



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 05:40 AM UTC

PDB ID : 8Y5T / pdb_00008y5t
EMDB ID : EMD-38949
Title : E.coli Transcription translation coupling complex in TTC-B state 5 (subclass 3) 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 : 4.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

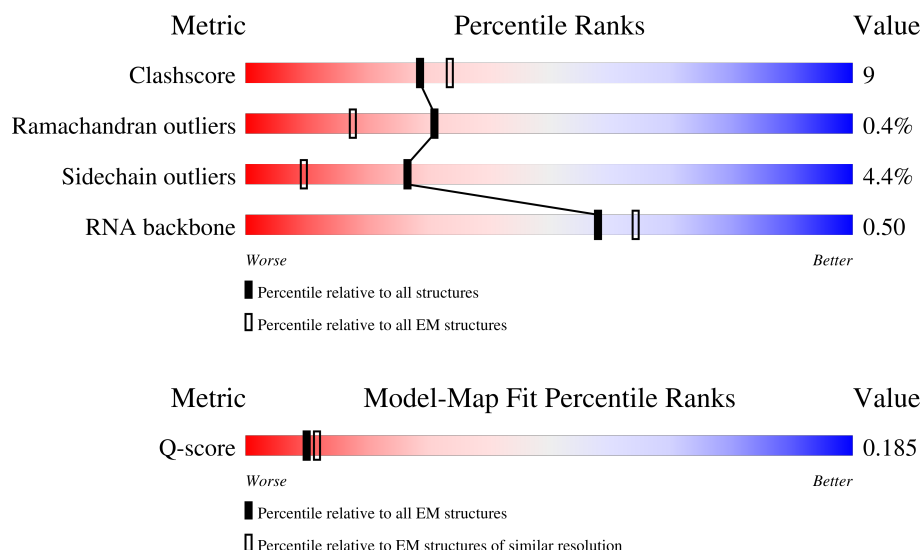
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 4.40 Å.

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



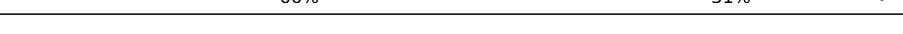
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3132 (3.91 - 4.90)

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

Mol	Chain	Length	Quality of chain
1	A	70	
2	B	57	
3	C	55	

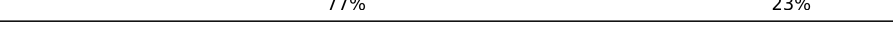
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Mol	Chain	Length	Quality of chain
4	D	46	
5	E	65	
6	F	38	
7	G	241	
8	H	233	
9	I	206	
10	J	167	
11	K	135	
12	L	179	
13	M	130	
14	N	130	
15	O	103	
16	P	129	
17	Q	124	
18	R	118	
19	S	101	
20	T	89	
21	U	82	
22	V	84	
23	W	75	
24	X	92	
25	Y	87	
26	Z	71	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

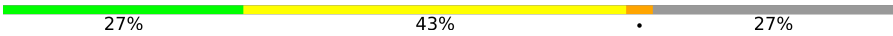
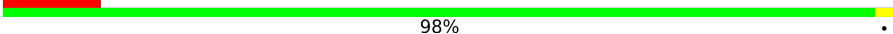
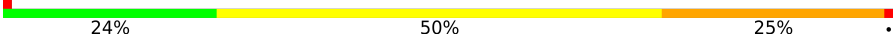
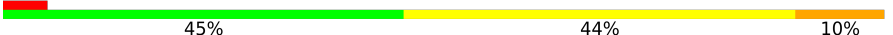
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Mol	Chain	Length	Quality of chain
29	d	201	 81% 19%
30	e	179	 78% 21% ..
31	f	177	 72% 27% ..
32	g	149	 26% 9% 65%
33	i	142	 58% 37% ...
34	j	142	 86% 14%
35	k	123	 80% 20% .
36	l	144	 86% 13% .
37	m	136	 83% 17%
38	n	127	 75% 20% 6%
39	o	117	 82% 17% .
40	p	115	 86% 12% ..
41	q	118	 83% 15% ..
42	r	103	 77% 23%
43	s	110	 85% 15%
44	t	100	 76% 17% 7%
45	u	104	 72% 26% .
46	v	94	 85% 15%
47	w	85	 73% 15% 12%
48	x	78	 77% 21% ..
49	y	63	 78% 22%
50	z	59	 76% 22% .
51	1	2904	 43% 51% 7%
52	2	120	 74% 22% .
53	3	1542	 68% 29% .

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Mol	Chain	Length	Quality of chain
54	4	44	
55	8	37	
56	9	37	
57	A1	329	
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 179688 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	S	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	218	Total	C	N	O	S	0	0
			1677	1048	297	326	6		
57	A2	67	Total	C	N	O		0	0
			331	197	67	67			

- 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		

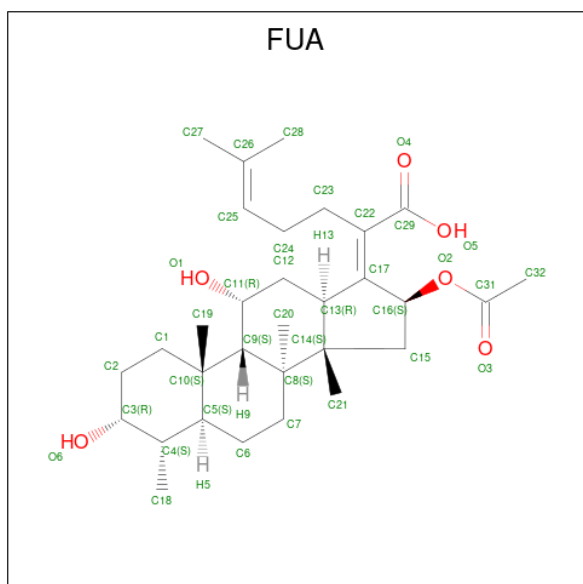
There are 12 discrepancies between the modelled and reference sequences:

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).

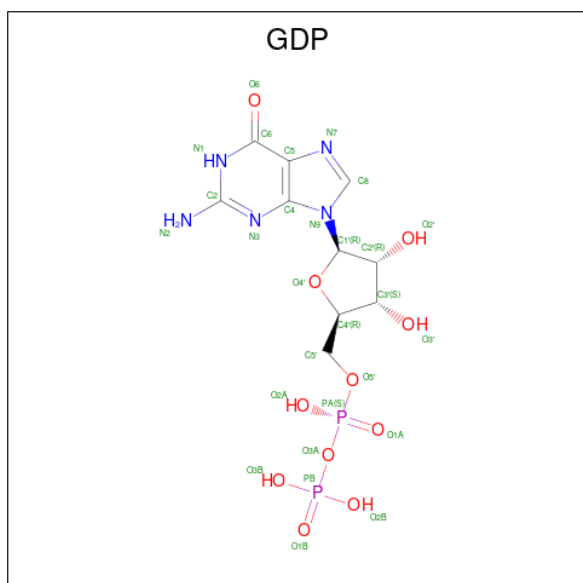
Mol	Chain	Residues	Atoms		AltConf
66	B1	1	Total	Mg	0
			1	1	

- 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: 



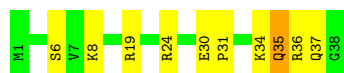
- Molecule 5: 50S ribosomal protein L35

Chain E: 



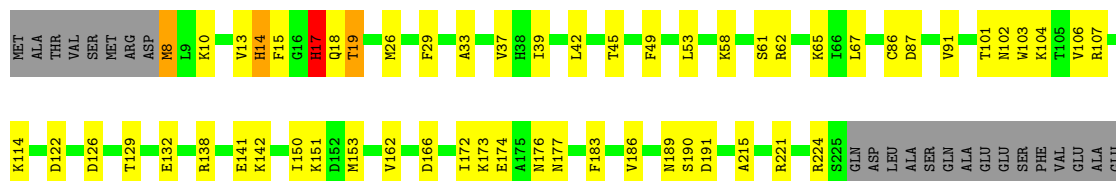
- Molecule 6: 50S ribosomal protein L36

Chain F:  74% 24% .



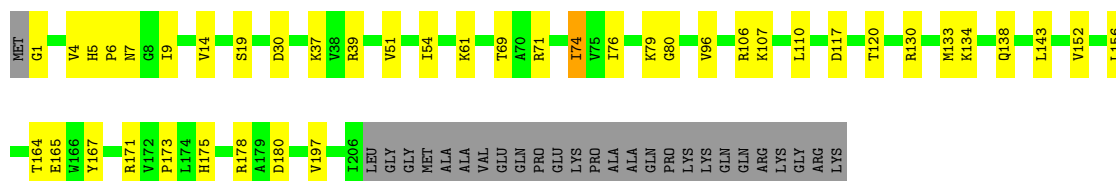
- Molecule 7: 30S ribosomal protein S2

Chain G:  67% 22% . 10%



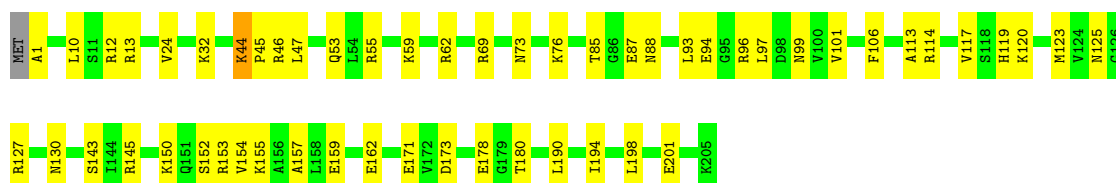
- Molecule 8: 30S ribosomal protein S3

Chain H:  70% 18% 12%



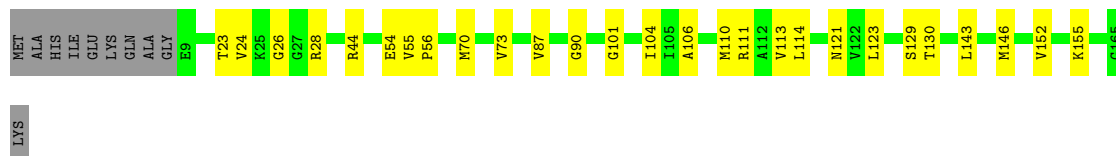
- Molecule 9: 30S ribosomal protein S4

Chain I:  73% 26%



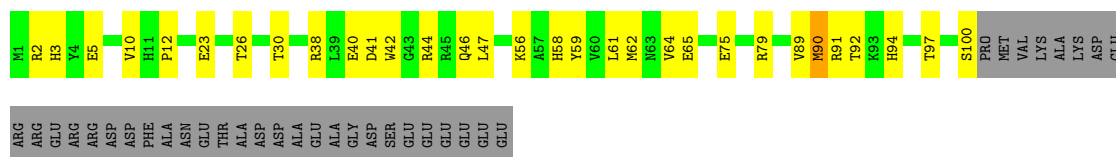
- Molecule 10: 30S ribosomal protein S5

Chain J:  78% 16% 6%



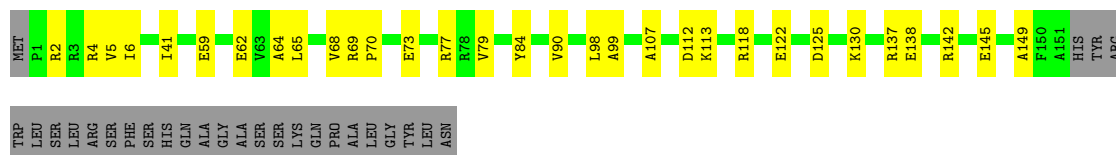
- Molecule 11: 30S ribosomal protein S6, fully modified isoform

Chain K:  51% 22% 26%



- Molecule 12: 30S ribosomal protein S7

Chain L: 67% 17% 16%



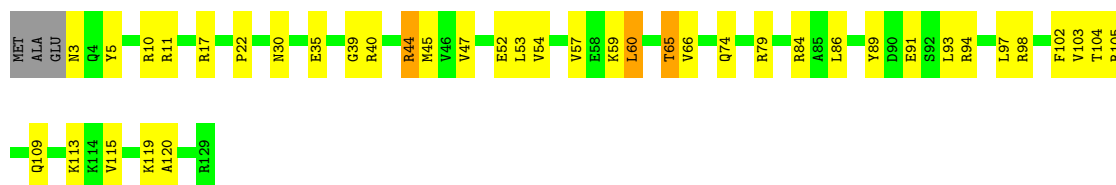
- Molecule 13: 30S ribosomal protein S8

Chain M: 88% 12%



- Molecule 14: 30S ribosomal protein S9

Chain N: 67% 28% 5%



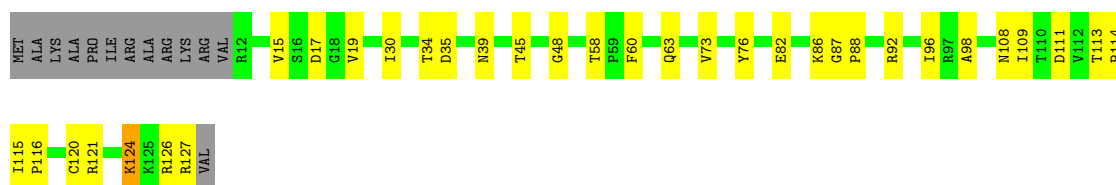
- Molecule 15: 30S ribosomal protein S10

Chain O: 72% 19% 9%



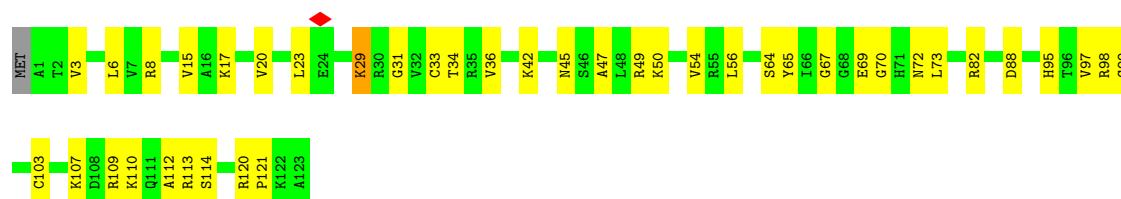
- Molecule 16: 30S ribosomal protein S11

Chain P: 64% 25% 11%



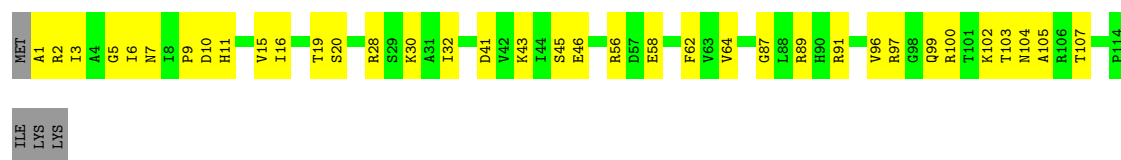
- Molecule 17: 30S ribosomal protein S12

Chain Q:  66% 32%



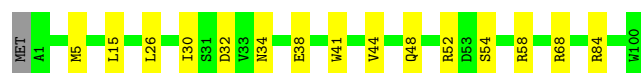
- Molecule 18: 30S ribosomal protein S13

Chain R:  66% 31%



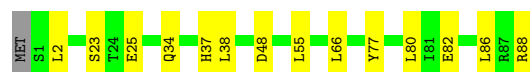
- Molecule 19: 30S ribosomal protein S14

Chain S:  84% 15%



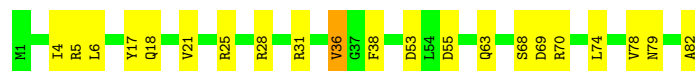
- Molecule 20: 30S ribosomal protein S15

Chain T:  83% 16%



- Molecule 21: 30S ribosomal protein S16

Chain U:  74% 24%



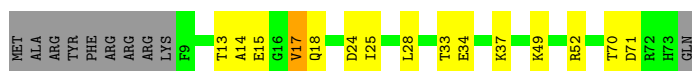
- Molecule 22: 30S ribosomal protein S17

Chain V:  75% 19% 5%



- Molecule 23: 30S ribosomal protein S18

Chain W:  67% 19% 13%



- Molecule 24: 30S ribosomal protein S19



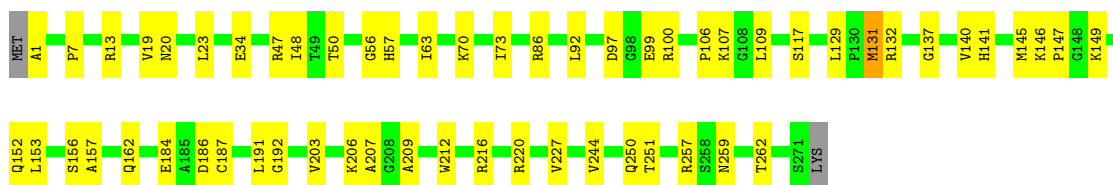
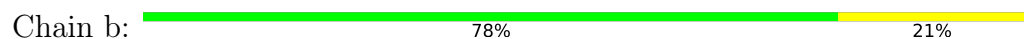
- Molecule 25: 30S ribosomal protein S20



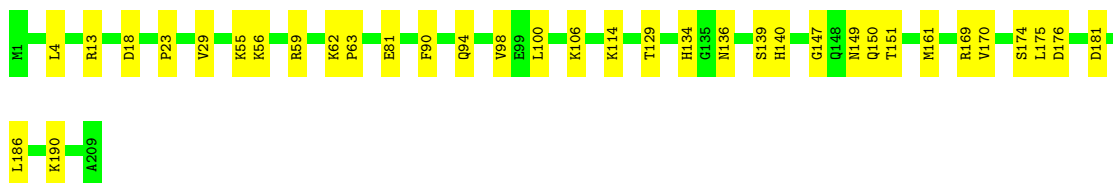
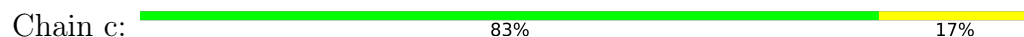
- Molecule 26: 30S ribosomal protein S21



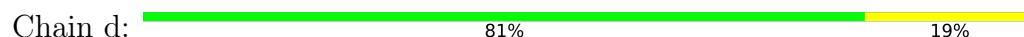
- Molecule 27: 50S ribosomal protein L2

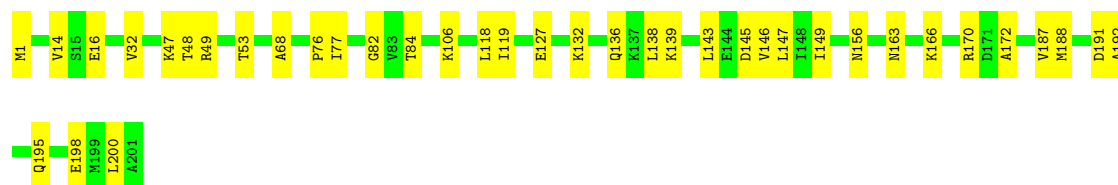


- Molecule 28: 50S ribosomal protein L3



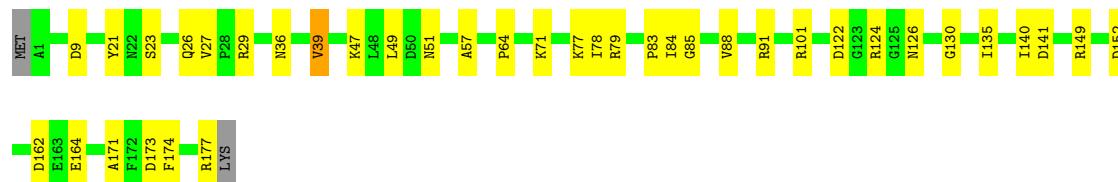
- Molecule 29: 50S ribosomal protein L4





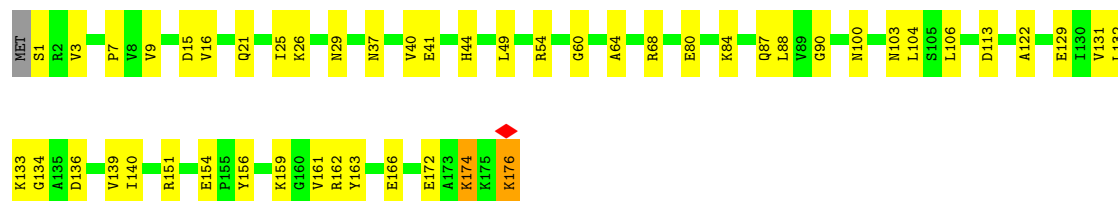
- Molecule 30: 50S ribosomal protein L5

Chain e: 78% 21% ..



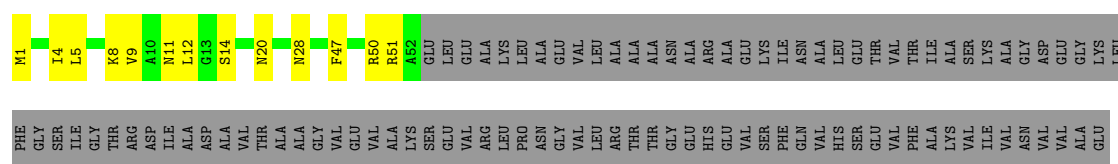
- Molecule 31: 50S ribosomal protein L6

Chain f: 72% 27% ..



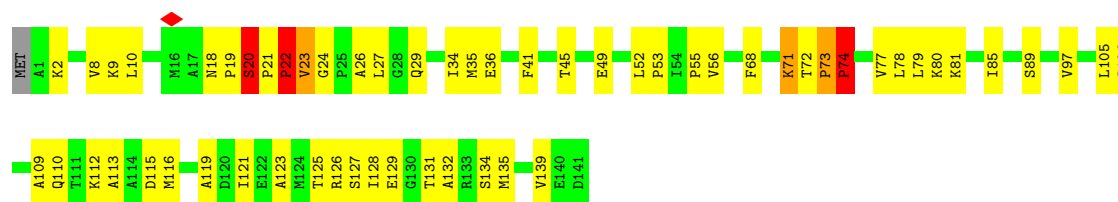
- Molecule 32: 50S ribosomal protein L9

Chain g: 26% 9% 65%



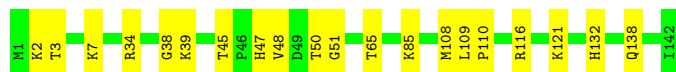
- Molecule 33: 50S ribosomal protein L11

Chain i: 58% 37% ...



- Molecule 34: 50S ribosomal protein L13

Chain j:  86% 14%



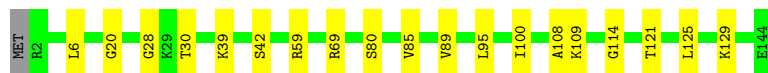
- Molecule 35: 50S ribosomal protein L14

Chain k:  80% 20%



- Molecule 36: 50S ribosomal protein L15

Chain l:  86% 13%



- Molecule 37: 50S ribosomal protein L16

Chain m:  83% 17%



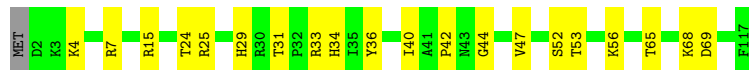
- Molecule 38: 50S ribosomal protein L17

Chain n:  75% 20% 6%



- Molecule 39: 50S ribosomal protein L18

Chain o:  82% 17%



- 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%



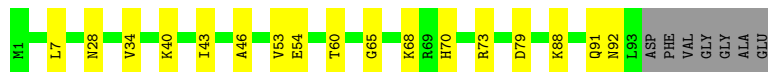
- Molecule 43: 50S ribosomal protein L22

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%



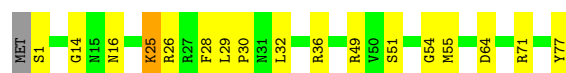
- Molecule 47: 50S ribosomal protein L27

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%



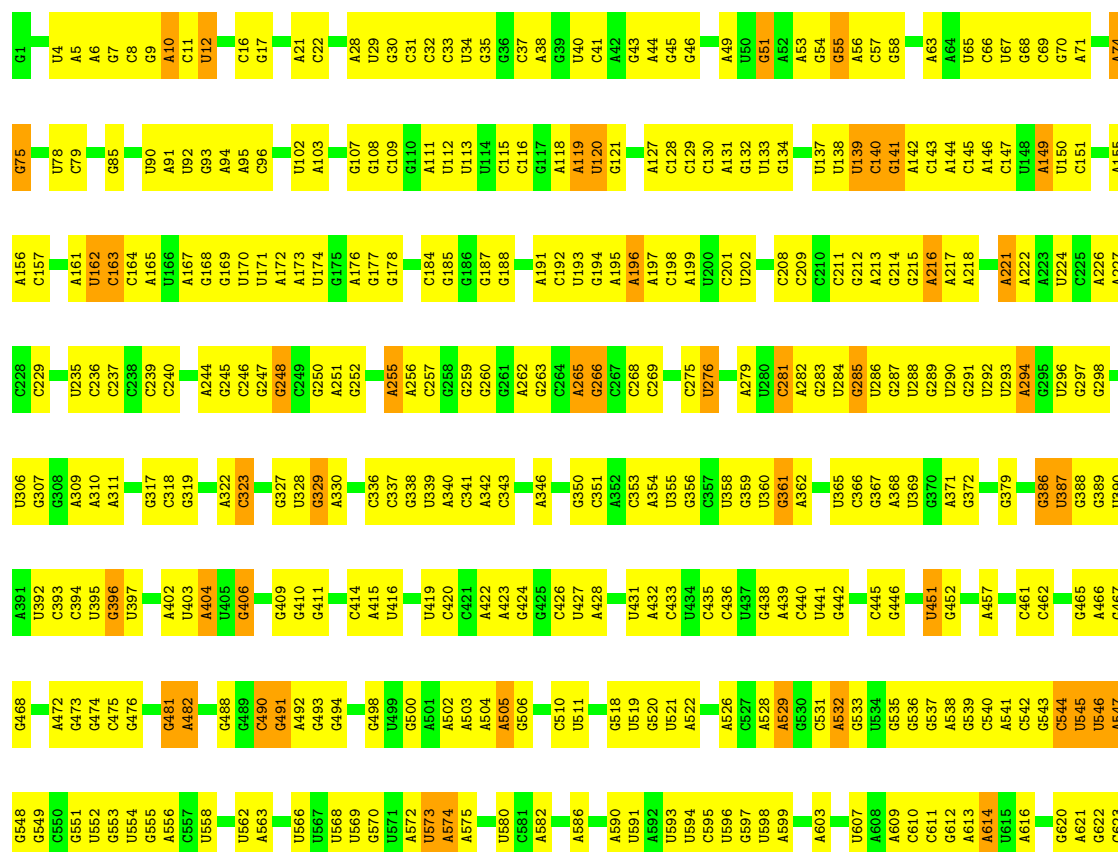
- Molecule 50: 50S ribosomal protein L30

Chain z:  76% 22% .



- Molecule 51: 23S rRNA

Chain 1:  43% 51% 7%



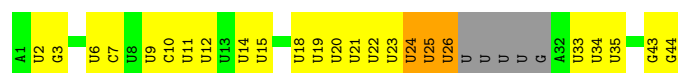


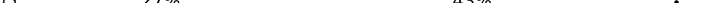
G2890	C2805	G2729	G2642	A2564	C2467	G2383	G2303	G2224	G2157	C2091	C1985	G1906	A1821
G2893	C2806	G2730	G2643	A2565	C2468	U2384	G2304	A2225	A2158	U2092	C1986	G1907	A1822
G2894	A2810	G2731	G2644	A2566	A2469	G2385	G2305	C2226	G2159	G2093	C1987	G1908	G1823
G2895	G2811	G2732	G2645	A2567	A2470	A2386	C2306	A2227	C2160	A2094	C1990	C1909	
G2896	G2812	G2733	G2646	G2568	A2471	A2387	A2309	G2230	C2161	A2095	U1991	G1910	U1827
G2897	A2813	A2734	G2647	G2569		A2388	G2310		A2163	A2096	U1992	G1911	G1828
G2898	A2814	G2735	G2648	G2570		G2389	G2311		C2164	A2097	U1993	A1912	A1829
G2899	G2815	A2736	G2649	U2571	A2476	U2390	A2312	U2233	C2165	U2098	C1997	A1913	C1832
G2900	G2816	G2737	G2650	A2572	A2482	G2391	U2313	G2234	U2166	G2100	A1998	C1914	C1833
C2901	G2816	G2737	G2651	G2573	A2483	U2392	A2314	G2235	U2167	A2101	C1999	A1915	U1834
A2820	C2852		G2652	G2574		C2394	G2315	G2236	U2168	G2102		U1917	
		A2741		G2575	G2488	C2395	G2316	G2237	A2170	C2103	G2012	A1918	G1845
		G2742		G2576	U2489	G2396		G2238	A2171	G2104	A2013	A1919	G1846
		U2743		A2577	G2490		U2321	G2239	U2172	U2105	A2014	A1920	G1847
		G2744		G2578	U2491	U2402	G2325	U2240	A2173	A2106	A2015	G1921	A1847
				G2579	U2492	C2403	G2326	G2241	A2174	G2107	U2016	G1922	A1848
		G2747		U2580		U2404	A2327	G2242	C2174			U1923	
		A2748		G2581	C2496	G2405	A2328	U2243		G2110	A2020	C1924	U1851
		A2749		G2582	A2497	U2406	A2329		U2180	U2112	C2021		U1852
		G2750		G2583	C2498	A2407	G2330	A2247	U2181	U2113	C2022	A1927	A1853
		G2751		U2584	C2499	A2408		G2248	U2182	U2114	C2023	A1928	U1854
				U2585		A2411	G2331	G2249	A2183	U2115	C2024	A1929	U1855
		U2754				A2412	G2332	G2250	A2184	G2115	C2025	G1930	G1856
		C2755		U2593	G2502		A2333	A2268	U2185		U2026	U1931	G1857
				G2594			U2334		G2186	U2118	G2027		A1858
				G2595	G2505	C2420	A2335	U2257	U2187	A2119		G1935	G1863
					U2506	G2421	A2336	C2258	U2188			G1936	U1864
				A2598	C2507	G2422	G2337	C2259	U2189		A2030	A1937	U1865
				G2599		U2423	G2338	C2260	G2190	U2122	C2031	A1938	U1866
				A2600	C2510	G2424	C2339	A2267	A2191	G2123	G2032	U1939	G1867
				G2601	U2511	A2425	A2340	A2268	U2192	G2124	U2034		G1868
				A2602		A2426			G2193	G2125			C1869
					A2516	C2427	G2345	G2271	U2194	A2126	G2035	C1942	C1870
				U2609	C2517	G2428	A2346		U2195	G2127	G2036	U1943	A1871
				G2610	A2518	G2429	C2347	C2275	C2196	U1944	A2037	U1945	A1872
				C2611	G2525	A2430	U2348		U2197	G2129			G1873
				G2612	G2526	U2431	G2349	A2278	A2198	U2130	C2043	G1948	C1874
				U2613	G2527	A2432	C2350	G2279	A2199	U2131			G1875
				A2614	C2528	A2433	G2351	G2280	C2200	U2132	C2047	A1952	
				U2615	U2528	A2434	A2352	A2281	G2201	G2133	G2048	A1953	G1878
				G2616	G2529	A2435		G2282	U2202	A2134	C2049	A1954	C1879
				U2617	A2530	G2436	G2357	C2283	U2203		C2050	U1955	C1879
				G2618		G2437		A2284	G2204	U2137	A2051	U1956	
				U2619	U2533		G2360	C2285	A2205	G2138	A2052	U1956	U1882
					A2534	C2440	G2361	C2286			G2053	U1963	U1883
				G2625		U2441	G2362	A2287	C2208	G2141	A2054	U1963	G1884
				C2626	C2539		G2363	A2288	G2209		C2055	G1964	A1885
				G2627			C2364	G2289	U2210	G2144	G2056	C1965	U1886
				C2628	G2545	G2446	G2365	G2290	A2211	G2145	A1966	C1966	U1887
				U2629	U2546	G2447	A2366	U2291	A2212	C2146	A2060	C1967	G1888
				G2630	A2547	A2448	G2367	U2292	U2213	A2147	G2061	G1968	A1889
				G2631			C2368	U2293	G2214	G2148		A1969	A1890
				A2632	U2554	G2455		G2294	C2215	U2149	G2069	A1970	
				G2633	U2555	C2456	G2371	C2295	G2216	U2150		U1971	C1893
				A2634	C2556	U2457	U2372	U2296	G2217	U2151	C2073	G1972	C1894
				A2635	C2557	G2458		U2297	G2218	G2152	U2074		
				C2636			G2379	A2298		C2153		A1978	A1901
				U2637	U2561	C2462	C2380	U2299	G2221	A2154	U2085	C1983	C1902
				G2638	U2562	G2463	A2381	U2299	G2222	U2155	U2086	G1984	C1905
					U2563	G2464	G2382	U2302	G2223	G2156			

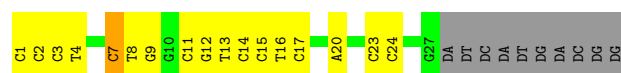
• Molecule 52: 5S rRNA

Chain 2: 74% 22%



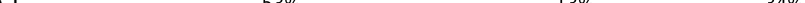


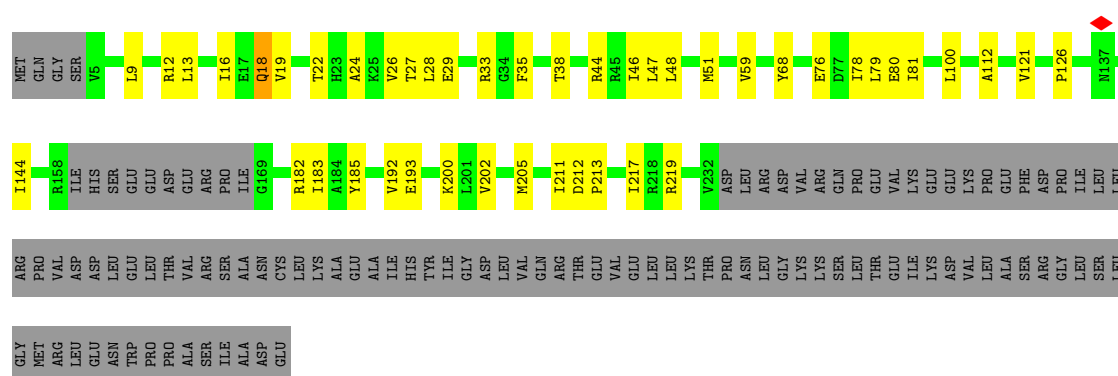
- Chain 8:  27% 43% . 27%



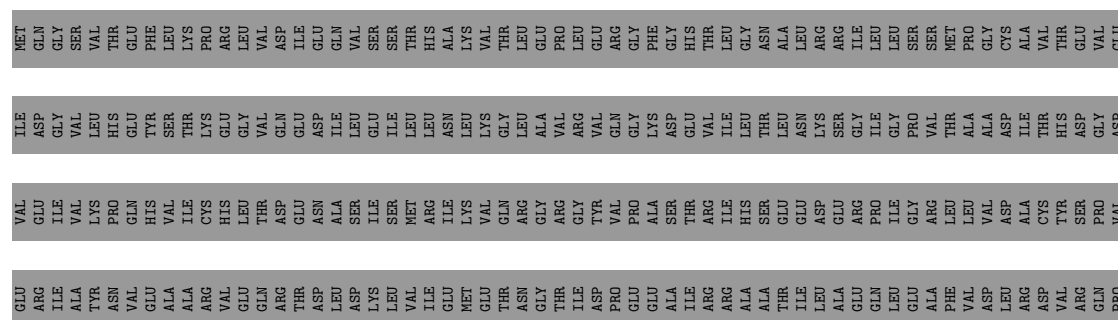
- Chain 9: 51% 1% 46%

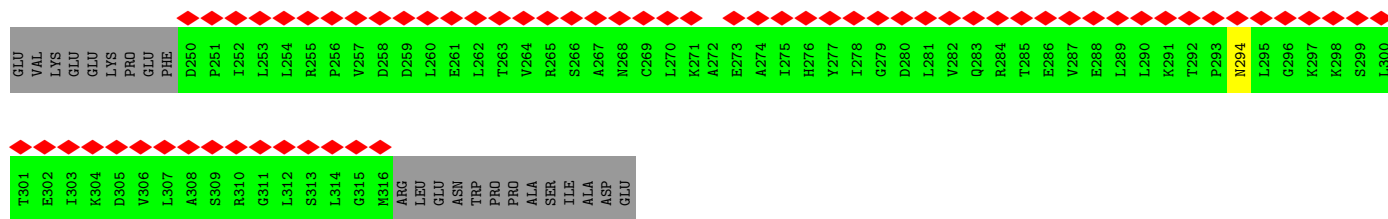


- Chain A1: 



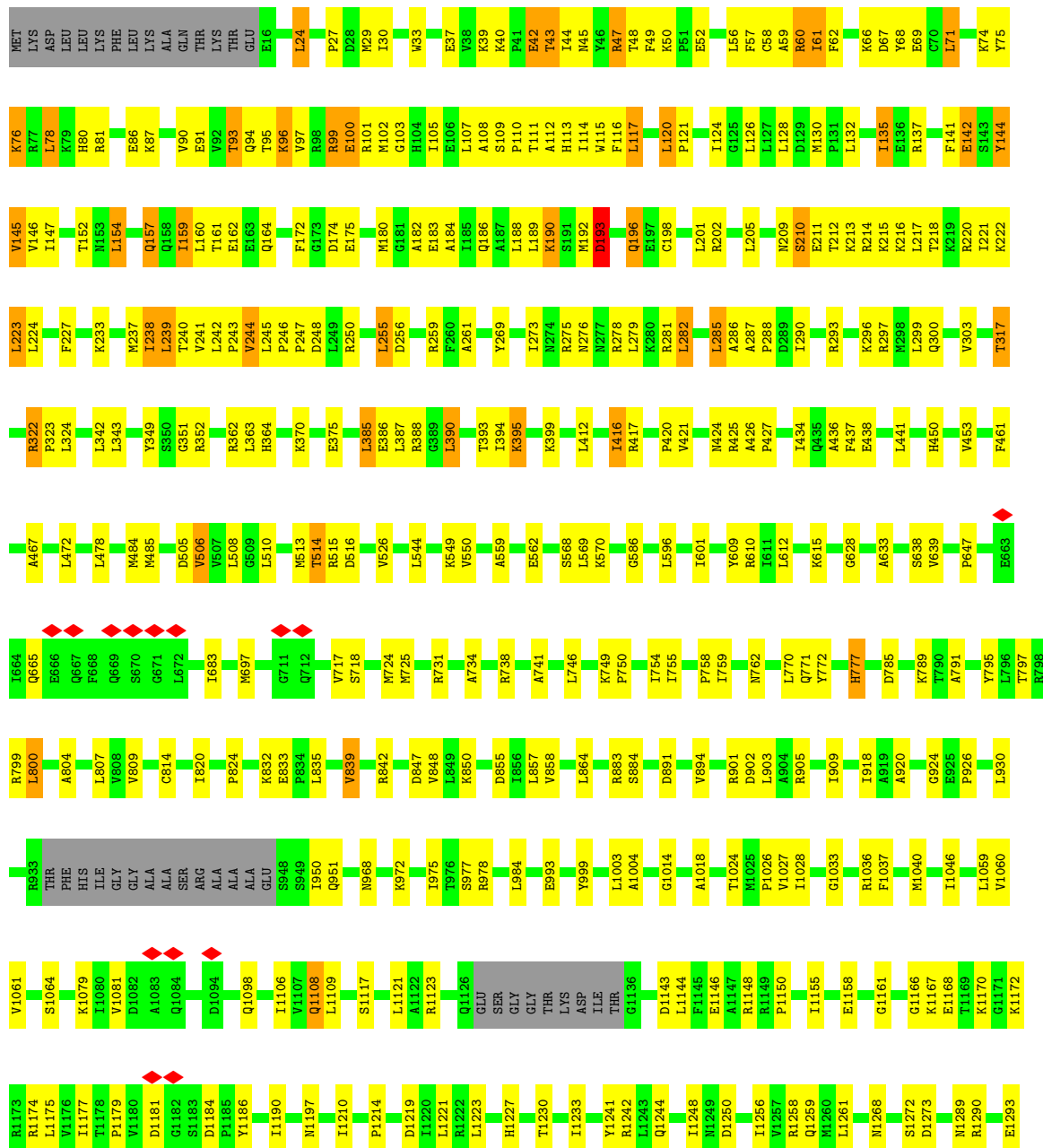
- Chain A2:

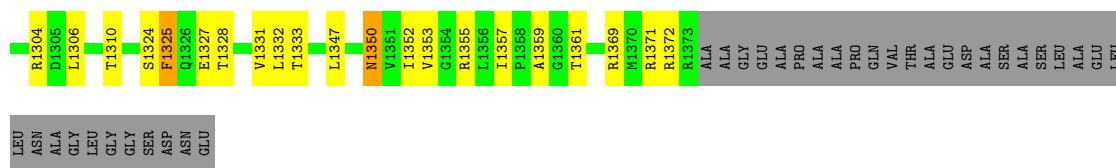




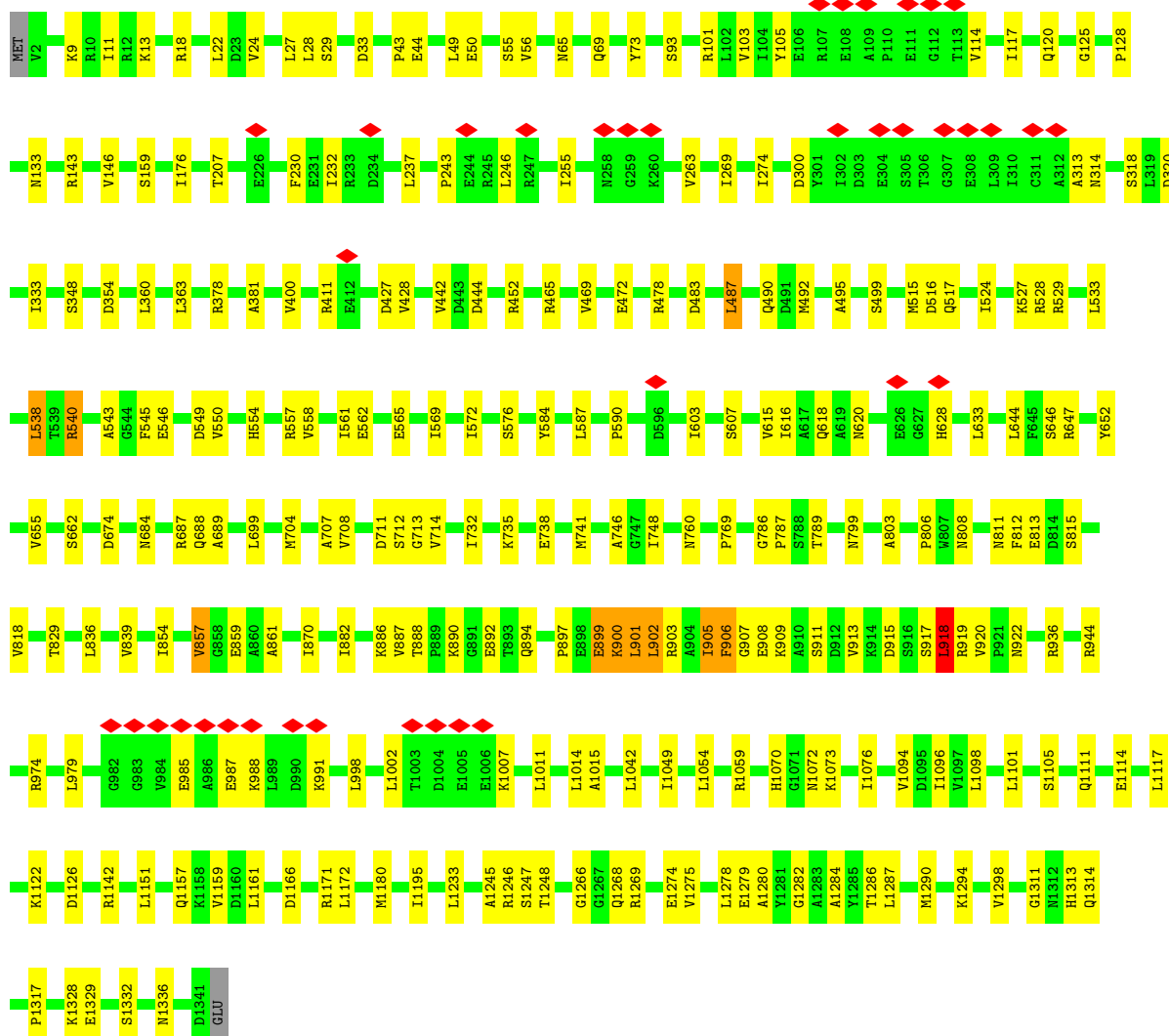
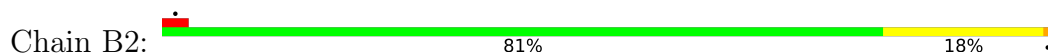
- Molecule 58: DNA-directed RNA polymerase subunit beta'

Chain B1: 67% 25% 5%

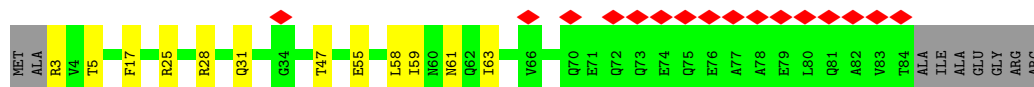
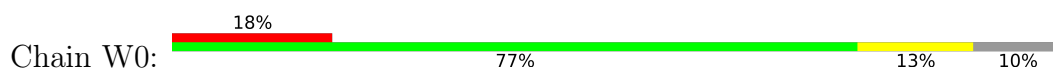




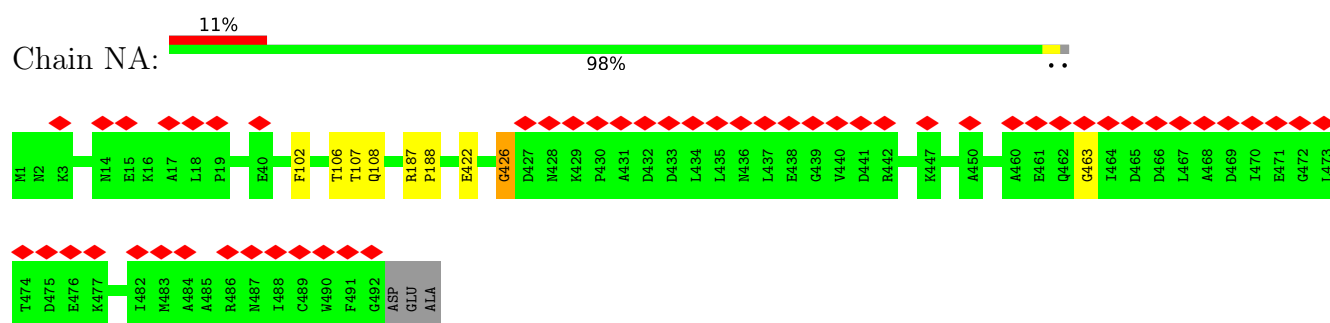
- Molecule 59: DNA-directed RNA polymerase subunit beta



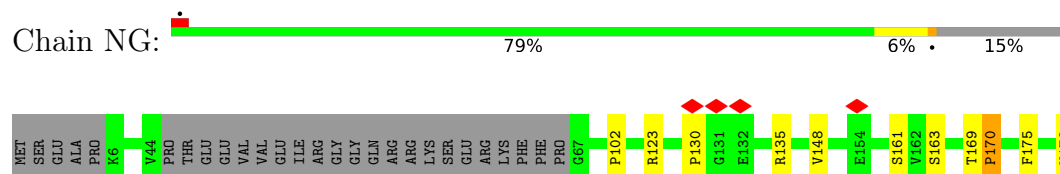
- Molecule 60: DNA-directed RNA polymerase subunit omega



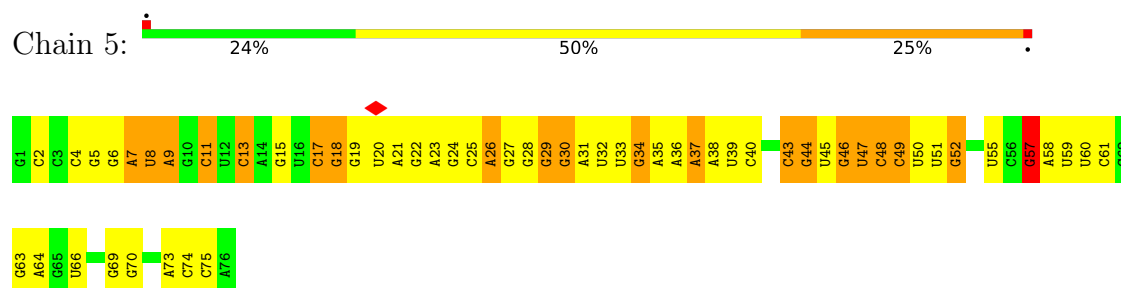
- Molecule 61: Transcription termination/antitermination protein NusA



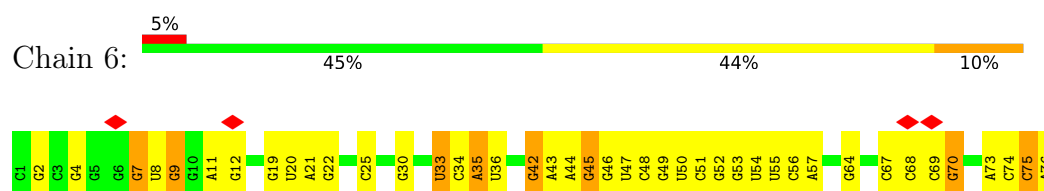
- Molecule 62: Transcription termination/antitermination protein NusG



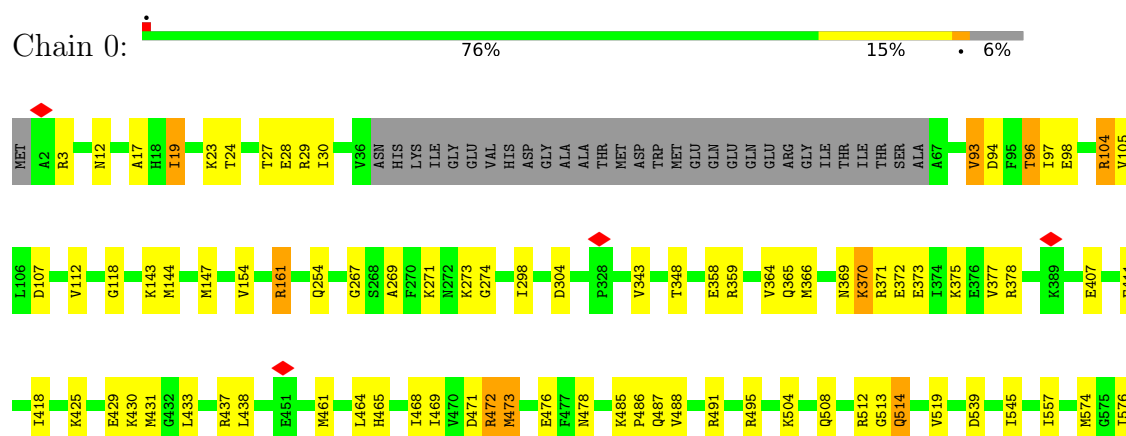
- Molecule 63: tRNA(Phe)

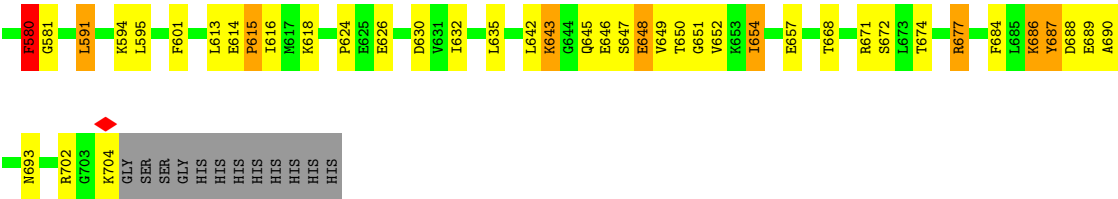


- Molecule 64: tRNA(fMet)



- Molecule 65: Elongation factor G





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	0.088	Depositor
Minimum map value	-0.032	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.005	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: FUA, MG, GDP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.27	0/530	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	0.57	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	0.31	0/1195	0.66	3/1602 (0.2%)
13	M	0.35	0/989	0.53	0/1326
14	N	0.47	0/1034	0.77	0/1375
15	O	0.49	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	4/1193 (0.3%)
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	0.55	0/1046	0.93	4/1410 (0.3%)
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	0.44	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	0.55	0/896	0.74	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	0.48	0/1696	0.69	0/2298
57	A2	0.75	0/330	1.20	0/458
58	B1	0.57	5/10510 (0.0%)	0.75	8/14196 (0.1%)
59	B2	0.46	0/10714	0.67	1/14459 (0.0%)
60	W0	0.30	0/652	0.60	0/879
61	NA	0.78	0/2431	1.22	0/3385
62	NG	1.11	0/756	1.05	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	5/193000 (0.0%)	0.64	72/284406 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
65	0	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	B1	1350	ASN	CG-ND2	-5.26	1.22	1.33
58	B1	1108	GLN	CD-OE1	5.18	1.33	1.23
58	B1	424	ASN	CG-ND2	-5.14	1.22	1.33
58	B1	665	GLN	CD-OE1	5.03	1.33	1.23
58	B1	1268	ASN	CG-OD1	5.00	1.33	1.23

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	i	74	PRO	N-CA-CB	-11.05	91.64	103.25
65	0	580	PHE	CA-CB-CG	9.59	123.39	113.80
16	P	73	VAL	N-CA-C	-9.08	104.48	113.20
41	q	33	VAL	N-CA-C	-8.69	104.82	112.12
12	L	64	ALA	N-CA-C	-7.71	105.04	114.75
51	1	1130	U	C2'-C3'-O3'	7.59	120.89	109.50
59	B2	897	PRO	N-CA-C	-7.55	104.42	113.86
64	6	33	U	C2'-C3'-O3'	7.28	120.42	109.50
51	1	2326	C	C2'-C3'-O3'	7.17	120.26	109.50
58	B1	450	HIS	CB-CG-CD2	-6.57	122.66	131.20
65	0	615	PRO	CB-CA-C	-6.51	102.45	110.98
51	1	761	A	C4'-C3'-O3'	-6.48	103.27	113.00
58	B1	777	HIS	CB-CG-CD2	-6.41	122.87	131.20
58	B1	61	ILE	CA-C-N	-6.33	114.04	121.64
58	B1	61	ILE	C-N-CA	-6.33	114.04	121.64
28	c	147	GLY	CA-C-N	-6.03	115.26	122.44
28	c	147	GLY	C-N-CA	-6.03	115.26	122.44
51	1	2060	A	C2'-C3'-O3'	5.68	118.02	109.50
65	0	657	GLU	CA-C-N	-5.68	118.39	123.33
65	0	657	GLU	C-N-CA	-5.68	118.39	123.33
58	B1	450	HIS	CB-CG-ND1	5.66	131.19	122.70
26	Z	35	GLU	CA-C-N	5.61	132.25	121.54
26	Z	35	GLU	C-N-CA	5.61	132.25	121.54
51	1	1790	C	N1-C1'-C2'	5.59	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
10	J	155	LYS	N-CA-C	-5.56	107.74	114.75
38	n	47	VAL	N-CA-C	-5.54	107.46	112.12
33	i	73	PRO	N-CA-C	-5.49	104.00	110.70
51	1	960	A	N9-C1'-C2'	5.49	120.23	112.00
51	1	1905	C	C4'-C3'-O3'	-5.48	104.78	113.00
58	B1	777	HIS	CB-CG-ND1	5.46	130.89	122.70
51	1	1451	C	N1-C1'-C2'	5.45	120.17	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	1	1020	A	C2'-C3'-O3'	5.44	117.66	109.50
51	1	1696	G	N9-C1'-C2'	5.40	120.11	112.00
4	D	3	ARG	CA-C-N	5.40	127.78	120.38
4	D	3	ARG	C-N-CA	5.40	127.78	120.38
55	8	7	DC	C2'-C3'-O3'	-5.38	103.42	111.50
51	1	2428	G	N9-C1'-C2'	5.33	120.00	112.00
65	0	271	LYS	N-CA-C	-5.32	106.29	112.89
51	1	1782	U	N1-C1'-C2'	5.31	119.97	112.00
30	e	141	ASP	CA-C-N	5.24	131.54	121.54
30	e	141	ASP	C-N-CA	5.24	131.54	121.54
34	j	110	PRO	N-CA-C	5.24	120.74	113.98
51	1	980	A	N9-C1'-C2'	5.23	119.85	112.00
51	1	2055	C	N1-C1'-C2'	5.23	119.85	112.00
12	L	5	VAL	CA-C-N	5.23	127.70	120.49
12	L	5	VAL	C-N-CA	5.23	127.70	120.49
51	1	2576	G	N9-C1'-C2'	5.22	119.83	112.00
58	B1	27	PRO	N-CA-C	-5.21	106.25	113.81
21	U	78	VAL	CA-C-N	5.19	129.66	121.56
21	U	78	VAL	C-N-CA	5.19	129.66	121.56
51	1	1565	C	N1-C1'-C2'	5.16	119.73	112.00
51	1	2430	A	N9-C1'-C2'	5.15	119.73	112.00
23	W	14	ALA	N-CA-C	-5.14	106.09	112.93
18	R	3	ILE	CA-C-N	5.14	131.35	121.54
18	R	3	ILE	C-N-CA	5.14	131.35	121.54
51	1	1328	A	N9-C1'-C2'	5.14	119.71	112.00
33	i	74	PRO	N-CA-C	5.13	123.03	112.47
63	5	57	G	C4'-C3'-O3'	5.12	117.08	109.40
33	i	22	PRO	N-CA-CB	-5.09	97.90	103.25
58	B1	61	ILE	CA-C-O	-5.09	115.65	120.95
65	0	375	LYS	N-CA-C	-5.08	106.93	112.72
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	2777	G	N9-C1'-C2'	5.06	119.59	112.00
10	J	87	VAL	N-CA-C	5.05	115.92	109.30
51	1	1087	G	N9-C1'-C2'	5.05	119.58	112.00
51	1	972	A	N9-C1'-C2'	5.04	119.56	112.00
48	x	25	LYS	N-CA-C	5.02	121.49	110.80
18	R	6	ILE	CA-C-N	5.01	129.23	121.26
18	R	6	ILE	C-N-CA	5.01	129.23	121.26

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
65	0	161	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	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	37	0
8	H	1624	0	1699	29	0
9	I	1643	0	1710	34	0
10	J	1156	0	1199	17	0
11	K	817	0	808	17	0
12	L	1181	0	1240	19	0
13	M	979	0	1034	9	0
14	N	1022	0	1070	21	0
15	O	786	0	828	12	0
16	P	869	0	878	20	0
17	Q	955	0	1019	26	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	10	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	13	0
27	b	2082	0	2157	47	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	28	0
32	g	400	0	423	6	0
33	i	1032	0	1088	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	j	1129	0	1162	19	0
35	k	938	0	1012	18	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	14	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
44	t	738	0	807	9	0
45	u	779	0	834	14	0
46	v	753	0	780	10	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	1454	0
52	2	2568	0	1303	16	0
53	3	33012	0	16618	187	0
54	4	809	0	404	12	0
55	8	539	0	305	28	0
56	9	417	0	224	1	0
57	A1	1677	0	1713	23	0
57	A2	331	0	146	2	0
58	B1	10353	0	10548	324	0
59	B2	10546	0	10550	181	0
60	W0	650	0	658	10	0
61	NA	2432	0	1171	16	0
62	NG	758	0	334	8	0
63	5	1622	0	821	28	0
64	6	1640	0	837	20	0
65	0	5211	0	5200	51	0
66	B1	1	0	0	0	0
67	0	37	0	47	7	0
68	0	28	0	12	0	0
All	All	179688	0	129150	2841	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 (2841) 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)
54:4:26:U:O2'	58:B1:78:LEU:HB3	1.46	1.12
59:B2:901:LEU:HD13	61:NA:107:THR:CB	1.82	1.08
59:B2:901:LEU:HD11	61:NA:107:THR:C	1.77	1.08
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
58:B1:750:PRO:HB3	59:B2:549:ASP:OD2	1.60	1.01
51:1:1666:G:H2'	51:1:1667:G:H5'	1.41	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
58:B1:111:THR:HG23	58:B1:300:GLN:CD	1.86	1.00
59:B2:901:LEU:CD1	61:NA:107:THR:C	2.34	1.00
51:1:1807:G:H2'	51:1:1808:A:H5'	1.44	0.99
33:i:72:THR:HB	33:i:115:ASP:HB2	1.46	0.98
58:B1:352:ARG:HD2	59:B2:1268:GLN:NE2	1.79	0.98
59:B2:901:LEU:HD11	61:NA:107:THR:O	1.62	0.96
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	0.94
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	1.34	0.92
51:1:1702:G:H2'	51:1:1703:G:H5''	1.51	0.92
51:1:1847:A:HO2'	51:1:1848:A:H8	1.08	0.92
54:4:44:G:H21	58:B1:427:PRO:HD3	1.34	0.92
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
58:B1:202:ARG:HG2	58:B1:202:ARG:HH11	1.34	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
54:4:26:U:HO2'	58:B1:78:LEU:HB3	1.37	0.90
51:1:890:C:H2'	51:1:891:G:H5'	1.53	0.90
58:B1:317:THR:HA	58:B1:323:PRO:HA	1.55	0.89
59:B2:854:ILE:HG21	59:B2:917:SER:HB3	1.54	0.89
14:N:3:ASN:N	14:N:5:TYR:HH	1.70	0.89
33:i:52:LEU:HB3	33:i:73:PRO:HB3	1.55	0.88
51:1:2097:A:H2'	51:1:2098:U:C6	2.08	0.88
63:5:9:A:H2'	63:5:11:C:H41	1.38	0.88
51:1:1060:U:H4'	51:1:1061:U:H5''	1.55	0.88
58:B1:68:TYR:C	58:B1:75:TYR:HE2	1.80	0.88
59:B2:901:LEU:CD1	61:NA:107:THR:CB	2.51	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1869:G:H3'	51:1:1870:C:H5'	1.57	0.86
58:B1:68:TYR:HB3	58:B1:75:TYR:OH	1.76	0.85
2:B:8:THR:HB	51:1:2020:A:H5'	1.56	0.85
17:Q:69:GLU:HG3	53:3:521:G:H4'	1.59	0.85
51:1:2792:A:H2'	51:1:2793:C:H5''	1.59	0.85
58:B1:633:ALA:HB2	59:B2:808:ASN:H	1.41	0.85
51:1:1387:A:H5'	51:1:1469:A:H1'	1.58	0.85
51:1:2333:A:H5'	51:1:2334:U:H2'	1.57	0.84
58:B1:68:TYR:O	58:B1:75:TYR:HE2	1.58	0.84
51:1:1175:A:H3'	51:1:1176:U:H5'	1.59	0.84
51:1:2584:U:H2'	51:1:2585:U:H5'	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
58:B1:770:LEU:HD13	59:B2:618:GLN:HG3	1.61	0.82
51:1:1666:G:C2'	51:1:1667:G:H5'	2.07	0.82
51:1:1141:U:H4'	51:1:1142:A:O4'	1.80	0.82
51:1:757:G:H2'	51:1:758:C:H5'	1.61	0.82
51:1:279:A:H61	51:1:361:G:H1'	1.46	0.81
51:1:545:U:C2	51:1:546:U:H1'	2.16	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
51:1:2360:G:H2'	51:1:2361:G:H5'	1.62	0.81
38:n:36:THR:HG22	51:1:1278:C:OP1	1.80	0.81
51:1:2112:G:H2'	51:1:2113:U:H5'	1.63	0.81
58:B1:144:TYR:HE1	58:B1:162:GLU:OE2	1.64	0.81
51:1:1197:G:O2'	51:1:1198:U:H5'	1.81	0.80
51:1:1775:U:H2'	51:1:1776:G:H5'	1.64	0.80
51:1:2224:G:H4'	51:1:2226:C:C2	2.16	0.80
51:1:1087:G:N2	51:1:1103:A:H1'	1.97	0.80
55:8:1:DC:H5''	58:B1:210:SER:OG	1.80	0.80
58:B1:141:PHE:CE2	58:B1:296:LYS:HB2	2.16	0.80
51:1:784:G:H5'	51:1:785:G:OP1	1.81	0.80
58:B1:37:GLU:O	58:B1:61:ILE:HD11	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
7:G:18:GLN:HG3	7:G:189:ASN:HB3	1.65	0.79
58:B1:111:THR:HG23	58:B1:300:GLN:OE1	1.81	0.79
51:1:1064:C:H41	51:1:1069:A:H5''	1.47	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	0.78
51:1:1297:C:OP1	51:1:2710:C:H4'	1.82	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
51:1:2215:C:H2'	51:1:2216:G:C8	2.18	0.78
51:1:275:C:H2'	51:1:276:U:C4'	2.14	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
51:1:1310: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
51:1:1702:G:C2'	51:1:1703:G:H5''	2.13	0.77
65:0:624:PRO:HG2	65:0:677:ARG:HD2	1.66	0.77
51:1:1275:A:N6	51:1:1296:G:H4'	2.00	0.77
33:i:55:PRO:HG3	51:1:1060:U:OP2	1.83	0.77
58:B1:186:GLN:HG3	58:B1:238:ILE:HG13	1.65	0.77
51:1:2156:G:C2'	51:1:2157:G:H5'	2.14	0.77
51:1:1736:U:H2'	51:1:1737:G:O4'	1.85	0.76
28:c:114:LYS:HB2	51:1:2680:U:OP1	1.84	0.76
51:1:310:A:O2'	51:1:311:A:H2'	1.85	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
51:1:368:A:H2'	51:1:369:U:H5'	1.66	0.76
51:1:548:G:H2'	51:1:549:G:O4'	1.84	0.76
51:1:1773:A:H2'	51:1:1774:C:H5'	1.68	0.76
51:1:275:C:H3'	51:1:276:U:H5''	1.66	0.75
51:1:2792:A:C2'	51:1:2793:C:H5''	2.16	0.75
51:1:958:U:H2'	52:2:89:U:O2	1.87	0.75
51:1:1063:G:H1	51:1:1075:C:N4	1.84	0.75
51:1:1083:U:H2'	51:1:1085:A:OP2	1.87	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
51:1:1020: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
51:1:2432:A:H1'	64:6:75:C:O4'	1.86	0.74
58:B1:202:ARG:HG2	58:B1:202:ARG:NH1	1.99	0.74
51:1:1061:U:H3'	51:1:1062:G:C5'	2.18	0.74
55:8:15:DC:H1'	58:B1:426:ALA:HB1	1.67	0.74
51:1:1425:G:H2'	51:1:1426:G:C8	2.23	0.74
58:B1:110:PRO:HG2	58:B1:183:GLU:HG3	1.68	0.74
51:1:2097:A:H2'	51:1:2098:U:H6	1.49	0.73
58:B1:1143:ASP:OD1	58:B1:1148:ARG:NH1	2.21	0.73
51:1:404:A:H1'	51:1:406:G:C4	2.23	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:543:G:H2'	51:1:544:C:H5''	1.68	0.73
58:B1:68:TYR:C	58:B1:75:TYR:CE2	2.65	0.73
51:1:1670:C:H2'	51:1:1671:U:H5'	1.70	0.73
55:8:3:DC:H2'	55:8:4:DT:H72	1.69	0.73
31:f:15:ASP:HB3	31:f:26:LYS:H	1.54	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
51:1:322:A:H5'	51:1:340:A:C1'	2.19	0.73
58:B1:107:LEU:HD11	58:B1:242:LEU:HB2	1.70	0.73
51:1:1433:A:H2'	51:1:1434:A:O4'	1.89	0.73
55:8:3:DC:C2'	55:8:4:DT:H72	2.19	0.73
58:B1:282:LEU:HA	58:B1:286:ALA:HA	1.70	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
65:0:508:GLN:HA	65:0:513:GLY:HA2	1.69	0.72
58:B1:220:ARG:HG2	58:B1:220:ARG:HH11	1.54	0.72
51:1:1942:C:H3'	51:1:1943:U:H2'	1.70	0.72
51:1:2713:U:C3'	51:1:2714:G:C5'	2.67	0.72
51:1:633:A:H2'	51:1:634:C:H5'	1.71	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
58:B1:210:SER:HB3	58:B1:213:LYS:HB2	1.71	0.71
58:B1:211:GLU:HG2	58:B1:215:LYS:HE3	1.70	0.71
36:l:59:ARG:HD2	51:1:250:G:H4'	1.71	0.71
51:1:2671:G:H2'	51:1:2672:U:C6	2.25	0.71
58:B1:157:GLN:OE1	58:B1:157:GLN:HA	1.89	0.71
51:1:1858:A:H1'	51:1:1885:A:C2	2.25	0.71
51:1:1441:G:H2'	51:1:1442:U:C6	2.25	0.71
51:1:2151:U:H2'	51:1:2152:G:H8	1.56	0.71
53:3:452:A:H61	53:3:480:U:H3	1.37	0.71
51:1:368:A:C2'	51:1:369:U:H5'	2.20	0.71
51:1:1670:C:C2'	51:1:1671:U:H5'	2.21	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	0.71
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:105:ILE:HD12	58:B1:242:LEU:HD22	1.71	0.71
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
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE22	1.55	0.70
42:r:79:ARG:NH1	51:1:572:A:OP2	2.25	0.70
51:1:2626:C:O2'	51:1:2627:G:H5'	1.91	0.70
51:1:1872:A:H2'	51:1:1873:G:O4'	1.89	0.70
33:i:22:PRO:HB3	51:1:1067:A:H4'	1.72	0.70
51:1:1386:C:H2'	51:1:1387:A:H8	1.56	0.70
51:1:1983:G:O2'	51:1:1984:G:H5'	1.92	0.70
51:1:2297:A:N1	51:1:2321:U:H5	1.89	0.70
51:1:2267:A:H5''	51:1:2268:A:H5''	1.74	0.70
51:1:644:A:C2'	51:1:645:C:H5''	2.22	0.70
59:B2:65:ASN:HB3	59:B2:105:TYR:HB2	1.74	0.70
51:1:322:A:H5'	51:1:340:A:H1'	1.73	0.70
58:B1:142:GLU:HG3	58:B1:142:GLU:O	1.90	0.70
34:j:7:LYS:HG2	51:1:538:A:H4'	1.73	0.69
65:0:618:LYS:HG3	65:0:643:LYS:HZ3	1.55	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
58:B1:93:THR:HB	58:B1:97:VAL:HG21	1.73	0.69
51:1:1555:G:H5'	51:1:1555:G:C8	2.27	0.69
51:1:2151:U:H2'	51:1:2152:G:C8	2.27	0.69
65:0:19:ILE:CG2	67:0:800:FUA:C28	2.70	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
51:1:1565:C:HO2'	51:1:1566:A:H8	1.41	0.69
36:l:30:THR:HG22	51:1:810:U:O4	1.93	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
51:1:2403:C:O2'	51:1:2404:U:H5'	1.92	0.69
58:B1:39:LYS:O	58:B1:273:ILE:CG2	2.41	0.69
58:B1:128:LEU:HD11	58:B1:189:LEU:HG	1.73	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
51:1:2758:A:H2'	51:1:2759:G:H5'	1.75	0.69
63:5:47:U:H4'	63:5:48:C:H5'	1.75	0.69
51:1:528:A:C8	51:1:528:A:H3'	2.27	0.69
51:1:644:A:H2'	51:1:645:C:C5'	2.21	0.69
51:1:2747:G:O6	51:1:2755:C:H5''	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2869:G:H2'	51:1:2870:C:C6	2.28	0.69
58:B1:243:PRO:HG2	59:B2:1332:SER:O	1.93	0.69
51:1:319:G:H1	51:1:323:C:H5	1.40	0.68
51:1:392:U:H2'	51:1:393:C:H6	1.58	0.68
51:1:2114:A:H2	51:1:2167:U:H1'	1.58	0.68
53:3:437:U:H3	53:3:495:A:H62	1.42	0.68
51:1:1078:U:H2'	51:1:1088:A:OP1	1.94	0.68
58:B1:141:PHE:CD2	58:B1:293:ARG:O	2.47	0.68
58:B1:161:THR:HG22	58:B1:164:GLN:HB2	1.75	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
51:1:1999:C:H5''	51:1:2723:C:O2'	1.94	0.68
50:z:38:GLU:OE2	51:1:928:A:H5'	1.94	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
51:1:2510:C:N4	51:1:2511:U:O4	2.27	0.68
53:3:1338:G:H22	63:5:29:G:H22	1.42	0.68
51:1:1889:A:H2'	51:1:1890:A:C8	2.29	0.68
51:1:246:C:H2'	51:1:247:G:H5'	1.76	0.68
51:1:1438:U:O2'	51:1:1439:A:H5'	1.94	0.68
51:1:1432:G:O2'	51:1:1433:A:H5'	1.94	0.67
51:1:1702:G:C3'	51:1:1703:G:H5''	2.24	0.67
8:H:117:ASP:HA	8:H:120:THR:HG22	1.75	0.67
58:B1:832:LYS:C	58:B1:1242:ARG:HH12	2.01	0.67
51:1:226:A:H2'	51:1:227:A:O4'	1.94	0.67
51:1:466:A:H2'	51:1:467:G:H5'	1.76	0.67
51:1:703:U:C2'	51:1:704:G:H5'	2.25	0.67
51:1:1061:U:H3'	51:1:1062:G:H5'	1.76	0.67
52:2:65:U:H3'	52:2:108:A:H61	1.58	0.67
51:1:112:U:H2'	51:1:113:U:H5'	1.76	0.67
51:1:1717:A:H2'	51:1:1718:G:H5'	1.77	0.67
51:1:2898:U:H2'	51:1:2899:A:C8	2.29	0.67
9:I:73:ASN:HA	9:I:76:LYS:HB2	1.77	0.67
51:1:65:U:H2'	51:1:66:C:H6	1.59	0.67
51:1:2233:U:H2'	51:1:2234:G:C8	2.30	0.67
65:0:104:ARG:HH22	65:0:407:GLU:HB3	1.57	0.67
37:m:14:LYS:NZ	51:1:956:G:N7	2.35	0.67
48:x:16:ASN:ND2	48:x:26:ARG:HB3	2.09	0.67
55:8:23:DC:H2''	55:8:24:DC:C5	2.30	0.67
58:B1:117:LEU:HD12	58:B1:117:LEU:O	1.94	0.67
55:8:3:DC:C6	55:8:4:DT:H72	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2516:A:O2'	51:1:2517:C:H5'	1.95	0.67
4:D:37:LYS:HD3	4:D:39:ARG:HD3	1.77	0.67
51:1:707:G:O2'	51:1:708:G:H5'	1.94	0.67
51:1:1484:U:H2'	51:1:1485:U:C6	2.30	0.67
55:8:13:DT:OP2	58:B1:791:ALA:HB1	1.95	0.67
65:0:364:VAL:HA	65:0:373:GLU:HA	1.77	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
51:1:2157:G:H2'	51:1:2158:A:H2	1.59	0.66
51:1:1063:G:H1	51:1:1075:C:H41	1.42	0.66
51:1:2278:A:C3'	51:1:2279:G:H5''	2.25	0.66
51:1:1176:U:H2'	51:1:1177:G:C8	2.29	0.66
51:1:2555:U:H2'	51:1:2556:C:H5'	1.77	0.66
58:B1:108:ALA:CB	58:B1:279:LEU:HD22	2.25	0.66
51:1:894:U:H2'	51:1:895:U:O4'	1.93	0.66
51:1:1082:U:H3'	51:1:1083:U:C5'	2.22	0.66
51:1:1270:C:H5''	51:1:1271:G:H5'	1.77	0.66
51:1:2278:A:H3'	51:1:2279:G:H5''	1.78	0.66
51:1:528:A:H3'	51:1:528:A:H8	1.59	0.66
51:1:2733:A:O2'	51:1:2734:A:H5'	1.96	0.66
58:B1:1355:ARG:NH1	58:B1:1369:ARG:HH12	1.92	0.66
51:1:673:C:H2'	51:1:674:G:H5'	1.77	0.66
45:u:25:LYS:HD3	45:u:36:GLU:HB3	1.75	0.66
51:1:870:U:C2'	51:1:871:U:H5'	2.26	0.66
51:1:1020:A:H1'	51:1:1021:A:OP2	1.95	0.66
51:1:1733:G:O2'	51:1:1734:G:H5'	1.95	0.66
51:1:2760:C:O2'	51:1:2761:A:H5'	1.96	0.66
17:Q:47:ALA:HB3	17:Q:49:ARG:HE	1.60	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
58:B1:984:LEU:HB3	58:B1:993:GLU:HB2	1.77	0.66
36:l:39:LYS:NZ	51:1:942:G:OP2	2.28	0.66
58:B1:395:LYS:HZ2	58:B1:399:LYS:CD	2.09	0.66
7:G:67:LEU:HD12	7:G:153:MET:HE1	1.77	0.65
28:c:4:LEU:HD23	28:c:29:VAL:HG11	1.77	0.65
51:1:635:C:H2'	51:1:636:G:C8	2.31	0.65
51:1:703:U:H2'	51:1:704:G:H5'	1.77	0.65
51:1:1098:A:H2'	51:1:1099:G:H5'	1.77	0.65
51:1:2595:G:N2	51:1:2598:A:OP2	2.23	0.65
38:n:63:ARG:NE	51:1:1454:C:H5'	2.10	0.65
51:1:1064:C:N4	51:1:1069:A:H5''	2.10	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2052:A:O2'	51:1:2053:G:H5'	1.96	0.65
51:1:2844: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
51:1:1746:A:H2'	51:1:1747:U:C6	2.31	0.65
58:B1:461:PHE:HD2	59:B2:813:GLU:HB2	1.61	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	1.59	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
51:1:543:G:H2'	51:1:544:C:C5'	2.26	0.65
27:b:227:VAL:HG11	51:1:784:G:C2	2.31	0.65
51:1:1270:C:H5''	51:1:1271:G:C5'	2.25	0.65
51:1:2013:A:H5''	51:1:2013:A:H8	1.59	0.65
58:B1:141:PHE:HD2	58:B1:293:ARG:O	1.79	0.65
19:S:38:GLU:HA	19:S:41:TRP:HB3	1.79	0.65
51:1:1796:U:H2'	51:1:1797:G:H8	1.61	0.65
51:1:2834:G:O2'	51:1:2835:A:H5'	1.97	0.65
58:B1:108:ALA:HB3	58:B1:279:LEU:HD22	1.77	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
51:1:2193:G:H2'	51:1:2194:U:C6	2.32	0.65
51:1:2221:G:O2'	51:1:2222:C:H5'	1.95	0.65
51:1:905:A:O2'	51:1:906:U:H5'	1.97	0.65
58:B1:975:ILE:HG22	58:B1:977:SER:H	1.62	0.65
59:B2:314:ASN:HD21	59:B2:348:SER:HA	1.62	0.65
31:f:154:GLU:HG3	31:f:156:TYR:H	1.61	0.65
51:1:1161:C:H2'	51:1:1162:G:H8	1.61	0.65
58:B1:68:TYR:HB3	58:B1:75:TYR:CE2	2.32	0.65
51:1:613:A:H5''	51:1:614:A:C8	2.32	0.65
51:1:1853:A:H2'	51:1:1854:A:C8	2.32	0.65
58:B1:285:LEU:HD13	58:B1:285:LEU:H	1.63	0.65
51:1:488:G:N2	51:1:491:G:H5''	2.11	0.64
51:1:2290:G:H2'	51:1:2291:U:C6	2.32	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
51:1:1788:C:O2'	51:1:1789:A:H5'	1.96	0.64
51:1:2799:A:C2'	51:1:2800:A:H5'	2.27	0.64
58:B1:918:ILE:HG22	59:B2:1280:ALA:HB1	1.79	0.64
4:D:24:THR:HG23	4:D:27:GLY:H	1.61	0.64
51:1:256:A:O2'	51:1:257:C:H5'	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:306:U:H2'	51:1:307:G:O4'	1.98	0.64
51:1:2792:A:H3'	51:1:2793:C:H5''	1.80	0.64
58:B1:1037:PHE:HB3	58:B1:1040:MET:HB2	1.78	0.64
59:B2:528:ARG:NH2	59:B2:576:SER:O	2.30	0.64
51:1:2404:U:O2'	51:1:2405:G:H5'	1.97	0.64
58:B1:162:GLU:HA	58:B1:162:GLU:OE1	1.97	0.64
58:B1:193:ASP:HB3	58:B1:196:GLN:HB2	1.78	0.64
51:1:414:C:H2'	51:1:415:A:H8	1.63	0.64
43:s:6:LYS:HB2	51:1:494:G:H4'	1.78	0.64
58:B1:978:ARG:HG2	58:B1:1197:ASN:HD21	1.61	0.64
12:L:59:GLU:HA	12:L:62:GLU:HB3	1.80	0.64
26:Z:32:ARG:HG2	26:Z:33:ARG:HG3	1.80	0.64
51:1:815:C:C2	51:1:1193:G:N2	2.66	0.64
51:1:2112:G:C2'	51:1:2113:U:H5'	2.27	0.64
51:1:2170:A:H2'	51:1:2171:A:O4'	1.97	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
16:P:19:VAL:HG22	16:P:82:GLU:HB2	1.79	0.64
51:1:622:G:O2'	51:1:623:C:H5'	1.98	0.64
51:1:1921:G:O2'	51:1:1922:G:H5'	1.98	0.64
51:1:2114:A:N7	51:1:2115:G:H1'	2.12	0.64
51:1:2469:A:H2'	51:1:2470:G:O4'	1.98	0.64
55:8:3:DC:C2'	55:8:4:DT:C7	2.75	0.64
51:1:1857:G:H22	51:1:1884:G:H2'	1.62	0.64
27:b:106:PRO:HD2	27:b:109:LEU:HD22	1.79	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
51:1:1766:G:O2'	51:1:1767:G:H5'	1.98	0.63
51:1:2314:A:H2'	51:1:2315:G:C8	2.33	0.63
58:B1:201:LEU:HB2	58:B1:221:ILE:HD13	1.80	0.63
58:B1:245:LEU:HG	58:B1:246:PRO:HD2	1.80	0.63
51:1:1164:C:O2'	51:1:1165:A:H5'	1.99	0.63
51:1:2811:G:O2'	51:1:2812:G:H5'	1.97	0.63
51:1:65:U:H2'	51:1:66:C:C6	2.33	0.63
51:1:1666:G:H2'	51:1:1667:G:C5'	2.24	0.63
11:K:38:ARG:HE	11:K:97:THR:HA	1.62	0.63
51:1:1149:G:H2'	51:1:1150:C:C6	2.33	0.63
65:0:614:GLU:HB3	65:0:690:ALA:HB2	1.79	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1280:G:O2'	51:1:1281:G:H5'	1.99	0.63
59:B2:1282:GLY:HA3	60:W0:17:PHE:HE1	1.63	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
51:1:1909:C:H2'	51:1:1910:G:H8	1.64	0.63
51:1:2636:C:H2'	51:1:2637:U:H6	1.64	0.63
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
34:j:45:THR:HB	34:j:48:VAL:HG22	1.81	0.63
51:1:212:G:O2'	51:1:213:A:H5'	1.99	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
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
51:1:1524:G:H2'	51:1:1525:A:H8	1.63	0.62
45:u:87:GLU:HG2	45:u:92:VAL:HG21	1.82	0.62
51:1:161:A:N7	51:1:162:U:H5	1.96	0.62
51:1:1448:G:H2'	51:1:1449:G:H8	1.64	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
58:B1:100:GLU:HA	59:B2:1328:LYS:HE2	1.82	0.62
61:NA:422:GLU:HA	61:NA:426:GLY:HA3	1.82	0.62
22:V:30:HIS:HD2	22:V:33:TYR:H	1.48	0.62
51:1:1680:U:H2'	51:1:1681:G:O4'	2.00	0.62
57:A1:211:ILE:HG12	57:A1:219:ARG:HH12	1.65	0.62
58:B1:128:LEU:HA	58:B1:192:MET:HE1	1.81	0.62
58:B1:1357:ILE:HD11	59:B2:1287:LEU:HD13	1.80	0.62
64:6:46:G:C2'	64:6:47:U:H5'	2.29	0.62
44:t:53:VAL:HG12	44:t:92:ASN:HD22	1.65	0.62
51:1:941:A:H2'	51:1:942:G:O4'	2.00	0.62
51:1:2092:U:H5	51:1:2199:A:H2	1.48	0.62
55:8:1:DC:H2''	55:8:2:DC:C5	2.35	0.62
58:B1:111:THR:CG2	58:B1:300:GLN:NE2	2.63	0.62
58:B1:395:LYS:NZ	58:B1:399:LYS:HD3	2.15	0.62
51:1:872:U:O2'	51:1:873:C:H5'	1.99	0.62
16:P:45:THR:HG23	16:P:48:GLY:H	1.65	0.62
51:1:889:C:H2'	51:1:890:C:O4'	1.99	0.62
51:1:1935:G:H1'	51:1:1964:G:N2	2.15	0.62
58:B1:68:TYR:HB3	58:B1:75:TYR:CZ	2.35	0.62
58:B1:223:LEU:HG	58:B1:223:LEU:O	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:120:GLN:NE2	59:B2:490:GLN:OE1	2.32	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
4:D:3:ARG:O	4:D:6:GLN:NE2	2.33	0.61
32:g:50:ARG:HH22	32:g:51:ARG:HH21	1.48	0.61
7:G:15:PHE:HB2	7:G:39:ILE:HG23	1.82	0.61
51:1:2734:A:H2'	51:1:2735:G:H5'	1.82	0.61
58:B1:770:LEU:HD13	59:B2:618:GLN:CG	2.30	0.61
16:P:58:THR:HG22	16:P:60:PHE:H	1.65	0.61
37:m:86:LYS:NZ	51:1:955:U:OP1	2.32	0.61
51:1:172:A:H2'	51:1:173:A:H8	1.66	0.61
51:1:1086:A:H5'	51:1:1103:A:H2	1.65	0.61
58:B1:111:THR:CG2	58:B1:300:GLN:CD	2.67	0.61
51:1:590:A:O2'	51:1:591:U:H5'	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
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
51:1:435:C:H2'	51:1:436:C:H5'	1.82	0.61
51:1:1040:A:H2	51:1:1115:G:H22	1.48	0.61
55:8:3:DC:H2'	55:8:4:DT:C7	2.30	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
51:1:2188:U:H2'	51:1:2189:U:O4'	2.01	0.61
58:B1:342:LEU:HD23	58:B1:1352:ILE:HG23	1.83	0.61
51:1:558:U:H6	51:1:558:U:O5'	1.84	0.61
51:1:1503:A:H3'	51:1:1504:A:H5''	1.82	0.61
58:B1:1355:ARG:NH1	58:B1:1369:ARG:NH1	2.47	0.61
51:1:1717:A:C2'	51:1:1718:G:H5'	2.31	0.61
58:B1:395:LYS:HZ2	58:B1:399:LYS:HD3	1.65	0.61
58:B1:750:PRO:CB	59:B2:549:ASP:OD2	2.45	0.61
59:B2:55:SER:OG	59:B2:465:ARG:NH1	2.33	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
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
37:m:17:ASN:O	37:m:38:ARG:NH1	2.34	0.60
51:1:723:C:H2'	51:1:724:U:H6	1.64	0.60
51:1:2097:A:H2'	51:1:2098:U:O4'	2.00	0.60
51:1:2852:G:O2'	51:1:2853:C:H5'	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:198:C:H42	51:1:248:G:H1	1.49	0.60
51:1:1198:U:H2'	51:1:1199:U:C6	2.37	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
51:1:2637:U:H2'	51:1:2638:G:H5'	1.82	0.60
51:1:2812:G:H2'	51:1:2813:A:C8	2.36	0.60
57:A1:112:ALA:HB3	57:A1:126:PRO:HA	1.83	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
34:j:39:LYS:HE3	51:1:1009:A:OP1	2.01	0.60
51:1:854:C:O2'	51:1:855:G:H5'	2.02	0.60
51:1:2093:G:O2'	51:1:2094:A:H5'	2.01	0.60
47:w:38:GLY:HA2	51:1:2330:G:H21	1.66	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
51:1:1026:G:H2'	51:1:1027:A:H8	1.67	0.60
53:3:1040:U:H2'	53:3:1041:G:H8	1.67	0.60
55:8:7:DC:H2''	55:8:8:DT:H71	1.84	0.60
58:B1:412:LEU:HD22	58:B1:441:LEU:HD21	1.84	0.60
59:B2:69:GLN:HE21	59:B2:101:ARG:HD2	1.67	0.60
65:0:19:ILE:HG21	67:0:800:FUA:H281	1.83	0.60
22:V:11:VAL:HA	22:V:22:VAL:HA	1.83	0.60
51:1:1508:A:H2'	51:1:1509:A:O4'	2.01	0.60
51:1:1775:U:H2'	51:1:1776:G:C5'	2.29	0.60
51:1:2187:U:O2'	51:1:2188:U:H5'	2.02	0.60
53:3:1133:G:H1	53:3:1141:C:H42	1.48	0.60
51:1:794:A:H2'	51:1:795:C:O4'	2.02	0.60
51:1:1287:A:C5	51:1:1288:G:C6	2.89	0.60
51:1:2360:G:C2'	51:1:2361:G:H5'	2.31	0.60
53:3:148:G:H1'	53:3:1447:A:H1'	1.84	0.60
51:1:283:G:H2'	51:1:284:U:H5'	1.83	0.60
51:1:893:C:H2'	51:1:894:U:C6	2.37	0.60
51:1:1183:U:H2'	51:1:1184:U:C6	2.37	0.60
51:1:2137:U:H2'	51:1:2138:G:H8	1.67	0.60
53:3:1351:U:H3	53:3:1371:G:H1	1.49	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:B1:201:LEU:HD11	58:B1:220:ARG:HH11	1.67	0.59
55:8:11:DC:H2'	55:8:12:DG:C8	2.37	0.59
58:B1:438:GLU:HG3	58:B1:485:MET:HE1	1.85	0.59
58:B1:951:GLN:NE2	58:B1:1014:GLY:O	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:1072:ASN:ND2	59:B2:1111:GLN:OE1	2.35	0.59
14:N:79:ARG:HH21	14:N:102:PHE:HA	1.67	0.59
33:i:19:PRO:HA	33:i:24:GLY:HA3	1.84	0.59
51:1:1538:G:H2'	51:1:1539:U:C6	2.37	0.59
51:1:2386:A:O2'	51:1:2387:U:H5'	2.01	0.59
51:1:2661:G:H5'	65:0:19:ILE:HD13	1.85	0.59
58:B1:161:THR:HG23	58:B1:164:GLN:H	1.68	0.59
33:i:74:PRO:HG3	51:1:1060:U:OP1	2.02	0.59
51:1:1553:A:HO2'	51:1:1554:U:H5	1.49	0.59
51:1:1857:G:N2	51:1:1884:G:H2'	2.17	0.59
58:B1:99:ARG:NH1	58:B1:99:ARG:HG3	2.17	0.59
58:B1:633:ALA:HA	59:B2:806:PRO:O	2.01	0.59
58:B1:926:PRO:HG2	58:B1:1248:ILE:HD11	1.84	0.59
58:B1:1161:GLY:HA3	58:B1:1179:PRO:HA	1.82	0.59
27:b:153:LEU:HD23	51:1:1799:G:C2	2.37	0.59
30:e:51:ASN:OD1	30:e:149:ARG:NH1	2.34	0.59
51:1:841:G:O2'	51:1:842:U:H5'	2.02	0.59
51:1:851:C:H2'	51:1:852:U:C6	2.36	0.59
51:1:1071:G:H1'	51:1:1089:A:C8	2.37	0.59
51:1:2643:G:H2'	51:1:2644:G:H5'	1.84	0.59
51:1:2789:C:H2'	51:1:2893:A:N7	2.18	0.59
24:X:30:LEU:HB2	24:X:48:ILE:HG22	1.84	0.59
29:d:77:ILE:HG23	51:1:1256:G:H21	1.68	0.59
51:1:11:C:C2'	51:1:12:U:H5''	2.29	0.59
51:1:2743:U:H3'	51:1:2744:G:H5''	1.84	0.59
58:B1:725:MET:SD	59:B2:1101:LEU:HD23	2.42	0.59
29:d:68:ALA:HA	51:1:1255:U:C5	2.37	0.59
39:o:4:LYS:HD3	39:o:7:ARG:HH21	1.65	0.59
51:1:2165:C:H2'	51:1:2166:U:C6	2.38	0.59
51:1:2717:C:C4	51:1:2718:G:N7	2.70	0.59
51:1:2749:A:OP2	51:1:2751:G:H5''	2.02	0.59
9:I:69:ARG:NH1	53:3:401:C:OP2	2.36	0.59
45:u:40:LEU:HD12	45:u:59:GLU:HG2	1.84	0.59
65:0:557:ILE:HG21	65:0:576:ILE:HD12	1.85	0.59
58:B1:144:TYR:CE1	58:B1:162:GLU:OE2	2.51	0.59
58:B1:615:LYS:HG2	60:W0:5:THR:HG21	1.85	0.59
59:B2:1142:ARG:NH1	59:B2:1161:LEU:O	2.36	0.59
9:I:201:GLU:O	53:3:8:A:N6	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
28:c:55:LYS:NZ	28:c:59:ARG:O	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:e:9:ASP:N	30:e:9:ASP:OD1	2.33	0.59
34:j:3:THR:N	51:1:995:C:N3	2.48	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
51:1:1042:G:H2'	51:1:1043:C:C6	2.37	0.59
51:1:1077:A:C8	51:1:1078:U:H1'	2.37	0.59
51:1:2153:C:H2'	51:1:2154:A:H5'	1.85	0.59
59:B2:918:LEU:O	59:B2:918:LEU:HD23	2.02	0.59
51:1:246:C:C2'	51:1:247:G:H5'	2.33	0.58
51:1:1171:G:H2'	51:1:1172:C:O4'	2.02	0.58
51:1:1337:G:H2'	51:1:1338:G:C8	2.37	0.58
51:1:1524:G:H2'	51:1:1525:A:C8	2.38	0.58
51:1:1725:U:H2'	51:1:1726:C:C6	2.38	0.58
51:1:2215:C:H2'	51:1:2216:G:H8	1.65	0.58
51:1:2533:U:H2'	51:1:2534:A:H5'	1.85	0.58
29:d:77:ILE:CG2	51:1:1256:G:H21	2.15	0.58
51:1:1098:A:H2'	51:1:1099:G:C5'	2.33	0.58
51:1:1333:G:O2'	51:1:1334:G:H5'	2.03	0.58
15:O:46:LYS:HG2	15:O:68:ARG:HG2	1.84	0.58
33:i:55:PRO:O	33:i:71:LYS:HB2	2.03	0.58
47:w:40:LYS:HE3	51:1:2330:G:O2'	2.03	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
51:1:2183:A:H2'	51:1:2184:A:C4	2.37	0.58
53:3:422:C:O2'	53:3:423:G:N2	2.36	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
58:B1:370:LYS:HG2	58:B1:441:LEU:HD23	1.84	0.58
51:1:215:G:H4'	51:1:216:A:H4'	1.84	0.58
51:1:1561:C:H2'	51:1:1562:U:C6	2.39	0.58
51:1:2834:G:H2'	51:1:2879:A:N6	2.17	0.58
58:B1:154:LEU:HD21	58:B1:160:LEU:HD21	1.83	0.58
65:0:618:LYS:HG3	65:0:643:LYS:NZ	2.19	0.58
21:U:70:ARG:HH22	53:3:451:A:H5'	1.66	0.58
51:1:1400:U:O2'	51:1:1401:G:H5'	2.04	0.58
51:1:1511:G:H2'	51:1:1512:C:C6	2.38	0.58
58:B1:638:SER:OG	58:B1:639:VAL:N	2.36	0.58
51:1:146:A:H2'	51:1:147:C:C6	2.39	0.58
51:1:1893:C:H2'	51:1:1894:C:H5'	1.85	0.58
23:W:49:LYS:HA	23:W:52:ARG:HH21	1.69	0.58
51:1:640:C:O2'	51:1:641:U:H5'	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1579:A:H2'	51:1:1580:A:C8	2.38	0.58
58:B1:275:ARG:NH1	58:B1:278:ARG:NH1	2.51	0.58
58:B1:514:THR:HG21	58:B1:596:LEU:HD12	1.84	0.58
30:e:47:LYS:O	30:e:51:ASN:ND2	2.37	0.58
51:1:1845:G:O2'	51:1:1846:G:H5'	2.02	0.58
51:1:2636:C:H2'	51:1:2637:U:C6	2.39	0.58
51:1:2812:G:H2'	51:1:2813:A:H8	1.68	0.58
53:3:409:U:H3	53:3:433:G:H1	1.51	0.58
55:8:9:DG:H4'	58:B1:120:LEU:HG	1.84	0.58
9:I:10:LEU:HD23	9:I:62:ARG:HB3	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
7:G:45:THR:O	7:G:49:PHE:N	2.35	0.57
19:S:5:MET:HE1	53:3:981:U:H5''	1.86	0.57
29:d:1:MET:HG2	29:d:16:GLU:HG2	1.86	0.57
39:o:56:LYS:NZ	52:2:117:G:OP1	2.36	0.57
58:B1:160:LEU:HD22	58:B1:164:GLN:HB3	1.86	0.57
15:O:29:ALA:HB2	15:O:87:LEU:HD11	1.86	0.57
27:b:141:HIS:ND1	27:b:192:GLY:O	2.35	0.57
27:b:220:ARG:NH1	51:1:1789:A:OP2	2.38	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
51:1:1108:U:H2'	51:1:1109:C:C2	2.40	0.57
51:1:1463:C:H2'	51:1:1464:G:H8	1.68	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'	2.05	0.57
58:B1:1046:ILE:HD12	58:B1:1059:LEU:HB3	1.86	0.57
65:0:94:ASP:HB3	65:0:465:HIS:HB2	1.85	0.57
25:Y:59:ARG:NH1	53:3:177:G:OP1	2.37	0.57
27:b:157:ALA:O	51:1:1820:U:C2	2.56	0.57
38:n:22:ARG:HG3	38:n:70:THR:HA	1.86	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
51:1:1275:A:C6	51:1:1296:G:H4'	2.40	0.57
58:B1:97:VAL:HG11	58:B1:101:ARG:NH2	2.18	0.57
58:B1:510:LEU:HD22	58:B1:601:ILE:HD12	1.86	0.57
59:B2:818:VAL:HG22	59:B2:1096:ILE:HG12	1.87	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:c:63:PRO:HG3	51:1:2787:C:H1'	1.85	0.57
45:u:36:GLU:HA	45:u:61:GLU:HG2	1.86	0.57
51:1:1173:U:C5	51:1:1174:U:H1'	2.40	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
51:1:1528:A:H2'	51:1:1529:G:H5'	1.87	0.57
58:B1:241:VAL:O	58:B1:241:VAL:HG12	2.04	0.57
58:B1:741:ALA:O	58:B1:762:ASN:ND2	2.38	0.57
51:1:635:C:H2'	51:1:636:G:H8	1.70	0.57
51:1:2186:G:O2'	51:1:2187:U:H5'	2.04	0.57
51:1:2897:U:H2'	51:1:2898:U:C6	2.39	0.57
59:B2:707:ALA:O	59:B2:711:ASP:HB2	2.03	0.57
41:q:30:VAL:HG13	51:1:580:U:O3'	2.04	0.57
51:1:235:U:H2'	51:1:236:C:C6	2.39	0.57
51:1:621:A:H2'	51:1:622:G:H5'	1.86	0.57
51:1:1319:C:O2'	51:1:1320:C:H5'	2.05	0.57
51:1:1520:U:O2'	51:1:1521:G:H5'	2.05	0.57
58:B1:99:ARG:CG	58:B1:99:ARG:HH11	2.17	0.57
59:B2:839:VAL:HG12	59:B2:1049:ILE:HG12	1.87	0.57
25:Y:73:ARG:NH2	53:3:261:U:OP2	2.36	0.57
38:n:54:LEU:HD23	38:n:66:ALA:HB2	1.86	0.57
51:1:74:A:H4'	51:1:75:G:O5'	2.05	0.57
51:1:327:G:O2'	51:1:328:U:H5'	2.04	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
59:B2:1122:LYS:NZ	59:B2:1126:ASP:OD1	2.38	0.57
21:U:55:ASP:OD1	21:U:55:ASP:N	2.38	0.57
27:b:259:ASN:ND2	27:b:262:THR:OG1	2.38	0.57
28:c:129:THR:OG1	28:c:140:HIS:O	2.22	0.57
51:1:287:G:H2'	51:1:288:U:C6	2.40	0.57
51:1:2570:G:H2'	51:1:2571:U:H5'	1.85	0.57
53:3:1125:U:H2'	53:3:1126:U:H2'	1.86	0.57
8:H:76:ILE:HD11	54:4:23:U:H4'	1.87	0.56
51:1:323:C:H3'	51:1:323:C:OP2	2.05	0.56
51:1:503:A:H4'	51:1:505:A:H5''	1.87	0.56
50:z:4:ILE:HD11	50:z:58:GLU:HG2	1.85	0.56
51:1:69:C:H2'	51:1:70:G:H8	1.70	0.56
51:1:358:U:H2'	51:1:359:G:C8	2.40	0.56
51:1:2662:A:H2'	51:1:2663:G:O4'	2.05	0.56
58:B1:352:ARG:HD2	59:B2:1268:GLN:HE21	1.68	0.56
7:G:114:LYS:HE3	7:G:151:LYS:HB2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:100:ARG:NH1	18:R:103:THR:OG1	2.38	0.56
31:f:44:HIS:HA	31:f:49:LEU:HG	1.87	0.56
35:k:65:THR:HG23	35:k:68:GLY:H	1.69	0.56
40:p:1:SER:OG	40:p:2:ASN:N	2.37	0.56
46:v:57:TYR:OH	46:v:79:ARG:NH2	2.38	0.56
51:1:184:C:H2'	51:1:185:G:H8	1.70	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
58:B1:1361:THR:HB	59:B2:1284:ALA:HB3	1.86	0.56
59:B2:899:GLU:HG3	59:B2:911:SER:HB2	1.87	0.56
10:J:54:GLU:HG2	10:J:56:PRO:HD2	1.86	0.56
27:b:250:GLN:NE2	27:b:251:THR:O	2.38	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
51:1:1410:G:H2'	51:1:1411:U:C6	2.41	0.56
51:1:2845:U:H2'	51:1:2846:G:H8	1.69	0.56
64:6:52:G:H2'	64:6:53:G:H8	1.69	0.56
14:N:35:GLU:HA	14:N:39:GLY:HA3	1.86	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
51:1:780:G:H21	51:1:783:A:H62	1.54	0.56
51:1:877:A:N1	51:1:899:A:H2'	2.20	0.56
51:1:1485:U:H2'	51:1:1486:U:C6	2.41	0.56
51:1:1590:A:O2'	51:1:1591:A:H5'	2.05	0.56
51:1:1678:A:H2'	51:1:1679:A:H5'	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
16:P:92:ARG:NH2	16:P:111:ASP:OD1	2.38	0.56
51:1:2395:C:H42	51:1:2421:G:H1	1.54	0.56
58:B1:102:MET:HG2	58:B1:246:PRO:HG3	1.87	0.56
11:K:12:PRO:HB2	11:K:44:ARG:HH21	1.70	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
51:1:296:U:H2'	51:1:297:G:C8	2.41	0.56
51:1:720:U:H2'	51:1:721:A:C8	2.41	0.56
51:1:1120:G:O2'	51:1:1121:C:H5'	2.05	0.56
51:1:1541:C:O2'	51:1:1542:U:H5'	2.06	0.56
51:1:1597:A:H5''	51:1:1598:A:H5'	1.87	0.56
51:1:2626:C:H2'	51:1:2627:G:O4'	2.06	0.56
53:3:159:G:N2	53:3:162:A:OP2	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:198:CYS:HA	58:B1:221:ILE:HD11	1.86	0.56
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
51:1:118:A:OP2	51:1:119:A:H5''	2.06	0.56
51:1:1097:U:H2'	51:1:1098:A:O4'	2.06	0.56
51:1:1182:G:H2'	51:1:1183:U:O4'	2.06	0.56
51:1:1485:U:H2'	51:1:1486:U:H6	1.71	0.56
51:1:1917:U:O2'	51:1:1918:A: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:B1:508:LEU:HD22	59:B2:1101:LEU:HD21	1.88	0.56
58:B1:804:ALA:HA	58:B1:1259:GLN:HG3	1.88	0.56
59:B2:13:LYS:HB2	59:B2:1180:MET:HE2	1.86	0.56
65:0:29:ARG:HE	65:0:269:ALA:HB1	1.70	0.56
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
51:1:1772:A:H5'	51:1:1773:A:OP2	2.06	0.56
51:1:2637:U:C2'	51:1:2638:G:H5'	2.36	0.56
58:B1:42:GLU:HB3	58:B1:52:GLU:HG3	1.86	0.56
58:B1:1175:LEU:HD22	58:B1:1190:ILE:HD11	1.88	0.56
51:1:759:G:H2'	51:1:760:G:C8	2.41	0.56
54:4:26:U:O2'	58:B1:78:LEU:CB	2.38	0.56
57:A1:29:GLU:HB3	57:A1:200:LYS:HG3	1.87	0.56
58:B1:37:GLU:O	58:B1:61:ILE:CD1	2.52	0.56
59:B2:1142:ARG:NH2	59:B2:1166:ASP:OD1	2.38	0.56
10:J:44:ARG:NH2	10:J:70:MET:SD	2.78	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
51:1:340:A:H2'	51:1:341:C:O4'	2.06	0.55
51:1:825:A:O2'	51:1:826:U:H5'	2.06	0.55
51:1:885:C:N4	51:1:886:A:H62	2.03	0.55
51:1:2114:A:C2	51:1:2167:U:H1'	2.41	0.55
57:A2:294:ASN:HA	61:NA:463:GLY:HA2	1.88	0.55
59:B2:900:LYS:HA	59:B2:903:ARG:HG3	1.87	0.55
49:y:28:LEU:HA	49:y:31:GLN:HB2	1.88	0.55
51:1:439:A:H2'	51:1:440:C:C6	2.42	0.55
51:1:613:A:H2'	51:1:613:A:N3	2.21	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
51:1:2584:U:C2'	51:1:2585:U:H5'	2.34	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:985:GLU:HB3	59:B2:988:LYS:HB2	1.89	0.55
4:D:9:VAL:HG22	51:1:1309:G:OP1	2.06	0.55
19:S:26:LEU:HA	19:S:30:ILE:HD12	1.88	0.55
37:m:27:SER:H	37:m:66:ARG:HH12	1.54	0.55
41:q:90:ASP:N	41:q:90:ASP:OD1	2.37	0.55
51:1:633:A:C2'	51:1:634:C:H5'	2.35	0.55
53:3:158:G:N2	53:3:163:C:O2	2.36	0.55
53:3:503:C:H2'	53:3:504:C:C6	2.41	0.55
53:3:830:G:H1	53:3:856:C:H42	1.53	0.55
54:4:26:U:H1'	58:B1:78:LEU:HD12	1.87	0.55
58:B1:247:PRO:HA	58:B1:250:ARG: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
28:c:134:HIS:CE1	51:1:1675:C:C4	2.94	0.55
51:1:655:A:H4'	51:1:656:G:C5'	2.30	0.55
51:1:877:A:C2'	51:1:878:A:H5''	2.36	0.55
51:1:1506:U:H2'	51:1:1507:C:C6	2.41	0.55
58:B1:39:LYS:O	58:B1:273:ILE:HG21	2.06	0.55
19:S:52:ARG:O	19:S:58:ARG:NH1	2.39	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
51:1:184:C:H2'	51:1:185:G:C8	2.41	0.55
51:1:543:G:H2'	51:1:544:C:C4'	2.37	0.55
51:1:2236:U:H2'	51:1:2237:G:H5'	1.88	0.55
58:B1:1155:ILE:HG13	58:B1:1210:ILE:HB	1.89	0.55
51:1:1389:G:O2'	51:1:1390:U:H5'	2.07	0.55
51:1:1448:G:H2'	51:1:1449:G:C8	2.42	0.55
53:3:49:U:H3	53:3:362:G:H1'	1.71	0.55
59:B2:633:LEU:HD13	59:B2:644:LEU:HD23	1.89	0.55
28:c:18:ASP:OD1	28:c:18:ASP:N	2.36	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
51:1:112: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
51:1:1948:G:H21	53:3:1418:A:H2	1.49	0.55
51:1:2195:U:O2'	51:1:2196:C:H5'	2.06	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
53:3:1040:U:H2'	53:3:1041:G:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:144:TYR:HE1	58:B1:162:GLU:CD	2.14	0.55
58:B1:145:VAL:HG23	58:B1:159:ILE:HG22	1.89	0.55
58:B1:833:GLU:HB2	58:B1:1242:ARG:NH1	2.22	0.55
51:1:296:U:H2'	51:1:297:G:H8	1.71	0.55
51:1:461:C:H2'	51:1:462:C:C6	2.42	0.55
51:1:1909:C:H2'	51:1:1910:G:C8	2.41	0.55
53:3:202:G:H21	53:3:466:A:H61	1.53	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
35:k:76:VAL:H	40:p:72:VAL:HG22	1.71	0.55
51:1:279:A:N6	51:1:361:G:H1'	2.21	0.55
51:1:1048:A:H2'	51:1:1049:C:H5'	1.88	0.55
51:1:1386:C:H2'	51:1:1387:A:C8	2.41	0.55
51:1:1601:G:C2'	51:1:1602:U:H5'	2.37	0.55
51:1:2114:A:C8	51:1:2115:G:H1'	2.42	0.55
51:1:2533:U:C2'	51:1:2534:A:H5'	2.36	0.55
30:e:23:SER:HB3	30:e:26:GLN:HB2	1.88	0.55
36:l:89:VAL:HG23	36:l:121:THR:HG23	1.88	0.55
51:1:2345:G:H5'	51:1:2347:C:H5'	1.89	0.55
53:3:1036:A:H2'	53:3:1037:C:H5'	1.88	0.55
58:B1:130:MET:HE2	58:B1:135:ILE:HG12	1.87	0.55
7:G:138:ARG:NH1	7:G:141:GLU:OE2	2.40	0.54
51:1:1745:A:O2'	51:1:1746:A:H5'	2.07	0.54
51:1:2217:G:O2'	51:1:2218:G:H5'	2.07	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
53:3:927:G:O2'	53:3:1503:A:N7	2.38	0.54
58:B1:58:CYS:SG	58:B1:59:ALA:N	2.80	0.54
58:B1:1166:GLY:HA3	58:B1:1174:ARG:HB2	1.88	0.54
59:B2:103:VAL:HB	59:B2:114:VAL:HG11	1.89	0.54
64:6:11:A:H2'	64:6:12:G:H8	1.72	0.54
29:d:84:THR:HG21	51:1:586:A:H5'	1.87	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
8:H:39:ARG:NH1	8:H:54:ILE:O	2.39	0.54
8:H:79:LYS:HD2	54:4:24:U:C6	2.42	0.54
12:L:73:GLU:HG2	12:L:90:VAL:HG22	1.89	0.54
12:L:113:LYS:O	53:3:1239:A:O2'	2.23	0.54
51:1:1005:C:H6	51:1:1005:C:O5'	1.90	0.54
51:1:1288:G:C6	51:1:1327:A:C2	2.96	0.54
51:1:1545:A:H2'	51:1:1546:G:O4'	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
25:Y:47:GLN:NE2	25:Y:51:ASN:OD1	2.40	0.54
37:m:64:TRP:HB2	37:m:104:GLU:HB2	1.89	0.54
51:1:472:A:H2'	51:1:473:G:H5'	1.90	0.54
51:1:1297:C:H2'	51:1:1298:C:C6	2.43	0.54
51:1:1310:G:O2'	51:1:1311:G:H5'	2.06	0.54
51:1:2091:C:H5	51:1:2092:U:HO2'	1.54	0.54
16:P:86:LYS:HG3	16:P:114:PRO:HD3	1.89	0.54
35:k:70:ARG:HG2	35:k:76:VAL:HG12	1.88	0.54
51:1:1091:G:H2'	51:1:1092:C:C6	2.42	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
51:1:2734: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
52:2:40:U:N3	52:2:44:G:OP2	2.40	0.54
59:B2:360:LEU:HD13	59:B2:378:ARG:HH11	1.72	0.54
59:B2:1117:LEU:HD12	59:B2:1195:ILE:HG12	1.90	0.54
21:U:69:ASP:OD1	21:U:69:ASP:N	2.38	0.54
38:n:35:LYS:NZ	38:n:100:CYS:SG	2.81	0.54
44:t:54:GLU:HB3	44:t:88:LYS:HE3	1.90	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
51:1:1530:G:H22	51:1:1542:U:H1'	1.73	0.54
51:1:2545:G:O2'	51:1:2546:U:H5'	2.07	0.54
58:B1:814:CYS:SG	58:B1:883:ARG:NH2	2.81	0.54
58:B1:1167:LYS:HZ2	58:B1:1170:LYS:HB2	1.72	0.54
59:B2:684:ASN:OD1	59:B2:687:ARG:NH2	2.41	0.54
59:B2:811:ASN:HA	59:B2:815:SER:HB2	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
51:1:1856:U:H2'	51:1:1857:G:O4'	2.08	0.54
51:1:2123:G:H2'	51:1:2124:G:H8	1.73	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:HD2	51:1:673:C:H5''	1.89	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
51:1:2190:G:O2'	51:1:2191:A:H5'	2.08	0.54
58:B1:99:ARG:HG3	58:B1:99:ARG:HH11	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:1070:HIS:NE2	59:B2:1114:GLU:OE1	2.36	0.54
7:G:86:CYS:SG	7:G:87:ASP:N	2.74	0.54
8:H:79:LYS:HA	54:4:24:U:OP1	2.08	0.54
9:I:55:ARG:O	9:I:59:LYS:N	2.41	0.54
10:J:23:THR:HA	10:J:28:ARG:HA	1.88	0.54
29:d:76:PRO:HA	29:d:82:GLY:HA3	1.90	0.54
51:1:923:G:O2'	51:1:924:G:H5'	2.07	0.54
51:1:1511:G:H2'	51:1:1512:C:H6	1.73	0.54
51:1:2092:U:C5	51:1:2199:A:H2	2.26	0.54
51:1:2328:A:H8	51:1:2328:A:O5'	1.91	0.54
51:1:2742:G:O2'	51:1:2743:U:H5'	2.08	0.54
58:B1:205:LEU:HG	58:B1:217:LEU:HB3	1.90	0.54
65:0:17:ALA:HB2	65:0:112:VAL:HB	1.89	0.54
19:S:84:ARG:NH2	53:3:1059:C:O3'	2.40	0.54
47:w:55:LEU:HD12	47:w:76:ILE:HD12	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
51:1:176:A:O2'	51:1:177:G:H5'	2.08	0.54
51:1:358:U:H2'	51:1:359:G:H8	1.72	0.54
51:1:2631:G:O2'	51:1:2632:A:H5'	2.08	0.54
53:3:458:U:H3	53:3:474:G:H1	1.56	0.54
7:G:126:ASP:OD1	7:G:126:ASP:N	2.41	0.53
16:P:15:VAL:HG12	16:P:76:TYR:HB3	1.90	0.53
17:Q:8:ARG:NH2	53:3:880:C:OP1	2.36	0.53
27:b:227:VAL:HG11	51:1:784:G:N1	2.23	0.53
31:f:103:ASN:ND2	31:f:113:ASP:OD1	2.41	0.53
51:1:1599:U:H2'	51:1:1600:C:C6	2.43	0.53
51:1:1913:A:N7	53:3:1494:G:H4'	2.21	0.53
53:3:505:G:H5''	53:3:534:U:H2'	1.89	0.53
59:B2:29:SER:O	59:B2:33:ASP:HB2	2.08	0.53
3:C:20:TYR:OH	51:1:2348:U:H5'	2.08	0.53
51:1:341:C:O2'	51:1:342:A:H5'	2.08	0.53
51:1:543:G:C2'	51:1:544:C:H5''	2.37	0.53
51:1:757:G:H2'	51:1:758:C:C5'	2.35	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:B1:799:ARG:HG2	58:B1:1325:PHE:HZ	1.72	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
8:H:71:ARG:HB3	8:H:74:ILE:HD13	1.89	0.53
30:e:21:TYR:OH	30:e:164:GLU:OE1	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:8:C:H2'	51:1:9:G:H8	1.73	0.53
51:1:44:A:O2'	51:1:45:G:H5'	2.08	0.53
51:1:441:U:O2'	51:1:442:G:H5'	2.08	0.53
51:1:613:A:H5''	51:1:614:A:N7	2.22	0.53
51:1:1601:G:O2'	51:1:1602:U:H5'	2.08	0.53
51:1:2644:G:O2'	51:1:2645:G:H5'	2.09	0.53
57:A1:100:LEU:HD21	57:A1:121:VAL:HG11	1.90	0.53
58:B1:785:ASP:O	58:B1:789:LYS:HB2	2.08	0.53
58:B1:800:LEU:HB3	58:B1:920:ALA:HB1	1.89	0.53
10:J:104:ILE:O	10:J:111:ARG:NH1	2.41	0.53
33:i:53:PRO:HD2	33:i:77:VAL:HG11	1.91	0.53
51:1:1130:U:O2'	51:1:1131:G:OP1	2.19	0.53
11:K:23:GLU:HA	11:K:26:THR:HG22	1.90	0.53
12:L:77:ARG:NH2	53:3:1381:U:O2	2.41	0.53
36:l:80:SER:HB3	36:l:114:GLY:HA3	1.89	0.53
39:o:31:THR:HG23	39:o:34:HIS:H	1.73	0.53
51:1:1560:G:H2'	51:1:1560:G:N3	2.24	0.53
51:1:2092:U:C5	51:1:2199:A:C2	2.97	0.53
59:B2:905:ILE:HG23	61:NA:102:PHE:CB	2.38	0.53
13:M:92:PRO:O	13:M:116:ARG:NH2	2.42	0.53
17:Q:64:SER:OG	17:Q:65:TYR:N	2.41	0.53
36:l:20:GLY:HA2	36:l:28:GLY:HA2	1.90	0.53
51:1:40:U:H2'	51:1:41:C:C6	2.43	0.53
51:1:53:A:H2'	51:1:54:G:H5'	1.89	0.53
51:1:402:A:C2'	51:1:403:U:H5'	2.38	0.53
51:1:1083:U:H2'	51:1:1084:A:H3'	1.89	0.53
51:1:1662:U:H2'	51:1:1663:G:O4'	2.09	0.53
53:3:1077:G:N2	53:3:1080:A:OP2	2.40	0.53
58:B1:209:ASN:HA	58:B1:214:ARG:HH21	1.74	0.53
59:B2:917:SER:O	59:B2:919:ARG:HG3	2.07	0.53
39:o:69:ASP:N	39:o:69:ASP:OD1	2.36	0.53
48:x:29:LEU:HD12	51:1:2230:G:H5''	1.90	0.53
51:1:282:A:H2'	51:1:283:G:C8	2.42	0.53
51:1:611:C:H2'	51:1:612:G:O4'	2.09	0.53
51:1:925:A:O2'	51:1:926:G:H5'	2.08	0.53
51:1:973:A:H5'	51:1:1188:U:H1'	1.90	0.53
51:1:995:C:H6	51:1:995:C:H5'	1.74	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
51:1:2617:U:H2'	51:1:2618:G:H5'	1.91	0.53
59:B2:628:HIS:HB3	59:B2:647:ARG:HH21	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:W0:3:ARG:NH1	60:W0:55:GLU:OE2	2.40	0.53
8:H:30:ASP:N	8:H:30:ASP:OD1	2.41	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
40:p:105:LYS:O	40:p:108:ARG:NH2	2.42	0.53
51:1:481:G:H1'	51:1:506:G:H21	1.71	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
51:1:1063:G:N1	51:1:1075:C:N4	2.53	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
51:1:2297:A:N1	51:1:2321:U:C5	2.75	0.53
53:3:1023:U:H2'	53:3:1024:G:H8	1.74	0.53
57:A1:205:MET:HE3	57:A1:213:PRO:HB3	1.91	0.53
9:I:154:VAL:HA	9:I:157:ALA:HB3	1.91	0.53
39:o:40:ILE:HD12	39:o:44:GLY:HA2	1.90	0.53
51:1:21:A:O2'	51:1:22:C:H5'	2.08	0.53
51:1:53:A:C2'	51:1:54:G:H5'	2.39	0.53
51:1:894:U:O2'	51:1:895:U:H5'	2.09	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
51:1:2092:U:C4'	51:1:2093:G:H5''	2.37	0.53
51:1:2425:A:H4'	51:1:2426:A:H5''	1.91	0.53
57:A1:47:LEU:HD23	57:A1:51:MET:HG3	1.89	0.53
58:B1:39:LYS:O	58:B1:273:ILE:HG23	2.08	0.53
58:B1:68:TYR:CA	58:B1:75:TYR:HE2	2.22	0.53
58:B1:78:LEU:O	58:B1:78:LEU:HD13	2.09	0.53
58:B1:633:ALA:HB2	59:B2:808:ASN:N	2.19	0.53
58:B1:759:ILE:HG23	58:B1:771:GLN:HB3	1.89	0.53
58:B1:975:ILE:HD11	58:B1:1003:LEU:HD11	1.91	0.53
42:r:4:VAL:HG12	42:r:13:ARG:HA	1.91	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
51:1:2747:G:O6	51:1:2754:U:H2'	2.09	0.53
58:B1:746:LEU:HG	58:B1:758:PRO:HG3	1.90	0.53
7:G:61:SER:OG	7:G:62:ARG:NH1	2.42	0.52
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
33:i:52:LEU:HB3	33:i:73:PRO:CB	2.33	0.52
34:j:2:LYS:HA	51:1:995:C:N3	2.23	0.52
51:1:57:C:H2'	51:1:58:G:O4'	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1530:G:N2	51:1:1542:U:H1'	2.23	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
53:3:1244:G:H1	53:3:1293:C:H42	1.57	0.52
58:B1:30:ILE:HG21	58:B1:241:VAL:O	2.08	0.52
27:b:92:LEU:HD11	27:b:100:ARG:HB3	1.91	0.52
30:e:91:ARG:NH2	52:2:43:C:O2	2.36	0.52
31:f:7:PRO:O	31:f:68:ARG:NH2	2.38	0.52
50:z:36:GLU:O	50:z:37:ARG:NH1	2.42	0.52
51:1:1111:A:H2'	51:1:1112:G:H4'	1.90	0.52
51:1:1278:C:O2'	51:1:1279:G:H5'	2.09	0.52
51:1:1782:U:H2'	51:1:1783:A:H5''	1.90	0.52
53:3:203:G:N2	53:3:204:G:O6	2.43	0.52
58:B1:112:ALA:HA	58:B1:238:ILE:HA	1.91	0.52
64:6:43:A:H2'	64:6:44:A:C8	2.44	0.52
51:1:519:U:H2'	51:1:520:G:H8	1.75	0.52
51:1:1574:C:H2'	51:1:1575:C:H6	1.74	0.52
51:1:1794:A:O2'	51:1:1795:C:H5'	2.10	0.52
53:3:1266:G:N2	53:3:1269:A:OP2	2.29	0.52
65:0:19:ILE:CG2	67:0:800:FUA:H281	2.38	0.52
51:1:752:A:H62	51:1:2609:U:H3	1.56	0.52
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:B1:201:LEU:HD12	58:B1:224:LEU:HD12	1.92	0.52
59:B2:246:LEU:HB3	59:B2:269:ILE:HD13	1.91	0.52
1:A:9:TYR:OH	30:e:101:ARG:NH2	2.41	0.52
17:Q:49:ARG:NH1	17:Q:88:ASP:OD2	2.42	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
51:1:2102:G:H2'	51:1:2103:C:O4'	2.09	0.52
51:1:2463:C:O2'	51:1:2464:G:H5'	2.10	0.52
51:1:2670:A:H2'	51:1:2671:G:H8	1.75	0.52
7:G:102:ASN:ND2	53:3:1073:U:O2	2.39	0.52
46:v:77:VAL:HG23	46:v:89:ILE:HG12	1.92	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
51:1:1110:G:HO2'	51:1:1111:A:H8	1.57	0.52
58:B1:390:LEU:N	58:B1:390:LEU:CD1	2.73	0.52
17:Q:36:VAL:HG21	17:Q:73:LEU:HB3	1.92	0.52
26:Z:28:LEU:HA	26:Z:31:VAL:HG12	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:257:ARG:NH2	27:b:262:THR:OG1	2.42	0.52
28:c:23:PRO:HB3	51:1:2682:A:N3	2.24	0.52
42:r:51:VAL:HG22	42:r:52:PRO:HD2	1.92	0.52
51:1:213:A:O2'	51:1:214:G:H5'	2.09	0.52
51:1:215:G:C4'	51:1:216:A:H4'	2.39	0.52
51:1:784:G:C5'	51:1:785:G:OP1	2.54	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
51:1:2707:U:H2'	51:1:2708:G:C8	2.44	0.52
59:B2:243:PRO:HB2	59:B2:274:ILE:HG23	1.90	0.52
59:B2:524:ILE:HG21	59:B2:708:VAL:HG13	1.92	0.52
59:B2:974:ARG:HD2	59:B2:1014:LEU:HD21	1.92	0.52
7:G:14:HIS:HB3	7:G:42:LEU:HD21	1.91	0.52
23:W:52:ARG:NH2	53:3:835:U:OP1	2.42	0.52
42:r:75:VAL:HG23	42:r:86:GLN:HG2	1.90	0.52
51:1:729:G:H5''	51:1:730:A:H5''	1.92	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
51:1:2216:G:H2'	51:1:2217:G:H8	1.74	0.52
51:1:2570:G:C2'	51:1:2571:U:H5'	2.40	0.52
51:1:2670:A:H2'	51:1:2671:G:C8	2.45	0.52
58:B1:111:THR:HG22	58:B1:300:GLN:NE2	2.23	0.52
58:B1:375:GLU:HG2	59:B2:1245:ALA:O	2.10	0.52
8:H:107:LYS:HB3	8:H:110:LEU:HD23	1.92	0.52
9:I:150:LYS:O	9:I:155:LYS:NZ	2.43	0.52
10:J:152:VAL:HG21	13:M:98:LEU:HD13	1.91	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
51:1:1878:G:O2'	51:1:1879:C:H5'	2.09	0.52
51:1:2731:G:H2'	51:1:2732:G:C8	2.45	0.52
58:B1:99:ARG:HA	58:B1:248:ASP:HB2	1.92	0.52
64:6:9:G:O4'	64:6:46:G:N3	2.42	0.52
33:i:56:VAL:HB	33:i:68:PHE:HB2	1.92	0.52
35:k:42:THR:HG22	35:k:57:VAL:HG12	1.91	0.52
39:o:40:ILE:HG22	39:o:47:VAL:HG12	1.91	0.52
51:1:8:C:H2'	51:1:9:G:C8	2.45	0.52
51:1:1047:G:N2	51:1:1110:G:H2'	2.25	0.52
51:1:1403:A:H2'	51:1:1404:C:C6	2.45	0.52
51:1:2013:A:H5''	51:1:2013:A:C8	2.44	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)
65:0:267:GLY:HA3	65:0:274:GLY:HA3	1.91	0.52
43:s:67:ASP:OD1	43:s:67:ASP:N	2.39	0.51
51:1:1722:A:H62	51:1:1738:G:H1'	1.74	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:B1:832:LYS:HB3	58:B1:1242:ARG:NH1	2.24	0.51
14:N:89:TYR:HB3	14:N:93:LEU:HD21	1.92	0.51
21:U:6:LEU:HD22	21:U:17:TYR:HB3	1.92	0.51
45:u:73:ASN:ND2	45:u:80:ASP:OD2	2.43	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'	2.10	0.51
51:1:1112:G:H2'	51:1:1113:U:O4'	2.10	0.51
51:1:1722:A:O2'	51:1:1723:G:H5'	2.10	0.51
51:1:1789:A:H2'	51:1:1790:C:O4'	2.09	0.51
53:3:202:G:H1	53:3:215:C:H42	1.57	0.51
57:A1:16:ILE:HG23	57:A1:26:VAL:HG22	1.91	0.51
62:NG:161:SER:HA	62:NG:170:PRO:HA	1.92	0.51
65:0:674:THR:O	65:0:677:ARG:HG3	2.11	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
51:1:208:C:O5'	51:1:208:C:H6	1.93	0.51
51:1:386:G:H3'	51:1:387:U:H5''	1.93	0.51
51:1:2651:C:O2'	51:1:2652:C:H5'	2.10	0.51
51:1:2758:A:H2'	51:1:2759:G:C5'	2.39	0.51
51:1:2776:A:C6	51:1:2782:G:H1'	2.45	0.51
58:B1:144:TYR:CE1	58:B1:162:GLU:CD	2.88	0.51
59:B2:125:GLY:HA2	59:B2:499:SER:HB2	1.92	0.51
59:B2:902:LEU:HD21	59:B2:908:GLU:HB2	1.90	0.51
15:O:24:GLU:HA	15:O:27:GLU:HB2	1.93	0.51
35:k:31:ARG:NH2	51:1:2676:C:OP2	2.44	0.51
44:t:65:GLY:N	44:t:79:ASP:OD1	2.43	0.51
51:1:49:A:O5'	51:1:51:G:H5'	2.09	0.51
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
51:1:138:U:C5	51:1:139:U:H5	2.28	0.51
51:1:355:U:H2'	51:1:356: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
51:1:1175:A:H3'	51:1:1176:U:C5'	2.36	0.51
58:B1:850:LYS:HB2	58:B1:857:LEU:HB2	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:0:632:ILE:HD11	65:0:654:ILE:HD12	1.91	0.51
3:C:7:LYS:HD3	51:1:2420:C:H5''	1.93	0.51
8:H:130:ARG:NH2	8:H:165:GLU:OE1	2.43	0.51
8:H:175:HIS:ND1	53:3:1109:C:OP2	2.44	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
51:1:69:C:H2'	51:1:70:G:C8	2.46	0.51
51:1:286:U:H2'	51:1:287:G:H8	1.76	0.51
51:1:2105:U:N3	51:1:2184:A:C2	2.78	0.51
59:B2:255:ILE:HB	59:B2:263:VAL:HB	1.92	0.51
37:m:38:ARG:HB3	37:m:98:PRO:HD3	1.92	0.51
51:1:291:G:O2'	51:1:292:U:H5'	2.11	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
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
59:B2:400:VAL:HG21	59:B2:452:ARG:HE	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
10:J:23:THR:HG22	10:J:28:ARG:HB3	1.91	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
27:b:50:THR:HG23	51:1:1813:G:H21	1.76	0.51
35:k:75:SER:OG	40:p:72:VAL:O	2.26	0.51
51:1:707:G:H2'	51:1:708:G:O4'	2.11	0.51
51:1:1266:G:O2'	51:1:2012:G:O6	2.25	0.51
51:1:1270:C:H5''	51:1:1271:G:H5''	1.93	0.51
58:B1:215:LYS:HA	58:B1:218:THR:HG22	1.91	0.51
58:B1:972:LYS:HD2	58:B1:1004:ALA:HA	1.93	0.51
59:B2:93:SER:HA	59:B2:128:PRO:HA	1.93	0.51
10:J:123:LEU:HD12	53:3:7:A:H2'	1.92	0.51
22:V:60:ILE:HA	22:V:74:LEU:HA	1.93	0.51
27:b:92:LEU:HD21	27:b:100:ARG:HD3	1.93	0.51
51:1:1930:G:C2'	51:1:1931:U:OP2	2.58	0.51
51:1:2285:C:O2'	51:1:2286:G:H5'	2.11	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
53:3:1538:C:O2'	53:3:1539:C:H5'	2.11	0.51
58:B1:505:ASP:OD2	59:B2:812:PHE:HA	2.11	0.51
58:B1:770:LEU:CD1	59:B2:618:GLN:HG3	2.37	0.51
59:B2:714:VAL:HB	59:B2:787:PRO:HD2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:207:ALA:HB2	51:1:1790:C:O2'	2.12	0.51
51:1:539:G:O2'	51:1:540:C:H5'	2.11	0.51
51:1:891:G:H2'	51:1:892:A:C8	2.46	0.51
51:1:1415:U:H1'	51:1:1588:G:N2	2.26	0.51
55:8:13:DT:OP2	58:B1:791:ALA:CB	2.59	0.51
58:B1:902:ASP:HB3	58:B1:905:ARG:HB2	1.93	0.51
27:b:147:PRO:HG3	27:b:184:GLU:HG2	1.92	0.50
30:e:162:ASP:OD1	30:e:162:ASP:N	2.37	0.50
38:n:49:GLU:O	38:n:53:THR:OG1	2.29	0.50
51:1:630:G:H4'	51:1:640:C:H4'	1.93	0.50
51:1:757:G:C2'	51:1:758:C:H5'	2.38	0.50
51:1:1441:G:H2'	51:1:1442:U:H6	1.71	0.50
51:1:2687:U:H2'	51:1:2688:G:O4'	2.11	0.50
58:B1:412:LEU:HD23	58:B1:416:ILE:HG13	1.92	0.50
59:B2:903:ARG:HA	59:B2:907:GLY:HA2	1.93	0.50
4:D:3:ARG:NH1	51:1:752:A:OP1	2.43	0.50
15:O:29:ALA:O	15:O:33:GLY:N	2.42	0.50
28:c:176:ASP:OD1	28:c:176:ASP:N	2.44	0.50
51:1:1293:C:H2'	51:1:1294:U:C6	2.46	0.50
51:1:2555:U:O2	51:1:2555:U:O4'	2.29	0.50
58:B1:683:ILE:HD12	58:B1:754:ILE:HG21	1.92	0.50
9:I:12:ARG:NH1	9:I:32:LYS:O	2.42	0.50
31:f:136:ASP:HB3	31:f:139:VAL:HG12	1.92	0.50
48:x:64:ASP:N	48:x:64:ASP:OD1	2.43	0.50
51:1:145:C:H2'	51:1:146:A:C8	2.46	0.50
51:1:438:G:H2'	51:1:439:A:H8	1.76	0.50
51:1:2052:A:C2'	51:1:2053:G:H5'	2.41	0.50
59:B2:232:ILE:HG12	59:B2:237:LEU:HG	1.94	0.50
11:K:42:TRP:HB2	11:K:59:TYR:HB2	1.93	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
51:1:386:G:H3'	51:1:387:U:C5'	2.41	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
51:1:1910:G:H1	51:1:1920:C:H42	1.58	0.50
51:1:2248:C:H2'	51:1:2249:U:H5'	1.94	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
51:1:2593:U:O2'	51:1:2594:C:H5'	2.11	0.50
58:B1:1179:PRO:HD2	58:B1:1184:ASP:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:c:161:MET:HE1	51:1:2050:C:O2	2.11	0.50
51:1:187:G:C6	51:1:188:G:N7	2.80	0.50
51:1:197:A:H2	51:1:2434:A:N6	2.10	0.50
51:1:288:U:H2'	51:1:289:G:C8	2.47	0.50
51:1:673:C:H2'	51:1:674:G:C5'	2.41	0.50
51:1:1388:G:O2'	51:1:1389:G:H5'	2.12	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
53:3:113:G:N3	53:3:353:A:O2'	2.42	0.50
53:3:664:G:H22	53:3:741:G:H1	1.60	0.50
57:A2:294:ASN:HA	61:NA:463:GLY:CA	2.41	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
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
27:b:146:LYS:HB2	27:b:149:LYS:HB2	1.93	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
58:B1:275:ARG:HH12	58:B1:278:ARG:NH1	2.09	0.50
58:B1:421:VAL:O	58:B1:436:ALA:HA	2.12	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
34:j:2:LYS:HG2	51:1:995:C:N4	2.27	0.50
46:v:51:GLN:OE1	46:v:79:ARG:NH2	2.40	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
51:1:1416: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
63:5:34:G:H3'	63:5:35:A:H8	1.76	0.50
8:H:4:VAL:HG21	8:H:9:ILE:HD13	1.93	0.50
12:L:65:LEU:O	12:L:69:ARG:N	2.43	0.50
15:O:39:PRO:HD2	53:3:1123:U:H4'	1.92	0.50
33:i:134:SER:OG	51:1:1062:G:N2	2.45	0.50
51:1:155:A:H2'	51:1:156:A:H8	1.76	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
51:1:900: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
51:1:1161:C:H2'	51:1:1162:G:C8	2.44	0.50
51:1:1409:U:H2'	51:1:1410:G:H8	1.77	0.50
51:1:2734:A:H2'	51:1:2735:G:C5'	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:437:PHE:HZ	58:B1:453:VAL:HG11	1.76	0.50
59:B2:411:ARG:NH2	59:B2:427:ASP:OD2	2.44	0.50
1:A:37:CYS:O	1:A:41:HIS:N	2.45	0.50
6:F:19:ARG:HB2	6:F:24:ARG:HD2	1.93	0.50
7:G:103:TRP:HA	7:G:106:VAL:HG12	1.93	0.50
19:S:68:ARG:NH2	53:3:974:A:OP1	2.45	0.50
21:U:5:ARG:HB3	53:3:376:G:H5''	1.93	0.50
30:e:84:ILE:HD11	51:1:2311:A:H1'	1.94	0.50
33:i:126:ARG:HD2	51:1:1080:A:H4'	1.93	0.50
43:s:109:ASP:OD1	43:s:109:ASP:N	2.42	0.50
51:1:246:C:H2'	51:1:247:G:C5'	2.40	0.50
51:1:1348:C:C5	51:1:1349:C:C5	3.00	0.50
51:1:1528:A:H2'	51:1:1529:G:O4'	2.11	0.50
51:1:1614:A:H2'	51:1:1615:C:H5'	1.94	0.50
51:1:1717:A:H2'	51:1:1718:G:C5'	2.40	0.50
51:1:1916:A:H2'	51:1:1917:U:O4'	2.12	0.50
51:1:2836:U:H2'	51:1:2837:A:C8	2.47	0.50
53:3:517:G:N2	53:3:533:A:OP2	2.33	0.50
59:B2:562:GLU:OE1	59:B2:662:SER:OG	2.28	0.50
63:5:29:G:H3'	63:5:30:G:H8	1.76	0.50
65:0:615:PRO:HG3	65:0:687:TYR:HE1	1.76	0.50
1:A:35:ASP:OD1	1:A:35:ASP:N	2.42	0.49
15:O:42:LEU:HB3	15:O:71:LEU:HB2	1.94	0.49
27:b:206:LYS:HD2	51:1:729:G:C8	2.47	0.49
29:d:191:ASP:O	29:d:195:GLN:NE2	2.44	0.49
33:i:110:GLN:HG2	33:i:121:ILE:HD13	1.93	0.49
51:1:1077:A:H8	51:1:1078:U:H1'	1.77	0.49
51:1:2815:C:O2'	51:1:2816:G:H5'	2.11	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
51:1:2393:U:H2'	51:1:2394:C:H5'	1.94	0.49
53:3:1178:G:N2	53:3:1181:G:OP2	2.43	0.49
58:B1:102:MET:HG2	58:B1:246:PRO:HD3	1.94	0.49
59:B2:554:HIS:HD2	59:B2:558:VAL:HB	1.77	0.49
13:M:29:SER:OG	13:M:30:LYS:N	2.44	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:173:A:H2'	51:1:174:U:C6	2.47	0.49
51:1:1087:G:H2'	51:1:1089:A:H5'	1.94	0.49
51:1:1119:U:O2'	51:1:1120:G:H5'	2.13	0.49
51:1:1437:C:H2'	51:1:1438:U:H6	1.78	0.49
51:1:1468:U:H2'	51:1:1522:A:N6	2.26	0.49
51:1:1785:A:O2'	51:1:1786:A:H8	1.96	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
53:3:928:G:O2'	53:3:1533:C:OP1	2.22	0.49
58:B1:1361:THR:OG1	59:B2:1282:GLY:O	2.28	0.49
59:B2:533:LEU:HD13	59:B2:540:ARG:HH21	1.77	0.49
7:G:101:THR:HG23	7:G:174:GLU:HG3	1.95	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:87:GLN:NE2	31:f:129:GLU:OE2	2.45	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
51:1:236:C:H2'	51:1:237:C:C6	2.46	0.49
51:1:482:A:H1'	51:1:498:G:N2	2.27	0.49
51:1:2257:U:O2'	51:1:2258:C:H5'	2.13	0.49
51:1:2348:U:O2'	51:1:2349:G:H5'	2.12	0.49
58:B1:749:LYS:HB3	58:B1:755:ILE:HD11	1.93	0.49
59:B2:18:ARG:HE	59:B2:620:ASN:HA	1.77	0.49
7:G:221:ARG:HG2	7:G:224:ARG:HH11	1.77	0.49
27:b:50:THR:HG23	51:1:1813:G:N2	2.27	0.49
51:1:519:U:H2'	51:1:520:G:C8	2.48	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
51:1:2290:G:H2'	51:1:2291:U:H6	1.74	0.49
51:1:2533:U:H2'	51:1:2534:A:C5'	2.43	0.49
59:B2:836:LEU:HD13	59:B2:1054:LEU:HD13	1.95	0.49
30:e:57:ALA:HB2	30:e:64:PRO:HD3	1.95	0.49
51:1:16:C:H2'	51:1:17:G:H8	1.78	0.49
51:1:898:C:C2'	51:1:899:A:H5'	2.43	0.49
51:1:940:G:H2'	51:1:941:A:C5'	2.41	0.49
51:1:2281:A:O2'	51:1:2282:G:H5'	2.12	0.49
51:1:2283:C:H2'	51:1:2284:A:O4'	2.11	0.49
51:1:2670:A:O2'	51:1:2671:G:H5'	2.12	0.49
58:B1:124:ILE:HG23	58:B1:128:LEU:HD12	1.94	0.49
59:B2:565:GLU:HA	59:B2:569:ILE:HG12	1.95	0.49
12:L:2:ARG:NH2	53:3:933:G:O6	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:120:ARG:HH12	53:3:500:G:H5'	1.77	0.49
31:f:122:ALA:HB2	31:f:132:LEU:HD23	1.94	0.49
48:x:1:SER:O	48:x:49:ARG:NH1	2.46	0.49
51:1:644:A:H2'	51:1:645:C:C4'	2.42	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
59:B2:857:VAL:HG13	59:B2:919:ARG:HH21	1.78	0.49
7:G:18:GLN:HG3	7:G:189:ASN:CB	2.41	0.49
21:U:36:VAL:HG12	21:U:53:ASP:HB3	1.94	0.49
29:d:77:ILE:HG23	51:1:1256:G:N2	2.26	0.49
33:i:20:SER:H	33:i:21:PRO:HD2	1.78	0.49
41:q:103:VAL:HA	41:q:106:THR:HG22	1.94	0.49
42:r:68:ARG:O	42:r:90:ARG:NH2	2.46	0.49
44:t:70:HIS:N	44:t:73:ARG:O	2.44	0.49
51:1:131:A:H2'	51:1:132:G:H8	1.77	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
51:1:840:C:O2'	51:1:841:G:H5'	2.12	0.49
51:1:1668:A:N3	51:1:1670:C:N4	2.60	0.49
59:B2:9:LYS:HG2	59:B2:1171:ARG:HH12	1.77	0.49
59:B2:400:VAL:HG11	59:B2:452:ARG:HD2	1.93	0.49
14:N:94:ARG:HG2	14:N:97:LEU:HD12	1.95	0.49
51:1:118:A:H2'	51:1:120:U:O4	2.13	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
58:B1:395:LYS:NZ	58:B1:399:LYS:CD	2.74	0.49
65:O:616:ILE:HB	65:O:686:LYS:HE3	1.95	0.49
9:I:93:LEU:O	9:I:99:ASN:ND2	2.39	0.49
9:I:153:ARG:NH2	53:3:435:A:N3	2.61	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
28:c:81:GLU:HG3	51:1:2636:C:O5'	2.13	0.49
33:i:85:ILE:HD12	33:i:97:VAL:HG12	1.95	0.49
51:1:1111:A:H2'	51:1:1111:A:N3	2.28	0.49
51:1:1117:C:H2'	51:1:1118:C:H6	1.78	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
51:1:1910:G:N2	51:1:1911:U:C2	2.81	0.49
51:1:2208:C:H2'	51:1:2209:G:C8	2.48	0.49
51:1:2510:C:N4	51:1:2511:U:C4	2.81	0.49
51:1:2843:G:O2'	51:1:2844:G:H5'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1064:G:O2'	53:3:1190:G:N2	2.46	0.49
59:B2:732:ILE:HD11	59:B2:769:PRO:HB3	1.95	0.49
37:m:74:THR:HG21	37:m:86:LYS:HG2	1.94	0.48
38:n:8:ARG:HH21	38:n:43:GLU:HG3	1.77	0.48
51:1:1537:G:H3'	51:1:1537:G:N3	2.28	0.48
51:1:2126:A:H5'	51:1:2127:G:O5'	2.13	0.48
53:3:890:G:O2'	53:3:906:A:N6	2.46	0.48
53:3:1137:C:H4'	53:3:1138:G:H5'	1.95	0.48
58:B1:145:VAL:HG12	58:B1:184:ALA:HB1	1.94	0.48
58:B1:201:LEU:HD11	58:B1:220:ARG:HG2	1.95	0.48
33:i:79:LEU:HD13	33:i:132:ALA:HB2	1.94	0.48
51:1:67:U:H2'	51:1:68:G:H8	1.77	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
51:1:360:U:H2'	51:1:361:G:C1'	2.43	0.48
51:1:706:A:H2'	51:1:707:G:H5'	1.95	0.48
51:1:898:C:O2'	51:1:899:A:H5'	2.13	0.48
51:1:1084:A:O2'	51:1:1105:U:H4'	2.12	0.48
51:1:2050:C:N4	51:1:2051:A:C6	2.81	0.48
58:B1:550:VAL:O	58:B1:569:LEU:HA	2.13	0.48
9:I:94:GLU:HG3	9:I:190:LEU:HD21	1.95	0.48
17:Q:97:VAL:HG12	17:Q:99:GLY:H	1.78	0.48
25:Y:59:ARG:O	25:Y:63:LYS:N	2.46	0.48
27:b:70:LYS:O	27:b:117:SER:OG	2.30	0.48
29:d:143:LEU:HD13	29:d:146:VAL:HG11	1.94	0.48
33:i:72:THR:O	33:i:73:PRO:C	2.55	0.48
35:k:5:GLN:HE21	51:1:1668:A:H5''	1.78	0.48
42:r:71:LYS:HA	42:r:90:ARG:HG2	1.95	0.48
51:1:54:G:H2'	51:1:55:G:O4'	2.12	0.48
51:1:214:G:H2'	51:1:215:G:C8	2.48	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
51:1:1536:C:H5''	51:1:1537:G:C4	2.48	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
51:1:2180: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
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
51:1:488:G:H22	51:1:491:G:H5''	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1680:U:O2'	51:1:1681:G:H5'	2.13	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
51:1:2649:C:O2'	51:1:2650:U:H5'	2.13	0.48
52:2:51:G:H22	52:2:53:A:H62	1.61	0.48
53:3:673:A:H2'	53:3:674:G:C8	2.49	0.48
58:B1:115:TRP:O	58:B1:1333:THR:HG21	2.13	0.48
58:B1:809:VAL:HG21	58:B1:909:ILE:HG12	1.95	0.48
58:B1:1371:ARG:HE	58:B1:1372:ARG:NH1	2.10	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
12:L:41:ILE:HD11	53:3:1240:U:H5'	1.94	0.48
45:u:88:ASP:OD1	45:u:88:ASP:N	2.43	0.48
51:1:286:U:H2'	51:1:287:G:C8	2.47	0.48
51:1:481:G:C2'	51:1:482:A:OP2	2.61	0.48
51:1:553:G:H2'	51:1:554:U:O4'	2.13	0.48
51:1:1087:G:O6	51:1:1089:A:C2	2.67	0.48
51:1:1871:A:H2'	51:1:1872:A:O4'	2.13	0.48
51:1:217:A:H2'	51:1:218:A:O4'	2.13	0.48
51:1:2828:G:O2'	51:1:2829:A:H5'	2.13	0.48
53:3:880:C:H2'	53:3:881:G:H8	1.78	0.48
53:3:1531:A:O2'	53:3:1532:U:H5'	2.14	0.48
55:8:3:DC:H2''	55:8:4:DT:C7	2.42	0.48
58:B1:1261:LEU:HD12	58:B1:1304:ARG:HH21	1.78	0.48
59:B2:529:ARG:HH11	59:B2:572:ILE:HG22	1.77	0.48
64:6:50:U:H2'	64:6:51:C:C5	2.49	0.48
65:0:468:ILE:HG21	67:0:800:FUA:H11	1.95	0.48
32:g:8:LYS:HD3	32:g:14:SER:HA	1.96	0.48
51:1:92:U:H2'	51:1:93:G:H5'	1.96	0.48
51:1:275:C:C3'	51:1:276:U:H5''	2.40	0.48
53:3:776:G:N2	53:3:802:A:OP2	2.39	0.48
57:A1:182:ARG:O	57:A1:205:MET:HA	2.14	0.48
59:B2:363:LEU:HB3	59:B2:381:ALA:HB1	1.96	0.48
14:N:10:ARG:NH2	53:3:1119:C:OP2	2.46	0.48
14:N:86:LEU:HD12	14:N:97:LEU:HD11	1.95	0.48
17:Q:82:ARG:O	17:Q:95:HIS:N	2.47	0.48
26:Z:55:HIS:HA	26:Z:58:LYS:HD2	1.95	0.48
29:d:149:ILE:HD11	29:d:172:ALA:HA	1.96	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
51:1:555:G:O2'	51:1:556:A:H8	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:718:A:H2'	51:1:719:C:O4'	2.12	0.48
51:1:1387:A:C5'	51:1:1469:A:H1'	2.38	0.48
51:1:2016:U:O5'	51:1:2016:U:H6	1.97	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
53:3:401:C:O2'	53:3:621:A:N3	2.45	0.48
55:8:14:DC:H2'	55:8:15:DC:H6	1.79	0.48
58:B1:255:LEU:HD23	58:B1:261:ALA:HB2	1.95	0.48
58:B1:1146:GLU:OE2	58:B1:1310:THR:HG22	2.14	0.48
59:B2:1314:GLN:HB2	60:W0:28:ARG:HH12	1.79	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
38:n:100:CYS:H	38:n:111:ALA:HA	1.79	0.48
51:1:476:G:H4'	51:1:502:A:N1	2.28	0.48
51:1:596:U:C2	51:1:662:G:N2	2.82	0.48
51:1:820:A:H2'	51:1:821:A:O4'	2.14	0.48
51:1:852:U:H2'	51:1:853:C:C6	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
51:1:2660:A:N6	65:0:672:SER:HB2	2.29	0.48
55:8:14:DC:H2'	55:8:15:DC:C6	2.48	0.48
57:A1:18:GLN:HA	57:A1:24:ALA:HA	1.94	0.48
58:B1:103:GLY:H	58:B1:244:VAL:HG22	1.79	0.48
32:g:47:PHE:HA	32:g:51:ARG:HB2	1.96	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
51:1:1464:G:H2'	51:1:1465:G:C8	2.49	0.48
51:1:1807:G:C2'	51:1:1808:A:H5'	2.29	0.48
51:1:2149:U:H2'	51:1:2150:C:C6	2.49	0.48
53:3:898:G:N2	53:3:901:A:OP2	2.46	0.48
58:B1:1347:LEU:HG	58:B1:1357:ILE:HG23	1.96	0.48
59:B2:400:VAL:HG22	59:B2:584:TYR:HB3	1.96	0.48
63:5:50:U:H2'	63:5:51:U:C6	2.49	0.48
27:b:131:MET:HE2	27:b:187:CYS:HB2	1.96	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	1.95	0.47
31:f:16:VAL:HA	31:f:25:ILE:HG12	1.96	0.47
40:p:2:ASN:HD21	51:1:2876:G:H4'	1.79	0.47
51:1:813:U:C2	51:1:1195:G:N2	2.82	0.47
51:1:1026:G:OP2	51:1:1134:A:H1'	2.13	0.47
51:1:2286:G:H21	51:1:2287:A:H61	1.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1223:C:H5'	53:3:1224:U:H5''	1.96	0.47
53:3:1305:G:N2	53:3:1331:G:H2'	2.29	0.47
58:B1:220:ARG:HH11	58:B1:220:ARG:CG	2.26	0.47
59:B2:786:GLY:N	59:B2:789:THR:OG1	2.41	0.47
59:B2:901:LEU:HD13	61:NA:107:THR:CA	2.42	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
21:U:18:GLN:HA	21:U:38:PHE:HA	1.95	0.47
27:b:152:GLN:HB3	51:1:1818:U:N3	2.29	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
51:1:5:A:H2'	51:1:6:A:C8	2.49	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
51:1:854:C:H2'	51:1:855:G:H8	1.79	0.47
51:1:2156:G:C3'	51:1:2157:G:H5'	2.44	0.47
57:A1:100:LEU:HB2	57:A1:144:ILE:HG23	1.95	0.47
59:B2:903:ARG:HA	59:B2:907:GLY:CA	2.44	0.47
28:c:190:LYS:HE2	51:1:2729:G:H4'	1.95	0.47
31:f:174:LYS:HD2	31:f:176:LYS:HB2	1.96	0.47
47:w:29:ALA:N	47:w:60:ASP:OD1	2.48	0.47
51:1:1463:C:H2'	51:1:1464:G:C8	2.49	0.47
51:1:2098:U:H2'	51:1:2099:U:O4'	2.14	0.47
51:1:2298:A:C2'	51:1:2299:U:H5'	2.45	0.47
51:1:2362:C:O5'	51:1:2362:C:H6	1.97	0.47
59:B2:133:ASN:O	59:B2:527:LYS:NZ	2.42	0.47
59:B2:318:SER:OG	59:B2:320:ASP:OD1	2.31	0.47
65:0:12:ASN:HB2	65:0:107:ASP:OD2	2.14	0.47
20:T:38:LEU:HD22	20:T:55:LEU:HD13	1.96	0.47
22:V:19:SER:OG	22:V:70:LYS:NZ	2.40	0.47
45:u:39:ASN:HB3	45:u:62:ALA:HB3	1.95	0.47
51:1:40:U:H2'	51:1:41:C:H6	1.78	0.47
51:1:1019:U:N3	51:1:1142:A:N6	2.57	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
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:B1:1027:VAL:HB	58:B1:1121:LEU:HB2	1.95	0.47
18:R:15:VAL:HG11	18:R:30:LYS:HG2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:f:133:LYS:NZ	31:f:134:GLY:O	2.44	0.47
46:v:79:ARG:HA	46:v:86:LEU:HA	1.94	0.47
51:1:143:C:H2'	51:1:144:A:C8	2.49	0.47
51:1:712:G:H2'	51:1:713:G:H5'	1.96	0.47
51:1:1067:A:H2'	51:1:1068:G:C8	2.50	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
51:1:1702:G:H2'	51:1:1703:G:C5'	2.35	0.47
51:1:2899:A:H2'	51:1:2900:A:O4'	2.15	0.47
58:B1:395:LYS:NZ	58:B1:399:LYS:CE	2.77	0.47
58:B1:968:ASN:HA	58:B1:1117:SER:HB2	1.96	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
28:c:13:ARG:NH2	40:p:74:GLN:OE1	2.43	0.47
31:f:88:LEU:HD21	31:f:104:LEU:HD23	1.97	0.47
47:w:19:VAL:HA	47:w:34:VAL:HG22	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
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
51:1:2625:G:H2'	51:1:2626:C:H6	1.76	0.47
53:3:358:U:H2'	53:3:359:G:H8	1.78	0.47
53:3:816:A:OP1	53:3:1526:G:O2'	2.28	0.47
58:B1:526:VAL:HG12	58:B1:549:LYS:HB2	1.96	0.47
4:D:29:GLN:O	4:D:29:GLN:NE2	2.47	0.47
9:I:159:GLU:HA	9:I:162:GLU:HB2	1.97	0.47
12:L:149:ALA:HB1	16:P:58:THR:HG21	1.97	0.47
19:S:32:ASP:O	19:S:34:ASN:ND2	2.48	0.47
21:U:25:ARG:NH1	53:3:230:G:O2'	2.48	0.47
26:Z:19:LYS:H	26:Z:19:LYS:HG3	1.53	0.47
27:b:156:SER:OG	27:b:157:ALA:N	2.44	0.47
28:c:136:ASN:OD1	51:1:2579:C:O2'	2.32	0.47
45:u:6:ARG:HB2	51:1:85:G:P	2.55	0.47
51:1:283:G:C2'	51:1:284:U:H5'	2.45	0.47
51:1:297:G:H2'	51:1:298:G:O4'	2.14	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
51:1:1297:C:H2'	51:1:1298:C:H6	1.79	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
51:1:1726:C:H2'	51:1:1727:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:2194:U:O2'	51:1:2195:U:H5'	2.15	0.47
51:1:2395:C:H2'	51:1:2396:G:O4'	2.15	0.47
58:B1:29:MET:HG2	59:B2:1336:ASN:ND2	2.29	0.47
58:B1:198:CYS:HA	58:B1:221:ILE:CD1	2.45	0.47
58:B1:891:ASP:OD2	58:B1:1290:ARG:NH2	2.47	0.47
59:B2:901:LEU:CD1	61:NA:107:THR:CA	2.93	0.47
59:B2:1286:THR:O	59:B2:1290:MET:HB2	2.14	0.47
59:B2:1314:GLN:HA	60:W0:28:ARG:HH22	1.80	0.47
12:L:107:ALA:HA	12:L:122:GLU:HG3	1.95	0.47
17:Q:114:SER:O	53:3:35:G:O2'	2.30	0.47
43:s:72:THR:OG1	43:s:73:LYS:N	2.48	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
51:1:686:U:H6	51:1:788:A:H61	1.61	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
51:1:1922:G:O2'	51:1:1923:U:H5'	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
51:1:2563:U:H2'	51:1:2565:A:OP2	2.15	0.47
58:B1:420:PRO:HA	58:B1:437:PHE:O	2.15	0.47
58:B1:833:GLU:N	58:B1:1242:ARG:HH12	2.12	0.47
59:B2:903:ARG:HA	59:B2:907:GLY:N	2.30	0.47
63:5:8:U:H2'	63:5:13:C:N4	2.30	0.47
16:P:34:THR:OG1	16:P:35:ASP:N	2.47	0.47
33:i:115:ASP:OD2	51:1:1059:G:H4'	2.14	0.47
51:1:435:C:C2'	51:1:436:C:H5'	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
51:1:1267:U:H2'	51:1:1267:U:O2	2.14	0.47
51:1:1491:G:H2'	51:1:1492:G:H8	1.80	0.47
51:1:1913:A:C8	53:3:1494:G:H4'	2.49	0.47
51:1:2180:U:H2'	51:1:2181:U:O4'	2.14	0.47
51:1:2295:C:O2'	51:1:2296:U:H5'	2.15	0.47
53:3:617:G:H1	53:3:623:C:H42	1.63	0.47
53:3:944:G:N1	53:3:1338:G:OP2	2.34	0.47
54:4:26:U:HO2'	58:B1:78:LEU:CB	2.19	0.47
58:B1:1167:LYS:NZ	58:B1:1170:LYS:HB2	2.30	0.47
59:B2:1311:GLY:O	60:W0:31:GLN:NE2	2.47	0.47
64:6:48:C:H5''	64:6:50:U:OP1	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:171:GLU:HB3	9:I:180:THR:HG22	1.97	0.47
31:f:100:ASN:OD1	31:f:100:ASN:N	2.47	0.47
39:o:68:LYS:HE3	52:2:49:C:H5''	1.97	0.47
51:1:570:G:H5'	51:1:983:A:C2	2.50	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
51:1:1068:G:H2'	51:1:1069:A:H4'	1.96	0.47
51:1:1209:U:O3'	51:1:1212:G:H5'	2.15	0.47
51:1:1400:U:H2'	51:1:1401:G:C8	2.50	0.47
51:1:1873:G:O2'	51:1:1874:C:H5'	2.15	0.47
51:1:2047:C:O5'	51:1:2047:C:H6	1.98	0.47
51:1:2241:A:H2'	51:1:2242:G:C8	2.50	0.47
51:1:2259:U:H2'	51:1:2260:C:O4'	2.15	0.47
51:1:2360:G:H2'	51:1:2361:G:C5'	2.40	0.47
51:1:2581:G:H2'	51:1:2581:G:N3	2.30	0.47
51:1:2858:C:H2'	51:1:2859:G:O4'	2.15	0.47
12:L:79:VAL:HB	12:L:84:TYR:HD2	1.80	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
46:v:83:LYS:HB3	46:v:85:LYS:HZ3	1.79	0.46
51:1:1141:U:H4'	51:1:1142:A:C1'	2.45	0.46
51:1:1480:C:H2'	51:1:1481:U:C6	2.49	0.46
51:1:1528:A:H2'	51:1:1529:G:C5'	2.44	0.46
53:3:1225:A:H2'	53:3:1225:A:N3	2.30	0.46
36:l:39:LYS:HG2	51:1:832:U:OP1	2.15	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
51:1:214:G:O2'	51:1:215:G:H5'	2.14	0.46
51:1:389:G:O2'	51:1:390:U:H5'	2.15	0.46
51:1:1036:G:O2'	51:1:1037:G:H5'	2.15	0.46
51:1:1146:C:O2'	51:1:1147:A:H5'	2.16	0.46
51:1:1516:G:O2'	51:1:1517:G:H5'	2.15	0.46
51:1:1536:C:H5''	51:1:1537:G:C5	2.50	0.46
53:3:410:G:H21	53:3:432:A:H62	1.62	0.46
53:3:512:U:H2'	53:3:513:C:C6	2.50	0.46
58:B1:108:ALA:HB1	58:B1:279:LEU:HD22	1.96	0.46
58:B1:515:ARG:NH2	58:B1:718:SER:O	2.48	0.46
58:B1:842:ARG:HH22	58:B1:1250:ASP:HB2	1.80	0.46
58:B1:1221:LEU:HD22	58:B1:1306:LEU:HB2	1.96	0.46
59:B2:103:VAL:HG12	59:B2:117:ILE:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:517:GLN:HB3	59:B2:760:ASN:H	1.79	0.46
59:B2:735:LYS:HA	59:B2:748:ILE:HG22	1.97	0.46
65:0:97:ILE:HD11	65:0:411:PHE:HD1	1.80	0.46
2:B:31:LYS:HG2	51:1:2885:G:N2	2.31	0.46
7:G:129:THR:HB	7:G:132:GLU:HB2	1.96	0.46
11:K:3:HIS:HA	11:K:65:GLU:HA	1.97	0.46
27:b:131:MET:H	27:b:131:MET:HG2	1.57	0.46
27:b:145:MET:HE1	51:1:1800:C:H2'	1.98	0.46
34:j:65:THR:HG22	51:1:1141:U:OP2	2.15	0.46
46:v:26:PHE:HE2	46:v:89:ILE:HG13	1.80	0.46
51:1:30:G:C5	51:1:31:C:C4	3.03	0.46
51:1:1389:G:C2	51:1:1390:U:C2	3.02	0.46
51:1:1851:U:OP1	64:6:4:G:H4'	2.15	0.46
51:1:1874:C:H2'	51:1:1875:G:O4'	2.15	0.46
51:1:1923:U:O2'	51:1:1924:C:H5'	2.16	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
53:3:959:A:O2'	53:3:984:C:O2'	2.24	0.46
58:B1:1060:VAL:HG13	58:B1:1106:ILE:HG12	1.96	0.46
59:B2:28:LEU:HD21	59:B2:524:ILE:HG13	1.98	0.46
59:B2:207:THR:OG1	59:B2:354:ASP:OD2	2.32	0.46
65:0:93:VAL:HA	65:0:96:THR:HG23	1.98	0.46
10:J:73:VAL:HG11	10:J:143:LEU:HB3	1.98	0.46
31:f:29:ASN:ND2	31:f:80:GLU:O	2.49	0.46
35:k:47:ILE:HG22	35:k:49:ARG:H	1.80	0.46
49:y:15:ASN:OD1	49:y:16:THR:N	2.48	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'	2.44	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
51:1:848:C:H2'	51:1:849:A:C8	2.51	0.46
51:1:853:C:O2'	51:1:854:C:H5'	2.16	0.46
51:1:1090:A:C2	51:1:1102:C:H1'	2.50	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
51:1:2290: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
58:B1:1150:PRO:HG3	58:B1:1214:PRO:HB2	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	2.51	0.46
11:K:10:VAL:HG23	11:K:58:HIS:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:33:THR:OG1	23:W:34:GLU:N	2.49	0.46
29:d:132:LYS:HG2	29:d:136:GLN:HE22	1.81	0.46
31:f:87:GLN:HB3	31:f:162:ARG:HG3	1.96	0.46
33:i:112:LYS:HD2	33:i:128:ILE:HD12	1.97	0.46
34:j:2:LYS:HA	51:1:995:C:C4	2.50	0.46
51:1:289:G:H2'	51:1:290:U:C6	2.50	0.46
51:1:538:A:O2'	51:1:539:G:H5'	2.14	0.46
51:1:688:U:H5'	51:1:1780:A:C2	2.51	0.46
51:1:1071:G:HO2'	51:1:1089:A:H2'	1.80	0.46
51:1:1105:U:H2'	51:1:1106:G:H8	1.80	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
51:1:1927: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
51:1:2294:G:O2'	51:1:2295:C:H5'	2.15	0.46
53:3:1035:A:H1'	53:3:1036:A:O5'	2.16	0.46
55:8:20:DA:H4'	59:B2:143:ARG:NH1	2.31	0.46
57:A1:59:VAL:HG22	57:A1:144:ILE:HA	1.97	0.46
57:A1:212:ASP:OD1	57:A1:212:ASP:N	2.48	0.46
63:5:26:A:H61	63:5:44:G:H22	1.64	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
22:V:10:ARG:NE	22:V:55:GLY:O	2.48	0.46
27:b:1:ALA:N	27:b:19:VAL:O	2.41	0.46
40:p:52:ARG:HH21	51:1:2720:U:H5''	1.80	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
51:1:1090:A:H61	51:1:1101:U:H3	1.62	0.46
51:1:1117:C:H2'	51:1:1118:C:C6	2.50	0.46
51:1:2329:U:H2'	51:1:2330:G:C8	2.51	0.46
58:B1:209:ASN:HA	58:B1:214:ARG:NH2	2.30	0.46
58:B1:352:ARG:HB2	59:B2:1268:GLN:NE2	2.30	0.46
4:D:12:ARG:NH1	51:1:465:G:OP1	2.49	0.46
33:i:79:LEU:HD21	33:i:105:LEU:HD21	1.96	0.46
51:1:28:A:O2'	51:1:29:U:H5'	2.16	0.46
51:1:338:G:O2'	51:1:339:U: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
51:1:2813:A:O2'	51:1:2814:A:H5'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:128:LEU:HD21	58:B1:188:LEU:HB3	1.97	0.46
58:B1:375:GLU:HB3	59:B2:1245:ALA:HB3	1.97	0.46
58:B1:385:LEU:HD23	58:B1:390:LEU:HB2	1.98	0.46
59:B2:689:ALA:HB2	59:B2:1233:LEU:HD23	1.97	0.46
63:5:8:U:H2'	63:5:13:C:H41	1.81	0.46
65:0:648:GLU:H	65:0:648:GLU:HG3	1.57	0.46
8:H:171:ARG:HG2	8:H:173:PRO:HD3	1.96	0.46
26:Z:29:ALA:O	26:Z:32:ARG:NH1	2.49	0.46
31:f:106:LEU:O	31:f:151:ARG:NH2	2.37	0.46
36:l:69:ARG:NH1	51:1:2406:A:C2	2.84	0.46
39:o:29:HIS:HB3	39:o:36:TYR:HB2	1.98	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
51:1:1863:G:H2'	51:1:1864:U:C6	2.51	0.46
51:1:1869:G:H3'	51:1:1870:C:C5'	2.38	0.46
51:1:1930:G:O2'	51:1:1931:U:OP2	2.33	0.46
51:1:2642:G:O5'	51:1:2642:G:H8	1.98	0.46
51:1:2783:U:H2'	51:1:2784:U:C6	2.51	0.46
51:1:2836:U:H2'	51:1:2837:A:H8	1.81	0.46
54:4:44:G:OP1	59:B2:1073:LYS:NZ	2.35	0.46
65:0:27:THR:HA	65:0:30:ILE:HD12	1.96	0.46
7:G:65:LYS:HE2	7:G:65:LYS:HB2	1.78	0.46
33:i:109:ALA:HA	33:i:112:LYS:HB2	1.98	0.46
51:1:409:G:H2'	51:1:410:G:C8	2.51	0.46
51:1:848:C:H2'	51:1:849:A:H8	1.80	0.46
51:1:1710:G:H2'	51:1:1711:A:C8	2.51	0.46
51:1:2339:C:H2'	51:1:2340:A:H8	1.81	0.46
51:1:2679:A:O2'	51:1:2680:U:H5'	2.15	0.46
58:B1:68:TYR:HB3	58:B1:75:TYR:HE2	1.81	0.46
65:0:574:MET:HE1	65:0:601:PHE:CE2	2.50	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
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
35:k:70:ARG:NH1	51:1:2684:U:O4'	2.49	0.46
51:1:342:A:H2'	51:1:343:C:O4'	2.16	0.46
51:1:438:G:O2'	51:1:439:A:H5'	2.16	0.46
51:1:1381:G:H2'	51:1:1382:G:H5'	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:141:PHE:CE2	58:B1:296:LYS:CB	2.94	0.46
59:B2:1002:LEU:HD21	59:B2:1007:LYS:HB2	1.98	0.46
12:L:142:ARG:HH21	64:6:42:G:H4'	1.81	0.45
16:P:127:ARG:HB2	26:Z:34:ARG:HH22	1.81	0.45
27:b:99:GLU:OE2	51:1:1491:G:O2'	2.33	0.45
28:c:170:VAL:HG21	51:1:2679:A:H5'	1.97	0.45
35:k:5:GLN:NE2	51:1:1668:A:H5''	2.31	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
51:1:466:A:C2'	51:1:467:G:H5'	2.46	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
51:1:1486:U:O2'	51:1:1487:U:H5'	2.14	0.45
51:1:2315:G:H2'	51:1:2316:G:H8	1.80	0.45
51:1:2648:G:C2	51:1:2649:C:C2	3.04	0.45
57:A1:185:TYR:HA	57:A1:202:VAL:O	2.16	0.45
58:B1:109:SER:HB2	58:B1:296:LYS:HG2	1.98	0.45
58:B1:115:TRP:HB3	58:B1:1333:THR:CG2	2.46	0.45
58:B1:352:ARG:CD	59:B2:1268:GLN:NE2	2.67	0.45
58:B1:375:GLU:O	59:B2:1247:SER:HB3	2.16	0.45
58:B1:1036:ARG:HE	58:B1:1081:VAL:HG11	1.79	0.45
63:5:6:G:H2'	63:5:7:A:C8	2.51	0.45
8:H:152:VAL:HG12	8:H:197:VAL:HG22	1.98	0.45
12:L:142:ARG:HA	12:L:145:GLU:HG3	1.97	0.45
13:M:83:ARG:NH2	53:3:587:G:OP1	2.43	0.45
14:N:11:ARG:NH2	53:3:1347:G:O6	2.49	0.45
17:Q:45:ASN:ND2	17:Q:88:ASP:OD2	2.39	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
44:t:34:VAL:HG21	44:t:43:ILE:HD11	1.99	0.45
51:1:569:U:H1'	51:1:947:A:O4'	2.16	0.45
51:1:1287:A:O2'	51:1:1288:G:H5'	2.15	0.45
51:1:1550:C:O2'	51:1:1551:A:H5'	2.16	0.45
51:1:2141:G:H1	51:1:2151:U:H3	1.63	0.45
51:1:2661:G:O2'	51:1:2662:A:H5'	2.16	0.45
57:A1:35:PHE:HA	57:A1:38:THR:HG22	1.98	0.45
58:B1:1357:ILE:HD13	59:B2:1279:GLU:HG2	1.97	0.45
59:B2:230:PHE:HB2	59:B2:333:ILE:HB	1.97	0.45
63:5:55:U:O2	63:5:57:G:H1'	2.16	0.45
64:6:7:G:H3'	64:6:49:G:OP2	2.16	0.45
18:R:97:ARG:HB2	18:R:99:GLN:HE22	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:d:32:VAL:HG21	36:l:6:LEU:HD13	1.99	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
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
51:1:30:G:H2'	51:1:31:C:O4'	2.16	0.45
51:1:1288:G:C5	51:1:1327:A:C2	3.04	0.45
51:1:1488:C:H2'	51:1:1489:C:C6	2.51	0.45
51:1:2743:U:H2'	51:1:2744:G:O4'	2.16	0.45
58:B1:282:LEU:CA	58:B1:286:ALA:HA	2.45	0.45
58:B1:343:LEU:HD11	58:B1:1324:SER:HB3	1.98	0.45
58:B1:1219:ASP:O	58:B1:1223:LEU:HB2	2.15	0.45
59:B2:176:ILE:HD11	59:B2:428:VAL:HG21	1.98	0.45
65:0:19:ILE:HG22	67:0:800:FUA:C28	2.45	0.45
7:G:142:LYS:NZ	53:3:1098:C:OP1	2.49	0.45
7:G:166:ASP:HB3	7:G:190:SER:HB2	1.98	0.45
28:c:4:LEU:HD11	28:c:100:LEU:HD21	1.98	0.45
41:q:82:LEU:HD22	41:q:87:VAL:HB	1.98	0.45
41:q:111:LYS:HA	41:q:111:LYS:HD2	1.81	0.45
48:x:30:PRO:HG2	48:x:32:LEU:HD11	1.98	0.45
49:y:6:LEU:HD13	49:y:56:LEU:HD22	1.98	0.45
51:1:438:G:H2'	51:1:439:A:C8	2.51	0.45
51:1:1087:G:H22	51:1:1103:A:H1'	1.76	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
51:1:2314:A:H2'	51:1:2315:G:H8	1.78	0.45
53:3:618:C:N4	53:3:621:A:OP2	2.49	0.45
58:B1:395:LYS:NZ	58:B1:399:LYS:HE2	2.32	0.45
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
19:S:58:ARG:HH21	53:3:980:C:H4'	1.81	0.45
37:m:34:LYS:N	37:m:129:THR:O	2.47	0.45
45:u:32:LYS:HG2	45:u:65:GLN:HA	1.99	0.45
51:1:707:G:C2'	51:1:708:G:H5'	2.47	0.45
51:1:1140:C:C2'	51:1:1141:U:H5'	2.47	0.45
51:1:1605:C:H2'	51:1:1606:C:H5'	1.98	0.45
51:1:1952:A:H2'	51:1:1953:A:C8	2.51	0.45
51:1:2364:C:O2'	51:1:2365:G:H5'	2.17	0.45
51:1:2741:A:H2'	51:1:2742:G:H5'	1.98	0.45
51:1:2849:U:H4'	51:1:2868:A:C2	2.51	0.45
53:3:1200:C:H5''	53:3:1201:A:H3'	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:3:1383:C:H4'	64:6:35:A:H2	1.81	0.45
58:B1:43:THR:HG22	58:B1:57:PHE:HE1	1.80	0.45
59:B2:906:PHE:HB3	59:B2:907:GLY:H	1.40	0.45
60:W0:25:ARG:NH1	60:W0:61:ASN:OD1	2.49	0.45
7:G:8:MET:HE3	7:G:8:MET:HB3	1.84	0.45
11:K:75:GLU:O	11:K:79:ARG:N	2.47	0.45
18:R:16:ILE:O	18:R:19:THR:OG1	2.26	0.45
35:k:121:GLU:HG2	35:k:122:VAL:HG23	1.97	0.45
51:1:195:A:H3'	51:1:196:A:H4'	1.98	0.45
51:1:540:C:O2'	51:1:541:A:H5'	2.16	0.45
51:1:1049:C:C2'	51:1:1050:A:H5'	2.47	0.45
51:1:1140:C:H2'	51:1:1141:U:H5'	1.98	0.45
51:1:2528:U:O2'	51:1:2529:G:H3'	2.16	0.45
53:3:765:G:H1	53:3:812:G:HO2'	1.63	0.45
58:B1:75:TYR:CD2	58:B1:75:TYR:O	2.70	0.45
59:B2:901:LEU:CD1	61:NA:108:GLN:N	2.78	0.45
2:B:8:THR:OG1	2:B:9:ARG:N	2.49	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
9:I:120:LYS:HG2	9:I:130:ASN:HB3	1.99	0.45
9:I:173:ASP:HB3	9:I:178:GLU:HB3	1.98	0.45
12:L:70:PRO:HG3	12:L:98:LEU:HD23	1.97	0.45
12:L:137:ARG:NH1	12:L:138:GLU:OE2	2.48	0.45
17:Q:23:LEU:HD12	17:Q:29:LYS:HD2	1.97	0.45
27:b:257:ARG:HH22	27:b:262:THR:HG1	1.62	0.45
29:d:136:GLN:HA	29:d:139:LYS:HE2	1.99	0.45
45:u:12:VAL:HA	45:u:69:VAL:HG12	1.99	0.45
51:1:432:A:O2'	51:1:433:C:H5'	2.17	0.45
51:1:893:C:H2'	51:1:894:U:O4'	2.17	0.45
51:1:1324:G:O2'	51:1:1326:U:OP2	2.29	0.45
51:1:1710:G:O2'	51:1:1711:A:H5'	2.17	0.45
51:1:2030:A:N3	51:1:2499:C:H5''	2.31	0.45
51:1:2085:U:O2'	51:1:2086:U:H5'	2.16	0.45
51:1:2636: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
53:3:1376:U:H2'	53:3:1377:A:C8	2.52	0.45
55:8:13:DT:C6	58:B1:791:ALA:HA	2.51	0.45
58:B1:847:ASP:OD1	58:B1:847:ASP:N	2.49	0.45
63:5:22:G:H2'	63:5:23:A:C8	2.52	0.45
33:i:71:LYS:HB3	33:i:72:THR:H	1.37	0.45
51:1:111:A:O2'	51:1:112:U:H5'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:167:A:H2'	51:1:168:G:O4'	2.16	0.45
51:1:367:G:O2'	51:1:368:A:H5'	2.17	0.45
51:1:395:U:H2'	51:1:396:G:C8	2.52	0.45
51:1:854:C:H2'	51:1:855:G:C8	2.52	0.45
51:1:1412:U:H2'	51:1:1413:A:H8	1.81	0.45
51:1:1766:G:C2'	51:1:1767:G:H5'	2.45	0.45
51:1:1807:G:H2'	51:1:1808:A:C5'	2.30	0.45
51:1:1868:C:H2'	51:1:1869:G:C8	2.52	0.45
51:1:1882:U:O2'	51:1:1883:U:H5'	2.17	0.45
51:1:2047:C:O2'	51:1:2048:G:H5'	2.16	0.45
51:1:2700:A:O2'	51:1:2701:U:H5'	2.16	0.45
51:1:2717:C:N3	51:1:2718:G:N7	2.65	0.45
58:B1:45:ASN:HD22	58:B1:48:THR:H	1.65	0.45
58:B1:388:ARG:HG2	58:B1:388:ARG:NH1	2.32	0.45
58:B1:770:LEU:HD13	59:B2:618:GLN:CD	2.42	0.45
2:B:4:GLN:HG3	51:1:2054:A:C2	2.52	0.45
33:i:49:GLU:OE1	33:i:81:LYS:NZ	2.41	0.45
51:1:500:G:N2	51:1:502:A:H3'	2.32	0.45
51:1:1338:G:H2'	51:1:1339:G:C8	2.51	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
53:3:477:C:H2'	53:3:478:A:C8	2.52	0.45
58:B1:33:TRP:HZ2	59:B2:1336:ASN:OD1	2.00	0.45
58:B1:201:LEU:HD11	58:B1:220:ARG:NH1	2.31	0.45
21:U:79:ASN:HB2	21:U:82:ALA:HB3	1.99	0.45
28:c:151:THR:O	51:1:1130:U:C4	2.70	0.45
33:i:135:MET:CE	51:1:1062:G:H21	2.30	0.45
51:1:545:U:O2	51:1:546:U:H1'	2.17	0.45
51:1:974:G:H1'	51:1:975:A:C8	2.53	0.45
51:1:1020:A:C2	51:1:1141:U:C2	3.05	0.45
51:1:1800:C:O2	51:1:1802:A:C8	2.70	0.45
51:1:2626:C:H2'	51:1:2627:G:C8	2.51	0.45
51:1:2844:G:H2'	51:1:2845:U:O4'	2.16	0.45
51:1:2889:C:O2'	51:1:2890:G:H5'	2.17	0.45
53:3:112:G:N2	53:3:354:G:O5'	2.49	0.45
55:8:1:DC:H2''	55:8:2:DC:C6	2.51	0.45
58:B1:128:LEU:CD2	58:B1:188:LEU:HB3	2.47	0.45
58:B1:201:LEU:CD1	58:B1:224:LEU:HD12	2.47	0.45
58:B1:484:MET:CE	59:B2:1278:LEU:HD21	2.46	0.45
65:0:473:MET:HE3	65:0:473:MET:HB3	1.87	0.45
7:G:26:MET:HE1	7:G:186:VAL:HB	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:33:ALA:HB3	7:G:37:VAL:HG12	1.99	0.44
9:I:1:ALA:N	53:3:405:U:O4	2.45	0.44
11:K:5:GLU:HB2	11:K:90:MET:HB2	1.98	0.44
28:c:106:LYS:HA	28:c:176:ASP:HA	1.99	0.44
33:i:8:VAL:HG11	33:i:26:ALA:HB2	1.98	0.44
40:p:88:ARG:HH11	40:p:114:ASN:HD21	1.66	0.44
51:1:1749:A:H2'	51:1:1750:G:H8	1.82	0.44
51:1:1915:U:O2	51:1:1915:U:O4'	2.34	0.44
51:1:2402:U:O2'	51:1:2403:C:H3'	2.17	0.44
51:1:2658:C:H2'	51:1:2659:G:O4'	2.16	0.44
56:9:12:DC:H3'	58:B1:47:ARG:HH12	1.83	0.44
58:B1:772:TYR:HE2	59:B2:561:ILE:HG21	1.80	0.44
59:B2:11:ILE:HG22	59:B2:1172:LEU:HD11	1.99	0.44
59:B2:901:LEU:HD11	61:NA:108:GLN:N	2.26	0.44
7:G:65:LYS:HG2	7:G:153:MET:HG3	1.98	0.44
7:G:173:LYS:HE3	7:G:173:LYS:HB2	1.76	0.44
9:I:47:LEU:HD23	9:I:47:LEU:HA	1.85	0.44
10:J:110:MET:HE3	10:J:110:MET:HB2	1.79	0.44
18:R:1:ALA:HB3	18:R:56:ARG:HH22	1.82	0.44
18:R:107:THR:OG1	53:3:947:G:O3'	2.35	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
51:1:208: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
51:1:1922: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
51:1:2122:U:H2'	51:1:2123:G:O4'	2.17	0.44
51:1:2137:U:H2'	51:1:2138:G:C8	2.50	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
53:3:647:C:H2'	53:3:648:A:H8	1.81	0.44
53:3:1253:G:H2'	53:3:1254:A:C8	2.52	0.44
54:4:25:U:H6	54:4:25:U:H2'	1.64	0.44
57:A1:192:VAL:HG12	57:A1:193:GLU:H	1.83	0.44
58:B1:850:LYS:HB3	58:B1:855:ASP:HB2	2.00	0.44
59:B2:674:ASP:OD2	59:B2:1070:HIS:ND1	2.50	0.44
8:H:134:LYS:HG2	8:H:138:GLN:HE21	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:62:MET:HB3	11:K:64:VAL:HG13	1.98	0.44
15:O:88:MET:HE3	15:O:88:MET:HB3	1.70	0.44
51:1:150:U:H2'	51:1:151:C:C6	2.52	0.44
51:1:239:C:H2'	51:1:240:C:O4'	2.16	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
51:1:1500:G:O2'	51:1:1501:G:H5'	2.16	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
53:3:1498:U:H4'	53:3:1519:A:H2	1.82	0.44
55:8:16:DT:H2'	55:8:17:DC:C6	2.52	0.44
59:B2:712:SER:OG	59:B2:713:GLY:N	2.49	0.44
64:6:11:A:H2'	64:6:12:G:C8	2.52	0.44
14:N:104:THR:HG23	53:3:1180:A:H5'	1.99	0.44
28:c:150:GLN:HE22	51:1:2032:G:H1'	1.82	0.44
31:f:132:LEU:HB3	31:f:140:ILE:HD11	1.99	0.44
33:i:9:LYS:HD2	51:1:1061:U:OP1	2.18	0.44
49:y:20:ASN:HA	49:y:23:ARG:HB2	1.99	0.44
51:1:293:U:H2'	51:1:294:A:H5''	1.99	0.44
51:1:355:U:H6	51:1:355:U:O5'	1.99	0.44
51:1:704:G:H1'	51:1:727:A:H62	1.83	0.44
51:1:720:U:H2'	51:1:721:A:H8	1.82	0.44
51:1:1465:G:O2'	51:1:1466:U:H5'	2.17	0.44
51:1:1680:U:C2'	51:1:1681:G:H5'	2.47	0.44
51:1:2204:G:H2'	51:1:2205:A:H8	1.81	0.44
58:B1:211:GLU:CG	58:B1:215:LYS:HE3	2.44	0.44
58:B1:1026:PRO:HB2	58:B1:1028:ILE:HG23	2.00	0.44
58:B1:1033:GLY:HA3	58:B1:1081:VAL:O	2.18	0.44
65:0:370:LYS:HE3	65:0:370:LYS:HB3	1.82	0.44
6:F:8:LYS:NZ	51:1:2467:C:OP1	2.37	0.44
14:N:119:LYS:NZ	53:3:1350:A:N7	2.64	0.44
47:w:12:SER:OG	47:w:13:GLU:N	2.51	0.44
48:x:51:SER:OG	48:x:54:GLY:N	2.48	0.44
51:1:940:G:H3'	51:1:941:A:H5''	1.97	0.44
51:1:1280:G:C2'	51:1:1281:G:H5'	2.46	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
51:1:2236:U:H2'	51:1:2237:G:C5'	2.46	0.44
58:B1:76:LYS:NZ	58:B1:76:LYS:HB3	2.32	0.44
58:B1:220:ARG:HG2	58:B1:220:ARG:NH1	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:434:ILE:HD11	59:B2:1274:GLU:HG3	2.00	0.44
58:B1:506:VAL:HG23	58:B1:628:GLY:HA3	1.98	0.44
58:B1:926:PRO:HB2	58:B1:1241:TYR:HE1	1.82	0.44
59:B2:24:VAL:HG11	59:B2:704:MET:HE1	1.99	0.44
59:B2:746:ALA:O	59:B2:974:ARG:NH2	2.45	0.44
63:5:49:C:H2'	63:5:50:U:C6	2.52	0.44
30:e:71:LYS:HA	30:e:71:LYS:HD2	1.79	0.44
51:1:163:C:O2'	51:1:164:C:H5'	2.17	0.44
51:1:1717:A:C2	51:1:1718:G:H1'	2.53	0.44
58:B1:67:ASP:OD1	58:B1:67:ASP:O	2.35	0.44
58:B1:478:LEU:HD21	60:W0:47:THR:HG23	1.99	0.44
58:B1:1079:LYS:HD3	58:B1:1098:GLN:HB3	1.99	0.44
14:N:74:GLN:OE1	53:3:1249:C:O2'	2.35	0.44
19:S:44:VAL:O	19:S:48:GLN:NE2	2.50	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
33:i:131:THR:HB	51:1:1060:U:O4	2.18	0.44
34:j:85:LYS:NZ	51:1:2768:U:OP1	2.49	0.44
41:q:47:ARG:NH2	41:q:51:GLN:OE1	2.51	0.44
51:1:12:U:O2	51:1:12:U:H2'	2.18	0.44
51:1:29:U:O5'	51:1:29:U:H6	2.01	0.44
51:1:336:C:O2'	51:1:337:C:H5'	2.18	0.44
51:1:518:G:O2'	51:1:519:U:H5'	2.18	0.44
51:1:721:A:H2'	51:1:722:A:C8	2.53	0.44
51:1:1507:C:H2'	51:1:1508:A:H4'	1.99	0.44
51:1:2880:C:H2'	51:1:2880:C:O2	2.17	0.44
57:A1:78:ILE:HA	57:A1:81:ILE:HG22	2.00	0.44
58:B1:161:THR:H	58:B1:164:GLN:HB2	1.82	0.44
58:B1:202:ARG:NH1	58:B1:202:ARG:CG	2.73	0.44
58:B1:375:GLU:HB3	59:B2:1245:ALA:CB	2.48	0.44
58:B1:1064:SER:OG	58:B1:1168:GLU:OE1	2.31	0.44
58:B1:1108:GLN:HG3	58:B1:1109:LEU:HD12	1.99	0.44
58:B1:1158:GLU:HA	58:B1:1223:LEU:HD21	1.99	0.44
59:B2:557:ARG:NH2	59:B2:607:SER:O	2.49	0.44
59:B2:829:THR:HG23	59:B2:1059:ARG:HG2	2.00	0.44
4:D:12:ARG:HH12	51:1:465:G:P	2.41	0.44
18:R:43:LYS:HB2	18:R:46:GLU:HG2	1.99	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:188:MET:HB2	29:d:192:ALA:HB3	1.99	0.44
42:r:19:THR:OG1	42:r:95:ASP:OD1	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:350:G:H2'	51:1:351:C:O4'	2.18	0.44
51:1:648:G:H2'	51:1:649:G:H8	1.83	0.44
51:1:684:G:C2	51:1:794:A:C2	3.06	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
51:1:1452:G:H2'	51:1:1453:A:OP2	2.17	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	2.47	0.44
53:3:75:G:H2'	53:3:76:G:C8	2.53	0.44
7:G:67:LEU:HD21	7:G:91:VAL:HG23	2.00	0.44
8:H:37:LYS:HD3	8:H:37:LYS:HA	1.81	0.44
9:I:85:THR:HA	9:I:88:ASN:HB2	2.00	0.44
10:J:24:VAL:HG23	10:J:26:GLY:H	1.82	0.44
17:Q:3:VAL:HA	17:Q:6:LEU:HD12	2.00	0.44
25:Y:49:ALA:HA	25:Y:52:GLU:HG3	2.00	0.44
36:l:95:LEU:HD22	36:l:100:ILE:HD11	2.00	0.44
46:v:62:THR:O	46:v:62:THR:OG1	2.35	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
51:1:2312: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
53:3:490:C:H2'	53:3:491:G:C8	2.53	0.44
53:3:908:A:H2'	53:3:909:A:H8	1.83	0.44
53:3:1013:G:N2	53:3:1016:A:OP2	2.35	0.44
58:B1:107:LEU:HA	58:B1:276:ASN:ND2	2.33	0.44
58:B1:111:THR:CG2	58:B1:300:GLN:HA	2.48	0.44
58:B1:287:ALA:HB1	58:B1:288:PRO:HD2	1.99	0.44
58:B1:804:ALA:HB2	58:B1:1256:ILE:CD1	2.47	0.44
58:B1:1227:HIS:HA	58:B1:1230:THR:HG22	1.99	0.44
62:NG:161:SER:CB	62:NG:170:PRO:HA	2.47	0.44
63:5:69:G:H2'	63:5:70:G:C8	2.52	0.44
65:0:580:PHE:HD2	65:0:581:GLY:N	2.16	0.44
32:g:28:ASN:ND2	51:1:2092:U:OP2	2.36	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
51:1:30:G:O2'	51:1:31:C:H5'	2.17	0.43
51:1:192:C:H2'	51:1:193:U:H5'	1.99	0.43
51:1:819:A:H5'	51:1:973:A:N1	2.33	0.43
51:1:1507:C:H2'	51:1:1508:A:O4'	2.18	0.43
51:1:1565:C:C5	51:1:1567:G:C6	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1571:A:H2'	51:1:1572:A:C8	2.53	0.43
51:1:2241:A:H2'	51:1:2242:G:H8	1.82	0.43
55:8:12:DG:OP1	58:B1:795:TYR:CE1	2.71	0.43
58:B1:213:LYS:HA	58:B1:213:LYS:HE3	1.99	0.43
59:B2:487:LEU:HD22	59:B2:487:LEU:HA	1.77	0.43
59:B2:811:ASN:ND2	59:B2:1098:LEU:O	2.51	0.43
11:K:38:ARG:HH11	11:K:61:LEU:HD21	1.83	0.43
21:U:28:ARG:NH1	53:3:390:U:O2'	2.46	0.43
33:i:123:ALA:HB1	51:1:1081:U:H4'	2.00	0.43
34:j:51:GLY:HA3	34:j:121:LYS:HE2	2.00	0.43
49:y:19:LEU:HA	49:y:19:LEU:HD23	1.86	0.43
50:z:38:GLU:CD	51:1:928:A:H5'	2.43	0.43
51:1:161:A:C5	51:1:162:U:H5	2.36	0.43
51:1:198:C:N4	51:1:248:G:H1	2.14	0.43
51:1:1049:C:H2'	51:1:1050:A:H5'	2.00	0.43
51:1:1232:G:H2'	51:1:1233:C:C6	2.53	0.43
51:1:1383:A:H2	51:1:1406:U:H1'	1.83	0.43
51:1:1625:C:H2'	51:1:1626:A:O4'	2.18	0.43
51:1:2152:G:N3	51:1:2152:G:H2'	2.33	0.43
53:3:958:A:N3	53:3:985:C:O2'	2.48	0.43
58:B1:978:ARG:HD3	58:B1:999:TYR:H	1.83	0.43
58:B1:1357:ILE:HG22	58:B1:1359:ALA:H	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	1.82	0.43
8:H:51:VAL:HA	8:H:69:THR:HG22	2.01	0.43
8:H:134:LYS:HB3	8:H:134:LYS:HE2	1.84	0.43
10:J:28:ARG:NH2	53:3:1397:C:OP2	2.38	0.43
10:J:104:ILE:HD11	10:J:114:LEU:HD13	1.99	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
22:V:44:HIS:HB3	22:V:70:LYS:HG2	1.99	0.43
30:e:171:ALA:C	30:e:173:ASP:H	2.27	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
51:1:108:G:O2'	51:1:109:C:H5'	2.18	0.43
51:1:388:G:N7	51:1:390:U:H2'	2.33	0.43
53:3:1053:G:H4'	53:3:1054:C:H3'	2.00	0.43
55:8:3:DC:N1	55:8:4:DT:H72	2.34	0.43
55:8:15:DC:H5'	59:B2:1269:ARG:HD3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:A1:68:TYR:HE1	57:A1:79:LEU:HD13	1.83	0.43
58:B1:472:LEU:CD1	59:B2:1294:LYS:HG2	2.47	0.43
59:B2:444:ASP:OD1	59:B2:444:ASP:N	2.51	0.43
59:B2:1157:GLN:HG3	59:B2:1159:VAL:HG13	2.00	0.43
2:B:4:GLN:NE2	51:1:2056:G:O2'	2.52	0.43
8:H:5:HIS:HE1	8:H:7:ASN:HB3	1.82	0.43
18:R:104:ASN:HB3	18:R:105:ALA:H	1.70	0.43
25:Y:14:GLU:OE1	25:Y:17:ARG:NH2	2.52	0.43
27:b:140:VAL:HG12	27:b:191:LEU:HD23	2.01	0.43
40:p:92:ARG:H	40:p:92:ARG:HG2	1.60	0.43
48:x:36:ARG:NH2	51:1:2200:C:OP2	2.52	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
51:1:1739:A:H2'	51:1:1740:G:O4'	2.19	0.43
51:1:1893:C:C2'	51:1:1894:C:H5'	2.47	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
53:3:560:A:H5''	53:3:561:U:H5'	2.00	0.43
58:B1:62:PHE:N	58:B1:62:PHE:CD1	2.86	0.43
58:B1:96:LYS:NZ	59:B2:1298:VAL:HG11	2.34	0.43
59:B2:300:ASP:OD1	59:B2:313:ALA:N	2.51	0.43
59:B2:1246:ARG:HH11	59:B2:1266:GLY:HA2	1.82	0.43
63:5:13:C:H42	63:5:46:G:N2	2.16	0.43
9:I:152:SER:HB3	53:3:436:C:H4'	2.00	0.43
10:J:146:MET:HE2	10:J:146:MET:HB3	1.75	0.43
17:Q:72:ASN:OD1	17:Q:72:ASN:N	2.50	0.43
21:U:31:ARG:HB2	53:3:310:G:H5''	2.01	0.43
28:c:62:LYS:NZ	51:1:2810:A:H5''	2.34	0.43
38:n:39:PRO:HG2	51:1:1651:G:H4'	2.01	0.43
43:s:74:ILE:HB	43:s:105:VAL:HG23	1.99	0.43
51:1:150:U:O2'	51:1:151:C:H5'	2.18	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
51:1:2671:G:C2	51:1:2672:U:C2	3.06	0.43
58:B1:362:ARG:HB2	58:B1:364:HIS:HD2	1.83	0.43
58:B1:894:VAL:HG22	58:B1:1258:ARG:HH11	1.83	0.43
65:0:545:ILE:HD11	65:0:581:GLY:HA3	2.00	0.43
1:A:62:LYS:HE3	1:A:62:LYS:HB3	1.90	0.43
8:H:76:ILE:HB	8:H:80:GLY:HA2	2.00	0.43
11:K:47:LEU:HG	11:K:56:LYS:HA	2.01	0.43
23:W:33:THR:HG22	23:W:37:LYS:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:b:153:LEU:HD23	51:1:1799:G:N2	2.33	0.43
33:i:127:SER:OG	51:1:1059:G:N2	2.51	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
37:m:96:ILE:HA	37:m:96:ILE:HD13	1.83	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
51:1:1998:A:O2'	51:1:1999:C:H5'	2.18	0.43
51:1:2226:C:C5	51:1:2227:A:N7	2.86	0.43
51:1:2305:U:O2'	51:1:2306:C:H5'	2.19	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
53:3:1200:C:O2'	53:3:1205:U:O4	2.35	0.43
53:3:1513:A:H2'	53:3:1514:G:H8	1.83	0.43
58:B1:58:CYS:SG	58:B1:60:ARG:HG2	2.59	0.43
59:B2:646:SER:OG	59:B2:647:ARG:N	2.51	0.43
18:R:28:ARG:HH21	18:R:62:PHE:HB2	1.84	0.43
24:X:27:LYS:HE2	24:X:27:LYS:HB3	1.77	0.43
27:b:48:ILE:HG12	51:1:779:U:OP2	2.18	0.43
34:j:47:HIS:CG	51:1:536:G:N2	2.87	0.43
38:n:103:ARG:HH11	51:1:1287:A:H5'	1.83	0.43
45:u:76:THR:HB	45:u:78:LYS:HE3	1.99	0.43
51:1:255:A:H2'	51:1:256:A:O4'	2.18	0.43
51:1:623:C:O2'	51:1:624:C:H5'	2.18	0.43
51:1:1092:C:H2'	51:1:1093:G:O4'	2.18	0.43
51:1:1095:A:H3'	51:1:1096:A:H8	1.83	0.43
51:1:1426:G:C6	51:1:1427:A:C6	3.06	0.43
51:1:1433:A:H2'	51:1:1434:A:C1'	2.49	0.43
53:3:422:C:H4'	53:3:423:G:C2	2.54	0.43
58:B1:568:SER:HB3	58:B1:570:LYS:NZ	2.34	0.43
7:G:107:ARG:HE	7:G:107:ARG:HB3	1.63	0.43
13:M:24:VAL:HG23	13:M:60:LEU:HB2	2.00	0.43
17:Q:67:GLY:O	17:Q:98:ARG:NH1	2.52	0.43
27:b:20:ASN:HB3	27:b:23:LEU:HD13	2.01	0.43
29:d:127:GLU:O	29:d:156:ASN:ND2	2.51	0.43
37:m:17:ASN:OD1	37:m:97:GLN:NE2	2.51	0.43
42:r:1:MET:HE3	42:r:101:ILE:HB	1.99	0.43
43:s:28:LYS:HE2	43:s:28:LYS:HB2	1.90	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1258:U:H2'	51:1:1259:G:C8	2.54	0.43
51:1:1306:C:N4	51:1:1606:C:H2'	2.34	0.43
51:1:2462:C:H2'	51:1:2463:C:C6	2.53	0.43
53:3:490:C:H2'	53:3:491:G:H8	1.84	0.43
58:B1:111:THR:HG21	58:B1:303:VAL:HB	2.00	0.43
58:B1:141:PHE:HE2	58:B1:296:LYS:CB	2.23	0.43
58:B1:731:ARG:HB3	59:B2:1105:SER:HB2	2.00	0.43
59:B2:901:LEU:CD1	61:NA:107:THR:O	2.45	0.43
59:B2:998:LEU:HG	59:B2:1011:LEU:HB3	1.99	0.43
59:B2:1313:HIS:CD2	60:W0:31:GLN:HE22	2.37	0.43
67:0:800:FUA:H213	67:0:800:FUA:H9	1.85	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
17:Q:113:ARG:NH1	53:3:36:C:O2'	2.51	0.43
27:b:7:PRO:HB3	27:b:13:ARG:HG3	2.00	0.43
31:f:84:LYS:HD2	31:f:84:LYS:HA	1.87	0.43
44:t:40:LYS:HE3	44:t:60:THR:HG22	2.01	0.43
48:x:1:SER:OG	51:1:1365:A:OP2	2.35	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
51:1:156:A:O2'	51:1:157:C:H5'	2.18	0.43
51:1:402:A:H2'	51:1:403:U:C5'	2.44	0.43
51:1:541:A:H2'	51:1:542:C:O4'	2.19	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
51:1:841:G:C2'	51:1:842:U:H5'	2.49	0.43
51:1:864:G:C2'	51:1:865:C:H5'	2.48	0.43
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
51:1:1751:U:H2'	51:1:1752:C:C6	2.54	0.43
53:3:501:C:H2'	53:3:502:A:C8	2.53	0.43
53:3:1005:A:OP2	53:3:1024:G:N2	2.48	0.43
53:3:1209:C:O2'	53:3:1214:C:N4	2.52	0.43
58:B1:102:MET:HG2	58:B1:246:PRO:CG	2.49	0.43
58:B1:190:LYS:HE3	58:B1:190:LYS:HB2	1.41	0.43
58:B1:513:MET:HG3	58:B1:544:LEU:HD11	2.01	0.43
58:B1:950:ILE:HB	58:B1:1018:ALA:HB3	2.01	0.43
16:P:115:ILE:HD12	16:P:116:PRO:HD2	1.99	0.43
18:R:91:ARG:HD2	51:1:888:C:OP1	2.18	0.43
24:X:6:LYS:NZ	53:3:1314:C:OP1	2.52	0.43
27:b:206:LYS:HB2	51:1:729:G:C5	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:f:151:ARG:HA	31:f:151:ARG:HD3	1.88	0.43
33:i:8:VAL:HG11	33:i:26:ALA:CB	2.49	0.43
51:1:467:G:O2'	51:1:468:G:H5'	2.19	0.43
51:1:758:C:H2'	51:1:759:G:H8	1.84	0.43
51:1:859:G:HO2'	51:1:860:U:P	2.42	0.43
51:1:1172:C:H2'	51:1:1173:U:O4'	2.19	0.43
51:1:1536:C:H4'	51:1:1537:G:N1	2.32	0.43
51:1:1601:G:H2'	51:1:1602:U:H5'	2.01	0.43
51:1:1741:C:O2'	51:1:1742:U:H5'	2.18	0.43
51:1:1761:C:H2'	51:1:1762:A:O4'	2.18	0.43
51:1:1964:G:H4'	51:1:1965:C:OP2	2.19	0.43
51:1:2073:C:C2'	51:1:2074:U:H5'	2.49	0.43
53:3:1348:U:H2'	53:3:1349:A:H8	1.84	0.43
53:3:1442:G:H1	53:3:1460:C:H42	1.66	0.43
58:B1:559:ALA:HB3	58:B1:562:GLU:HB3	2.01	0.43
58:B1:1024:THR:HG23	58:B1:1123:ARG:HA	2.00	0.43
65:0:438:LEU:HD13	65:0:469:ILE:HG23	2.01	0.43
7:G:122:ASP:N	7:G:122:ASP:OD1	2.51	0.42
16:P:35:ASP:OD1	16:P:39:ASN:N	2.50	0.42
27:b:86:ARG:HD3	27:b:86:ARG:HA	1.84	0.42
27:b:244:VAL:HG12	27:b:250:GLN:HA	2.01	0.42
40:p:63:ILE:HA	40:p:68:GLY:HA2	2.01	0.42
51:1:918:A:H2'	51:1:919:U:O4'	2.19	0.42
51:1:1287:A:H3'	51:1:1288:G:N2	2.33	0.42
51:1:1668:A:C4'	51:1:1669:A:H5'	2.36	0.42
51:1:1917:U:H2'	51:1:1918:A:H5'	2.01	0.42
51:1:2660:A:H2'	51:1:2661:G:O4'	2.18	0.42
53:3:680:C:H2'	53:3:681:A:H8	1.84	0.42
58:B1:242:LEU:C	58:B1:242:LEU:HD23	2.44	0.42
59:B2:22:LEU:HB3	59:B2:655:VAL:HG11	2.01	0.42
59:B2:590:PRO:HB2	59:B2:655:VAL:HG21	2.01	0.42
63:5:9:A:H1'	63:5:45:U:H2'	2.01	0.42
65:0:615:PRO:HB3	65:0:684:PHE:HE1	1.83	0.42
2:B:27:LEU:HD23	2:B:27:LEU:HA	1.85	0.42
9:I:101:VAL:HG22	9:I:106:PHE:HB2	2.01	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
17:Q:31:GLY:HA2	17:Q:56:LEU:HA	2.01	0.42
47:w:14:ALA:HB1	51:1:2271:G:OP1	2.19	0.42
51:1:1335:C:H2'	51:1:1336:A:H8	1.84	0.42
51:1:2371:G:O2'	51:1:2372:U:H5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:538:LEU:HD13	59:B2:543:ALA:HB2	2.00	0.42
59:B2:861:ALA:HB1	59:B2:882:ILE:HD13	2.02	0.42
59:B2:901:LEU:HD13	61:NA:107:THR:C	2.35	0.42
59:B2:905:ILE:CD1	61:NA:106:THR:CB	2.97	0.42
65:0:557:ILE:CG2	65:0:576:ILE:HD12	2.48	0.42
27:b:97:ASP:N	27:b:97:ASP:OD1	2.45	0.42
33:i:26:ALA:H	51:1:1070:A:H61	1.67	0.42
36:l:108:ALA:HB3	36:l:125:LEU:HG	2.01	0.42
41:q:83:LYS:HE2	41:q:83:LYS:HB3	1.72	0.42
51:1:8:C:C2	51:1:9:G:C8	3.07	0.42
51:1:90:U:H2'	51:1:91:A:C8	2.55	0.42
51:1:365:U:H2'	51:1:366:C:C6	2.53	0.42
51:1:481:G:H2'	51:1:482:A:OP2	2.18	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
51:1:595: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
51:1:712:G:C2'	51:1:713:G:H5'	2.49	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
51:1:1230:A:H2'	51:1:1231:U:O4'	2.19	0.42
51:1:1336:A:H2'	51:1:1337:G:H8	1.85	0.42
51:1:1487:U:H2'	51:1:1488:C:C6	2.54	0.42
51:1:2024:G:H2'	51:1:2025:C:C6	2.54	0.42
51:1:2102:G:H1	51:1:2187:U:H3	1.66	0.42
51:1:2741:A:N6	51:1:2742:G:C2	2.88	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	1.85	0.42
53:3:75:G:H1	53:3:95:C:H42	1.68	0.42
53:3:460:A:H2'	53:3:461:A:C8	2.54	0.42
53:3:1253:G:H2'	53:3:1254:A:H8	1.83	0.42
58:B1:515:ARG:HH12	58:B1:724:MET:HG2	1.83	0.42
58:B1:1350:ASN:HA	58:B1:1353:VAL:HG12	2.02	0.42
59:B2:1275:VAL:HG13	59:B2:1287:LEU:HD11	2.00	0.42
60:W0:58:LEU:HD12	60:W0:59:ILE:HG12	2.00	0.42
62:NG:130:PRO:HA	62:NG:148:VAL:O	2.19	0.42
63:5:17:C:H6	63:5:17:C:H2'	1.69	0.42
2:B:39:ARG:HA	2:B:39:ARG:HD2	1.91	0.42
8:H:1:GLY:HA2	53:3:1060:U:C5	2.54	0.42
9:I:55:ARG:HA	9:I:55:ARG:HD3	1.88	0.42
12:L:68:VAL:HG23	12:L:99:ALA:HB1	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:30:ASN:HD21	14:N:66:VAL:H	1.66	0.42
20:T:66:LEU:HB3	20:T:77:TYR:HE1	1.84	0.42
33:i:129:GLU:HG3	33:i:139:VAL:HG21	2.00	0.42
48:x:71:ARG:NH2	48:x:77:TYR:OH	2.42	0.42
51:1:510:C:OP1	51:1:510:C:H3'	2.20	0.42
51:1:673:C:O2'	51:1:674:G:H5'	2.19	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
51:1:1993:U:O2	51:1:1993:U:H2'	2.18	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
58:B1:137:ARG:HA	58:B1:142:GLU:HG2	2.02	0.42
58:B1:213:LYS:HE3	58:B1:213:LYS:CA	2.47	0.42
58:B1:385:LEU:CD2	58:B1:390:LEU:HB2	2.50	0.42
58:B1:434:ILE:HD11	59:B2:1274:GLU:CG	2.49	0.42
58:B1:647:PRO:HG3	58:B1:697:MET:HB3	2.01	0.42
58:B1:824:PRO:HD3	58:B1:835:LEU:HD12	2.00	0.42
58:B1:839:VAL:HG12	58:B1:864:LEU:HD12	2.01	0.42
58:B1:1046:ILE:HG22	58:B1:1061:VAL:HA	2.00	0.42
59:B2:27:LEU:O	59:B2:528:ARG:NH1	2.43	0.42
62:NG:135:ARG:O	62:NG:178:VAL:CA	2.68	0.42
14:N:98:ARG:HG2	14:N:103:VAL:HG21	2.01	0.42
16:P:126:ARG:O	53:3:796:C:H5''	2.19	0.42
17:Q:50:LYS:HE2	17:Q:70:GLY:HA2	2.01	0.42
24:X:36:ARG:HB3	53:3:1320:C:N4	2.34	0.42
34:j:138:GLN:H	34:j:138:GLN:HG2	1.62	0.42
36:l:109:LYS:HE2	51:1:636:G:N7	2.34	0.42
41:q:13:HIS:ND1	51:1:582:A:OP1	2.45	0.42
41:q:54:ARG:HD3	51:1:1155:A:H5''	2.01	0.42
44:t:68:LYS:HD3	44:t:68:LYS:HA	1.83	0.42
51:1:259:G:O2'	51:1:260:G:H5'	2.20	0.42
51:1:870:U:H2'	51:1:871:U:C5'	2.48	0.42
51:1:1306:C:H41	51:1:1606:C:H2'	1.84	0.42
51:1:1316:U:O2'	51:1:1317:G:H5'	2.19	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
53:3:28:A:O2'	53:3:296:U:OP1	2.33	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:B1:59:ALA:HB1	58:B1:90:VAL:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:B1:797:THR:HG22	58:B1:924:GLY:HA3	2.01	0.42
58:B1:1289:ASN:O	58:B1:1293:GLU:HB2	2.20	0.42
59:B2:478:ARG:HD2	59:B2:492:MET:HA	2.02	0.42
13:M:52:GLY:HA3	13:M:56:PRO:HA	2.01	0.42
18:R:11:HIS:HA	18:R:43:LYS:HD2	2.01	0.42
29:d:47:LYS:HE2	51:1:451:U:H4'	2.00	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:33:ARG:O	39:o:65:THR:OG1	2.28	0.42
39:o:40:ILE:HA	39:o:47:VAL:HA	2.00	0.42
42:r:62:GLU:HG3	42:r:97:LYS:HB3	2.01	0.42
43:s:87:PRO:HG3	51:1:1615:C:C6	2.54	0.42
51:1:955:U:H2'	51:1:956:G:H5'	2.02	0.42
51:1:1054:A:H2'	51:1:1055:G:C8	2.54	0.42
51:1:1197:G:C2'	51:1:1198:U:H5'	2.50	0.42
51:1:1204:A:H4'	51:1:1205:A:H5''	2.02	0.42
51:1:1381:G:C2'	51:1:1382:G:H5'	2.49	0.42
51:1:1727:C:O2'	51:1:1728:C:H5'	2.20	0.42
51:1:2248:C:C2'	51:1:2249:U:H5'	2.49	0.42
51:1:2562:U:C2'	51:1:2563:U:H5'	2.49	0.42
58:B1:68:TYR:O	58:B1:75:TYR:CD2	2.70	0.42
58:B1:820:ILE:HG12	58:B1:884:SER:HB2	2.01	0.42
17:Q:98:ARG:HA	17:Q:103:CYS:HB2	2.02	0.42
18:R:87:GLY:O	18:R:91:ARG:N	2.52	0.42
33:i:2:LYS:HA	33:i:2:LYS:HD3	1.89	0.42
33:i:78:LEU:HA	33:i:81:LYS:HB3	2.02	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
51:1:191:A:C2	51:1:192:C:C4	3.08	0.42
51:1:532:A:H2'	51:1:532:A:N3	2.35	0.42
51:1:623:C:H2'	51:1:624:C:H6	1.85	0.42
51:1:849:A:H2'	51:1:850:U:C5	2.54	0.42
51:1:1864:U:O5'	51:1:1864:U:H6	2.02	0.42
51:1:1886:U:O2'	51:1:1887:C:H5'	2.20	0.42
51:1:2091:C:H5	51:1:2092:U:O2'	2.02	0.42
51:1:2144:G:H1'	51:1:2147:A:N6	2.34	0.42
51:1:2292:U:H2'	51:1:2293:G:C8	2.55	0.42
58:B1:71:LEU:HD23	58:B1:71:LEU:HA	1.75	0.42
58:B1:161:THR:CG2	58:B1:164:GLN:HB2	2.49	0.42
58:B1:201:LEU:CB	58:B1:221:ILE:HD13	2.47	0.42
58:B1:245:LEU:CG	58:B1:246:PRO:HD2	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:469:VAL:HA	59:B2:472:GLU:HG2	2.02	0.42
59:B2:557:ARG:HB3	59:B2:587:LEU:HD13	2.00	0.42
59:B2:699:LEU:HG	59:B2:799:ASN:HD22	1.85	0.42
59:B2:741:MET:SD	59:B2:974:ARG:NH2	2.93	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
21:U:4:ILE:HG12	21:U:21:VAL:HG22	2.00	0.42
38:n:16:HIS:CD2	51:1:1275:A:C2	3.07	0.42
46:v:58:SER:OG	46:v:59:GLU:OE1	2.36	0.42
48:x:55:MET:HE2	48:x:55:MET:HB3	1.91	0.42
51:1:397:U:O5'	51:1:397:U:H6	2.02	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
51:1:648:G:H5''	51:1:2352:A:H5''	2.00	0.42
51:1:809:G:C6	51:1:810:U:C4	3.08	0.42
51:1:1467:U:C4	51:1:1468:U:C4	3.08	0.42
51:1:1589:U:H2'	51:1:1590:A:C8	2.55	0.42
51:1:1642:G:H2'	51:1:1643:G:O4'	2.19	0.42
51:1:1936:A:N6	51:1:1963:U:H3	2.18	0.42
51:1:2098:U:C2'	51:1:2099:U:H5'	2.49	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
53:3:692:U:O2'	53:3:694:A:N7	2.39	0.42
53:3:1513:A:H2'	53:3:1514:G:C8	2.55	0.42
58:B1:144:TYR:CE1	58:B1:162:GLU:OE1	2.73	0.42
9:I:87:GLU:N	9:I:87:GLU:OE2	2.53	0.42
9:I:119:HIS:O	9:I:145:ARG:NH2	2.52	0.42
14:N:113:LYS:HA	14:N:120:ALA:HB2	2.01	0.42
15:O:57:VAL:HG22	15:O:58:ASN:H	1.85	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
27:b:57:HIS:ND1	51:1:1567:G:H5'	2.35	0.42
28:c:175:LEU:HD12	28:c:175:LEU:HA	1.92	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
51:1:1469:A:H2'	51:1:1470:A:H8	1.83	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

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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	0.42
53:3:322:C:O2	53:3:332:G:N2	2.52	0.42
54:4:43:G:H5'	59:B2:688:GLN:HE22	1.85	0.42
58:B1:243:PRO:HG2	59:B2:1332:SER:C	2.44	0.42
58:B1:609:TYR:HD2	58:B1:610:ARG:NH1	2.17	0.42
58:B1:1272:SER:OG	58:B1:1273:ASP:N	2.53	0.42
8:H:61:LYS:HE2	8:H:96:VAL:HG12	2.01	0.42
9:I:24:VAL:HG22	53:3:409:U:H4'	2.02	0.42
14:N:84:ARG:NH2	53:3:1119:C:OP1	2.48	0.42
28:c:134:HIS:HE1	51:1:1675:C:C4	2.38	0.42
29:d:106:LYS:HG3	29:d:200:LEU:HD13	2.01	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
51:1:837:C:O5'	51:1:837:C:H6	2.02	0.42
51:1:1213:A:C1'	51:1:1237:A:C2	3.03	0.42
51:1:1719:G:O2'	51:1:1720:U:H5'	2.20	0.42
51:1:1983:G:HO2'	51:1:1984:G:H5'	1.82	0.42
52:2:65:U:H3'	52:2:108:A:N6	2.30	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:B1:141:PHE:CD2	58:B1:297:ARG:HB2	2.54	0.42
58:B1:390:LEU:N	58:B1:390:LEU:HD13	2.35	0.42
58:B1:390:LEU:HD13	58:B1:390:LEU:H	1.85	0.42
58:B1:515:ARG:HG2	58:B1:516:ASP:H	1.85	0.42
58:B1:1177:ILE:HD12	58:B1:1186:TYR:HE2	1.85	0.42
59:B2:125:GLY:H	59:B2:495:ALA:HB1	1.84	0.42
10:J:90:GLY:O	10:J:129:SER:OG	2.36	0.41
11:K:26:THR:O	11:K:30:THR:OG1	2.29	0.41
28:c:136:ASN:ND2	28:c:139:SER:O	2.52	0.41
34:j:109:LEU:HD23	34:j:109:LEU:HA	1.85	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
46:v:57:TYR:HH	46:v:79:ARG:NH2	2.18	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
51:1:422:A:H2'	51:1:423:A:O4'	2.20	0.41
51:1:1181:U:H2'	51:1:1182:G:H8	1.81	0.41
51:1:1246:A:H2'	51:1:1247:A:O4'	2.19	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1:1614:A:C8	51:1:1614:A:O5'	2.73	0.41
51:1:2160:C:H2'	51:1:2161:C:O4'	2.20	0.41
51:1:2389:G:H5''	51:1:2390:U:H5'	2.01	0.41
51:1:2437:G:O4'	51:1:2598:A:C2	2.73	0.41
51:1:2467:C:N4	51:1:2468:A:C6	2.88	0.41
51:1:2583:G:H8	51:1:2583:G:O5'	2.03	0.41
53:3:497:G:H2'	53:3:498:A:C8	2.55	0.41
57:A1:76:GLU:HB3	57:A1:80:GLU:HB3	2.01	0.41
58:B1:586:GLY:HA3	58:B1:612:LEU:HD11	2.01	0.41
59:B2:50:GLU:HG2	59:B2:73:TYR:HE1	1.85	0.41
9:I:53:GLN:HA	9:I:198:LEU:HD12	2.01	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
29:d:145:ASP:HA	29:d:166:LYS:HB3	2.02	0.41
46:v:14:LYS:HB2	52:2:98:G:H1	1.84	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	2.56	0.41
51:1:1173:U:H5	51:1:1174:U:H1'	1.81	0.41
51:1:1314:C:H42	51:1:1338:G:H1	1.68	0.41
51:1:1482:G:H2'	51:1:1483:G:H8	1.85	0.41
51:1:1901:A:C2	51:1:1902:C:C5	3.08	0.41
51:1:2612:C:O5'	51:1:2612:C:H6	2.03	0.41
51:1:2628:C:H3'	51:1:2629:U:H5'	2.01	0.41
53:3:142:G:O2'	53:3:196:A:N1	2.45	0.41
53:3:689:C:H2'	53:3:690:G:O4'	2.20	0.41
53:3:1243:C:H2'	53:3:1244:G:H8	1.85	0.41
58:B1:220:ARG:CG	58:B1:220:ARG:NH1	2.82	0.41
58:B1:388:ARG:HG2	58:B1:388:ARG:HH11	1.84	0.41
63:5:27:G:H1	63:5:43:C:H42	1.69	0.41
63:5:29:G:H2'	63:5:29:G:N3	2.35	0.41
7:G:17:HIS:C	7:G:19:THR:H	2.28	0.41
23:W:24:ASP:OD1	23:W:24:ASP:N	2.53	0.41
38:n:28:LEU:O	38:n:32:GLU:N	2.38	0.41
51:1:49:A:P	51:1:51:G:H5'	2.61	0.41
51:1:573:U:O2'	51:1:574:A:H3'	2.20	0.41
51:1:638:G:H2'	51:1:639:U:C6	2.55	0.41
51:1:759:G:H2'	51:1:760:G:H8	1.83	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
51:1:1239:G:H2'	51:1:1240:U:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
51:1:1822:C:H2'	51:1:1823:G:H8	1.85	0.41
59:B2:616:ILE:HG13	59:B2:652:TYR:HB2	2.01	0.41
1:A:2:LYS:NZ	52:2:42:C:OP2	2.39	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
17:Q:110:LYS:HB2	17:Q:110:LYS:HE2	1.89	0.41
27:b:107:LYS:HE2	27:b:107:LYS:HB2	1.87	0.41
35:k:7:MET:HE2	35:k:18:ARG:HD3	2.01	0.41
51:1:724:U:C4	51:1:725:G:C6	3.09	0.41
51:1:877:A:H2'	51:1:878:A:H5''	2.02	0.41
51:1:903:C:H2'	51:1:904:G:H8	1.85	0.41
51:1:1038:G:H2'	51:1:1039:A:H8	1.83	0.41
51:1:1077:A:H3'	51:1:1078:U:H4'	2.02	0.41
51:1:1152:C:H2'	51:1:1153:C:C6	2.55	0.41
51:1:1488:C:H2'	51:1:1489:C:H6	1.84	0.41
51:1:1991:U:H2'	51:1:1992:G:H5'	2.02	0.41
51:1:2156:G:H2'	51:1:2157:G:C5'	2.35	0.41
51:1:2482:A:H2'	51:1:2483:C:C6	2.54	0.41
51:1:2741:A:H2'	51:1:2742:G:C5'	2.50	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:B1:848:VAL:HB	58:B1:858:VAL:HG22	2.02	0.41
59:B2:1278:LEU:HD23	59:B2:1278:LEU:HA	1.86	0.41
16:P:30:ILE:HG23	16:P:45:THR:HB	2.02	0.41
28:c:4:LEU:HD21	28:c:98:VAL:HA	2.02	0.41
28:c:90:PHE:HD1	28:c:94:GLN:HG2	1.83	0.41
31:f:21:GLN:NE2	31:f:37:ASN:O	2.54	0.41
33:i:116:MET:HE2	33:i:116:MET:HB3	1.79	0.41
47:w:7:ARG:HA	47:w:7:ARG:HD3	1.77	0.41
50:z:31:ILE:HD11	51:1:989:G:P	2.61	0.41
51:1:688:U:O5'	51:1:688:U:H6	2.03	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
51:1:1063:G:N2	51:1:1075:C:H41	2.18	0.41
51:1:1418:G:H1'	51:1:1581:G:N2	2.36	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
51:1:1750:G:H2'	51:1:1751:U:C6	2.56	0.41
53:3:202:G:H2'	53:3:203:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:8:14:DC:C2	55:8:15:DC:C5	3.09	0.41
57:A1:211:ILE:HD12	57:A1:211:ILE:HA	1.92	0.41
58:B1:24:LEU:HD21	58:B1:116:PHE:CE2	2.54	0.41
58:B1:144:TYR:N	58:B1:144:TYR:CD1	2.88	0.41
59:B2:979:LEU:HD11	59:B2:1011:LEU:HD11	2.03	0.41
65:0:491:ARG:HD3	65:0:491:ARG:HA	1.71	0.41
35:k:17:ARG:HD3	35:k:47:ILE:HD11	2.02	0.41
37:m:123:LYS:HE2	51:1:2467:C:O2	2.20	0.41
41:q:23:TYR:HB3	41:q:27:ARG:HB2	2.02	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
51:1:191:A:H2'	51:1:192:C:C6	2.56	0.41
51:1:426:C:O2'	51:1:427:U:H5'	2.21	0.41
51:1:892:A:O2'	51:1:893:C:H5'	2.19	0.41
51:1:1416:G:H2'	51:1:1417:C:H6	1.82	0.41
53:3:370:C:H2'	53:3:371:A:H8	1.86	0.41
53:3:1228:C:H2'	53:3:1229:A:C8	2.55	0.41
58:B1:109:SER:CB	58:B1:296:LYS:HG2	2.51	0.41
58:B1:239:LEU:HD23	58:B1:239:LEU:N	2.36	0.41
58:B1:279:LEU:HD13	58:B1:299:LEU:HD13	2.02	0.41
59:B2:741:MET:HE3	59:B2:974:ARG:HH12	1.85	0.41
59:B2:886:LYS:HE2	59:B2:918:LEU:HD13	2.03	0.41
65:0:298:ILE:CG2	65:0:304:ASP:HA	2.50	0.41
5:E:28:LEU:HD23	5:E:28:LEU:HA	1.83	0.41
6:F:35:GLN:HE21	6:F:35:GLN:HB3	1.57	0.41
7:G:162:VAL:N	7:G:183:PHE:O	2.38	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
25:Y:4:LYS:HA	25:Y:4:LYS:HD3	1.86	0.41
51:1:197:A:H2	51:1:2434:A:H62	1.69	0.41
51:1:244:A:H2'	51:1:245:G:O4'	2.20	0.41
51:1:431:U:O5'	51:1:431:U:H6	2.03	0.41
51:1:1868:C:H2'	51:1:1869:G:H8	1.86	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
51:1:2568:U:O5'	51:1:2568:U:H6	2.04	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
53:3:373:A:N1	53:3:391:G:O2'	2.49	0.41
53:3:685:G:N1	53:3:704:A:OP2	2.52	0.41
58:B1:244:VAL:HA	58:B1:269:TYR:OH	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:B2:515:MET:HE2	59:B2:515:MET:HB3	1.82	0.41
15:O:12:ALA:HB2	15:O:96:VAL:HG13	2.02	0.41
33:i:109:ALA:O	33:i:113:ALA:N	2.52	0.41
43:s:29:VAL:HG21	43:s:55:ILE:HG21	2.03	0.41
51:1:94:A:H2'	51:1:95:A:C8	2.54	0.41
51:1:265:A:C8	51:1:428:A:C2	3.09	0.41
51:1:309:A:N3	51:1:329:G:O2'	2.53	0.41
51:1:490:C:O2'	51:1:491:G:P	2.79	0.41
51:1:518:G:H2'	51:1:519:U:C6	2.55	0.41
51:1:543:G:C3'	51:1:544:C:H5''	2.51	0.41
51:1:679:C:H2'	51:1:680:C:C6	2.56	0.41
51:1:1024:G:H21	51:1:1144:A:C4'	2.32	0.41
51:1:1317:G:H2'	51:1:1318:U:C6	2.56	0.41
51:1:1328:A:H2'	51:1:1330:C:C4	2.56	0.41
51:1:1931:U:C5	51:1:1968:G:N2	2.88	0.41
51:1:2335:A:N7	51:1:2337:G:C5	2.88	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:A1:205:MET:HE1	57:A1:217:ILE:HG13	2.02	0.41
59:B2:902:LEU:O	59:B2:906:PHE:N	2.48	0.41
62:NG:175:PHE:O	62:NG:178:VAL:O	2.38	0.41
7:G:104:LYS:HE2	7:G:104:LYS:HB2	1.92	0.41
8:H:19:SER:HB2	8:H:39:ARG:HH21	1.85	0.41
12:L:125:ASP:HB2	12:L:130:LYS:HG3	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
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
28:c:59:ARG:HD3	28:c:59:ARG:HA	1.83	0.41
29:d:163:ASN:HD21	51:1:322:A:P	2.44	0.41
30:e:39:VAL:HG12	30:e:85:GLY:HA2	2.03	0.41
33:i:77:VAL:HA	33:i:80:LYS:HE2	2.02	0.41
38:n:71:ARG:HE	38:n:71:ARG:HB3	1.68	0.41
42:r:81:LYS:NZ	51:1:568:U:O4	2.54	0.41
51:1:56:A:H1'	51:1:127:A:C2	2.55	0.41
51:1:170:U:H2'	51:1:171:U:C6	2.55	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
51:1:722:A:H2'	51:1:723:C:C6	2.56	0.41
51:1:908:C:O2'	51:1:909:A:H5'	2.20	0.41
51:1:924:G:O2'	51:1:925:A:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
51:1:1327: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
51:1:2575:C:H2'	51:1:2578:G:O6	2.21	0.41
51:1:2660:A:H2'	51:1:2661:G:C8	2.56	0.41
53:3:146:G:H2'	53:3:147:G:H8	1.86	0.41
53:3:336:A:H2'	53:3:337:G:H8	1.86	0.41
53:3:1304:G:N1	53:3:1332:A:OP2	2.54	0.41
58:B1:56:LEU:HD12	58:B1:56:LEU:HA	1.84	0.41
58:B1:351:GLY:O	58:B1:467:ALA:HA	2.21	0.41
58:B1:930:LEU:HA	58:B1:1244:GLN:HG3	2.02	0.41
59:B2:803:ALA:HB2	59:B2:1094:VAL:HG21	2.03	0.41
59:B2:936:ARG:HB2	59:B2:1042:LEU:HD12	2.03	0.41
59:B2:987:GLU:HG2	59:B2:991:LYS:HE3	2.03	0.41
65:0:519:VAL:HB	65:0:580:PHE:HB3	2.02	0.41
6:F:30:GLU:HA	6:F:31:PRO:HD3	1.91	0.41
9:I:101:VAL:HG13	9:I:113:ALA:HB1	2.03	0.41
31:f:60:GLY:O	31:f:64:ALA:N	2.54	0.41
33:i:41:PHE:O	33:i:45:THR:N	2.54	0.41
33:i:89:SER:HB3	51:1:1063:G:O2'	2.20	0.41
38:n:22:ARG:HH22	51:1:2709:G:H5'	1.86	0.41
51:1:10:A:C6	51:1:2800:A:C2	3.09	0.41
51:1:79:C:O2	51:1:346:A:H2	2.03	0.41
51:1:224:U:O4	51:1:420:C:H5'	2.21	0.41
51:1:724:U:H2'	51:1:725:G:O4'	2.21	0.41
51:1:1092:C:O2'	51:1:1093:G:H5'	2.21	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
51:1:2649: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
51:1:2828:G:N1	51:1:2829:A:C5	2.89	0.41
53:3:31:G:N2	53:3:48:C:OP1	2.41	0.41
59:B2:524:ILE:HD12	59:B2:712:SER:HB2	2.02	0.41
59:B2:870:ILE:HB	59:B2:944:ARG:HD3	2.02	0.41
67:0:800:FUA:H212	67:0:800:FUA:H72	1.89	0.41
7:G:190:SER:OG	7:G:191:ASP:N	2.53	0.40
8:H:5:HIS:HA	8:H:6:PRO:HD3	1.95	0.40
14:N:22:PRO:HA	14:N:60:LEU:HA	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:108:ASN:HA	26:Z:7:GLU:HG2	2.03	0.40
20:T:80:LEU:HD12	20:T:80:LEU:HA	1.92	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
30:e:124:ARG:NH2	51:1:2315:G:N3	2.68	0.40
32:g:1:MET:N	32:g:20:ASN:OD1	2.40	0.40
42:r:4:VAL:HG23	42:r:39:LEU:HB2	2.03	0.40
51:1:137:U:H3	51:1:142:A:H61	1.69	0.40
51:1:518:G:C2	51:1:519:U:C2	3.08	0.40
51:1:555:G:HO2'	51:1:556:A:H8	1.69	0.40
51:1:1302:A:H5'	51:1:1608:A:OP1	2.21	0.40
51:1:1605:C:H2'	51:1:1606:C:C5'	2.52	0.40
51:1:1715:G:O2'	51:1:1716:U:C6	2.75	0.40
51:1:2221: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
51:1:2600:A:H8	51:1:2600:A:O5'	2.03	0.40
57:A1:44:ARG:HA	57:A1:183:ILE:HD12	2.03	0.40
59:B2:22:LEU:HD22	59:B2:603:ILE:HG21	2.02	0.40
59:B2:998:LEU:HD21	59:B2:1015:ALA:HB2	2.02	0.40
63:5:17:C:H2'	63:5:18:G:C8	2.56	0.40
63:5:23:A:H2'	63:5:24:G:C8	2.56	0.40
65:0:118:GLY:HA2	65:0:154:VAL:HG22	2.03	0.40
8:H:14:VAL:HG11	8:H:180:ASP:HB3	2.03	0.40
13:M:91:LEU:HD23	13:M:91:LEU:HA	1.90	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
23:W:25:ILE:HA	23:W:28:LEU:HB2	2.02	0.40
25:Y:43:LYS:HE2	25:Y:43:LYS:HB2	1.89	0.40
39:o:24:THR:HB	39:o:42:PRO:HG3	2.03	0.40
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
51:1:886:A:N7	51:1:887:U:H1'	2.36	0.40
51:1:1048:A:N6	51:1:1111:A:C8	2.89	0.40
51:1:1722:A:H2'	51:1:1723:G:O4'	2.21	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
51:1:2106:U:H3'	51:1:2107:G:H8	1.86	0.40
58:B1:68:TYR:CB	58:B1:75:TYR:HE2	2.34	0.40
58:B1:245:LEU:HD13	59:B2:1329:GLU:HA	2.03	0.40
9:I:10:LEU:HG	9:I:62:ARG:HD2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:123:MET:HB2	9:I:143:SER:HB3	2.04	0.40
13:M:42:GLU:HG2	13:M:100:ILE:HG21	2.02	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
22:V:11:VAL:HG23	22:V:55:GLY:H	1.85	0.40
26:Z:9:GLU:HB3	26:Z:10:PRO:HD3	2.03	0.40
28:c:174:SER:O	28:c:174:SER:OG	2.37	0.40
30:e:64:PRO:HA	30:e:88:VAL:HG22	2.03	0.40
35:k:13:ASN:HB3	35:k:100:PHE:CZ	2.57	0.40
35:k:44:LYS:HB3	35:k:44:LYS:HE3	1.92	0.40
35:k:110:GLU:H	35:k:113:MET:HE3	1.86	0.40
51:1:359:G:H2'	51:1:360:U:C5'	2.51	0.40
51:1:467:G:O5'	51:1:467:G:H8	2.04	0.40
51:1:706:A:H2'	51:1:707:G:C5'	2.51	0.40
51:1:1160:G:C6	51:1:1161:C:C4	3.09	0.40
51:1:1333:G:C2'	51:1:1334:G:H5'	2.51	0.40
51:1:1430:G:O2'	51:1:1431:A:H5'	2.21	0.40
51:1:1695:G:H2'	51:1:1696:G:O5'	2.22	0.40
51:1:1721:G:H1'	51:1:1739:A:N6	2.35	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
51:1:2210:U:H6	51:1:2210:U:OP1	2.04	0.40
51:1:2357:G:C2	51:1:2361:G:C6	3.10	0.40
51:1:2393:U:C2'	51:1:2394:C:H5'	2.51	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
53:3:202:G:H2'	53:3:203:G:H8	1.85	0.40
57:A1:79:LEU:HD11	58:B1:526:VAL:HG21	2.04	0.40
58:B1:109:SER:HA	58:B1:110:PRO:HD3	1.96	0.40
58:B1:111:THR:HG23	58:B1:300:GLN:HA	2.03	0.40
58:B1:395:LYS:HB3	58:B1:395:LYS:HE3	1.45	0.40
58:B1:472:LEU:HD11	59:B2:1294:LYS:HG2	2.02	0.40
65:0:438:LEU:HD21	65:0:472:ARG:HD2	2.02	0.40
65:0:574:MET:HE1	65:0:601:PHE:CZ	2.57	0.40
24:X:32:THR:OG1	24:X:49:ALA:O	2.31	0.40
27:b:70:LYS:HD2	27:b:73:ILE:HD12	2.02	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
29:d:138:LEU:HG	29:d:143:LEU:HD12	2.03	0.40
30:e:36:ASN:HB3	30:e:152:ASP:HB3	2.03	0.40
30:e:49:LEU:HD22	30:e:83:PRO:HB2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:f:3:VAL:HG13	51:1:2751:G:H4'	2.02	0.40
45:u:4:ILE:HD13	45:u:69:VAL:HG23	2.03	0.40
51:1:55:G:N2	51:1:116:C:C2	2.90	0.40
51:1:120:U:C2	51:1:149:A:C6	3.10	0.40
51:1:221:A:C4	51:1:266:G:N7	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
51:1:724:U:H2'	51:1:725:G:C8	2.56	0.40
51:1:914:G:H5'	51:1:915:C:OP2	2.21	0.40
51:1:935:C:H2'	51:1:936:A:C8	2.56	0.40
51:1:1279:G:H2'	51:1:1280:G:C8	2.56	0.40
51:1:1346:G:O2'	51:1:1347:A:H5'	2.22	0.40
51:1:1430:G:H2'	51:1:1431:A:O4'	2.21	0.40
51:1:1505:A:O2'	51:1:1506:U:H5'	2.19	0.40
51:1:1722:A:N6	51:1:1738:G:H1'	2.36	0.40
51:1:2105:U:C2	51:1:2184:A:H2	2.39	0.40
51:1:2788:C:H2'	51:1:2789:C:C6	2.56	0.40
51:1:2888:C:H2'	51:1:2889: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
55:8:2:DC:C6	55:8:2:DC:H5'	2.56	0.40
57:A1:18:GLN:H	57:A1:18:GLN:HG3	1.66	0.40
58:B1:322:ARG:HA	58:B1:323:PRO:HD2	1.98	0.40
58:B1:349:TYR:HA	59:B2:1246:ARG:O	2.22	0.40
58:B1:734:ALA:O	58:B1:738:ARG:HB2	2.22	0.40
58:B1:777:HIS:CD2	59:B2:550:VAL:HG13	2.56	0.40
59:B2:738:GLU:HA	59:B2:741:MET:HE2	2.03	0.40
64:6:69:C:H2'	64:6:70:G:C8	2.57	0.40
65:0:635:LEU:HD23	65:0:635:LEU:HA	1.98	0.40
9:I:59:LYS:HE2	9:I:194:ILE:HG22	2.04	0.40
19:S:15:LEU:HB3	19:S:54:SER:HB3	2.03	0.40
51:1:164:C:H2'	51:1:165:A:O4'	2.22	0.40
51:1:194:G:O6	51:1:195:A:C6	2.75	0.40
51:1:510:C:H2'	51:1:511:U:H6	1.85	0.40
51:1:1095:A:H1'	65:0:632:ILE:HD13	2.02	0.40
51:1:1334:G:C6	51:1:1335:C:C4	3.09	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
51:1:2093:G:N7	51:1:2225:A:H2'	2.37	0.40
51:1:2193:G:H2'	51:1:2194:U:H6	1.83	0.40
51:1:2647:U:O2'	51:1:2648:G:H5'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:2:31:C:H2'	52:2:53:A:H61	1.87	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
58:B1:113:HIS:ND1	58:B1:115:TRP:HB2	2.37	0.40
58:B1:182:ALA:HB1	58:B1:238:ILE:CG2	2.52	0.40
58:B1:244:VAL:HA	58:B1:269:TYR:CZ	2.57	0.40
58:B1:515:ARG:HH21	58:B1:717:VAL:HG23	1.87	0.40
58:B1:1144:LEU:HD23	58:B1:1144:LEU:HA	1.96	0.40
59:B2:159:SER:HB2	59:B2:442:VAL:HG11	2.04	0.40
59:B2:1247:SER:OG	59:B2:1248:THR:N	2.55	0.40
65:0:418:ILE:HA	65:0:486:PRO:HD3	2.04	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	19
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	49
8	H	204/233 (88%)	194 (95%)	10 (5%)	0	100	100
9	I	203/206 (98%)	173 (85%)	29 (14%)	1 (0%)	24	62
10	J	155/167 (93%)	138 (89%)	17 (11%)	0	100	100
11	K	98/135 (73%)	84 (86%)	14 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	12	47
16	P	114/129 (88%)	100 (88%)	13 (11%)	1 (1%)	14	49
17	Q	121/124 (98%)	94 (78%)	27 (22%)	0	100	100
18	R	112/118 (95%)	98 (88%)	13 (12%)	1 (1%)	14	49
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%)	9	41
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%)	7	36
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	31
33	i	139/142 (98%)	109 (78%)	27 (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	35
42	r	101/103 (98%)	88 (87%)	13 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	12	47
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%)	9	41
49	y	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
50	z	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
57	A1	214/329 (65%)	195 (91%)	19 (9%)	0	100	100
57	A2	65/329 (20%)	65 (100%)	0	0	100	100
58	B1	1329/1407 (94%)	1202 (90%)	123 (9%)	4 (0%)	36	71
59	B2	1338/1342 (100%)	1205 (90%)	129 (10%)	4 (0%)	36	71
60	W0	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
61	NA	490/495 (99%)	472 (96%)	15 (3%)	3 (1%)	21	58
62	NG	150/181 (83%)	132 (88%)	13 (9%)	5 (3%)	3	21
65	0	669/716 (93%)	625 (93%)	43 (6%)	1 (0%)	48	83
All	All	9955/10945 (91%)	8997 (90%)	921 (9%)	37 (0%)	31	66

All (37) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
48	x	25	LYS
58	B1	121	PRO
61	NA	187	ARG
61	NA	188	PRO
62	NG	102	PRO
59	B2	43	PRO
59	B2	918	LEU
61	NA	426	GLY
62	NG	163	SER
59	B2	888	THR
2	B	23	ALA
7	G	19	THR
18	R	5	GLY
32	g	12	LEU
33	i	22	PRO

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Mol	Chain	Res	Type
41	q	23	TYR
58	B1	43	THR
58	B1	193	ASP
7	G	17	HIS
15	O	58	ASN
22	V	50	ASN
23	W	13	THR
45	u	97	SER
58	B1	1325	PHE
9	I	45	PRO
23	W	17	VAL
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%)	53	67
2	B	47/48 (98%)	47 (100%)	0	100	100
3	C	45/49 (92%)	44 (98%)	1 (2%)	45	64
4	D	38/38 (100%)	37 (97%)	1 (3%)	40	60
5	E	51/52 (98%)	49 (96%)	2 (4%)	28	49
6	F	34/34 (100%)	30 (88%)	4 (12%)	5	19
7	G	180/199 (90%)	174 (97%)	6 (3%)	33	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	170/190 (90%)	167 (98%)	3 (2%)	51	67
9	I	172/173 (99%)	168 (98%)	4 (2%)	44	63
10	J	119/126 (94%)	117 (98%)	2 (2%)	53	67
11	K	87/116 (75%)	82 (94%)	5 (6%)	18	41
12	L	124/147 (84%)	124 (100%)	0	100	100
13	M	104/105 (99%)	103 (99%)	1 (1%)	68	76
14	N	105/107 (98%)	95 (90%)	10 (10%)	8	25
15	O	86/90 (96%)	78 (91%)	8 (9%)	8	26
16	P	89/99 (90%)	86 (97%)	3 (3%)	32	54
17	Q	103/104 (99%)	98 (95%)	5 (5%)	22	44
18	R	92/96 (96%)	91 (99%)	1 (1%)	65	74
19	S	83/84 (99%)	83 (100%)	0	100	100
20	T	76/77 (99%)	73 (96%)	3 (4%)	28	49
21	U	65/65 (100%)	64 (98%)	1 (2%)	57	70
22	V	74/78 (95%)	72 (97%)	2 (3%)	39	59
23	W	56/65 (86%)	52 (93%)	4 (7%)	13	35
24	X	70/79 (89%)	70 (100%)	0	100	100
25	Y	65/66 (98%)	64 (98%)	1 (2%)	57	70
26	Z	55/61 (90%)	47 (86%)	8 (14%)	3	14
27	b	216/218 (99%)	212 (98%)	4 (2%)	50	66
28	c	164/164 (100%)	164 (100%)	0	100	100
29	d	165/165 (100%)	162 (98%)	3 (2%)	51	67
30	e	148/150 (99%)	142 (96%)	6 (4%)	27	48
31	f	137/138 (99%)	132 (96%)	5 (4%)	31	52
32	g	41/114 (36%)	38 (93%)	3 (7%)	13	34
33	i	109/110 (99%)	98 (90%)	11 (10%)	7	23
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%)	68	76
37	m	109/109 (100%)	103 (94%)	6 (6%)	19	42
38	n	100/103 (97%)	99 (99%)	1 (1%)	68	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	o	86/87 (99%)	86 (100%)	0	100	100
40	p	99/100 (99%)	98 (99%)	1 (1%)	68	76
41	q	89/90 (99%)	86 (97%)	3 (3%)	32	54
42	r	84/84 (100%)	82 (98%)	2 (2%)	43	63
43	s	93/93 (100%)	92 (99%)	1 (1%)	65	74
44	t	80/84 (95%)	80 (100%)	0	100	100
45	u	83/85 (98%)	79 (95%)	4 (5%)	23	45
46	v	78/78 (100%)	77 (99%)	1 (1%)	61	72
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%)	26	48
57	A1	185/286 (65%)	174 (94%)	11 (6%)	18	40
58	B1	1110/1168 (95%)	1016 (92%)	94 (8%)	10	30
59	B2	1150/1157 (99%)	1118 (97%)	32 (3%)	38	59
60	W0	70/75 (93%)	69 (99%)	1 (1%)	59	71
65	0	553/588 (94%)	481 (87%)	72 (13%)	4	17
All	All	7745/8214 (94%)	7405 (96%)	340 (4%)	27	47

All (340) 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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
18	R	64	VAL
20	T	82	GLU
20	T	86	LEU
20	T	88	ARG
21	U	36	VAL
22	V	47	ASP
22	V	52	CYS
23	W	15	GLU
23	W	17	VAL
23	W	18	GLN
23	W	70	THR
25	Y	85	LEU
26	Z	3	ILE
26	Z	4	LYS
26	Z	5	VAL
26	Z	12	ASP
26	Z	15	LEU
26	Z	19	LYS
26	Z	20	ARG
26	Z	27	VAL
27	b	129	LEU
27	b	131	MET
27	b	132	ARG
27	b	203	VAL
29	d	14	VAL
29	d	118	LEU
29	d	198	GLU
30	e	39	VAL
30	e	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

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Mol	Chain	Res	Type
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
33	i	71	LYS
33	i	74	PRO
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
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

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Mol	Chain	Res	Type
57	A1	48	LEU
58	B1	24	LEU
58	B1	40	LYS
58	B1	42	GLU
58	B1	44	ILE
58	B1	47	ARG
58	B1	49	PHE
58	B1	50	LYS
58	B1	60	ARG
58	B1	66	LYS
58	B1	69	GLU
58	B1	71	LEU
58	B1	74	LYS
58	B1	76	LYS
58	B1	78	LEU
58	B1	80	HIS
58	B1	81	ARG
58	B1	86	GLU
58	B1	87	LYS
58	B1	91	GLU
58	B1	93	THR
58	B1	94	GLN
58	B1	95	THR
58	B1	96	LYS
58	B1	99	ARG
58	B1	100	GLU
58	B1	114	ILE
58	B1	117	LEU
58	B1	120	LEU
58	B1	126	LEU
58	B1	132	LEU
58	B1	135	ILE
58	B1	142	GLU
58	B1	144	TYR
58	B1	145	VAL
58	B1	146	VAL
58	B1	147	ILE
58	B1	152	THR
58	B1	154	LEU
58	B1	157	GLN
58	B1	159	ILE
58	B1	172	PHE

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
59	B2	899	GLU
59	B2	900	LYS
59	B2	901	LEU
59	B2	902	LEU
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

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Mol	Chain	Res	Type
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	161	ARG
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
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

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (133) 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

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Mol	Chain	Res	Type
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	96	ASN
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
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
23	W	51	GLN
24	X	68	HIS
25	Y	2	ASN
25	Y	77	ASN

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Mol	Chain	Res	Type
26	Z	8	ASN
27	b	24	HIS
27	b	69	ASN
27	b	89	ASN
27	b	142	ASN
27	b	259	ASN
28	c	49	GLN
28	c	134	HIS
28	c	150	GLN
28	c	164	GLN
28	c	173	GLN
29	d	41	GLN
29	d	62	GLN
29	d	90	GLN
29	d	94	GLN
29	d	165	HIS
30	e	4	HIS
31	f	44	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
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

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Mol	Chain	Res	Type
46	v	87	GLN
47	w	53	HIS
48	x	16	ASN
48	x	33	HIS
49	y	31	GLN
49	y	38	GLN
50	z	8	GLN
57	A1	37	HIS
57	A1	66	HIS
57	A1	84	ASN
57	A1	117	HIS
57	A1	128	HIS
58	B1	45	ASN
58	B1	364	HIS
58	B1	424	ASN
58	B1	469	HIS
58	B1	771	GLN
58	B1	805	GLN
58	B1	817	HIS
58	B1	865	HIS
58	B1	1195	GLN
58	B1	1238	GLN
58	B1	1252	HIS
58	B1	1259	GLN
59	B2	69	GLN
59	B2	314	ASN
59	B2	330	HIS
59	B2	343	HIS
59	B2	518	ASN
59	B2	554	HIS
59	B2	688	GLN
59	B2	808	ASN
59	B2	1237	HIS
59	B2	1268	GLN
59	B2	1313	HIS
60	W0	7	GLN
60	W0	31	GLN
65	0	344	ASN
65	0	367	HIS
65	0	465	HIS
65	0	496	GLN
65	0	514	GLN

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Mol	Chain	Res	Type
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%)	2 (1%)
53	3	1538/1542 (99%)	253 (16%)	4 (0%)
54	4	37/44 (84%)	21 (56%)	3 (8%)
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%)	33 (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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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 (33) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	1	481	G
51	1	490	C
51	1	685	A
51	1	764	A
51	1	784	G
51	1	827	U
51	1	859	G
51	1	1020	A
51	1	1130	U
51	1	1715	G
51	1	1783	A
51	1	1801	A
51	1	1930	G
51	1	2275	C
51	1	2326	C
51	1	2732	G
52	2	12	C
52	2	88	C
53	3	4	U
53	3	1035	A
53	3	1139	G
53	3	1224	U

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Mol	Chain	Res	Type
54	4	14	U
54	4	19	U
54	4	25	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	-	29,30,30	1.15	4 (13%)	45,47,47	1.82	8 (17%)
67	FUA	0	800	-	39,40,40	1.66	3 (7%)	50,64,64	1.17	6 (12%)

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	-	-	2/16/32/32	0/3/3/3
67	FUA	0	800	-	-	10/16/92/92	0/4/4/4

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	0	800	FUA	C29-C22	-9.41	1.34	1.47
68	0	801	GDP	C5-C4	3.01	1.47	1.38
67	0	800	FUA	O5-C29	-2.58	1.23	1.30
67	0	800	FUA	C9-C11	2.50	1.57	1.54
68	0	801	GDP	C6-N1	-2.36	1.34	1.38
68	0	801	GDP	C4-N9	-2.09	1.32	1.38
68	0	801	GDP	C5-N7	-2.03	1.35	1.39

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	0	801	GDP	C5-C4-N3	-5.79	119.18	128.39
68	0	801	GDP	C2-N3-C4	5.04	120.99	112.30
68	0	801	GDP	N9-C4-N3	4.07	134.10	125.95
68	0	801	GDP	C6-C5-N7	3.66	136.95	130.29
67	0	800	FUA	C14-C8-C9	-2.71	104.53	109.30
68	0	801	GDP	C4-C5-N7	-2.63	106.50	110.67
68	0	801	GDP	O6-C6-C5	-2.41	120.17	126.53
67	0	800	FUA	C1-C10-C9	2.37	114.48	109.16
67	0	800	FUA	C8-C9-C10	2.30	118.89	116.42
67	0	800	FUA	O2-C16-C17	2.10	114.46	108.30
68	0	801	GDP	C5-C6-N1	2.07	118.52	113.25
68	0	801	GDP	C3'-C2'-C1'	2.04	105.31	101.46
67	0	800	FUA	O1-C11-C9	2.03	116.49	111.11
67	0	800	FUA	C6-C7-C8	2.01	116.32	112.85

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
67	0	800	FUA	C13-C17-C22-C23
67	0	800	FUA	C13-C17-C22-C29
67	0	800	FUA	C23-C22-C29-O4
67	0	800	FUA	C23-C22-C29-O5
67	0	800	FUA	C32-C31-O2-C16
68	0	801	GDP	PA-O3A-PB-O2B

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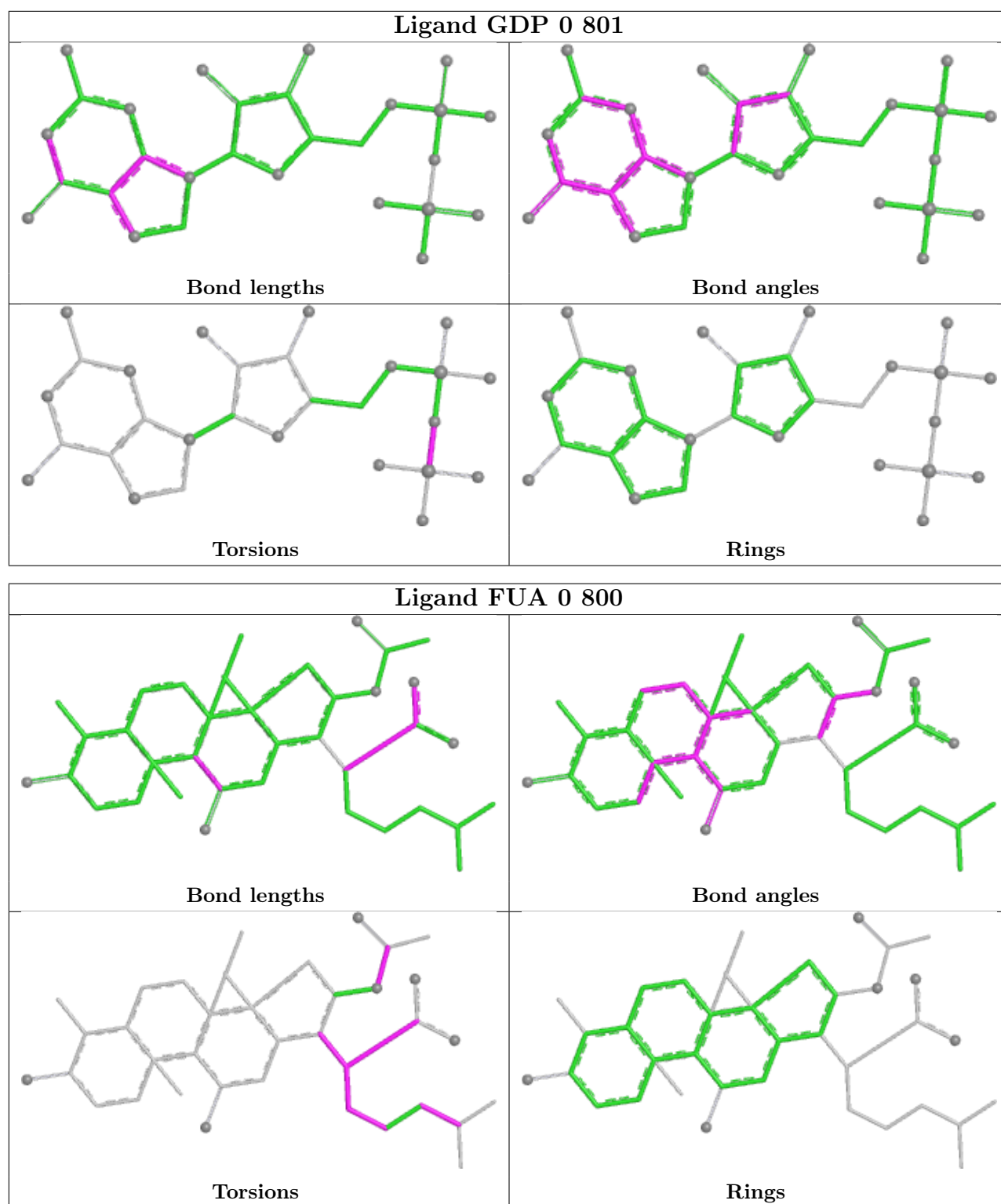
Mol	Chain	Res	Type	Atoms
67	0	800	FUA	O3-C31-O2-C16
67	0	800	FUA	C24-C25-C26-C27
67	0	800	FUA	C24-C25-C26-C28
67	0	800	FUA	C22-C23-C24-C25
68	0	801	GDP	PA-O3A-PB-O1B
67	0	800	FUA	C29-C22-C23-C24

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
67	0	800	FUA	7	0

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



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

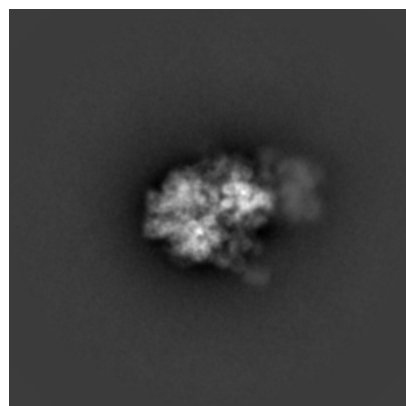
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38949. These allow visual inspection of the internal detail of the map and identification of artifacts.

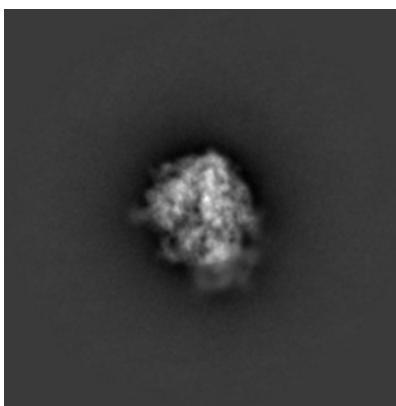
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

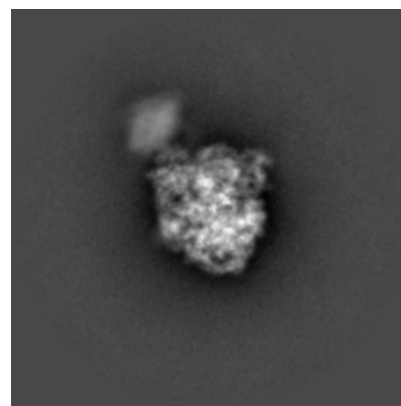
6.1.1 Primary map



X

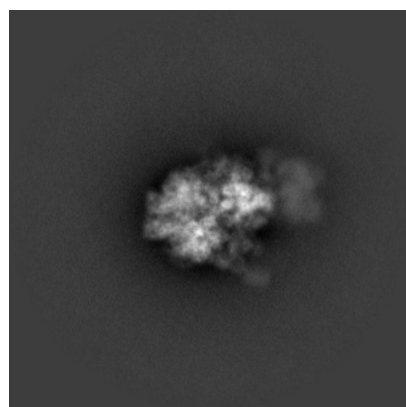


Y

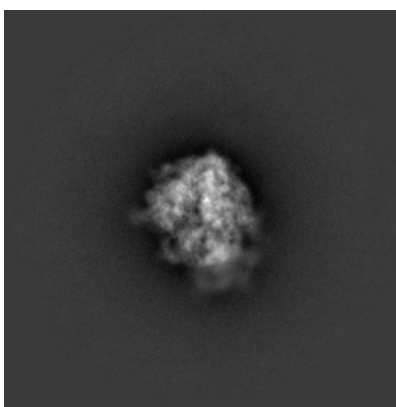


Z

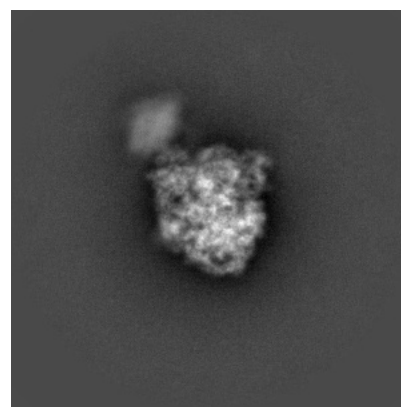
6.1.2 Raw map



X



Y

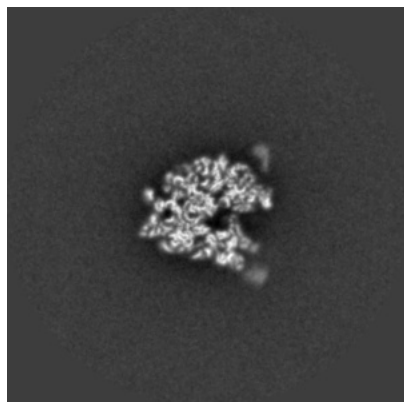


Z

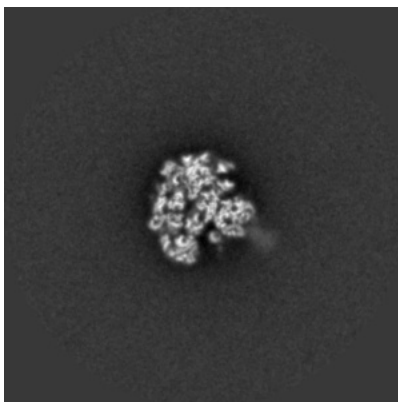
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

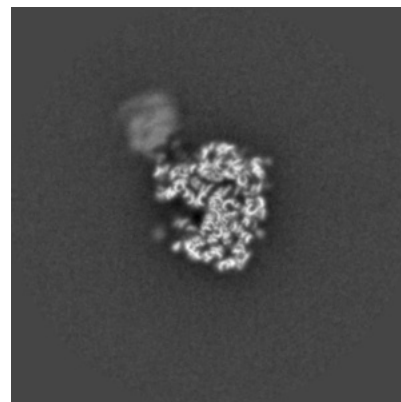
6.2.1 Primary map



X Index: 240

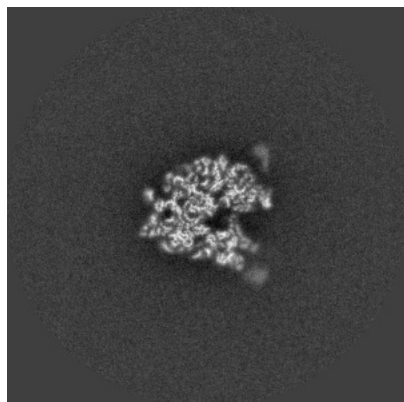


Y Index: 240

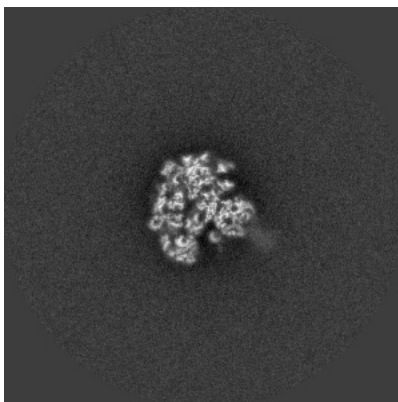


Z Index: 240

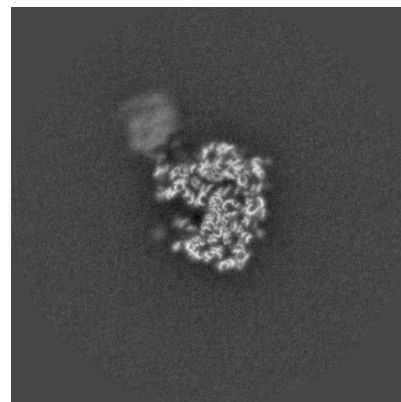
6.2.2 Raw map



X Index: 240



Y Index: 240

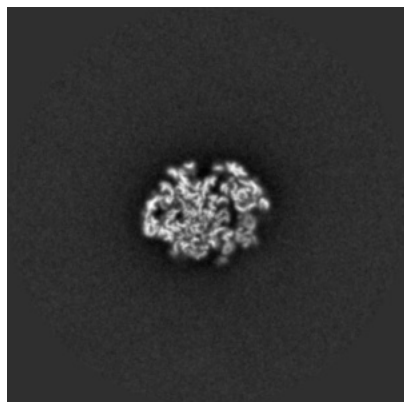


Z Index: 240

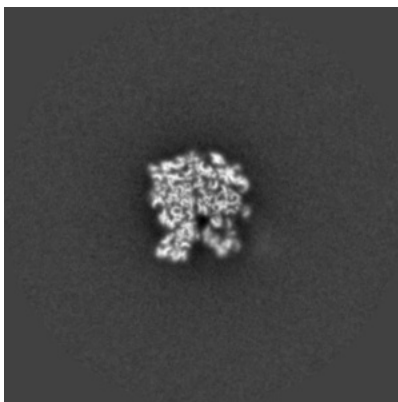
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

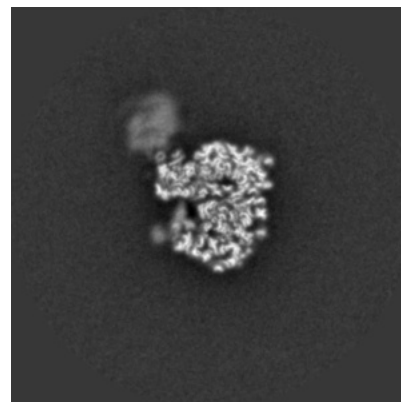
6.3.1 Primary map



X Index: 265

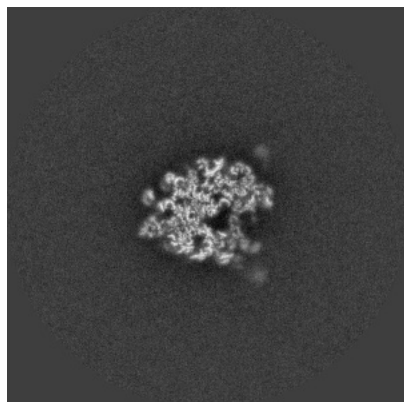


Y Index: 223

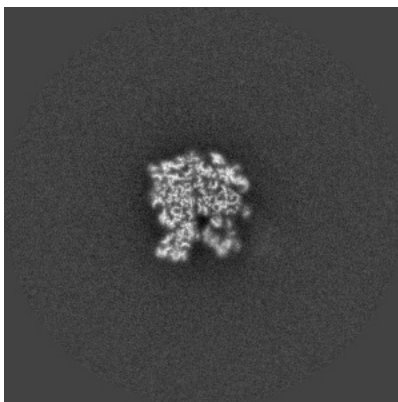


Z Index: 246

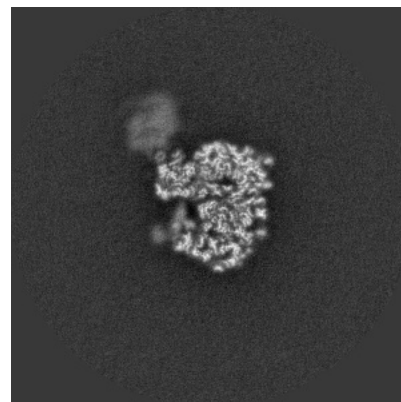
6.3.2 Raw map



X Index: 243



Y Index: 223

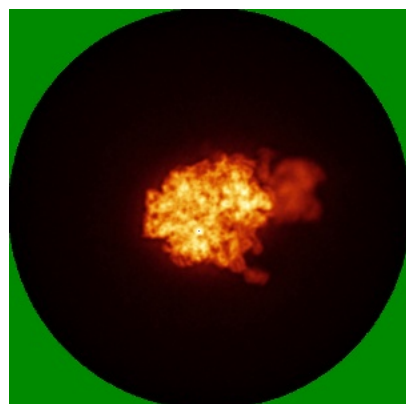


Z Index: 246

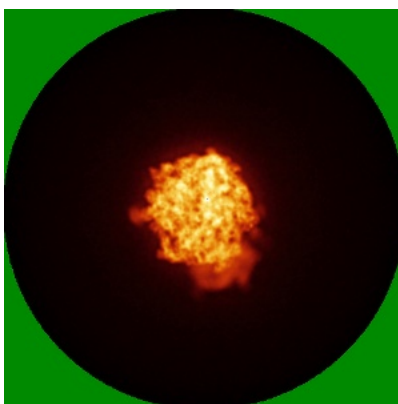
The images above show the largest variance slices of the map in three orthogonal directions.

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

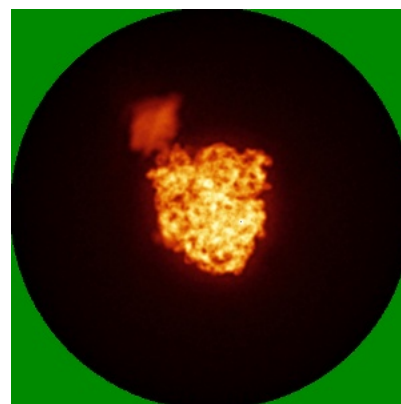
6.4.1 Primary map



X

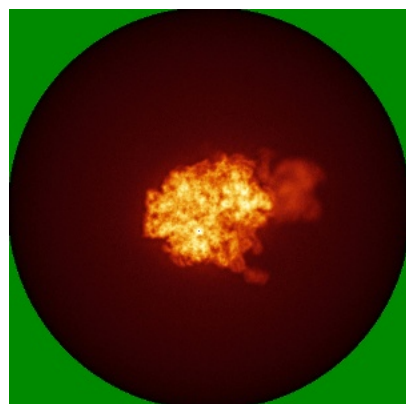


Y

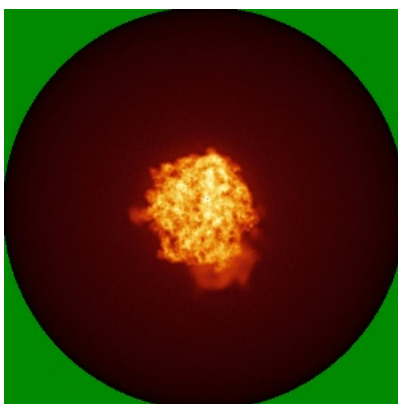


Z

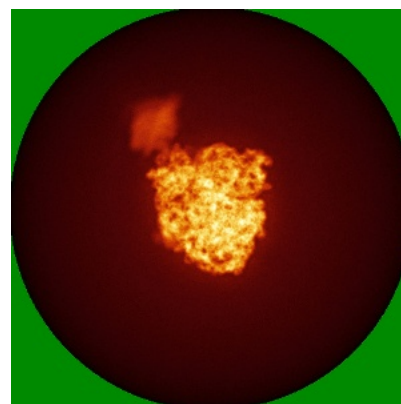
6.4.2 Raw map



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](#)

This section was not generated.

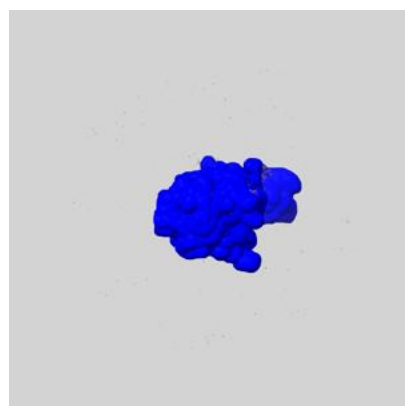
6.6 Mask visualisation [i](#)

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

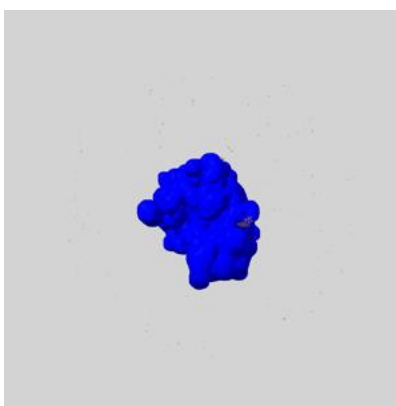
A mask typically either:

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

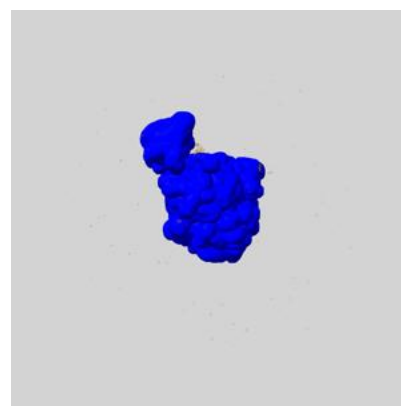
6.6.1 emd_38949_msk_1.map [i](#)



X



Y

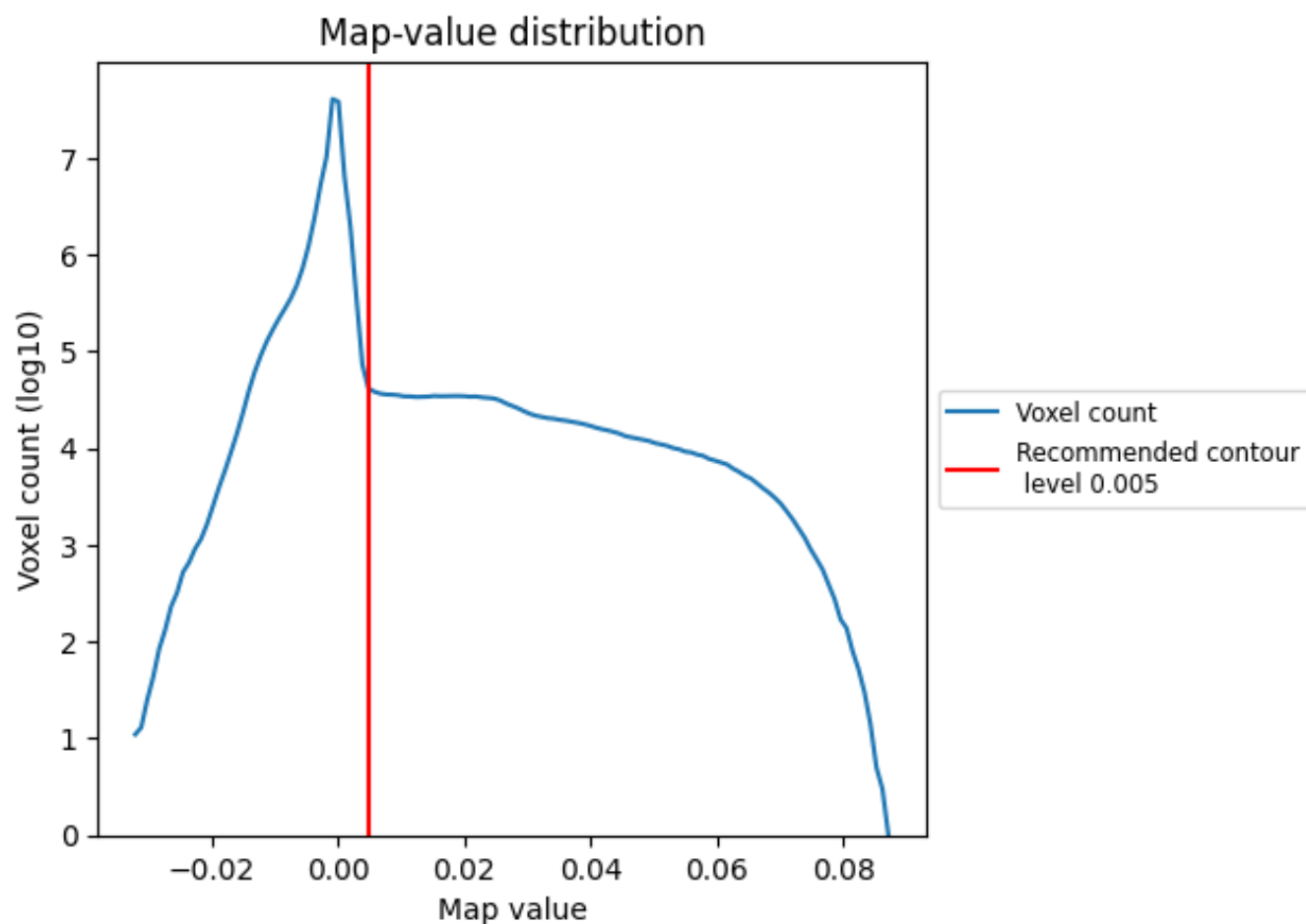


Z

7 Map analysis [i](#)

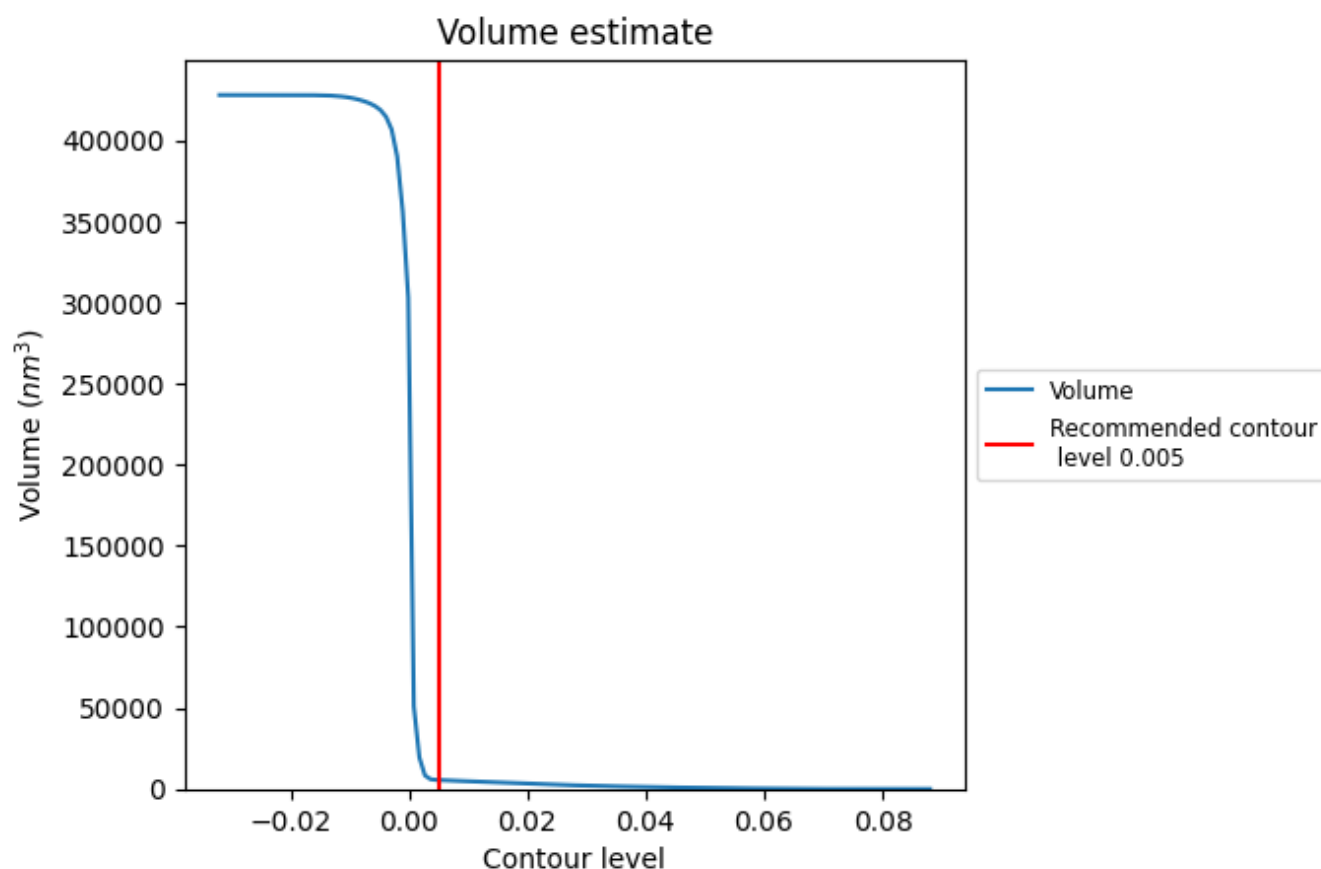
This section contains the results of statistical analysis of the map.

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.

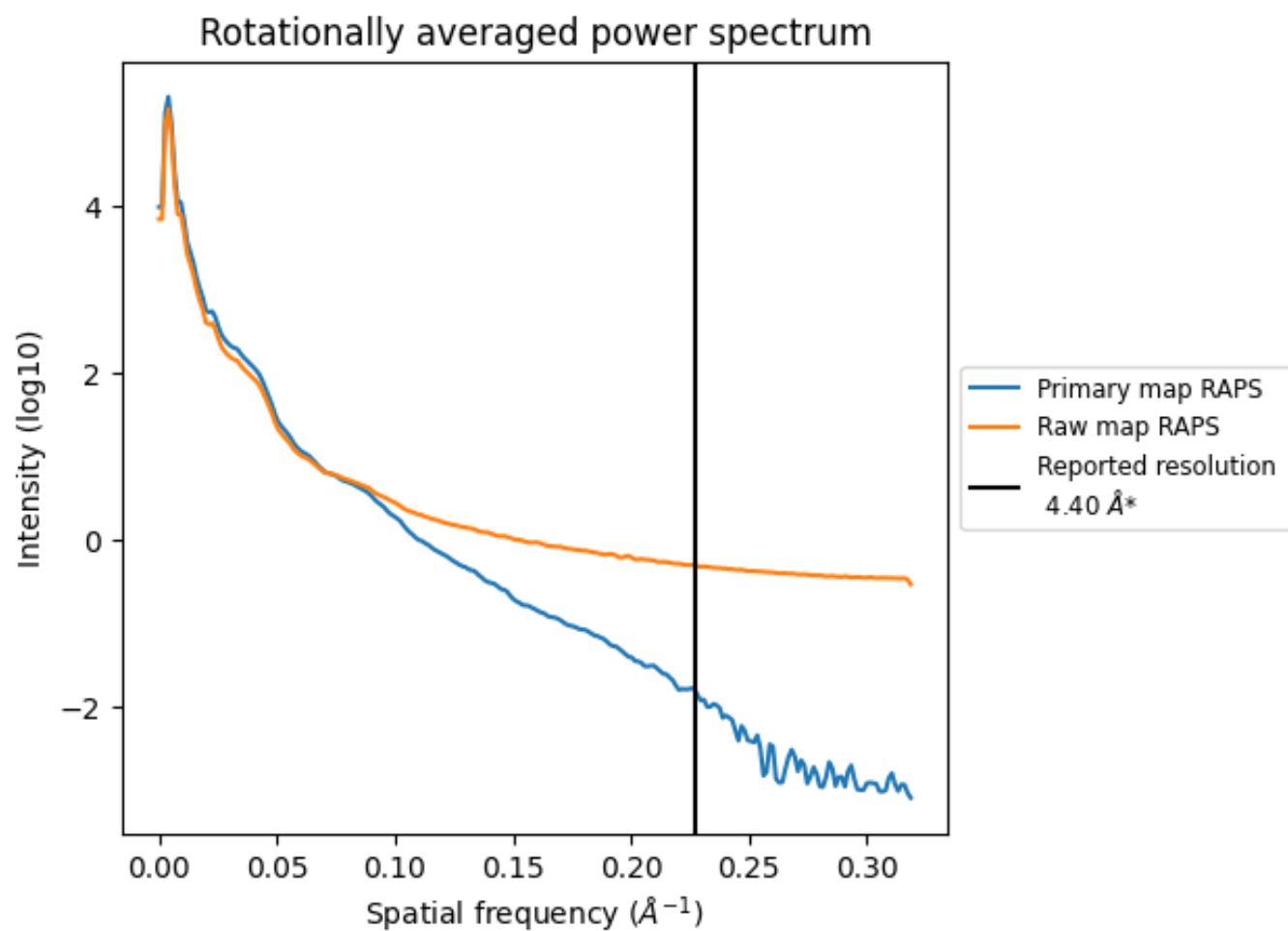
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5501 nm^3 ; this corresponds to an approximate mass of 4969 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](#)

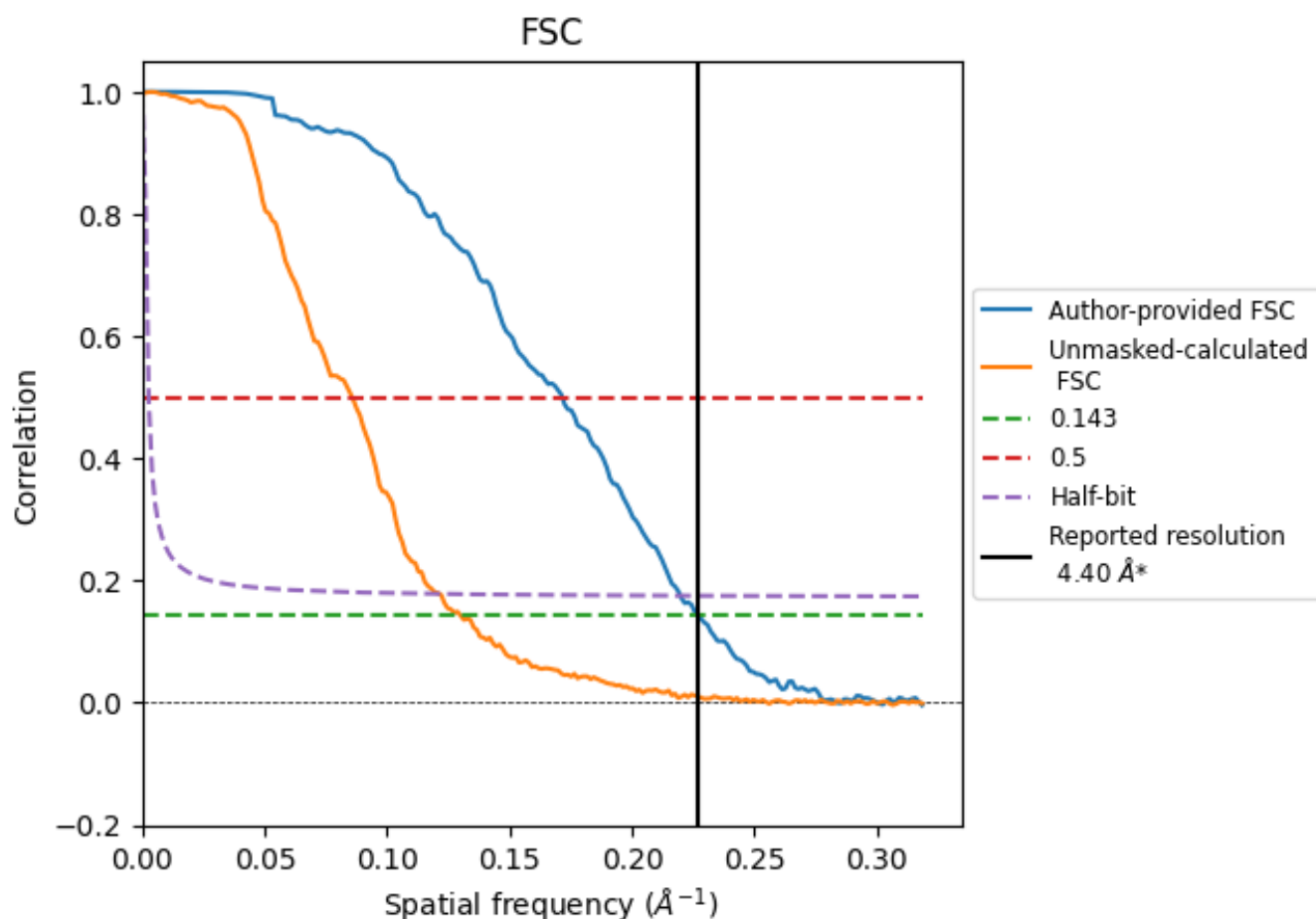


*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

8.2 Resolution estimates [i](#)

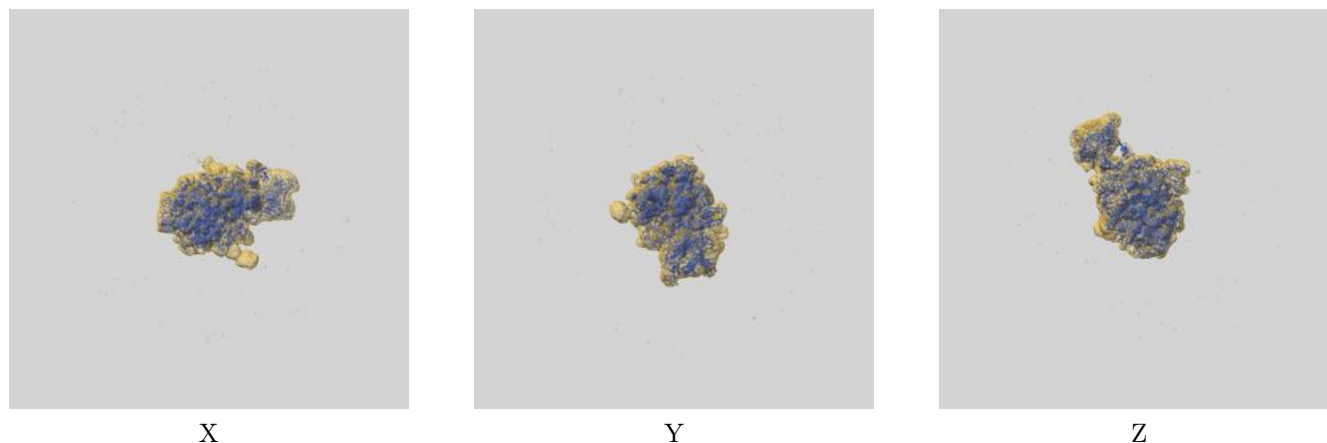
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	4.41	5.83	4.55
Unmasked-calculated*	7.70	11.67	8.24

*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 7.70 differs from the reported value 4.4 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-38949 and PDB model 8Y5T. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



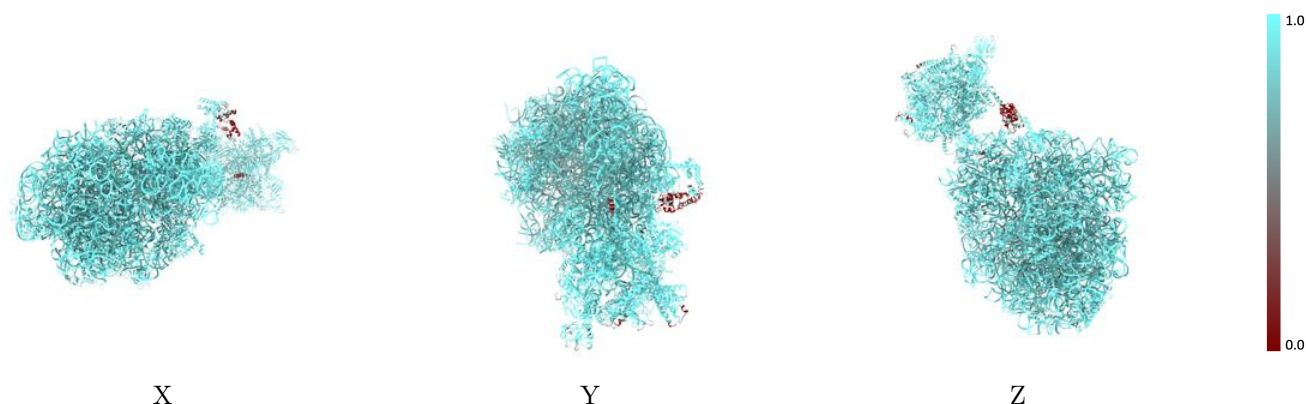
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



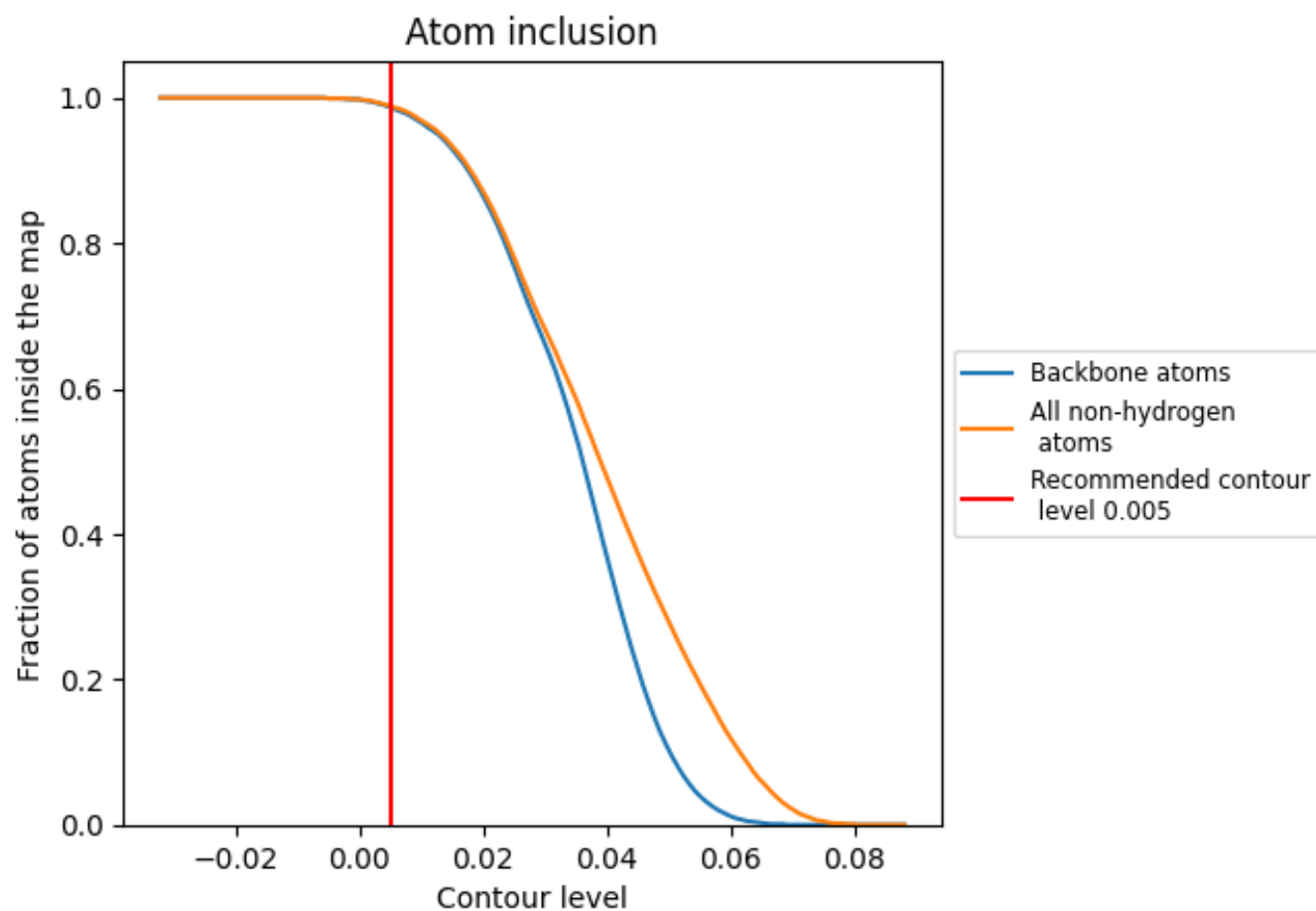
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9890	 0.1850
0	 0.9740	 0.1590
1	 1.0000	 0.2360
2	 1.0000	 0.2150
3	 1.0000	 0.2190
4	 0.9840	 0.0830
5	 0.9820	 0.1420
6	 0.8620	 0.0790
8	 1.0000	 0.0490
9	 1.0000	 0.0490
A	 0.9860	 0.1380
A1	 0.9930	 0.0330
A2	 0.0450	 -0.0080
B	 0.9980	 0.1920
B1	 0.9840	 0.0470
B2	 0.9610	 0.0480
C	 0.9880	 0.1780
D	 0.9890	 0.1770
E	 1.0000	 0.1730
F	 1.0000	 0.1450
G	 0.9940	 0.1840
H	 0.9840	 0.1650
I	 0.9980	 0.1470
J	 0.9980	 0.1930
K	 0.9990	 0.1940
L	 0.9940	 0.1900
M	 0.9920	 0.1900
N	 1.0000	 0.1590
NA	 0.8890	 0.1530
NG	 0.9710	 0.0880
O	 1.0000	 0.1460
P	 1.0000	 0.2020
Q	 0.9630	 0.1470
R	 1.0000	 0.1630
S	 0.9990	 0.1260



Continued on next page...

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Chain	Atom inclusion	Q-score
T	 0.9960	 0.1680
U	 1.0000	 0.1560
V	 0.9970	 0.1850
W	 0.9980	 0.1540
W0	 0.7820	 0.0280
X	 0.9920	 0.0970
Y	 0.9950	 0.1700
Z	 0.9880	 0.1450
b	 0.9960	 0.2200
c	 0.9990	 0.1880
d	 0.9980	 0.1950
e	 0.9960	 0.1700
f	 0.9850	 0.1790
g	 1.0000	 0.1830
i	 0.9630	 0.0930
j	 0.9990	 0.1910
k	 0.9890	 0.2170
l	 1.0000	 0.1900
m	 0.9950	 0.1980
n	 1.0000	 0.1810
o	 1.0000	 0.1660
p	 0.9880	 0.2090
q	 0.9990	 0.1670
r	 0.9990	 0.1880
s	 0.9960	 0.1940
t	 0.9960	 0.1940
u	 0.9970	 0.1720
v	 1.0000	 0.1760
w	 1.0000	 0.1700
x	 1.0000	 0.1920
y	 1.0000	 0.1750
z	 1.0000	 0.1970