	51:1:1879:C:H5'	2.09	0.52
51:1:2013:A:H5''	51:1:2013:A:C8	2.43	0.52
58:B1:209:ASN:HA	58:B1:214:ARG:HH21	1.73	0.52
59:B2:524:ILE:HG21	59:B2:708:VAL:HG13	1.92	0.52
39:o:40:ILE:HG22	39:o:47:VAL:HG12	1.91	0.51
51:1:208:C:O5'	51:1:208:C:H6	1.93	0.51
51:1:1047:G:N2	51:1:1110:G:H2'	2.25	0.51
51:1:1722:A:O2'	51:1:1723:G:H5'	2.10	0.51
57:A2:140:ILE:HD12	57:A2:142:MET:HE3	1.91	0.51
59:B2:786:GLY:N	59:B2:789:THR:OG1	2.41	0.51
62:NG:161:SER:HA	62:NG:170:PRO:HA	1.92	0.51
65:0:267:GLY:HA3	65:0:274:GLY:HA3	1.91	0.51
45:u:73:ASN:ND2	45:u:80:ASP:OD2	2.43	0.51
51:1:386:G:H3'	51:1:387:U:H5''	1.92	0.51
51:1:723:C:O2'	51:1:724:U:H5'	2.09	0.51
51:1:724:U:O2'	51:1:725:G:H5'	2.11	0.51
51:1:1722:A:H62	51:1:1738:G:H1'	1.75	0.51
51:1:2470:G:O2'	51:1:2471:A:H5'	2.10	0.51
51:1:2529:G:H5''	51:1:2530:A:H5''	1.91	0.51
58:B1:99:ARG:HA	58:B1:248:ASP:HB2	1.92	0.51
58:B1:205:LEU:HG	58:B1:217:LEU:HB3	1.90	0.51
65:0:674:THR:O	65:0:677:ARG:HG3	2.11	0.51
14:N:89:TYR:HB3	14:N:93:LEU:HD21	1.92	0.51
15:O:24:GLU:HA	15:O:27:GLU:HB2	1.93	0.51
21:U:6:LEU:HD22	21:U:17:TYR:HB3	1.91	0.51
23:W:71:ASP:N	23:W:71:ASP:OD1	2.44	0.51
36:l:42:SER:HB2	51:1:672:C:H5	1.76	0.51
43:s:67:ASP:OD1	43:s:67:ASP:N	2.39	0.51
44:t:65:GLY:N	44:t:79:ASP:OD1	2.43	0.51
51:1:1112:G:H2'	51:1:1113:U:O4'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1338:G:H2'	51:1:1339:G:H8	1.74	0.51
51:1:1923:U:H2'	51:1:1924:C:C6	2.45	0.51
51:1:2651:C:O2'	51:1:2652:C:H5'	2.10	0.51
53:3:202:G:H1	53:3:215:C:H42	1.57	0.51
58:B1:215:LYS:HA	58:B1:218:THR:HG22	1.91	0.51
3:C:7:LYS:HD3	51:1:2420:C:H5''	1.93	0.51
35:k:31:ARG:NH2	51:1:2676:C:OP2	2.44	0.51
51:1:49:A:O5'	51:1:51:G:H5'	2.09	0.51
51:1:138:U:C5	51:1:139:U:H5	2.27	0.51
51:1:355:U:H2'	51:1:356:G:C8	2.45	0.51
51:1:2776:A:C6	51:1:2782:G:H1'	2.45	0.51
65:0:632:ILE:HD11	65:0:654:ILE:HD12	1.91	0.51
51:1:69:C:H2'	51:1:70:G:C8	2.46	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	1.59	0.51
51:1:800:A:H4'	51:1:801:G:H3'	1.92	0.51
58:B1:99:ARG:HG3	58:B1:99:ARG:HH11	1.73	0.51
58:B1:972:LYS:HD2	58:B1:1004:ALA:HA	1.93	0.51
59:B2:246:LEU:HB3	59:B2:269:ILE:HD13	1.91	0.51
8:H:130:ARG:NH2	8:H:165:GLU:OE1	2.43	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
10:J:106:ALA:O	10:J:111:ARG:NH2	2.43	0.51
21:U:25:ARG:O	53:3:110:C:O2'	2.28	0.51
51:1:286:U:H2'	51:1:287:G:H8	1.76	0.51
51:1:1270:C:H5''	51:1:1271:G:H5''	1.93	0.51
51:1:1678:A:C2'	51:1:1679:A:H5'	2.41	0.51
51:1:1754:A:C6	51:1:1755:A:C6	2.98	0.51
58:B1:111:THR:HG23	58:B1:300:GLN:NE2	2.24	0.51
58:B1:201:LEU:HD12	58:B1:224:LEU:HD12	1.92	0.51
51:1:2105:U:N3	51:1:2184:A:C2	2.78	0.51
51:1:2618:G:H2'	51:1:2619:C:O4'	2.11	0.51
53:3:494:G:H2'	53:3:496:A:H8	1.76	0.51
65:0:647:SER:HA	65:0:652:VAL:HA	1.92	0.51
2:B:2:VAL:HG23	51:1:2015:A:C6	2.46	0.51
15:O:5:ARG:N	15:O:76:ILE:O	2.43	0.51
17:Q:70:GLY:O	17:Q:107:LYS:NZ	2.44	0.51
22:V:60:ILE:HA	22:V:74:LEU:HA	1.93	0.51
27:b:50:THR:HG23	51:1:1813:G:H21	1.76	0.51
51:1:291:G:O2'	51:1:292:U:H5'	2.11	0.51
51:1:707:G:H2'	51:1:708:G:O4'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1175:A:H3'	51:1:1176:U:C5'	2.37	0.51
51:1:1266:G:O2'	51:1:2012:G:O6	2.25	0.51
51:1:2285:C:O2'	51:1:2286:G:H5'	2.11	0.51
58:B1:275:ARG:HH12	58:B1:278:ARG:NH1	2.09	0.51
58:B1:375:GLU:HG2	59:B2:1245:ALA:O	2.10	0.51
58:B1:437:PHE:HZ	58:B1:453:VAL:HG11	1.76	0.51
60:W0:3:ARG:NH1	60:W0:55:GLU:OE2	2.40	0.51
10:J:123:LEU:HD12	53:3:7:A:H2'	1.92	0.51
35:k:75:SER:OG	40:p:72:VAL:O	2.26	0.51
51:1:1415:U:H1'	51:1:1588:G:N2	2.26	0.51
51:1:1441:G:H2'	51:1:1442:U:H6	1.71	0.51
51:1:2525:G:N2	51:1:2539:C:C2	2.79	0.51
53:3:780:A:N6	53:3:801:U:OP2	2.42	0.51
59:B2:93:SER:HA	59:B2:128:PRO:HA	1.92	0.51
27:b:92:LEU:HD21	27:b:100:ARG:HD3	1.93	0.51
37:m:38:ARG:HB3	37:m:98:PRO:HD3	1.92	0.51
51:1:630:G:H4'	51:1:640:C:H4'	1.93	0.51
51:1:891:G:H2'	51:1:892:A:C8	2.46	0.51
51:1:1930:G:C2'	51:1:1931:U:OP2	2.58	0.51
58:B1:683:ILE:HD12	58:B1:754:ILE:HG21	1.92	0.51
59:B2:400:VAL:HG11	59:B2:452:ARG:HD2	1.93	0.51
28:c:176:ASP:OD1	28:c:176:ASP:N	2.44	0.50
51:1:539:G:O2'	51:1:540:C:H5'	2.12	0.50
51:1:1293:C:H2'	51:1:1294:U:C6	2.46	0.50
51:1:2687:U:H2'	51:1:2688:G:O4'	2.11	0.50
53:3:1538:C:O2'	53:3:1539:C:H5'	2.11	0.50
58:B1:749:LYS:HB3	58:B1:755:ILE:HD11	1.94	0.50
59:B2:714:VAL:HB	59:B2:787:PRO:HD2	1.92	0.50
9:I:12:ARG:NH1	9:I:32:LYS:O	2.42	0.50
15:O:29:ALA:O	15:O:33:GLY:N	2.42	0.50
27:b:147:PRO:HG3	27:b:184:GLU:HG2	1.92	0.50
27:b:207:ALA:HB2	51:1:1790:C:O2'	2.12	0.50
38:n:49:GLU:O	38:n:53:THR:OG1	2.29	0.50
48:x:64:ASP:N	48:x:64:ASP:OD1	2.43	0.50
51:1:757:G:C2'	51:1:758:C:H5'	2.38	0.50
51:1:2052:A:C2'	51:1:2053:G:H5'	2.41	0.50
51:1:2555:U:O2	51:1:2555:U:O4'	2.29	0.50
55:8:13:DT:OP2	58:B1:791:ALA:CB	2.59	0.50
4:D:3:ARG:NH1	51:1:752:A:OP1	2.43	0.50
11:K:42:TRP:HB2	11:K:59:TYR:HB2	1.93	0.50
30:e:162:ASP:OD1	30:e:162:ASP:N	2.37	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:145:C:H2'	51:1:146:A:C8	2.46	0.50
51:1:386:G:H3'	51:1:387:U:C5'	2.41	0.50
51:1:1388:G:O2'	51:1:1389:G:H5'	2.12	0.50
51:1:1910:G:H1	51:1:1920:C:H42	1.58	0.50
51:1:2248:C:H2'	51:1:2249:U:H5'	1.93	0.50
53:3:113:G:N3	53:3:353:A:O2'	2.42	0.50
58:B1:505:ASP:OD2	59:B2:812:PHE:HA	2.11	0.50
58:B1:850:LYS:HB2	58:B1:857:LEU:HB2	1.91	0.50
59:B2:255:ILE:HB	59:B2:263:VAL:HB	1.92	0.50
11:K:46:GLN:HA	11:K:56:LYS:HB3	1.94	0.50
30:e:135:ILE:HG23	30:e:140:ILE:HD11	1.93	0.50
51:1:288:U:H2'	51:1:289:G:C8	2.47	0.50
51:1:438:G:H2'	51:1:439:A:H8	1.76	0.50
51:1:439:A:H2'	51:1:440:C:H6	1.75	0.50
51:1:521:U:H2'	51:1:522:A:H8	1.73	0.50
51:1:905:A:H2'	51:1:906:U:C5'	2.40	0.50
51:1:2250:G:H8	51:1:2250:G:O5'	1.95	0.50
51:1:2302:U:O2'	51:1:2303:G:H5'	2.12	0.50
59:B2:400:VAL:HG21	59:B2:452:ARG:HE	1.76	0.50
31:f:136:ASP:HB3	31:f:139:VAL:HG12	1.92	0.50
51:1:187:G:C6	51:1:188:G:N7	2.80	0.50
51:1:1676:A:H8	51:1:1676:A:O5'	1.95	0.50
51:1:2286:G:H21	51:1:2287:A:N6	2.09	0.50
51:1:2593:U:O2'	51:1:2594:C:H5'	2.11	0.50
59:B2:974:ARG:HD2	59:B2:1014:LEU:HD21	1.92	0.50
64:6:9:G:C2	64:6:45:G:C6	3.00	0.50
64:6:9:G:O4'	64:6:46:G:C2	2.65	0.50
4:D:14:ARG:NH1	51:1:1377:G:O3'	2.44	0.50
20:T:2:LEU:HD22	20:T:34:GLN:HB2	1.92	0.50
20:T:23:SER:OG	20:T:25:GLU:OE1	2.30	0.50
27:b:56:GLY:HA2	27:b:212:TRP:HA	1.94	0.50
28:c:161:MET:HE1	51:1:2050:C:O2	2.11	0.50
51:1:197:A:H2	51:1:2434:A:N6	2.10	0.50
51:1:673:C:H2'	51:1:674:G:C5'	2.41	0.50
51:1:1161:C:H2'	51:1:1162:G:C8	2.44	0.50
51:1:2888:C:H2'	51:1:2889:C:H6	1.77	0.50
53:3:460:A:H2'	53:3:461:A:H8	1.75	0.50
53:3:664:G:H22	53:3:741:G:H1	1.60	0.50
63:5:34:G:H3'	63:5:35:A:H8	1.76	0.50
1:A:35:ASP:OD1	1:A:35:ASP:N	2.42	0.50
27:b:146:LYS:HB2	27:b:149:LYS:HB2	1.93	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
51:1:355:U:H2'	51:1:356:G:H8	1.77	0.50
51:1:580:U:O5'	51:1:580:U:H6	1.94	0.50
51:1:928:A:O2'	51:1:929:U:H5'	2.10	0.50
51:1:1345:C:H6	51:1:1345:C:H5'	1.77	0.50
51:1:1409:U:H2'	51:1:1410:G:H8	1.76	0.50
51:1:1416:G:H2'	51:1:1417:C:C6	2.46	0.50
51:1:1593:A:H2'	51:1:1594:U:C6	2.47	0.50
51:1:2734:A:H2'	51:1:2735:G:C5'	2.42	0.50
53:3:517:G:N2	53:3:533:A:OP2	2.33	0.50
58:B1:412:LEU:HD23	58:B1:416:ILE:HG13	1.92	0.50
6:F:19:ARG:HB2	6:F:24:ARG:HD2	1.92	0.50
8:H:4:VAL:HG21	8:H:9:ILE:HD13	1.92	0.50
15:O:39:PRO:HD2	53:3:1123:U:H4'	1.92	0.50
15:O:89:ARG:HH22	62:NG:165:PHE:H	1.60	0.50
51:1:1348:C:C5	51:1:1349:C:C5	3.00	0.50
51:1:1614:A:H2'	51:1:1615:C:H5'	1.94	0.50
51:1:2836:U:H2'	51:1:2837:A:C8	2.47	0.50
58:B1:124:ILE:HG23	58:B1:128:LEU:HD12	1.94	0.50
58:B1:1371:ARG:HE	58:B1:1372:ARG:NH1	2.10	0.50
1:A:37:CYS:O	1:A:41:HIS:N	2.45	0.50
12:L:65:LEU:O	12:L:69:ARG:N	2.43	0.50
21:U:5:ARG:HB3	53:3:376:G:H5''	1.93	0.50
29:d:191:ASP:O	29:d:195:GLN:NE2	2.44	0.50
30:e:84:ILE:HD11	51:1:2311:A:H1'	1.94	0.50
46:v:51:GLN:OE1	46:v:79:ARG:NH2	2.40	0.50
51:1:246:C:H2'	51:1:247:G:C5'	2.40	0.50
51:1:900:A:H2'	51:1:901:C:H5'	1.94	0.50
51:1:1061:U:H4'	51:1:1070:A:H1'	1.93	0.50
51:1:1916:A:H2'	51:1:1917:U:O4'	2.12	0.50
51:1:2815:C:O2'	51:1:2816:G:H5'	2.11	0.50
59:B2:411:ARG:NH2	59:B2:427:ASP:OD2	2.44	0.50
63:5:29:G:H3'	63:5:30:G:H8	1.76	0.50
19:S:68:ARG:NH2	53:3:974:A:OP1	2.45	0.49
27:b:206:LYS:HD2	51:1:729:G:C8	2.46	0.49
43:s:109:ASP:OD1	43:s:109:ASP:N	2.42	0.49
51:1:155:A:H2'	51:1:156:A:H8	1.76	0.49
51:1:1077:A:H8	51:1:1078:U:H1'	1.77	0.49
51:1:1468:U:H2'	51:1:1522:A:N6	2.26	0.49
51:1:1528:A:H2'	51:1:1529:G:O4'	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1717:A:H2'	51:1:1718:G:C5'	2.40	0.49
53:3:928:G:O2'	53:3:1533:C:OP1	2.22	0.49
58:B1:421:VAL:O	58:B1:436:ALA:HA	2.12	0.49
59:B2:9:LYS:HG2	59:B2:1171:ARG:HH12	1.77	0.49
65:0:615:PRO:HG3	65:0:687:TYR:HE1	1.76	0.49
7:G:103:TRP:HA	7:G:106:VAL:HG12	1.93	0.49
13:M:29:SER:OG	13:M:30:LYS:N	2.44	0.49
15:O:42:LEU:HB3	15:O:71:LEU:HB2	1.94	0.49
33:i:110:GLN:HG2	33:i:121:ILE:HD13	1.93	0.49
33:i:126:ARG:HD2	51:1:1080:A:H4'	1.93	0.49
51:1:173:A:H2'	51:1:174:U:C6	2.47	0.49
51:1:898:C:H2'	51:1:899:A:O4'	2.12	0.49
51:1:1144:A:H2'	51:1:1145:C:C6	2.47	0.49
51:1:1645:G:H5''	51:1:1646:C:H5'	1.94	0.49
51:1:2298:A:O2'	51:1:2299:U:H5'	2.12	0.49
59:B2:232:ILE:HG12	59:B2:237:LEU:HG	1.94	0.49
27:b:137:GLY:O	27:b:162:GLN:NE2	2.45	0.49
30:e:27:VAL:O	30:e:29:ARG:NH1	2.41	0.49
51:1:30:G:H2'	51:1:31:C:C6	2.47	0.49
51:1:69:C:O2'	51:1:70:G:H5'	2.13	0.49
51:1:236:C:H2'	51:1:237:C:C6	2.46	0.49
51:1:1087:G:H2'	51:1:1089:A:H5'	1.94	0.49
51:1:2348:U:O2'	51:1:2349:G:H5'	2.12	0.49
51:1:2393:U:H2'	51:1:2394:C:H5'	1.94	0.49
51:1:2634:A:O2'	51:1:2635:A:H5'	2.12	0.49
53:3:481:G:O2'	53:3:483:C:N4	2.46	0.49
53:3:1178:G:N2	53:3:1181:G:OP2	2.43	0.49
58:B1:1179:PRO:HD2	58:B1:1184:ASP:HA	1.93	0.49
7:G:101:THR:HG23	7:G:174:GLU:HG3	1.95	0.49
7:G:221:ARG:HG2	7:G:224:ARG:HH11	1.77	0.49
16:P:96:ILE:HD13	16:P:109:ILE:HD13	1.94	0.49
31:f:41:GLU:HG2	31:f:54:ARG:HH21	1.78	0.49
31:f:163:TYR:HB2	31:f:166:GLU:HB2	1.95	0.49
44:t:7:LEU:HD13	44:t:46:ALA:HA	1.94	0.49
51:1:1119:U:O2'	51:1:1120:G:H5'	2.13	0.49
51:1:1785:A:O2'	51:1:1786:A:H8	1.96	0.49
31:f:87:GLN:NE2	31:f:129:GLU:OE2	2.45	0.49
51:1:16:C:H2'	51:1:17:G:H8	1.78	0.49
51:1:519:U:H2'	51:1:520:G:C8	2.48	0.49
51:1:644:A:H2'	51:1:645:C:C4'	2.42	0.49
51:1:940:G:H2'	51:1:941:A:C5'	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1437:C:H2'	51:1:1438:U:H6	1.78	0.49
51:1:1539:U:H2'	51:1:1540:G:H8	1.76	0.49
51:1:2241:A:O2'	51:1:2242:G:H5'	2.12	0.49
51:1:2257:U:O2'	51:1:2258:C:H5'	2.13	0.49
51:1:2283:C:H2'	51:1:2284:A:O4'	2.11	0.49
51:1:2533:U:H2'	51:1:2534:A:C5'	2.42	0.49
27:b:50:THR:HG23	51:1:1813:G:N2	2.27	0.49
30:e:57:ALA:HB2	30:e:64:PRO:HD3	1.95	0.49
31:f:122:ALA:HB2	31:f:132:LEU:HD23	1.94	0.49
51:1:482:A:H1'	51:1:498:G:N2	2.27	0.49
51:1:898:C:C2'	51:1:899:A:H5'	2.43	0.49
51:1:2281:A:O2'	51:1:2282:G:H5'	2.12	0.49
51:1:2290:G:H2'	51:1:2291:U:H6	1.74	0.49
51:1:2670:A:O2'	51:1:2671:G:H5'	2.12	0.49
17:Q:120:ARG:HH12	53:3:500:G:H5'	1.77	0.49
42:r:68:ARG:O	42:r:90:ARG:NH2	2.46	0.49
51:1:262:A:H2'	51:1:263:G:O4'	2.12	0.49
51:1:367:G:H2'	51:1:368:A:O4'	2.13	0.49
51:1:886:A:C5	51:1:887:U:H1'	2.47	0.49
51:1:1400:U:H2'	51:1:1401:G:H8	1.78	0.49
57:A1:18:GLN:HA	57:A1:24:ALA:HA	1.94	0.49
58:B1:220:ARG:HG2	58:B1:220:ARG:NH1	2.25	0.49
7:G:18:GLN:HG3	7:G:189:ASN:CB	2.41	0.49
12:L:2:ARG:NH2	53:3:933:G:O6	2.45	0.49
14:N:94:ARG:HG2	14:N:97:LEU:HD12	1.95	0.49
29:d:77:ILE:HG23	51:1:1256:G:N2	2.26	0.49
48:x:1:SER:O	48:x:49:ARG:NH1	2.46	0.49
51:1:131:A:H2'	51:1:132:G:H8	1.77	0.49
51:1:840:C:O2'	51:1:841:G:H5'	2.12	0.49
58:B1:115:TRP:O	58:B1:1333:THR:HG21	2.13	0.49
59:B2:529:ARG:HH11	59:B2:572:ILE:HG22	1.77	0.49
9:I:153:ARG:NH2	53:3:435:A:N3	2.61	0.49
21:U:36:VAL:HG12	21:U:53:ASP:HB3	1.94	0.49
28:c:81:GLU:HG3	51:1:2636:C:O5'	2.13	0.49
33:i:20:SER:H	33:i:21:PRO:HD2	1.78	0.49
33:i:79:LEU:HD13	33:i:132:ALA:HB2	1.94	0.49
41:q:103:VAL:HA	41:q:106:THR:HG22	1.94	0.49
44:t:70:HIS:N	44:t:73:ARG:O	2.44	0.49
51:1:609:A:H2'	51:1:610:C:O4'	2.11	0.49
51:1:841:G:C2	51:1:938:G:C2	3.01	0.49
51:1:1117:C:H2'	51:1:1118:C:H6	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1668:A:N3	51:1:1670:C:N4	2.60	0.49
51:1:1910:G:N2	51:1:1911:U:C2	2.81	0.49
53:3:1137:C:H4'	53:3:1138:G:H5'	1.94	0.49
58:B1:145:VAL:HG12	58:B1:184:ALA:HB1	1.94	0.49
58:B1:902:ASP:HB3	58:B1:905:ARG:HB2	1.93	0.49
59:B2:554:HIS:HD2	59:B2:558:VAL:HB	1.77	0.49
65:0:616:ILE:HB	65:0:686:LYS:HE3	1.95	0.49
14:N:91:GLU:HA	14:N:94:ARG:HB2	1.94	0.49
28:c:56:LYS:NZ	51:1:2830:C:H5''	2.28	0.49
33:i:85:ILE:HD12	33:i:97:VAL:HG12	1.95	0.49
37:m:74:THR:HG21	37:m:86:LYS:HG2	1.94	0.49
51:1:67:U:H2'	51:1:68:G:H8	1.77	0.49
51:1:1534:U:H4'	51:1:1535:A:N1	2.27	0.49
51:1:1796:U:H2'	51:1:1797:G:C8	2.45	0.49
51:1:2843:G:O2'	51:1:2844:G:H5'	2.13	0.49
38:n:8:ARG:HH21	38:n:43:GLU:HG3	1.77	0.48
51:1:118:A:H2'	51:1:120:U:O4	2.13	0.48
51:1:898:C:O2'	51:1:899:A:H5'	2.13	0.48
51:1:1111:A:H2'	51:1:1111:A:N3	2.28	0.48
51:1:1537:G:H3'	51:1:1537:G:N3	2.28	0.48
51:1:2050:C:N4	51:1:2051:A:C6	2.81	0.48
51:1:2126:A:H5'	51:1:2127:G:O5'	2.13	0.48
51:1:2510:C:N4	51:1:2511:U:C4	2.81	0.48
53:3:890:G:O2'	53:3:906:A:N6	2.46	0.48
53:3:1064:G:O2'	53:3:1190:G:N2	2.46	0.48
59:B2:836:LEU:HD13	59:B2:1054:LEU:HD13	1.95	0.48
9:I:93:LEU:O	9:I:99:ASN:ND2	2.39	0.48
25:Y:59:ARG:O	25:Y:63:LYS:N	2.46	0.48
51:1:78:U:H2'	51:1:79:C:H6	1.77	0.48
51:1:121:G:H4'	51:1:149:A:H5'	1.95	0.48
51:1:129:C:H2'	51:1:130:C:H6	1.79	0.48
51:1:1084:A:O2'	51:1:1105:U:H4'	2.12	0.48
51:1:1536:C:H5''	51:1:1537:G:C4	2.48	0.48
51:1:2208:C:H2'	51:1:2209:G:C8	2.48	0.48
55:8:3:DC:H2''	55:8:4:DT:C7	2.42	0.48
17:Q:97:VAL:HG12	17:Q:99:GLY:H	1.78	0.48
27:b:70:LYS:O	27:b:117:SER:OG	2.30	0.48
51:1:54:G:H2'	51:1:55:G:O4'	2.12	0.48
51:1:360:U:H2'	51:1:361:G:C1'	2.43	0.48
51:1:473:G:O2'	51:1:474:G:H5'	2.14	0.48
51:1:572:A:H8	51:1:572:A:O5'	1.97	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:706:A:H2'	51:1:707:G:H5'	1.95	0.48
51:1:1680:U:O2'	51:1:1681:G:H5'	2.13	0.48
51:1:2180:U:O2'	51:1:2181:U:H5'	2.13	0.48
51:1:2367:G:O2'	51:1:2368:C:H5'	2.13	0.48
52:2:51:G:H22	52:2:53:A:H62	1.61	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
17:Q:110:LYS:HG3	17:Q:121:PRO:HG3	1.94	0.48
25:Y:53:MET:HE2	25:Y:57:VAL:HG21	1.94	0.48
35:k:5:GLN:HE21	51:1:1668:A:H5''	1.78	0.48
51:1:214:G:H2'	51:1:215:G:C8	2.48	0.48
51:1:286:U:H2'	51:1:287:G:C8	2.47	0.48
51:1:1742:U:O2'	51:1:1743:G:H5'	2.14	0.48
51:1:1748:C:H2'	51:1:1749:A:C8	2.47	0.48
51:1:2214:C:H2'	51:1:2215:C:O4'	2.14	0.48
51:1:2329:U:H2'	51:1:2330:G:H8	1.78	0.48
53:3:673:A:H2'	53:3:674:G:C8	2.49	0.48
58:B1:809:VAL:HG21	58:B1:909:ILE:HG12	1.95	0.48
58:B1:968:ASN:HA	58:B1:1117:SER:HB2	1.96	0.48
59:B2:18:ARG:HE	59:B2:620:ASN:HA	1.77	0.48
59:B2:533:LEU:HD13	59:B2:540:ARG:HH21	1.77	0.48
12:L:41:ILE:HD11	53:3:1240:U:H5'	1.94	0.48
29:d:143:LEU:HD13	29:d:146:VAL:HG11	1.94	0.48
45:u:88:ASP:OD1	45:u:88:ASP:N	2.43	0.48
51:1:217:A:H2'	51:1:218:A:O4'	2.13	0.48
51:1:488:G:H22	51:1:491:G:H5''	1.77	0.48
51:1:553:G:H2'	51:1:554:U:O4'	2.13	0.48
51:1:1087:G:O6	51:1:1089:A:C2	2.67	0.48
51:1:2649:C:O2'	51:1:2650:U:H5'	2.13	0.48
53:3:1531:A:O2'	53:3:1532:U:H5'	2.14	0.48
57:A1:100:LEU:HB2	57:A1:144:ILE:HG23	1.94	0.48
59:B2:857:VAL:HG13	59:B2:919:ARG:HH21	1.78	0.48
63:5:51:U:H2'	63:5:52:G:C8	2.48	0.48
6:F:6:SER:O	6:F:6:SER:OG	2.31	0.48
42:r:71:LYS:HA	42:r:90:ARG:HG2	1.95	0.48
51:1:92:U:H2'	51:1:93:G:H5'	1.96	0.48
51:1:481:G:C2'	51:1:482:A:OP2	2.61	0.48
51:1:1871:A:H2'	51:1:1872:A:O4'	2.13	0.48
53:3:880:C:H2'	53:3:881:G:H8	1.78	0.48
14:N:10:ARG:NH2	53:3:1119:C:OP2	2.46	0.48
17:Q:82:ARG:O	17:Q:95:HIS:N	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:55:HIS:HA	26:Z:58:LYS:HD2	1.95	0.48
51:1:718:A:H2'	51:1:719:C:O4'	2.12	0.48
51:1:2016:U:O5'	51:1:2016:U:H6	1.97	0.48
51:1:2828:G:O2'	51:1:2829:A:H5'	2.13	0.48
58:B1:102:MET:HG2	58:B1:246:PRO:HD3	1.94	0.48
58:B1:201:LEU:HD11	58:B1:220:ARG:HG2	1.95	0.48
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE21	1.68	0.48
64:6:50:U:H2'	64:6:51:C:C5	2.49	0.48
32:g:8:LYS:HD3	32:g:14:SER:HA	1.96	0.48
38:n:100:CYS:H	38:n:111:ALA:HA	1.79	0.48
49:y:16:THR:O	49:y:20:ASN:ND2	2.46	0.48
51:1:415:A:H2'	51:1:416:U:C6	2.49	0.48
51:1:596:U:C2	51:1:662:G:N2	2.82	0.48
51:1:852:U:H2'	51:1:853:C:C6	2.49	0.48
51:1:1807:G:C2'	51:1:1808:A:H5'	2.29	0.48
51:1:2547:A:H61	51:1:2561:U:H3	1.62	0.48
53:3:38:G:H22	53:3:397:A:H5'	1.78	0.48
55:8:14:DC:H2'	55:8:15:DC:C6	2.48	0.48
58:B1:190:LYS:HB2	58:B1:190:LYS:HE3	1.41	0.48
58:B1:1036:ARG:HE	58:B1:1081:VAL:HG11	1.79	0.48
59:B2:400:VAL:HG22	59:B2:584:TYR:HB3	1.96	0.48
62:NG:161:SER:CA	62:NG:170:PRO:HA	2.43	0.48
14:N:44:ARG:O	14:N:47:VAL:HG22	2.13	0.48
14:N:86:LEU:HD12	14:N:97:LEU:HD11	1.95	0.48
36:l:129:LYS:HG2	51:1:636:G:OP1	2.14	0.48
39:o:15:ARG:NH2	52:2:8:C:OP1	2.47	0.48
51:1:555:G:O2'	51:1:556:A:H8	1.96	0.48
51:1:1464:G:H2'	51:1:1465:G:C8	2.49	0.48
51:1:1465:G:H2'	51:1:1466:U:O4'	2.13	0.48
51:1:2527:C:O2'	51:1:2528:U:H5'	2.13	0.48
53:3:401:C:O2'	53:3:621:A:N3	2.45	0.48
53:3:776:G:N2	53:3:802:A:OP2	2.39	0.48
58:B1:255:LEU:HD23	58:B1:261:ALA:HB2	1.95	0.48
58:B1:891:ASP:OD2	58:B1:1290:ARG:NH2	2.47	0.48
59:B2:732:ILE:HD11	59:B2:769:PRO:HB3	1.95	0.48
59:B2:895:LEU:HD12	59:B2:899:GLU:HB3	1.95	0.48
29:d:149:ILE:HD11	29:d:172:ALA:HA	1.96	0.48
31:f:16:VAL:HA	31:f:25:ILE:HG12	1.96	0.48
51:1:275:C:C3'	51:1:276:U:H5''	2.40	0.48
51:1:476:G:H4'	51:1:502:A:N1	2.28	0.48
51:1:820:A:H2'	51:1:821:A:O4'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:854:C:H2'	51:1:855:G:H8	1.79	0.48
51:1:1387:A:C5'	51:1:1469:A:H1'	2.38	0.48
51:1:2660:A:N6	65:0:672:SER:HB2	2.29	0.48
53:3:898:G:N2	53:3:901:A:OP2	2.46	0.48
58:B1:108:ALA:HB1	58:B1:279:LEU:HD22	1.96	0.48
63:5:50:U:H2'	63:5:51:U:C6	2.49	0.48
27:b:152:GLN:HB3	51:1:1818:U:N3	2.29	0.47
29:d:48:THR:OG1	29:d:49:ARG:N	2.47	0.47
29:d:119:ILE:HB	29:d:187:VAL:HG12	1.96	0.47
40:p:2:ASN:HD21	51:1:2876:G:H4'	1.79	0.47
51:1:2098:U:H2'	51:1:2099:U:O4'	2.14	0.47
51:1:2149:U:H2'	51:1:2150:C:C6	2.49	0.47
51:1:2286:G:H21	51:1:2287:A:H61	1.62	0.47
53:3:1305:G:N2	53:3:1331:G:H2'	2.29	0.47
58:B1:103:GLY:H	58:B1:244:VAL:HG22	1.79	0.47
58:B1:550:VAL:O	58:B1:569:LEU:HA	2.13	0.47
58:B1:1146:GLU:OE2	58:B1:1310:THR:HG22	2.14	0.47
12:L:112:ASP:HB2	12:L:118:ARG:HG2	1.97	0.47
17:Q:70:GLY:O	17:Q:98:ARG:NH2	2.47	0.47
28:c:190:LYS:HE2	51:1:2729:G:H4'	1.95	0.47
32:g:47:PHE:HA	32:g:51:ARG:HB2	1.96	0.47
33:i:54:ILE:HD12	33:i:73:PRO:HD3	1.95	0.47
40:p:59:THR:HG22	40:p:72:VAL:HG12	1.95	0.47
42:r:7:SER:OG	42:r:8:GLY:N	2.47	0.47
47:w:29:ALA:N	47:w:60:ASP:OD1	2.48	0.47
51:1:5:A:H2'	51:1:6:A:C8	2.49	0.47
51:1:40:U:H2'	51:1:41:C:H6	1.78	0.47
51:1:813:U:C2	51:1:1195:G:N2	2.83	0.47
51:1:1026:G:OP2	51:1:1134:A:H1'	2.13	0.47
51:1:2362:C:O5'	51:1:2362:C:H6	1.96	0.47
53:3:1223:C:H5'	53:3:1224:U:H5''	1.96	0.47
58:B1:1060:VAL:HG13	58:B1:1106:ILE:HG12	1.96	0.47
20:T:38:LEU:HD22	20:T:55:LEU:HD13	1.96	0.47
21:U:18:GLN:HA	21:U:38:PHE:HA	1.95	0.47
27:b:131:MET:HE2	27:b:187:CYS:HB2	1.96	0.47
51:1:107:G:O2'	51:1:108:G:H5'	2.14	0.47
51:1:554:U:O2'	51:1:555:G:H5'	2.13	0.47
51:1:762:U:N3	51:1:1431:A:OP1	2.47	0.47
51:1:1463:C:H2'	51:1:1464:G:C8	2.49	0.47
51:1:2156:G:C3'	51:1:2157:G:H5'	2.44	0.47
51:1:2899:A:H2'	51:1:2900:A:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:816:A:OP1	53:3:1526:G:O2'	2.28	0.47
58:B1:375:GLU:HB3	59:B2:1245:ALA:HB3	1.97	0.47
58:B1:1347:LEU:HG	58:B1:1357:ILE:HG23	1.96	0.47
59:B2:1311:GLY:O	60:W0:31:GLN:NE2	2.47	0.47
59:B2:1314:GLN:HB2	60:W0:28:ARG:HH12	1.79	0.47
65:0:12:ASN:HB2	65:0:107:ASP:OD2	2.14	0.47
27:b:156:SER:OG	27:b:157:ALA:N	2.44	0.47
31:f:133:LYS:NZ	31:f:134:GLY:O	2.44	0.47
31:f:174:LYS:HD2	31:f:176:LYS:HB2	1.96	0.47
45:u:39:ASN:HB3	45:u:62:ALA:HB3	1.95	0.47
51:1:143:C:H2'	51:1:144:A:C8	2.49	0.47
51:1:1019:U:N3	51:1:1142:A:N6	2.57	0.47
51:1:1067:A:H2'	51:1:1068:G:C8	2.49	0.47
51:1:2298:A:C2'	51:1:2299:U:H5'	2.45	0.47
51:1:2626:C:H2'	51:1:2627:G:H8	1.80	0.47
51:1:2895:G:H2'	51:1:2896:C:C6	2.49	0.47
53:3:768:A:N3	53:3:1512:U:O2'	2.46	0.47
58:B1:395:LYS:NZ	58:B1:399:LYS:CE	2.77	0.47
58:B1:1221:LEU:HD22	58:B1:1306:LEU:HB2	1.96	0.47
59:B2:565:GLU:HA	59:B2:569:ILE:HG12	1.95	0.47
18:R:15:VAL:HG11	18:R:30:LYS:HG2	1.97	0.47
28:c:13:ARG:NH2	40:p:74:GLN:OE1	2.43	0.47
47:w:19:VAL:HA	47:w:34:VAL:HG22	1.97	0.47
51:1:712:G:H2'	51:1:713:G:H5'	1.96	0.47
51:1:1257:C:O5'	51:1:1257:C:H6	1.97	0.47
51:1:1464:G:H2'	51:1:1465:G:H8	1.78	0.47
51:1:1922:G:H2'	51:1:1923:U:C6	2.50	0.47
51:1:2455:G:C6	51:1:2456:C:N4	2.83	0.47
53:3:358:U:H2'	53:3:359:G:H8	1.78	0.47
57:A1:182:ARG:O	57:A1:205:MET:HA	2.14	0.47
58:B1:1357:ILE:HD13	59:B2:1279:GLU:HG2	1.97	0.47
59:B2:207:THR:OG1	59:B2:354:ASP:OD2	2.32	0.47
5:E:5:THR:HG22	5:E:62:PRO:HD2	1.97	0.47
15:O:58:ASN:ND2	53:3:1061:G:O2'	2.45	0.47
31:f:88:LEU:HD21	31:f:104:LEU:HD23	1.97	0.47
51:1:551:G:O2'	51:1:552:U:H5'	2.15	0.47
51:1:1098:A:O2'	51:1:1099:G:H5'	2.15	0.47
57:A1:59:VAL:HG22	57:A1:144:ILE:HA	1.97	0.47
58:B1:1261:LEU:HD12	58:B1:1304:ARG:HH21	1.78	0.47
59:B2:103:VAL:HG12	59:B2:117:ILE:HG22	1.97	0.47
4:D:29:GLN:O	4:D:29:GLN:NE2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:159:GLU:HA	9:I:162:GLU:HB2	1.97	0.47
12:L:107:ALA:HA	12:L:122:GLU:HG3	1.95	0.47
12:L:149:ALA:HB1	16:P:58:THR:HG21	1.97	0.47
21:U:25:ARG:NH1	53:3:230:G:O2'	2.48	0.47
28:c:136:ASN:OD1	51:1:2579:C:O2'	2.32	0.47
46:v:79:ARG:HA	46:v:86:LEU:HA	1.95	0.47
51:1:283:G:C2'	51:1:284:U:H5'	2.45	0.47
51:1:368:A:H2'	51:1:369:U:C5'	2.39	0.47
51:1:1020:A:C1'	51:1:1021:A:OP2	2.61	0.47
51:1:1367:A:H3'	51:1:1368:G:O4'	2.15	0.47
51:1:1435:G:O2'	51:1:1436:G:H5'	2.15	0.47
51:1:1702:G:H2'	51:1:1703:G:C5'	2.35	0.47
51:1:1726:C:H2'	51:1:1727:C:C6	2.50	0.47
51:1:1729:U:H5	51:1:1731:G:N2	2.12	0.47
51:1:2155:U:H2'	51:1:2156:G:O4'	2.15	0.47
51:1:2194:U:O2'	51:1:2195:U:H5'	2.14	0.47
51:1:2395:C:H2'	51:1:2396:G:O4'	2.15	0.47
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
51:1:2625:G:H2'	51:1:2626:C:H6	1.76	0.47
53:3:944:G:N1	53:3:1338:G:OP2	2.34	0.47
58:B1:43:THR:HG22	58:B1:57:PHE:HE1	1.80	0.47
58:B1:526:VAL:HG12	58:B1:549:LYS:HB2	1.96	0.47
16:P:34:THR:OG1	16:P:35:ASP:N	2.47	0.47
19:S:32:ASP:O	19:S:34:ASN:ND2	2.48	0.47
43:s:72:THR:OG1	43:s:73:LYS:N	2.48	0.47
45:u:6:ARG:HB2	51:1:85:G:P	2.55	0.47
51:1:297:G:H2'	51:1:298:G:O4'	2.14	0.47
51:1:877:A:O2'	51:1:878:A:H5''	2.14	0.47
51:1:1219:U:O2'	51:1:1220:G:H5'	2.15	0.47
51:1:1517:G:O2'	51:1:1518:C:H5'	2.15	0.47
51:1:2563:U:H2'	51:1:2565:A:OP2	2.15	0.47
58:B1:141:PHE:HE2	58:B1:296:LYS:CB	2.22	0.47
58:B1:1361:THR:OG1	59:B2:1282:GLY:O	2.28	0.47
63:5:8:U:H2'	63:5:13:C:N4	2.30	0.47
51:1:149:A:H2'	51:1:150:U:C6	2.49	0.47
51:1:466:A:H2'	51:1:467:G:C5'	2.44	0.47
51:1:900:A:C2'	51:1:901:C:H5'	2.45	0.47
51:1:979:A:H2'	51:1:982:C:H42	1.80	0.47
51:1:1068:G:H2'	51:1:1069:A:H4'	1.96	0.47
51:1:1297:C:H2'	51:1:1298:C:H6	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1400:U:H2'	51:1:1401:G:C8	2.50	0.47
51:1:1491:G:H2'	51:1:1492:G:H8	1.80	0.47
51:1:1873:G:O2'	51:1:1874:C:H5'	2.15	0.47
51:1:1922:G:O2'	51:1:1923:U:H5'	2.15	0.47
51:1:2180:U:H2'	51:1:2181:U:O4'	2.14	0.47
51:1:2259:U:H2'	51:1:2260:C:O4'	2.15	0.47
51:1:2581:G:H2'	51:1:2581:G:N3	2.30	0.47
53:3:617:G:H1	53:3:623:C:H42	1.63	0.47
57:A2:64:VAL:HG11	57:A2:78:ILE:HG21	1.97	0.47
58:B1:352:ARG:HB2	59:B2:1268:GLN:NE2	2.30	0.47
58:B1:420:PRO:HA	58:B1:437:PHE:O	2.15	0.47
59:B2:689:ALA:HB2	59:B2:1233:LEU:HD23	1.97	0.47
64:6:48:C:H5''	64:6:50:U:OP1	2.15	0.47
9:I:171:GLU:HB3	9:I:180:THR:HG22	1.97	0.47
12:L:79:VAL:HB	12:L:84:TYR:HD2	1.80	0.47
31:f:100:ASN:OD1	31:f:100:ASN:N	2.47	0.47
33:i:115:ASP:OD2	51:1:1059:G:H4'	2.14	0.47
46:v:83:LYS:HB3	46:v:85:LYS:HZ3	1.79	0.47
51:1:435:C:C2'	51:1:436:C:H5'	2.44	0.47
51:1:686:U:H6	51:1:788:A:H61	1.61	0.47
51:1:708:G:H2'	51:1:709:U:C6	2.50	0.47
51:1:859:G:C2'	51:1:860:U:OP2	2.62	0.47
51:1:1209:U:O3'	51:1:1212:G:H5'	2.15	0.47
51:1:1267:U:H2'	51:1:1267:U:O2	2.14	0.47
51:1:1913:A:C8	53:3:1494:G:H4'	2.50	0.47
51:1:2295:C:O2'	51:1:2296:U:H5'	2.15	0.47
51:1:2858:C:H2'	51:1:2859:G:O4'	2.15	0.47
7:G:129:THR:HB	7:G:132:GLU:HB2	1.96	0.46
18:R:7:ASN:HD22	18:R:20:SER:HB2	1.80	0.46
20:T:37:HIS:HD2	20:T:38:LEU:HD12	1.80	0.46
27:b:184:GLU:HG3	27:b:186:ASP:H	1.80	0.46
39:o:68:LYS:HE3	52:2:49:C:H5''	1.97	0.46
51:1:214:G:O2'	51:1:215:G:H5'	2.14	0.46
51:1:570:G:H5'	51:1:983:A:C2	2.51	0.46
51:1:1036:G:O2'	51:1:1037:G:H5'	2.15	0.46
51:1:1465:G:HO2'	51:1:1466:U:H5'	1.80	0.46
51:1:1480:C:H2'	51:1:1481:U:C6	2.49	0.46
51:1:1536:C:H5''	51:1:1537:G:C5	2.50	0.46
51:1:2047:C:O5'	51:1:2047:C:H6	1.98	0.46
51:1:2241:A:H2'	51:1:2242:G:C8	2.50	0.46
51:1:2360:G:H2'	51:1:2361:G:C5'	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:410:G:H21	53:3:432:A:H62	1.62	0.46
53:3:1225:A:H2'	53:3:1225:A:N3	2.29	0.46
58:B1:833:GLU:N	58:B1:1242:ARG:HH12	2.12	0.46
58:B1:1150:PRO:HG3	58:B1:1214:PRO:HB2	1.97	0.46
48:x:14:GLY:HA3	48:x:28:PHE:HE1	1.81	0.46
51:1:156:A:H2'	51:1:157:C:C6	2.50	0.46
51:1:389:G:O2'	51:1:390:U:H5'	2.15	0.46
51:1:1141:U:H4'	51:1:1142:A:C1'	2.45	0.46
51:1:1146:C:O2'	51:1:1147:A:H5'	2.16	0.46
51:1:1389:G:C2	51:1:1390:U:C2	3.02	0.46
51:1:1516:G:O2'	51:1:1517:G:H5'	2.15	0.46
51:1:1528:A:H2'	51:1:1529:G:C5'	2.44	0.46
51:1:1851:U:OP1	64:6:4:G:H4'	2.15	0.46
51:1:2496:C:H2'	51:1:2497:A:O4'	2.16	0.46
53:3:459:A:H2'	53:3:460:A:C8	2.50	0.46
59:B2:28:LEU:HD21	59:B2:524:ILE:HG13	1.98	0.46
65:0:93:VAL:HA	65:0:96:THR:HG23	1.97	0.46
65:0:97:ILE:HD11	65:0:411:PHE:HD1	1.80	0.46
35:k:47:ILE:HG22	35:k:49:ARG:H	1.80	0.46
36:l:39:LYS:HG2	51:1:832:U:OP1	2.15	0.46
46:v:26:PHE:HE2	46:v:89:ILE:HG13	1.80	0.46
51:1:93:G:O2'	51:1:94:A:H5'	2.16	0.46
51:1:536:G:H2'	51:1:537:G:C5'	2.43	0.46
51:1:1874:C:H2'	51:1:1875:G:O4'	2.15	0.46
51:1:2290:G:O2'	51:1:2291:U:H5'	2.16	0.46
51:1:2350:C:H2'	51:1:2351:G:O4'	2.16	0.46
53:3:512:U:H2'	53:3:513:C:C6	2.50	0.46
53:3:959:A:O2'	53:3:984:C:O2'	2.24	0.46
53:3:1035:A:H1'	53:3:1036:A:O5'	2.16	0.46
58:B1:29:MET:HG2	59:B2:1336:ASN:ND2	2.29	0.46
59:B2:363:LEU:HB3	59:B2:381:ALA:HB1	1.96	0.46
59:B2:562:GLU:OE1	59:B2:662:SER:OG	2.28	0.46
10:J:73:VAL:HG11	10:J:143:LEU:HB3	1.98	0.46
27:b:145:MET:HE1	51:1:1800:C:H2'	1.98	0.46
31:f:29:ASN:ND2	31:f:80:GLU:O	2.48	0.46
34:j:65:THR:HG22	51:1:1141:U:OP2	2.15	0.46
49:y:15:ASN:OD1	49:y:16:THR:N	2.48	0.46
51:1:30:G:C5	51:1:31:C:C4	3.03	0.46
51:1:289:G:H2'	51:1:290:U:C6	2.50	0.46
51:1:554:U:C2'	51:1:555:G:H5'	2.46	0.46
51:1:595:C:C2	51:1:596:U:C5	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:848:C:H2'	51:1:849:A:C8	2.51	0.46
51:1:1509:A:H2'	51:1:1510:G:C8	2.49	0.46
51:1:1768:C:H42	51:1:1984:G:H1	1.62	0.46
51:1:1923:U:O2'	51:1:1924:C:H5'	2.16	0.46
57:A1:35:PHE:HA	57:A1:38:THR:HG22	1.97	0.46
58:B1:105:ILE:HD12	58:B1:242:LEU:CD2	2.44	0.46
58:B1:128:LEU:HD21	58:B1:188:LEU:HB3	1.97	0.46
62:NG:135:ARG:O	62:NG:178:VAL:HA	2.16	0.46
63:5:34:G:H3'	63:5:35:A:C8	2.50	0.46
2:B:31:LYS:HG2	51:1:2885:G:N2	2.31	0.46
11:K:3:HIS:HA	11:K:65:GLU:HA	1.97	0.46
11:K:10:VAL:HG23	11:K:58:HIS:HB3	1.97	0.46
11:K:41:ASP:OD1	11:K:58:HIS:NE2	2.39	0.46
16:P:124:LYS:HB3	26:Z:34:ARG:HB3	1.98	0.46
23:W:33:THR:OG1	23:W:34:GLU:N	2.49	0.46
29:d:132:LYS:HG2	29:d:136:GLN:HE22	1.81	0.46
33:i:112:LYS:HD2	33:i:128:ILE:HD12	1.97	0.46
51:1:28:A:O2'	51:1:29:U:H5'	2.16	0.46
51:1:44:A:H2'	51:1:45:G:O4'	2.15	0.46
51:1:637:A:C6	51:1:652:U:H4'	2.50	0.46
51:1:688:U:H5'	51:1:1780:A:C2	2.51	0.46
51:1:853:C:O2'	51:1:854:C:H5'	2.16	0.46
51:1:1090:A:C2	51:1:1102:C:H1'	2.50	0.46
51:1:1117:C:H2'	51:1:1118:C:C6	2.50	0.46
51:1:1173:U:C6	51:1:1174:U:H1'	2.51	0.46
51:1:1183:U:H2'	51:1:1184:U:H6	1.80	0.46
51:1:1210:G:P	51:1:1212:G:H5'	2.56	0.46
51:1:1572:A:H2'	51:1:1573:G:O4'	2.16	0.46
51:1:2294:G:O2'	51:1:2295:C:H5'	2.15	0.46
55:8:14:DC:H2'	55:8:15:DC:H6	1.79	0.46
58:B1:209:ASN:HA	58:B1:214:ARG:NH2	2.30	0.46
58:B1:352:ARG:CD	59:B2:1268:GLN:NE2	2.67	0.46
22:V:10:ARG:NE	22:V:55:GLY:O	2.48	0.46
27:b:131:MET:H	27:b:131:MET:HG2	1.57	0.46
31:f:87:GLN:HB3	31:f:162:ARG:HG3	1.96	0.46
34:j:2:LYS:HA	51:1:995:C:C4	2.50	0.46
51:1:538:A:O2'	51:1:539:G:H5'	2.14	0.46
51:1:1285:A:H2'	51:1:1286:A:H5'	1.96	0.46
51:1:1574:C:H2'	51:1:1575:C:C6	2.50	0.46
51:1:1927:A:H2'	51:1:1928:A:C8	2.50	0.46
51:1:2247:A:H2'	51:1:2248:C:H6	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2329:U:H2'	51:1:2330:G:C8	2.51	0.46
51:1:2642:G:O5'	51:1:2642:G:H8	1.98	0.46
59:B2:517:GLN:HB3	59:B2:760:ASN:H	1.79	0.46
59:B2:1286:THR:O	59:B2:1290:MET:HB2	2.14	0.46
63:5:8:U:H2'	63:5:13:C:H41	1.81	0.46
63:5:26:A:H61	63:5:44:G:H22	1.64	0.46
4:D:12:ARG:NH1	51:1:465:G:OP1	2.49	0.46
8:H:171:ARG:HG2	8:H:173:PRO:HD3	1.96	0.46
27:b:1:ALA:N	27:b:19:VAL:O	2.41	0.46
36:l:69:ARG:NH1	51:1:2406:A:C2	2.84	0.46
51:1:1090:A:H61	51:1:1101:U:H3	1.62	0.46
51:1:1105:U:H2'	51:1:1106:G:H8	1.80	0.46
51:1:1863:G:H2'	51:1:1864:U:C6	2.51	0.46
51:1:2836:U:H2'	51:1:2837:A:H8	1.81	0.46
55:8:20:DA:H4'	59:B2:143:ARG:NH1	2.31	0.46
57:A1:212:ASP:OD1	57:A1:212:ASP:N	2.48	0.46
59:B2:230:PHE:HB2	59:B2:333:ILE:HB	1.97	0.46
59:B2:318:SER:OG	59:B2:320:ASP:OD1	2.31	0.46
59:B2:1002:LEU:HD21	59:B2:1007:LYS:HB2	1.98	0.46
65:0:27:THR:HA	65:0:30:ILE:HD12	1.96	0.46
65:0:648:GLU:H	65:0:648:GLU:HG3	1.57	0.46
26:Z:29:ALA:O	26:Z:32:ARG:NH1	2.49	0.46
33:i:79:LEU:HD21	33:i:105:LEU:HD21	1.96	0.46
33:i:109:ALA:HA	33:i:112:LYS:HB2	1.98	0.46
39:o:29:HIS:HB3	39:o:36:TYR:HB2	1.98	0.46
40:p:52:ARG:HH21	51:1:2720:U:H5''	1.80	0.46
51:1:290:U:O2'	51:1:291:G:H5'	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
51:1:1520:U:H2'	51:1:1521:G:O4'	2.16	0.46
51:1:1869:G:H3'	51:1:1870:C:C5'	2.38	0.46
51:1:2679:A:O2'	51:1:2680:U:H5'	2.15	0.46
51:1:2783:U:H2'	51:1:2784:U:C6	2.51	0.46
51:1:2813:A:O2'	51:1:2814:A:H5'	2.15	0.46
57:A2:294:ASN:HA	61:NA:464:ILE:N	2.28	0.46
59:B2:735:LYS:HA	59:B2:748:ILE:HG22	1.97	0.46
7:G:65:LYS:HE2	7:G:65:LYS:HB2	1.78	0.46
9:I:114:ARG:HA	9:I:117:VAL:HG22	1.98	0.46
15:O:100:ILE:O	62:NG:170:PRO:O	2.34	0.46
31:f:106:LEU:O	31:f:151:ARG:NH2	2.37	0.46
51:1:338:G:O2'	51:1:339:U:H5'	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:409:G:H2'	51:1:410:G:C8	2.51	0.46
51:1:438:G:O2'	51:1:439:A:H5'	2.16	0.46
51:1:1710:G:H2'	51:1:1711:A:C8	2.51	0.46
51:1:1930:G:O2'	51:1:1931:U:OP2	2.33	0.46
51:1:2315:G:H2'	51:1:2316:G:H8	1.80	0.46
51:1:2339:C:H2'	51:1:2340:A:H8	1.81	0.46
57:A2:102:LEU:HD12	57:A2:115:ILE:HG12	1.96	0.46
58:B1:198:CYS:HA	58:B1:221:ILE:CD1	2.45	0.46
58:B1:772:TYR:HE2	59:B2:561:ILE:HG21	1.80	0.46
58:B1:1167:LYS:NZ	58:B1:1170:LYS:HB2	2.30	0.46
16:P:127:ARG:HB2	26:Z:34:ARG:HH22	1.81	0.46
21:U:70:ARG:O	21:U:74:LEU:N	2.47	0.46
22:V:11:VAL:HG13	22:V:58:VAL:HG21	1.98	0.46
31:f:90:GLY:HA2	31:f:159:LYS:HG2	1.98	0.46
51:1:342:A:H2'	51:1:343:C:O4'	2.16	0.46
51:1:848:C:H2'	51:1:849:A:H8	1.80	0.46
51:1:1486:U:O2'	51:1:1487:U:H5'	2.14	0.46
55:8:13:DT:C6	58:B1:791:ALA:HA	2.51	0.46
57:A1:231:PHE:O	57:A2:218:ARG:NH1	2.49	0.46
58:B1:1219:ASP:O	58:B1:1223:LEU:HB2	2.15	0.46
63:5:6:G:H2'	63:5:7:A:C8	2.51	0.46
8:H:152:VAL:HG12	8:H:197:VAL:HG22	1.98	0.45
12:L:142:ARG:HH21	64:6:42:G:H4'	1.81	0.45
17:Q:45:ASN:ND2	17:Q:88:ASP:OD2	2.39	0.45
28:c:170:VAL:HG21	51:1:2679:A:H5'	1.97	0.45
29:d:32:VAL:HG21	36:l:6:LEU:HD13	1.99	0.45
35:k:70:ARG:NH1	51:1:2684:U:O4'	2.49	0.45
43:s:82:MET:HE1	51:1:1322:A:H5''	1.98	0.45
51:1:360:U:H2'	51:1:361:G:H1'	1.98	0.45
51:1:607:U:O4	51:1:620:G:H5'	2.17	0.45
51:1:1170:C:H2'	51:1:1171:G:C8	2.51	0.45
51:1:1381:G:H2'	51:1:1382:G:H5'	1.98	0.45
51:1:2141:G:H1	51:1:2151:U:H3	1.63	0.45
51:1:2648:G:C2	51:1:2649:C:C2	3.04	0.45
59:B2:712:SER:OG	59:B2:713:GLY:N	2.49	0.45
65:0:574:MET:HE1	65:0:601:PHE:CE2	2.50	0.45
12:L:142:ARG:HA	12:L:145:GLU:HG3	1.97	0.45
14:N:11:ARG:NH2	53:3:1347:G:O6	2.49	0.45
17:Q:72:ASN:HD21	17:Q:103:CYS:HA	1.81	0.45
31:f:1:SER:HA	51:1:2749:A:OP1	2.15	0.45
35:k:5:GLN:NE2	51:1:1668:A:H5''	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:t:34:VAL:HG21	44:t:43:ILE:HD11	1.99	0.45
47:w:37:ARG:HA	47:w:37:ARG:HD3	1.70	0.45
51:1:6:A:H2'	51:1:7:G:C8	2.52	0.45
51:1:466:A:C2'	51:1:467:G:H5'	2.46	0.45
51:1:569:U:H1'	51:1:947:A:O4'	2.16	0.45
51:1:1288:G:C5	51:1:1327:A:C2	3.04	0.45
51:1:1550:C:O2'	51:1:1551:A:H5'	2.16	0.45
51:1:2743:U:H2'	51:1:2744:G:O4'	2.16	0.45
58:B1:375:GLU:O	59:B2:1247:SER:HB3	2.16	0.45
60:W0:25:ARG:NH1	60:W0:61:ASN:OD1	2.49	0.45
63:5:55:U:O2	63:5:57:G:H1'	2.17	0.45
13:M:83:ARG:NH2	53:3:587:G:OP1	2.44	0.45
18:R:16:ILE:O	18:R:19:THR:OG1	2.26	0.45
33:i:106:GLN:OE1	33:i:125:THR:OG1	2.31	0.45
34:j:108:MET:CE	51:1:1138:G:H21	2.29	0.45
37:m:34:LYS:N	37:m:129:THR:O	2.47	0.45
41:q:82:LEU:HD22	41:q:87:VAL:HB	1.98	0.45
49:y:6:LEU:HD13	49:y:56:LEU:HD22	1.98	0.45
51:1:1087:G:H22	51:1:1103:A:H1'	1.76	0.45
51:1:1287:A:O2'	51:1:1288:G:H5'	2.15	0.45
51:1:1488:C:H2'	51:1:1489:C:C6	2.51	0.45
51:1:2661:G:O2'	51:1:2662:A:H5'	2.16	0.45
57:A2:80:GLU:HG3	59:B2:694:ARG:HH22	1.81	0.45
58:B1:201:LEU:HD11	58:B1:220:ARG:NH1	2.32	0.45
58:B1:515:ARG:NH2	58:B1:718:SER:O	2.48	0.45
64:6:7:G:H3'	64:6:49:G:OP2	2.16	0.45
7:G:166:ASP:HB3	7:G:190:SER:HB2	1.98	0.45
18:R:97:ARG:HB2	18:R:99:GLN:HE22	1.81	0.45
28:c:4:LEU:HD11	28:c:100:LEU:HD21	1.98	0.45
48:x:30:PRO:HG2	48:x:32:LEU:HD11	1.98	0.45
51:1:30:G:H2'	51:1:31:C:O4'	2.17	0.45
51:1:438:G:H2'	51:1:439:A:C8	2.51	0.45
51:1:1605:C:H2'	51:1:1606:C:H5'	1.98	0.45
53:3:1200:C:H5''	53:3:1201:A:H3'	1.97	0.45
53:3:1383:C:H4'	64:6:35:A:H2	1.81	0.45
55:8:1:DC:H2''	55:8:2:DC:C6	2.51	0.45
58:B1:67:ASP:OD1	58:B1:67:ASP:O	2.35	0.45
58:B1:115:TRP:HB3	58:B1:1333:THR:CG2	2.46	0.45
59:B2:24:VAL:HG11	59:B2:704:MET:HE1	1.99	0.45
7:G:8:MET:HE3	7:G:8:MET:HB3	1.84	0.45
7:G:142:LYS:NZ	53:3:1098:C:OP1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:172:ILE:O	7:G:176:ASN:ND2	2.50	0.45
10:J:101:GLY:H	10:J:121:ASN:HB3	1.82	0.45
12:L:70:PRO:HG3	12:L:98:LEU:HD23	1.97	0.45
19:S:58:ARG:HH21	53:3:980:C:H4'	1.81	0.45
51:1:1049:C:C2'	51:1:1050:A:H5'	2.47	0.45
51:1:1140:C:C2'	51:1:1141:U:H5'	2.47	0.45
51:1:1140:C:H2'	51:1:1141:U:H5'	1.97	0.45
51:1:1239:G:O2'	51:1:1240:U:H5'	2.17	0.45
51:1:1866:A:H2'	51:1:1867:G:O4'	2.16	0.45
51:1:1952:A:H2'	51:1:1953:A:C8	2.51	0.45
51:1:2314:A:H2'	51:1:2315:G:H8	1.78	0.45
51:1:2364:C:O2'	51:1:2365:G:H5'	2.17	0.45
51:1:2528:U:O2'	51:1:2529:G:H3'	2.16	0.45
51:1:2741:A:H2'	51:1:2742:G:H5'	1.98	0.45
53:3:618:C:N4	53:3:621:A:OP2	2.49	0.45
58:B1:842:ARG:HH22	58:B1:1250:ASP:HB2	1.80	0.45
58:B1:1158:GLU:HA	58:B1:1223:LEU:HD21	1.99	0.45
11:K:75:GLU:O	11:K:79:ARG:N	2.47	0.45
29:d:136:GLN:HA	29:d:139:LYS:HE2	1.99	0.45
35:k:121:GLU:HG2	35:k:122:VAL:HG23	1.97	0.45
45:u:32:LYS:HG2	45:u:65:GLN:HA	1.99	0.45
51:1:540:C:O2'	51:1:541:A:H5'	2.16	0.45
51:1:707:G:C2'	51:1:708:G:H5'	2.47	0.45
51:1:1324:G:O2'	51:1:1326:U:OP2	2.29	0.45
51:1:1412:U:H2'	51:1:1413:A:H8	1.81	0.45
51:1:1868:C:H2'	51:1:1869:G:C8	2.52	0.45
51:1:2030:A:N3	51:1:2499:C:H5''	2.31	0.45
51:1:2849:U:H4'	51:1:2868:A:C2	2.51	0.45
53:3:765:G:H1	53:3:812:G:HO2'	1.63	0.45
53:3:1376:U:H2'	53:3:1377:A:C8	2.52	0.45
58:B1:395:LYS:HZ2	58:B1:399:LYS:CE	2.28	0.45
2:B:4:GLN:HG3	51:1:2054:A:C2	2.52	0.45
8:H:5:HIS:CE1	8:H:7:ASN:HB3	2.51	0.45
9:I:13:ARG:NH1	53:3:542:G:O3'	2.50	0.45
12:L:137:ARG:NH1	12:L:138:GLU:OE2	2.48	0.45
27:b:257:ARG:HH22	27:b:262:THR:HG1	1.62	0.45
41:q:111:LYS:HA	41:q:111:LYS:HD2	1.81	0.45
51:1:111:A:O2'	51:1:112:U:H5'	2.17	0.45
51:1:167:A:H2'	51:1:168:G:O4'	2.16	0.45
51:1:893:C:H2'	51:1:894:U:O4'	2.17	0.45
51:1:1766:G:C2'	51:1:1767:G:H5'	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2636:C:O2'	51:1:2637:U:H5'	2.16	0.45
51:1:2651:C:H2'	51:1:2652:C:H6	1.81	0.45
54:4:44:G:OP1	59:B2:1073:LYS:NZ	2.35	0.45
58:B1:128:LEU:CD2	58:B1:188:LEU:HB3	2.47	0.45
58:B1:213:LYS:CA	58:B1:213:LYS:HE3	2.47	0.45
58:B1:343:LEU:HD11	58:B1:1324:SER:HB3	1.98	0.45
58:B1:478:LEU:HD21	60:W0:47:THR:HG23	1.99	0.45
59:B2:674:ASP:OD2	59:B2:1070:HIS:ND1	2.50	0.45
59:B2:900:LYS:HE3	59:B2:900:LYS:HB3	1.62	0.45
63:5:22:G:H2'	63:5:23:A:C8	2.52	0.45
65:0:473:MET:HE3	65:0:473:MET:HB3	1.87	0.45
2:B:8:THR:OG1	2:B:9:ARG:N	2.49	0.45
9:I:173:ASP:HB3	9:I:178:GLU:HB3	1.98	0.45
17:Q:23:LEU:HD12	17:Q:29:LYS:HD2	1.97	0.45
45:u:12:VAL:HA	45:u:69:VAL:HG12	1.99	0.45
51:1:395:U:H2'	51:1:396:G:C8	2.52	0.45
51:1:1071:G:HO2'	51:1:1089:A:H2'	1.81	0.45
51:1:1710:G:O2'	51:1:1711:A:H5'	2.17	0.45
51:1:2047:C:O2'	51:1:2048:G:H5'	2.16	0.45
51:1:2717:C:N3	51:1:2718:G:N7	2.65	0.45
58:B1:484:MET:CE	59:B2:1278:LEU:HD21	2.46	0.45
59:B2:557:ARG:NH2	59:B2:607:SER:O	2.49	0.45
9:I:120:LYS:HG2	9:I:130:ASN:HB3	1.99	0.45
15:O:29:ALA:HB2	15:O:87:LEU:HD11	1.99	0.45
28:c:106:LYS:HA	28:c:176:ASP:HA	1.99	0.45
33:i:49:GLU:OE1	33:i:81:LYS:NZ	2.41	0.45
51:1:195:A:H3'	51:1:196:A:H4'	1.99	0.45
51:1:367:G:O2'	51:1:368:A:H5'	2.17	0.45
51:1:432:A:O2'	51:1:433:C:H5'	2.17	0.45
51:1:500:G:N2	51:1:502:A:H3'	2.32	0.45
51:1:854:C:H2'	51:1:855:G:C8	2.52	0.45
51:1:1344:U:H3'	51:1:1345:C:H5'	1.97	0.45
51:1:1832:C:O5'	51:1:1832:C:H6	2.00	0.45
51:1:1882:U:O2'	51:1:1883:U:H5'	2.17	0.45
51:1:2085:U:O2'	51:1:2086:U:H5'	2.16	0.45
51:1:2626:C:H2'	51:1:2627:G:C8	2.51	0.45
53:3:477:C:H2'	53:3:478:A:C8	2.52	0.45
55:8:16:DT:H2'	55:8:17:DC:C6	2.52	0.45
58:B1:76:LYS:NZ	58:B1:76:LYS:HB3	2.32	0.45
58:B1:211:GLU:CG	58:B1:215:LYS:HE3	2.44	0.45
58:B1:472:LEU:CD1	59:B2:1294:LYS:HG2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:926:PRO:HB2	58:B1:1241:TYR:HE1	1.82	0.45
59:B2:1314:GLN:HA	60:W0:28:ARG:HH22	1.80	0.45
9:I:1:ALA:N	53:3:405:U:O4	2.45	0.45
11:K:5:GLU:HB2	11:K:90:MET:HB2	1.98	0.45
33:i:8:VAL:HG11	33:i:26:ALA:HB2	1.98	0.45
51:1:974:G:H1'	51:1:975:A:C8	2.52	0.45
51:1:1020:A:C2	51:1:1141:U:C2	3.05	0.45
51:1:1338:G:H2'	51:1:1339:G:C8	2.51	0.45
51:1:1915:U:O2	51:1:1915:U:O4'	2.34	0.45
51:1:2137:U:H2'	51:1:2138:G:C8	2.50	0.45
51:1:2700:A:O2'	51:1:2701:U:H5'	2.17	0.45
51:1:2844:G:H2'	51:1:2845:U:O4'	2.16	0.45
53:3:647:C:H2'	53:3:648:A:H8	1.81	0.45
58:B1:33:TRP:HZ2	59:B2:1336:ASN:OD1	2.00	0.45
58:B1:68:TYR:O	58:B1:75:TYR:CD2	2.70	0.45
58:B1:109:SER:HB2	58:B1:296:LYS:HG2	1.98	0.45
58:B1:395:LYS:NZ	58:B1:399:LYS:CD	2.74	0.45
59:B2:176:ILE:HD11	59:B2:428:VAL:HG21	1.98	0.45
7:G:26:MET:HE1	7:G:186:VAL:HB	1.99	0.44
7:G:33:ALA:HB3	7:G:37:VAL:HG12	1.99	0.44
7:G:65:LYS:HG2	7:G:153:MET:HG3	1.98	0.44
10:J:110:MET:HE3	10:J:110:MET:HB2	1.79	0.44
18:R:107:THR:OG1	53:3:947:G:O3'	2.35	0.44
21:U:79:ASN:HB2	21:U:82:ALA:HB3	1.99	0.44
28:c:151:THR:O	51:1:1130:U:C4	2.70	0.44
33:i:135:MET:CE	51:1:1062:G:H21	2.30	0.44
40:p:88:ARG:HH11	40:p:114:ASN:HD21	1.65	0.44
51:1:545:U:O2	51:1:546:U:H1'	2.17	0.44
51:1:1749:A:H2'	51:1:1750:G:H8	1.82	0.44
51:1:1800:C:O2	51:1:1802:A:C8	2.70	0.44
51:1:2122:U:H2'	51:1:2123:G:O4'	2.17	0.44
51:1:2402:U:O2'	51:1:2403:C:H3'	2.17	0.44
51:1:2889:C:O2'	51:1:2890:G:H5'	2.17	0.44
53:3:112:G:N2	53:3:354:G:O5'	2.49	0.44
53:3:1253:G:H2'	53:3:1254:A:C8	2.52	0.44
58:B1:201:LEU:CB	58:B1:221:ILE:HD13	2.47	0.44
58:B1:395:LYS:NZ	58:B1:399:LYS:HE2	2.32	0.44
58:B1:770:LEU:HD13	59:B2:618:GLN:CD	2.42	0.44
58:B1:804:ALA:HB2	58:B1:1256:ILE:CD1	2.48	0.44
58:B1:1357:ILE:HG22	58:B1:1359:ALA:H	1.82	0.44
7:G:173:LYS:HE3	7:G:173:LYS:HB2	1.76	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:134:LYS:HG2	8:H:138:GLN:HE21	1.82	0.44
51:1:208:C:O2'	51:1:209:C:H5'	2.18	0.44
51:1:354:A:H2'	51:1:355:U:O4'	2.17	0.44
51:1:696:G:H2'	51:1:697:G:O4'	2.18	0.44
51:1:1747:U:H2'	51:1:1748:C:C6	2.53	0.44
51:1:1807:G:H2'	51:1:1808:A:C5'	2.30	0.44
51:1:2658:C:H2'	51:1:2659:G:O4'	2.16	0.44
51:1:2869:G:H2'	51:1:2870:C:O4'	2.17	0.44
53:3:146:G:N2	53:3:177:G:N7	2.66	0.44
53:3:1498:U:H4'	53:3:1519:A:H2	1.82	0.44
58:B1:201:LEU:CD1	58:B1:224:LEU:HD12	2.47	0.44
58:B1:1227:HIS:HA	58:B1:1230:THR:HG22	1.99	0.44
59:B2:998:LEU:HG	59:B2:1011:LEU:HB3	1.99	0.44
14:N:104:THR:HG23	53:3:1180:A:H5'	1.99	0.44
18:R:1:ALA:HB3	18:R:56:ARG:HH22	1.82	0.44
29:d:68:ALA:HA	51:1:1255:U:C6	2.52	0.44
34:j:34:ARG:NH2	34:j:39:LYS:O	2.51	0.44
38:n:65:LEU:HD11	51:1:2870:C:H5''	1.99	0.44
45:u:17:ASP:HA	45:u:20:LYS:HE2	2.00	0.44
51:1:239:C:H2'	51:1:240:C:O4'	2.16	0.44
51:1:355:U:H6	51:1:355:U:O5'	1.99	0.44
51:1:639:U:H2'	51:1:640:C:C6	2.52	0.44
51:1:654:A:N3	51:1:654:A:H5''	2.31	0.44
51:1:1680:U:C2'	51:1:1681:G:H5'	2.47	0.44
51:1:1922:G:H2'	51:1:1923:U:O4'	2.18	0.44
51:1:2101:A:H2'	51:1:2102:G:H8	1.81	0.44
51:1:2201:G:H2'	51:1:2202:U:O4'	2.17	0.44
51:1:2805:C:O2'	51:1:2806:C:H5'	2.18	0.44
52:2:66:A:H4'	52:2:67:G:C8	2.53	0.44
57:A1:185:TYR:HA	57:A1:202:VAL:O	2.16	0.44
59:B2:1246:ARG:HH11	59:B2:1266:GLY:HA2	1.82	0.44
64:6:11:A:H2'	64:6:12:G:C8	2.52	0.44
6:F:8:LYS:NZ	51:1:2467:C:OP1	2.37	0.44
9:I:47:LEU:HD23	9:I:47:LEU:HA	1.85	0.44
11:K:62:MET:HB3	11:K:64:VAL:HG13	1.98	0.44
31:f:132:LEU:HB3	31:f:140:ILE:HD11	1.99	0.44
51:1:150:U:H2'	51:1:151:C:C6	2.52	0.44
51:1:720:U:H2'	51:1:721:A:H8	1.82	0.44
51:1:1500:G:O2'	51:1:1501:G:H5'	2.16	0.44
51:1:2236:U:H2'	51:1:2237:G:C5'	2.46	0.44
58:B1:141:PHE:CE2	58:B1:296:LYS:CB	2.94	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:245:LEU:CG	58:B1:246:PRO:HD2	2.47	0.44
58:B1:385:LEU:HD23	58:B1:390:LEU:HB2	1.98	0.44
58:B1:388:ARG:HG2	58:B1:388:ARG:NH1	2.32	0.44
65:0:370:LYS:HE3	65:0:370:LYS:HB3	1.82	0.44
14:N:119:LYS:NZ	53:3:1350:A:N7	2.64	0.44
28:c:150:GLN:HE22	51:1:2032:G:H1'	1.82	0.44
33:i:9:LYS:HD2	51:1:1061:U:OP1	2.18	0.44
48:x:51:SER:OG	48:x:54:GLY:N	2.48	0.44
51:1:293:U:H2'	51:1:294:A:H5''	1.99	0.44
51:1:704:G:H1'	51:1:727:A:H62	1.83	0.44
51:1:1280:G:C2'	51:1:1281:G:H5'	2.46	0.44
51:1:1465:G:O2'	51:1:1466:U:H5'	2.17	0.44
51:1:1670:C:O2'	51:1:1671:U:H5'	2.16	0.44
51:1:1672:A:N3	51:1:2582:G:H5'	2.27	0.44
51:1:2204:G:H2'	51:1:2205:A:H8	1.81	0.44
58:B1:75:TYR:CD2	58:B1:75:TYR:O	2.70	0.44
58:B1:375:GLU:HB3	59:B2:1245:ALA:CB	2.48	0.44
58:B1:506:VAL:HG23	58:B1:628:GLY:HA3	1.99	0.44
8:H:37:LYS:HD3	8:H:37:LYS:HA	1.81	0.44
14:N:74:GLN:OE1	53:3:1249:C:O2'	2.35	0.44
29:d:188:MET:HB2	29:d:192:ALA:HB3	1.99	0.44
30:e:71:LYS:HA	30:e:71:LYS:HD2	1.79	0.44
47:w:12:SER:OG	47:w:13:GLU:N	2.51	0.44
49:y:20:ASN:HA	49:y:23:ARG:HB2	1.99	0.44
51:1:29:U:O5'	51:1:29:U:H6	2.00	0.44
51:1:336:C:O2'	51:1:337:C:H5'	2.18	0.44
63:5:49:C:H2'	63:5:50:U:C6	2.52	0.44
19:S:44:VAL:O	19:S:48:GLN:NE2	2.50	0.44
33:i:131:THR:HB	51:1:1060:U:O4	2.18	0.44
41:q:47:ARG:NH2	41:q:51:GLN:OE1	2.51	0.44
51:1:163:C:O2'	51:1:164:C:H5'	2.17	0.44
51:1:350:G:H2'	51:1:351:C:O4'	2.18	0.44
51:1:518:G:O2'	51:1:519:U:H5'	2.18	0.44
51:1:648:G:H2'	51:1:649:G:H8	1.83	0.44
51:1:721:A:H2'	51:1:722:A:C8	2.53	0.44
51:1:940:G:H3'	51:1:941:A:H5''	1.97	0.44
51:1:1010:A:H1'	51:1:1153:C:H1'	2.00	0.44
51:1:1199:U:H2'	51:1:1200:C:C6	2.52	0.44
51:1:1507:C:H2'	51:1:1508:A:H4'	1.99	0.44
51:1:1717:A:C2	51:1:1718:G:H1'	2.53	0.44
51:1:2880:C:H2'	51:1:2880:C:O2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:490:C:H2'	53:3:491:G:C8	2.53	0.44
58:B1:894:VAL:HG22	58:B1:1258:ARG:HH11	1.83	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
25:Y:49:ALA:HA	25:Y:52:GLU:HG3	2.00	0.44
32:g:28:ASN:ND2	51:1:2092:U:OP2	2.36	0.44
34:j:85:LYS:NZ	51:1:2768:U:OP1	2.49	0.44
51:1:12:U:O2	51:1:12:U:H2'	2.18	0.44
51:1:28:A:H2'	51:1:29:U:C6	2.53	0.44
51:1:169:G:O2'	51:1:170:U:H5'	2.18	0.44
51:1:859:G:HO2'	51:1:860:U:P	2.41	0.44
51:1:1539:U:H2'	51:1:1540:G:C8	2.53	0.44
52:2:39:A:O2'	52:2:46:A:N1	2.46	0.44
53:3:75:G:H2'	53:3:76:G:C8	2.53	0.44
53:3:1013:G:N2	53:3:1016:A:OP2	2.35	0.44
57:A1:78:ILE:HA	57:A1:81:ILE:HG22	2.00	0.44
58:B1:282:LEU:HA	58:B1:282:LEU:HD12	1.79	0.44
65:0:580:PHE:HD2	65:0:581:GLY:N	2.16	0.44
9:I:85:THR:HA	9:I:88:ASN:HB2	2.00	0.44
17:Q:3:VAL:HA	17:Q:6:LEU:HD12	2.00	0.44
24:X:76:THR:OG1	24:X:77:ARG:N	2.51	0.44
25:Y:67:HIS:O	25:Y:69:ASN:ND2	2.51	0.44
29:d:147:LEU:HD11	29:d:170:ARG:HG2	1.98	0.44
30:e:122:ASP:OD2	30:e:126:ASN:ND2	2.42	0.44
36:l:95:LEU:HD22	36:l:100:ILE:HD11	2.00	0.44
49:y:19:LEU:HA	49:y:19:LEU:HD23	1.86	0.44
51:1:161:A:C5	51:1:162:U:H5	2.36	0.44
51:1:684:G:C2	51:1:794:A:C2	3.06	0.44
51:1:1383:A:H2	51:1:1406:U:H1'	1.83	0.44
51:1:1507:C:H2'	51:1:1508:A:O4'	2.18	0.44
51:1:1625:C:H2'	51:1:1626:A:O4'	2.18	0.44
51:1:2312:U:O2'	51:1:2313:C:H5'	2.17	0.44
51:1:2411:A:H2'	51:1:2412:A:C8	2.53	0.44
53:3:162:A:C5	53:3:163:C:H1'	2.53	0.44
53:3:958:A:N3	53:3:985:C:O2'	2.48	0.44
58:B1:1033:GLY:HA3	58:B1:1081:VAL:O	2.18	0.44
59:B2:805:MET:HE3	59:B2:805:MET:HB2	1.86	0.44
59:B2:811:ASN:ND2	59:B2:1098:LEU:O	2.51	0.44
60:W0:58:LEU:HD12	60:W0:59:ILE:HG12	2.00	0.44
63:5:69:G:H2'	63:5:70:G:C8	2.52	0.44
7:G:67:LEU:HD21	7:G:91:VAL:HG23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:88:MET:HE3	15:O:88:MET:HB3	1.70	0.43
18:R:43:LYS:HB2	18:R:46:GLU:HG2	1.99	0.43
42:r:19:THR:OG1	42:r:95:ASP:OD1	2.35	0.43
46:v:62:THR:O	46:v:62:THR:OG1	2.35	0.43
50:z:30:ARG:HG2	50:z:33:HIS:HB2	1.99	0.43
50:z:37:ARG:HA	50:z:37:ARG:HD3	1.83	0.43
50:z:38:GLU:CD	51:1:928:A:H5'	2.43	0.43
51:1:192:C:H2'	51:1:193:U:H5'	1.99	0.43
51:1:1452:G:H2'	51:1:1453:A:OP2	2.17	0.43
51:1:1565:C:C5	51:1:1567:G:C6	3.06	0.43
53:3:908:A:H2'	53:3:909:A:H8	1.83	0.43
58:B1:1026:PRO:HB2	58:B1:1028:ILE:HG23	2.00	0.43
59:B2:538:LEU:HD13	59:B2:543:ALA:HB2	2.00	0.43
62:NG:161:SER:CB	62:NG:170:PRO:HA	2.47	0.43
8:H:134:LYS:HB3	8:H:134:LYS:HE2	1.84	0.43
11:K:38:ARG:HH11	11:K:61:LEU:HD21	1.83	0.43
12:L:113:LYS:HB3	53:3:1297:G:H21	1.82	0.43
14:N:105:ARG:NH1	14:N:109:GLN:OE1	2.49	0.43
30:e:171:ALA:C	30:e:173:ASP:H	2.26	0.43
33:i:123:ALA:HB1	51:1:1081:U:H4'	2.00	0.43
35:k:38:ILE:HG22	35:k:61:VAL:HB	2.01	0.43
42:r:80:ARG:HD3	51:1:566:U:O4	2.17	0.43
51:1:43:G:H2'	51:1:44:A:C8	2.53	0.43
51:1:107:G:H2'	51:1:108:G:H8	1.82	0.43
51:1:198:C:N4	51:1:248:G:H1	2.14	0.43
51:1:819:A:H5'	51:1:973:A:N1	2.33	0.43
51:1:1571:A:H2'	51:1:1572:A:C8	2.54	0.43
51:1:2241:A:H2'	51:1:2242:G:H8	1.82	0.43
53:3:1053:G:H4'	53:3:1054:C:H3'	2.00	0.43
58:B1:161:THR:H	58:B1:164:GLN:HB2	1.82	0.43
63:5:63:G:H2'	63:5:64:A:C8	2.53	0.43
2:B:8:THR:HG23	2:B:11:LYS:H	1.81	0.43
8:H:51:VAL:HA	8:H:69:THR:HG22	2.01	0.43
10:J:104:ILE:HD11	10:J:114:LEU:HD13	1.99	0.43
22:V:44:HIS:HB3	22:V:70:LYS:HG2	1.99	0.43
25:Y:14:GLU:OE1	25:Y:17:ARG:NH2	2.51	0.43
34:j:51:GLY:HA3	34:j:121:LYS:HE2	2.00	0.43
51:1:30:G:O2'	51:1:31:C:H5'	2.17	0.43
51:1:108:G:O2'	51:1:109:C:H5'	2.18	0.43
51:1:150:U:O2'	51:1:151:C:H5'	2.18	0.43
51:1:388:G:N7	51:1:390:U:H2'	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1049:C:H2'	51:1:1050:A:H5'	2.00	0.43
51:1:2152:G:N3	51:1:2152:G:H2'	2.33	0.43
51:1:2285:C:C2'	51:1:2286:G:H5'	2.48	0.43
51:1:2834:G:C2'	51:1:2835:A:H5'	2.49	0.43
58:B1:287:ALA:HB1	58:B1:288:PRO:HD2	1.99	0.43
58:B1:731:ARG:HB3	59:B2:1105:SER:HB2	2.00	0.43
58:B1:847:ASP:N	58:B1:847:ASP:OD1	2.49	0.43
58:B1:978:ARG:HD3	58:B1:999:TYR:H	1.83	0.43
59:B2:800:MET:HE3	59:B2:800:MET:HB2	1.69	0.43
21:U:31:ARG:HB2	53:3:310:G:H5''	2.01	0.43
27:b:140:VAL:HG12	27:b:191:LEU:HD23	2.01	0.43
51:1:1232:G:H2'	51:1:1233:C:C6	2.53	0.43
51:1:1739:A:H2'	51:1:1740:G:O4'	2.19	0.43
51:1:2671:G:C2	51:1:2672:U:C2	3.06	0.43
58:B1:213:LYS:HE3	58:B1:213:LYS:HA	1.99	0.43
63:5:13:C:H42	63:5:46:G:N2	2.16	0.43
2:B:4:GLN:NE2	51:1:2056:G:O2'	2.52	0.43
9:I:152:SER:HB3	53:3:436:C:H4'	2.00	0.43
17:Q:72:ASN:OD1	17:Q:72:ASN:N	2.50	0.43
18:R:104:ASN:HB3	18:R:105:ALA:H	1.69	0.43
21:U:28:ARG:NH1	53:3:390:U:O2'	2.46	0.43
27:b:153:LEU:HD23	51:1:1799:G:N2	2.33	0.43
28:c:62:LYS:NZ	51:1:2810:A:H5''	2.34	0.43
33:i:127:SER:OG	51:1:1059:G:N2	2.51	0.43
37:m:96:ILE:HA	37:m:96:ILE:HD13	1.83	0.43
38:n:39:PRO:HG2	51:1:1651:G:H4'	2.01	0.43
51:1:68:G:H2'	51:1:69:C:O4'	2.18	0.43
51:1:528:A:C2	51:1:2043:C:H4'	2.53	0.43
51:1:1520:U:C2'	51:1:1521:G:H5'	2.49	0.43
51:1:2106:U:H2'	51:1:2107:G:O4'	2.18	0.43
51:1:2226:C:C5	51:1:2227:A:N7	2.86	0.43
53:3:1513:A:H2'	53:3:1514:G:H8	1.83	0.43
56:9:12:DC:H3'	58:B1:47:ARG:HH12	1.83	0.43
1:A:62:LYS:HE3	1:A:62:LYS:HB3	1.89	0.43
8:H:5:HIS:HE1	8:H:7:ASN:HB3	1.82	0.43
8:H:76:ILE:HB	8:H:80:GLY:HA2	2.00	0.43
10:J:28:ARG:NH2	53:3:1397:C:OP2	2.38	0.43
10:J:146:MET:HE2	10:J:146:MET:HB3	1.75	0.43
18:R:28:ARG:HH21	18:R:62:PHE:HB2	1.84	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:s:28:LYS:HE2	43:s:28:LYS:HB2	1.90	0.43
43:s:74:ILE:HB	43:s:105:VAL:HG23	1.99	0.43
45:u:76:THR:HB	45:u:78:LYS:HE3	1.99	0.43
48:x:36:ARG:NH2	51:1:2200:C:OP2	2.52	0.43
51:1:327:G:H2'	51:1:328:U:O4'	2.18	0.43
51:1:473:G:C2'	51:1:474:G:H5'	2.48	0.43
51:1:1433:A:H2'	51:1:1434:A:C1'	2.49	0.43
51:1:1893:C:C2'	51:1:1894:C:H5'	2.47	0.43
51:1:1998:A:O2'	51:1:1999:C:H5'	2.18	0.43
51:1:2736:A:O2'	51:1:2737:G:H5'	2.19	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
53:3:490:C:H2'	53:3:491:G:H8	1.84	0.43
53:3:560:A:H5''	53:3:561:U:H5'	2.00	0.43
53:3:1200:C:O2'	53:3:1205:U:O4	2.35	0.43
55:8:12:DG:OP1	58:B1:795:TYR:CE1	2.71	0.43
57:A1:192:VAL:HG12	57:A1:193:GLU:H	1.83	0.43
58:B1:62:PHE:CD1	58:B1:62:PHE:N	2.86	0.43
58:B1:513:MET:HG3	58:B1:544:LEU:HD11	2.01	0.43
65:0:545:ILE:HD11	65:0:581:GLY:HA3	2.00	0.43
11:K:47:LEU:HG	11:K:56:LYS:HA	2.01	0.43
24:X:27:LYS:HE2	24:X:27:LYS:HB3	1.77	0.43
27:b:20:ASN:HB3	27:b:23:LEU:HD13	2.00	0.43
29:d:127:GLU:O	29:d:156:ASN:ND2	2.51	0.43
34:j:47:HIS:CG	51:1:536:G:N2	2.87	0.43
34:j:47:HIS:CG	51:1:536:G:H21	2.37	0.43
36:l:69:ARG:CZ	51:1:2406:A:N3	2.82	0.43
37:m:69:PRO:HA	37:m:94:ALA:HB2	2.01	0.43
38:n:103:ARG:HH11	51:1:1287:A:H5'	1.83	0.43
51:1:255:A:H2'	51:1:256:A:O4'	2.18	0.43
51:1:841:G:C2'	51:1:842:U:H5'	2.49	0.43
51:1:1095:A:H3'	51:1:1096:A:H8	1.83	0.43
51:1:1258:U:H2'	51:1:1259:G:C8	2.54	0.43
51:1:1426:G:C6	51:1:1427:A:C6	3.06	0.43
51:1:2305:U:O2'	51:1:2306:C:H5'	2.19	0.43
51:1:2462:C:H2'	51:1:2463:C:C6	2.53	0.43
57:A1:68:TYR:HE1	57:A1:79:LEU:HD13	1.83	0.43
58:B1:59:ALA:HB1	58:B1:90:VAL:HG23	2.01	0.43
58:B1:111:THR:CG2	58:B1:300:GLN:HA	2.48	0.43
58:B1:434:ILE:HD11	59:B2:1274:GLU:HG3	2.00	0.43
58:B1:515:ARG:HH12	58:B1:724:MET:HG2	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:1024:THR:HG23	58:B1:1123:ARG:HA	2.00	0.43
58:B1:1079:LYS:HD3	58:B1:1098:GLN:HB3	1.99	0.43
58:B1:1108:GLN:HG3	58:B1:1109:LEU:HD12	1.99	0.43
59:B2:590:PRO:HB2	59:B2:655:VAL:HG21	2.01	0.43
31:f:84:LYS:HD2	31:f:84:LYS:HA	1.87	0.43
37:m:17:ASN:OD1	37:m:97:GLN:NE2	2.51	0.43
51:1:402:A:H2'	51:1:403:U:C5'	2.44	0.43
51:1:623:C:O2'	51:1:624:C:H5'	2.18	0.43
51:1:644:A:C3'	51:1:645:C:H5''	2.49	0.43
51:1:993:G:O2'	51:1:994:C:H5'	2.19	0.43
51:1:1092:C:H2'	51:1:1093:G:O4'	2.18	0.43
51:1:1306:C:N4	51:1:1606:C:H2'	2.34	0.43
51:1:1761:C:H2'	51:1:1762:A:O4'	2.18	0.43
58:B1:107:LEU:HA	58:B1:276:ASN:ND2	2.33	0.43
58:B1:220:ARG:NH1	58:B1:220:ARG:CG	2.82	0.43
59:B2:11:ILE:HG22	59:B2:1172:LEU:HD11	1.99	0.43
59:B2:22:LEU:HB3	59:B2:655:VAL:HG11	2.01	0.43
59:B2:27:LEU:O	59:B2:528:ARG:NH1	2.43	0.43
59:B2:300:ASP:OD1	59:B2:313:ALA:N	2.51	0.43
59:B2:1157:GLN:HG3	59:B2:1159:VAL:HG13	2.00	0.43
59:B2:1275:VAL:HG13	59:B2:1287:LEU:HD11	2.01	0.43
7:G:107:ARG:HE	7:G:107:ARG:HB3	1.63	0.43
8:H:106:ARG:HG2	8:H:107:LYS:HG3	2.01	0.43
9:I:125:ASN:HB2	9:I:127:ARG:HD3	2.01	0.43
13:M:24:VAL:HG23	13:M:60:LEU:HB2	2.00	0.43
16:P:35:ASP:OD1	16:P:39:ASN:N	2.50	0.43
17:Q:67:GLY:O	17:Q:98:ARG:NH1	2.52	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
27:b:206:LYS:HB2	51:1:729:G:C5	2.54	0.43
41:q:83:LYS:HE2	41:q:83:LYS:HB3	1.72	0.43
42:r:1:MET:HE3	42:r:101:ILE:HB	1.99	0.43
44:t:40:LYS:HE3	44:t:60:THR:HG22	2.01	0.43
49:y:11:VAL:HA	49:y:14:LEU:HB2	2.00	0.43
51:1:131:A:H2'	51:1:132:G:C8	2.53	0.43
51:1:705:A:C2	51:1:727:A:H1'	2.54	0.43
51:1:783:A:C8	51:1:783:A:H3'	2.54	0.43
51:1:871:U:H2'	51:1:872:U:C6	2.54	0.43
51:1:1020:A:O5'	51:1:1020:A:H8	2.02	0.43
51:1:1287:A:H3'	51:1:1288:G:N2	2.33	0.43
51:1:1741:C:O2'	51:1:1742:U:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1751:U:H2'	51:1:1752:C:C6	2.54	0.43
53:3:680:C:H2'	53:3:681:A:H8	1.84	0.43
53:3:1209:C:O2'	53:3:1214:C:N4	2.52	0.43
58:B1:45:ASN:HD22	58:B1:48:THR:H	1.65	0.43
58:B1:102:MET:HG2	58:B1:246:PRO:CG	2.49	0.43
59:B2:1313:HIS:CD2	60:W0:31:GLN:HE22	2.37	0.43
65:0:438:LEU:HD13	65:0:469:ILE:HG23	2.01	0.43
16:P:115:ILE:HD12	16:P:116:PRO:HD2	1.99	0.43
24:X:6:LYS:NZ	53:3:1314:C:OP1	2.52	0.43
27:b:7:PRO:HB3	27:b:13:ARG:HG3	1.99	0.43
33:i:8:VAL:HG11	33:i:26:ALA:CB	2.49	0.43
48:x:1:SER:OG	51:1:1365:A:OP2	2.35	0.43
51:1:156:A:O2'	51:1:157:C:H5'	2.18	0.43
51:1:467:G:O2'	51:1:468:G:H5'	2.19	0.43
51:1:541:A:H2'	51:1:542:C:O4'	2.19	0.43
51:1:758:C:H2'	51:1:759:G:H8	1.84	0.43
51:1:864:G:C2'	51:1:865:C:H5'	2.48	0.43
51:1:1172:C:H2'	51:1:1173:U:O4'	2.19	0.43
51:1:1601:G:H2'	51:1:1602:U:H5'	2.01	0.43
51:1:1917:U:H2'	51:1:1918:A:H5'	2.01	0.43
51:1:1964:G:H4'	51:1:1965:C:OP2	2.19	0.43
53:3:501:C:H2'	53:3:502:A:C8	2.53	0.43
53:3:1348:U:H2'	53:3:1349:A:H8	1.84	0.43
58:B1:388:ARG:HG2	58:B1:388:ARG:HH11	1.84	0.43
58:B1:850:LYS:HB3	58:B1:855:ASP:HB2	2.00	0.43
58:B1:1046:ILE:HG22	58:B1:1061:VAL:HA	2.00	0.43
59:B2:546:GLU:H	59:B2:546:GLU:HG3	1.53	0.43
63:5:9:A:H1'	63:5:45:U:H2'	2.01	0.43
65:0:615:PRO:HB3	65:0:684:PHE:HE1	1.82	0.43
7:G:122:ASP:N	7:G:122:ASP:OD1	2.51	0.42
9:I:101:VAL:HG22	9:I:106:PHE:HB2	2.01	0.42
31:f:151:ARG:HA	31:f:151:ARG:HD3	1.88	0.42
36:l:108:ALA:HB3	36:l:125:LEU:HG	2.01	0.42
51:1:918:A:H2'	51:1:919:U:O4'	2.19	0.42
51:1:1536:C:H4'	51:1:1537:G:N1	2.32	0.42
51:1:1668:A:C4'	51:1:1669:A:H5'	2.36	0.42
51:1:2073:C:C2'	51:1:2074:U:H5'	2.49	0.42
51:1:2371:G:O2'	51:1:2372:U:H5'	2.19	0.42
51:1:2660:A:H2'	51:1:2661:G:O4'	2.18	0.42
53:3:1005:A:OP2	53:3:1024:G:N2	2.48	0.42
53:3:1442:G:H1	53:3:1460:C:H42	1.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:824:PRO:HD3	58:B1:835:LEU:HD12	2.00	0.42
59:B2:909:LYS:HD3	59:B2:909:LYS:HA	1.43	0.42
65:0:557:ILE:CG2	65:0:576:ILE:HD12	2.48	0.42
8:H:1:GLY:HA2	53:3:1060:U:C5	2.54	0.42
10:J:110:MET:HA	10:J:113:VAL:HG12	2.01	0.42
11:K:100:SER:O	11:K:100:SER:OG	2.34	0.42
27:b:244:VAL:HG12	27:b:250:GLN:HA	2.01	0.42
34:j:138:GLN:H	34:j:138:GLN:HG2	1.62	0.42
40:p:63:ILE:HA	40:p:68:GLY:HA2	2.01	0.42
47:w:14:ALA:HB1	51:1:2271:G:OP1	2.19	0.42
51:1:8:C:C2	51:1:9:G:C8	3.07	0.42
51:1:481:G:H2'	51:1:482:A:OP2	2.18	0.42
51:1:712:G:C2'	51:1:713:G:H5'	2.49	0.42
51:1:1487:U:H2'	51:1:1488:C:C6	2.54	0.42
51:1:2844:G:H2'	51:1:2845:U:H6	1.80	0.42
51:1:2895:G:H2'	51:1:2896:C:H6	1.84	0.42
53:3:75:G:H1	53:3:95:C:H42	1.67	0.42
58:B1:434:ILE:HD11	59:B2:1274:GLU:CG	2.49	0.42
2:B:27:LEU:HD23	2:B:27:LEU:HA	1.84	0.42
33:i:26:ALA:H	51:1:1070:A:H61	1.67	0.42
33:i:129:GLU:HG3	33:i:139:VAL:HG21	2.00	0.42
51:1:90:U:H2'	51:1:91:A:C8	2.55	0.42
51:1:595:C:H2'	51:1:596:U:C6	2.54	0.42
51:1:629:G:H2'	51:1:630:G:O4'	2.19	0.42
51:1:673:C:O2'	51:1:674:G:H5'	2.19	0.42
51:1:1020:A:H5'	51:1:1021:A:N7	2.34	0.42
51:1:1087:G:H5''	51:1:1088:A:OP2	2.18	0.42
51:1:1335:C:H2'	51:1:1336:A:H8	1.84	0.42
51:1:1336:A:H2'	51:1:1337:G:H8	1.85	0.42
51:1:1993:U:O2	51:1:1993:U:H2'	2.18	0.42
51:1:2024:G:H2'	51:1:2025:C:C6	2.54	0.42
51:1:2741:A:N6	51:1:2742:G:C2	2.88	0.42
53:3:1253:G:H2'	53:3:1254:A:H8	1.83	0.42
55:8:3:DC:N1	55:8:4:DT:H72	2.34	0.42
58:B1:126:LEU:H	58:B1:126:LEU:HG	1.67	0.42
58:B1:144:TYR:CE1	58:B1:162:GLU:OE1	2.73	0.42
59:B2:125:GLY:H	59:B2:495:ALA:HB1	1.84	0.42
12:L:68:VAL:HG23	12:L:99:ALA:HB1	2.02	0.42
14:N:30:ASN:HD21	14:N:66:VAL:H	1.66	0.42
14:N:98:ARG:HG2	14:N:103:VAL:HG21	2.00	0.42
36:l:109:LYS:HE2	51:1:636:G:N7	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:q:54:ARG:HD3	51:1:1155:A:H5''	2.01	0.42
43:s:87:PRO:HG3	51:1:1615:C:C6	2.54	0.42
48:x:71:ARG:NH2	48:x:77:TYR:OH	2.42	0.42
51:1:365:U:H2'	51:1:366:C:C6	2.53	0.42
51:1:510:C:OP1	51:1:510:C:H3'	2.20	0.42
51:1:535:G:O2'	51:1:536:G:H5'	2.20	0.42
51:1:572:A:O5'	51:1:572:A:C8	2.72	0.42
51:1:1306:C:H41	51:1:1606:C:H2'	1.84	0.42
51:1:1500:G:H2'	51:1:1501:G:H8	1.83	0.42
51:1:1907:G:C5	51:1:1908:C:C4	3.07	0.42
51:1:1922:G:H4'	63:5:25:C:H4'	2.01	0.42
51:1:2102:G:H1	51:1:2187:U:H3	1.66	0.42
51:1:2287:A:C4	51:1:2289:G:N7	2.88	0.42
51:1:2584:U:O5'	51:1:2584:U:H6	2.02	0.42
53:3:460:A:H2'	53:3:461:A:C8	2.54	0.42
55:8:15:DC:H5'	59:B2:1269:ARG:HD3	2.00	0.42
57:A1:76:GLU:HB3	57:A1:80:GLU:HB3	2.01	0.42
58:B1:58:CYS:SG	58:B1:60:ARG:HG2	2.59	0.42
58:B1:96:LYS:NZ	59:B2:1298:VAL:HG11	2.34	0.42
58:B1:111:THR:HG21	58:B1:303:VAL:HB	2.00	0.42
58:B1:242:LEU:HA	58:B1:243:PRO:HD3	1.94	0.42
58:B1:647:PRO:HG3	58:B1:697:MET:HB3	2.01	0.42
58:B1:797:THR:HG22	58:B1:924:GLY:HA3	2.01	0.42
59:B2:616:ILE:HG13	59:B2:652:TYR:HB2	2.01	0.42
62:NG:130:PRO:HA	62:NG:148:VAL:O	2.20	0.42
62:NG:135:ARG:O	62:NG:178:VAL:CA	2.68	0.42
16:P:126:ARG:O	53:3:796:C:H5''	2.19	0.42
17:Q:31:GLY:HA2	17:Q:56:LEU:HA	2.01	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
39:o:33:ARG:O	39:o:65:THR:OG1	2.28	0.42
48:x:55:MET:HE2	48:x:55:MET:HB3	1.91	0.42
51:1:259:G:O2'	51:1:260:G:H5'	2.20	0.42
51:1:1197:G:C2'	51:1:1198:U:H5'	2.50	0.42
51:1:1230:A:H2'	51:1:1231:U:O4'	2.19	0.42
51:1:2562:U:C2'	51:1:2563:U:H5'	2.49	0.42
51:1:2839:G:O2'	51:1:2840:C:H5'	2.18	0.42
51:1:2852:G:H2'	51:1:2853:C:O4'	2.20	0.42
58:B1:244:VAL:HA	58:B1:269:TYR:OH	2.19	0.42
58:B1:390:LEU:N	58:B1:390:LEU:HD13	2.35	0.42
59:B2:11:ILE:O	59:B2:1149:TYR:OH	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:5:17:C:H6	63:5:17:C:H2'	1.69	0.42
17:Q:50:LYS:HE2	17:Q:70:GLY:HA2	2.01	0.42
20:T:66:LEU:HB3	20:T:77:TYR:HE1	1.84	0.42
27:b:97:ASP:N	27:b:97:ASP:OD1	2.45	0.42
29:d:53:THR:HB	51:1:452:G:H8	1.85	0.42
32:g:11:ASN:ND2	51:1:2095:A:OP1	2.53	0.42
39:o:40:ILE:HA	39:o:47:VAL:HA	2.00	0.42
46:v:58:SER:OG	46:v:59:GLU:OE1	2.36	0.42
51:1:623:C:H2'	51:1:624:C:H6	1.85	0.42
51:1:648:G:H5''	51:1:2352:A:H5''	2.00	0.42
51:1:870:U:H2'	51:1:871:U:C5'	2.48	0.42
51:1:1054:A:H2'	51:1:1055:G:C8	2.54	0.42
51:1:1316:U:O2'	51:1:1317:G:H5'	2.20	0.42
51:1:1727:C:O2'	51:1:1728:C:H5'	2.20	0.42
51:1:1886:U:O2'	51:1:1887:C:H5'	2.20	0.42
51:1:2248:C:C2'	51:1:2249:U:H5'	2.49	0.42
51:1:2292:U:H2'	51:1:2293:G:C8	2.55	0.42
53:3:987:G:H2'	53:3:988:G:H8	1.84	0.42
53:3:1531:A:C2'	53:3:1532:U:H5'	2.50	0.42
58:B1:279:LEU:HD13	58:B1:299:LEU:HD13	2.02	0.42
59:B2:557:ARG:HB3	59:B2:587:LEU:HD13	2.00	0.42
2:B:39:ARG:HA	2:B:39:ARG:HD2	1.91	0.42
9:I:55:ARG:HA	9:I:55:ARG:HD3	1.88	0.42
13:M:52:GLY:HA3	13:M:56:PRO:HA	2.01	0.42
17:Q:98:ARG:HA	17:Q:103:CYS:HB2	2.02	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
21:U:4:ILE:HG12	21:U:21:VAL:HG22	2.00	0.42
42:r:62:GLU:HG3	42:r:97:LYS:HB3	2.01	0.42
44:t:68:LYS:HD3	44:t:68:LYS:HA	1.83	0.42
51:1:191:A:C2	51:1:192:C:C4	3.08	0.42
51:1:532:A:H2'	51:1:532:A:N3	2.34	0.42
51:1:849:A:H2'	51:1:850:U:C5	2.54	0.42
51:1:955:U:H2'	51:1:956:G:H5'	2.02	0.42
51:1:1204:A:H4'	51:1:1205:A:H5''	2.02	0.42
51:1:1381:G:C2'	51:1:1382:G:H5'	2.49	0.42
51:1:1642:G:H2'	51:1:1643:G:O4'	2.19	0.42
51:1:1864:U:O5'	51:1:1864:U:H6	2.02	0.42
51:1:2091:C:H5	51:1:2092:U:O2'	2.02	0.42
51:1:2098:U:C2'	51:1:2099:U:H5'	2.49	0.42
51:1:2144:G:H1'	51:1:2147:A:N6	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:242:LEU:C	58:B1:242:LEU:HD23	2.44	0.42
58:B1:243:PRO:HG2	59:B2:1332:SER:C	2.44	0.42
58:B1:385:LEU:CD2	58:B1:390:LEU:HB2	2.50	0.42
58:B1:568:SER:HB3	58:B1:570:LYS:NZ	2.34	0.42
58:B1:616:PRO:HA	58:B1:619:ILE:HG22	2.02	0.42
18:R:32:ILE:HG23	18:R:58:GLU:HB3	2.02	0.42
18:R:89:ARG:HB2	18:R:96:VAL:HG22	2.01	0.42
24:X:51:HIS:HB2	24:X:56:HIS:CE1	2.55	0.42
28:c:175:LEU:HD12	28:c:175:LEU:HA	1.92	0.42
33:i:78:LEU:HA	33:i:81:LYS:HB3	2.02	0.42
38:n:16:HIS:CD2	51:1:1275:A:C2	3.07	0.42
38:n:58:ASP:OD1	38:n:63:ARG:NH2	2.44	0.42
51:1:128:C:H2'	51:1:129:C:C6	2.53	0.42
51:1:439:A:H2'	51:1:440:C:O4'	2.19	0.42
51:1:598:U:H2'	51:1:599:A:C8	2.54	0.42
51:1:630:G:N2	51:1:634:C:C4	2.88	0.42
51:1:809:G:C6	51:1:810:U:C4	3.08	0.42
51:1:1936:A:N6	51:1:1963:U:H3	2.17	0.42
51:1:2411:A:O2'	51:1:2412:A:H5'	2.20	0.42
51:1:2697:G:C2	51:1:2711:A:C2	3.08	0.42
53:3:322:C:O2	53:3:332:G:N2	2.52	0.42
53:3:1513:A:H2'	53:3:1514:G:C8	2.55	0.42
58:B1:362:ARG:HB2	58:B1:364:HIS:HD2	1.83	0.42
58:B1:609:TYR:HD2	58:B1:610:ARG:NH1	2.17	0.42
58:B1:839:VAL:HG12	58:B1:864:LEU:HD12	2.02	0.42
58:B1:1350:ASN:HA	58:B1:1353:VAL:HG12	2.02	0.42
59:B2:559:CYS:HA	59:B2:560:PRO:HD3	1.91	0.42
59:B2:699:LEU:HG	59:B2:799:ASN:HD22	1.85	0.42
59:B2:861:ALA:HB1	59:B2:882:ILE:HD13	2.01	0.42
63:5:4:C:H2'	63:5:5:G:C8	2.55	0.42
8:H:110:LEU:HD21	8:H:143:LEU:HB3	2.02	0.42
9:I:24:VAL:HG22	53:3:409:U:H4'	2.02	0.42
9:I:119:HIS:O	9:I:145:ARG:NH2	2.52	0.42
14:N:84:ARG:NH2	53:3:1119:C:OP1	2.48	0.42
14:N:113:LYS:HA	14:N:120:ALA:HB2	2.01	0.42
27:b:57:HIS:ND1	51:1:1567:G:H5'	2.35	0.42
28:c:134:HIS:HE1	51:1:1675:C:C4	2.38	0.42
51:1:397:U:O5'	51:1:397:U:H6	2.02	0.42
51:1:552:U:O2'	51:1:553:G:H5'	2.20	0.42
51:1:1070:A:H5'	51:1:1072:C:OP1	2.20	0.42
51:1:1467:U:C4	51:1:1468:U:C4	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1589:U:H2'	51:1:1590:A:C8	2.55	0.42
51:1:1600:C:H2'	51:1:1601:G:C8	2.55	0.42
51:1:1914:C:O2	51:1:1914:C:O4'	2.37	0.42
51:1:2216:G:H2'	51:1:2217:G:C8	2.54	0.42
51:1:2389:G:H5''	51:1:2390:U:H5'	2.01	0.42
52:2:65:U:H3'	52:2:108:A:N6	2.30	0.42
58:B1:141:PHE:CD2	58:B1:297:ARG:HB2	2.54	0.42
58:B1:390:LEU:HD13	58:B1:390:LEU:H	1.85	0.42
59:B2:741:MET:HE3	59:B2:974:ARG:HH12	1.85	0.42
59:B2:829:THR:HG23	59:B2:1059:ARG:HG2	2.00	0.42
8:H:61:LYS:HE2	8:H:96:VAL:HG12	2.01	0.42
9:I:87:GLU:N	9:I:87:GLU:OE2	2.53	0.42
10:J:90:GLY:O	10:J:129:SER:OG	2.36	0.42
15:O:57:VAL:HG22	15:O:58:ASN:H	1.85	0.42
38:n:28:LEU:O	38:n:32:GLU:N	2.38	0.42
43:s:9:HIS:H	43:s:102:HIS:CE1	2.38	0.42
51:1:4:U:O2'	51:1:5:A:H5'	2.20	0.42
51:1:1181:U:H2'	51:1:1182:G:H8	1.81	0.42
51:1:1213:A:C1'	51:1:1237:A:C2	3.03	0.42
51:1:1314:C:H42	51:1:1338:G:H1	1.68	0.42
51:1:1469:A:H2'	51:1:1470:A:H8	1.83	0.42
51:1:1614:A:C8	51:1:1614:A:O5'	2.73	0.42
53:3:73:C:H2'	53:3:74:A:C8	2.55	0.42
53:3:842:U:H5''	53:3:846:G:C6	2.55	0.42
58:B1:472:LEU:HD11	59:B2:1294:LYS:HG2	2.02	0.42
58:B1:820:ILE:HD11	58:B1:822:MET:HE2	2.02	0.42
58:B1:1289:ASN:O	58:B1:1293:GLU:HB2	2.20	0.42
29:d:106:LYS:HG3	29:d:200:LEU:HD13	2.01	0.41
29:d:145:ASP:HA	29:d:166:LYS:HB3	2.02	0.41
50:z:57:GLU:OE1	50:z:57:GLU:N	2.53	0.41
51:1:281:C:H2'	51:1:282:A:C8	2.54	0.41
51:1:284:U:H2'	51:1:285:G:C8	2.55	0.41
51:1:422:A:H2'	51:1:423:A:O4'	2.20	0.41
51:1:837:C:O5'	51:1:837:C:H6	2.02	0.41
51:1:1283:G:N2	51:1:1285:A:H3'	2.35	0.41
51:1:1343:G:N3	51:1:1343:G:H2'	2.35	0.41
51:1:1452:G:C2'	51:1:1453:A:OP2	2.68	0.41
51:1:1719:G:O2'	51:1:1720:U:H5'	2.20	0.41
51:1:1901:A:C2	51:1:1902:C:C5	3.08	0.41
51:1:1983:G:HO2'	51:1:1984:G:H5'	1.82	0.41
51:1:2583:G:H8	51:1:2583:G:O5'	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2812:G:O2'	51:1:2813:A:H5'	2.19	0.41
53:3:497:G:H2'	53:3:498:A:C8	2.55	0.41
53:3:1243:C:H2'	53:3:1244:G:H8	1.84	0.41
58:B1:175:GLU:H	58:B1:175:GLU:HG3	1.66	0.41
58:B1:515:ARG:HG2	58:B1:516:ASP:H	1.85	0.41
58:B1:950:ILE:HB	58:B1:1018:ALA:HB3	2.01	0.41
63:5:27:G:H1	63:5:43:C:H42	1.68	0.41
9:I:53:GLN:HA	9:I:198:LEU:HD12	2.01	0.41
9:I:146:GLU:HA	9:I:149:LYS:HZ3	1.85	0.41
23:W:24:ASP:OD1	23:W:24:ASP:N	2.53	0.41
26:Z:39:LYS:HA	26:Z:42:THR:HB	2.02	0.41
27:b:109:LEU:HD12	27:b:109:LEU:HA	1.93	0.41
44:t:28:ASN:HD21	44:t:91:GLN:HB3	1.85	0.41
45:u:6:ARG:N	51:1:85:G:OP1	2.52	0.41
51:1:638:G:H2'	51:1:639:U:C6	2.55	0.41
51:1:724:U:C4	51:1:725:G:C6	3.08	0.41
51:1:1034:G:C6	51:1:1035:U:N3	2.88	0.41
51:1:1048:A:C2'	51:1:1049:C:H5'	2.49	0.41
51:1:1077:A:H3'	51:1:1078:U:H4'	2.02	0.41
51:1:1482:G:H2'	51:1:1483:G:H8	1.85	0.41
51:1:1594:U:O2'	51:1:1595:C:H5'	2.20	0.41
51:1:1812:U:H5''	51:1:1812:U:H6	1.85	0.41
51:1:2160:C:H2'	51:1:2161:C:O4'	2.20	0.41
51:1:2437:G:O4'	51:1:2598:A:C2	2.73	0.41
51:1:2467:C:N4	51:1:2468:A:C6	2.89	0.41
51:1:2612:C:O5'	51:1:2612:C:H6	2.03	0.41
58:B1:137:ARG:HA	58:B1:142:GLU:HG2	2.02	0.41
58:B1:144:TYR:CD1	58:B1:144:TYR:N	2.88	0.41
59:B2:22:LEU:HD22	59:B2:603:ILE:HG21	2.02	0.41
7:G:17:HIS:C	7:G:19:THR:H	2.28	0.41
28:c:136:ASN:ND2	28:c:139:SER:O	2.52	0.41
33:i:116:MET:HE2	33:i:116:MET:HB3	1.79	0.41
34:j:109:LEU:HD23	34:j:109:LEU:HA	1.85	0.41
51:1:49:A:P	51:1:51:G:H5'	2.61	0.41
51:1:196:A:N3	51:1:196:A:H2'	2.35	0.41
51:1:256:A:C2'	51:1:257:C:H5'	2.50	0.41
51:1:759:G:H2'	51:1:760:G:H8	1.83	0.41
51:1:1152:C:H2'	51:1:1153:C:C6	2.55	0.41
51:1:1246:A:H2'	51:1:1247:A:O4'	2.19	0.41
51:1:1822:C:H2'	51:1:1823:G:H8	1.85	0.41
51:1:1991:U:H2'	51:1:1992:G:H5'	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2628:C:H3'	51:1:2629:U:H5'	2.01	0.41
53:3:1238:A:OP1	53:3:1335:U:O2'	2.35	0.41
53:3:1382:C:H2'	53:3:1383:C:H6	1.84	0.41
58:B1:576:ARG:HD3	58:B1:593:ASN:HA	2.02	0.41
59:B2:50:GLU:HG2	59:B2:73:TYR:HE1	1.85	0.41
59:B2:478:ARG:HD2	59:B2:492:MET:HA	2.02	0.41
59:B2:1244:HIS:NE2	59:B2:1266:GLY:O	2.44	0.41
63:5:29:G:H2'	63:5:29:G:N3	2.35	0.41
7:G:162:VAL:N	7:G:183:PHE:O	2.38	0.41
11:K:40:GLU:HB3	11:K:61:LEU:HB3	2.02	0.41
13:M:26:MET:HE2	13:M:26:MET:HB3	1.96	0.41
28:c:4:LEU:HD21	28:c:98:VAL:HA	2.02	0.41
35:k:7:MET:HE2	35:k:18:ARG:HD3	2.01	0.41
40:p:110:LYS:HE3	40:p:110:LYS:HB3	1.91	0.41
41:q:23:TYR:HB3	41:q:27:ARG:HB2	2.02	0.41
46:v:14:LYS:HB2	52:2:98:G:H1	1.84	0.41
47:w:7:ARG:HA	47:w:7:ARG:HD3	1.77	0.41
51:1:573:U:O2'	51:1:574:A:H3'	2.20	0.41
51:1:1038:G:H2'	51:1:1039:A:H8	1.83	0.41
51:1:1173:U:H5	51:1:1174:U:H1'	1.81	0.41
51:1:1239:G:H2'	51:1:1240:U:O4'	2.21	0.41
51:1:1418:G:H1'	51:1:1581:G:N2	2.36	0.41
51:1:1750:G:H2'	51:1:1751:U:C6	2.56	0.41
51:1:2156:G:H2'	51:1:2157:G:C5'	2.35	0.41
51:1:2741:A:H2'	51:1:2742:G:C5'	2.50	0.41
53:3:142:G:O2'	53:3:196:A:N1	2.45	0.41
55:8:14:DC:C2	55:8:15:DC:C5	3.09	0.41
57:A2:104:LYS:O	57:A2:139:SER:OG	2.36	0.41
58:B1:239:LEU:HD23	58:B1:239:LEU:N	2.36	0.41
58:B1:395:LYS:HB3	58:B1:395:LYS:HE3	1.45	0.41
59:B2:515:MET:HE2	59:B2:515:MET:HB3	1.82	0.41
65:0:491:ARG:HD3	65:0:491:ARG:HA	1.71	0.41
1:A:2:LYS:NZ	52:2:42:C:OP2	2.39	0.41
31:f:21:GLN:NE2	31:f:37:ASN:O	2.54	0.41
31:f:81:GLY:HA3	31:f:133:LYS:HZ1	1.85	0.41
51:1:191:A:H2'	51:1:192:C:C6	2.56	0.41
51:1:903:C:H2'	51:1:904:G:H8	1.86	0.41
51:1:1063:G:N2	51:1:1075:C:H41	2.18	0.41
51:1:1553:A:O2'	51:1:1554:U:H5	2.02	0.41
51:1:1599:U:H2'	51:1:1600:C:H6	1.85	0.41
51:1:1868:C:H2'	51:1:1869:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2482:A:H2'	51:1:2483:C:C6	2.54	0.41
53:3:370:C:H2'	53:3:371:A:H8	1.86	0.41
53:3:373:A:N1	53:3:391:G:O2'	2.49	0.41
53:3:1228:C:H2'	53:3:1229:A:C8	2.55	0.41
57:A1:48:LEU:HD12	57:A1:48:LEU:HA	1.79	0.41
58:B1:1050:THR:HG23	58:B1:1057:SER:HB3	2.03	0.41
58:B1:1177:ILE:HD12	58:B1:1186:TYR:HE2	1.85	0.41
58:B1:1223:LEU:HA	58:B1:1223:LEU:HD23	1.89	0.41
59:B2:979:LEU:HD11	59:B2:1011:LEU:HD11	2.03	0.41
59:B2:1278:LEU:HA	59:B2:1278:LEU:HD23	1.86	0.41
27:b:107:LYS:HE2	27:b:107:LYS:HB2	1.87	0.41
35:k:17:ARG:HD3	35:k:47:ILE:HD11	2.02	0.41
50:z:31:ILE:HD11	51:1:989:G:P	2.61	0.41
51:1:115:C:O2'	51:1:116:C:H5'	2.20	0.41
51:1:127:A:H5''	51:1:128:C:O4'	2.21	0.41
51:1:431:U:O5'	51:1:431:U:H6	2.03	0.41
51:1:688:U:O5'	51:1:688:U:H6	2.03	0.41
51:1:877:A:H2'	51:1:878:A:H5''	2.02	0.41
51:1:892:A:O2'	51:1:893:C:H5'	2.19	0.41
51:1:940:G:H2'	51:1:941:A:C4'	2.51	0.41
51:1:1045:C:H1'	51:1:1047:G:C2	2.56	0.41
51:1:1488:C:H2'	51:1:1489:C:H6	1.84	0.41
53:3:202:G:H2'	53:3:203:G:C8	2.55	0.41
53:3:685:G:N1	53:3:704:A:OP2	2.52	0.41
58:B1:24:LEU:HD21	58:B1:116:PHE:CE2	2.54	0.41
58:B1:71:LEU:HD23	58:B1:71:LEU:HA	1.75	0.41
58:B1:224:LEU:HD23	58:B1:224:LEU:HA	1.89	0.41
58:B1:559:ALA:HB3	58:B1:562:GLU:HB3	2.01	0.41
58:B1:820:ILE:HG12	58:B1:884:SER:HB2	2.01	0.41
59:B2:469:VAL:HA	59:B2:472:GLU:HG2	2.02	0.41
59:B2:755:LYS:HD2	59:B2:755:LYS:HA	1.86	0.41
65:0:298:ILE:CG2	65:0:304:ASP:HA	2.50	0.41
8:H:178:ARG:NH1	53:3:1112:C:O2'	2.54	0.41
9:I:44:LYS:HA	9:I:44:LYS:HD2	1.55	0.41
16:P:30:ILE:HG23	16:P:45:THR:HB	2.02	0.41
28:c:59:ARG:HD3	28:c:59:ARG:HA	1.83	0.41
28:c:90:PHE:HD1	28:c:94:GLN:HG2	1.83	0.41
37:m:123:LYS:HE2	51:1:2467:C:O2	2.20	0.41
51:1:94:A:H2'	51:1:95:A:C8	2.54	0.41
51:1:244:A:H2'	51:1:245:G:O4'	2.20	0.41
51:1:426:C:O2'	51:1:427:U:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:543:G:C3'	51:1:544:C:H5''	2.51	0.41
51:1:1024:G:H21	51:1:1144:A:C4'	2.33	0.41
51:1:1416:G:H2'	51:1:1417:C:H6	1.82	0.41
51:1:2335:A:N7	51:1:2337:G:C5	2.88	0.41
51:1:2568:U:O5'	51:1:2568:U:H6	2.04	0.41
51:1:2743:U:H2'	51:1:2744:G:C4'	2.50	0.41
53:3:146:G:H2'	53:3:147:G:C8	2.56	0.41
57:A1:33:ARG:HE	57:A1:33:ARG:HB3	1.56	0.41
58:B1:848:VAL:HB	58:B1:858:VAL:HG22	2.02	0.41
59:B2:524:ILE:HD12	59:B2:712:SER:HB2	2.02	0.41
59:B2:646:SER:OG	59:B2:647:ARG:N	2.51	0.41
59:B2:870:ILE:HB	59:B2:944:ARG:HD3	2.02	0.41
59:B2:998:LEU:HD21	59:B2:1015:ALA:HB2	2.02	0.41
65:0:519:VAL:HB	65:0:580:PHE:HB3	2.02	0.41
6:F:35:GLN:HE21	6:F:35:GLN:HB3	1.57	0.41
12:L:125:ASP:HB2	12:L:130:LYS:HG3	2.03	0.41
25:Y:4:LYS:HA	25:Y:4:LYS:HD3	1.86	0.41
51:1:170:U:H2'	51:1:171:U:C6	2.55	0.41
51:1:197:A:H2	51:1:2434:A:H62	1.69	0.41
51:1:265:A:C8	51:1:428:A:C2	3.09	0.41
51:1:490:C:O2'	51:1:491:G:P	2.79	0.41
51:1:908:C:O2'	51:1:909:A:H5'	2.19	0.41
51:1:1317:G:H2'	51:1:1318:U:C6	2.56	0.41
51:1:1327:A:H2'	51:1:1328:A:H5'	2.01	0.41
51:1:1782:U:C2'	51:1:1783:A:H5''	2.51	0.41
51:1:1931:U:C5	51:1:1968:G:N2	2.88	0.41
51:1:1955:U:H5	51:1:2557:G:N2	2.19	0.41
51:1:2098:U:H2'	51:1:2099:U:H5'	2.03	0.41
51:1:2615:U:O2	51:1:2615:U:H2'	2.20	0.41
51:1:2848:G:C2	51:1:2867:G:C4	3.08	0.41
58:B1:109:SER:HA	58:B1:110:PRO:HD3	1.96	0.41
58:B1:450:HIS:HA	58:B1:451:PRO:HD3	1.91	0.41
58:B1:586:GLY:HA3	58:B1:612:LEU:HD11	2.01	0.41
59:B2:310:ILE:HG21	59:B2:325:LEU:HB3	2.03	0.41
59:B2:678:ARG:HD3	59:B2:678:ARG:HA	1.84	0.41
59:B2:741:MET:SD	59:B2:974:ARG:NH2	2.93	0.41
5:E:28:LEU:HD23	5:E:28:LEU:HA	1.83	0.41
8:H:19:SER:HB2	8:H:39:ARG:HH21	1.85	0.41
15:O:12:ALA:HB2	15:O:96:VAL:HG13	2.03	0.41
16:P:17:ASP:OD1	16:P:17:ASP:N	2.44	0.41
18:R:10:ASP:HB3	18:R:45:SER:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:63:GLN:OE1	53:3:227:G:O2'	2.36	0.41
21:U:68:SER:OG	21:U:69:ASP:N	2.53	0.41
30:e:39:VAL:HG12	30:e:85:GLY:HA2	2.03	0.41
31:f:60:GLY:O	31:f:64:ALA:N	2.53	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
33:i:89:SER:HB3	51:1:1063:G:O2'	2.20	0.41
33:i:109:ALA:O	33:i:113:ALA:N	2.53	0.41
42:r:81:LYS:NZ	51:1:568:U:O4	2.54	0.41
43:s:29:VAL:HG21	43:s:55:ILE:HG21	2.03	0.41
51:1:56:A:H1'	51:1:127:A:C2	2.55	0.41
51:1:79:C:O2	51:1:346:A:H2	2.03	0.41
51:1:191:A:C6	51:1:192:C:N4	2.88	0.41
51:1:235:U:H2'	51:1:236:C:H6	1.86	0.41
51:1:309:A:N3	51:1:329:G:O2'	2.53	0.41
51:1:518:G:H2'	51:1:519:U:C6	2.55	0.41
51:1:679:C:H2'	51:1:680:C:C6	2.56	0.41
51:1:924:G:O2'	51:1:925:A:H5'	2.21	0.41
51:1:1095:A:C1'	65:0:632:ILE:HD13	2.51	0.41
51:1:1107:G:H2'	51:1:1108:U:C6	2.56	0.41
51:1:1107:G:H2'	51:1:1108:U:O4'	2.20	0.41
51:1:1328:A:H2'	51:1:1330:C:C4	2.56	0.41
51:1:2575:C:H2'	51:1:2578:G:O6	2.21	0.41
51:1:2600:A:H8	51:1:2600:A:O5'	2.03	0.41
51:1:2660:A:H2'	51:1:2661:G:C8	2.56	0.41
53:3:146:G:H2'	53:3:147:G:H8	1.86	0.41
53:3:1304:G:N1	53:3:1332:A:OP2	2.54	0.41
58:B1:108:ALA:HB2	58:B1:276:ASN:OD1	2.21	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:B1:1272:SER:OG	58:B1:1273:ASP:N	2.53	0.41
59:B2:176:ILE:HD12	59:B2:184:LEU:HD23	2.03	0.41
59:B2:213:LEU:HD13	59:B2:422:LYS:HG2	2.03	0.41
62:NG:175:PHE:O	62:NG:178:VAL:O	2.38	0.41
8:H:14:VAL:HG11	8:H:180:ASP:HB3	2.03	0.41
32:g:1:MET:N	32:g:20:ASN:OD1	2.40	0.41
38:n:22:ARG:HH22	51:1:2709:G:H5'	1.86	0.41
38:n:71:ARG:HE	38:n:71:ARG:HB3	1.68	0.41
39:o:24:THR:HB	39:o:42:PRO:HG3	2.02	0.41
51:1:10:A:C6	51:1:2800:A:C2	3.09	0.41
51:1:224:U:O4	51:1:420:C:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:518:G:C2	51:1:519:U:C2	3.08	0.41
51:1:722:A:H2'	51:1:723:C:C6	2.56	0.41
51:1:1116:G:O2'	51:1:1117:C:H5'	2.22	0.41
51:1:1412:U:H2'	51:1:1413:A:C8	2.56	0.41
51:1:1605:C:H2'	51:1:1606:C:C5'	2.51	0.41
51:1:2649:C:N3	51:1:2650:U:C4	2.89	0.41
51:1:2701:U:H3'	51:1:2702:G:H5''	2.01	0.41
51:1:2776:A:C6	51:1:2778:A:C6	3.09	0.41
53:3:336:A:H2'	53:3:337:G:H8	1.86	0.41
58:B1:68:TYR:CB	58:B1:75:TYR:HE2	2.34	0.41
58:B1:245:LEU:HG	58:B1:246:PRO:CD	2.50	0.41
7:G:190:SER:OG	7:G:191:ASP:N	2.53	0.40
9:I:101:VAL:HG13	9:I:113:ALA:HB1	2.03	0.40
13:M:42:GLU:HG2	13:M:100:ILE:HG21	2.02	0.40
16:P:108:ASN:HA	26:Z:7:GLU:HG2	2.03	0.40
24:X:49:ALA:HA	24:X:58:PRO:HA	2.03	0.40
28:c:169:ARG:O	51:1:2773:C:H4'	2.21	0.40
29:d:163:ASN:HD21	51:1:322:A:P	2.45	0.40
30:e:124:ARG:NH2	51:1:2315:G:N3	2.68	0.40
35:k:44:LYS:HB3	35:k:44:LYS:HE3	1.92	0.40
42:r:4:VAL:HG23	42:r:39:LEU:HB2	2.03	0.40
51:1:724:U:H2'	51:1:725:G:O4'	2.21	0.40
51:1:1092:C:O2'	51:1:1093:G:H5'	2.21	0.40
51:1:1302:A:H5'	51:1:1608:A:OP1	2.21	0.40
51:1:1722:A:H2'	51:1:1723:G:O4'	2.21	0.40
51:1:2221:G:H2'	51:1:2222:C:C6	2.56	0.40
51:1:2293:G:O2'	51:1:2294:G:H5'	2.21	0.40
51:1:2379:G:H2'	51:1:2380:C:C6	2.56	0.40
51:1:2828:G:N1	51:1:2829:A:C5	2.90	0.40
58:B1:144:TYR:OH	58:B1:162:GLU:OE1	2.34	0.40
63:5:17:C:H2'	63:5:18:G:C8	2.56	0.40
65:0:118:GLY:HA2	65:0:154:VAL:HG22	2.03	0.40
7:G:104:LYS:HE2	7:G:104:LYS:HB2	1.92	0.40
9:I:10:LEU:HG	9:I:62:ARG:HD2	2.03	0.40
13:M:91:LEU:HD23	13:M:91:LEU:HA	1.90	0.40
14:N:22:PRO:HA	14:N:60:LEU:HA	2.03	0.40
15:O:89:ARG:NH2	62:NG:165:PHE:H	2.18	0.40
20:T:80:LEU:HD12	20:T:80:LEU:HA	1.91	0.40
22:V:7:LEU:N	22:V:59:GLU:OE2	2.53	0.40
22:V:52:CYS:HB3	22:V:58:VAL:HG11	2.03	0.40
25:Y:43:LYS:HE2	25:Y:43:LYS:HB2	1.88	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:211:C:O2'	51:1:212:G:H5'	2.21	0.40
51:1:379:G:N1	51:1:396:G:C6	2.89	0.40
51:1:555:G:HO2'	51:1:556:A:H8	1.69	0.40
51:1:1048:A:N6	51:1:1111:A:C8	2.89	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	2.75	0.40
51:1:1721:G:H1'	51:1:1739:A:N6	2.35	0.40
51:1:2648:G:O2'	51:1:2649:C:H5'	2.21	0.40
51:1:2680:U:O2'	51:1:2681:C:H5'	2.21	0.40
53:3:31:G:N2	53:3:48:C:OP1	2.41	0.40
58:B1:26:SER:HB3	58:B1:29:MET:H	1.86	0.40
58:B1:282:LEU:CA	58:B1:286:ALA:HA	2.45	0.40
59:B2:657:THR:HG21	59:B2:1188:ASP:HB2	2.03	0.40
59:B2:886:LYS:HE2	59:B2:918:LEU:HD13	2.03	0.40
63:5:23:A:H2'	63:5:24:G:C8	2.56	0.40
6:F:30:GLU:HA	6:F:31:PRO:HD3	1.91	0.40
7:G:130:LYS:HE3	7:G:130:LYS:HB3	1.96	0.40
8:H:5:HIS:HA	8:H:6:PRO:HD3	1.95	0.40
18:R:7:ASN:CG	18:R:9:PRO:HD2	2.45	0.40
18:R:41:ASP:OD1	18:R:41:ASP:N	2.54	0.40
27:b:70:LYS:HD2	27:b:73:ILE:HD12	2.02	0.40
30:e:64:PRO:HA	30:e:88:VAL:HG22	2.03	0.40
31:f:3:VAL:HG13	51:1:2751:G:H4'	2.02	0.40
35:k:13:ASN:HB3	35:k:100:PHE:CZ	2.57	0.40
35:k:110:GLU:H	35:k:113:MET:HE3	1.86	0.40
45:u:4:ILE:HD13	45:u:69:VAL:HG23	2.03	0.40
51:1:137:U:H3	51:1:142:A:H61	1.69	0.40
51:1:467:G:O5'	51:1:467:G:H8	2.04	0.40
51:1:886:A:N7	51:1:887:U:H1'	2.36	0.40
51:1:1095:A:H1'	65:0:632:ILE:HD13	2.02	0.40
51:1:1333:G:C2'	51:1:1334:G:H5'	2.51	0.40
51:1:1346:G:O2'	51:1:1347:A:H5'	2.22	0.40
51:1:1505:A:O2'	51:1:1506:U:H5'	2.19	0.40
51:1:1767:G:N2	51:1:1986:C:C2	2.89	0.40
51:1:2049:G:O2'	51:1:2050:C:H5'	2.21	0.40
51:1:2105:U:C2	51:1:2184:A:H2	2.39	0.40
51:1:2106:U:H3'	51:1:2107:G:H8	1.86	0.40
51:1:2193:G:H2'	51:1:2194:U:H6	1.83	0.40
51:1:2210:U:H6	51:1:2210:U:OP1	2.04	0.40
51:1:2357:G:C2	51:1:2361:G:C6	3.09	0.40
51:1:2393:U:C2'	51:1:2394:C:H5'	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2888:C:H2'	51:1:2889:C:C6	2.56	0.40
57:A1:224:LEU:HD23	57:A2:228:LEU:HD21	2.03	0.40
57:A2:57:THR:HG22	57:A2:58:GLU:HG3	2.04	0.40
65:0:574:MET:HE1	65:0:601:PHE:CZ	2.57	0.40
65:0:635:LEU:HD23	65:0:635:LEU:HA	1.98	0.40
9:I:123:MET:HB2	9:I:143:SER:HB3	2.04	0.40
19:S:15:LEU:HB3	19:S:54:SER:HB3	2.02	0.40
22:V:11:VAL:HG23	22:V:55:GLY:H	1.85	0.40
23:W:25:ILE:HA	23:W:28:LEU:HB2	2.02	0.40
26:Z:9:GLU:HB3	26:Z:10:PRO:HD3	2.03	0.40
27:b:209:ALA:HA	27:b:212:TRP:CE2	2.55	0.40
28:c:56:LYS:HG3	28:c:59:ARG:HB3	2.04	0.40
28:c:174:SER:O	28:c:174:SER:OG	2.37	0.40
30:e:36:ASN:HB3	30:e:152:ASP:HB3	2.03	0.40
32:g:1:MET:HE3	32:g:1:MET:HB3	1.77	0.40
35:k:53:LYS:HA	35:k:53:LYS:HD3	1.96	0.40
39:o:76:LYS:HE2	39:o:76:LYS:HB3	1.93	0.40
51:1:120:U:C2	51:1:149:A:C6	3.10	0.40
51:1:164:C:H2'	51:1:165:A:O4'	2.21	0.40
51:1:194:G:O6	51:1:195:A:C6	2.75	0.40
51:1:221:A:C4	51:1:266:G:N7	2.90	0.40
51:1:359:G:H2'	51:1:360:U:C5'	2.51	0.40
51:1:706:A:H2'	51:1:707:G:C5'	2.51	0.40
51:1:724:U:H2'	51:1:725:G:C8	2.56	0.40
51:1:935:C:H2'	51:1:936:A:C8	2.56	0.40
51:1:1160:G:C6	51:1:1161:C:C4	3.09	0.40
51:1:1279:G:H2'	51:1:1280:G:C8	2.56	0.40
51:1:1430:G:H2'	51:1:1431:A:O4'	2.21	0.40
51:1:1494:A:C6	51:1:1495:A:C6	3.09	0.40
51:1:1749:A:H2'	51:1:1750:G:C8	2.57	0.40
51:1:1783:A:N1	51:1:2587:A:H2'	2.37	0.40
51:1:1944:U:H3'	51:1:1945:G:H5'	2.03	0.40
51:1:2092:U:H5	51:1:2199:A:C2	2.30	0.40
51:1:2788:C:H2'	51:1:2789:C:C6	2.56	0.40
53:3:195:A:H2'	53:3:196:A:C8	2.57	0.40
53:3:1124:G:H1	53:3:1149:C:H42	1.68	0.40
56:9:33:DA:H5''	58:B1:121:PRO:HG3	2.04	0.40
58:B1:182:ALA:HB1	58:B1:238:ILE:CG2	2.52	0.40
58:B1:351:GLY:O	58:B1:467:ALA:HA	2.21	0.40
58:B1:1361:THR:N	59:B2:1282:GLY:O	2.53	0.40
64:6:69:C:H2'	64:6:70:G:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:0:418:ILE:HA	65:0:486:PRO:HD3	2.04	0.40
65:0:438:LEU:HD21	65:0:472:ARG:HD2	2.02	0.40
7:G:161:PHE:HA	7:G:183:PHE:HB2	2.02	0.40
15:O:9:ARG:NH2	53:3:1279:G:OP1	2.53	0.40
24:X:32:THR:OG1	24:X:49:ALA:O	2.31	0.40
29:d:138:LEU:HG	29:d:143:LEU:HD12	2.03	0.40
30:e:49:LEU:HD22	30:e:83:PRO:HB2	2.04	0.40
31:f:157:LYS:HD3	51:1:2658:C:H5''	2.02	0.40
34:j:13:ARG:NH1	34:j:49:ASP:O	2.41	0.40
41:q:57:ARG:NH1	51:1:1154:G:OP2	2.52	0.40
51:1:55:G:N2	51:1:116:C:C2	2.90	0.40
51:1:279:A:N6	51:1:361:G:HO2'	2.20	0.40
51:1:367:G:H2'	51:1:368:A:C8	2.57	0.40
51:1:510:C:H2'	51:1:511:U:H6	1.85	0.40
51:1:914:G:H5'	51:1:915:C:OP2	2.21	0.40
51:1:1334:G:C6	51:1:1335:C:C4	3.09	0.40
51:1:1695:G:H2'	51:1:1696:G:O5'	2.22	0.40
51:1:2093:G:N7	51:1:2225:A:H2'	2.37	0.40
51:1:2278:A:C2'	51:1:2279:G:H5''	2.51	0.40
51:1:2757:A:H2'	51:1:2758:A:H5''	2.02	0.40
53:3:202:G:H2'	53:3:203:G:H8	1.85	0.40
53:3:297:G:N2	53:3:300:A:OP2	2.39	0.40
53:3:440:C:H2'	53:3:441:A:H8	1.85	0.40
53:3:987:G:H2'	53:3:988:G:C8	2.56	0.40
54:4:43:G:H5'	59:B2:688:GLN:HE22	1.85	0.40
57:A2:104:LYS:HG2	57:A2:110:VAL:HG22	2.03	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%)	33 (92%)	3 (8%)	0	100	100
7	G	216/241 (90%)	187 (87%)	27 (12%)	2 (1%)	14	51
8	H	204/233 (88%)	194 (95%)	10 (5%)	0	100	100
9	I	203/206 (98%)	172 (85%)	30 (15%)	1 (0%)	25	64
10	J	155/167 (93%)	138 (89%)	17 (11%)	0	100	100
11	K	98/135 (73%)	84 (86%)	14 (14%)	0	100	100
12	L	149/179 (83%)	130 (87%)	19 (13%)	0	100	100
13	M	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
14	N	125/130 (96%)	104 (83%)	21 (17%)	0	100	100
15	O	96/103 (93%)	87 (91%)	8 (8%)	1 (1%)	13	49
16	P	114/129 (88%)	100 (88%)	13 (11%)	1 (1%)	14	51
17	Q	121/124 (98%)	94 (78%)	27 (22%)	0	100	100
18	R	112/118 (95%)	98 (88%)	13 (12%)	1 (1%)	14	51
19	S	98/101 (97%)	83 (85%)	15 (15%)	0	100	100
20	T	86/89 (97%)	75 (87%)	11 (13%)	0	100	100
21	U	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
22	V	78/84 (93%)	69 (88%)	8 (10%)	1 (1%)	10	42
23	W	63/75 (84%)	56 (89%)	5 (8%)	2 (3%)	3	21
24	X	77/92 (84%)	71 (92%)	6 (8%)	0	100	100
25	Y	83/87 (95%)	78 (94%)	5 (6%)	0	100	100
26	Z	63/71 (89%)	44 (70%)	18 (29%)	1 (2%)	8	37
27	b	269/273 (98%)	244 (91%)	25 (9%)	0	100	100
28	c	207/209 (99%)	189 (91%)	18 (9%)	0	100	100
29	d	199/201 (99%)	186 (94%)	13 (6%)	0	100	100
30	e	175/179 (98%)	157 (90%)	18 (10%)	0	100	100
31	f	174/177 (98%)	160 (92%)	14 (8%)	0	100	100
32	g	50/149 (34%)	44 (88%)	5 (10%)	1 (2%)	6	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	i	139/142 (98%)	110 (79%)	26 (19%)	3 (2%)	5	29
34	j	140/142 (99%)	128 (91%)	12 (9%)	0	100	100
35	k	120/123 (98%)	106 (88%)	14 (12%)	0	100	100
36	l	141/144 (98%)	129 (92%)	12 (8%)	0	100	100
37	m	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
38	n	118/127 (93%)	103 (87%)	15 (13%)	0	100	100
39	o	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
40	p	112/115 (97%)	102 (91%)	10 (9%)	0	100	100
41	q	115/118 (98%)	110 (96%)	3 (3%)	2 (2%)	7	36
42	r	101/103 (98%)	88 (87%)	13 (13%)	0	100	100
43	s	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
44	t	91/100 (91%)	82 (90%)	9 (10%)	0	100	100
45	u	100/104 (96%)	84 (84%)	15 (15%)	1 (1%)	13	49
46	v	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
47	w	73/85 (86%)	67 (92%)	6 (8%)	0	100	100
48	x	75/78 (96%)	72 (96%)	2 (3%)	1 (1%)	10	42
49	y	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
50	z	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
57	A1	295/329 (90%)	273 (92%)	21 (7%)	1 (0%)	37	72
57	A2	282/329 (86%)	272 (96%)	10 (4%)	0	100	100
58	B1	1329/1407 (94%)	1202 (90%)	123 (9%)	4 (0%)	37	72
59	B2	1338/1342 (100%)	1203 (90%)	130 (10%)	5 (0%)	30	68
60	W0	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
61	NA	490/495 (99%)	474 (97%)	14 (3%)	2 (0%)	30	68
62	NG	150/181 (83%)	133 (89%)	10 (7%)	7 (5%)	2	17
65	0	669/716 (93%)	625 (93%)	43 (6%)	1 (0%)	48	83
All	All	10253/10945 (94%)	9283 (90%)	930 (9%)	40 (0%)	32	68

All (40) Ramachandran outliers are listed below:

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

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Mol	Chain	Res	Type
61	NA	187	ARG
61	NA	188	PRO
62	NG	102	PRO
62	NG	122	PRO
59	B2	43	PRO
59	B2	918	LEU
62	NG	121	LYS
62	NG	163	SER
57	A1	250	ASP
59	B2	888	THR
2	B	23	ALA
7	G	19	THR
18	R	5	GLY
32	g	12	LEU
33	i	22	PRO
41	q	23	TYR
58	B1	43	THR
58	B1	193	ASP
59	B2	909	LYS
7	G	17	HIS
15	O	58	ASN
22	V	50	ASN
23	W	13	THR
45	u	97	SER
58	B1	1325	PHE
9	I	45	PRO
23	W	17	VAL
33	i	20	SER
62	NG	123	ARG
62	NG	169	THR
62	NG	170	PRO
26	Z	10	PRO
33	i	23	VAL
41	q	6	GLY
65	0	651	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	58/62 (94%)	57 (98%)	1 (2%)	56	72
2	B	47/48 (98%)	47 (100%)	0	100	100
3	C	45/49 (92%)	44 (98%)	1 (2%)	47	65
4	D	38/38 (100%)	37 (97%)	1 (3%)	41	61
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%)	95 (90%)	10 (10%)	7	23
15	O	86/90 (96%)	78 (91%)	8 (9%)	7	24
16	P	89/99 (90%)	86 (97%)	3 (3%)	32	53
17	Q	103/104 (99%)	98 (95%)	5 (5%)	21	43
18	R	92/96 (96%)	91 (99%)	1 (1%)	70	80
19	S	83/84 (99%)	83 (100%)	0	100	100
20	T	76/77 (99%)	73 (96%)	3 (4%)	27	49
21	U	65/65 (100%)	64 (98%)	1 (2%)	60	75
22	V	74/78 (95%)	72 (97%)	2 (3%)	40	60
23	W	56/65 (86%)	52 (93%)	4 (7%)	12	32
24	X	70/79 (89%)	70 (100%)	0	100	100
25	Y	65/66 (98%)	64 (98%)	1 (2%)	60	75
26	Z	55/61 (90%)	47 (86%)	8 (14%)	2	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	142 (96%)	6 (4%)	26	48
31	f	137/138 (99%)	132 (96%)	5 (4%)	30	52
32	g	41/114 (36%)	38 (93%)	3 (7%)	11	31
33	i	109/110 (99%)	100 (92%)	9 (8%)	9	28
34	j	116/116 (100%)	116 (100%)	0	100	100
35	k	103/104 (99%)	103 (100%)	0	100	100
36	l	102/103 (99%)	101 (99%)	1 (1%)	73	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%)	98 (99%)	1 (1%)	73	81
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%)	184 (99%)	2 (1%)	70	80
58	B1	1110/1168 (95%)	1017 (92%)	93 (8%)	9	28
59	B2	1150/1157 (99%)	1118 (97%)	32 (3%)	38	59
60	W0	70/75 (93%)	69 (99%)	1 (1%)	62	75
65	0	553/588 (94%)	482 (87%)	71 (13%)	3	15
All	All	7931/8500 (93%)	7593 (96%)	338 (4%)	27	47

All (338) 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
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	40	ARG
14	N	44	ARG
14	N	45	MET
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
30	e	77	LYS
30	e	78	ILE
30	e	79	ARG
30	e	174	PHE
30	e	177	ARG
31	f	9	VAL
31	f	131	VAL
31	f	172	GLU
31	f	174	LYS
31	f	176	LYS
32	g	4	ILE
32	g	5	LEU
32	g	9	VAL
33	i	18	ASN
33	i	20	SER
33	i	22	PRO
33	i	23	VAL
33	i	27	LEU
33	i	29	GLN
33	i	34	ILE
33	i	35	MET
33	i	36	GLU
36	l	85	VAL
37	m	44	ARG
37	m	47	GLU
37	m	50	ARG
37	m	55	ARG
37	m	58	LYS
37	m	59	ARG
38	n	13	ASN
40	p	52	ARG
41	q	4	LYS
41	q	5	ARG
41	q	28	SER
42	r	53	PHE
42	r	54	VAL
43	s	3	THR
45	u	35	VAL
45	u	93	ARG
45	u	100	GLU
45	u	101	THR
46	v	72	VAL

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Mol	Chain	Res	Type
50	z	16	LEU
50	z	40	THR
57	A1	9	LEU
57	A1	12	ARG
57	A1	13	LEU
57	A1	18	GLN
57	A1	19	VAL
57	A1	22	THR
57	A1	27	THR
57	A1	28	LEU
57	A1	33	ARG
57	A1	46	ILE
57	A1	48	LEU
57	A2	29	GLU
57	A2	74	VAL
58	B1	24	LEU
58	B1	40	LYS
58	B1	42	GLU
58	B1	44	ILE
58	B1	47	ARG
58	B1	49	PHE
58	B1	50	LYS
58	B1	60	ARG
58	B1	66	LYS
58	B1	69	GLU
58	B1	71	LEU
58	B1	74	LYS
58	B1	76	LYS
58	B1	78	LEU
58	B1	80	HIS
58	B1	81	ARG
58	B1	87	LYS
58	B1	91	GLU
58	B1	93	THR
58	B1	94	GLN
58	B1	95	THR
58	B1	96	LYS
58	B1	99	ARG
58	B1	100	GLU
58	B1	114	ILE
58	B1	117	LEU
58	B1	120	LEU

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Mol	Chain	Res	Type
58	B1	126	LEU
58	B1	132	LEU
58	B1	135	ILE
58	B1	142	GLU
58	B1	144	TYR
58	B1	145	VAL
58	B1	146	VAL
58	B1	147	ILE
58	B1	152	THR
58	B1	154	LEU
58	B1	157	GLN
58	B1	159	ILE
58	B1	172	PHE
58	B1	174	ASP
58	B1	175	GLU
58	B1	180	MET
58	B1	190	LYS
58	B1	193	ASP
58	B1	196	GLN
58	B1	210	SER
58	B1	212	THR
58	B1	216	LYS
58	B1	222	LYS
58	B1	223	LEU
58	B1	227	PHE
58	B1	233	LYS
58	B1	237	MET
58	B1	238	ILE
58	B1	239	LEU
58	B1	240	THR
58	B1	244	VAL
58	B1	255	LEU
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

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Mol	Chain	Res	Type
58	B1	385	LEU
58	B1	386	GLU
58	B1	387	LEU
58	B1	390	LEU
58	B1	393	THR
58	B1	394	ILE
58	B1	395	LYS
58	B1	416	ILE
58	B1	417	ARG
58	B1	425	ARG
58	B1	506	VAL
58	B1	514	THR
58	B1	800	LEU
58	B1	807	LEU
58	B1	839	VAL
58	B1	901	ARG
58	B1	903	LEU
58	B1	1172	LYS
58	B1	1181	ASP
58	B1	1233	ILE
58	B1	1327	GLU
58	B1	1328	THR
58	B1	1331	VAL
58	B1	1332	LEU
59	B2	44	GLU
59	B2	49	LEU
59	B2	56	VAL
59	B2	146	VAL
59	B2	483	ASP
59	B2	487	LEU
59	B2	516	ASP
59	B2	538	LEU
59	B2	540	ARG
59	B2	545	PHE
59	B2	546	GLU
59	B2	615	VAL
59	B2	857	VAL
59	B2	859	GLU
59	B2	887	VAL
59	B2	890	LYS
59	B2	892	GLU
59	B2	894	GLN

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Mol	Chain	Res	Type
59	B2	900	LYS
59	B2	901	LEU
59	B2	902	LEU
59	B2	903	ARG
59	B2	905	ILE
59	B2	906	PHE
59	B2	909	LYS
59	B2	913	VAL
59	B2	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
65	0	3	ARG
65	0	19	ILE
65	0	23	LYS
65	0	24	THR
65	0	28	GLU
65	0	93	VAL
65	0	96	THR
65	0	98	GLU
65	0	104	ARG
65	0	105	VAL
65	0	143	LYS
65	0	144	MET
65	0	147	MET
65	0	254	GLN
65	0	273	LYS
65	0	343	VAL
65	0	358	GLU
65	0	365	GLN
65	0	366	MET
65	0	369	ASN
65	0	370	LYS
65	0	371	ARG
65	0	372	GLU
65	0	377	VAL
65	0	378	ARG
65	0	425	LYS
65	0	429	GLU

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Mol	Chain	Res	Type
65	0	430	LYS
65	0	431	MET
65	0	433	LEU
65	0	437	ARG
65	0	461	MET
65	0	464	LEU
65	0	471	ASP
65	0	472	ARG
65	0	473	MET
65	0	476	GLU
65	0	478	ASN
65	0	485	LYS
65	0	487	GLN
65	0	488	VAL
65	0	495	ARG
65	0	504	LYS
65	0	512	ARG
65	0	514	GLN
65	0	539	ASP
65	0	580	PHE
65	0	591	LEU
65	0	594	LYS
65	0	595	LEU
65	0	613	LEU
65	0	626	GLU
65	0	630	ASP
65	0	642	LEU
65	0	643	LYS
65	0	645	GLN
65	0	646	GLU
65	0	648	GLU
65	0	649	VAL
65	0	650	THR
65	0	654	ILE
65	0	668	THR
65	0	671	ARG
65	0	677	ARG
65	0	686	LYS
65	0	687	TYR
65	0	688	ASP
65	0	689	GLU
65	0	693	ASN

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Mol	Chain	Res	Type
65	0	702	ARG
65	0	704	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (135) 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	25	ASN
3	C	44	GLN
4	D	16	HIS
6	F	35	GLN
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	197	HIS
10	J	76	ASN
10	J	88	HIS
10	J	121	ASN
12	L	85	GLN
12	L	121	ASN
12	L	147	ASN
13	M	3	GLN
13	M	37	ASN
13	M	66	GLN
14	N	4	GLN
14	N	30	ASN
15	O	20	GLN
15	O	58	ASN
16	P	80	ASN
17	Q	4	ASN

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Mol	Chain	Res	Type
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
27	b	142	ASN
27	b	259	ASN
28	c	49	GLN
28	c	134	HIS
28	c	150	GLN
28	c	164	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
31	f	47	ASN
31	f	87	GLN
32	g	2	GLN
33	i	30	GLN
34	j	58	ASN
34	j	135	GLN
35	k	3	GLN
35	k	5	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

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Mol	Chain	Res	Type
42	r	18	GLN
42	r	82	HIS
43	s	7	HIS
44	t	28	ASN
44	t	59	ASN
44	t	92	ASN
45	u	52	ASN
46	v	75	GLN
46	v	87	GLN
47	w	53	HIS
48	x	16	ASN
48	x	33	HIS
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	227	GLN
57	A2	23	HIS
57	A2	227	GLN
58	B1	45	ASN
58	B1	196	GLN
58	B1	364	HIS
58	B1	424	ASN
58	B1	469	HIS
58	B1	805	GLN
58	B1	865	HIS
58	B1	1195	GLN
58	B1	1238	GLN
58	B1	1259	GLN
59	B2	69	GLN
59	B2	314	ASN
59	B2	330	HIS
59	B2	343	HIS
59	B2	518	ASN
59	B2	554	HIS
59	B2	688	GLN
59	B2	808	ASN

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Mol	Chain	Res	Type
59	B2	965	GLN
59	B2	1008	GLN
59	B2	1080	ASN
59	B2	1237	HIS
59	B2	1268	GLN
59	B2	1313	HIS
60	W0	7	GLN
60	W0	31	GLN
60	W0	62	GLN
65	0	344	ASN
65	0	367	HIS
65	0	465	HIS
65	0	496	GLN
65	0	514	GLN
65	0	579	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	1	2902/2904 (99%)	398 (13%)	16 (0%)
52	2	119/120 (99%)	17 (14%)	1 (0%)
53	3	1538/1542 (99%)	253 (16%)	4 (0%)
54	4	37/44 (84%)	21 (56%)	2 (5%)
63	5	75/76 (98%)	39 (52%)	6 (8%)
64	6	76/77 (98%)	27 (35%)	2 (2%)
All	All	4747/4763 (99%)	755 (15%)	31 (0%)

All (755) 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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
51	1	2820	A
51	1	2861	U
51	1	2867	G
51	1	2868	A
51	1	2872	A
51	1	2879	A
51	1	2880	C
51	1	2884	U
51	1	2901	C
52	2	9	G
52	2	13	G
52	2	25	U
52	2	30	C
52	2	35	C
52	2	36	C
52	2	44	G
52	2	45	A
52	2	53	A
52	2	67	G
52	2	87	U
52	2	88	C
52	2	89	U
52	2	90	C
52	2	108	A
52	2	109	A
52	2	120	A
53	3	4	U
53	3	5	U
53	3	6	G
53	3	7	A
53	3	9	G
53	3	22	G
53	3	32	A
53	3	39	G
53	3	47	C
53	3	48	C
53	3	51	A
53	3	71	A
53	3	75	G
53	3	77	A
53	3	78	A
53	3	80	A

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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	2	U
54	4	3	G
54	4	6	U
54	4	7	C
54	4	9	U
54	4	10	C
54	4	11	U
54	4	12	U
54	4	14	U
54	4	15	U
54	4	18	U
54	4	19	U
54	4	20	U
54	4	21	U
54	4	22	U

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Mol	Chain	Res	Type
54	4	24	U
54	4	25	U
54	4	26	U
54	4	33	U
54	4	34	U
54	4	35	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
63	5	36	A
63	5	37	A
63	5	39	U
63	5	40	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	57	G
63	5	58	A
63	5	59	U
63	5	60	U
63	5	61	C
63	5	66	U

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Mol	Chain	Res	Type
63	5	73	A
63	5	74	C
63	5	75	C
64	6	2	G
64	6	7	G
64	6	8	U
64	6	9	G
64	6	19	G
64	6	20	U
64	6	21	A
64	6	22	G
64	6	30	G
64	6	33	U
64	6	34	C
64	6	35	A
64	6	36	U
64	6	42	G
64	6	45	G
64	6	54	U
64	6	55	U
64	6	56	C
64	6	57	A
64	6	64	G
64	6	67	C
64	6	68	C
64	6	70	G
64	6	73	A
64	6	74	C
64	6	75	C
64	6	76	A

All (31) 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

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
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
53	3	1139	G
53	3	1224	U
54	4	14	U
54	4	19	U
63	5	7	A
63	5	32	U
63	5	39	U
63	5	48	C
63	5	57	G
63	5	60	U
64	6	33	U
64	6	56	C

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
68	GDP	0	801	-	24,30,30	0.90	1 (4%)	30,47,47	1.39	5 (16%)
67	FUA	0	800	-	39,40,40	1.67	3 (7%)	49,64,64	1.13	3 (6%)

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
68	GDP	0	801	-	-	2/12/32/32	0/3/3/3
67	FUA	0	800	-	-	9/15/92/92	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	0	800	FUA	C29-C22	-9.59	1.34	1.47
67	0	800	FUA	O5-C29	-2.46	1.23	1.30
68	0	801	GDP	C6-N1	-2.31	1.34	1.37
67	0	800	FUA	C9-C11	2.24	1.57	1.54

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	0	801	GDP	C3'-C2'-C1'	2.89	105.33	100.98
68	0	801	GDP	PA-O3A-PB	-2.62	123.84	132.83
68	0	801	GDP	C5-C6-N1	2.59	118.52	113.95
67	0	800	FUA	C14-C8-C9	-2.54	104.42	109.40
67	0	800	FUA	C8-C9-C10	2.51	118.92	116.34
68	0	801	GDP	C8-N7-C5	2.19	107.17	102.99
68	0	801	GDP	O6-C6-C5	-2.13	120.20	124.37
67	0	800	FUA	C1-C10-C9	2.05	113.96	109.13

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
67	0	800	FUA	C13-C17-C22-C29

*Continued on next page...*

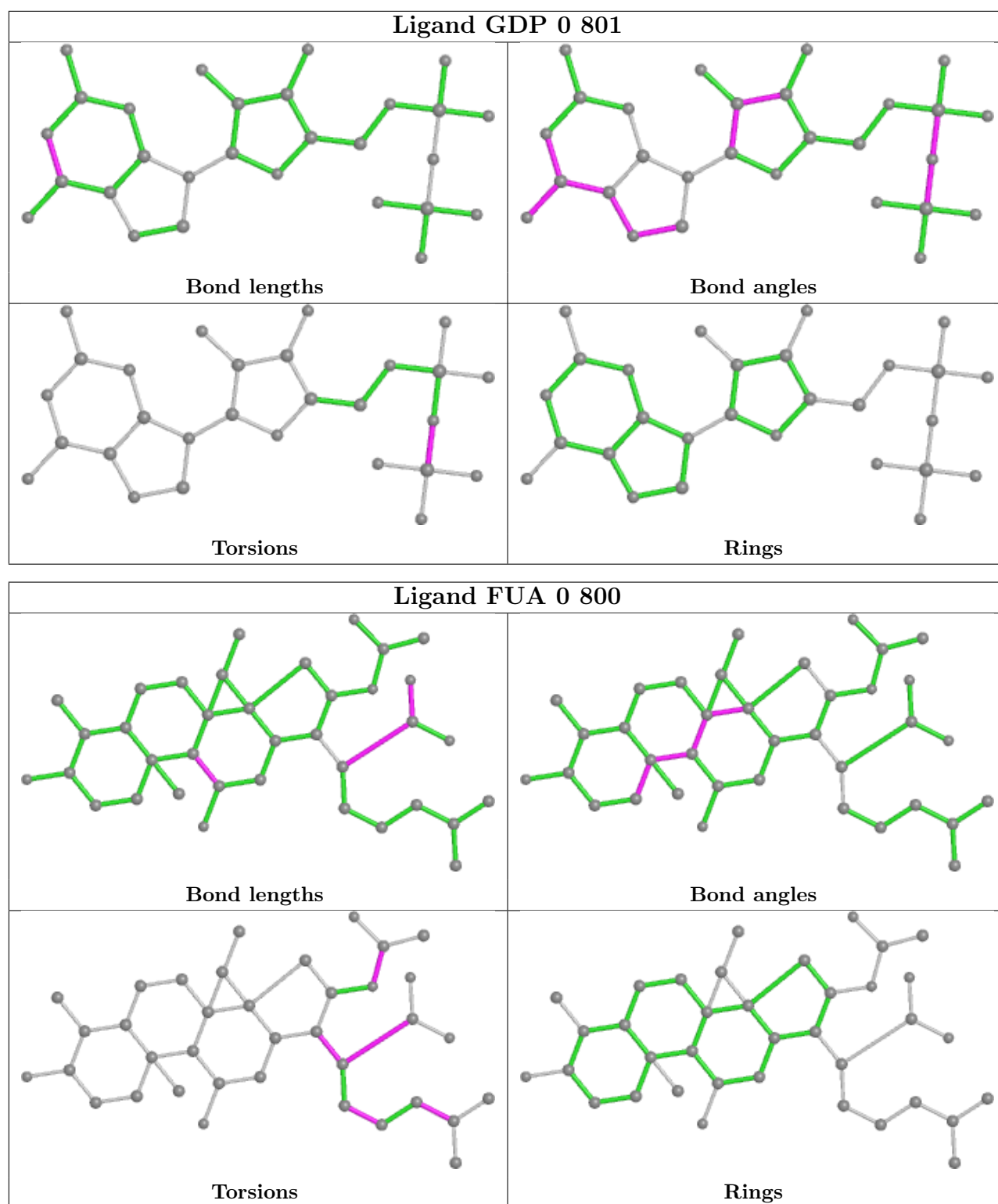
*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
67	0	800	FUA	C23-C22-C29-O4
67	0	800	FUA	C23-C22-C29-O5
67	0	800	FUA	C22-C23-C24-C25
67	0	800	FUA	C24-C25-C26-C27
67	0	800	FUA	C24-C25-C26-C28
67	0	800	FUA	C32-C31-O2-C16
68	0	801	GDP	PA-O3A-PB-O2B
67	0	800	FUA	O3-C31-O2-C16
68	0	801	GDP	PA-O3A-PB-O1B
67	0	800	FUA	C17-C22-C29-O4

There are no ring outliers.

No monomer is involved in short contacts.

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



## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

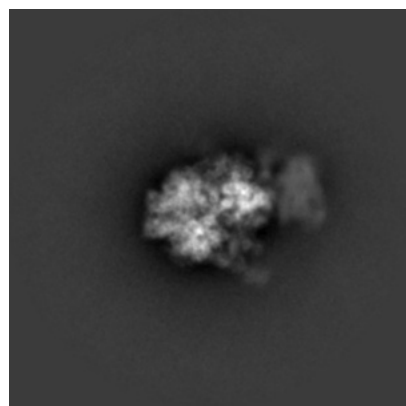
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38947. These allow visual inspection of the internal detail of the map and identification of artifacts.

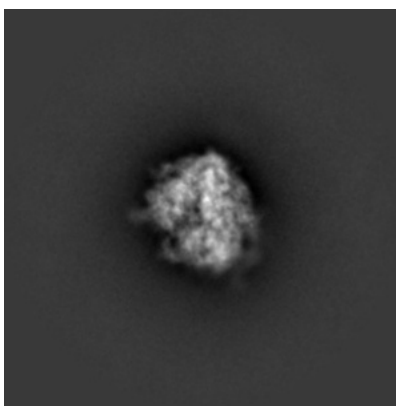
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

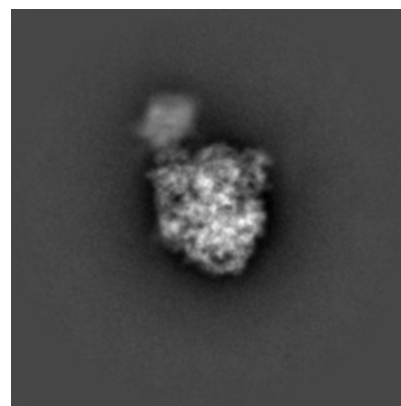
#### 6.1.1 Primary map



X

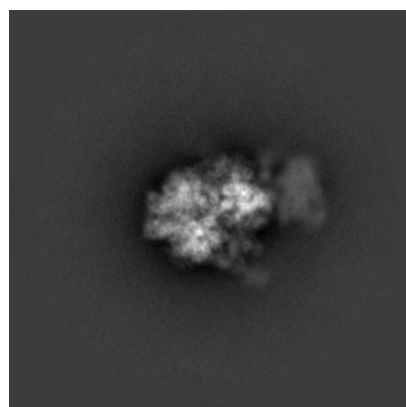


Y

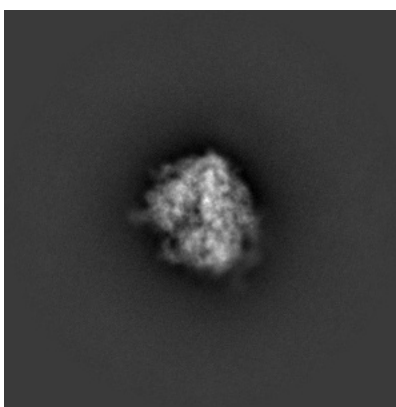


Z

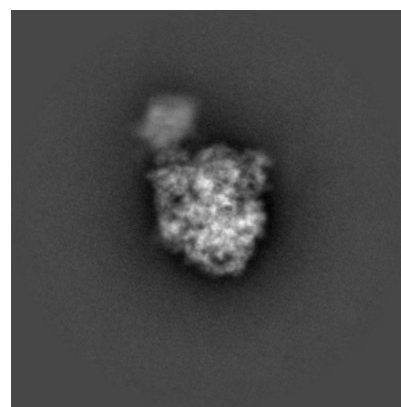
#### 6.1.2 Raw map



X



Y

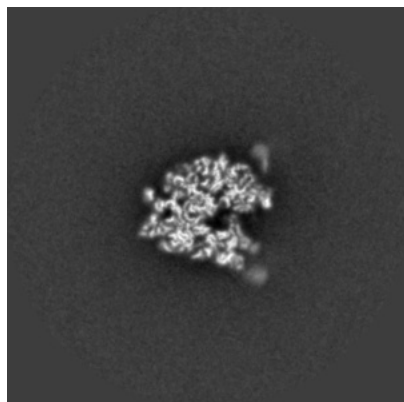


Z

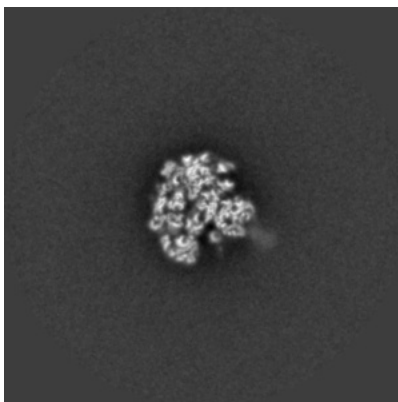
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

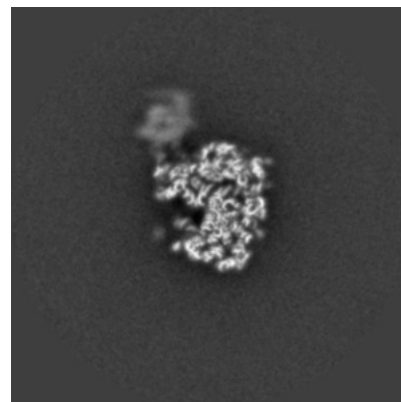
### 6.2.1 Primary map



X Index: 240

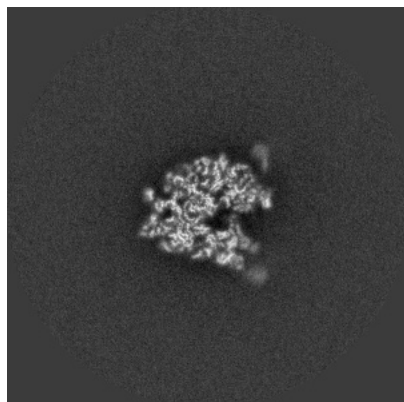


Y Index: 240

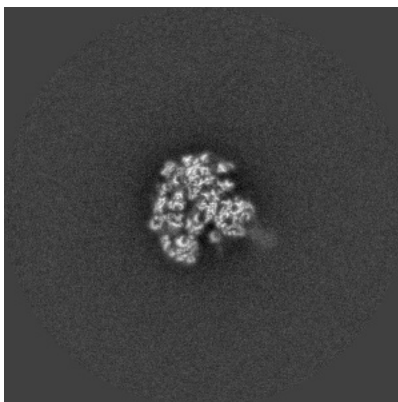


Z Index: 240

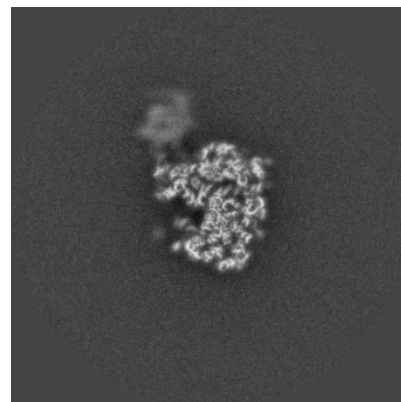
### 6.2.2 Raw map



X Index: 240



Y Index: 240

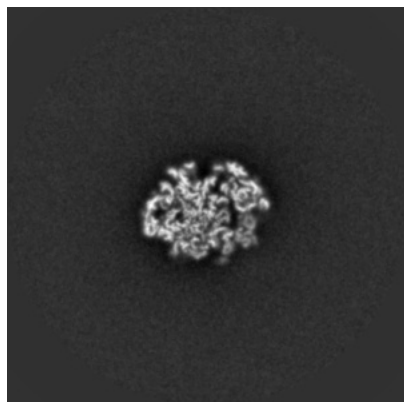


Z Index: 240

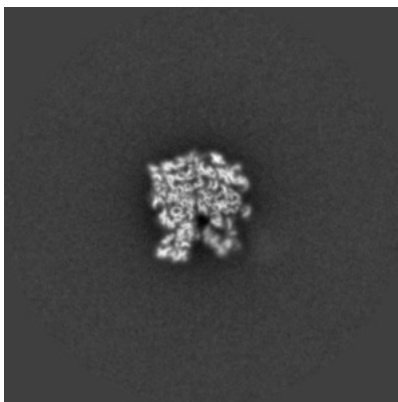
The images above show central slices of the map in three orthogonal directions.

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

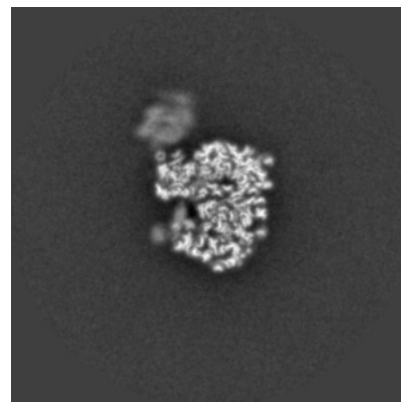
### 6.3.1 Primary map



X Index: 265

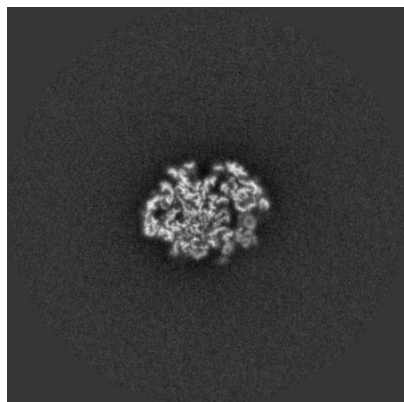


Y Index: 224

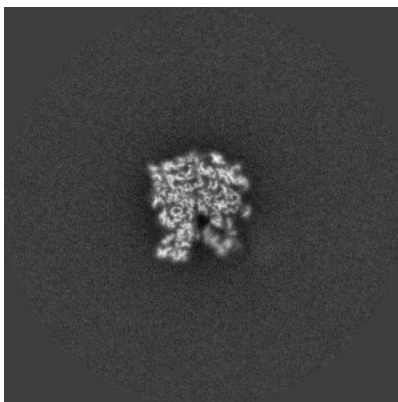


Z Index: 246

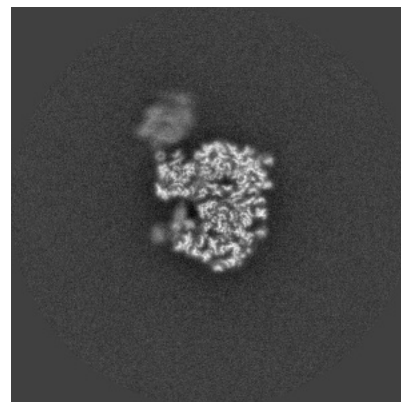
### 6.3.2 Raw map



X Index: 265



Y Index: 224

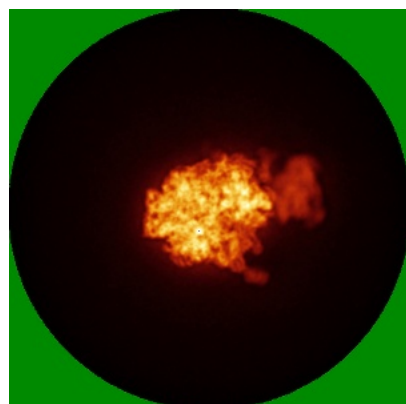


Z Index: 246

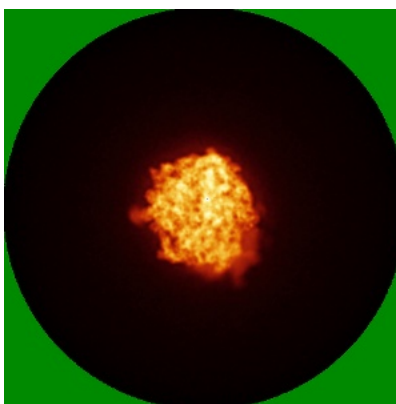
The images above show the largest variance slices of the map in three orthogonal directions.

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

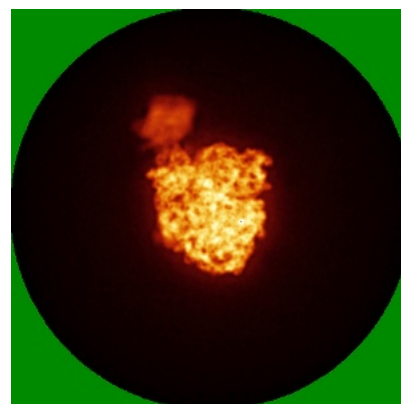
### 6.4.1 Primary map



X

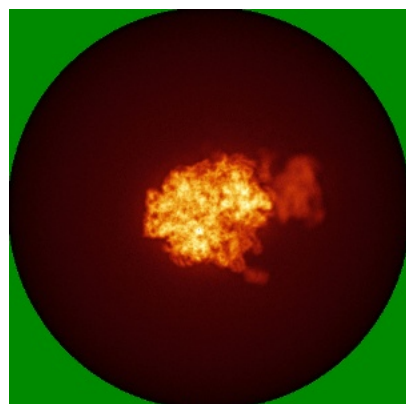


Y

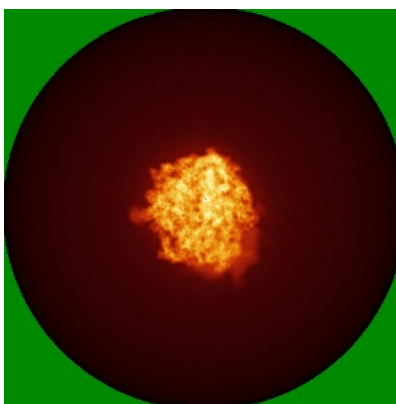


Z

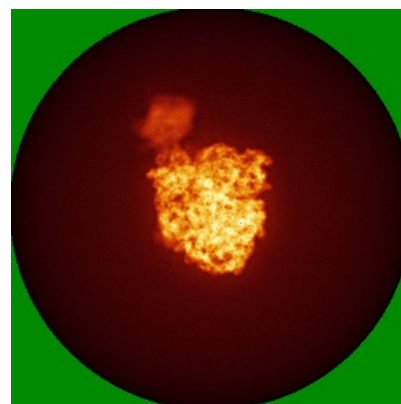
### 6.4.2 Raw map



X



Y

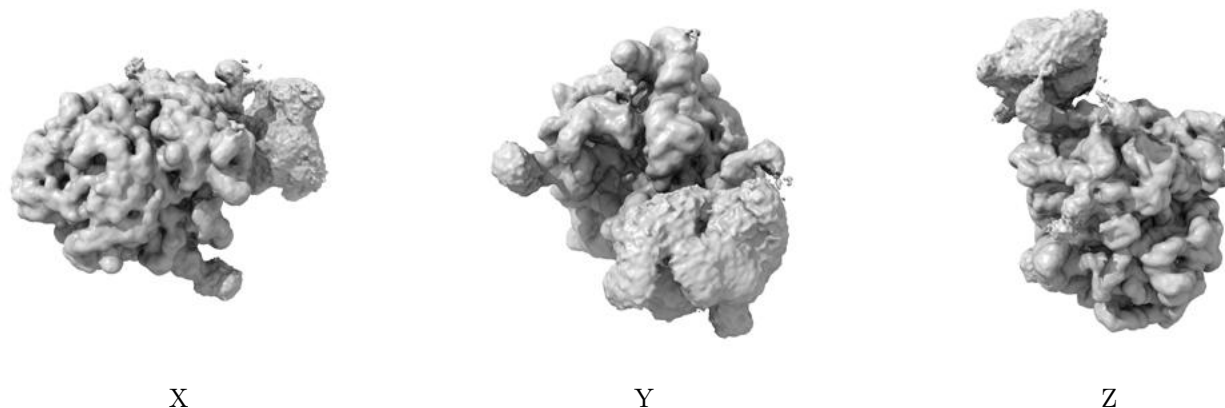


Z

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.

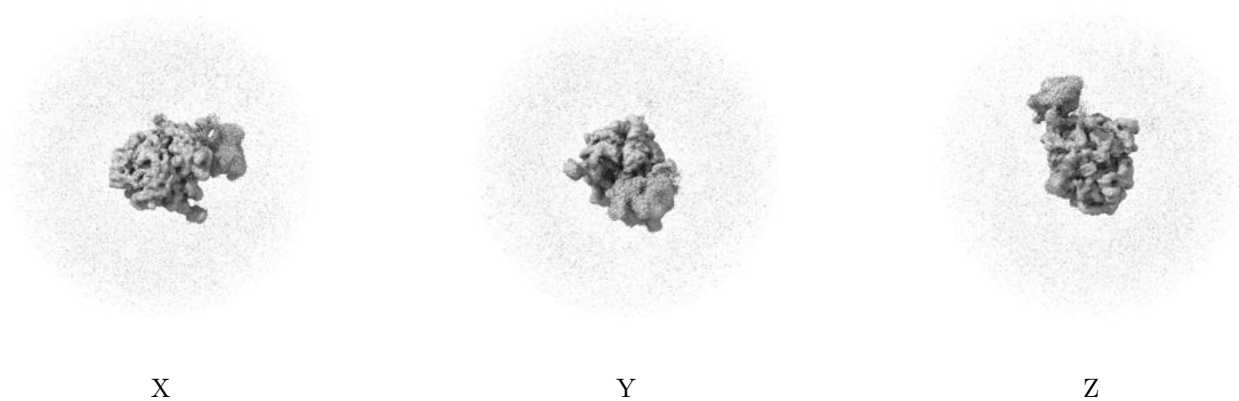
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.007. 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.

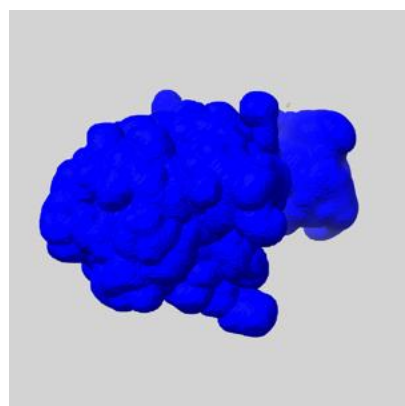
## 6.6 Mask visualisation [i](#)

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

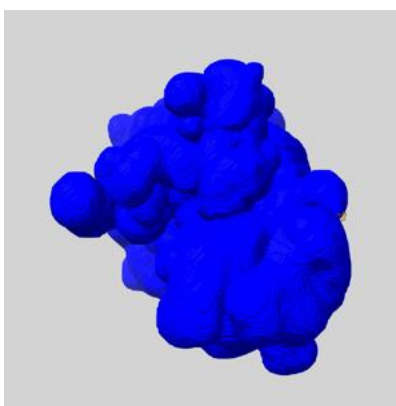
A mask typically either:

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

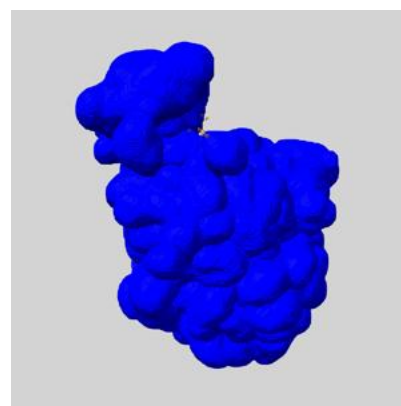
### 6.6.1 emd\_38947\_msk\_1.map [i](#)



X



Y

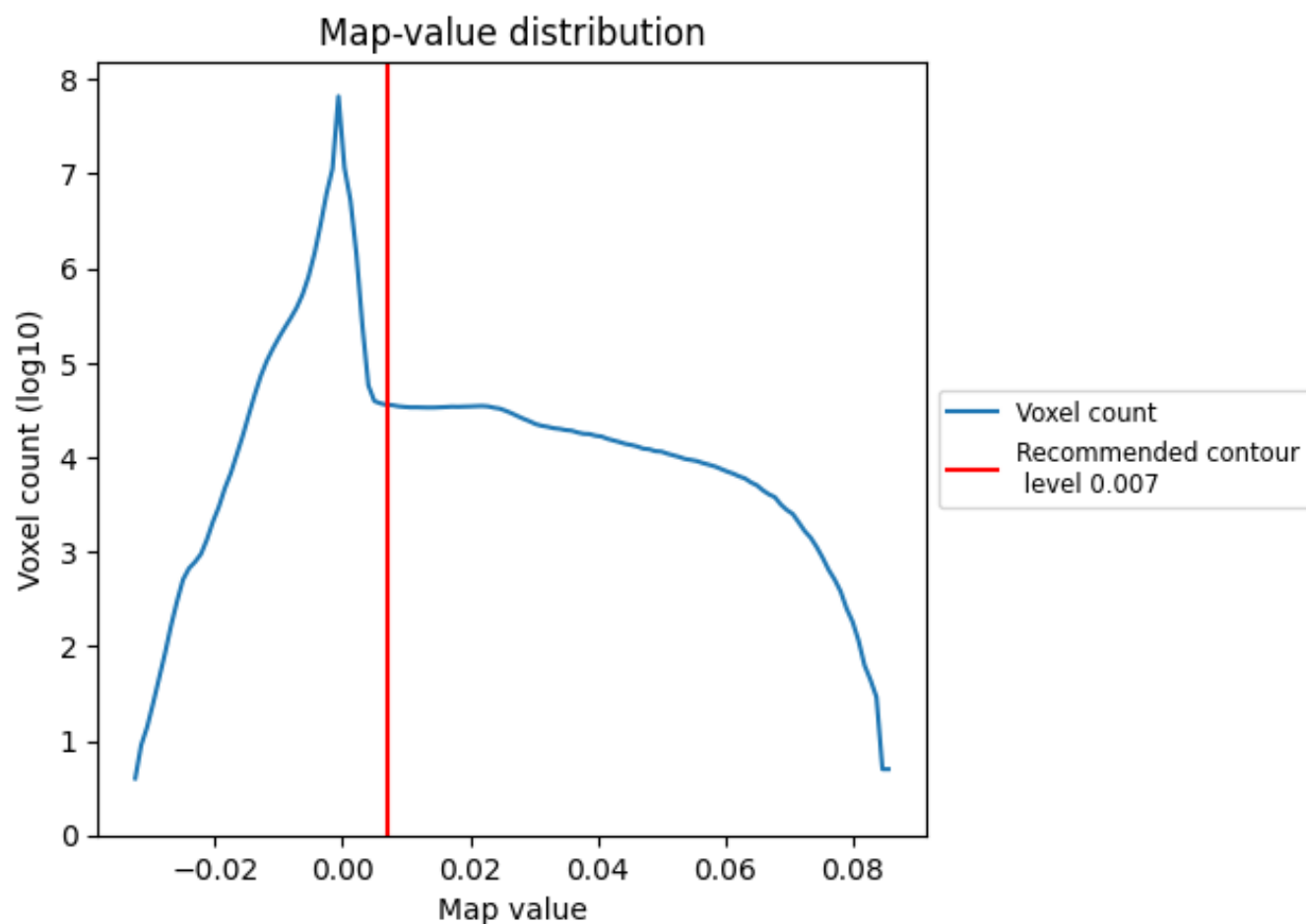


Z

## 7 Map analysis [i](#)

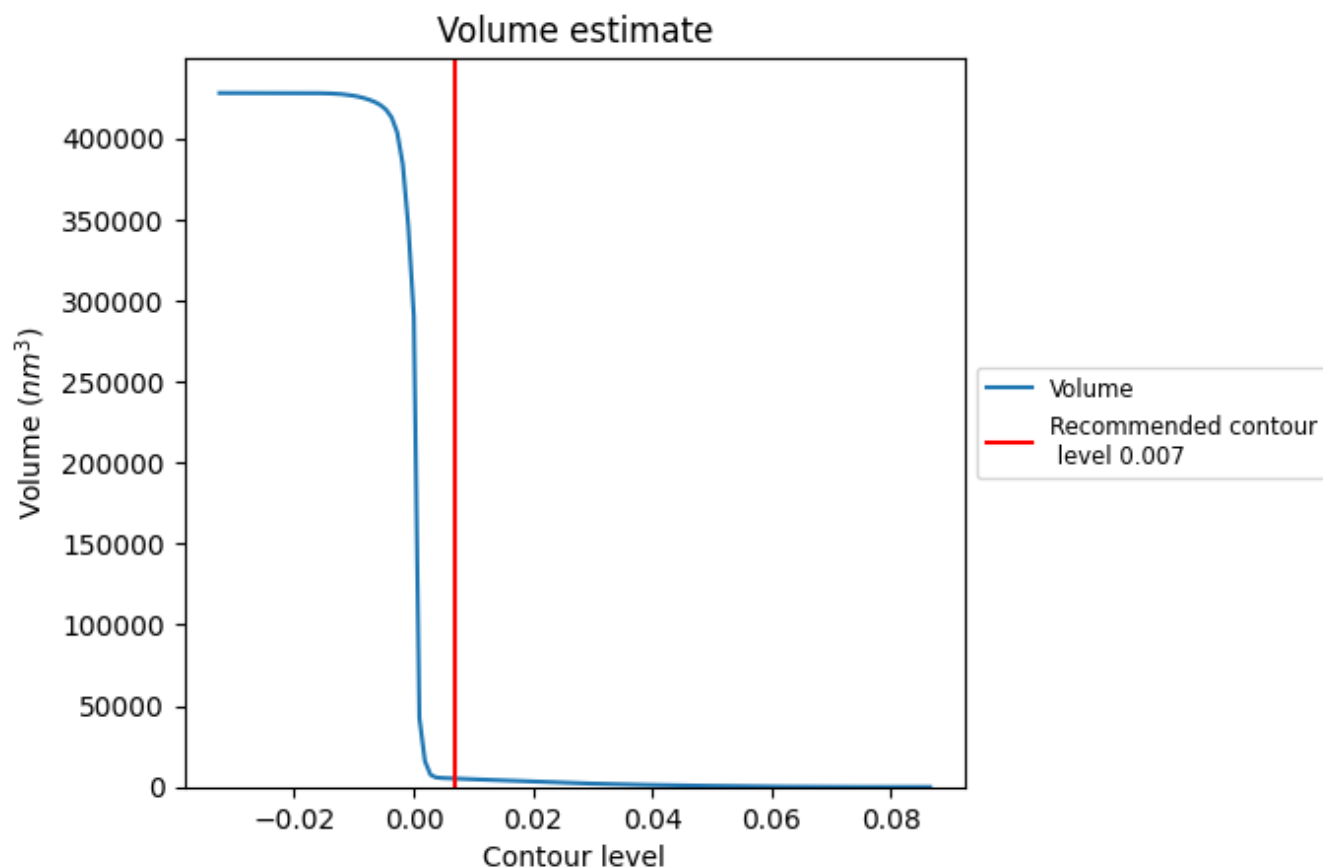
This section contains the results of statistical analysis of the map.

### 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.

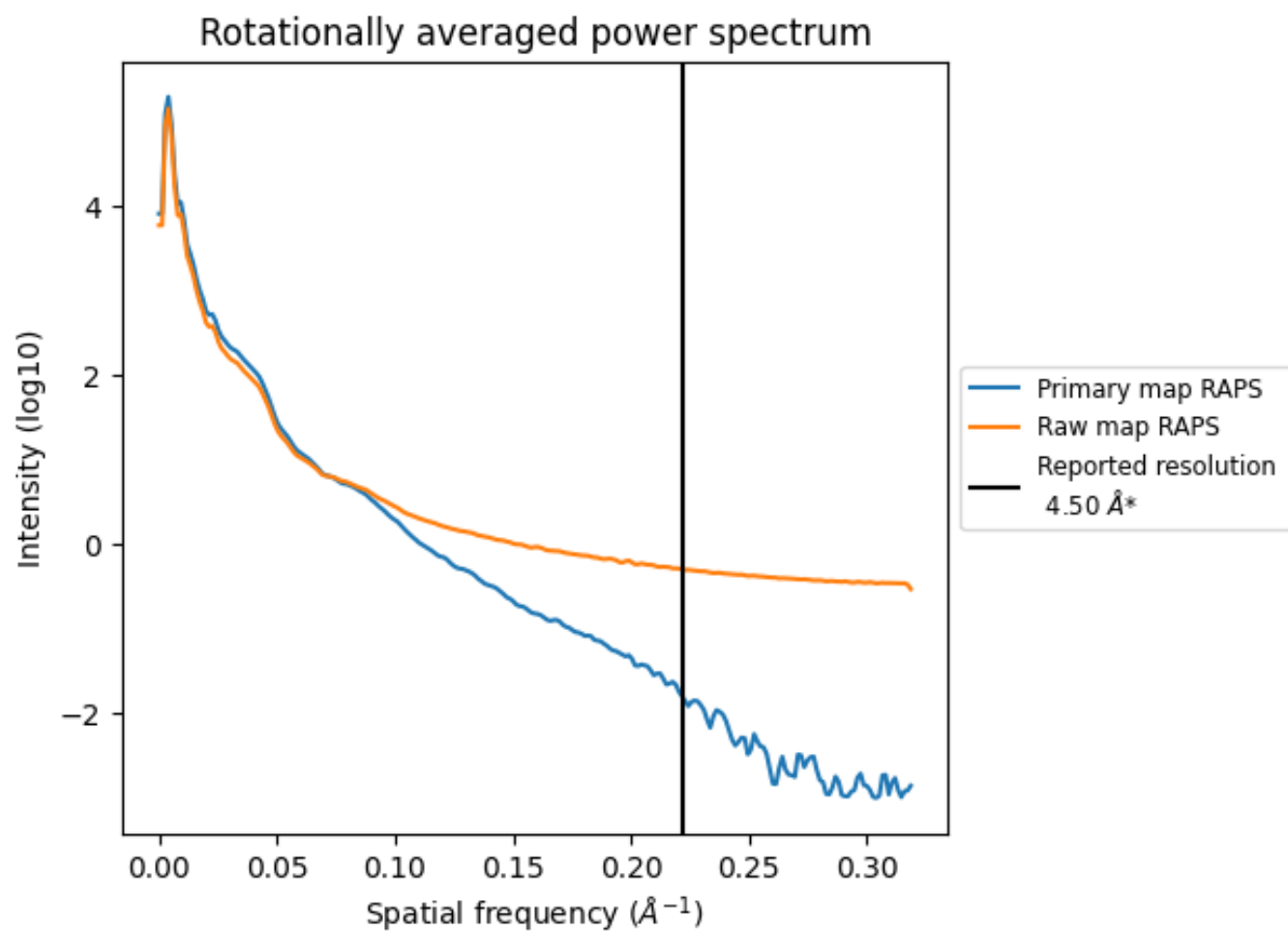
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5179  $\text{nm}^3$ ; this corresponds to an approximate mass of 4678 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 [i](#)

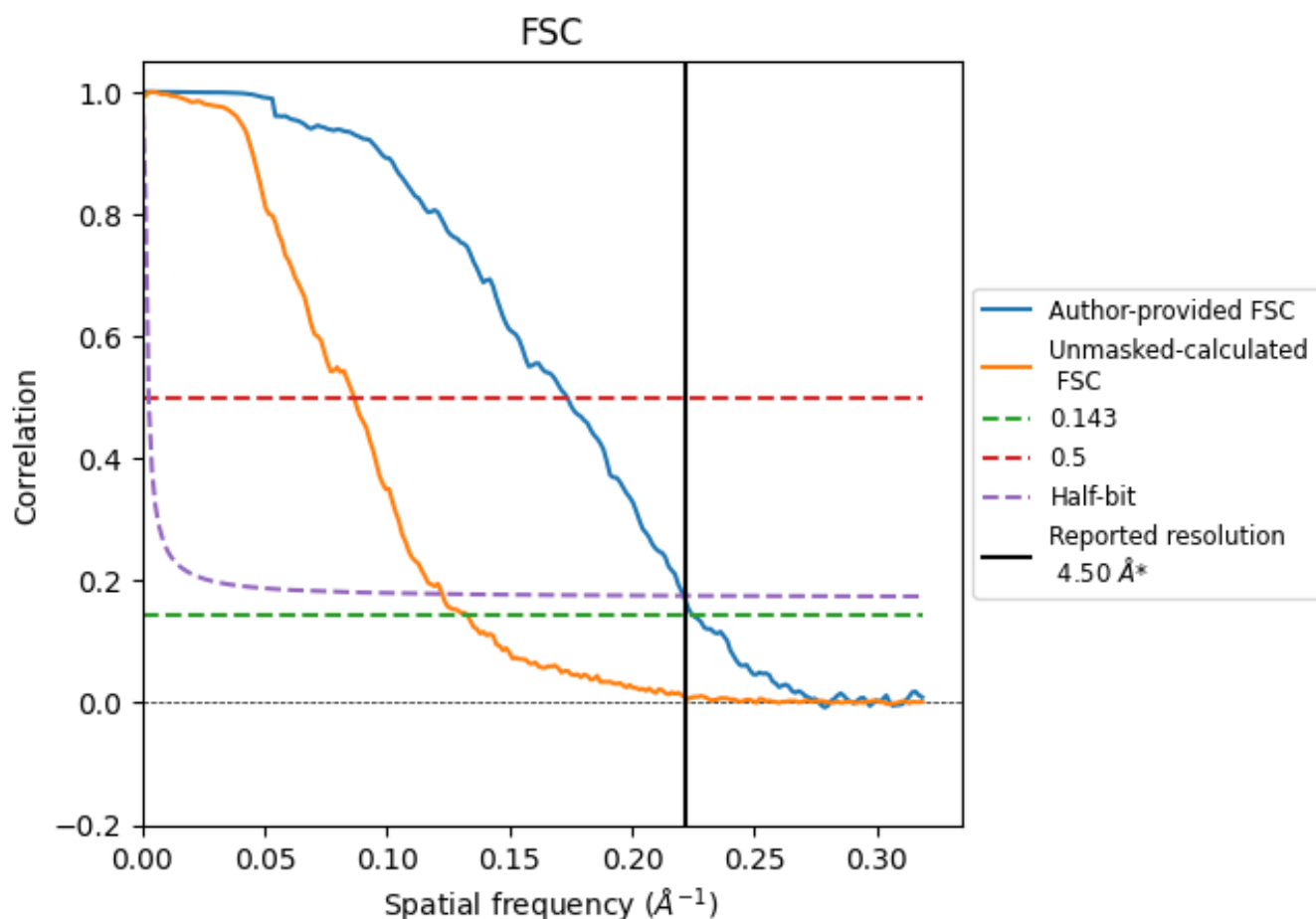


\*Reported resolution corresponds to spatial frequency of 0.222 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.222 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

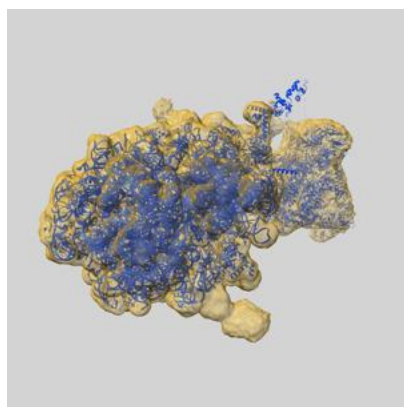
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.45	5.77	4.52
Unmasked-calculated*	7.53	11.57	8.16

\*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 7.53 differs from the reported value 4.5 by more than 10 %

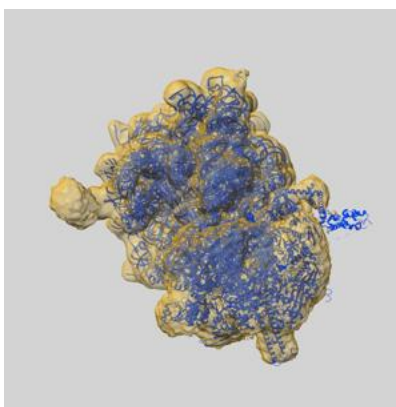
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-38947 and PDB model 8Y5R. Per-residue inclusion information can be found in section 3 on page 18.

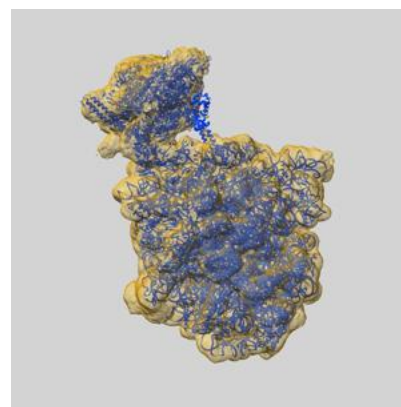
### 9.1 Map-model overlay [i](#)



X



Y



Z

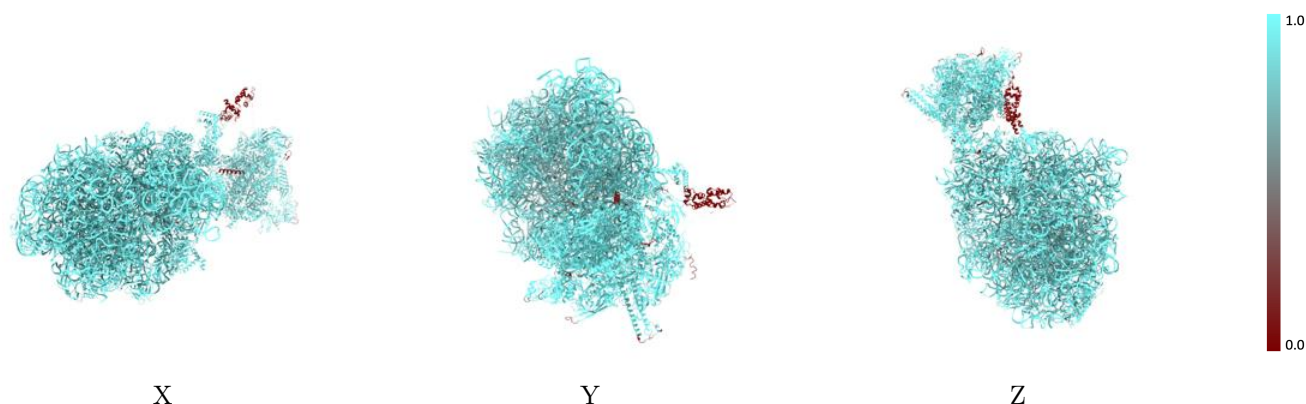
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



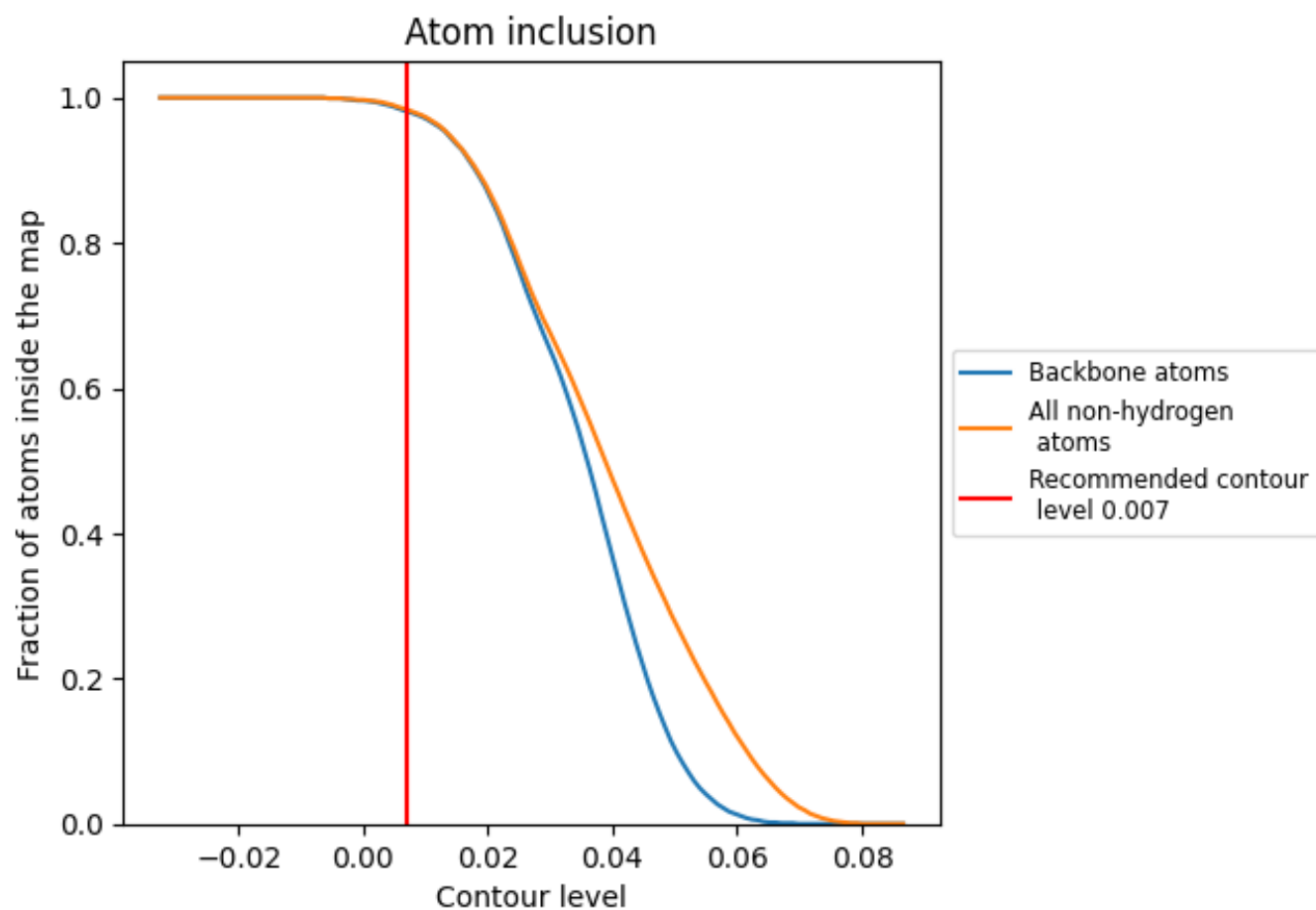
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9840	 0.1860
0	 0.9620	 0.1590
1	 0.9990	 0.2370
2	 1.0000	 0.2190
3	 0.9990	 0.2220
4	 0.9600	 0.0710
5	 0.9770	 0.1390
6	 0.8350	 0.0860
8	 1.0000	 0.0480
9	 1.0000	 0.0880
A	 0.9780	 0.1340
A1	 0.9270	 0.0570
A2	 0.8330	 0.0560
B	 0.9950	 0.1950
B1	 0.9580	 0.0460
B2	 0.9760	 0.0550
C	 0.9850	 0.1850
D	 0.9860	 0.1780
E	 1.0000	 0.1740
F	 1.0000	 0.1580
G	 0.9900	 0.1840
H	 0.9780	 0.1770
I	 0.9980	 0.1480
J	 0.9930	 0.1970
K	 0.9940	 0.1890
L	 0.9940	 0.1930
M	 0.9850	 0.1870
N	 0.9990	 0.1660
NA	 0.8350	 0.1560
NG	 0.9140	 0.0750
O	 1.0000	 0.1410
P	 0.9980	 0.2010
Q	 0.9460	 0.1560
R	 0.9990	 0.1670
S	 0.9970	 0.1300



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Chain	Atom inclusion	Q-score
T	 0.9940	 0.1650
U	 0.9980	 0.1540
V	 0.9870	 0.1840
W	 0.9980	 0.1550
W0	 0.5610	 0.0450
X	 0.9870	 0.1100
Y	 0.9950	 0.1780
Z	 0.9770	 0.1500
b	 0.9950	 0.2210
c	 0.9950	 0.1920
d	 0.9960	 0.1930
e	 0.9910	 0.1700
f	 0.9780	 0.1860
g	 0.9980	 0.1820
i	 0.9560	 0.0900
j	 0.9960	 0.1930
k	 0.9880	 0.2310
l	 1.0000	 0.1900
m	 0.9880	 0.2080
n	 1.0000	 0.1840
o	 1.0000	 0.1720
p	 0.9870	 0.2130
q	 0.9990	 0.1670
r	 0.9960	 0.1940
s	 0.9920	 0.1970
t	 0.9890	 0.1840
u	 0.9950	 0.1700
v	 0.9970	 0.1800
w	 1.0000	 0.1690
x	 1.0000	 0.1940
y	 1.0000	 0.1660
z	 0.9950	 0.1960