



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 07:05 AM UTC

PDB ID : 6WD3 / pdb_00006wd3
EMDB ID : EMD-21622
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure II-B1)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

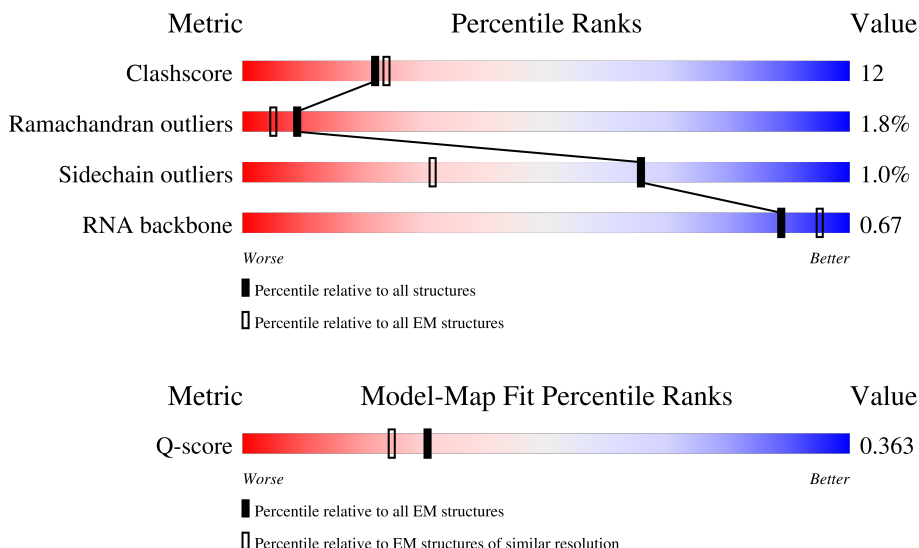
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 Å.

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



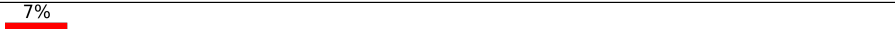
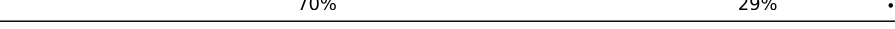
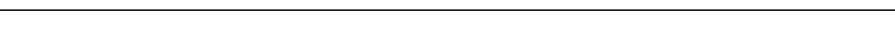
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	b	271	
2	c	209	
3	d	201	

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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
27	C	50	
28	D	46	

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Mol	Chain	Length	Quality of chain
29	E	64	
30	F	38	
31	G	225	
32	H	206	
33	I	205	
34	J	157	
35	K	100	
36	L	151	
37	M	129	
38	N	127	
39	O	98	
40	P	116	
41	Q	123	
42	R	114	
43	S	100	
44	T	88	
45	U	82	
46	V	80	
47	W	65	
48	X	79	
49	Y	85	
50	Z	65	
51	a	223	
52	3	1539	
53	1	2903	

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Mol	Chain	Length	Quality of chain
54	2	120	46%48%7%
55	5	77	65%30%5%
55	6	77	61%35%. 6%
56	4	18	50%44%6%
57	7	76	46%43%11%
58	8	400	54%40%. .

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 153211 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 L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

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

- Molecule 3 is a protein called 50S ribosomal protein L4.

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

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

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

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	j	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	m	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	o	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	p	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	r	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	s	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	t	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	u	102	Total	C	N	O	0	0
			780	492	146	142		

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	v	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	x	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L32.

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

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	C	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 28 is a protein called 50S ribosomal protein L34.

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

- Molecule 29 is a protein called 50S ribosomal protein L35.

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

- Molecule 30 is a protein called 50S ribosomal protein L36.

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

- Molecule 31 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	225	Total	C	N	O	S	0	0
			1757	1111	315	323	8		

- Molecule 32 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 33 is a protein called 30S ribosomal protein S4.

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

- Molecule 34 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 35 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 36 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 37 is a protein called 30S ribosomal protein S8.

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

- Molecule 38 is a protein called 30S ribosomal protein S9.

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

- Molecule 39 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 40 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 41 is a protein called 30S ribosomal protein S12.

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

- Molecule 42 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 43 is a protein called 30S ribosomal protein S14.

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

- Molecule 44 is a protein called 30S ribosomal protein S15.

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

- Molecule 45 is a protein called 30S ribosomal protein S16.

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

- Molecule 46 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 47 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 48 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 49 is a protein called 30S ribosomal protein S20.

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

- Molecule 50 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 51 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	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	variant	GB 1036415628

- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	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	-	insertion	GB 1370526515

- Molecule 55 is a RNA chain called tRNA^fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
55	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	18	Total	C	N	O	P	0	0
			388	175	76	120	17		

- Molecule 57 is a RNA chain called tRNA^{Phe}.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 58 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	8	383	Total	C	N	O	S	0	0
			2961	1876	507	565	13		

There are 7 discrepancies between the modelled and reference sequences:

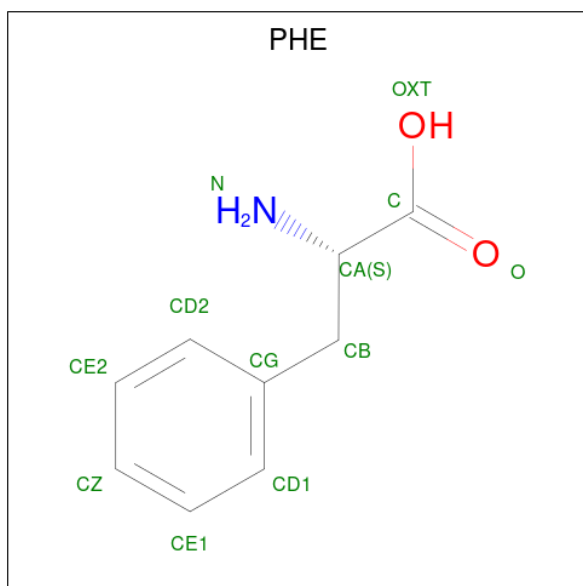
Chain	Residue	Modelled	Actual	Comment	Reference
8	395	SER	-	expression tag	UNP E2QFJ4
8	396	HIS	-	expression tag	UNP E2QFJ4
8	397	HIS	-	expression tag	UNP E2QFJ4
8	398	HIS	-	expression tag	UNP E2QFJ4
8	399	HIS	-	expression tag	UNP E2QFJ4
8	400	HIS	-	expression tag	UNP E2QFJ4
8	401	HIS	-	expression tag	UNP E2QFJ4

- Molecule 59 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).



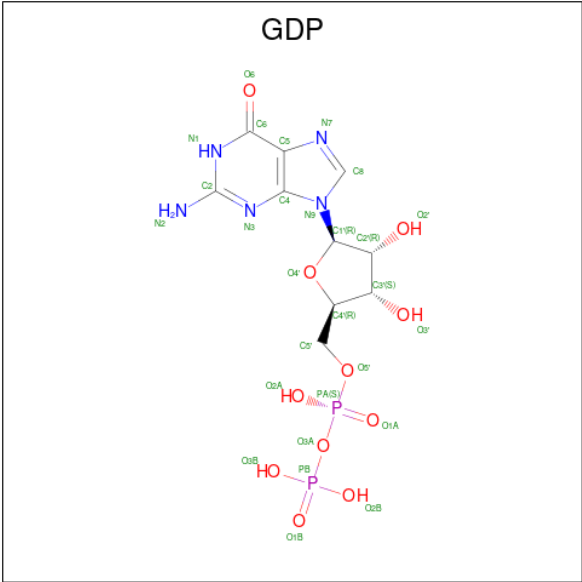
Mol	Chain	Residues	Atoms					AltConf
59	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 60 is PHENYLALANINE (CCD ID: PHE) (formula: $C_9H_{11}NO_2$).



Mol	Chain	Residues	Atoms					AltConf
60	7	1	Total	C	N	O		0
			11	9	1	1		

- Molecule 61 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
61	8	1	Total	C	N	O	P	0
			28	10	5	11	2	

3 Residue-property plots

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.

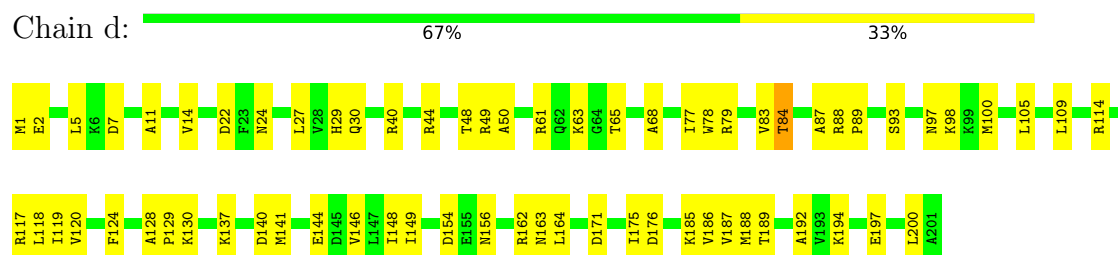
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

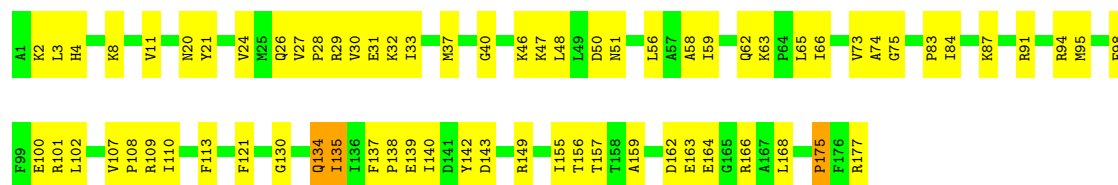


- Molecule 3: 50S ribosomal protein L4

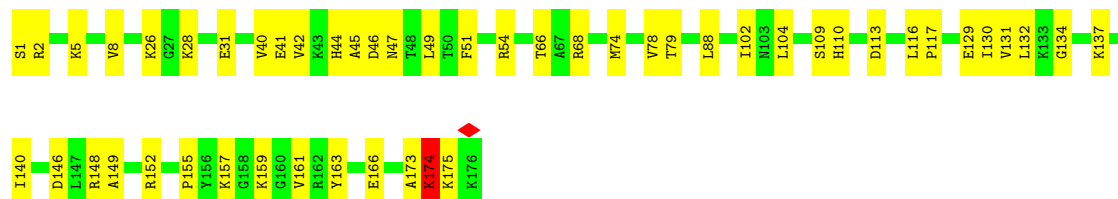


- Molecule 4: 50S ribosomal protein L5

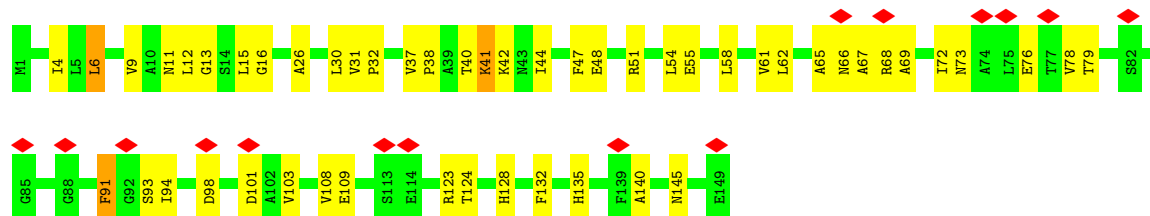




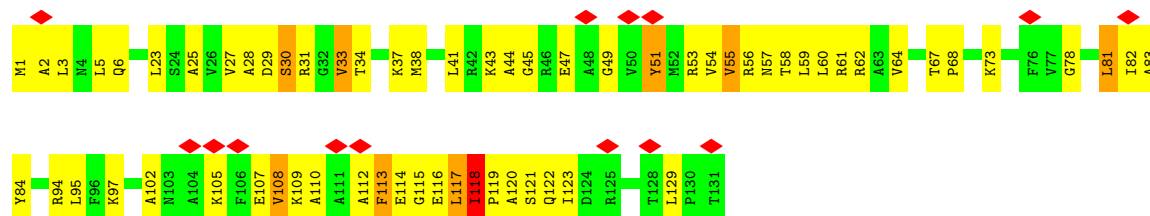
• Molecule 5: 50S ribosomal protein L6



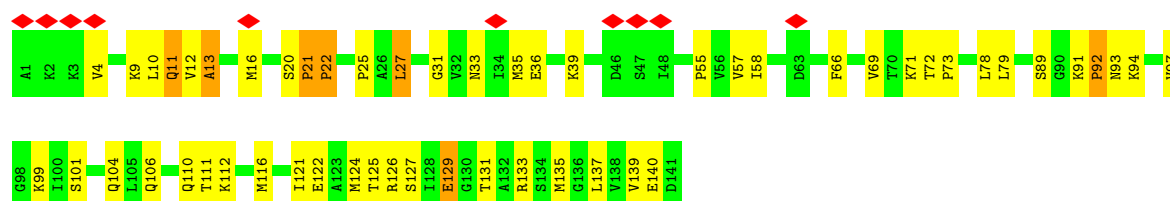
• Molecule 6: 50S ribosomal protein L9



• Molecule 7: 50S ribosomal protein L10

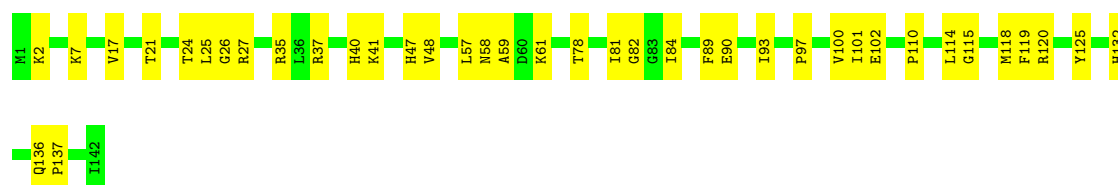


• Molecule 8: 50S ribosomal protein L11



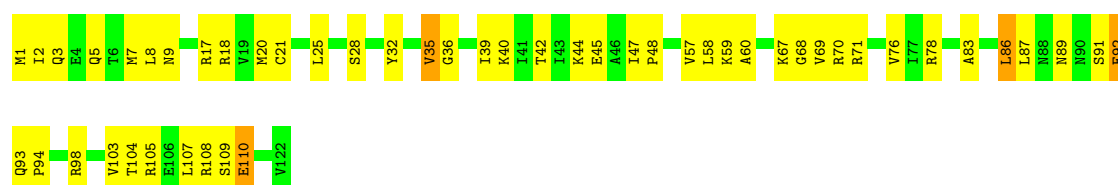
- Molecule 9: 50S ribosomal protein L13

Chain j:  73% 27%



- Molecule 10: 50S ribosomal protein L14

Chain k:  59% 38% .



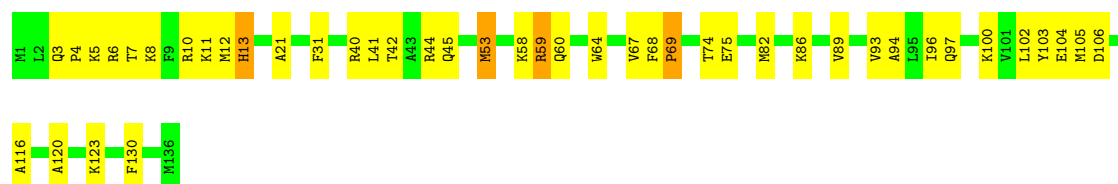
- Molecule 11: 50S ribosomal protein L15

Chain l:  63% 31% 6%



- Molecule 12: 50S ribosomal protein L16

Chain m:  68% 29% .



- Molecule 13: 50S ribosomal protein L17

Chain n:  69% 30% .



- Molecule 14: 50S ribosomal protein L18

Chain o:  71% 27%



- Molecule 15: 50S ribosomal protein L19

Chain p:  70% 29%



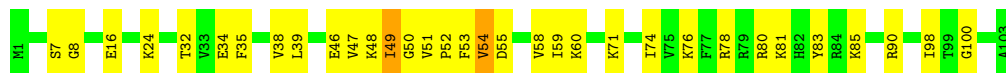
- Molecule 16: 50S ribosomal protein L20

Chain q:  83% 16%



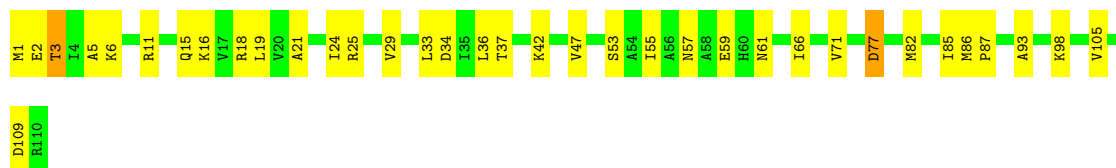
- Molecule 17: 50S ribosomal protein L21

Chain r:  68% 30%



- Molecule 18: 50S ribosomal protein L22

Chain s:  67% 31%

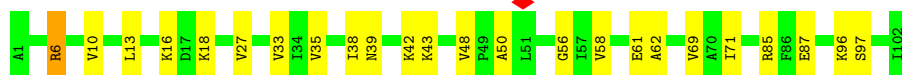
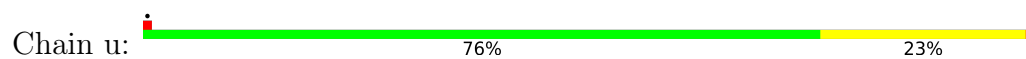


- Molecule 19: 50S ribosomal protein L23

Chain t:  60% 39%



- Molecule 20: 50S ribosomal protein L24



- Molecule 21: 50S ribosomal protein L25



- Molecule 22: 50S ribosomal protein L27



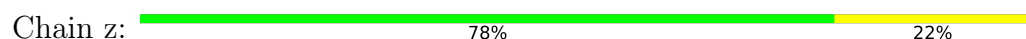
- Molecule 23: 50S ribosomal protein L28



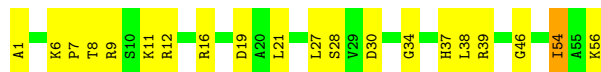
- Molecule 24: 50S ribosomal protein L29



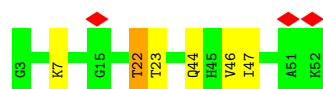
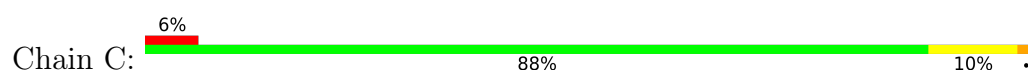
- Molecule 25: 50S ribosomal protein L30



- Molecule 26: 50S ribosomal protein L32



- Molecule 27: 50S ribosomal protein L33



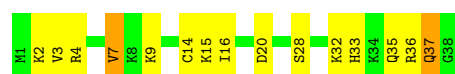
- Molecule 28: 50S ribosomal protein L34



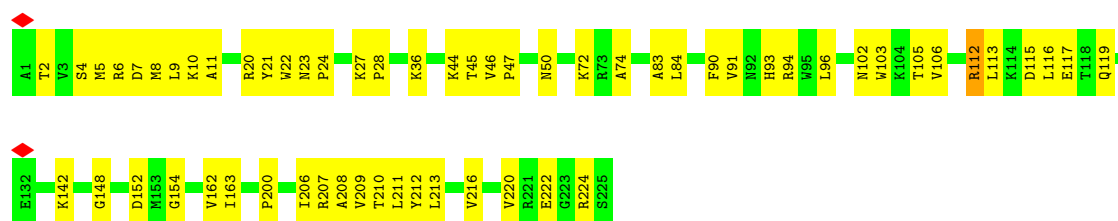
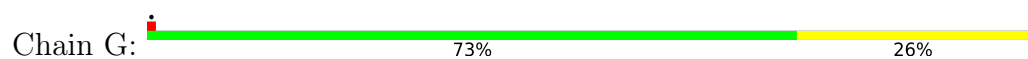
- Molecule 29: 50S ribosomal protein L35



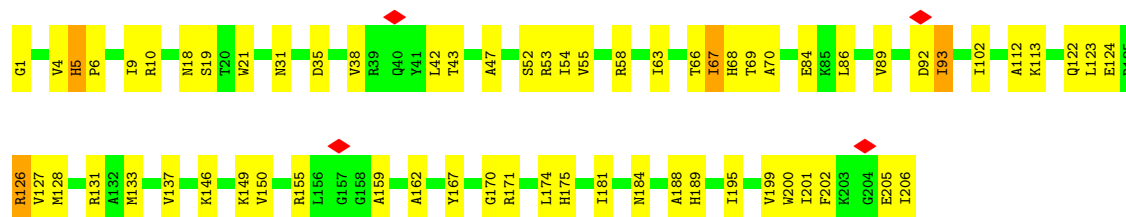
- Molecule 30: 50S ribosomal protein L36



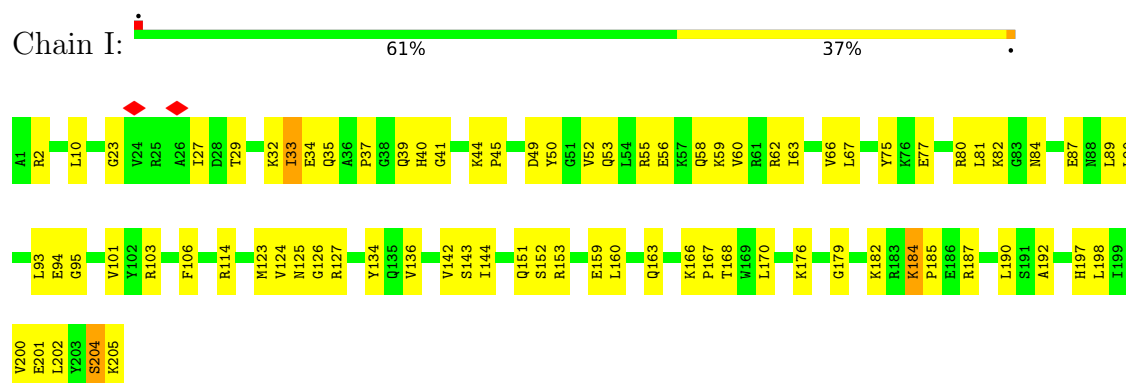
- Molecule 31: 30S ribosomal protein S2



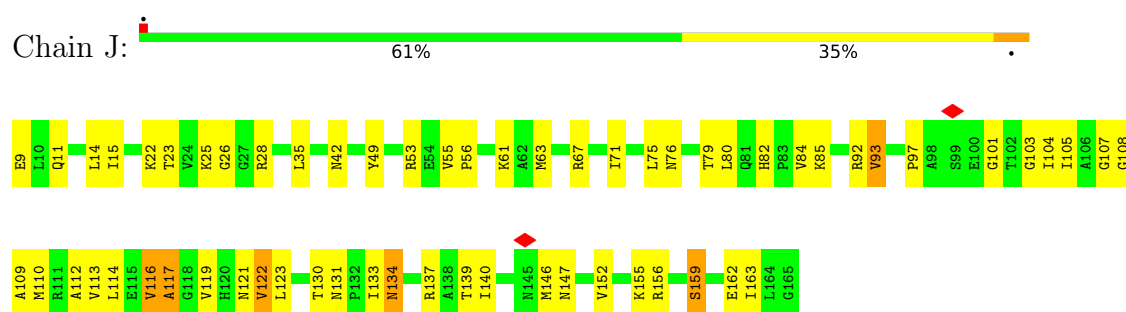
- Molecule 32: 30S ribosomal protein S3



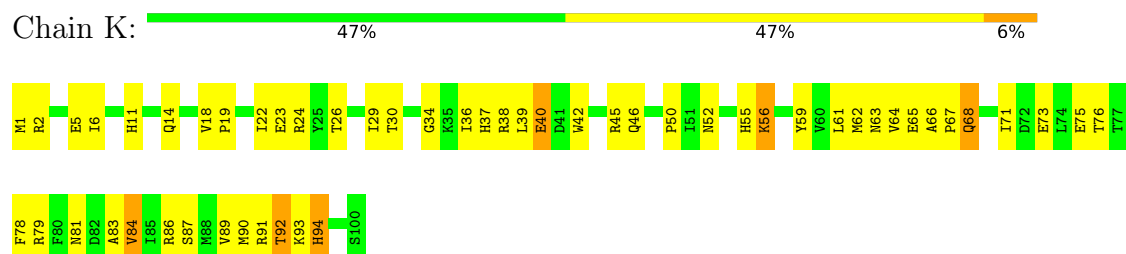
- Molecule 33: 30S ribosomal protein S4



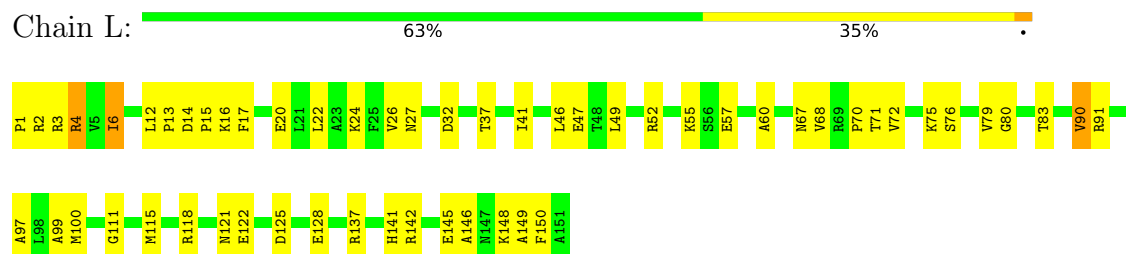
- Molecule 34: 30S ribosomal protein S5



- Molecule 35: 30S ribosomal protein S6

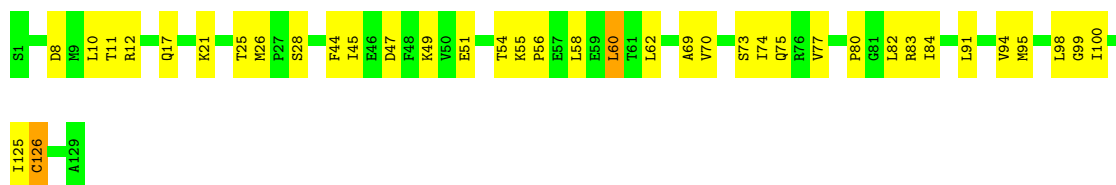


- Molecule 36: 30S ribosomal protein S7

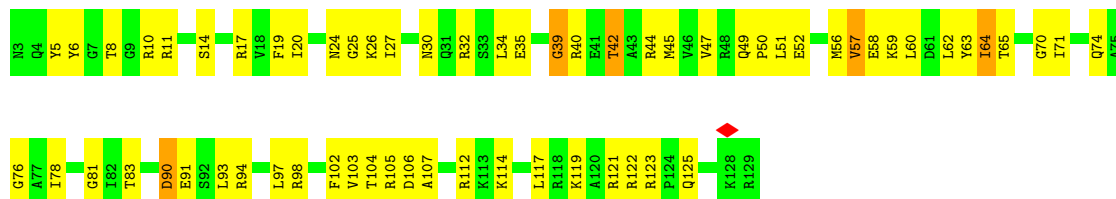


- Molecule 37: 30S ribosomal protein S8

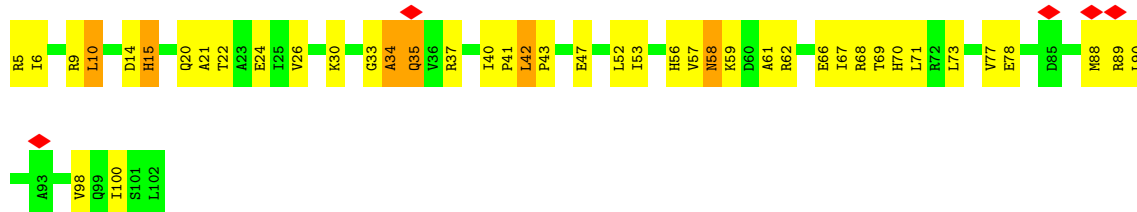




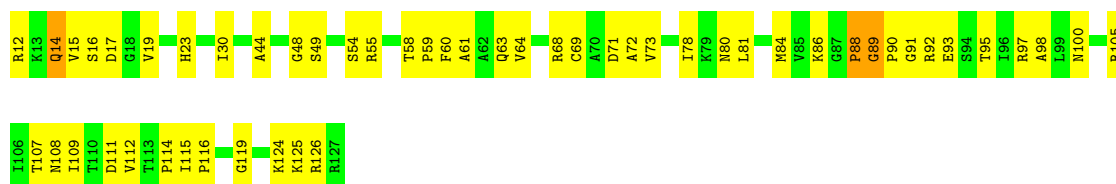
- Molecule 38: 30S ribosomal protein S9



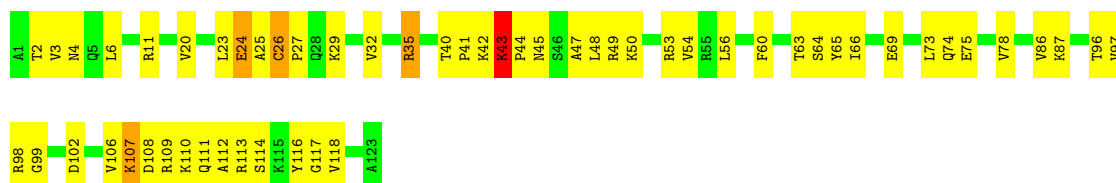
- Molecule 39: 30S ribosomal protein S10



- Molecule 40: 30S ribosomal protein S11

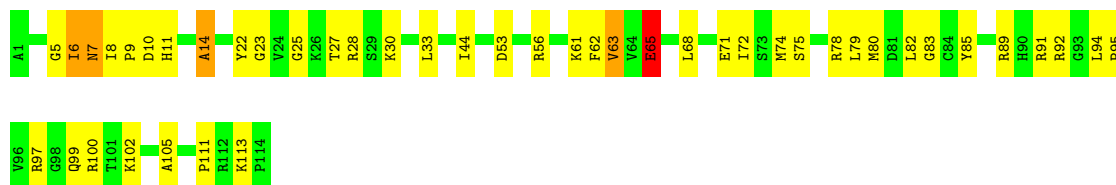


- Molecule 41: 30S ribosomal protein S12



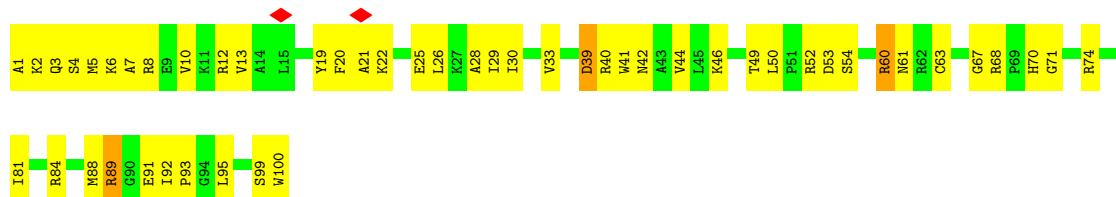
- Molecule 42: 30S ribosomal protein S13

Chain R:  61% 35%



- Molecule 43: 30S ribosomal protein S14

Chain S:  49% 48%



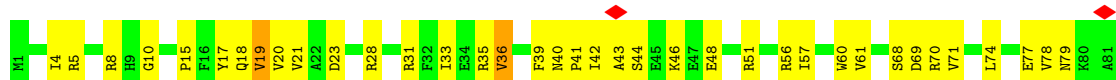
- Molecule 44: 30S ribosomal protein S15

Chain T:  78% 20%

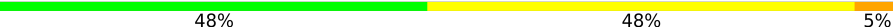


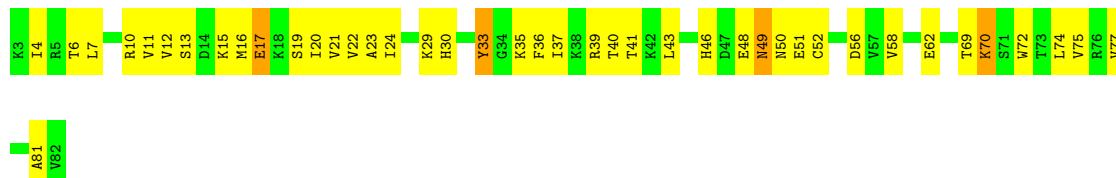
- Molecule 45: 30S ribosomal protein S16

Chain U:  55% 43%



- Molecule 46: 30S ribosomal protein S17

Chain V:  48% 48% 5%



- Molecule 47: 30S ribosomal protein S18

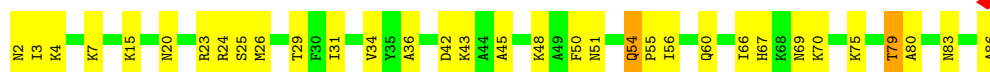
Chain W:  71% 28%



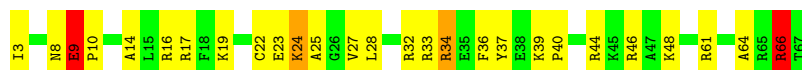
- Molecule 48: 30S ribosomal protein S19



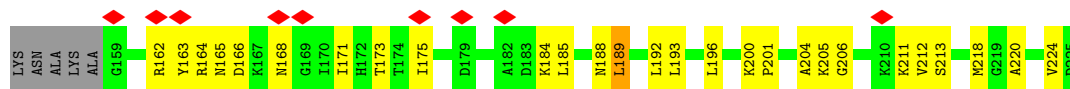
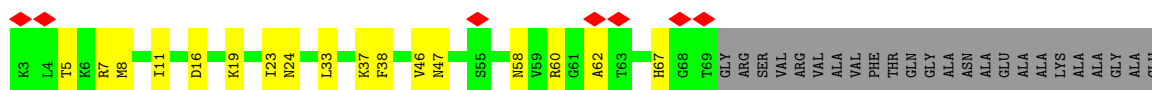
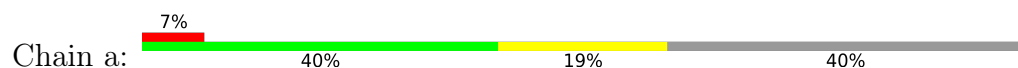
- Molecule 49: 30S ribosomal protein S20



- Molecule 50: 30S ribosomal protein S21

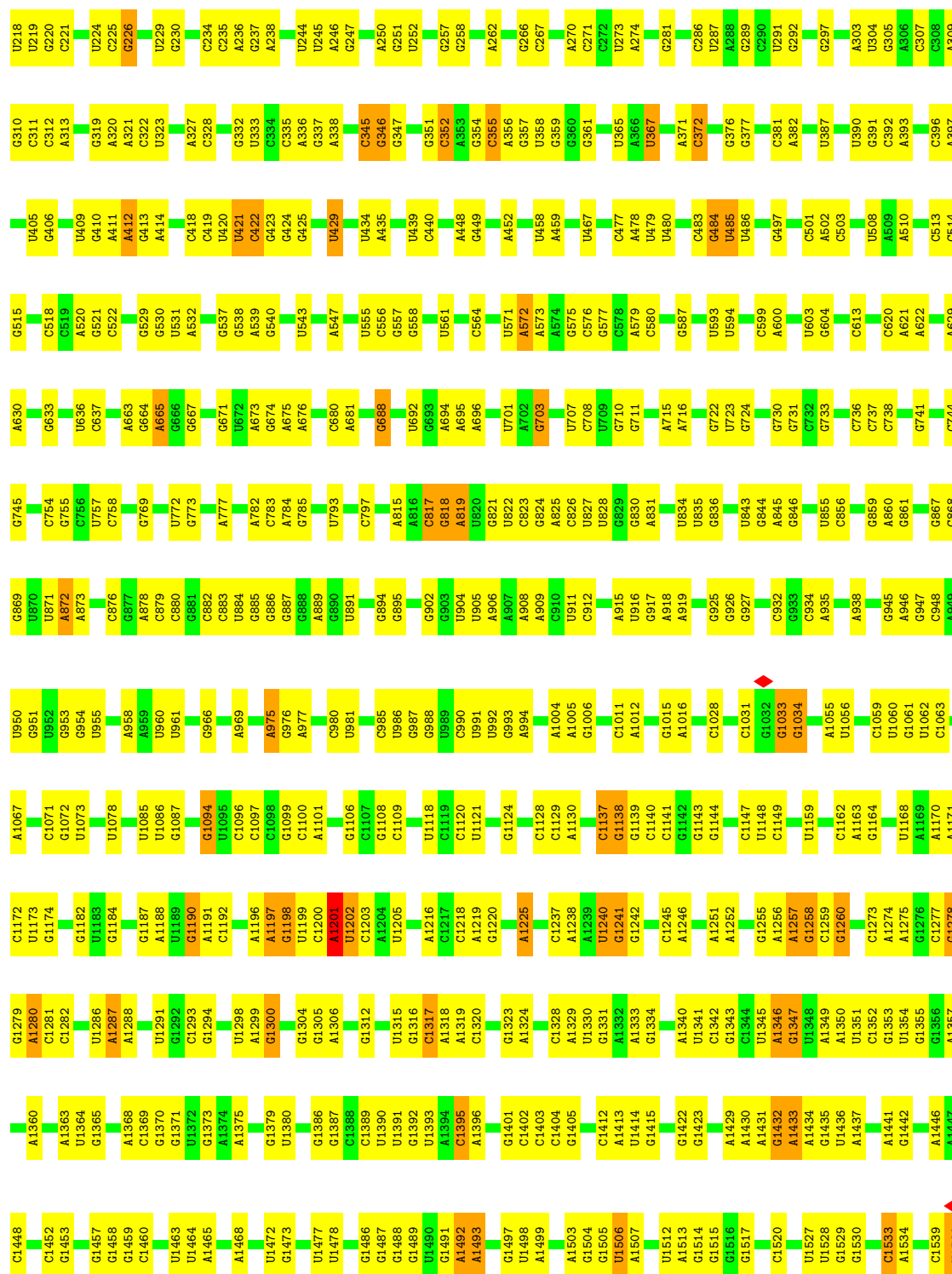


- Molecule 51: 50S ribosomal protein L1



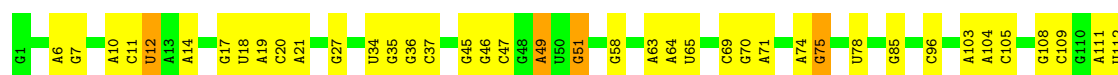
- Molecule 52: 16S ribosomal RNA





• Molecule 53: 23S ribosomal RNA

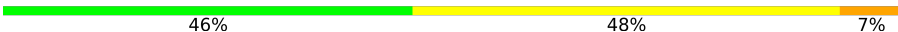
Chain 1:

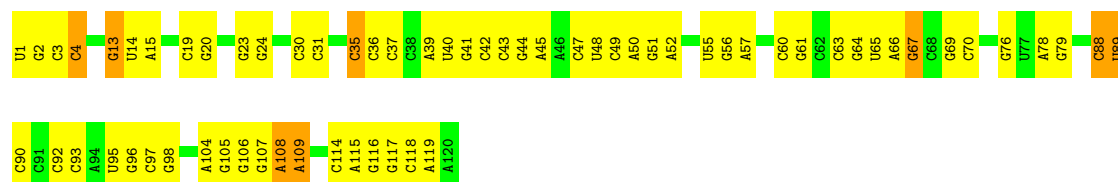




U2833	G2641	G2553	G2458	G2371	A2298	C2208	A2117	G2040	U1956	A1853	U1758	A1665	G1567
G2834	G2642	U2554	C2462	A2376	U2299	G2209	U2118	U2041	C1957	A1854	A1759	G1666	G1568
U2835	G2643	G2557	C2463	A2377	U2302	U2210	G2120	C2043	G1958	U1855	C1760	A1667	A1569
A2837	C2646	C2558	C2466	A2378	G2303	A2211	G2121	G2043	G1959	G1857	C1764	A1668	A1570
C2841	U2647	U2562	C2467	A2381	G2304	U2213	U2122	G2049	U1963	A1858	U1773	G1674	A1571
G2842	C2468	U2563	A2468	G2382	U2305	U2220	G2127	G2048	G1964	A1859	A1774	C1675	G1572
G2843	C2469	A2564	A2469	G2383	A2309	G2221	G2128	G2049	G1965	G1860	C1774	A1676	G1573
G2844	U2652	A2565	G2470	C2385	U2312	G2222	C2129	A2052	C1966	G1861	U1775	C1685	C1574
U2845	A2654	A2566	A2471	U2386	C2313	G2223	U2130	A2053	U1967	A1871	G1776	C1686	U1576
G2846	G2655	G2567	G2472	G2389	G2314	A2225	U2132	G2055	A1970	G1872	U1779	U1578	U1578
U2849	U2656	C2572	C2475	U2390	G2315	G2226	G2133	G2056	G1971	C1874	U1782	G1689	G1581
A2850	G2660	A2577	U2476	A2391	A2317	U2233	A2134	A2060	A1978	A1873	U1783	A1690	U1584
C2853	G2661	G2578	U2477	A2392	G2318	G2234	U2139	A2061	U1979	G1874	U1784	A1693	C1585
G2854	A2662	C2579	A2478	U2393	G2319	U2235	G2141	A2062	G1980	A1885	A1785	G1697	C1585
C2855	G2663	U2580	C2483	C2394	G2323	G2238	A2142	C2063	G1983	G1888	A1786	A1698	U1594
A2856	A2665	G2581	G2484	U2398	U2324	U2240	G2147	C2065	A1987	A1889	G1792	G1699	C1595
G2859	A2666	U2582	C2485	G2399	G2325	A2241	C2155	C2066	G1988	A1900	C1793	A1701	A1596
A2860	G2667	G2583	U2489	U2402	C2326	G2242	G2156	G2067	G1989	A1899	C1794	G1702	A1597
G2862	C2671	U2584	G2490	A2406	A2327	U2243	G2157	U2068	G1990	A1900	C1795	G1703	A1598
C2863	U2672	U2585	C2498	A2407	A2328	U2244	G2157	A2070	G1991	A1901	C1796	G1704	G1601
G2864	G2679	A2589	C2499	A2415	G2330	U2245	G2157	A2071	U1992	C1905	U1798	A1705	U1602
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C2862	A2682	G2591	U2503	C2416	U2334	U2249	A2163	C2072	C1996	G1907	C1800	G1709	C1605
G2863	U2684	U2504	G2505	C2417	U2344	G2250	C2164	U2074	C1997	C1908	U1801	U1710	C1606
C2864	G2685	G2602	G2508	U2419	A2340	U2257	A2171	C2078	A1998	C1909	G1807	G1715	C1607
U2865	U2686	U2603	G2508	C2420	G2341	C2258	U2172	U2079	C1999	G1910	A1808	U1716	A1608
G2867	U2689	C2605	C2512	U2423	C2342	U2259	A2173	A2080	U1988	U1911	A1809	A1717	C1611
A2868	U2690	G2606	U2514	A2425	U2343	U2262	G2175	G2083	C2008	A1912	A1810	G1718	C1612
C2872	U2691	U2609	C2515	A2426	G2344	U2267	C2176	C2084	A2009	A1913	G1811	U1719	G1613
A2873	G2692	C2610	C2515	A2427	A2345	A2268	C2177	U2086	U2011	A1918	U1812	G1721	G1614
G2874	U2693	U2613	A2518	C2428	C2347	A2267	U2180	U2087	G2012	A1919	C1816	U1725	C1615
C2875	U2694	A2614	U2519	G2429	U2348	A2268	U2181	A2088	A2019	C1920	G1817	C1726	A1616
G2876	U2695	C2618	C2520	A2430	G2349	G2277	U2182	U2088	U2022	G1929	U1818	C1727	U1629
U2879	C2704	U2619	C2521	U2431	C2350	A2278	A2183	A2088	C2023	G1930	A1819	C1728	U1630
C2880	A2705	C2619	G2529	A2432	G2351	A2281	A2184	U2093	G2024	U1931	U1821	U1729	U1636
U2881	U2706	C2620	A2530	A2435	C2354	A2282	U2185	C2096	C2025	A1932	C1822	C1730	A1637
G2882	U2707	U2623	U2533	U2441	A2358	C2283	G2190	A2101	C2026	G1933	G1823	U1736	C1638
C2883	G2708	G2624	A2534	C2442	C2359	A2284	A2191	G2102	G2026	C1934	U1824	G1737	C1639
U2884	U2709	U2625	U2537	C2443	G2360	C2285	U2192	C2103	U2028	G1935	G1826	G1738	G1645
A2889	C2710	C2626	U2537	G2444	G2361	G2286	G2193	C2104	G2029	A1936	U1827	C1738	C1646
U2890	A2711	U2628	C2538	G2447	C2362	A2287	U2194	U2105	A2030	A1937	G1828	U1647	U1648
C2891	G2714	U2629	U2539	A2448	G2363	A2288	C2196	G2107	A2031	U1943	U1829	A1744	U1648
U2897	U2723	G2632	G2545	A2449	C2364	U2291	U2197	U2110	G2032	U1944	G1830	A1652	A1652
U2898	C2724	G2633	U2546	U2450	G2365	U2292	A2198	G2111	C2033	G1832	C1833	G1753	G1653
A2899	A2725	C2636	A2547	A2451	G2367	G2294	A2199	G2112	U2034	C1947	U1834	A1754	U1657
U2903	U2726	U2637	U2548	C2452	G2368	C2295	U2203	A2114	C2037	G1948	U1837	C1658	C1658
U2903	A2727	G2638	U2552	U2457	A2369	U2296	G2204	U2113	G2038	G1954	C1837	A1757	A1664

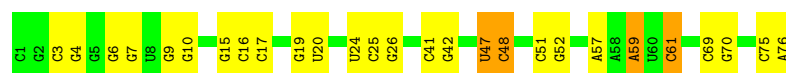
- Molecule 54: 5S ribosomal RNA

Chain 2: 



- Molecule 55: tRNA^{fMet}

Chain 5: 



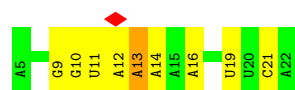
- Molecule 55: tRNA^{fMet}

Chain 6: 

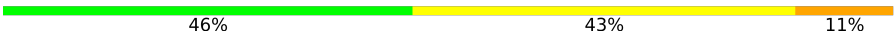


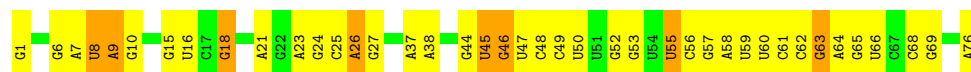
- Molecule 56: mRNA

Chain 4: 



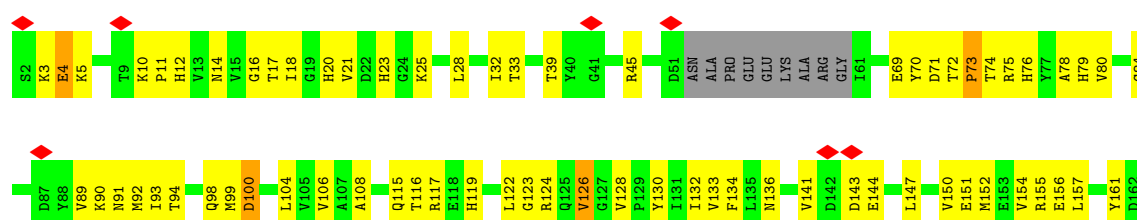
- Molecule 57: tRNA^{Phe}

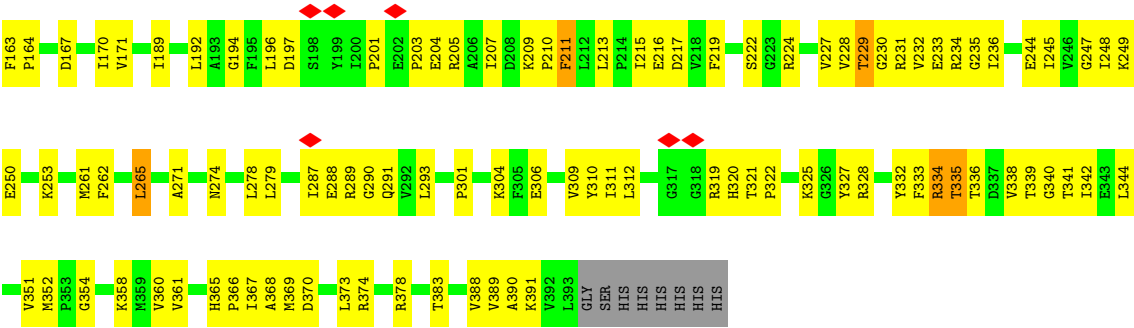
Chain 7: 



- Molecule 58: Elongation factor Tu

Chain 8: 





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	7401	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	18.877	Depositor
Minimum map value	-10.681	Depositor
Average map value	0.115	Depositor
Map value standard deviation	0.882	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: FME, 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	b	0.30	0/2122	0.98	12/2852 (0.4%)
2	c	0.29	0/1586	0.89	2/2134 (0.1%)
3	d	0.29	0/1571	0.85	3/2113 (0.1%)
4	e	0.30	0/1435	0.88	3/1926 (0.2%)
5	f	0.30	0/1343	0.93	5/1816 (0.3%)
6	g	0.31	0/1122	0.90	2/1515 (0.1%)
7	h	0.34	0/1002	1.05	7/1350 (0.5%)
8	i	0.36	0/1046	0.97	6/1410 (0.4%)
9	j	0.30	0/1152	0.85	1/1551 (0.1%)
10	k	0.29	0/948	0.97	3/1268 (0.2%)
11	l	0.30	0/1054	1.05	10/1403 (0.7%)
12	m	0.29	0/1093	0.87	3/1460 (0.2%)
13	n	0.29	0/974	0.95	5/1301 (0.4%)
14	o	0.29	0/902	0.87	2/1209 (0.2%)
15	p	0.29	0/929	0.84	4/1242 (0.3%)
16	q	0.28	0/960	0.96	4/1278 (0.3%)
17	r	0.29	0/829	0.88	3/1107 (0.3%)
18	s	0.29	0/864	0.95	1/1156 (0.1%)
19	t	0.28	0/745	0.83	0/994
20	u	0.29	0/788	0.88	1/1051 (0.1%)
21	v	0.28	0/766	0.83	0/1025
22	w	0.27	0/582	0.86	1/769 (0.1%)
23	x	0.28	0/635	0.85	1/848 (0.1%)
24	y	0.29	0/510	0.90	3/677 (0.4%)
25	z	0.30	0/453	0.91	1/605 (0.2%)
26	B	0.29	0/450	0.82	1/599 (0.2%)
27	C	0.32	0/417	0.80	0/554
28	D	0.32	0/380	0.89	1/498 (0.2%)
29	E	0.30	0/513	1.00	3/676 (0.4%)
30	F	0.33	0/303	0.99	2/397 (0.5%)
31	G	0.29	0/1788	0.90	5/2408 (0.2%)
32	H	0.32	0/1652	0.93	5/2225 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.30	0/1665	0.94	8/2227 (0.4%)
34	J	0.34	0/1170	0.99	6/1573 (0.4%)
35	K	0.31	0/836	1.00	7/1128 (0.6%)
36	L	0.29	0/1196	0.96	5/1602 (0.3%)
37	M	0.29	0/989	0.97	5/1326 (0.4%)
38	N	0.29	0/1034	0.89	2/1375 (0.1%)
39	O	0.32	0/797	0.90	2/1077 (0.2%)
40	P	0.33	0/886	0.92	1/1195 (0.1%)
41	Q	0.32	0/969	1.03	9/1300 (0.7%)
42	R	0.32	0/893	0.93	2/1193 (0.2%)
43	S	0.30	0/817	0.92	5/1088 (0.5%)
44	T	0.28	0/722	0.89	5/964 (0.5%)
45	U	0.30	0/659	0.87	2/884 (0.2%)
46	V	0.29	0/658	0.98	3/881 (0.3%)
47	W	0.31	0/545	0.93	2/731 (0.3%)
48	X	0.31	0/653	0.93	1/877 (0.1%)
49	Y	0.29	0/671	0.97	4/888 (0.5%)
50	Z	0.33	0/551	0.97	3/728 (0.4%)
51	a	0.32	0/1034	0.82	2/1387 (0.1%)
52	3	0.41	0/36963	0.47	2/57662 (0.0%)
53	1	0.40	0/69796	0.48	3/108888 (0.0%)
54	2	0.41	0/2872	0.47	0/4479
55	5	0.41	0/1832	0.46	0/2855
55	6	0.42	0/1832	0.48	0/2855
56	4	0.41	0/436	0.47	0/679
57	7	0.40	0/1809	0.48	0/2819
58	8	0.32	0/3015	0.90	8/4079 (0.2%)
All	All	0.38	0/166214	0.63	187/248157 (0.1%)

There are no bond length outliers.

All (187) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	V	75	VAL	N-CA-C	-10.67	103.19	111.62
40	P	73	VAL	N-CA-C	-10.56	103.06	113.20
34	J	117	ALA	N-CA-C	-10.27	100.16	112.89
17	r	50	GLY	N-CA-C	-9.67	100.79	112.49
1	b	87	SER	N-CA-C	-9.62	102.34	114.56
41	Q	20	VAL	N-CA-C	9.50	117.55	108.15
43	S	49	THR	N-CA-C	-9.45	100.86	111.82
7	h	117	LEU	N-CA-C	8.74	122.78	109.23
11	l	95	LEU	N-CA-C	-8.60	102.22	112.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	Y	7	LYS	N-CA-C	-7.64	103.69	113.16
1	b	120	ASP	N-CA-C	-7.62	104.13	113.50
31	G	222	GLU	N-CA-C	-7.58	103.02	111.82
16	q	49	ARG	N-CA-C	-7.53	104.12	113.38
36	L	4	ARG	N-CA-C	7.24	120.49	110.35
13	n	67	PHE	N-CA-C	-7.13	105.11	113.88
13	n	116	VAL	N-CA-C	7.07	116.81	106.55
8	i	127	SER	N-CA-C	-7.03	103.37	112.23
48	X	66	VAL	N-CA-C	-6.98	106.26	112.12
11	l	113	ALA	N-CA-C	-6.97	104.92	113.50
32	H	124	GLU	N-CA-C	-6.95	102.03	112.04
11	l	47	ARG	N-CA-C	6.85	118.69	110.19
35	K	39	LEU	N-CA-C	-6.79	102.61	111.71
33	I	204	SER	N-CA-C	-6.77	103.97	111.82
34	J	101	GLY	N-CA-C	-6.75	106.48	115.32
36	L	47	GLU	N-CA-C	-6.71	104.04	111.82
32	H	5	HIS	CA-C-N	6.70	126.95	119.32
32	H	5	HIS	C-N-CA	6.70	126.95	119.32
24	y	20	ASN	N-CA-C	-6.68	105.26	113.41
58	8	100	ASP	N-CA-C	-6.66	103.62	113.61
33	I	166	LYS	CA-C-N	6.62	128.11	119.84
33	I	166	LYS	C-N-CA	6.62	128.11	119.84
1	b	207	ALA	N-CA-C	-6.60	103.57	111.69
4	e	48	LEU	N-CA-C	-6.60	104.17	111.36
11	l	23	ILE	N-CA-C	-6.59	106.56	111.90
25	z	31	ILE	N-CA-C	-6.56	101.10	109.30
8	i	27	LEU	N-CA-C	-6.55	105.29	113.28
32	H	112	ALA	N-CA-C	6.51	118.93	111.11
44	T	27	GLN	N-CA-C	6.47	118.00	111.07
1	b	19	VAL	N-CA-C	6.46	116.54	107.37
13	n	71	ARG	N-CA-C	6.45	120.31	111.54
2	c	2	ILE	N-CA-C	6.40	117.13	108.17
37	M	55	LYS	CA-C-N	6.39	127.83	119.84
37	M	55	LYS	C-N-CA	6.39	127.83	119.84
1	b	12	ARG	N-CA-C	-6.38	105.43	113.72
8	i	111	THR	N-CA-C	-6.37	104.42	111.36
41	Q	114	SER	N-CA-C	-6.35	104.35	111.28
50	Z	17	ARG	N-CA-C	-6.32	105.53	113.18
7	h	44	ALA	N-CA-C	-6.31	105.06	112.89
41	Q	43	LYS	N-CA-C	6.31	123.75	109.81
34	J	22	LYS	N-CA-C	-6.29	106.15	113.88
51	a	23	ILE	N-CA-C	6.23	116.34	110.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	Q	97	VAL	N-CA-C	6.19	117.00	108.84
18	s	24	ILE	N-CA-C	6.18	116.27	106.32
13	n	68	ALA	N-CA-C	-6.15	105.03	112.54
20	u	96	LYS	N-CA-C	-6.14	100.56	110.32
33	I	33	ILE	N-CA-C	6.11	116.71	110.05
41	Q	4	ASN	N-CA-C	-6.08	104.73	111.36
12	m	60	GLN	N-CA-C	6.08	118.17	110.33
6	g	67	ALA	N-CA-C	-6.06	104.60	112.23
58	8	265	LEU	N-CA-C	6.06	119.01	110.23
11	l	137	ALA	N-CA-C	-5.99	104.87	111.82
10	k	92	GLU	N-CA-C	-5.95	104.74	112.23
29	E	61	LEU	CA-C-N	5.95	127.27	119.84
29	E	61	LEU	C-N-CA	5.95	127.27	119.84
53	1	1020	A	C2'-C3'-O3'	5.94	118.41	109.50
12	m	53	MET	N-CA-C	-5.94	107.85	114.62
49	Y	15	LYS	N-CA-C	-5.93	104.94	111.82
1	b	225	ASN	CA-C-N	5.91	127.23	119.84
1	b	225	ASN	C-N-CA	5.91	127.23	119.84
16	q	40	LYS	N-CA-C	-5.91	106.07	113.28
37	M	125	ILE	N-CA-C	5.91	115.97	110.42
1	b	176	ARG	N-CA-C	5.88	118.45	111.33
16	q	24	TYR	N-CA-C	5.88	119.40	109.76
31	G	112	ARG	N-CA-C	-5.88	104.83	112.23
52	3	1190	G	C2'-C3'-O3'	5.87	118.30	109.50
35	K	52	ASN	N-CA-C	-5.86	104.74	112.24
46	V	33	TYR	N-CA-C	5.85	118.13	111.11
43	S	50	LEU	N-CA-C	-5.83	102.70	109.93
15	p	92	ARG	N-CA-C	5.77	117.92	110.65
52	3	1201	A	C2'-C3'-O3'	5.77	118.15	109.50
31	G	22	TRP	N-CA-C	5.75	118.17	110.35
1	b	132	ARG	N-CA-C	-5.75	104.83	112.94
38	N	64	ILE	N-CA-C	5.73	116.83	108.53
30	F	28	SER	N-CA-C	5.72	117.19	111.07
10	k	32	TYR	N-CA-C	5.71	118.54	110.14
43	S	39	ASP	N-CA-C	-5.71	105.20	111.82
6	g	91	PHE	N-CA-C	-5.70	105.21	111.82
11	l	115	GLU	N-CA-C	5.70	117.58	110.91
35	K	24	ARG	N-CA-C	-5.70	104.45	111.40
42	R	83	GLY	N-CA-C	-5.70	107.32	115.64
8	i	129	GLU	N-CA-C	-5.68	105.23	111.82
35	K	30	THR	N-CA-C	-5.68	105.61	112.54
12	m	13	HIS	N-CA-C	5.67	117.65	110.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	S	60	ARG	N-CA-C	5.67	119.38	112.23
50	Z	66	ARG	N-CA-C	5.65	122.83	110.80
7	h	30	SER	N-CA-C	-5.65	105.12	112.23
16	q	38	VAL	N-CA-C	5.63	116.37	110.62
44	T	49	HIS	N-CA-C	5.63	118.35	111.82
32	H	67	ILE	N-CA-C	5.62	115.94	107.80
5	f	174	LYS	N-CA-C	5.61	122.76	110.80
47	W	69	TYR	N-CA-C	-5.59	105.27	111.36
4	e	134	GLN	N-CA-C	-5.59	106.46	113.28
41	Q	26	CYS	CA-C-N	5.56	125.66	119.32
41	Q	26	CYS	C-N-CA	5.56	125.66	119.32
47	W	66	LEU	N-CA-C	-5.55	106.64	113.41
13	n	119	SER	N-CA-C	-5.55	106.18	113.17
24	y	22	LEU	N-CA-C	-5.55	105.38	111.82
1	b	35	LYS	N-CA-C	5.53	117.71	109.25
33	I	184	LYS	CA-C-N	5.51	125.83	119.93
33	I	184	LYS	C-N-CA	5.51	125.83	119.93
34	J	134	ASN	N-CA-C	5.50	117.08	111.14
2	c	152	PRO	N-CA-C	-5.49	106.37	113.57
22	w	52	ASP	N-CA-C	-5.49	106.17	112.92
49	Y	79	THR	N-CA-C	-5.49	105.38	111.36
7	h	29	ASP	N-CA-C	5.47	117.83	109.62
26	B	54	ILE	N-CA-C	-5.47	108.17	113.53
44	T	53	ARG	N-CA-C	-5.46	105.41	111.36
58	8	144	GLU	N-CA-C	5.46	117.99	111.71
41	Q	108	ASP	N-CA-C	5.43	118.89	111.39
29	E	17	GLY	N-CA-C	5.43	119.06	112.49
7	h	51	TYR	N-CA-C	5.42	118.11	111.82
7	h	55	VAL	N-CA-C	5.42	116.40	109.30
1	b	30	ALA	N-CA-C	5.41	121.77	109.81
53	1	2287	A	N9-C1'-C2'	5.41	120.12	112.00
49	Y	36	ALA	N-CA-C	-5.40	105.55	111.82
35	K	68	GLN	N-CA-C	5.40	117.16	111.28
35	K	83	ALA	N-CA-C	5.39	116.97	111.14
46	V	51	GLU	N-CA-C	-5.39	107.07	113.97
34	J	82	HIS	N-CA-C	5.38	113.07	108.22
51	a	24	ASN	N-CA-C	5.38	119.33	112.34
1	b	259	ASN	N-CA-C	-5.37	107.39	114.31
23	x	21	LEU	N-CA-C	5.37	119.11	111.92
58	8	211	PHE	N-CA-C	5.35	118.08	110.10
33	I	94	GLU	N-CA-C	-5.32	106.63	113.23
11	l	96	LYS	N-CA-C	-5.31	105.54	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
38	N	39	GLY	N-CA-C	-5.31	108.37	115.32
10	k	108	ARG	N-CA-C	5.28	118.00	110.24
37	M	70	VAL	N-CA-C	5.28	115.42	110.30
11	l	118	THR	N-CA-C	5.25	117.33	110.08
8	i	4	VAL	N-CA-C	5.24	115.76	108.84
44	T	57	ARG	N-CA-C	-5.24	105.65	111.36
58	8	229	THR	N-CA-C	5.24	116.62	109.18
31	G	21	TYR	N-CA-C	-5.24	106.91	113.72
8	i	131	THR	N-CA-C	-5.23	105.75	111.82
58	8	116	THR	N-CA-C	-5.23	105.75	111.82
28	D	35	ARG	N-CA-C	-5.22	105.76	111.82
50	Z	9	GLU	N-CA-C	5.21	121.33	109.81
3	d	79	ARG	N-CA-C	-5.21	102.48	110.14
15	p	75	THR	N-CA-C	5.21	117.37	111.02
36	L	128	GLU	N-CA-C	-5.20	106.25	112.59
42	R	14	ALA	N-CA-C	5.20	119.90	111.37
5	f	109	SER	N-CA-C	-5.18	106.81	112.72
44	T	43	ALA	N-CA-C	-5.18	105.63	111.28
36	L	79	VAL	N-CA-C	-5.16	108.26	113.47
43	S	89	ARG	N-CA-C	-5.16	106.99	113.28
11	l	98	ALA	N-CA-C	-5.15	106.68	113.17
11	l	138	ALA	N-CA-C	-5.14	105.36	111.69
3	d	171	ASP	N-CA-C	-5.14	102.15	110.32
5	f	47	ASN	N-CA-C	-5.13	106.52	112.89
34	J	116	VAL	N-CA-C	-5.13	106.90	112.80
36	L	90	VAL	N-CA-C	5.13	116.01	110.21
3	d	200	LEU	N-CA-C	-5.13	106.71	113.17
37	M	126	CYS	N-CA-C	5.11	115.79	108.74
17	r	49	ILE	N-CA-C	5.11	115.20	107.75
9	j	120	ARG	N-CA-C	-5.09	106.58	112.89
7	h	43	LYS	N-CA-C	-5.09	105.92	111.82
58	8	39	THR	N-CA-C	-5.08	107.75	114.31
14	o	68	LYS	N-CA-C	5.08	116.50	111.07
39	O	20	GLN	N-CA-C	-5.08	106.59	112.89
33	I	176	LYS	N-CA-C	-5.08	105.78	112.94
4	e	11	VAL	N-CA-C	5.06	115.27	110.42
5	f	110	HIS	N-CA-C	5.06	112.68	108.13
15	p	10	GLU	N-CA-C	-5.05	107.17	113.38
45	U	10	GLY	N-CA-C	-5.05	106.89	112.04
15	p	100	ARG	N-CA-C	-5.05	106.90	113.16
39	O	15	HIS	N-CA-C	5.04	116.46	111.07
53	1	372	G	N9-C1'-C2'	5.04	119.55	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	8	126	VAL	N-CA-C	-5.03	107.85	112.83
5	f	40	VAL	N-CA-C	5.03	115.82	108.58
14	o	12	THR	N-CA-C	5.03	116.76	111.28
17	r	46	GLU	N-CA-C	5.03	118.00	109.76
45	U	78	VAL	N-CA-C	-5.02	106.24	113.07
30	F	7	VAL	N-CA-C	5.02	116.47	109.80
35	K	84	VAL	N-CA-C	5.01	116.14	109.37
41	Q	107	LYS	N-CA-C	5.01	117.94	110.52
24	y	14	LEU	N-CA-C	-5.01	106.01	111.82
31	G	142	LYS	N-CA-C	-5.00	105.91	111.36

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	2083	0	2157	78	0
2	c	1565	0	1616	41	0
3	d	1552	0	1619	53	0
4	e	1411	0	1447	56	0
5	f	1323	0	1374	30	0
6	g	1111	0	1148	35	0
7	h	989	0	1025	60	0
8	i	1032	0	1088	45	0
9	j	1129	0	1162	31	0
10	k	939	0	1012	38	0
11	l	1045	0	1117	37	0
12	m	1074	0	1157	41	0
13	n	961	0	1000	22	0
14	o	892	0	923	20	0
15	p	917	0	965	34	0
16	q	947	0	1022	20	0
17	r	816	0	839	24	0
18	s	857	0	922	26	0
19	t	739	0	807	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	u	780	0	834	18	0
21	v	753	0	780	14	0
22	w	575	0	592	21	0
23	x	625	0	655	23	0
24	y	509	0	543	15	0
25	z	449	0	491	9	0
26	B	444	0	461	16	0
27	C	410	0	440	4	0
28	D	377	0	418	16	0
29	E	504	0	574	20	0
30	F	302	0	343	12	0
31	G	1757	0	1787	41	0
32	H	1625	0	1699	50	0
33	I	1643	0	1710	57	0
34	J	1157	0	1199	48	0
35	K	818	0	808	39	0
36	L	1182	0	1240	44	0
37	M	979	0	1034	34	0
38	N	1022	0	1070	48	0
39	O	787	0	828	38	0
40	P	870	0	878	39	0
41	Q	955	0	1019	46	0
42	R	884	0	944	34	0
43	S	805	0	847	42	0
44	T	714	0	737	15	0
45	U	649	0	666	32	0
46	V	649	0	691	33	0
47	W	536	0	552	12	0
48	X	638	0	665	28	0
49	Y	665	0	714	30	0
50	Z	545	0	579	34	0
51	a	1027	0	1092	37	0
52	3	33012	0	16618	542	0
53	1	62317	0	31346	962	0
54	2	2568	0	1303	66	0
55	5	1640	0	836	21	0
55	6	1640	0	837	23	0
56	4	388	0	196	10	0
57	7	1619	0	821	39	0
58	8	2961	0	2978	117	0
59	5	10	0	10	3	0
60	7	11	0	8	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	8	28	0	12	0	0
All	All	153211	0	104255	2988	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 12.

All (2988) 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)
50:Z:44:ARG:HE	52:3:722:G:H5'	1.16	1.08
53:1:1906:G:H2'	53:1:1907:G:H5''	1.39	1.03
58:8:16:GLY:HA3	58:8:80:VAL:HG22	1.42	1.01
35:K:2:ARG:HG3	35:K:92:THR:HG22	1.40	1.00
20:u:16:LYS:HG3	53:1:329:G:H1	1.24	1.00
18:s:36:LEU:HD21	18:s:47:VAL:HG13	1.44	0.98
7:h:118:ILE:HG22	7:h:119:PRO:HD3	1.44	0.98
2:c:183:GLU:HG3	2:c:184:ARG:HD3	1.43	0.98
53:1:2277:G:H2'	53:1:2278:A:H5''	1.48	0.95
12:m:74:THR:HG21	12:m:86:LYS:HD2	1.46	0.95
38:N:98:ARG:HG3	38:N:103:VAL:HG21	1.49	0.95
42:R:111:PRO:HB2	42:R:113:LYS:HE2	1.48	0.95
7:h:116:GLU:HG3	7:h:117:LEU:HG	1.48	0.94
53:1:45:G:H5''	53:1:46:G:H5'	1.45	0.93
12:m:12:MET:HA	53:1:910:A:H62	1.31	0.92
41:Q:42:LYS:HD3	41:Q:43:LYS:H	1.34	0.92
50:Z:44:ARG:HH21	52:3:722:G:H4'	1.34	0.91
39:O:37:ARG:HG3	52:3:1124:G:H5''	1.52	0.89
52:3:1259:C:H3'	52:3:1260:G:H5''	1.51	0.89
53:1:1645:G:H5''	53:1:1646:C:H5'	1.52	0.89
53:1:1053:C:H2'	53:1:1054:A:H5''	1.55	0.89
53:1:1077:A:H2'	53:1:1078:U:H5'	1.55	0.89
57:7:7:A:H3'	57:7:8:U:H5''	1.54	0.89
54:2:3:C:H2'	54:2:4:C:H5''	1.53	0.89
33:I:190:LEU:HD12	33:I:192:ALA:H	1.38	0.88
49:Y:48:LYS:HA	49:Y:51:ASN:HD22	1.37	0.87
48:X:69:LYS:HZ2	52:3:1319:A:H5''	1.40	0.86
50:Z:34:ARG:HB3	50:Z:36:PHE:CE1	2.11	0.86
51:a:185:LEU:HA	51:a:188:ASN:HD22	1.40	0.85
48:X:69:LYS:NZ	52:3:1319:A:H5''	1.92	0.85
41:Q:69:GLU:HG2	52:3:521:G:H4'	1.56	0.85
34:J:107:GLY:HA3	52:3:9:G:H5'	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Q:43:LYS:HD3	56:4:21:C:H4'	1.58	0.84
4:e:130:GLY:HA3	53:1:2305:U:H5''	1.58	0.84
7:h:37:LYS:HZ2	53:1:1086:A:H62	1.26	0.84
35:K:79:ARG:HH12	52:3:671:G:H4'	1.43	0.84
15:p:38:ARG:NH1	52:3:345:C:H5'	1.93	0.83
45:U:41:PRO:HG2	45:U:42:ILE:HD12	1.60	0.83
53:1:1906:G:C2'	53:1:1907:G:H5''	2.07	0.83
4:e:26:GLN:NE2	54:2:57:A:H4'	1.93	0.83
52:3:405:U:H3'	52:3:406:G:H5'	1.58	0.83
12:m:45:GLN:HE21	53:1:2485:G:H5''	1.44	0.83
58:8:311:ILE:HG23	58:8:354:GLY:H	1.42	0.82
38:N:114:LYS:HD3	52:3:1187:G:H5''	1.62	0.82
2:c:115:GLY:HA2	2:c:166:GLY:HA3	1.60	0.82
13:n:2:ARG:O	13:n:2:ARG:HD3	1.79	0.81
8:i:33:ASN:HB2	8:i:36:GLU:HG2	1.62	0.81
38:N:57:VAL:HG23	38:N:58:GLU:H	1.46	0.81
53:1:215:G:H4'	53:1:216:A:H4'	1.60	0.81
57:7:25:C:H3'	57:7:26:A:H5''	1.63	0.81
31:G:7:ASP:HA	31:G:10:LYS:HE2	1.62	0.81
34:J:55:VAL:HG13	34:J:56:PRO:HD3	1.62	0.80
57:7:6:G:H3'	57:7:7:A:H5''	1.62	0.80
9:j:37:ARG:HA	9:j:118:MET:HE3	1.64	0.80
52:3:327:A:O2'	52:3:328:C:H4'	1.81	0.80
44:T:68:TYR:HB2	52:3:754:C:H4'	1.64	0.80
15:p:38:ARG:HH12	52:3:345:C:H5'	1.43	0.79
51:a:5:THR:HG22	51:a:8:MET:HE3	1.64	0.79
5:f:163:TYR:HB2	5:f:166:GLU:HB2	1.63	0.79
2:c:149:ASN:HB3	53:1:2572:A:OP2	1.82	0.79
43:S:68:ARG:HE	52:3:1202:U:H4'	1.47	0.79
55:5:75:C:H2'	55:5:76:A:H5''	1.62	0.79
7:h:118:ILE:HG22	7:h:119:PRO:CD	2.13	0.79
53:1:2553:G:H3'	53:1:2554:U:H5''	1.65	0.79
53:1:2743:U:H2'	53:1:2744:G:H5''	1.62	0.78
3:d:146:VAL:HG12	3:d:185:LYS:HB2	1.65	0.78
8:i:69:VAL:HG13	8:i:71:LYS:HZ1	1.47	0.78
36:L:142:ARG:HG2	55:6:41:C:H4'	1.66	0.78
53:1:2286:G:H5''	53:1:2287:A:OP1	1.84	0.78
2:c:151:THR:HB	2:c:152:PRO:HD3	1.66	0.78
4:e:140:ILE:HG13	4:e:142:TYR:H	1.49	0.78
51:a:62:ALA:HB2	51:a:162:ARG:HD2	1.63	0.78
53:1:546:U:H2'	53:1:547:A:H4'	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:8:99:MET:HE1	58:8:126:VAL:HG23	1.64	0.78
53:1:300:A:H2'	53:1:334:C:H1'	1.67	0.77
34:J:156:ARG:NH1	37:M:100:ILE:HG23	1.99	0.77
7:h:30:SER:HB2	7:h:81:LEU:HD13	1.67	0.76
41:Q:35:ARG:HD3	41:Q:53:ARG:HH12	1.50	0.76
1:b:203:VAL:HG23	53:1:1792:G:H5'	1.66	0.76
53:1:1020:A:H1'	53:1:1021:A:OP2	1.85	0.76
53:1:1807:G:H2'	53:1:1808:A:H5'	1.66	0.76
6:g:58:LEU:O	6:g:61:VAL:HG22	1.86	0.76
53:1:275:C:H2'	53:1:276:U:H4'	1.67	0.76
36:L:111:GLY:HA2	36:L:118:ARG:HD3	1.68	0.75
36:L:149:ALA:HB1	40:P:58:THR:HG21	1.67	0.75
8:i:73:PRO:HG2	8:i:78:LEU:HD21	1.67	0.75
10:k:48:PRO:HG3	52:3:1422:G:H5'	1.69	0.75
41:Q:42:LYS:NZ	52:3:1491:G:H5''	2.00	0.75
57:7:50:U:H3	57:7:64:A:H61	1.31	0.75
20:u:16:LYS:HG3	53:1:329:G:N1	2.02	0.75
48:X:18:VAL:HG21	48:X:43:MET:HG2	1.68	0.75
41:Q:32:VAL:HA	41:Q:78:VAL:HG12	1.67	0.75
10:k:18:ARG:HB3	10:k:45:GLU:HG3	1.69	0.74
53:1:1105:U:H2'	53:1:1106:G:H5''	1.68	0.74
37:M:95:MET:HE3	37:M:98:LEU:HD12	1.69	0.74
55:6:59:A:H2'	55:6:60:U:H5'	1.69	0.74
41:Q:42:LYS:HD3	41:Q:43:LYS:N	2.03	0.74
41:Q:113:ARG:HB2	41:Q:118:VAL:HB	1.70	0.74
58:8:219:PHE:HB2	58:8:227:VAL:HG23	1.70	0.74
34:J:108:GLY:H	52:3:9:G:H4'	1.53	0.74
49:Y:66:ILE:HD11	49:Y:70:LYS:HD2	1.69	0.74
10:k:3:GLN:HE21	53:1:1666:G:H1'	1.53	0.74
36:L:12:LEU:HD12	36:L:13:PRO:HD2	1.69	0.74
8:i:93:ASN:ND2	53:1:1077:A:H5''	2.03	0.73
54:2:3:C:C2'	54:2:4:C:H5''	2.16	0.73
53:1:2682:A:H61	53:1:2728:U:H1'	1.52	0.73
53:1:310:A:H2'	53:1:311:A:H5''	1.68	0.73
17:r:78:ARG:HH12	53:1:990:A:H61	1.35	0.73
52:3:112:G:H21	52:3:354:G:H5'	1.53	0.73
4:e:91:ARG:NH2	54:2:45:A:H1'	2.04	0.73
1:b:268:ARG:HH22	52:3:681:A:H5'	1.53	0.73
53:1:2048:G:H2'	53:1:2049:G:H5''	1.70	0.73
55:6:54:U:H3	55:6:58:A:H62	1.36	0.73
11:l:93:ASN:O	11:l:94:THR:HG22	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:C:7:LYS:HD2	53:1:2420:C:H5''	1.70	0.72
39:O:47:GLU:HB3	39:O:67:ILE:HB	1.69	0.72
7:h:57:ASN:HB3	7:h:62:ARG:HD2	1.71	0.72
52:3:50:A:H4'	52:3:51:A:H5'	1.71	0.72
17:r:60:LYS:HB2	17:r:100:GLY:HA3	1.72	0.72
52:3:664:G:H22	52:3:741:G:H1	1.35	0.72
41:Q:73:LEU:HD22	41:Q:73:LEU:H	1.55	0.72
6:g:132:PHE:HB2	6:g:140:ALA:HB3	1.72	0.72
21:v:76:ASP:HB3	21:v:90:ASP:HB2	1.71	0.72
39:O:61:ALA:HB2	52:3:1061:G:H5'	1.72	0.72
52:3:1306:A:N6	52:3:1331:G:H1'	2.04	0.72
53:1:310:A:C2'	53:1:311:A:H5''	2.18	0.72
8:i:69:VAL:HG13	8:i:71:LYS:NZ	2.04	0.71
35:K:91:ARG:HG3	35:K:92:THR:H	1.55	0.71
48:X:35:ARG:HH21	48:X:74:ALA:HB3	1.55	0.71
8:i:122:GLU:HG3	8:i:126:ARG:HH12	1.55	0.71
57:7:6:G:C3'	57:7:7:A:H5''	2.19	0.71
53:1:528:A:N1	53:1:2042:A:H2'	2.05	0.71
38:N:49:GLN:O	38:N:52:GLU:HG3	1.90	0.71
52:3:1200:C:H5''	52:3:1201:A:H3'	1.71	0.71
13:n:44:LEU:HD23	13:n:113:ILE:HD13	1.73	0.71
38:N:105:ARG:O	38:N:105:ARG:HD3	1.90	0.71
43:S:3:GLN:O	43:S:6:LYS:HG3	1.91	0.71
7:h:59:LEU:HD22	7:h:62:ARG:HH21	1.56	0.71
25:z:4:ILE:HD11	25:z:58:GLU:HG2	1.72	0.71
30:F:36:ARG:HG3	30:F:37:GLN:H	1.54	0.71
8:i:89:SER:HB3	8:i:135:MET:HA	1.73	0.71
5:f:2:ARG:HH12	53:1:1113:U:H5'	1.56	0.71
16:q:108:LEU:HA	17:r:48:LYS:HE2	1.73	0.71
53:1:821:A:H5''	53:1:822:G:H5''	1.71	0.71
43:S:63:CYS:HB3	43:S:67:GLY:H	1.55	0.71
52:3:484:G:H4'	52:3:485:U:H5''	1.71	0.71
53:1:2277:G:C2'	53:1:2278:A:H5''	2.18	0.71
41:Q:35:ARG:HD3	41:Q:53:ARG:NH1	2.06	0.70
49:Y:43:LYS:HD2	49:Y:86:ALA:HB2	1.71	0.70
50:Z:16:ARG:NH2	50:Z:19:LYS:HG2	2.07	0.70
53:1:2800:A:H3'	53:1:2801:G:H5'	1.73	0.70
21:v:68:LYS:HE3	21:v:70:ILE:HD11	1.72	0.70
57:7:7:A:H3'	57:7:8:U:C5'	2.21	0.70
53:1:435:C:H2'	53:1:436:C:H5'	1.73	0.70
3:d:63:LYS:HE2	53:1:2444:G:OP2	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:73:VAL:HG12	4:e:75:GLY:H	1.57	0.69
53:1:1141:U:H4'	53:1:1142:A:O4'	1.90	0.69
53:1:2112:G:H2'	53:1:2113:U:H5'	1.73	0.69
44:T:56:LEU:O	44:T:59:VAL:HG12	1.92	0.69
53:1:1394:U:H4'	53:1:1603:A:H4'	1.73	0.69
53:1:2061:G:H22	59:5:101:FME:HG3	1.58	0.69
10:k:87:LEU:HA	10:k:94:PRO:HA	1.73	0.69
43:S:99:SER:OG	52:3:1187:G:H1'	1.93	0.69
51:a:38:PHE:HD1	53:1:2127:G:H4'	1.56	0.69
54:2:65:U:H3'	54:2:108:A:H61	1.57	0.69
11:l:36:LYS:HD2	53:1:807:U:OP2	1.92	0.69
20:u:42:LYS:HD2	53:1:499:U:H5''	1.75	0.69
50:Z:25:ALA:HB1	56:4:9:G:H5'	1.75	0.69
51:a:38:PHE:CD1	53:1:2127:G:H4'	2.28	0.69
53:1:542:C:H2'	53:1:543:G:H5''	1.75	0.69
52:3:769:G:H4'	52:3:1513:A:H4'	1.74	0.68
42:R:71:GLU:OE2	42:R:72:ILE:HG23	1.94	0.68
52:3:1318:A:H2'	52:3:1319:A:H5'	1.75	0.68
53:1:329:G:O4'	53:1:477:A:H1'	1.90	0.68
53:1:2297:A:N6	53:1:2319:G:H1'	2.08	0.68
24:y:31:GLN:HG2	24:y:37:LEU:HB2	1.75	0.68
52:3:1429:A:H2'	52:3:1430:A:H8	1.59	0.68
53:1:1956:U:H2'	53:1:1957:C:H5'	1.75	0.68
54:2:88:C:H5''	54:2:89:U:OP1	1.93	0.68
9:j:7:LYS:HG2	53:1:538:A:H4'	1.76	0.68
12:m:64:TRP:HZ3	12:m:106:ASP:HB3	1.56	0.68
36:L:145:GLU:HA	36:L:148:LYS:HG3	1.74	0.68
44:T:28:VAL:HG21	44:T:80:LEU:HD21	1.76	0.68
53:1:995:C:H6	53:1:995:C:H5'	1.59	0.68
36:L:71:THR:HG23	36:L:72:VAL:HG12	1.75	0.68
49:Y:26:MET:HB3	52:3:1458:G:H5'	1.75	0.68
32:H:19:SER:O	43:S:93:PRO:HG3	1.94	0.68
40:P:23:HIS:HB3	40:P:30:ILE:HG23	1.76	0.68
52:3:1201:A:H1'	52:3:1202:U:OP2	1.94	0.68
1:b:182:LYS:HE3	1:b:267:VAL:HG22	1.75	0.67
8:i:20:SER:HB3	8:i:21:PRO:HD3	1.74	0.67
11:l:85:VAL:HG12	11:l:86:GLU:H	1.59	0.67
31:G:5:MET:HA	31:G:8:MET:HE2	1.75	0.67
51:a:8:MET:HE2	53:1:2174:C:H5''	1.77	0.67
58:8:98:GLN:HA	58:8:231:ARG:HD3	1.75	0.67
9:j:17:VAL:HG23	9:j:137:PRO:HB2	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:615:U:H5''	53:1:616:A:OP2	1.94	0.67
53:1:1077:A:C2'	53:1:1078:U:H5'	2.24	0.67
46:V:13:SER:H	46:V:21:VAL:HG13	1.59	0.67
43:S:68:ARG:HG3	43:S:70:HIS:H	1.59	0.67
53:1:2048:G:C3'	53:1:2049:G:H5''	2.24	0.67
32:H:189:HIS:CD2	52:3:1205:U:H4'	2.30	0.67
8:i:92:PRO:HB2	53:1:1076:C:O2'	1.95	0.67
20:u:48:VAL:HG22	20:u:50:ALA:H	1.59	0.67
35:K:29:ILE:HG22	35:K:34:GLY:HA3	1.76	0.67
8:i:11:GLN:NE2	8:i:12:VAL:O	2.28	0.67
8:i:94:LYS:NZ	53:1:1076:C:H4'	2.10	0.67
35:K:61:LEU:HD23	35:K:62:MET:N	2.09	0.66
38:N:83:THR:HG21	38:N:102:PHE:HB3	1.77	0.66
52:3:1137:C:H5'	52:3:1138:G:H5'	1.76	0.66
42:R:100:ARG:HE	42:R:102:LYS:HB3	1.60	0.66
53:1:2248:C:H2'	53:1:2249:U:H5'	1.75	0.66
23:x:15:ASN:HD22	23:x:23:ALA:HB1	1.61	0.66
38:N:123:ARG:HB3	52:3:1343:G:H4'	1.76	0.66
60:7:101:PHE:N	58:8:262:PHE:H	1.94	0.66
52:3:501:C:H2'	52:3:502:A:C8	2.31	0.66
53:1:49:A:H5'	53:1:51:G:O4'	1.95	0.66
15:p:38:ARG:CZ	52:3:345:C:H5'	2.26	0.66
29:E:31:ILE:HD11	53:1:2391:G:H5'	1.77	0.66
33:I:103:ARG:HB2	33:I:170:LEU:HD21	1.76	0.66
7:h:27:VAL:HG13	7:h:83:ALA:HB3	1.78	0.66
22:w:36:GLN:HE22	22:w:39:THR:HA	1.59	0.66
35:K:6:ILE:HB	35:K:62:MET:HB2	1.76	0.66
53:1:2743:U:C2'	53:1:2744:G:H5''	2.26	0.66
35:K:66:ALA:HB1	35:K:67:PRO:HD2	1.77	0.66
28:D:34:ARG:NH1	28:D:39:ARG:HD2	2.11	0.66
5:f:2:ARG:NH1	53:1:1113:U:H5'	2.11	0.66
12:m:21:ALA:HB1	12:m:100:LYS:HD3	1.78	0.66
50:Z:44:ARG:HG3	52:3:723:U:OP1	1.96	0.66
12:m:21:ALA:HB2	12:m:97:GLN:HB2	1.77	0.65
49:Y:80:ALA:HA	49:Y:83:ASN:HD21	1.61	0.65
6:g:72:ILE:HD12	6:g:108:VAL:HG13	1.79	0.65
49:Y:50:PHE:O	49:Y:54:GLN:HG2	1.97	0.65
43:S:1:ALA:HB2	52:3:1203:C:OP1	1.95	0.65
37:M:77:VAL:HG12	37:M:84:ILE:HD12	1.79	0.65
53:1:974:G:H1'	53:1:975:A:C8	2.31	0.65
15:p:38:ARG:NH2	52:3:345:C:H5'	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:T:63:ARG:HE	44:T:87:ARG:HH22	1.43	0.65
47:W:61:ALA:HB1	47:W:67:LEU:HD13	1.77	0.65
30:F:20:ASP:HA	53:1:2757:A:OP2	1.97	0.65
53:1:45:G:H5''	53:1:46:G:C5'	2.24	0.65
53:1:161:A:H3'	53:1:162:U:H5''	1.78	0.65
53:1:1657:U:H2'	53:1:1658:C:C6	2.32	0.65
53:1:1796:U:H2'	53:1:1797:G:H8	1.61	0.65
53:1:2048:G:C2'	53:1:2049:G:H5''	2.27	0.65
35:K:46:GLN:HA	35:K:56:LYS:HG2	1.77	0.65
38:N:42:THR:HA	38:N:44:ARG:HH11	1.62	0.65
1:b:203:VAL:HG23	53:1:1792:G:C5'	2.27	0.64
24:y:21:LEU:HA	24:y:25:GLN:HB3	1.78	0.64
40:P:12:ARG:HG3	40:P:14:GLN:HE21	1.60	0.64
52:3:70:U:H5''	52:3:71:A:OP1	1.96	0.64
26:B:30:ASP:HB3	26:B:34:GLY:H	1.62	0.64
58:8:378:ARG:HG2	58:8:383:THR:HA	1.79	0.64
33:I:75:TYR:HA	33:I:89:LEU:HD21	1.79	0.64
58:8:312:LEU:HD23	58:8:312:LEU:H	1.62	0.64
3:d:2:GLU:HB3	3:d:11:ALA:HB1	1.78	0.64
10:k:109:SER:O	10:k:110:GLU:HG2	1.97	0.64
15:p:105:LYS:O	15:p:108:ARG:HG2	1.98	0.64
21:v:11:GLU:HG3	21:v:16:ALA:HB2	1.80	0.64
33:I:82:LYS:HD2	52:3:5:U:O4	1.98	0.64
40:P:114:PRO:HB2	52:3:676:A:H5''	1.79	0.64
49:Y:67:HIS:ND1	52:3:262:A:H5'	2.13	0.64
52:3:355:C:H5'	52:3:355:C:H6	1.61	0.64
22:w:36:GLN:NE2	22:w:39:THR:HA	2.11	0.64
40:P:61:ALA:O	40:P:64:VAL:HG12	1.96	0.64
52:3:29:U:O2'	52:3:30:U:H5'	1.97	0.64
53:1:745:G:O2'	53:1:748:G:H1'	1.98	0.64
53:1:807:U:H2'	53:1:808:G:H8	1.61	0.64
52:3:219:U:H2'	52:3:220:G:H8	1.62	0.64
35:K:68:GLN:O	35:K:71:ILE:HG22	1.98	0.64
42:R:6:ILE:HG23	42:R:7:ASN:H	1.63	0.64
47:W:11:ARG:HD2	52:3:845:A:H1'	1.79	0.64
34:J:110:MET:HG3	34:J:139:THR:HG21	1.78	0.64
38:N:51:LEU:HB3	38:N:56:MET:HB3	1.80	0.64
53:1:1373:A:H5'	53:1:2212:A:H1'	1.79	0.64
53:1:2807:U:H3	53:1:2891:U:H3	1.45	0.64
54:2:3:C:C3'	54:2:4:C:H5''	2.28	0.64
29:E:31:ILE:O	29:E:31:ILE:HG13	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:358:U:H2'	52:3:359:G:H8	1.63	0.64
53:1:704:G:H2'	53:1:726:G:H22	1.63	0.64
53:1:2248:C:C2'	53:1:2249:U:H5'	2.28	0.64
13:n:82:GLU:HG3	13:n:86:ARG:HH22	1.61	0.63
15:p:38:ARG:HH22	52:3:345:C:C5'	2.11	0.63
32:H:122:GLN:HG2	32:H:127:VAL:HG11	1.80	0.63
55:6:17:C:H2'	55:6:17(A):U:C5	2.32	0.63
18:s:98:LYS:HD2	53:1:2012:G:OP1	1.98	0.63
30:F:16:ILE:HD13	53:1:1032:A:H4'	1.80	0.63
52:3:1280:A:O2'	52:3:1281:C:H5'	1.98	0.63
53:1:473:G:O2'	53:1:474:G:H5'	1.98	0.63
22:w:67:VAL:HG12	22:w:74:LYS:HE3	1.79	0.63
29:E:51:LYS:HD2	53:1:937:C:OP1	1.98	0.63
52:3:1379:G:O2'	52:3:1380:U:H5'	1.97	0.63
32:H:1:GLY:HA3	52:3:1060:U:H5	1.64	0.63
40:P:88:PRO:HG2	40:P:89:GLY:H	1.61	0.63
51:a:11:ILE:HG23	51:a:33:LEU:HD22	1.80	0.63
52:3:730:G:H2'	52:3:731:G:H5'	1.81	0.63
1:b:16:VAL:HB	1:b:203:VAL:HG12	1.81	0.63
53:1:1697:G:H4'	53:1:1978:A:H5''	1.80	0.63
2:c:135:GLY:HA2	53:1:743:A:OP1	1.99	0.63
6:g:40:THR:HG21	6:g:42:LYS:NZ	2.14	0.63
7:h:28:ALA:HA	7:h:81:LEU:O	1.99	0.63
52:3:335:C:H2'	52:3:336:A:C8	2.34	0.63
19:t:78:SER:OG	53:1:58:G:H5'	1.98	0.63
53:1:1071:G:OP1	53:1:1071:G:H3'	1.99	0.63
3:d:162:ARG:NH1	53:1:321:U:H1'	2.14	0.63
7:h:67:THR:OG1	7:h:68:PRO:HD3	1.98	0.63
18:s:59:GLU:HB3	18:s:66:ILE:HD11	1.79	0.63
36:L:3:ARG:HH21	52:3:932:C:H5''	1.63	0.63
52:3:955:U:H3	52:3:1225:A:H61	1.46	0.63
58:8:12:HIS:NE2	58:8:78:ALA:HB2	2.14	0.63
15:p:28:LYS:HG2	15:p:41:ALA:HA	1.81	0.62
40:P:109:ILE:N	40:P:109:ILE:HD12	2.14	0.62
45:U:41:PRO:HG2	45:U:42:ILE:CD1	2.28	0.62
51:a:60:ARG:HB2	51:a:164:ARG:HG3	1.82	0.62
53:1:215:G:C4'	53:1:216:A:H4'	2.28	0.62
53:1:717:C:H2'	53:1:718:A:H5'	1.81	0.62
53:1:2287:A:O2'	53:1:2288:A:H2'	1.99	0.62
38:N:19:PHE:HB2	38:N:63:TYR:HB3	1.81	0.62
46:V:39:ARG:HH22	52:3:237:G:H5''	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1352:C:H2'	52:3:1353:G:C8	2.35	0.62
53:1:1053:C:C2'	53:1:1054:A:H5''	2.27	0.62
14:o:6:ALA:O	14:o:9:ARG:HD3	1.98	0.62
18:s:1:MET:HE3	18:s:2:GLU:H	1.64	0.62
4:e:135:ILE:H	4:e:135:ILE:HD12	1.63	0.62
50:Z:44:ARG:NE	52:3:722:G:H5'	2.02	0.62
14:o:33:ARG:HE	54:2:52:A:H62	1.47	0.62
22:w:17:LEU:HD23	22:w:35:ARG:HH12	1.63	0.62
53:1:1367:A:H2'	53:1:1368:G:H5'	1.80	0.62
18:s:34:ASP:HB3	26:B:27:LEU:HD11	1.82	0.62
20:u:16:LYS:CG	53:1:329:G:H1	2.06	0.62
42:R:111:PRO:CB	42:R:113:LYS:HE2	2.26	0.62
49:Y:48:LYS:HA	49:Y:51:ASN:ND2	2.12	0.62
50:Z:34:ARG:HB3	50:Z:36:PHE:CZ	2.34	0.62
52:3:358:U:H2'	52:3:359:G:C8	2.35	0.62
52:3:1258:G:H2'	52:3:1259:C:C6	2.35	0.62
53:1:2350:C:H2'	53:1:2351:G:O4'	1.98	0.62
12:m:58:LYS:O	12:m:59:ARG:HG2	1.99	0.62
18:s:53:SER:O	18:s:57:ASN:HB2	1.99	0.62
37:M:25:THR:O	37:M:26:MET:HG3	1.99	0.62
48:X:14:LEU:HD12	48:X:17:LYS:HD2	1.82	0.62
21:v:21:ARG:HH12	21:v:87:GLN:HA	1.64	0.62
28:D:12:ARG:HH21	28:D:44:VAL:HG21	1.64	0.62
52:3:501:C:H2'	52:3:502:A:H8	1.64	0.62
52:3:1493:A:H4'	56:4:19:U:O2'	2.00	0.62
53:1:2267:A:H5''	53:1:2268:A:H5'	1.82	0.62
53:1:2799:A:H2'	53:1:2800:A:H5'	1.81	0.62
22:w:20:LYS:HD2	53:1:2355:G:H4'	1.80	0.61
37:M:10:LEU:HD22	37:M:74:ILE:HD11	1.83	0.61
37:M:80:PRO:HG2	52:3:878:A:C5'	2.29	0.61
50:Z:8:ASN:HB3	50:Z:9:GLU:OE1	2.00	0.61
52:3:78:A:H2'	52:3:79:G:O4'	2.00	0.61
58:8:25:LYS:HE3	58:8:84:GLY:H	1.64	0.61
28:D:34:ARG:HH12	28:D:39:ARG:HD2	1.64	0.61
15:p:92:ARG:HD3	53:1:1753:G:OP1	2.01	0.61
35:K:91:ARG:HG3	35:K:92:THR:N	2.15	0.61
52:3:225:C:H2'	52:3:226:G:H5''	1.82	0.61
53:1:2537:U:H2'	53:1:2538:C:C6	2.36	0.61
14:o:56:LYS:HB2	14:o:60:GLU:HG3	1.82	0.61
16:q:5:ARG:NH1	53:1:585:G:N7	2.47	0.61
46:V:24:ILE:HB	46:V:41:THR:HB	1.80	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:817:C:H4'	52:3:818:G:H5''	1.81	0.61
52:3:1441:A:H2'	52:3:1442:G:H5'	1.82	0.61
53:1:1068:G:O2'	53:1:1096:A:H4'	2.00	0.61
58:8:151:GLU:HG3	58:8:170:ILE:HG21	1.83	0.61
5:f:173:ALA:O	5:f:175:LYS:N	2.33	0.61
50:Z:9:GLU:HB2	50:Z:10:PRO:HD3	1.83	0.61
51:a:211:LYS:NZ	53:1:2177:C:H5''	2.16	0.61
53:1:45:G:C5'	53:1:46:G:H5'	2.27	0.61
53:1:2547:A:H2'	53:1:2548:U:C6	2.35	0.61
58:8:117:ARG:HG3	58:8:157:LEU:HD11	1.82	0.61
10:k:76:VAL:H	15:p:72:VAL:HG12	1.66	0.61
18:s:42:LYS:HB2	53:1:2010:G:H5''	1.82	0.61
28:D:14:ARG:HD2	53:1:771:G:OP1	2.00	0.61
35:K:5:GLU:HA	35:K:63:ASN:HA	1.82	0.61
52:3:1346:A:O2'	52:3:1347:G:H4'	2.01	0.61
2:c:194:PRO:HA	53:1:2680:U:H5'	1.81	0.61
6:g:12:LEU:HD12	6:g:13:GLY:N	2.16	0.61
38:N:59:LYS:HB3	38:N:60:LEU:HD12	1.83	0.61
52:3:211:G:H2'	52:3:212:G:H5'	1.82	0.61
1:b:48:ILE:HG22	53:1:779:U:OP1	2.01	0.61
37:M:28:SER:OG	37:M:56:PRO:HB2	2.00	0.61
45:U:20:VAL:HG22	45:U:21:VAL:H	1.66	0.61
52:3:79:G:O2'	52:3:80:A:H5'	2.01	0.61
52:3:946:A:H2'	52:3:947:G:H8	1.66	0.61
52:3:1412:C:H2'	52:3:1413:A:C8	2.36	0.61
58:8:249:LYS:HG2	58:8:250:GLU:H	1.66	0.61
41:Q:42:LYS:HZ1	52:3:1491:G:H5''	1.64	0.61
53:1:1856:U:H2'	53:1:1857:G:O4'	2.01	0.61
6:g:26:ALA:HA	6:g:30:LEU:HD12	1.82	0.60
53:1:1509:A:H2'	53:1:1510:G:C8	2.36	0.60
53:1:2061:G:N2	59:5:101:FME:HG3	2.16	0.60
53:1:2163:A:H2'	53:1:2164:C:H5'	1.83	0.60
48:X:54:ARG:HG3	48:X:55:GLN:HG2	1.82	0.60
53:1:2646:C:H2'	53:1:2647:U:O4'	2.00	0.60
58:8:122:LEU:HD12	58:8:123:GLY:N	2.15	0.60
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.83	0.60
47:W:11:ARG:HB3	52:3:845:A:O2'	2.01	0.60
53:1:704:G:H2'	53:1:726:G:N2	2.16	0.60
7:h:27:VAL:HG23	7:h:110:ALA:HA	1.83	0.60
8:i:35:MET:O	8:i:39:LYS:HG2	2.01	0.60
32:H:133:MET:HE3	32:H:167:TYR:HB2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:119:A:H4'	53:1:120:U:H5'	1.84	0.60
53:1:1965:C:H5''	53:1:1966:A:H2'	1.83	0.60
19:t:24:MET:SD	19:t:30:ILE:HA	2.41	0.60
39:O:6:ILE:HD12	39:O:6:ILE:N	2.16	0.60
53:1:833:A:H2'	53:1:834:G:H8	1.66	0.60
53:1:2834:G:O2'	53:1:2835:A:H5'	2.01	0.60
33:I:151:GLN:HE21	33:I:153:ARG:HB3	1.66	0.60
45:U:31:ARG:HB2	52:3:310:G:H5''	1.84	0.60
4:e:37:MET:HG3	4:e:56:LEU:HD21	1.83	0.60
34:J:80:LEU:HG	34:J:122:VAL:HG11	1.84	0.60
52:3:1414:U:H2'	52:3:1415:G:H8	1.65	0.60
46:V:6:THR:C	46:V:7:LEU:HD22	2.26	0.60
52:3:946:A:H2'	52:3:947:G:C8	2.36	0.60
52:3:1218:C:H2'	52:3:1219:A:C8	2.36	0.60
53:1:598:U:H2'	53:1:599:A:C8	2.37	0.60
53:1:1105:U:C2'	53:1:1106:G:H5''	2.31	0.60
3:d:77:ILE:HG13	3:d:78:TRP:HD1	1.67	0.60
17:r:39:LEU:O	17:r:49:ILE:HG23	2.01	0.60
3:d:137:LYS:HA	3:d:140:ASP:OD2	2.01	0.60
8:i:27:LEU:HD23	8:i:27:LEU:H	1.66	0.60
11:l:63:LYS:HA	29:E:12:ARG:HG2	1.83	0.60
20:u:10:VAL:HG12	20:u:71:ILE:HA	1.83	0.60
25:z:37:ARG:NH2	53:1:929:U:H4'	2.17	0.60
37:M:45:ILE:HG21	37:M:60:LEU:HD23	1.84	0.60
50:Z:25:ALA:HB1	56:4:9:G:C4'	2.32	0.60
52:3:225:C:C3'	52:3:226:G:H5''	2.31	0.60
52:3:1130:A:H61	52:3:1144:G:H1'	1.67	0.60
4:e:63:LYS:O	54:2:42:C:H1'	2.02	0.59
1:b:36:ASN:HB2	1:b:61:TYR:HB2	1.84	0.59
7:h:33:VAL:HG12	7:h:34:THR:H	1.67	0.59
11:l:30:THR:HG22	53:1:810:U:O4	2.02	0.59
39:O:5:ARG:HB3	39:O:6:ILE:HD12	1.83	0.59
40:P:80:ASN:HA	40:P:105:ARG:HB3	1.83	0.59
41:Q:25:ALA:O	41:Q:27:PRO:HD3	2.02	0.59
52:3:950:U:H2'	52:3:951:G:H8	1.67	0.59
52:3:1347:G:N2	52:3:1373:G:H2'	2.17	0.59
53:1:1664:A:H61	53:1:1996:C:H42	1.50	0.59
1:b:220:ARG:HD2	53:1:1827:U:OP2	2.01	0.59
38:N:56:MET:HG3	38:N:57:VAL:N	2.17	0.59
15:p:38:ARG:HH22	52:3:345:C:H5'	1.67	0.59
32:H:18:ASN:ND2	43:S:89:ARG:O	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:63:MET:HE3	34:J:67:ARG:HH12	1.67	0.59
55:5:6:G:O2'	55:5:7:G:H5'	2.02	0.59
1:b:224:MET:HE2	53:1:782:A:C6	2.37	0.59
2:c:13:ARG:HH11	15:p:55:HIS:HA	1.66	0.59
14:o:40:ILE:HG12	14:o:47:VAL:HG12	1.85	0.59
17:r:78:ARG:NH1	53:1:990:A:H61	2.00	0.59
49:Y:2:ASN:HB3	52:3:332:G:OP2	2.03	0.59
8:i:22:PRO:O	57:7:56:C:H4'	2.03	0.59
8:i:79:LEU:HD13	8:i:137:LEU:HD11	1.84	0.59
52:3:396:C:H2'	52:3:397:A:H5''	1.84	0.59
53:1:2286:G:H4'	53:1:2287:A:O4'	2.03	0.59
1:b:216:ARG:NH2	53:1:690:G:O3'	2.34	0.59
2:c:24:VAL:HG21	2:c:188:LEU:HB3	1.84	0.59
53:1:2296:U:H5''	53:1:2297:A:OP1	2.03	0.59
9:j:90:GLU:O	9:j:93:ILE:HG22	2.02	0.59
32:H:162:ALA:HB2	52:3:1056:U:H4'	1.85	0.59
33:I:159:GLU:N	33:I:159:GLU:OE1	2.35	0.59
43:S:40:ARG:HH21	48:X:6:LYS:HG3	1.68	0.59
52:3:701:U:H4'	52:3:703:G:H1'	1.85	0.59
53:1:1709:U:H2'	53:1:1710:G:H8	1.68	0.59
53:1:2605:U:H2'	53:1:2606:C:C6	2.38	0.59
58:8:248:ILE:HB	58:8:365:HIS:HB3	1.84	0.59
1:b:116:GLN:HG3	1:b:121:ALA:HB2	1.85	0.59
50:Z:27:VAL:HG13	50:Z:28:LEU:HD22	1.84	0.59
52:3:211:G:C2'	52:3:212:G:H5'	2.33	0.59
7:h:60:LEU:HA	7:h:64:VAL:HG21	1.85	0.59
12:m:69:PRO:HA	12:m:94:ALA:HB2	1.83	0.59
49:Y:25:SER:OG	52:3:1458:G:H5''	2.02	0.59
53:1:833:A:H2'	53:1:834:G:C8	2.37	0.59
58:8:304:LYS:HE3	58:8:360:VAL:CG1	2.33	0.59
7:h:117:LEU:HD23	7:h:120:ALA:HA	1.84	0.58
16:q:105:PHE:HA	16:q:108:LEU:HD12	1.85	0.58
7:h:118:ILE:CG2	7:h:119:PRO:HD3	2.26	0.58
52:3:335:C:H2'	52:3:336:A:H8	1.68	0.58
52:3:784:A:H4'	53:1:1837:C:OP1	2.03	0.58
54:2:65:U:H3'	54:2:108:A:N6	2.18	0.58
57:7:25:C:C3'	57:7:26:A:H5''	2.32	0.58
39:O:62:ARG:HB3	39:O:62:ARG:HH11	1.67	0.58
6:g:79:THR:HG22	6:g:145:ASN:HB2	1.85	0.58
35:K:86:ARG:NH2	52:3:673:A:O3'	2.36	0.58
53:1:2266:A:H4'	53:1:2267:A:C2	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2508:G:H1	53:1:2580:U:H3	1.49	0.58
22:w:20:LYS:CD	53:1:2355:G:H4'	2.34	0.58
37:M:94:VAL:HB	37:M:99:GLY:O	2.03	0.58
52:3:346:G:H2'	52:3:347:G:H5'	1.84	0.58
52:3:674:G:H2'	52:3:675:A:H8	1.68	0.58
1:b:119:VAL:HG23	6:g:91:PHE:CE1	2.38	0.58
1:b:235:GLU:H	1:b:238:ASN:ND2	2.02	0.58
51:a:218:MET:HE1	53:1:2128:G:H4'	1.84	0.58
52:3:1346:A:H2'	52:3:1346:A:N3	2.19	0.58
53:1:2055:C:H2'	53:1:2504:U:H5'	1.84	0.58
53:1:2093:G:N7	53:1:2225:A:H2'	2.19	0.58
57:7:58:A:H1'	57:7:60:U:H5	1.69	0.58
5:f:66:THR:OG1	53:1:2748:A:H1'	2.04	0.58
11:l:74:THR:HG22	11:l:107:PHE:HB2	1.85	0.58
12:m:5:LYS:HG2	12:m:6:ARG:HG2	1.84	0.58
22:w:33:ILE:HG22	22:w:34:VAL:HG23	1.85	0.58
55:5:75:C:C2'	55:5:76:A:H5''	2.32	0.58
1:b:30:ALA:HB3	1:b:31:PRO:HD3	1.86	0.58
31:G:206:ILE:H	31:G:206:ILE:HD12	1.69	0.58
53:1:2743:U:C3'	53:1:2744:G:H5''	2.34	0.58
29:E:61:LEU:HD12	29:E:64:ALA:HB3	1.85	0.58
35:K:23:GLU:HA	35:K:26:THR:HG22	1.86	0.58
39:O:40:ILE:HB	39:O:73:LEU:HB2	1.86	0.58
53:1:386:G:H3'	53:1:387:U:C5'	2.34	0.58
53:1:1637:A:H5'	53:1:1760:C:O2'	2.03	0.58
38:N:56:MET:HG3	38:N:57:VAL:H	1.67	0.58
42:R:10:ASP:OD2	42:R:11:HIS:N	2.37	0.58
48:X:15:LEU:O	48:X:18:VAL:HG12	2.04	0.58
52:3:950:U:H2'	52:3:951:G:C8	2.39	0.58
53:1:1936:A:H2	53:1:1943:U:H3	1.52	0.58
53:1:2194:U:H2'	53:1:2195:U:C6	2.39	0.58
53:1:2799:A:C2'	53:1:2800:A:H5'	2.33	0.58
40:P:97:ARG:HA	40:P:100:ASN:HD22	1.69	0.57
53:1:532:A:H2'	53:1:532:A:N3	2.18	0.57
53:1:1300:G:H4'	53:1:1301:A:C5'	2.34	0.57
53:1:1373:A:C5'	53:1:2212:A:H1'	2.34	0.57
29:E:37:THR:HG21	53:1:2348:U:OP1	2.03	0.57
36:L:68:VAL:HG23	36:L:99:ALA:HB1	1.85	0.57
39:O:9:ARG:HG2	39:O:71:LEU:HD11	1.86	0.57
39:O:62:ARG:HB3	39:O:62:ARG:NH1	2.19	0.57
52:3:219:U:H2'	52:3:220:G:C8	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1293:C:H2'	52:3:1294:G:H8	1.70	0.57
53:1:20:C:H2'	53:1:21:A:H8	1.69	0.57
53:1:1186:G:H2'	53:1:1187:G:O4'	2.04	0.57
58:8:12:HIS:HE2	58:8:78:ALA:HB2	1.69	0.57
43:S:52:ARG:HH11	52:3:1317:C:H42	1.51	0.57
53:1:635:C:H2'	53:1:636:G:C8	2.39	0.57
53:1:1268:A:H2'	53:1:1269:A:O4'	2.04	0.57
6:g:54:LEU:HD12	6:g:55:GLU:N	2.19	0.57
45:U:74:LEU:HA	45:U:77:GLU:HB2	1.87	0.57
49:Y:31:ILE:O	49:Y:34:VAL:HG22	2.05	0.57
1:b:182:LYS:HE3	1:b:267:VAL:CG2	2.34	0.57
6:g:72:ILE:HB	6:g:108:VAL:HG22	1.86	0.57
7:h:114:GLU:HA	7:h:123:ILE:HD13	1.87	0.57
8:i:57:VAL:HG12	8:i:71:LYS:HZ1	1.69	0.57
46:V:4:ILE:H	46:V:4:ILE:HD12	1.69	0.57
53:1:554:U:H2'	53:1:555:G:O4'	2.05	0.57
53:1:996:A:H2'	53:1:997:G:H8	1.69	0.57
53:1:1111:A:H2'	53:1:1111:A:N3	2.18	0.57
53:1:1509:A:H2'	53:1:1510:G:H8	1.70	0.57
53:1:1872:A:H2'	53:1:1873:G:O4'	2.04	0.57
53:1:2389:G:H5''	53:1:2390:U:O4'	2.04	0.57
53:1:2743:U:H2'	53:1:2744:G:C5'	2.35	0.57
57:7:53:G:H5''	58:8:321:THR:OG1	2.04	0.57
7:h:2:ALA:H	7:h:6:GLN:HE22	1.53	0.57
9:j:26:GLY:HA3	53:1:1140:C:H5'	1.85	0.57
23:x:10:ARG:HD3	23:x:11:PRO:HD2	1.86	0.57
41:Q:110:LYS:HG3	52:3:539:A:OP1	2.03	0.57
45:U:20:VAL:HG22	45:U:21:VAL:N	2.19	0.57
49:Y:56:ILE:O	49:Y:60:GLN:HG2	2.04	0.57
53:1:635:C:H2'	53:1:636:G:H8	1.70	0.57
53:1:1909:C:H2'	53:1:1910:G:H8	1.69	0.57
53:1:2114:A:H61	53:1:2117:A:H62	1.53	0.57
53:1:2443:C:H2'	53:1:2444:G:H8	1.69	0.57
29:E:2:LYS:HG3	53:1:242:G:C8	2.39	0.57
29:E:18:LYS:HG3	53:1:651:G:H5'	1.85	0.57
52:3:502:A:H2'	52:3:503:C:O4'	2.04	0.57
52:3:1534:A:H61	56:4:11:U:H3	1.52	0.57
58:8:134:PHE:HA	58:8:171:VAL:HG13	1.85	0.57
2:c:194:PRO:HA	53:1:2680:U:C5'	2.35	0.57
16:q:55:GLN:HA	16:q:58:GLN:HG2	1.85	0.57
33:I:23:GLY:HA3	52:3:409:U:OP1	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:S:81:ILE:HG21	52:3:1202:U:N3	2.19	0.57
52:3:304:U:O2'	52:3:305:G:H5'	2.05	0.57
38:N:11:ARG:HD2	38:N:76:GLY:HA3	1.87	0.57
52:3:1273:C:H2'	52:3:1274:A:O4'	2.04	0.57
52:3:1432:G:H1'	52:3:1468:A:N6	2.20	0.57
53:1:481:G:H1'	53:1:506:G:N2	2.20	0.57
53:1:2281:A:O2'	53:1:2282:G:H5'	2.04	0.57
58:8:213:LEU:HD23	58:8:293:LEU:HD23	1.87	0.57
58:8:215:ILE:HD12	58:8:228:VAL:HG21	1.86	0.57
31:G:213:LEU:HA	31:G:216:VAL:HG22	1.87	0.57
53:1:2208:C:H2'	53:1:2209:G:C8	2.40	0.57
8:i:91:LYS:HB3	8:i:94:LYS:HB2	1.87	0.56
33:I:37:PRO:HD2	33:I:41:GLY:HA3	1.87	0.56
39:O:88:MET:O	39:O:89:ARG:HG2	2.05	0.56
52:3:392:C:H2'	52:3:393:A:H8	1.70	0.56
48:X:62:THR:HG22	48:X:65:MET:HE1	1.87	0.56
49:Y:20:ASN:HD21	49:Y:24:ARG:NH1	2.03	0.56
58:8:72:THR:HG22	58:8:73:PRO:HD2	1.88	0.56
8:i:21:PRO:HB2	8:i:22:PRO:HD3	1.87	0.56
8:i:121:ILE:HA	8:i:124:MET:HE3	1.88	0.56
20:u:39:ASN:HB3	20:u:62:ALA:HB3	1.87	0.56
33:I:33:ILE:HG13	33:I:34:GLU:N	2.19	0.56
34:J:23:THR:HA	34:J:28:ARG:HA	1.86	0.56
35:K:50:PRO:HG3	35:K:55:HIS:HE1	1.70	0.56
40:P:109:ILE:HG22	50:Z:16:ARG:HH11	1.70	0.56
40:P:115:ILE:HD12	40:P:116:PRO:HD2	1.87	0.56
47:W:40:PRO:HG2	47:W:43:ILE:HG12	1.87	0.56
51:a:206:GLY:H	53:1:1861:G:P	2.27	0.56
52:3:1005:A:H2'	52:3:1006:G:O4'	2.05	0.56
52:3:1414:U:H2'	52:3:1415:G:C8	2.40	0.56
53:1:1796:U:H2'	53:1:1797:G:C8	2.40	0.56
58:8:11:PRO:HD2	58:8:75:ARG:HA	1.87	0.56
58:8:94:THR:HG21	58:8:289:ARG:HE	1.70	0.56
29:E:32:LEU:HD13	53:1:2419:U:OP2	2.05	0.56
31:G:115:ASP:O	31:G:119:GLN:HG2	2.05	0.56
34:J:55:VAL:HG13	34:J:56:PRO:CD	2.32	0.56
35:K:86:ARG:NH1	52:3:673:A:H4'	2.21	0.56
43:S:68:ARG:NH2	52:3:1202:U:O4'	2.37	0.56
52:3:225:C:H3'	52:3:226:G:H5''	1.88	0.56
53:1:1954:G:N2	53:1:1956:U:H3	2.03	0.56
23:x:3:VAL:HG12	23:x:10:ARG:HE	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:x:42:GLU:HB3	23:x:44:ARG:HG2	1.88	0.56
31:G:28:PRO:O	31:G:44:LYS:HD2	2.06	0.56
35:K:81:ASN:HB3	35:K:84:VAL:HG12	1.88	0.56
39:O:66:GLU:OE2	39:O:68:ARG:HG3	2.06	0.56
44:T:47:LYS:HD3	44:T:49:HIS:CD2	2.41	0.56
52:3:235:C:H2'	52:3:236:A:H8	1.70	0.56
53:1:2398:U:H2'	53:1:2399:G:C8	2.40	0.56
58:8:203:PRO:HG2	58:8:205:ARG:NE	2.19	0.56
1:b:42:ARG:HH12	53:1:690:G:H21	1.51	0.56
7:h:45:GLY:HA2	7:h:49:GLY:HA2	1.88	0.56
8:i:25:PRO:HG2	57:7:55:U:H5'	1.86	0.56
27:C:22:THR:HG22	27:C:23:THR:H	1.70	0.56
46:V:17:GLU:OE1	52:3:273:U:H1'	2.05	0.56
52:3:1256:A:H1'	52:3:1258:G:N9	2.21	0.56
53:1:1636:U:H2'	53:1:1637:A:C8	2.41	0.56
49:Y:23:ARG:O	49:Y:26:MET:HG3	2.06	0.56
52:3:572:A:H5''	52:3:917:G:H4'	1.87	0.56
52:3:673:A:H2'	52:3:674:G:C8	2.40	0.56
53:1:141:G:H3'	53:1:142:A:O4'	2.05	0.56
53:1:1801:A:H5''	53:1:2203:U:H2'	1.86	0.56
52:3:352:C:H4'	52:3:354:G:OP1	2.06	0.56
53:1:189:G:H2'	53:1:205:G:N2	2.21	0.56
58:8:152:MET:O	58:8:156:GLU:HG3	2.05	0.56
1:b:106:PRO:HD2	1:b:109:LEU:HD22	1.88	0.56
18:s:93:ALA:HB2	53:1:1614:A:C2	2.40	0.56
21:v:20:LEU:HD11	21:v:41:GLU:HG3	1.87	0.56
39:O:22:THR:O	39:O:26:VAL:HG23	2.06	0.56
46:V:69:THR:HG22	46:V:70:LYS:H	1.69	0.56
52:3:17:U:H2'	52:3:18:C:C6	2.41	0.56
53:1:20:C:H2'	53:1:21:A:C8	2.40	0.56
53:1:940:G:H2'	53:1:941:A:H5''	1.88	0.56
53:1:2467:C:H2'	53:1:2468:A:O4'	2.06	0.56
55:6:59:A:C2'	55:6:60:U:H5'	2.35	0.56
1:b:64:VAL:HG21	1:b:86:ARG:HH12	1.70	0.56
5:f:174:LYS:HB3	53:1:2529:G:H5'	1.87	0.56
31:G:45:THR:HG22	31:G:200:PRO:HB2	1.87	0.56
45:U:8:ARG:NE	45:U:15:PRO:HB3	2.21	0.56
52:3:715:A:H2'	52:3:716:A:C8	2.41	0.56
53:1:414:C:H2'	53:1:415:A:C8	2.41	0.56
53:1:2086:U:H2'	53:1:2087:G:C8	2.41	0.56
53:1:2391:G:H4'	53:1:2392:A:OP1	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:8:133:VAL:HG11	58:8:154:VAL:HG11	1.88	0.56
4:e:37:MET:HE2	4:e:56:LEU:HG	1.88	0.55
11:l:46:VAL:HG11	11:l:50:PHE:CD2	2.42	0.55
39:O:88:MET:HE3	39:O:100:ILE:HD13	1.87	0.55
52:3:309:A:H2'	52:3:310:G:H8	1.71	0.55
52:3:405:U:C3'	52:3:406:G:H5'	2.34	0.55
52:3:1412:C:H2'	52:3:1413:A:H8	1.69	0.55
53:1:27:G:N2	53:1:512:G:H1'	2.20	0.55
57:7:53:G:H5'	58:8:319:ARG:HH22	1.70	0.55
2:c:179:ARG:HB3	2:c:188:LEU:HD12	1.87	0.55
32:H:146:LYS:HB2	32:H:202:PHE:CD2	2.41	0.55
51:a:212:VAL:HG13	51:a:224:VAL:HG13	1.88	0.55
3:d:148:ILE:HD13	3:d:187:VAL:CG1	2.37	0.55
35:K:37:HIS:O	35:K:38:ARG:HD2	2.07	0.55
43:S:19:TYR:O	43:S:22:LYS:HG2	2.06	0.55
49:Y:54:GLN:HG3	49:Y:55:PRO:HD3	1.87	0.55
52:3:1401:G:H2'	52:3:1402:C:O4'	2.07	0.55
52:3:1512:U:H2'	52:3:1513:A:C8	2.41	0.55
53:1:580:U:H2'	53:1:581:C:C6	2.42	0.55
53:1:1319:C:O2'	53:1:1320:C:H5'	2.05	0.55
53:1:2196:C:O2'	53:1:2197:U:H5'	2.06	0.55
53:1:2679:A:O2'	53:1:2680:U:H5'	2.07	0.55
58:8:287:ILE:HD12	58:8:291:GLN:NE2	2.21	0.55
3:d:149:ILE:CG2	3:d:188:MET:HG2	2.35	0.55
26:B:7:PRO:HB3	26:B:11:LYS:HD3	1.88	0.55
34:J:105:ILE:CD1	34:J:123:LEU:HD22	2.37	0.55
42:R:6:ILE:HG23	42:R:7:ASN:N	2.21	0.55
48:X:72:GLU:OE2	52:3:1320:C:H4'	2.06	0.55
52:3:1202:U:H2'	52:3:1203:C:H5'	1.88	0.55
54:2:56:G:H4'	54:2:57:A:H8	1.71	0.55
54:2:95:U:H2'	54:2:96:G:H8	1.71	0.55
7:h:23:LEU:HD12	7:h:117:LEU:O	2.07	0.55
15:p:112:ARG:C	15:p:113:LEU:HD23	2.31	0.55
16:q:23:TYR:CD1	53:1:533:G:H5'	2.41	0.55
41:Q:99:GLY:HA3	41:Q:117:GLY:HA3	1.87	0.55
52:3:715:A:H2'	52:3:716:A:H8	1.70	0.55
52:3:1060:U:H2'	52:3:1061:G:C8	2.42	0.55
52:3:1402:C:H2'	52:3:1403:C:O4'	2.07	0.55
53:1:2221:G:O2'	53:1:2222:C:H5'	2.06	0.55
39:O:37:ARG:HE	52:3:1124:G:H3'	1.71	0.55
42:R:82:LEU:HD21	48:X:64:GLU:HG2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:736:C:H2'	52:3:737:C:C6	2.41	0.55
53:1:467:G:O2'	53:1:468:G:H5'	2.07	0.55
53:1:873:C:H2'	53:1:874:G:C8	2.41	0.55
53:1:1344:U:H3'	53:1:1345:C:H5'	1.88	0.55
53:1:2121:G:H2'	53:1:2122:U:O4'	2.06	0.55
6:g:6:LEU:HD11	6:g:51:ARG:HH21	1.71	0.55
7:h:41:LEU:HD13	53:1:1082:U:H2'	1.87	0.55
8:i:99:LYS:HE3	8:i:140:GLU:HB3	1.88	0.55
10:k:87:LEU:HD13	10:k:92:GLU:HA	1.88	0.55
28:D:9:VAL:HG12	53:1:1309:G:OP1	2.07	0.55
52:3:297:G:H4'	52:3:557:G:H4'	1.88	0.55
52:3:884:U:H4'	52:3:885:G:H5''	1.89	0.55
53:1:546:U:H2'	53:1:547:A:C4'	2.35	0.55
53:1:2208:C:H2'	53:1:2209:G:H8	1.72	0.55
53:1:2266:A:H4'	53:1:2267:A:N3	2.21	0.55
53:1:2432:A:H1'	55:6:75:C:H4'	1.89	0.55
57:7:8:U:H5''	57:7:49:C:OP2	2.07	0.55
45:U:71:VAL:HA	45:U:74:LEU:HD13	1.88	0.55
53:1:703:U:H2'	53:1:704:G:O4'	2.06	0.55
53:1:1668:A:H61	53:1:1676:A:H61	1.54	0.55
53:1:2047:C:H2'	53:1:2048:G:H8	1.71	0.55
53:1:2197:U:H1'	53:1:2198:A:C8	2.41	0.55
58:8:3:LYS:HG2	58:8:4:GLU:H	1.71	0.55
2:c:111:GLY:HA3	2:c:201:LEU:HD23	1.89	0.55
10:k:35:VAL:HG13	10:k:36:GLY:N	2.20	0.55
12:m:42:THR:HA	12:m:93:VAL:HA	1.88	0.55
14:o:71:ALA:HB1	14:o:106:LEU:HB2	1.88	0.55
33:I:39:GLN:HG2	33:I:40:HIS:ND1	2.22	0.55
38:N:94:ARG:HA	38:N:97:LEU:HB3	1.88	0.55
52:3:834:U:H2'	52:3:835:U:C6	2.42	0.55
53:1:1386:C:H2'	53:1:1387:A:C8	2.41	0.55
33:I:49:ASP:O	33:I:52:VAL:HG12	2.06	0.55
41:Q:6:LEU:HD11	41:Q:11:ARG:NE	2.22	0.55
53:1:1085:A:H1'	53:1:1105:U:H1'	1.87	0.55
57:7:16:U:H1'	57:7:60:U:O2'	2.06	0.55
7:h:53:ARG:HB3	7:h:55:VAL:HG23	1.90	0.54
51:a:16:ASP:OD2	51:a:19:LYS:HB3	2.06	0.54
2:c:56:LYS:NZ	53:1:2830:C:OP1	2.40	0.54
52:3:393:A:H5'	52:3:483:C:O2'	2.07	0.54
53:1:2087:G:H2'	53:1:2088:A:H8	1.73	0.54
54:2:2:G:H2'	54:2:3:C:C6	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:34:THR:HG21	53:1:1057:A:H1'	1.88	0.54
12:m:82:MET:HE2	53:1:960:A:H61	1.73	0.54
22:w:43:ALA:HB1	22:w:47:VAL:HG23	1.89	0.54
52:3:357:G:OP1	52:3:367:U:H5''	2.07	0.54
52:3:1369:C:H2'	52:3:1370:G:C8	2.42	0.54
53:1:310:A:O2'	53:1:311:A:H5''	2.07	0.54
53:1:616:A:H2'	53:1:617:G:O4'	2.06	0.54
53:1:828:U:H2'	53:1:829:A:C8	2.43	0.54
53:1:1947:C:H2'	53:1:1948:G:H8	1.71	0.54
53:1:2457:U:O2'	53:1:2458:G:H5'	2.07	0.54
53:1:2512:C:H2'	53:1:2513:A:O4'	2.08	0.54
8:i:72:THR:HG21	8:i:112:LYS:HG2	1.90	0.54
11:l:79:LEU:HD12	11:l:112:LEU:HA	1.90	0.54
37:M:80:PRO:HG2	52:3:878:A:H5''	1.89	0.54
40:P:125:LYS:HD3	52:3:797:C:OP1	2.06	0.54
42:R:25:GLY:H	52:3:1329:A:H5''	1.71	0.54
52:3:1330:U:H2'	52:3:1331:G:O4'	2.07	0.54
53:1:1720:U:H2'	53:1:1721:G:O4'	2.08	0.54
32:H:170:GLY:O	52:3:1106:G:H4'	2.06	0.54
50:Z:25:ALA:HB1	56:4:9:G:C5'	2.37	0.54
52:3:674:G:H2'	52:3:675:A:C8	2.43	0.54
53:1:572:A:H61	53:1:2029:G:H21	1.55	0.54
53:1:1827:U:H2'	53:1:1828:G:O4'	2.08	0.54
58:8:28:LEU:O	58:8:32:ILE:HG13	2.08	0.54
2:c:55:LYS:HD2	2:c:77:ARG:HA	1.88	0.54
9:j:25:LEU:HB3	53:1:1140:C:OP1	2.07	0.54
9:j:84:ILE:HG23	9:j:84:ILE:O	2.08	0.54
12:m:41:LEU:HD13	12:m:96:ILE:HG13	1.90	0.54
21:v:9:ARG:HG3	21:v:41:GLU:HB2	1.88	0.54
23:x:13:THR:HG21	53:1:188:G:H5'	1.89	0.54
25:z:6:ILE:HG22	25:z:28:LEU:HD21	1.89	0.54
31:G:24:PRO:HB3	52:3:828:U:H2'	1.88	0.54
52:3:346:G:C2'	52:3:347:G:H5'	2.38	0.54
52:3:664:G:N2	52:3:741:G:H1	2.04	0.54
57:7:26:A:H61	57:7:45:U:H3	1.54	0.54
4:e:28:PRO:HB2	4:e:168:LEU:HD22	1.90	0.54
7:h:53:ARG:NH2	7:h:55:VAL:HG21	2.23	0.54
7:h:81:LEU:HD21	53:1:1106:G:H21	1.73	0.54
9:j:101:ILE:H	9:j:101:ILE:HD12	1.73	0.54
10:k:35:VAL:HG13	10:k:36:GLY:H	1.73	0.54
40:P:54:SER:HB2	52:3:694:A:H5''	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1199:U:H2'	52:3:1200:C:H5'	1.88	0.54
52:3:1259:C:H3'	52:3:1260:G:C5'	2.33	0.54
52:3:1298:U:H4'	52:3:1299:A:O4'	2.07	0.54
52:3:1513:A:H2'	52:3:1514:G:C8	2.42	0.54
53:1:395:U:H2'	53:1:396:G:C8	2.43	0.54
53:1:503:A:H4'	53:1:505:A:H5''	1.89	0.54
53:1:807:U:H2'	53:1:808:G:C8	2.41	0.54
53:1:2073:C:O2'	53:1:2074:U:H5'	2.07	0.54
18:s:85:ILE:HD12	18:s:85:ILE:N	2.22	0.54
25:z:8:GLN:HE21	25:z:53:MET:HE2	1.72	0.54
26:B:54:ILE:HG23	26:B:56:LYS:H	1.72	0.54
32:H:188:ALA:HB3	32:H:195:ILE:HB	1.89	0.54
39:O:53:ILE:HG12	52:3:1060:U:H5''	1.90	0.54
41:Q:106:VAL:HG11	41:Q:109:ARG:HD3	1.90	0.54
53:1:1786:A:H1'	53:1:1938:A:N6	2.22	0.54
53:1:2070:A:H2'	53:1:2071:A:O4'	2.08	0.54
53:1:2285:C:O2'	53:1:2287:A:H1'	2.08	0.54
53:1:2472:G:H2'	53:1:2475:C:H42	1.73	0.54
57:7:62:C:C3'	57:7:63:G:H5''	2.38	0.54
3:d:117:ARG:HA	3:d:185:LYS:HD3	1.90	0.54
10:k:7:MET:HB3	10:k:18:ARG:HD2	1.89	0.54
10:k:71:ARG:NH1	15:p:71:ARG:HH22	2.06	0.54
30:F:33:HIS:O	30:F:35:GLN:HG2	2.07	0.54
33:I:197:HIS:HE1	34:J:103:GLY:HA2	1.73	0.54
41:Q:56:LEU:HD12	41:Q:60:PHE:HB2	1.90	0.54
49:Y:20:ASN:ND2	52:3:323:U:OP1	2.34	0.54
52:3:113:G:H1'	52:3:354:G:H5''	1.88	0.54
52:3:224:U:H2'	52:3:225:C:C6	2.42	0.54
53:1:174:U:H2'	53:1:175:G:C8	2.42	0.54
53:1:598:U:H2'	53:1:599:A:H8	1.71	0.54
53:1:1023:U:O2'	53:1:1122:G:H5'	2.07	0.54
6:g:44:ILE:O	6:g:48:GLU:HG2	2.08	0.54
8:i:122:GLU:HG3	8:i:126:ARG:NH1	2.23	0.54
10:k:17:ARG:HB3	10:k:45:GLU:OE2	2.07	0.54
34:J:107:GLY:HA2	52:3:8:A:H1'	1.90	0.54
38:N:105:ARG:HG3	52:3:1118:U:H5'	1.90	0.54
41:Q:26:CYS:CB	41:Q:29:LYS:HE2	2.38	0.54
52:3:70:U:H4'	52:3:71:A:H8	1.73	0.54
53:1:2047:C:H2'	53:1:2048:G:C8	2.43	0.54
54:2:3:C:H3'	54:2:4:C:H5''	1.90	0.54
39:O:57:VAL:O	39:O:58:ASN:HB2	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Q:3:VAL:HG23	46:V:35:LYS:HE2	1.89	0.53
52:3:772:U:H2'	52:3:773:G:C8	2.43	0.53
52:3:1170:A:H2'	52:3:1171:A:O4'	2.08	0.53
52:3:1354:U:H2'	52:3:1355:G:H8	1.73	0.53
53:1:145:C:H2'	53:1:146:A:C8	2.43	0.53
53:1:2529:G:OP2	53:1:2530:A:H5''	2.07	0.53
54:2:95:U:H2'	54:2:96:G:C8	2.43	0.53
1:b:42:ARG:N	1:b:42:ARG:HD2	2.23	0.53
1:b:245:THR:HG23	1:b:247:TRP:H	1.74	0.53
2:c:124:ARG:HA	2:c:165:MET:HE3	1.90	0.53
23:x:6:VAL:HG11	23:x:57:VAL:HG11	1.90	0.53
52:3:1430:A:H2'	52:3:1431:A:H5'	1.89	0.53
52:3:1513:A:H2'	52:3:1514:G:H8	1.73	0.53
53:1:1300:G:H4'	53:1:1301:A:H5'	1.89	0.53
1:b:93:VAL:HG22	1:b:101:ARG:O	2.09	0.53
33:I:50:TYR:CE2	52:3:508:U:H4'	2.43	0.53
36:L:24:LYS:HE3	52:3:1375:A:H5''	1.89	0.53
38:N:114:LYS:HB2	38:N:117:LEU:HD22	1.89	0.53
52:3:77:A:H2'	52:3:78:A:H8	1.73	0.53
52:3:663:A:H5'	52:3:836:G:OP1	2.08	0.53
52:3:917:G:H2'	52:3:918:A:C8	2.43	0.53
53:1:2443:C:H2'	53:1:2444:G:C8	2.43	0.53
55:6:36:U:H2'	55:6:37:A:O4'	2.08	0.53
6:g:93:SER:OG	6:g:123:ARG:HG2	2.08	0.53
8:i:10:LEU:N	8:i:10:LEU:HD23	2.23	0.53
19:t:24:MET:HE1	19:t:30:ILE:HG13	1.90	0.53
38:N:57:VAL:HG23	38:N:58:GLU:N	2.20	0.53
43:S:7:ALA:HA	43:S:10:VAL:HG12	1.90	0.53
53:1:1909:C:H2'	53:1:1910:G:C8	2.44	0.53
22:w:33:ILE:HD11	22:w:78:ILE:HD11	1.91	0.53
35:K:18:VAL:N	35:K:19:PRO:CD	2.71	0.53
38:N:6:TYR:CZ	52:3:1147:C:H4'	2.44	0.53
38:N:25:GLY:HA3	38:N:57:VAL:O	2.09	0.53
41:Q:98:ARG:HB2	41:Q:116:TYR:HA	1.91	0.53
52:3:225:C:C2'	52:3:226:G:H5''	2.38	0.53
53:1:864:G:O2'	53:1:865:C:H5'	2.09	0.53
4:e:107:VAL:HB	4:e:108:PRO:HD3	1.90	0.53
8:i:97:VAL:HB	8:i:137:LEU:HD23	1.91	0.53
11:l:3:LEU:HD23	53:1:1203:U:H5'	1.89	0.53
41:Q:106:VAL:CG1	41:Q:109:ARG:HD3	2.39	0.53
46:V:12:VAL:HB	46:V:21:VAL:HG13	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:3:ILE:O	50:Z:3:ILE:HG22	2.08	0.53
51:a:193:LEU:HA	51:a:196:LEU:HD12	1.91	0.53
52:3:514:C:H2'	52:3:515:G:C8	2.43	0.53
52:3:1413:A:H2	52:3:1487:G:H22	1.56	0.53
53:1:669:G:H2'	53:1:669:G:N3	2.23	0.53
12:m:64:TRP:HB2	12:m:104:GLU:HB2	1.91	0.53
19:t:34:VAL:HG11	19:t:43:ILE:HD13	1.90	0.53
36:L:97:ALA:HA	36:L:100:MET:HE3	1.90	0.53
52:3:1293:C:H2'	52:3:1294:G:C8	2.43	0.53
52:3:1395:C:H6	52:3:1395:C:H5'	1.74	0.53
53:1:340:A:H2'	53:1:341:C:O4'	2.09	0.53
53:1:1181:U:H2'	53:1:1182:G:C8	2.43	0.53
53:1:2360:G:H2'	53:1:2361:G:H5'	1.89	0.53
7:h:47:GLU:CD	7:h:95:LEU:HD11	2.34	0.53
8:i:25:PRO:HG2	57:7:55:U:C5'	2.39	0.53
46:V:35:LYS:HG2	46:V:36:PHE:N	2.23	0.53
52:3:1527:U:O2'	52:3:1528:U:H5'	2.09	0.53
53:1:1020:A:C1'	53:1:1021:A:OP2	2.56	0.53
53:1:1386:C:H2'	53:1:1387:A:H8	1.73	0.53
53:1:1434:A:H2'	53:1:1435:G:C8	2.44	0.53
54:2:30:C:H2'	54:2:31:C:O4'	2.09	0.53
58:8:245:ILE:N	58:8:245:ILE:HD12	2.24	0.53
2:c:2:ILE:HD12	2:c:2:ILE:N	2.24	0.53
10:k:28:SER:OG	53:1:2566:A:N1	2.40	0.53
33:I:124:VAL:HG22	33:I:125:ASN:ND2	2.23	0.53
53:1:581:C:H2'	53:1:582:A:H8	1.74	0.53
53:1:1316:U:H2'	53:1:1317:G:C8	2.44	0.53
53:1:1709:U:H2'	53:1:1710:G:C8	2.44	0.53
7:h:2:ALA:HB3	7:h:6:GLN:NE2	2.24	0.53
22:w:39:THR:H	53:1:2331:G:H4'	1.74	0.53
36:L:37:THR:O	36:L:41:ILE:HG13	2.09	0.53
37:M:54:THR:C	37:M:56:PRO:HD3	2.34	0.53
38:N:112:ARG:HH12	38:N:114:LYS:HD2	1.74	0.53
53:1:174:U:H2'	53:1:175:G:H8	1.74	0.53
53:1:2514:U:H2'	53:1:2515:C:C6	2.44	0.53
53:1:2545:G:C2'	53:1:2546:U:H5'	2.38	0.53
57:7:68:C:H2'	57:7:69:G:C8	2.44	0.53
3:d:27:LEU:HD12	53:1:600:G:C5'	2.39	0.52
4:e:58:ALA:O	4:e:139:GLU:HG2	2.08	0.52
6:g:61:VAL:HG23	6:g:62:LEU:HD12	1.91	0.52
32:H:5:HIS:HB3	43:S:88:MET:HE3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:6:ILE:HG13	42:R:8:ILE:HG12	1.91	0.52
52:3:911:U:H2'	52:3:912:C:C6	2.44	0.52
52:3:1389:C:H2'	52:3:1390:U:C6	2.44	0.52
53:1:1539:U:H2'	53:1:1540:G:H8	1.74	0.52
53:1:2041:U:H2'	53:1:2042:A:C8	2.44	0.52
53:1:2190:G:H2'	53:1:2191:A:H8	1.74	0.52
55:6:41:C:H2'	55:6:42:G:C8	2.44	0.52
4:e:29:ARG:HH22	54:2:57:A:H2	1.57	0.52
4:e:91:ARG:HH21	54:2:45:A:H1'	1.74	0.52
5:f:26:LYS:HG3	5:f:31:GLU:HB2	1.91	0.52
17:r:81:LYS:HD2	53:1:973:A:H5''	1.90	0.52
38:N:30:ASN:O	38:N:32:ARG:NH1	2.42	0.52
41:Q:53:ARG:HG2	41:Q:63:THR:HG22	1.91	0.52
52:3:987:G:H2'	52:3:988:G:H8	1.74	0.52
52:3:1202:U:C2'	52:3:1203:C:H5'	2.39	0.52
53:1:2224:G:H4'	53:1:2226:C:C2	2.44	0.52
53:1:2545:G:H2'	53:1:2546:U:H5'	1.91	0.52
53:1:2691:C:H2'	53:1:2692:G:H8	1.75	0.52
58:8:164:PRO:HB2	58:8:167:ASP:HB2	1.90	0.52
4:e:155:ILE:HD12	4:e:155:ILE:N	2.24	0.52
11:l:46:VAL:HG11	11:l:50:PHE:CG	2.45	0.52
13:n:73:ASN:HA	13:n:76:VAL:HG12	1.92	0.52
16:q:2:ARG:HA	53:1:1248:G:O2'	2.09	0.52
51:a:37:LYS:HD3	53:1:2128:G:OP2	2.09	0.52
52:3:123:U:H5''	52:3:311:C:O2'	2.09	0.52
52:3:680:C:H2'	52:3:681:A:C8	2.44	0.52
52:3:1173:U:H2'	52:3:1174:G:C8	2.44	0.52
53:1:278:A:H2'	53:1:278:A:N3	2.23	0.52
53:1:1709:U:O2'	53:1:2859:G:H1'	2.09	0.52
53:1:2241:A:H2'	53:1:2242:G:C8	2.44	0.52
53:1:2297:A:H62	53:1:2319:G:H1'	1.74	0.52
53:1:2423:U:O2'	53:1:2425:A:H2'	2.10	0.52
58:8:17:THR:HG23	58:8:79:HIS:CE1	2.43	0.52
58:8:215:ILE:HG21	58:8:287:ILE:HD11	1.91	0.52
2:c:133:THR:HG23	2:c:134:HIS:CD2	2.44	0.52
4:e:91:ARG:HH21	54:2:45:A:C1'	2.23	0.52
8:i:129:GLU:HG2	8:i:139:VAL:HG21	1.90	0.52
26:B:30:ASP:HB3	26:B:34:GLY:N	2.25	0.52
35:K:40:GLU:HB3	35:K:61:LEU:HB3	1.92	0.52
37:M:28:SER:HB3	37:M:58:LEU:HB2	1.90	0.52
39:O:52:LEU:HB2	43:S:80:ARG:HD2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:817:C:H4'	52:3:818:G:C5'	2.40	0.52
52:3:860:A:H2'	52:3:861:G:O4'	2.09	0.52
52:3:987:G:H2'	52:3:988:G:C8	2.44	0.52
53:1:1326:U:H2'	53:1:1327:A:H8	1.75	0.52
53:1:1810:A:H2'	53:1:1811:G:O4'	2.09	0.52
53:1:2120:G:H2'	53:1:2121:G:C8	2.44	0.52
1:b:268:ARG:NH2	52:3:680:C:O2'	2.42	0.52
3:d:63:LYS:CE	53:1:2444:G:OP2	2.56	0.52
5:f:134:GLY:HA3	5:f:140:ILE:HG21	1.90	0.52
23:x:7:THR:OG1	23:x:9:LYS:HG3	2.10	0.52
33:I:82:LYS:HD2	52:3:5:U:C4	2.44	0.52
37:M:80:PRO:HG2	52:3:878:A:H5'	1.91	0.52
38:N:17:ARG:HB2	38:N:65:THR:OG1	2.10	0.52
53:1:323:C:H2'	53:1:1205:A:H61	1.73	0.52
53:1:1045:C:OP1	53:1:1047:G:H5'	2.10	0.52
53:1:1078:U:H5''	53:1:1079:C:H5''	1.90	0.52
53:1:2533:U:H2'	53:1:2534:A:O4'	2.09	0.52
54:2:19:C:H2'	54:2:20:G:C8	2.45	0.52
54:2:118:C:H2'	54:2:119:A:C8	2.45	0.52
58:8:304:LYS:HE3	58:8:360:VAL:HG12	1.90	0.52
3:d:24:ASN:ND2	3:d:27:LEU:HB2	2.24	0.52
3:d:148:ILE:HD13	3:d:187:VAL:HG13	1.92	0.52
11:l:4:ASN:O	53:1:1243:C:H1'	2.10	0.52
11:l:93:ASN:C	11:l:95:LEU:H	2.17	0.52
45:U:19:VAL:HG13	45:U:36:VAL:O	2.10	0.52
52:3:530:G:H3'	52:3:531:U:C5'	2.40	0.52
53:1:1827:U:O2'	53:1:1828:G:H5'	2.10	0.52
53:1:2193:G:H2'	53:1:2194:U:C6	2.44	0.52
53:1:2432:A:H1'	55:6:75:C:C4'	2.40	0.52
53:1:2514:U:H2'	53:1:2515:C:H6	1.74	0.52
57:7:62:C:H3'	57:7:63:G:H5''	1.92	0.52
58:8:209:LYS:HB3	58:8:234:ARG:HD3	1.91	0.52
1:b:68:ARG:O	1:b:188:ARG:NH1	2.43	0.52
3:d:164:LEU:H	3:d:164:LEU:HD12	1.74	0.52
34:J:92:ARG:O	34:J:93:VAL:C	2.52	0.52
37:M:12:ARG:CZ	52:3:826:C:H5'	2.40	0.52
53:1:435:C:C2'	53:1:436:C:H5'	2.37	0.52
53:1:542:C:C2'	53:1:543:G:H5''	2.39	0.52
53:1:1874:C:H2'	53:1:1875:G:O4'	2.09	0.52
53:1:2141:G:H2'	53:1:2142:A:H8	1.75	0.52
6:g:124:THR:OG1	6:g:128:HIS:NE2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:31:ARG:NH2	53:1:1054:A:O3'	2.43	0.52
9:j:47:HIS:ND1	9:j:48:VAL:HG23	2.25	0.52
10:k:47:ILE:HG23	10:k:48:PRO:HD2	1.92	0.52
11:l:48:ARG:HD3	53:1:666:A:H4'	1.92	0.52
11:l:77:ILE:HD12	11:l:77:ILE:N	2.25	0.52
14:o:24:THR:HG23	14:o:90:VAL:HA	1.91	0.52
15:p:89:GLY:HA2	15:p:111:GLU:HA	1.92	0.52
42:R:63:VAL:HG12	42:R:68:LEU:HG	1.92	0.52
53:1:171:U:H2'	53:1:172:A:H8	1.74	0.52
53:1:1825:U:H2'	53:1:1826:G:C8	2.44	0.52
53:1:2638:G:H1'	53:1:2778:A:H61	1.75	0.52
4:e:66:ILE:N	4:e:66:ILE:HD12	2.24	0.52
11:l:95:LEU:HD22	11:l:100:ILE:HD11	1.92	0.52
26:B:46:GLY:HA3	26:B:54:ILE:HG21	1.92	0.52
33:I:87:GLU:HA	33:I:90:LEU:HD12	1.91	0.52
39:O:15:HIS:HB3	39:O:70:HIS:NE2	2.25	0.52
8:i:93:ASN:HD22	53:1:1077:A:H5''	1.74	0.52
9:j:17:VAL:HG13	9:j:57:LEU:HD22	1.91	0.52
14:o:33:ARG:NE	54:2:52:A:H62	2.08	0.52
25:z:50:VAL:O	25:z:54:VAL:HG22	2.09	0.52
32:H:175:HIS:ND1	52:3:1108:G:H5'	2.25	0.52
35:K:36:ILE:HA	35:K:64:VAL:HG23	1.92	0.52
53:1:226:A:H2'	53:1:227:A:O4'	2.09	0.52
53:1:2553:G:H1'	53:1:2582:G:H21	1.75	0.52
4:e:31:GLU:HB3	4:e:156:THR:HG23	1.92	0.51
4:e:32:LYS:HA	4:e:95:MET:SD	2.50	0.51
30:F:9:LYS:NZ	30:F:16:ILE:HG13	2.26	0.51
31:G:94:ARG:HG3	52:3:1100:C:OP2	2.09	0.51
34:J:134:ASN:ND2	52:3:19:A:OP1	2.42	0.51
49:Y:3:ILE:O	49:Y:4:LYS:HD2	2.10	0.51
53:1:523:C:H2'	53:1:524:G:H8	1.75	0.51
53:1:742:A:H2'	53:1:743:A:C8	2.45	0.51
53:1:783:A:H2'	53:1:784:G:H5'	1.92	0.51
53:1:1700:A:H2'	53:1:1701:A:H5'	1.92	0.51
53:1:2233:U:H2'	53:1:2234:G:C8	2.45	0.51
4:e:24:VAL:O	4:e:27:VAL:HG22	2.10	0.51
6:g:47:PHE:HA	6:g:51:ARG:HB2	1.92	0.51
8:i:33:ASN:HB2	8:i:36:GLU:CG	2.37	0.51
23:x:13:THR:CG2	53:1:188:G:H5'	2.40	0.51
45:U:70:ARG:O	45:U:74:LEU:HD12	2.10	0.51
52:3:20:U:H2'	52:3:21:G:O4'	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:555:U:H2'	52:3:556:C:C6	2.45	0.51
52:3:1499:A:O2'	52:3:1520:C:H5'	2.09	0.51
53:1:851:C:H2'	53:1:852:U:C6	2.46	0.51
53:1:1090:A:H2'	53:1:1091:G:C8	2.45	0.51
53:1:1905:C:H4'	53:1:1929:G:H8	1.73	0.51
53:1:2315:G:H2'	53:1:2316:G:C8	2.45	0.51
7:h:30:SER:H	7:h:109:LYS:HZ2	1.56	0.51
10:k:2:ILE:HG21	10:k:8:LEU:HD21	1.93	0.51
11:l:111:ILE:HD11	53:1:636:G:C6	2.46	0.51
34:J:152:VAL:HG23	34:J:163:ILE:HD12	1.91	0.51
52:3:1422:G:H2'	52:3:1423:G:H8	1.74	0.51
53:1:306:U:H3	53:1:310:A:H62	1.58	0.51
53:1:729:G:H4'	53:1:763:G:C5'	2.41	0.51
53:1:2671:G:H2'	53:1:2672:U:C6	2.46	0.51
58:8:5:LYS:HA	58:8:265:LEU:HB3	1.92	0.51
1:b:206:LYS:HB2	1:b:209:ALA:HB2	1.91	0.51
3:d:118:LEU:HD12	3:d:186:VAL:O	2.09	0.51
19:t:66:LYS:HD3	19:t:68:LYS:HE2	1.92	0.51
32:H:150:VAL:HG23	32:H:167:TYR:HB3	1.92	0.51
32:H:200:TRP:C	32:H:201:ILE:HD12	2.35	0.51
33:I:80:ARG:NH2	52:3:613:C:OP2	2.43	0.51
36:L:76:SER:OG	36:L:83:THR:HG22	2.11	0.51
37:M:60:LEU:HD12	37:M:60:LEU:N	2.24	0.51
48:X:44:ILE:HD13	48:X:63:ASP:HA	1.92	0.51
51:a:166:ASP:OD2	51:a:168:ASN:HB2	2.09	0.51
53:1:492:A:H2'	53:1:493:G:O4'	2.10	0.51
53:1:1138:G:H2'	53:1:1139:G:O4'	2.11	0.51
56:4:9:G:H2'	56:4:10:G:H8	1.75	0.51
1:b:260:LYS:O	1:b:263:ASP:OD1	2.29	0.51
6:g:40:THR:HG21	6:g:42:LYS:HZ3	1.76	0.51
7:h:25:ALA:HA	7:h:115:GLY:HA2	1.92	0.51
18:s:93:ALA:HB2	53:1:1614:A:H2	1.74	0.51
37:M:12:ARG:HD2	37:M:26:MET:HG2	1.91	0.51
40:P:58:THR:HG23	40:P:61:ALA:H	1.75	0.51
45:U:33:ILE:HG21	45:U:60:TRP:CH2	2.46	0.51
47:W:28:LEU:HD11	47:W:58:ILE:HD13	1.92	0.51
52:3:46:G:O2'	52:3:365:U:H1'	2.10	0.51
52:3:77:A:H2'	52:3:78:A:C8	2.45	0.51
53:1:1605:C:H2'	53:1:1606:C:H5'	1.92	0.51
53:1:2134:A:N6	53:1:2157:G:H4'	2.26	0.51
53:1:2162:G:H2'	53:1:2163:A:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:8:25:LYS:HE3	58:8:84:GLY:N	2.26	0.51
9:j:78:THR:HB	53:1:2641:G:H5''	1.92	0.51
29:E:37:THR:HA	29:E:40:LYS:HE3	1.93	0.51
52:3:985:C:H2'	52:3:986:U:C6	2.46	0.51
53:1:565:C:H2'	53:1:566:U:C6	2.45	0.51
53:1:2139:U:H2'	53:1:2140:G:C8	2.46	0.51
13:n:82:GLU:CG	13:n:86:ARG:HH22	2.24	0.51
29:E:53:ASP:OD2	53:1:2359:C:H4'	2.11	0.51
53:1:680:C:H2'	53:1:681:G:C8	2.46	0.51
21:v:78:GLN:HE22	54:2:76:G:H1'	1.76	0.51
22:w:25:GLU:HG3	53:1:923:G:H4'	1.91	0.51
34:J:152:VAL:HA	34:J:155:LYS:HG2	1.92	0.51
42:R:22:TYR:HB3	42:R:65:GLU:HG3	1.93	0.51
51:a:47:ASN:HB3	51:a:211:LYS:H	1.76	0.51
53:1:1287:A:C2'	53:1:1288:G:H5'	2.41	0.51
53:1:1956:U:C2'	53:1:1957:C:H5'	2.41	0.51
53:1:1983:G:H4'	53:1:2606:C:H4'	1.92	0.51
53:1:1999:C:H5''	53:1:2723:C:O2'	2.10	0.51
3:d:22:ASP:HA	3:d:114:ARG:HH22	1.75	0.51
7:h:3:LEU:HD21	53:1:1043:C:H5''	1.92	0.51
22:w:20:LYS:CE	53:1:2355:G:H4'	2.41	0.51
23:x:18:SER:HB2	53:1:2080:A:H5'	1.91	0.51
23:x:50:VAL:HG22	23:x:54:GLY:HA3	1.93	0.51
35:K:2:ARG:HG3	35:K:92:THR:CG2	2.28	0.51
43:S:39:ASP:HA	43:S:42:ASN:HD22	1.75	0.51
52:3:16:A:O2'	52:3:17:U:H5'	2.11	0.51
52:3:825:A:H2'	52:3:826:C:C6	2.46	0.51
52:3:1094:G:N3	52:3:1094:G:H2'	2.26	0.51
52:3:1357:A:H61	52:3:1365:G:H1	1.57	0.51
52:3:1477:U:H2'	52:3:1478:U:C6	2.46	0.51
53:1:239:C:H2'	53:1:240:C:O4'	2.11	0.51
53:1:1213:A:N6	53:1:1236:G:H1'	2.26	0.51
58:8:20:HIS:CE1	58:8:21:VAL:HG12	2.45	0.51
58:8:128:VAL:HG13	58:8:163:PHE:HZ	1.76	0.51
1:b:48:ILE:HD11	1:b:51:ARG:HA	1.93	0.51
5:f:74:MET:O	5:f:78:VAL:HG22	2.11	0.51
6:g:66:ASN:HD22	6:g:135:HIS:HD2	1.59	0.51
32:H:155:ARG:HD3	52:3:1055:A:O2'	2.10	0.51
36:L:15:PRO:O	38:N:45:MET:HE2	2.11	0.51
52:3:40:C:H2'	52:3:41:G:H8	1.75	0.51
53:1:189:G:H2'	53:1:205:G:H22	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:225:C:H2'	53:1:226:A:O4'	2.10	0.51
54:2:106:G:H2'	54:2:107:G:O4'	2.11	0.51
1:b:75:ALA:HB3	1:b:115:ILE:HG13	1.93	0.50
7:h:34:THR:O	7:h:37:LYS:HG2	2.11	0.50
9:j:2:LYS:HE3	53:1:995:C:N4	2.25	0.50
9:j:59:ALA:HB1	9:j:101:ILE:HD13	1.92	0.50
10:k:25:LEU:CD2	53:1:2562:U:H4'	2.41	0.50
16:q:69:ARG:HH12	53:1:1012:U:P	2.35	0.50
20:u:13:LEU:O	20:u:18:LYS:HG3	2.12	0.50
51:a:211:LYS:HZ3	53:1:2177:C:H5''	1.76	0.50
52:3:1429:A:H2'	52:3:1430:A:C8	2.43	0.50
52:3:1434:A:H2'	52:3:1435:G:O4'	2.10	0.50
53:1:962:G:H21	53:1:2250:G:H1	1.57	0.50
53:1:1112:G:H2'	53:1:1113:U:C6	2.46	0.50
53:1:1565:C:O2'	53:1:1566:A:H2'	2.10	0.50
55:6:17:C:H2'	55:6:17(A):U:H5	1.73	0.50
8:i:106:GLN:O	8:i:110:GLN:HG3	2.11	0.50
19:t:61:LEU:HD21	19:t:82:LYS:HG3	1.93	0.50
25:z:26:LEU:HB2	25:z:28:LEU:HD12	1.94	0.50
30:F:7:VAL:HG13	30:F:37:GLN:O	2.11	0.50
32:H:162:ALA:CB	52:3:1056:U:H4'	2.41	0.50
35:K:11:HIS:HB3	35:K:14:GLN:HB2	1.93	0.50
43:S:4:SER:HB3	52:3:1216:A:H5''	1.94	0.50
53:1:75:G:H22	53:1:111:A:H2	1.59	0.50
53:1:765:C:H2'	53:1:766:U:C6	2.46	0.50
53:1:1026:G:H2'	53:1:1027:A:H8	1.76	0.50
53:1:1316:U:H2'	53:1:1317:G:H8	1.76	0.50
53:1:2443:C:O2'	53:1:2444:G:H5'	2.10	0.50
54:2:37:C:H42	54:2:49:C:H1'	1.77	0.50
57:7:62:C:H2'	57:7:63:G:H5''	1.93	0.50
58:8:89:VAL:O	58:8:93:ILE:HG13	2.10	0.50
58:8:117:ARG:HA	58:8:157:LEU:HD21	1.92	0.50
3:d:24:ASN:HD22	3:d:27:LEU:HB2	1.77	0.50
3:d:61:ARG:HH11	3:d:65:THR:HG23	1.75	0.50
22:w:74:LYS:NZ	53:1:857:G:H5''	2.26	0.50
39:O:15:HIS:HB3	39:O:70:HIS:CD2	2.45	0.50
48:X:5:LYS:HG3	48:X:6:LYS:HG2	1.94	0.50
52:3:1128:C:O2'	52:3:1129:C:H5'	2.12	0.50
52:3:1333:A:H2'	52:3:1334:G:O4'	2.11	0.50
53:1:1365:A:N3	53:1:1365:A:H2'	2.26	0.50
53:1:2589:A:H2'	53:1:2590:A:H8	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:j:24:THR:HB	9:j:27:ARG:HG2	1.92	0.50
11:l:119:PRO:HG3	11:l:138:ALA:O	2.11	0.50
15:p:108:ARG:HD2	52:3:1463:U:OP1	2.11	0.50
40:P:91:GLY:O	40:P:95:THR:HG23	2.11	0.50
43:S:2:LYS:HE3	43:S:5:MET:HG3	1.94	0.50
44:T:63:ARG:NE	44:T:87:ARG:HH22	2.08	0.50
49:Y:80:ALA:HA	49:Y:83:ASN:ND2	2.26	0.50
52:3:245:U:O2'	52:3:246:A:H5'	2.12	0.50
52:3:381:C:H2'	52:3:382:A:O4'	2.11	0.50
52:3:1201:A:C1'	52:3:1202:U:OP2	2.60	0.50
52:3:1497:G:C2'	52:3:1498:U:H5'	2.41	0.50
53:1:859:G:O2'	53:1:860:U:H6	1.95	0.50
53:1:1175:A:H5'	53:1:1176:U:O4'	2.11	0.50
53:1:1281:G:H2'	53:1:1282:U:C6	2.47	0.50
54:2:60:C:H2'	54:2:61:G:H8	1.76	0.50
57:7:1:G:O3'	58:8:90:LYS:NZ	2.43	0.50
58:8:306:GLU:HB2	58:8:391:LYS:HB2	1.93	0.50
8:i:93:ASN:ND2	53:1:1077:A:C5'	2.73	0.50
8:i:94:LYS:HZ1	53:1:1076:C:H4'	1.76	0.50
12:m:10:ARG:HG2	12:m:11:LYS:HD3	1.93	0.50
20:u:35:VAL:HG23	20:u:38:ILE:HB	1.93	0.50
24:y:19:LEU:O	24:y:23:ARG:HB2	2.11	0.50
28:D:3:ARG:HG2	53:1:1613:G:H4'	1.92	0.50
33:I:10:LEU:HD23	33:I:10:LEU:H	1.76	0.50
52:3:1138:G:H3'	52:3:1138:G:N3	2.26	0.50
53:1:1073:A:H2'	53:1:1074:G:O4'	2.11	0.50
53:1:1906:G:C3'	53:1:1907:G:H5''	2.41	0.50
53:1:2710:C:H2'	53:1:2711:A:C8	2.46	0.50
1:b:104:LEU:HD11	1:b:155:ARG:HG2	1.94	0.50
5:f:155:PRO:HG3	53:1:2530:A:N6	2.27	0.50
21:v:2:PHE:HD1	21:v:50:MET:HE3	1.77	0.50
35:K:5:GLU:HB2	35:K:90:MET:HB2	1.94	0.50
52:3:1305:G:H22	52:3:1331:G:H2'	1.76	0.50
52:3:1346:A:C2'	52:3:1347:G:H4'	2.41	0.50
53:1:1527:G:H21	53:1:1545:A:H62	1.59	0.50
53:1:2698:U:H2'	53:1:2699:C:C6	2.46	0.50
54:2:108:A:H5'	54:2:109:A:O5'	2.12	0.50
57:7:25:C:H2'	57:7:26:A:C4'	2.42	0.50
58:8:10:LYS:HB2	58:8:76:HIS:HB2	1.93	0.50
4:e:84:ILE:HG21	53:1:2312:U:H5'	1.94	0.50
10:k:70:ARG:HG2	10:k:76:VAL:HG12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:79:THR:OG1	34:J:80:LEU:N	2.43	0.50
47:W:32:ILE:HD13	47:W:67:LEU:HD23	1.94	0.50
53:1:581:C:H2'	53:1:582:A:C8	2.47	0.50
53:1:685:A:H5''	53:1:788:A:H62	1.76	0.50
53:1:859:G:O2'	53:1:860:U:C6	2.65	0.50
53:1:1035:U:H2'	53:1:1036:G:H8	1.77	0.50
53:1:1704:C:H2'	53:1:1705:A:C8	2.47	0.50
54:2:63:C:H2'	54:2:64:G:H8	1.77	0.50
58:8:141:VAL:HG13	58:8:147:LEU:HD21	1.94	0.50
12:m:74:THR:HA	12:m:89:VAL:HA	1.94	0.50
33:I:95:GLY:O	33:I:136:VAL:HG12	2.11	0.50
34:J:61:LYS:HD3	52:3:1073:U:OP1	2.12	0.50
46:V:48:GLU:O	46:V:49:ASN:O	2.30	0.50
53:1:1433:A:H2'	53:1:1434:A:C8	2.46	0.50
58:8:108:ALA:HA	58:8:150:VAL:HG11	1.94	0.50
1:b:27:LYS:NZ	53:1:1428:C:OP2	2.45	0.50
4:e:65:LEU:HD12	54:2:41:G:N2	2.26	0.50
14:o:51:ALA:HB2	14:o:81:ARG:HD2	1.92	0.50
33:I:50:TYR:CD2	52:3:508:U:H4'	2.47	0.50
46:V:39:ARG:HD2	46:V:40:THR:N	2.27	0.50
53:1:917:A:H5''	53:1:2268:A:H61	1.76	0.50
53:1:996:A:H2'	53:1:997:G:C8	2.47	0.50
53:1:2773:C:H2'	53:1:2774:C:C6	2.46	0.50
4:e:84:ILE:HD13	53:1:2312:U:H5'	1.92	0.49
6:g:73:ASN:O	6:g:76:GLU:HG3	2.12	0.49
32:H:150:VAL:HG12	32:H:199:VAL:HG12	1.94	0.49
34:J:159:SER:O	34:J:162:GLU:HG2	2.11	0.49
40:P:12:ARG:CG	40:P:14:GLN:HE21	2.25	0.49
43:S:10:VAL:O	43:S:13:VAL:HG12	2.11	0.49
43:S:68:ARG:HE	52:3:1202:U:C4'	2.22	0.49
52:3:128:G:O2'	52:3:129:A:H5'	2.11	0.49
52:3:206:C:H2'	52:3:207:C:O4'	2.11	0.49
53:1:112:U:H2'	53:1:113:U:H5'	1.93	0.49
53:1:948:C:H2'	53:1:949:G:H8	1.76	0.49
53:1:2315:G:H2'	53:1:2316:G:H8	1.75	0.49
56:4:13:A:O2'	56:4:14:A:H5'	2.12	0.49
57:7:1:G:H4'	58:8:90:LYS:NZ	2.27	0.49
2:c:156:PHE:HB3	9:j:81:ILE:HG22	1.94	0.49
16:q:50:ARG:HG2	53:1:1156:A:C8	2.47	0.49
22:w:41:PHE:O	22:w:55:LEU:HD11	2.12	0.49
26:B:12:ARG:NH2	53:1:517:C:OP1	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:108:GLY:N	52:3:9:G:H4'	2.24	0.49
41:Q:45:ASN:HA	52:3:529:G:O6	2.12	0.49
42:R:14:ALA:HB3	42:R:33:LEU:HD21	1.94	0.49
52:3:31:G:N2	52:3:47:C:H5''	2.26	0.49
52:3:166:U:H2'	52:3:167:A:C8	2.48	0.49
53:1:1447:C:H2'	53:1:1448:G:C8	2.47	0.49
53:1:2348:U:O2'	53:1:2349:G:H5'	2.12	0.49
53:1:2623:G:H2'	53:1:2624:G:H8	1.77	0.49
28:D:26:ASN:CG	53:1:682:G:H5'	2.37	0.49
32:H:55:VAL:HG23	32:H:66:THR:OG1	2.11	0.49
41:Q:42:LYS:HZ3	52:3:1491:G:H5''	1.76	0.49
52:3:757:U:H2'	52:3:758:C:O4'	2.12	0.49
52:3:1060:U:H2'	52:3:1061:G:H8	1.77	0.49
52:3:1163:A:H2'	52:3:1164:G:C8	2.47	0.49
52:3:1219:A:H2'	52:3:1220:G:C8	2.47	0.49
53:1:290:U:H2'	53:1:291:G:H8	1.78	0.49
53:1:472:A:H2'	53:1:473:G:H5'	1.93	0.49
54:2:66:A:H5''	54:2:67:G:OP1	2.12	0.49
55:5:41:C:H2'	55:5:42:G:C8	2.47	0.49
58:8:92:MET:HE2	58:8:119:HIS:HD2	1.78	0.49
58:8:171:VAL:HG11	58:8:192:LEU:HD13	1.93	0.49
3:d:88:ARG:HB3	3:d:89:PRO:HD2	1.93	0.49
5:f:8:VAL:HB	5:f:49:LEU:HB2	1.94	0.49
7:h:108:VAL:HG13	7:h:109:LYS:H	1.76	0.49
11:l:65:GLY:HA2	53:1:2415:G:H4'	1.94	0.49
11:l:117:THR:OG1	11:l:118:THR:N	2.45	0.49
29:E:2:LYS:HG3	53:1:242:G:H8	1.75	0.49
29:E:63:TYR:OH	53:1:593:U:H5'	2.12	0.49
40:P:44:ALA:HB3	40:P:69:CYS:HB2	1.93	0.49
43:S:100:TRP:HZ2	52:3:1368:A:H5''	1.78	0.49
53:1:687:C:H2'	53:1:688:U:O4'	2.12	0.49
53:1:1947:C:H2'	53:1:1948:G:C8	2.47	0.49
53:1:2323:G:O2'	53:1:2324:U:H5'	2.12	0.49
53:1:2834:G:H2'	53:1:2879:A:H61	1.76	0.49
54:2:104:A:H2'	54:2:105:G:O4'	2.11	0.49
4:e:28:PRO:HG3	4:e:164:GLU:OE2	2.12	0.49
7:h:53:ARG:HH21	7:h:55:VAL:HG21	1.77	0.49
12:m:42:THR:HG22	12:m:93:VAL:HG12	1.94	0.49
20:u:6:ARG:N	53:1:85:G:OP1	2.45	0.49
31:G:5:MET:O	31:G:9:LEU:HG	2.12	0.49
31:G:91:VAL:O	31:G:91:VAL:HG13	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:104:THR:HG22	38:N:106:ASP:H	1.77	0.49
40:P:15:VAL:HG22	40:P:16:SER:H	1.76	0.49
43:S:68:ARG:HH21	52:3:1202:U:C4'	2.25	0.49
52:3:458:U:H2'	52:3:459:A:C8	2.47	0.49
52:3:1256:A:H1'	52:3:1258:G:C4	2.48	0.49
52:3:1386:G:H2'	52:3:1387:G:H8	1.77	0.49
53:1:962:G:O2'	53:1:963:U:H5'	2.12	0.49
53:1:1083:U:H2'	53:1:1085:A:OP2	2.12	0.49
53:1:1825:U:H2'	53:1:1826:G:H8	1.78	0.49
53:1:2553:G:C3'	53:1:2554:U:H5''	2.40	0.49
55:6:71:C:H2'	55:6:72:A:C8	2.48	0.49
1:b:200:MET:HE2	53:1:1820:U:C5	2.46	0.49
9:j:84:ILE:HD12	53:1:1131:G:H4'	1.94	0.49
24:y:21:LEU:HD22	24:y:25:GLN:HG2	1.95	0.49
35:K:75:GLU:HA	35:K:78:PHE:HD2	1.77	0.49
54:2:48:U:H2'	54:2:49:C:C6	2.48	0.49
10:k:40:LYS:HD2	10:k:57:VAL:HG22	1.93	0.49
19:t:61:LEU:HB3	53:1:1341:G:H5'	1.95	0.49
29:E:6:VAL:HG23	29:E:9:ALA:HB3	1.94	0.49
37:M:11:THR:HG21	52:3:876:C:H1'	1.95	0.49
41:Q:41:PRO:HG3	41:Q:49:ARG:HG3	1.95	0.49
41:Q:73:LEU:HD22	41:Q:73:LEU:N	2.26	0.49
43:S:42:ASN:O	43:S:46:LYS:HG2	2.13	0.49
51:a:7:ARG:HB3	53:1:2129:C:OP1	2.12	0.49
51:a:192:LEU:O	51:a:192:LEU:HD23	2.13	0.49
52:3:483:C:H2'	52:3:484:G:C8	2.47	0.49
52:3:514:C:H2'	52:3:515:G:H8	1.78	0.49
53:1:1817:G:N2	53:1:1818:U:H1'	2.27	0.49
53:1:2291:U:H2'	53:1:2292:U:C6	2.48	0.49
53:1:2469:A:H2'	53:1:2470:G:O4'	2.12	0.49
58:8:232:VAL:HB	58:8:271:ALA:HA	1.94	0.49
4:e:3:LEU:HD23	4:e:100:GLU:HG3	1.95	0.49
14:o:55:GLU:HG3	54:2:116:G:O5'	2.11	0.49
18:s:29:VAL:HG12	18:s:55:ILE:HD11	1.94	0.49
32:H:162:ALA:HB3	52:3:1056:U:H5'	1.95	0.49
38:N:5:TYR:HB2	38:N:20:ILE:HG23	1.94	0.49
52:3:886:G:H2'	52:3:887:G:C8	2.48	0.49
53:1:176:A:O2'	53:1:177:G:H5'	2.13	0.49
53:1:1367:A:C2'	53:1:1368:G:H5'	2.41	0.49
53:1:1652:A:H2'	53:1:1653:G:O4'	2.13	0.49
53:1:1831:G:H2'	53:1:1832:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:94:ILE:HD12	6:g:94:ILE:N	2.27	0.49
10:k:91:SER:HB2	10:k:93:GLN:HG2	1.95	0.49
16:q:30:VAL:HG13	53:1:580:U:O3'	2.13	0.49
35:K:91:ARG:NH1	52:3:738:C:OP2	2.46	0.49
36:L:80:GLY:HA3	56:4:11:U:O2'	2.13	0.49
52:3:257:G:H2'	52:3:258:G:H8	1.78	0.49
52:3:1506:U:O2'	52:3:1507:A:H5'	2.12	0.49
53:1:208:C:H2'	53:1:209:C:C6	2.47	0.49
53:1:1447:C:H2'	53:1:1448:G:H8	1.77	0.49
54:2:35:C:C2'	54:2:36:C:H5'	2.43	0.49
1:b:106:PRO:HG2	1:b:109:LEU:HB2	1.94	0.49
11:l:81:ASP:HB2	11:l:84:LYS:HD2	1.94	0.49
13:n:100:CYS:HB3	13:n:110:MET:HG3	1.95	0.49
16:q:87:VAL:HG22	17:r:49:ILE:O	2.13	0.49
31:G:46:VAL:HG13	31:G:47:PRO:HD3	1.95	0.49
31:G:211:LEU:HD23	31:G:211:LEU:O	2.12	0.49
33:I:44:LYS:HE3	33:I:45:PRO:HD2	1.95	0.49
33:I:58:GLN:O	33:I:62:ARG:HG2	2.12	0.49
34:J:9:GLU:OE1	34:J:9:GLU:N	2.46	0.49
40:P:71:ASP:O	40:P:72:ALA:HB3	2.13	0.49
52:3:70:U:H4'	52:3:71:A:C8	2.48	0.49
52:3:89:U:H2'	52:3:90:C:O4'	2.13	0.49
52:3:418:C:H2'	52:3:419:C:C6	2.47	0.49
53:1:394:C:O2'	53:1:395:U:H5'	2.13	0.49
53:1:395:U:H2'	53:1:396:G:H8	1.77	0.49
53:1:2087:G:H2'	53:1:2088:A:C8	2.48	0.49
58:8:33:THR:HG22	58:8:70:TYR:HB3	1.95	0.49
58:8:231:ARG:HA	58:8:274:ASN:HA	1.94	0.49
58:8:333:PHE:O	58:8:334:ARG:HG2	2.13	0.49
12:m:45:GLN:NE2	53:1:2485:G:H5''	2.20	0.48
15:p:94:ALA:HB2	53:1:2848:G:N7	2.28	0.48
31:G:102:ASN:ND2	31:G:105:THR:OG1	2.46	0.48
31:G:209:VAL:HA	31:G:212:TYR:CD2	2.47	0.48
46:V:52:CYS:HB3	46:V:77:VAL:HG21	1.95	0.48
52:3:56:U:H2'	52:3:57:G:H8	1.77	0.48
52:3:237:G:H2'	52:3:238:A:H8	1.78	0.48
52:3:439:U:H2'	52:3:440:C:O4'	2.12	0.48
53:1:171:U:H2'	53:1:172:A:C8	2.47	0.48
53:1:331:C:O2'	53:1:332:A:H5'	2.13	0.48
53:1:577:G:H2'	53:1:578:G:C8	2.47	0.48
53:1:1629:U:H2'	53:1:1630:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2489:U:C2'	53:1:2490:G:H5'	2.43	0.48
3:d:176:ASP:N	3:d:176:ASP:OD1	2.45	0.48
26:B:46:GLY:HA3	26:B:54:ILE:CG2	2.44	0.48
36:L:55:LYS:HB2	36:L:60:ALA:HB2	1.95	0.48
48:X:16:LYS:O	48:X:19:GLU:HG3	2.13	0.48
52:3:56:U:H2'	52:3:57:G:C8	2.47	0.48
53:1:858:G:H5'	53:1:859:G:OP2	2.13	0.48
53:1:1103:A:H2'	53:1:1103:A:N3	2.29	0.48
53:1:1278:C:H2'	53:1:1279:G:H8	1.78	0.48
53:1:2247:A:H2'	53:1:2248:C:C6	2.48	0.48
53:1:2579:C:O2'	53:1:2580:U:H5'	2.14	0.48
5:f:8:VAL:HG22	5:f:68:ARG:HE	1.78	0.48
25:z:3:THR:OG1	25:z:4:ILE:N	2.46	0.48
33:I:90:LEU:HD13	33:I:187:ARG:HD3	1.96	0.48
33:I:143:SER:C	33:I:144:ILE:HD12	2.38	0.48
39:O:6:ILE:HD12	39:O:6:ILE:H	1.79	0.48
40:P:81:LEU:HD12	40:P:81:LEU:O	2.12	0.48
44:T:81:ILE:HA	44:T:86:LEU:HD21	1.95	0.48
45:U:17:TYR:HB2	45:U:39:PHE:HB3	1.95	0.48
52:3:371:A:H2'	52:3:372:C:O4'	2.14	0.48
53:1:694:U:OP1	53:1:1569:A:H1'	2.13	0.48
53:1:1437:C:H2'	53:1:1438:U:C6	2.48	0.48
53:1:2875:C:H2'	53:1:2876:G:H8	1.78	0.48
58:8:207:ILE:HB	58:8:236:ILE:HD11	1.95	0.48
58:8:211:PHE:HA	58:8:235:GLY:HA3	1.95	0.48
12:m:4:PRO:HG3	12:m:68:PHE:HE2	1.78	0.48
16:q:88:GLU:OE1	17:r:52:PRO:HB3	2.12	0.48
17:r:83:TYR:HE1	17:r:85:LYS:HE2	1.79	0.48
28:D:39:ARG:NH1	53:1:469:G:O6	2.46	0.48
32:H:31:ASN:HB3	32:H:58:ARG:HH12	1.79	0.48
42:R:53:ASP:HA	42:R:56:ARG:HH11	1.77	0.48
43:S:20:PHE:O	43:S:21:ALA:HB3	2.12	0.48
43:S:25:GLU:HA	43:S:28:ALA:HB3	1.95	0.48
52:3:195:A:H2'	52:3:196:A:C8	2.47	0.48
52:3:410:G:H2'	52:3:429:U:O4	2.13	0.48
52:3:695:A:H2'	52:3:696:A:C8	2.49	0.48
52:3:868:C:H2'	52:3:869:G:O4'	2.13	0.48
53:1:121:G:H4'	53:1:149:A:H5'	1.93	0.48
53:1:948:C:H2'	53:1:949:G:C8	2.48	0.48
53:1:2048:G:H3'	53:1:2049:G:H5''	1.95	0.48
53:1:2329:U:H2'	53:1:2330:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2343:U:H2'	53:1:2344:U:C6	2.48	0.48
58:8:374:ARG:HA	58:8:388:VAL:HG12	1.96	0.48
6:g:55:GLU:HG3	6:g:58:LEU:HD12	1.95	0.48
11:l:63:LYS:O	29:E:29:ARG:NH1	2.47	0.48
13:n:86:ARG:HD2	13:n:117:ASP:CG	2.38	0.48
52:3:194:C:O2'	52:3:195:A:H5'	2.13	0.48
52:3:312:C:H2'	52:3:313:A:C8	2.48	0.48
53:1:1258:U:H2'	53:1:1259:G:C8	2.49	0.48
53:1:1571:A:H2'	53:1:1572:A:C8	2.48	0.48
28:D:19:ARG:HD3	53:1:125:A:OP2	2.13	0.48
29:E:44:ARG:N	29:E:45:PRO:HD2	2.29	0.48
30:F:9:LYS:HD2	30:F:14:CYS:HB2	1.96	0.48
32:H:205:GLU:OE2	32:H:206:ILE:HG22	2.14	0.48
33:I:56:GLU:HG3	33:I:198:LEU:HD12	1.96	0.48
33:I:187:ARG:HH12	33:I:192:ALA:HA	1.78	0.48
35:K:18:VAL:O	35:K:22:ILE:HG13	2.13	0.48
35:K:91:ARG:HA	35:K:91:ARG:HE	1.78	0.48
44:T:9:LYS:O	44:T:13:GLU:HG2	2.13	0.48
51:a:33:LEU:HD13	51:a:220:ALA:H	1.78	0.48
52:3:235:C:H2'	52:3:236:A:C8	2.48	0.48
52:3:392:C:H2'	52:3:393:A:C8	2.48	0.48
52:3:1256:A:H1'	52:3:1258:G:C8	2.48	0.48
53:1:1822:C:H2'	53:1:1823:G:H8	1.78	0.48
60:7:101:PHE:N	58:8:261:MET:HA	2.28	0.48
58:8:320:HIS:CD2	58:8:321:THR:HG23	2.48	0.48
1:b:86:ARG:NE	53:1:1817:G:H5''	2.28	0.48
7:h:121:SER:OG	7:h:122:GLN:N	2.45	0.48
8:i:58:ILE:HD11	8:i:66:PHE:HD2	1.77	0.48
14:o:105:ALA:O	14:o:108:ASP:OD1	2.31	0.48
24:y:22:LEU:HD23	24:y:22:LEU:O	2.13	0.48
38:N:70:GLY:HA3	52:3:1371:G:O3'	2.13	0.48
42:R:97:ARG:HB2	42:R:99:GLN:OE1	2.13	0.48
52:3:1163:A:H2'	52:3:1164:G:H8	1.79	0.48
53:1:796:C:H2'	53:1:797:G:H8	1.77	0.48
53:1:1078:U:H4'	53:1:1079:C:H5''	1.95	0.48
53:1:1935:G:H1'	53:1:1964:G:N2	2.29	0.48
53:1:2039:U:H2'	53:1:2040:G:C8	2.49	0.48
53:1:2861:U:H2'	53:1:2862:G:C8	2.49	0.48
53:1:2861:U:H2'	53:1:2862:G:H8	1.78	0.48
54:2:118:C:H2'	54:2:119:A:H8	1.78	0.48
58:8:332:TYR:CE1	58:8:378:ARG:HB2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:1:MET:N	53:1:1105:U:OP1	2.46	0.48
7:h:73:LYS:HB3	7:h:117:LEU:HD21	1.96	0.48
8:i:12:VAL:O	8:i:13:ALA:C	2.56	0.48
17:r:76:LYS:HB2	17:r:85:LYS:HB3	1.95	0.48
24:y:5:GLU:O	24:y:56:LEU:HD13	2.14	0.48
38:N:40:ARG:NH2	52:3:1291:U:H4'	2.29	0.48
42:R:105:ALA:HA	52:3:948:C:OP1	2.14	0.48
52:3:82:G:H2'	52:3:83:C:O4'	2.13	0.48
52:3:1464:U:H2'	52:3:1465:A:C8	2.48	0.48
53:1:1971:U:C5'	53:1:1972:G:H5''	2.44	0.48
3:d:40:ARG:HD2	53:1:443:A:C5	2.49	0.48
8:i:133:ARG:NH1	53:1:1079:C:H4'	2.29	0.48
12:m:82:MET:HE1	53:1:956:G:O4'	2.12	0.48
18:s:11:ARG:HD3	53:1:1322:A:OP1	2.14	0.48
31:G:94:ARG:HH22	52:3:1100:C:H3'	1.79	0.48
33:I:53:GLN:HB3	33:I:202:LEU:HD13	1.96	0.48
35:K:2:ARG:O	35:K:65:GLU:HG3	2.14	0.48
41:Q:65:TYR:OH	52:3:522:C:OP2	2.30	0.48
42:R:85:TYR:OH	42:R:89:ARG:NH1	2.47	0.48
43:S:84:ARG:NH2	52:3:1059:C:O3'	2.47	0.48
52:3:1497:G:O2'	52:3:1498:U:H5'	2.13	0.48
53:1:1971:U:H5''	53:1:1972:G:H5''	1.96	0.48
53:1:1987:A:H2'	53:1:1988:G:H8	1.78	0.48
53:1:2105:U:H2'	53:1:2106:U:O4'	2.14	0.48
53:1:2190:G:H2'	53:1:2191:A:C8	2.48	0.48
53:1:2370:G:H2'	53:1:2371:G:C8	2.49	0.48
3:d:105:LEU:HD13	3:d:175:ILE:HD11	1.95	0.48
9:j:101:ILE:HD12	9:j:101:ILE:N	2.28	0.48
16:q:2:ARG:HB2	53:1:1248:G:C5	2.49	0.48
18:s:82:MET:HB2	18:s:98:LYS:HB3	1.96	0.48
32:H:126:ARG:HH12	52:3:421:U:H3	1.58	0.48
40:P:78:ILE:HD11	40:P:81:LEU:HB3	1.96	0.48
40:P:126:ARG:O	50:Z:34:ARG:NH2	2.47	0.48
46:V:4:ILE:HD12	46:V:4:ILE:N	2.29	0.48
51:a:8:MET:CE	53:1:2174:C:H5''	2.43	0.48
52:3:250:A:H4'	52:3:252:U:C6	2.49	0.48
52:3:1096:C:H2'	52:3:1097:C:C6	2.49	0.48
52:3:1259:C:C3'	52:3:1260:G:H5''	2.35	0.48
53:1:433:C:O2'	53:1:434:U:H5'	2.14	0.48
53:1:863:A:H2'	53:1:864:G:C8	2.49	0.48
53:1:1139:G:O2'	53:1:1140:C:H5'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1563:U:H2'	53:1:1564:C:C6	2.48	0.48
53:1:2019:A:H2	53:1:2035:G:H22	1.60	0.48
53:1:2184:A:H2'	53:1:2185:U:C6	2.49	0.48
53:1:2266:A:H4'	53:1:2267:A:C4	2.49	0.48
53:1:2314:A:H2'	53:1:2315:G:C8	2.48	0.48
53:1:2628:C:H3'	53:1:2629:U:H5'	1.96	0.48
53:1:2841:C:H2'	53:1:2842:G:C8	2.49	0.48
6:g:69:ALA:HA	6:g:72:ILE:HG13	1.96	0.47
10:k:58:LEU:HA	10:k:89:ASN:OD1	2.14	0.47
15:p:105:LYS:HD3	52:3:1432:G:O3'	2.14	0.47
19:t:39:THR:OG1	19:t:42:GLU:HG3	2.14	0.47
30:F:4:ARG:HB3	53:1:2466:C:OP1	2.13	0.47
31:G:96:LEU:N	31:G:96:LEU:HD12	2.29	0.47
36:L:22:LEU:O	36:L:26:VAL:HG23	2.14	0.47
48:X:39:ILE:HD11	48:X:73:PHE:HE2	1.78	0.47
48:X:71:GLY:HA3	52:3:1320:C:C2	2.49	0.47
53:1:249:C:H2'	53:1:2394:C:O2'	2.14	0.47
53:1:293:U:H2'	53:1:294:A:H5''	1.96	0.47
53:1:1475:G:O2'	53:1:1476:U:H6	1.97	0.47
53:1:2564:A:C2	53:1:2647:U:H4'	2.50	0.47
5:f:148:ARG:HA	5:f:161:VAL:CG2	2.44	0.47
18:s:71:VAL:HG13	18:s:71:VAL:O	2.14	0.47
37:M:49:LYS:HB3	37:M:51:GLU:OE1	2.14	0.47
37:M:82:LEU:O	37:M:82:LEU:HD23	2.14	0.47
38:N:121:ARG:HH12	52:3:1345:U:H5''	1.79	0.47
52:3:707:U:H2'	52:3:708:C:C6	2.49	0.47
52:3:730:G:C2'	52:3:731:G:H5'	2.44	0.47
53:1:156:A:H2'	53:1:157:C:C6	2.48	0.47
53:1:2039:U:H2'	53:1:2040:G:H8	1.78	0.47
53:1:2233:U:H2'	53:1:2234:G:H8	1.78	0.47
55:5:69:C:H2'	55:5:70:G:H8	1.79	0.47
58:8:189:ILE:O	58:8:192:LEU:HB3	2.14	0.47
10:k:25:LEU:HD11	10:k:59:LYS:HE2	1.96	0.47
45:U:18:GLN:OE1	45:U:35:ARG:NH2	2.48	0.47
52:3:337:G:H2'	52:3:338:A:C8	2.49	0.47
53:1:827:U:H4'	53:1:828:U:C5	2.49	0.47
53:1:1004:U:H3	53:1:1151:A:H61	1.62	0.47
53:1:1078:U:C5'	53:1:1079:C:H5''	2.42	0.47
58:8:339:THR:HG22	58:8:340:GLY:H	1.79	0.47
3:d:27:LEU:HD12	53:1:600:G:H5'	1.96	0.47
14:o:30:ARG:NH1	54:2:49:C:OP2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:6:ARG:HE	31:G:9:LEU:HD12	1.79	0.47
31:G:72:LYS:HE2	31:G:74:ALA:HB3	1.96	0.47
38:N:8:THR:O	38:N:81:GLY:HA2	2.14	0.47
39:O:40:ILE:CD1	52:3:1124:G:H4'	2.44	0.47
40:P:93:GLU:O	40:P:97:ARG:NH1	2.48	0.47
46:V:58:VAL:HG21	46:V:74:LEU:HD22	1.95	0.47
52:3:1062:U:H2'	52:3:1063:C:C6	2.49	0.47
53:1:441:U:O2'	53:1:442:G:H5'	2.14	0.47
53:1:1219:U:H2'	53:1:1220:G:H8	1.80	0.47
53:1:2795:C:H2'	53:1:2796:U:O4'	2.14	0.47
55:5:3:C:H2'	55:5:4:G:C8	2.49	0.47
1:b:48:ILE:HG23	1:b:48:ILE:O	2.14	0.47
4:e:47:LYS:HA	4:e:50:ASP:OD2	2.15	0.47
6:g:78:VAL:HG21	6:g:103:VAL:HG12	1.97	0.47
32:H:43:THR:O	32:H:47:ALA:HB2	2.14	0.47
41:Q:50:LYS:HD2	41:Q:50:LYS:N	2.30	0.47
48:X:5:LYS:HD2	48:X:6:LYS:HE3	1.96	0.47
48:X:77:ARG:HD2	52:3:1225:A:O2'	2.13	0.47
53:1:1297:C:OP1	53:1:2710:C:H4'	2.15	0.47
53:1:1675:C:H2'	53:1:1676:A:O4'	2.15	0.47
53:1:1725:U:H2'	53:1:1726:C:C6	2.50	0.47
53:1:2589:A:H2'	53:1:2590:A:C8	2.49	0.47
1:b:228:ASP:CG	53:1:780:G:H1	2.23	0.47
10:k:60:ALA:HA	10:k:86:LEU:HA	1.97	0.47
11:l:47:ARG:HE	53:1:251:A:H5''	1.78	0.47
16:q:92:LYS:NZ	53:1:995:C:O2	2.47	0.47
23:x:15:ASN:C	23:x:26:ARG:HG2	2.39	0.47
32:H:86:LEU:HA	32:H:89:VAL:HG22	1.97	0.47
50:Z:46:ARG:NH2	52:3:1533:C:N3	2.62	0.47
52:3:309:A:H2'	52:3:310:G:C8	2.48	0.47
52:3:422:C:H5''	52:3:423:G:O5'	2.15	0.47
52:3:680:C:H2'	52:3:681:A:H8	1.79	0.47
53:1:744:U:H2'	53:1:745:G:O4'	2.15	0.47
53:1:1092:C:H2'	53:1:1093:G:O4'	2.14	0.47
53:1:1979:U:O2'	53:1:1980:G:H5'	2.14	0.47
53:1:2328:A:H2'	53:1:2329:U:C6	2.49	0.47
3:d:163:ASN:HB2	53:1:322:A:OP2	2.14	0.47
10:k:105:ARG:HH21	15:p:32:VAL:HG23	1.79	0.47
13:n:30:ARG:O	13:n:78:LYS:NZ	2.48	0.47
16:q:23:TYR:CE1	53:1:533:G:H5'	2.50	0.47
18:s:5:ALA:HB3	18:s:105:VAL:CG2	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:x:56:ARG:NH2	53:1:372:G:O6	2.48	0.47
30:F:3:VAL:HG21	53:1:2539:C:H5'	1.97	0.47
35:K:42:TRP:HB3	35:K:45:ARG:CZ	2.44	0.47
36:L:16:LYS:HG2	36:L:17:PHE:HD1	1.80	0.47
43:S:10:VAL:HA	43:S:13:VAL:HG12	1.96	0.47
48:X:65:MET:N	48:X:65:MET:SD	2.87	0.47
52:3:599:C:H2'	52:3:600:A:C8	2.50	0.47
52:3:990:C:H2'	52:3:991:U:O4'	2.14	0.47
52:3:1120:C:H2'	52:3:1121:U:C6	2.50	0.47
53:1:6:A:H2'	53:1:7:G:C8	2.50	0.47
53:1:37:C:H4'	53:1:451:U:OP1	2.15	0.47
53:1:323:C:H2'	53:1:1205:A:N1	2.30	0.47
53:1:445:C:C2'	53:1:446:G:H5'	2.44	0.47
53:1:542:C:H2'	53:1:543:G:C5'	2.45	0.47
53:1:677:A:O2'	53:1:2071:A:H5'	2.14	0.47
53:1:680:C:H2'	53:1:681:G:H8	1.79	0.47
53:1:2853:C:H2'	53:1:2854:G:C8	2.50	0.47
54:2:97:C:H2'	54:2:98:G:O4'	2.13	0.47
2:c:148:GLN:N	2:c:148:GLN:OE1	2.48	0.47
6:g:31:VAL:N	6:g:32:PRO:HD2	2.30	0.47
6:g:41:LYS:HA	6:g:44:ILE:HB	1.97	0.47
15:p:110:LYS:HG2	15:p:111:GLU:N	2.29	0.47
50:Z:9:GLU:HB2	50:Z:10:PRO:CD	2.44	0.47
52:3:90:C:H2'	52:3:91:U:C5	2.50	0.47
52:3:904:U:H2'	52:3:905:U:C6	2.50	0.47
52:3:1137:C:H4'	52:3:1138:G:C2	2.50	0.47
52:3:1441:A:C2'	52:3:1442:G:H5'	2.45	0.47
53:1:2180:U:H2'	53:1:2181:U:O4'	2.14	0.47
53:1:2584:U:H2'	53:1:2585:U:H2'	1.95	0.47
54:2:13:G:N7	54:2:70:C:H4'	2.30	0.47
1:b:147:PRO:HD3	1:b:184:GLU:OE2	2.14	0.47
1:b:245:THR:C	1:b:247:TRP:H	2.23	0.47
3:d:97:ASN:H	3:d:100:MET:HE2	1.80	0.47
5:f:137:LYS:HG2	53:1:2746:U:H5''	1.96	0.47
9:j:89:PHE:HE1	9:j:100:VAL:HG11	1.80	0.47
14:o:75:GLY:HA3	14:o:109:ALA:HB3	1.96	0.47
39:O:10:LEU:HB3	39:O:98:VAL:HG13	1.97	0.47
48:X:69:LYS:HZ1	52:3:1319:A:H5''	1.76	0.47
50:Z:32:ARG:HH11	50:Z:33:ARG:HE	1.62	0.47
51:a:37:LYS:HD3	53:1:2128:G:P	2.55	0.47
52:3:82:G:C2'	52:3:83:C:H5'	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:539:A:H2'	52:3:540:G:C8	2.50	0.47
52:3:894:G:H2'	52:3:895:G:H8	1.80	0.47
52:3:953:G:H2'	52:3:954:G:O4'	2.15	0.47
53:1:1132:U:H2'	53:1:1133:A:C8	2.50	0.47
53:1:1572:A:H2'	53:1:1573:G:H8	1.79	0.47
53:1:2518:A:H5'	53:1:2518:A:N3	2.30	0.47
53:1:2538:C:H2'	53:1:2539:C:H6	1.79	0.47
53:1:2849:U:H4'	53:1:2850:A:H5'	1.97	0.47
54:2:3:C:H3'	54:2:4:C:C5'	2.45	0.47
1:b:166:ARG:HG3	1:b:171:VAL:HG22	1.97	0.47
2:c:28:GLU:OE2	2:c:30:GLU:HG3	2.15	0.47
3:d:27:LEU:HD23	3:d:27:LEU:C	2.40	0.47
5:f:149:ALA:O	5:f:152:ARG:NH2	2.48	0.47
6:g:98:ASP:O	6:g:101:ASP:OD1	2.33	0.47
7:h:102:ALA:HA	7:h:105:LYS:NZ	2.29	0.47
9:j:114:LEU:O	9:j:118:MET:HG2	2.15	0.47
12:m:53:MET:HG3	12:m:120:ALA:HB2	1.96	0.47
18:s:6:LYS:O	53:1:494:G:H4'	2.14	0.47
19:t:54:GLU:HG3	19:t:88:LYS:HD2	1.96	0.47
20:u:61:GLU:N	20:u:61:GLU:OE2	2.48	0.47
36:L:75:LYS:HZ1	52:3:938:A:H5''	1.80	0.47
39:O:67:ILE:HD11	43:S:95:LEU:HG	1.97	0.47
48:X:54:ARG:HB3	52:3:958:A:C2	2.50	0.47
52:3:220:G:O2'	52:3:221:C:H5'	2.14	0.47
52:3:915:A:H2'	52:3:916:U:H5'	1.97	0.47
52:3:1514:G:O2'	52:3:1515:G:H5'	2.14	0.47
53:1:290:U:H2'	53:1:291:G:C8	2.50	0.47
53:1:639:U:H2'	53:1:640:C:C6	2.50	0.47
53:1:1170:C:H2'	53:1:1171:G:C8	2.50	0.47
53:1:1570:A:H2'	53:1:1571:A:C8	2.49	0.47
53:1:1833:C:H2'	53:1:1834:U:O4'	2.15	0.47
53:1:2628:C:O2'	53:1:2781:A:H2'	2.15	0.47
53:1:2849:U:H4'	53:1:2868:A:C2	2.49	0.47
58:8:367:ILE:O	58:8:369:MET:HG2	2.15	0.47
1:b:3:VAL:HG13	1:b:3:VAL:O	2.16	0.46
1:b:239:PHE:O	1:b:241:LYS:HG3	2.15	0.46
2:c:3:GLY:HA3	2:c:203:VAL:O	2.14	0.46
2:c:46:ARG:CZ	2:c:86:GLU:HA	2.45	0.46
7:h:56:ARG:HD2	53:1:1084:A:N3	2.30	0.46
13:n:92:GLY:O	53:1:2880:C:H1'	2.14	0.46
15:p:50:ARG:NH1	15:p:52:ARG:HG3	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:C:44:GLN:HE22	27:C:46:VAL:HB	1.79	0.46
29:E:25:HIS:NE2	29:E:47:ALA:HB2	2.30	0.46
33:I:123:MET:HE3	33:I:126:GLY:HA2	1.96	0.46
37:M:77:VAL:HG23	37:M:126:CYS:HA	1.96	0.46
42:R:9:PRO:HG2	42:R:44:ILE:HG21	1.97	0.46
43:S:8:ARG:O	43:S:12:ARG:HG3	2.15	0.46
52:3:5:U:H4'	52:3:6:G:C4	2.50	0.46
52:3:784:A:H2'	52:3:785:G:H8	1.80	0.46
52:3:1202:U:H2'	52:3:1203:C:C5'	2.45	0.46
52:3:1340:A:O2'	52:3:1341:U:H5'	2.15	0.46
52:3:1354:U:H2'	52:3:1355:G:C8	2.49	0.46
53:1:211:C:H2'	53:1:212:G:C8	2.50	0.46
53:1:1469:A:H2'	53:1:1470:A:C8	2.50	0.46
53:1:1773:A:C2'	53:1:1774:C:H5'	2.45	0.46
53:1:2243:U:H2'	53:1:2244:U:C6	2.50	0.46
53:1:2564:A:OP1	53:1:2648:G:H4'	2.15	0.46
54:2:55:U:H2'	54:2:56:G:C8	2.50	0.46
58:8:342:ILE:CD1	58:8:361:VAL:HG22	2.45	0.46
1:b:146:LYS:HB2	1:b:149:LYS:HB2	1.98	0.46
3:d:117:ARG:HH12	11:l:2:ARG:HG2	1.80	0.46
3:d:149:ILE:HG23	3:d:188:MET:HG2	1.98	0.46
4:e:2:LYS:HB2	4:e:100:GLU:OE1	2.16	0.46
4:e:163:GLU:HA	4:e:166:ARG:NH1	2.30	0.46
13:n:38:LEU:HD11	13:n:99:LYS:HE3	1.98	0.46
13:n:60:VAL:HG13	13:n:61:ALA:N	2.30	0.46
14:o:5:SER:O	14:o:8:ILE:HG22	2.15	0.46
32:H:31:ASN:HB3	32:H:58:ARG:NH1	2.30	0.46
36:L:75:LYS:NZ	52:3:938:A:H5''	2.30	0.46
40:P:16:SER:OG	40:P:17:ASP:N	2.49	0.46
53:1:1182:G:H2'	53:1:1183:U:O4'	2.14	0.46
53:1:1854:A:N6	53:1:1888:G:H1'	2.30	0.46
54:2:63:C:H2'	54:2:64:G:C8	2.50	0.46
57:7:25:C:H2'	57:7:26:A:H4'	1.97	0.46
1:b:68:ARG:NH1	1:b:128:THR:OG1	2.49	0.46
1:b:231:HIS:O	1:b:232:GLY:O	2.33	0.46
4:e:91:ARG:NH2	54:2:45:A:C1'	2.74	0.46
7:h:2:ALA:H	7:h:6:GLN:NE2	2.13	0.46
10:k:48:PRO:HA	52:3:1422:G:OP1	2.15	0.46
10:k:87:LEU:HD22	10:k:92:GLU:O	2.16	0.46
16:q:75:TYR:HE2	53:1:1153:C:H5'	1.80	0.46
51:a:185:LEU:O	51:a:189:LEU:HD12	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:359:G:O2'	53:1:360:U:H5'	2.15	0.46
53:1:1001:A:H2'	53:1:1002:G:O4'	2.15	0.46
53:1:1057:A:H2'	53:1:1057:A:N3	2.30	0.46
53:1:1090:A:H2'	53:1:1091:G:H8	1.80	0.46
53:1:1932:A:H2'	53:1:1933:G:O4'	2.15	0.46
53:1:1958:C:O2'	53:1:1959:G:H5'	2.16	0.46
53:1:2052:A:O2'	53:1:2053:G:H5'	2.15	0.46
55:5:16:C:H5'	55:5:59:A:N1	2.31	0.46
58:8:204:GLU:C	58:8:205:ARG:HD2	2.40	0.46
33:I:190:LEU:HD12	33:I:192:ALA:N	2.20	0.46
33:I:197:HIS:CE1	34:J:103:GLY:HA2	2.51	0.46
38:N:17:ARG:NH2	52:3:1129:C:H4'	2.31	0.46
38:N:119:LYS:NZ	52:3:1349:A:OP2	2.49	0.46
52:3:665:A:C1'	52:3:733:G:H1'	2.46	0.46
53:1:319:G:H2'	53:1:320:A:O4'	2.15	0.46
53:1:1219:U:H2'	53:1:1220:G:C8	2.50	0.46
53:1:1370:C:H2'	53:1:1371:G:O4'	2.16	0.46
53:1:2756:U:H4'	53:1:2757:A:OP1	2.15	0.46
54:2:3:C:H42	54:2:117:G:H1	1.64	0.46
4:e:102:LEU:HD23	4:e:102:LEU:C	2.41	0.46
4:e:177:ARG:OXT	4:e:177:ARG:HD2	2.16	0.46
7:h:118:ILE:N	7:h:119:PRO:CD	2.78	0.46
23:x:36:ARG:HA	23:x:47:THR:HA	1.97	0.46
31:G:210:THR:HA	31:G:213:LEU:HG	1.97	0.46
32:H:4:VAL:O	32:H:6:PRO:HD3	2.16	0.46
32:H:181:ILE:HD12	32:H:181:ILE:N	2.29	0.46
34:J:63:MET:HE3	34:J:67:ARG:NH1	2.30	0.46
34:J:110:MET:O	34:J:113:VAL:HG12	2.16	0.46
35:K:29:ILE:HG21	35:K:64:VAL:HG21	1.97	0.46
38:N:14:SER:OG	38:N:74:GLN:HA	2.16	0.46
41:Q:66:ILE:HA	41:Q:96:THR:OG1	2.16	0.46
43:S:71:GLY:HA2	52:3:975:A:O2'	2.15	0.46
45:U:8:ARG:HE	45:U:15:PRO:HB3	1.80	0.46
51:a:163:TYR:HB2	51:a:171:ILE:HD11	1.97	0.46
52:3:1347:G:H22	52:3:1373:G:H2'	1.79	0.46
52:3:1391:U:H2'	52:3:1392:G:C8	2.51	0.46
53:1:419:U:H2'	53:1:420:C:C6	2.51	0.46
53:1:607:U:O4	53:1:620:G:H5'	2.16	0.46
53:1:873:C:H2'	53:1:874:G:H8	1.80	0.46
53:1:974:G:N3	53:1:974:G:H2'	2.31	0.46
53:1:1918:A:H2	53:1:1919:A:H62	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2302:U:H2'	53:1:2303:G:C8	2.51	0.46
7:h:58:THR:OG1	7:h:78:GLY:O	2.33	0.46
8:i:101:SER:HB3	8:i:104:GLN:HG3	1.98	0.46
12:m:75:GLU:OE2	53:1:957:C:H5'	2.16	0.46
15:p:105:LYS:O	15:p:108:ARG:NH2	2.48	0.46
17:r:16:GLU:HG3	17:r:98:ILE:HG22	1.98	0.46
20:u:42:LYS:HB2	53:1:499:U:H4'	1.97	0.46
21:v:64:VAL:HA	21:v:69:GLU:HA	1.97	0.46
24:y:4:LYS:HA	24:y:7:ARG:HH22	1.81	0.46
33:I:27:ILE:HG23	33:I:29:THR:HG23	1.96	0.46
33:I:197:HIS:O	33:I:200:VAL:HG12	2.15	0.46
41:Q:43:LYS:HD3	56:4:21:C:C4'	2.40	0.46
42:R:80:MET:O	42:R:91:ARG:NH1	2.48	0.46
45:U:48:GLU:CD	45:U:51:ARG:HG3	2.40	0.46
50:Z:32:ARG:CZ	50:Z:33:ARG:HH21	2.29	0.46
53:1:46:G:H2'	53:1:47:C:C6	2.51	0.46
53:1:863:A:H2'	53:1:864:G:H8	1.81	0.46
53:1:1566:A:O2'	53:1:1567:G:H5'	2.16	0.46
53:1:1594:U:H2'	53:1:1595:C:C6	2.51	0.46
53:1:1779:U:H5	53:1:1784:A:N7	2.14	0.46
53:1:2427:C:H5''	53:1:2429:G:H5'	1.97	0.46
2:c:33:ARG:HD3	2:c:73:VAL:HB	1.98	0.46
3:d:84:THR:HG21	53:1:672:C:H4'	1.98	0.46
6:g:68:ARG:HD2	6:g:68:ARG:C	2.41	0.46
32:H:201:ILE:HD12	32:H:201:ILE:N	2.31	0.46
36:L:16:LYS:HG2	36:L:17:PHE:CD1	2.51	0.46
37:M:17:GLN:HB3	37:M:69:ALA:CB	2.46	0.46
37:M:58:LEU:HG	37:M:60:LEU:HD11	1.97	0.46
50:Z:61:ARG:H	50:Z:61:ARG:HD3	1.81	0.46
53:1:163:C:H2'	53:1:164:C:O4'	2.16	0.46
53:1:211:C:H2'	53:1:212:G:H8	1.80	0.46
53:1:387:U:H5'	53:1:387:U:H6	1.81	0.46
53:1:473:G:C2'	53:1:474:G:H5'	2.46	0.46
53:1:2537:U:H2'	53:1:2538:C:H6	1.80	0.46
58:8:104:LEU:HG	58:8:106:VAL:HG23	1.98	0.46
3:d:5:LEU:HG	3:d:120:VAL:HG23	1.97	0.46
4:e:21:TYR:HB3	4:e:26:GLN:HB3	1.96	0.46
8:i:122:GLU:HA	8:i:125:THR:HG22	1.97	0.46
11:l:19:LEU:HD23	53:1:587:C:C2	2.51	0.46
11:l:39:LYS:HD2	53:1:833:A:OP1	2.15	0.46
13:n:47:VAL:O	13:n:50:PRO:HD2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:t:5:GLU:N	19:t:5:GLU:OE2	2.48	0.46
19:t:51:PHE:O	19:t:53:VAL:HG13	2.15	0.46
30:F:2:LYS:HB2	30:F:35:GLN:HB3	1.96	0.46
49:Y:42:ASP:CG	49:Y:45:ALA:HB3	2.41	0.46
52:3:599:C:H2'	52:3:600:A:H8	1.81	0.46
52:3:701:U:C4'	52:3:703:G:H1'	2.45	0.46
52:3:1504:G:H4'	52:3:1505:G:O4'	2.16	0.46
53:1:696:G:O2'	53:1:697:G:H5'	2.16	0.46
53:1:1070:A:H2'	53:1:1097:U:OP1	2.15	0.46
53:1:1137:G:O2'	53:1:1138:G:H5'	2.16	0.46
53:1:2093:G:O6	53:1:2225:A:H5''	2.16	0.46
1:b:179:GLU:OE2	1:b:270:ARG:HB2	2.15	0.46
2:c:3:GLY:HA3	2:c:204:LYS:HA	1.97	0.46
2:c:121:THR:HB	2:c:127:PHE:CD2	2.51	0.46
4:e:113:PHE:HZ	4:e:175:PRO:HG2	1.81	0.46
5:f:41:GLU:HA	5:f:54:ARG:HH21	1.80	0.46
11:l:85:VAL:HG12	11:l:86:GLU:N	2.28	0.46
12:m:10:ARG:HB2	12:m:10:ARG:NH2	2.31	0.46
17:r:80:ARG:NH2	53:1:572:A:OP2	2.49	0.46
18:s:16:LYS:O	18:s:19:LEU:HD12	2.16	0.46
19:t:6:ARG:O	19:t:10:VAL:HG23	2.16	0.46
22:w:16:ARG:N	22:w:16:ARG:HD2	2.31	0.46
22:w:19:VAL:HG22	22:w:34:VAL:HG22	1.98	0.46
23:x:35:HIS:NE2	53:1:2199:A:O2'	2.48	0.46
29:E:8:GLY:O	29:E:12:ARG:NH2	2.49	0.46
31:G:152:ASP:N	31:G:152:ASP:OD1	2.49	0.46
32:H:171:ARG:HH21	52:3:1106:G:P	2.39	0.46
40:P:15:VAL:HG22	40:P:16:SER:N	2.30	0.46
40:P:48:GLY:HA2	52:3:688:G:H5'	1.98	0.46
48:X:43:MET:O	48:X:46:LEU:HD13	2.16	0.46
50:Z:66:ARG:NE	52:3:1099:G:H4'	2.31	0.46
52:3:199:A:H61	52:3:218:U:H3	1.63	0.46
52:3:879:C:H2'	52:3:880:C:C6	2.51	0.46
52:3:1015:G:O2'	52:3:1016:A:H5'	2.15	0.46
52:3:1245:C:H2'	52:3:1246:A:H8	1.80	0.46
52:3:1389:C:H2'	52:3:1390:U:H6	1.80	0.46
52:3:1540:U:O2	52:3:1540:U:H3'	2.15	0.46
53:1:103:A:H2'	53:1:104:A:O4'	2.16	0.46
53:1:729:G:H4'	53:1:763:G:H5'	1.97	0.46
53:1:818:G:O2'	53:1:819:A:H5''	2.16	0.46
53:1:1541:C:H2'	53:1:1542:U:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1542:U:H2'	53:1:1543:G:O4'	2.16	0.46
53:1:1706:C:C2	53:1:1757:A:H5'	2.51	0.46
53:1:1890:A:H2'	53:1:1891:G:O4'	2.15	0.46
53:1:2358:A:H2'	53:1:2359:C:O4'	2.16	0.46
55:5:15:G:H2'	55:5:59:A:N1	2.31	0.46
58:8:287:ILE:HA	58:8:291:GLN:HE22	1.81	0.46
58:8:290:GLY:HA2	58:8:335:THR:O	2.16	0.46
2:c:12:THR:OG1	2:c:13:ARG:N	2.48	0.46
2:c:146:ILE:HG13	2:c:146:ILE:O	2.17	0.46
3:d:124:PHE:HE1	3:d:141:MET:HE1	1.81	0.46
4:e:74:ALA:HB2	55:5:57:A:H5'	1.98	0.46
7:h:61:ARG:O	53:1:1046:A:H4'	2.16	0.46
8:i:9:LYS:HE3	8:i:55:PRO:HB2	1.96	0.46
31:G:11:ALA:HB1	31:G:208:ALA:HA	1.98	0.46
37:M:44:PHE:C	37:M:45:ILE:HD12	2.41	0.46
41:Q:24:GLU:O	41:Q:25:ALA:HB3	2.15	0.46
50:Z:19:LYS:HB3	50:Z:24:LYS:HD2	1.98	0.46
53:1:353:C:H2'	53:1:354:A:H8	1.81	0.46
53:1:570:G:H2'	53:1:2030:A:N7	2.30	0.46
53:1:971:G:H2'	53:1:972:A:O4'	2.16	0.46
53:1:1794:A:H2'	53:1:1795:C:C6	2.51	0.46
53:1:2636:C:H2'	53:1:2637:U:C6	2.51	0.46
1:b:153:LEU:HD13	1:b:175:LEU:HD21	1.98	0.45
3:d:189:THR:HG23	3:d:192:ALA:H	1.81	0.45
12:m:7:THR:OG1	12:m:8:LYS:N	2.50	0.45
32:H:54:ILE:CD1	32:H:67:ILE:HG23	2.46	0.45
32:H:92:ASP:OD2	32:H:93:ILE:HD12	2.16	0.45
34:J:130:THR:HG23	34:J:130:THR:O	2.16	0.45
52:3:286:C:H2'	52:3:287:U:C6	2.50	0.45
52:3:434:U:H2'	52:3:435:A:H8	1.80	0.45
52:3:1404:C:H2'	52:3:1405:G:C8	2.52	0.45
53:1:686:U:H3'	53:1:687:C:H5'	1.97	0.45
53:1:1101:U:H2'	53:1:1102:C:C6	2.51	0.45
53:1:1285:A:H2'	53:1:1286:A:H5'	1.98	0.45
53:1:1360:G:H2'	53:1:1361:G:H5'	1.98	0.45
53:1:1782:U:H1'	53:1:2609:U:O4'	2.16	0.45
53:1:2244:U:H2'	53:1:2245:U:O4'	2.17	0.45
4:e:121:PHE:HB3	4:e:162:ASP:HB2	1.98	0.45
4:e:142:TYR:CD2	42:R:8:ILE:HG21	2.51	0.45
7:h:3:LEU:HB2	7:h:5:LEU:CD2	2.45	0.45
14:o:33:ARG:HB2	54:2:52:A:N6	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:80:ASN:HB2	53:1:1151:A:O2'	2.17	0.45
18:s:5:ALA:HB3	18:s:105:VAL:HG23	1.97	0.45
19:t:22:THR:O	19:t:26:LYS:HB2	2.16	0.45
23:x:10:ARG:HD3	23:x:11:PRO:CD	2.46	0.45
31:G:220:VAL:O	31:G:224:ARG:HG2	2.17	0.45
34:J:76:ASN:HB3	34:J:79:THR:HG23	1.98	0.45
42:R:14:ALA:CB	42:R:33:LEU:HD21	2.46	0.45
48:X:2:ARG:HG2	52:3:1312:G:N7	2.32	0.45
52:3:45:G:H2'	52:3:46:G:C8	2.52	0.45
52:3:889:A:H5'	52:3:891:U:H1'	1.98	0.45
53:1:365:U:H2'	53:1:366:C:C6	2.52	0.45
53:1:717:C:C2'	53:1:718:A:H5'	2.45	0.45
53:1:1987:A:H2'	53:1:1988:G:C8	2.51	0.45
53:1:2026:U:H2'	53:1:2027:G:C8	2.52	0.45
53:1:2123:G:H1'	53:1:2176:A:H2	1.81	0.45
53:1:2293:G:H2'	53:1:2294:G:C8	2.51	0.45
9:j:125:TYR:HH	9:j:132:HIS:HE2	1.64	0.45
10:k:103:VAL:HG11	10:k:107:LEU:HD22	1.98	0.45
34:J:131:ASN:HB3	34:J:134:ASN:HD22	1.82	0.45
38:N:24:ASN:HB3	38:N:26:LYS:HE3	1.98	0.45
42:R:27:THR:HG21	52:3:1328:C:OP1	2.16	0.45
42:R:27:THR:HA	42:R:30:LYS:NZ	2.31	0.45
44:T:56:LEU:HD21	53:1:715:A:N7	2.32	0.45
51:a:5:THR:CG2	51:a:8:MET:HE3	2.42	0.45
52:3:571:U:H4'	52:3:819:A:C6	2.51	0.45
52:3:1277:C:H2'	52:3:1278:G:H5''	1.99	0.45
52:3:1316:G:H2'	52:3:1317:C:H5''	1.99	0.45
53:1:1292:G:H2'	53:1:1293:C:C6	2.51	0.45
53:1:1526:C:H2'	53:1:1527:G:O4'	2.16	0.45
53:1:2155:U:H2'	53:1:2156:G:H5'	1.98	0.45
53:1:2591:C:H2'	53:1:2592:G:C8	2.51	0.45
53:1:2800:A:H3'	53:1:2801:G:C5'	2.45	0.45
57:7:52:G:H5'	58:8:327:TYR:HD1	1.82	0.45
58:8:90:LYS:NZ	58:8:91:ASN:HD21	2.14	0.45
58:8:224:ARG:NE	58:8:278:LEU:HD21	2.31	0.45
2:c:52:THR:OG1	2:c:53:GLY:N	2.49	0.45
6:g:40:THR:HG21	6:g:42:LYS:HZ2	1.81	0.45
15:p:63:ILE:HG23	15:p:63:ILE:O	2.16	0.45
33:I:101:VAL:HG22	33:I:106:PHE:HB2	1.99	0.45
35:K:1:MET:HE2	35:K:67:PRO:HB3	1.97	0.45
39:O:89:ARG:O	39:O:90:LEU:HD12	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:U:44:SER:O	45:U:46:LYS:HG2	2.17	0.45
49:Y:23:ARG:HH12	52:3:176:C:H5''	1.82	0.45
52:3:945:G:H2'	52:3:945:G:N3	2.29	0.45
53:1:779:U:H2'	53:1:780:G:C8	2.52	0.45
53:1:779:U:H2'	53:1:780:G:O4'	2.16	0.45
53:1:1298:C:H2'	53:1:1299:G:O4'	2.17	0.45
53:1:2855:C:H2'	53:1:2856:A:H8	1.82	0.45
2:c:56:LYS:NZ	53:1:2830:C:H5''	2.32	0.45
10:k:68:GLY:HA3	10:k:78:ARG:HG2	1.98	0.45
12:m:75:GLU:CD	53:1:957:C:H5'	2.42	0.45
12:m:123:LYS:NZ	53:1:2483:C:H42	2.14	0.45
20:u:27:VAL:HA	20:u:33:VAL:HA	1.97	0.45
23:x:56:ARG:O	23:x:59:ASP:HB3	2.16	0.45
26:B:37:HIS:ND1	26:B:38:LEU:O	2.50	0.45
28:D:21:ARG:C	28:D:23:ALA:H	2.24	0.45
31:G:94:ARG:NH2	52:3:1100:C:H3'	2.31	0.45
33:I:151:GLN:O	33:I:152:SER:OG	2.29	0.45
36:L:70:PRO:HA	36:L:141:HIS:NE2	2.32	0.45
44:T:28:VAL:CG2	44:T:80:LEU:HD21	2.44	0.45
46:V:30:HIS:HD2	46:V:33:TYR:H	1.63	0.45
52:3:50:A:N6	52:3:361:G:H4'	2.32	0.45
52:3:869:G:H4'	52:3:872:A:C8	2.51	0.45
52:3:1349:A:H2'	52:3:1350:A:O4'	2.16	0.45
52:3:1395:C:O2'	52:3:1396:A:H5'	2.16	0.45
52:3:1486:G:H2'	52:3:1487:G:O4'	2.17	0.45
52:3:1497:G:H2'	52:3:1498:U:H5'	1.98	0.45
53:1:720:U:H2'	53:1:721:A:C8	2.50	0.45
53:1:742:A:H2'	53:1:743:A:H8	1.82	0.45
53:1:847:U:O2	53:1:847:U:H2'	2.16	0.45
53:1:2066:C:O2'	53:1:2067:G:H5'	2.16	0.45
55:5:51:C:H2'	55:5:52:G:C8	2.52	0.45
20:u:56:GLY:N	53:1:483:A:O2'	2.50	0.45
22:w:20:LYS:HE3	53:1:2355:G:H4'	1.99	0.45
33:I:134:TYR:HE1	52:3:620:C:H5'	1.82	0.45
45:U:57:ILE:O	45:U:61:VAL:HG23	2.17	0.45
53:1:1209:U:H2'	53:1:1210:G:H21	1.82	0.45
53:1:2101:A:H2'	53:1:2102:G:H8	1.82	0.45
53:1:2194:U:H2'	53:1:2195:U:H6	1.81	0.45
53:1:2364:C:H2'	53:1:2365:G:O4'	2.17	0.45
58:8:229:THR:OG1	58:8:230:GLY:N	2.50	0.45
1:b:32:LEU:C	1:b:33:LEU:HD12	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:213:ARG:NH2	53:1:1566:A:H5'	2.31	0.45
9:j:35:ARG:HA	9:j:40:HIS:HD2	1.79	0.45
10:k:105:ARG:NH2	15:p:32:VAL:O	2.49	0.45
19:t:43:ILE:O	19:t:47:VAL:HG23	2.17	0.45
20:u:85:ARG:HD3	20:u:87:GLU:HG3	1.99	0.45
34:J:35:LEU:HD22	34:J:133:ILE:HD13	1.99	0.45
36:L:46:LEU:HD13	36:L:49:LEU:HD23	1.99	0.45
36:L:52:ARG:HH12	36:L:121:ASN:ND2	2.14	0.45
43:S:41:TRP:O	43:S:44:VAL:HG12	2.17	0.45
45:U:4:ILE:HG22	45:U:71:VAL:HG11	1.99	0.45
48:X:14:LEU:HA	48:X:17:LYS:HG2	1.99	0.45
53:1:1082:U:H3	53:1:1086:A:H61	1.65	0.45
53:1:2111:U:H5'	53:1:2112:G:OP2	2.17	0.45
58:8:322:PRO:HB3	58:8:352:MET:HA	1.99	0.45
1:b:67:LYS:O	1:b:188:ARG:NH1	2.50	0.45
1:b:88:ALA:HB1	1:b:194:VAL:CG1	2.46	0.45
1:b:132:ARG:HB3	1:b:185:ALA:HB1	1.98	0.45
5:f:157:LYS:HB2	5:f:159:LYS:HG3	1.99	0.45
7:h:54:VAL:HA	7:h:84:TYR:O	2.17	0.45
7:h:108:VAL:HG13	7:h:109:LYS:N	2.31	0.45
9:j:21:THR:OG1	9:j:58:ASN:ND2	2.49	0.45
29:E:57:VAL:O	29:E:61:LEU:HD23	2.17	0.45
31:G:113:LEU:O	31:G:117:GLU:HG3	2.17	0.45
32:H:6:PRO:O	32:H:9:ILE:HG22	2.16	0.45
32:H:67:ILE:HB	32:H:102:ILE:HG22	1.98	0.45
34:J:105:ILE:HD11	34:J:123:LEU:HD22	1.97	0.45
45:U:44:SER:H	45:U:46:LYS:HE3	1.82	0.45
46:V:29:LYS:HB2	46:V:36:PHE:CE1	2.51	0.45
52:3:980:C:H2'	52:3:981:U:H5'	1.98	0.45
52:3:1251:A:O2'	52:3:1370:G:H5'	2.16	0.45
52:3:1306:A:H62	52:3:1331:G:H1'	1.78	0.45
53:1:145:C:H2'	53:1:146:A:H8	1.81	0.45
53:1:758:C:O2	53:1:758:C:H2'	2.17	0.45
53:1:1611:C:H6	53:1:1611:C:H5'	1.81	0.45
53:1:2652:C:H2'	53:1:2653:U:O4'	2.16	0.45
53:1:2863:C:H2'	53:1:2864:G:C8	2.52	0.45
54:2:51:G:O2'	54:2:52:A:H5'	2.17	0.45
1:b:180:MET:HB2	1:b:268:ARG:H	1.82	0.45
2:c:56:LYS:HG3	2:c:58:ASN:OD1	2.17	0.45
3:d:149:ILE:HD13	3:d:188:MET:HE3	1.99	0.45
4:e:26:GLN:HE21	54:2:57:A:H4'	1.78	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:37:LYS:NZ	53:1:1086:A:H62	2.07	0.45
10:k:20:MET:O	10:k:42:THR:HG22	2.16	0.45
10:k:70:ARG:NH1	53:1:2684:U:O4'	2.50	0.45
17:r:54:VAL:HG12	17:r:55:ASP:N	2.31	0.45
19:t:32:LEU:HD12	19:t:32:LEU:O	2.16	0.45
30:F:15:LYS:HD2	30:F:16:ILE:H	1.81	0.45
38:N:10:ARG:HA	38:N:14:SER:O	2.16	0.45
41:Q:73:LEU:H	41:Q:73:LEU:CD2	2.27	0.45
41:Q:74:GLN:OE1	41:Q:74:GLN:N	2.50	0.45
46:V:58:VAL:HG23	46:V:77:VAL:HG22	1.99	0.45
49:Y:23:ARG:HH22	52:3:176:C:H5''	1.82	0.45
52:3:783:C:H2'	52:3:784:A:H8	1.82	0.45
52:3:1352:C:H2'	52:3:1353:G:H8	1.81	0.45
53:1:11:C:H3'	53:1:12:U:C5'	2.47	0.45
53:1:146:A:H2'	53:1:147:C:C6	2.51	0.45
53:1:1597:A:H5''	53:1:1598:A:H5'	1.98	0.45
53:1:1744:A:H2'	53:1:1745:A:O4'	2.17	0.45
53:1:1833:C:O2'	53:1:1834:U:H5'	2.17	0.45
53:1:2029:G:O6	53:1:2032:G:H5''	2.17	0.45
1:b:73:ILE:HG23	53:1:1490:A:N6	2.32	0.45
31:G:24:PRO:CB	52:3:828:U:H2'	2.46	0.45
31:G:46:VAL:CG1	31:G:47:PRO:HD3	2.47	0.45
32:H:18:ASN:HA	32:H:55:VAL:HG12	1.98	0.45
50:Z:48:LYS:HE3	52:3:723:U:O5'	2.17	0.45
51:a:211:LYS:HE2	51:a:213:SER:OG	2.17	0.45
52:3:82:G:H2'	52:3:83:C:H5'	1.98	0.45
52:3:390:U:H2'	52:3:391:G:H8	1.82	0.45
52:3:579:A:H2'	52:3:580:C:C6	2.52	0.45
52:3:1323:G:H2'	52:3:1324:A:C8	2.52	0.45
53:1:1837:C:H2'	53:1:1899:A:H61	1.82	0.45
53:1:2106:U:H2'	53:1:2107:G:C8	2.52	0.45
54:2:69:G:H2'	54:2:70:C:O4'	2.17	0.45
58:8:141:VAL:HG22	58:8:143:ASP:H	1.81	0.45
1:b:38:LYS:HB2	53:1:692:C:O3'	2.17	0.44
1:b:213:ARG:HH21	53:1:1566:A:H5'	1.81	0.44
5:f:28:LYS:HE3	5:f:79:THR:O	2.17	0.44
13:n:12:ARG:O	13:n:17:ARG:NH2	2.50	0.44
22:w:12:SER:HB3	53:1:2262:U:H5	1.82	0.44
28:D:3:ARG:O	28:D:6:GLN:NE2	2.50	0.44
32:H:35:ASP:O	32:H:38:VAL:HG12	2.16	0.44
36:L:115:MET:HA	36:L:118:ARG:HB2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:62:LEU:HG	38:N:64:ILE:HG12	1.98	0.44
45:U:5:ARG:HB3	52:3:376:G:H5''	1.99	0.44
52:3:24:U:H2'	52:3:25:C:C6	2.52	0.44
52:3:396:C:C2'	52:3:397:A:H5''	2.46	0.44
52:3:396:C:C3'	52:3:397:A:H5''	2.47	0.44
52:3:1143:G:H2'	52:3:1144:G:C8	2.52	0.44
53:1:1097:U:H2'	53:1:1098:A:O4'	2.17	0.44
53:1:1164:C:H2'	53:1:1165:A:H8	1.81	0.44
54:2:14:U:O2	54:2:107:G:H4'	2.17	0.44
4:e:33:ILE:HD12	4:e:155:ILE:HG13	1.99	0.44
15:p:110:LYS:HG2	15:p:111:GLU:H	1.81	0.44
33:I:160:LEU:O	33:I:163:GLN:HG2	2.18	0.44
36:L:149:ALA:HA	40:P:60:PHE:HB3	1.99	0.44
42:R:78:ARG:O	42:R:82:LEU:HG	2.18	0.44
44:T:86:LEU:N	44:T:86:LEU:HD23	2.32	0.44
52:3:710:G:O2'	52:3:711:G:H5'	2.16	0.44
53:1:27:G:H22	53:1:512:G:H1'	1.81	0.44
53:1:326:G:H2'	53:1:327:G:H8	1.81	0.44
53:1:353:C:H2'	53:1:354:A:C8	2.51	0.44
53:1:1575:C:H2'	53:1:1576:U:C6	2.51	0.44
53:1:1965:C:H3'	53:1:1966:A:H8	1.82	0.44
53:1:2033:A:H1'	53:1:2035:G:OP2	2.17	0.44
58:8:16:GLY:HA2	58:8:80:VAL:H	1.81	0.44
58:8:367:ILE:HG12	58:8:368:ALA:H	1.82	0.44
3:d:48:THR:C	3:d:50:ALA:H	2.25	0.44
12:m:67:VAL:HG11	12:m:102:LEU:HD23	2.00	0.44
23:x:69:GLU:O	23:x:73:ARG:HG3	2.17	0.44
34:J:156:ARG:HH12	37:M:100:ILE:HG23	1.79	0.44
39:O:40:ILE:CG1	39:O:73:LEU:HB2	2.48	0.44
45:U:68:SER:HB3	45:U:71:VAL:HG23	2.00	0.44
51:a:58:ASN:ND2	51:a:165:ASN:OD1	2.50	0.44
52:3:237:G:H2'	52:3:238:A:C8	2.52	0.44
52:3:882:C:O2'	52:3:883:C:H5'	2.17	0.44
52:3:1033:G:H2'	52:3:1034:G:H5''	1.99	0.44
53:1:1550:C:H2'	53:1:1551:A:H8	1.83	0.44
53:1:2053:G:O2'	53:1:2054:A:H5'	2.18	0.44
53:1:2257:U:H2'	53:1:2258:C:C6	2.52	0.44
53:1:2376:A:H2'	53:1:2377:A:O4'	2.18	0.44
53:1:2581:G:H2'	53:1:2581:G:N3	2.32	0.44
1:b:73:ILE:HG23	53:1:1490:A:H62	1.82	0.44
1:b:92:LEU:HD11	1:b:100:ARG:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:109:GLU:H	6:g:109:GLU:CD	2.25	0.44
7:h:59:LEU:HB3	7:h:62:ARG:HB2	1.99	0.44
8:i:16:MET:HE3	8:i:22:PRO:HG2	2.00	0.44
9:j:47:HIS:CE1	9:j:48:VAL:HG23	2.52	0.44
16:q:24:TYR:HB3	53:1:533:G:OP1	2.17	0.44
33:l:84:ASN:HB3	33:l:87:GLU:HB2	1.99	0.44
33:l:201:GLU:O	33:l:204:SER:OG	2.29	0.44
35:k:84:VAL:HG21	35:k:87:SER:HB3	2.00	0.44
35:k:92:THR:OG1	35:k:93:LYS:N	2.46	0.44
39:o:88:MET:C	39:o:89:ARG:HG2	2.42	0.44
43:s:74:ARG:NH2	52:3:1360:A:OP2	2.50	0.44
47:w:33:THR:OG1	47:w:34:GLU:N	2.48	0.44
47:w:66:LEU:C	47:w:67:LEU:HD12	2.43	0.44
50:z:19:LYS:HA	50:z:22:CYS:SG	2.58	0.44
51:a:67:HIS:ND1	51:a:184:LYS:HE3	2.33	0.44
52:3:86:G:H4'	52:3:87:C:C6	2.53	0.44
52:3:1241:G:H2'	52:3:1242:G:H8	1.83	0.44
53:1:104:A:H2'	53:1:105:C:O4'	2.17	0.44
53:1:193:U:H2'	53:1:194:G:H8	1.83	0.44
53:1:942:G:H2'	53:1:943:A:O4'	2.17	0.44
54:2:23:G:H2'	54:2:24:G:C8	2.52	0.44
54:2:92:C:H2'	54:2:93:C:C6	2.52	0.44
1:b:70:LYS:HG3	1:b:95:TYR:CZ	2.53	0.44
3:d:7:ASP:OD2	3:d:7:ASP:N	2.50	0.44
8:i:112:LYS:O	8:i:116:MET:HG2	2.17	0.44
10:k:5:GLN:NE2	10:k:20:MET:SD	2.91	0.44
12:m:82:MET:HE1	53:1:956:G:C1'	2.47	0.44
15:p:102:ARG:NH2	53:1:1754:A:O3'	2.50	0.44
21:v:35:GLU:OE1	21:v:35:GLU:N	2.51	0.44
33:l:184:LYS:HA	33:l:185:PRO:HD3	1.82	0.44
34:j:15:ILE:HD12	34:j:15:ILE:N	2.33	0.44
52:3:1011:C:H2'	52:3:1012:A:H8	1.83	0.44
52:3:1086:U:H2'	52:3:1087:G:H8	1.82	0.44
52:3:1197:A:H2'	52:3:1198:G:C5'	2.47	0.44
53:1:1965:C:H3'	53:1:1966:A:C8	2.53	0.44
53:1:2632:A:O2'	53:1:2633:G:H5'	2.18	0.44
53:1:2843:G:O2'	53:1:2844:G:H5'	2.17	0.44
57:7:76:A:O2'	60:7:101:PHE:C	2.59	0.44
2:c:133:THR:OG1	2:c:134:HIS:N	2.49	0.44
12:m:94:ALA:O	12:m:96:ILE:HG12	2.18	0.44
17:r:49:ILE:HB	17:r:51:VAL:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B:1:ALA:H3	53:1:2056:G:H21	1.66	0.44
33:I:77:GLU:OE2	33:I:80:ARG:NH1	2.50	0.44
33:I:90:LEU:HD13	33:I:187:ARG:CD	2.48	0.44
35:K:18:VAL:HG12	35:K:19:PRO:HD3	1.99	0.44
39:O:21:ALA:O	39:O:24:GLU:HG2	2.17	0.44
41:Q:40:THR:HA	41:Q:41:PRO:HD3	1.86	0.44
48:X:35:ARG:O	48:X:71:GLY:N	2.50	0.44
52:3:188:C:H2'	52:3:189:A:O4'	2.17	0.44
52:3:692:U:H2'	52:3:694:A:OP2	2.18	0.44
52:3:1392:G:H2'	52:3:1393:U:C6	2.52	0.44
52:3:1463:U:H2'	52:3:1464:U:C6	2.53	0.44
53:1:953:G:H2'	53:1:954:G:H8	1.83	0.44
53:1:1858:A:H1'	53:1:1885:A:C2	2.53	0.44
53:1:1889:A:H2'	53:1:1890:A:C8	2.53	0.44
53:1:2660:A:H2'	53:1:2661:G:O4'	2.18	0.44
53:1:2691:C:H2'	53:1:2692:G:C8	2.52	0.44
54:2:19:C:H2'	54:2:20:G:H8	1.81	0.44
55:6:62:C:H2'	55:6:63:G:C8	2.53	0.44
57:7:62:C:H2'	57:7:63:G:C4'	2.47	0.44
58:8:288:GLU:H	58:8:291:GLN:HE21	1.65	0.44
9:j:102:GLU:HB2	9:j:119:PHE:HZ	1.82	0.44
14:o:80:GLU:O	14:o:83:LEU:HG	2.18	0.44
16:q:50:ARG:NH2	53:1:993:G:OP2	2.51	0.44
17:r:38:VAL:O	17:r:54:VAL:HG23	2.18	0.44
34:J:104:ILE:HA	34:J:121:ASN:O	2.17	0.44
35:K:73:GLU:O	35:K:76:THR:OG1	2.31	0.44
52:3:86:G:H4'	52:3:87:C:C5	2.53	0.44
52:3:1187:G:H2'	52:3:1188:A:C8	2.52	0.44
52:3:1245:C:H2'	52:3:1246:A:C8	2.53	0.44
52:3:1453:G:H3'	52:3:1453:G:N3	2.32	0.44
53:1:69:C:O2'	53:1:70:G:H5'	2.17	0.44
53:1:523:C:H2'	53:1:524:G:C8	2.51	0.44
53:1:817:C:H2'	53:1:818:G:O4'	2.17	0.44
53:1:1773:A:H2'	53:1:1774:C:O4'	2.18	0.44
53:1:2008:C:H2'	53:1:2009:A:H8	1.82	0.44
53:1:2377:A:H2'	53:1:2378:A:C8	2.52	0.44
53:1:2682:A:O2'	53:1:2683:C:H5'	2.18	0.44
53:1:2808:G:H2'	53:1:2890:G:C6	2.53	0.44
58:8:117:ARG:CG	58:8:157:LEU:HD11	2.47	0.44
1:b:94:LEU:HD11	53:1:1501:G:H4'	2.00	0.44
3:d:98:LYS:HG3	53:1:607:U:P	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:129:PRO:HD3	3:d:156:ASN:ND2	2.33	0.44
4:e:87:LYS:HD2	53:1:2313:C:H5''	2.00	0.44
23:x:3:VAL:CG1	23:x:10:ARG:HE	2.29	0.44
28:D:31:LEU:O	28:D:35:ARG:HG3	2.18	0.44
31:G:83:ALA:HB2	31:G:90:PHE:HB3	1.99	0.44
32:H:10:ARG:NH2	32:H:174:LEU:O	2.50	0.44
32:H:42:LEU:HD12	32:H:54:ILE:HG21	2.00	0.44
34:J:112:ALA:O	34:J:116:VAL:HG22	2.18	0.44
36:L:67:ASN:O	36:L:137:ARG:NE	2.49	0.44
52:3:423:G:H2'	52:3:424:G:H5'	1.99	0.44
52:3:452:A:H61	52:3:480:U:H3	1.66	0.44
53:1:2063:C:O2'	55:5:76:A:H4'	2.18	0.44
53:1:2553:G:H2'	53:1:2554:U:H4'	2.00	0.44
53:1:2617:U:H2'	53:1:2618:G:O4'	2.18	0.44
53:1:2619:C:H2'	53:1:2620:C:C6	2.53	0.44
57:7:9:A:O2'	57:7:46:G:H4'	2.18	0.44
57:7:47:U:H2'	57:7:50:U:OP1	2.17	0.44
1:b:145:MET:HE2	1:b:181:ARG:NH2	2.33	0.44
2:c:51:THR:HB	2:c:79:LEU:HD23	2.00	0.44
4:e:59:ILE:O	4:e:101:ARG:NH1	2.49	0.44
31:G:2:THR:HG23	31:G:50:ASN:ND2	2.33	0.44
36:L:1:PRO:HB2	36:L:2:ARG:H	1.51	0.44
41:Q:23:LEU:HD12	41:Q:23:LEU:HA	1.86	0.44
42:R:79:LEU:HD23	42:R:82:LEU:HD12	1.99	0.44
43:S:92:ILE:HB	43:S:95:LEU:HD12	2.00	0.44
45:U:56:ARG:HH21	45:U:60:TRP:HE1	1.65	0.44
52:3:372:C:N4	52:3:387:U:H2'	2.32	0.44
53:1:149:A:H2'	53:1:150:U:C6	2.53	0.44
53:1:191:A:H2'	53:1:192:C:C6	2.53	0.44
53:1:621:A:H2'	53:1:622:G:H5'	2.00	0.44
53:1:1450:G:O2'	53:1:1451:C:H5'	2.18	0.44
53:1:2298:A:H2'	53:1:2299:U:O4'	2.18	0.44
54:2:35:C:H2'	54:2:36:C:H5'	2.00	0.44
57:7:18:G:N2	57:7:57:G:H2'	2.32	0.44
2:c:36:GLN:HG2	2:c:37:VAL:N	2.33	0.43
5:f:88:LEU:HG	5:f:161:VAL:HG12	1.99	0.43
6:g:40:THR:HG22	6:g:42:LYS:HG2	1.99	0.43
7:h:61:ARG:HB3	53:1:1046:A:H4'	1.99	0.43
22:w:38:GLY:HA2	53:1:2330:G:H21	1.83	0.43
26:B:6:LYS:O	26:B:6:LYS:HG3	2.17	0.43
29:E:39:ARG:O	29:E:43:LEU:HD12	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:25:LYS:HG3	34:J:26:GLY:N	2.33	0.43
49:Y:3:ILE:O	49:Y:3:ILE:HG23	2.18	0.43
52:3:477:C:H2'	52:3:478:A:C8	2.52	0.43
52:3:823:C:H2'	52:3:824:G:H8	1.82	0.43
52:3:1202:U:H2'	52:3:1203:C:O4'	2.18	0.43
53:1:481:G:H1'	53:1:506:G:H21	1.83	0.43
53:1:572:A:H5''	53:1:573:U:OP2	2.18	0.43
53:1:783:A:C2'	53:1:784:G:H5'	2.47	0.43
53:1:2104:C:H2'	53:1:2105:U:C6	2.53	0.43
53:1:2120:G:H2'	53:1:2121:G:H8	1.83	0.43
53:1:2784:U:H2'	53:1:2785:C:C6	2.53	0.43
54:2:114:C:H2'	54:2:115:A:C8	2.54	0.43
2:c:13:ARG:NH1	15:p:74:GLN:OE1	2.41	0.43
3:d:194:LYS:O	3:d:197:GLU:HB3	2.18	0.43
10:k:21:CYS:HB3	10:k:39:ILE:HD12	2.00	0.43
32:H:1:GLY:HA3	52:3:1060:U:C5	2.50	0.43
33:I:143:SER:OG	33:I:144:ILE:N	2.51	0.43
37:M:80:PRO:CG	52:3:878:A:H5'	2.49	0.43
41:Q:78:VAL:O	41:Q:102:ASP:HB2	2.18	0.43
52:3:26:A:N6	52:3:558:G:H1'	2.33	0.43
52:3:193:C:H2'	52:3:194:C:C6	2.52	0.43
53:1:1176:U:H2'	53:1:1177:G:C8	2.52	0.43
53:1:1717:A:H2'	53:1:1718:G:O4'	2.19	0.43
53:1:2398:U:H2'	53:1:2399:G:H8	1.81	0.43
53:1:2825:G:H2'	53:1:2826:A:H5'	2.00	0.43
53:1:2898:U:H2'	53:1:2899:A:C8	2.54	0.43
55:6:41:C:H2'	55:6:42:G:H8	1.82	0.43
58:8:194:GLY:O	58:8:197:ASP:OD1	2.35	0.43
58:8:244:GLU:C	58:8:245:ILE:HD12	2.43	0.43
58:8:309:VAL:HG12	58:8:310:TYR:N	2.33	0.43
2:c:118:PHE:HE1	2:c:163:GLY:HA2	1.83	0.43
24:y:31:GLN:HG2	24:y:37:LEU:CB	2.47	0.43
24:y:52:ARG:NH2	24:y:52:ARG:HB2	2.33	0.43
28:D:1:MET:HE1	28:D:3:ARG:HD3	2.00	0.43
31:G:10:LYS:O	31:G:207:ARG:NE	2.45	0.43
33:I:142:VAL:HG22	33:I:179:GLY:O	2.19	0.43
38:N:122:ARG:NH1	38:N:123:ARG:O	2.51	0.43
41:Q:48:LEU:HB2	52:3:520:A:OP1	2.18	0.43
44:T:50:HIS:CE1	52:3:667:G:H4'	2.53	0.43
48:X:57:VAL:HG23	48:X:57:VAL:O	2.17	0.43
52:3:40:C:H2'	52:3:41:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:270:A:H2'	52:3:271:C:C6	2.53	0.43
52:3:855:U:H2'	52:3:856:C:C6	2.52	0.43
52:3:918:A:H2'	52:3:919:A:O4'	2.17	0.43
52:3:1225:A:H2'	52:3:1225:A:N3	2.34	0.43
53:1:17:G:O2'	53:1:18:U:H5'	2.19	0.43
53:1:935:C:H2'	53:1:936:A:H8	1.83	0.43
53:1:1000:A:H2'	53:1:1001:A:C8	2.54	0.43
53:1:2008:C:H2'	53:1:2009:A:C8	2.53	0.43
53:1:2366:A:H2'	53:1:2367:G:O4'	2.18	0.43
53:1:2875:C:H2'	53:1:2876:G:C8	2.53	0.43
55:5:41:C:H2'	55:5:42:G:H8	1.83	0.43
4:e:33:ILE:HG21	4:e:98:PHE:HE2	1.83	0.43
4:e:62:GLN:HB3	4:e:94:ARG:NH2	2.33	0.43
6:g:73:ASN:HD22	6:g:76:GLU:HA	1.83	0.43
18:s:1:MET:HE3	18:s:3:THR:H	1.84	0.43
24:y:2:LYS:HB2	53:1:78:U:OP1	2.18	0.43
24:y:41:HIS:CD2	53:1:96:C:H4'	2.53	0.43
26:B:28:SER:HB3	26:B:39:ARG:HD2	2.00	0.43
38:N:35:GLU:HA	38:N:39:GLY:HA3	2.01	0.43
51:a:185:LEU:HA	51:a:188:ASN:ND2	2.20	0.43
52:3:103:U:H2'	52:3:104:G:O4'	2.19	0.43
53:1:334:C:O5'	53:1:334:C:H6	2.02	0.43
53:1:2182:U:H2'	53:1:2183:A:C8	2.53	0.43
13:n:69:ARG:O	13:n:70:THR:OG1	2.31	0.43
23:x:53:LYS:HA	23:x:56:ARG:HG3	2.00	0.43
51:a:46:VAL:HG13	51:a:171:ILE:HG23	2.01	0.43
52:3:1071:C:H2'	52:3:1072:G:H8	1.84	0.43
52:3:1128:C:H2'	52:3:1129:C:C6	2.53	0.43
53:1:594:U:H2'	53:1:595:C:C6	2.54	0.43
53:1:1019:U:H3	53:1:1142:A:H62	1.65	0.43
53:1:1388:G:H2'	53:1:1389:G:C8	2.54	0.43
53:1:1507:C:H2'	53:1:1508:A:C4'	2.48	0.43
53:1:1779:U:OP2	53:1:1784:A:N6	2.44	0.43
53:1:2038:G:H2'	53:1:2039:U:O4'	2.19	0.43
55:6:37:A:O2'	55:6:38:A:H5'	2.18	0.43
57:7:15:G:H2'	57:7:16:U:H5'	2.01	0.43
57:7:37:A:H2'	57:7:38:A:O4'	2.19	0.43
58:8:71:ASP:OD1	58:8:71:ASP:N	2.50	0.43
58:8:279:LEU:HD22	58:8:279:LEU:N	2.33	0.43
2:c:197:THR:HB	53:1:2820:A:N1	2.33	0.43
4:e:84:ILE:HG23	53:1:2312:U:H4'	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:134:GLN:HB3	4:e:149:ARG:O	2.19	0.43
17:r:74:ILE:N	17:r:74:ILE:HD12	2.33	0.43
17:r:76:LYS:HE2	17:r:85:LYS:HD2	1.99	0.43
19:t:44:LYS:HG3	19:t:55:VAL:HG11	2.01	0.43
28:D:1:MET:CE	28:D:3:ARG:HD3	2.48	0.43
33:I:2:ARG:HE	33:I:114:ARG:HD3	1.82	0.43
33:I:60:VAL:HA	33:I:63:ILE:HD12	1.99	0.43
40:P:119:GLY:HA2	52:3:716:A:N3	2.33	0.43
52:3:421:U:O2'	52:3:422:C:P	2.76	0.43
52:3:521:G:O2'	52:3:522:C:H5'	2.18	0.43
52:3:1464:U:H2'	52:3:1465:A:H8	1.83	0.43
53:1:248:G:H3'	53:1:249:C:C5'	2.48	0.43
53:1:1038:G:H2'	53:1:1039:A:H8	1.83	0.43
53:1:1055:G:H1	53:1:1104:C:H42	1.66	0.43
53:1:1775:U:C2'	53:1:1776:G:H5'	2.48	0.43
53:1:2489:U:O2'	53:1:2490:G:H5'	2.18	0.43
53:1:2538:C:H2'	53:1:2539:C:C6	2.53	0.43
54:2:1:U:H2'	54:2:2:G:C8	2.54	0.43
55:5:17:C:H5'	55:5:61:C:OP1	2.19	0.43
55:5:69:C:H2'	55:5:70:G:C8	2.53	0.43
58:8:72:THR:C	58:8:74:THR:H	2.26	0.43
58:8:152:MET:SD	58:8:155:ARG:HD2	2.59	0.43
1:b:127:ASN:HB2	1:b:191:LEU:HD12	2.00	0.43
1:b:202:ARG:HE	1:b:202:ARG:HB2	1.67	0.43
13:n:24:MET:O	13:n:27:SER:OG	2.36	0.43
14:o:68:LYS:HG3	54:2:50:A:OP1	2.19	0.43
27:C:46:VAL:HG22	27:C:47:ILE:N	2.34	0.43
33:I:151:GLN:H	33:I:151:GLN:CD	2.27	0.43
36:L:14:ASP:OD2	36:L:16:LYS:HB3	2.19	0.43
37:M:17:GLN:HE21	37:M:62:LEU:HD22	1.84	0.43
49:Y:23:ARG:HH12	52:3:176:C:C5'	2.31	0.43
52:3:51:A:H4'	52:3:52:C:H5''	2.01	0.43
52:3:225:C:H2'	52:3:226:G:C5'	2.47	0.43
52:3:423:G:C2'	52:3:424:G:H5'	2.49	0.43
52:3:1256:A:O2'	52:3:1257:A:H5''	2.19	0.43
52:3:1488:G:H2'	52:3:1489:G:H8	1.83	0.43
53:1:288:U:H2'	53:1:289:G:C8	2.52	0.43
53:1:995:C:H5'	53:1:995:C:C6	2.47	0.43
58:8:128:VAL:HG13	58:8:163:PHE:CZ	2.53	0.43
58:8:390:ALA:HB3	58:8:391:LYS:HD2	2.01	0.43
1:b:61:TYR:HA	1:b:85:ASN:HD21	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:65:LEU:HD22	54:2:42:C:C4	2.54	0.43
7:h:81:LEU:CD2	53:1:1106:G:H21	2.31	0.43
13:n:35:LYS:HE2	13:n:100:CYS:SG	2.59	0.43
13:n:100:CYS:SG	13:n:110:MET:HE3	2.59	0.43
32:H:53:ARG:HD3	32:H:54:ILE:H	1.83	0.43
36:L:41:ILE:HD11	52:3:1240:U:C4'	2.48	0.43
36:L:115:MET:HA	36:L:118:ARG:HE	1.83	0.43
43:S:60:ARG:O	43:S:61:ASN:HB2	2.17	0.43
45:U:42:ILE:HD12	45:U:42:ILE:N	2.34	0.43
46:V:16:MET:HG2	46:V:19:SER:HB2	2.01	0.43
49:Y:2:ASN:OD1	49:Y:3:ILE:N	2.52	0.43
50:Z:34:ARG:HD2	50:Z:36:PHE:CZ	2.54	0.43
52:3:412:A:C2	52:3:414:A:H1'	2.53	0.43
52:3:1148:U:H2'	52:3:1149:C:O4'	2.18	0.43
52:3:1430:A:C2'	52:3:1431:A:H5'	2.49	0.43
53:1:192:C:H2'	53:1:193:U:H5'	2.00	0.43
53:1:706:A:H2'	53:1:707:G:O4'	2.19	0.43
53:1:792:A:H3'	53:1:793:A:H5'	2.00	0.43
53:1:1164:C:H2'	53:1:1165:A:C8	2.54	0.43
53:1:1910:G:H1	53:1:1920:C:H42	1.65	0.43
54:2:78:A:H2'	54:2:79:G:O4'	2.18	0.43
58:8:130:TYR:CE2	58:8:201:PRO:HD2	2.54	0.43
9:j:110:PRO:O	9:j:115:GLY:HA3	2.19	0.43
12:m:3:GLN:HA	12:m:4:PRO:HD3	1.91	0.43
14:o:34:HIS:ND1	14:o:65:THR:HG21	2.33	0.43
31:G:207:ARG:HG2	31:G:207:ARG:HH11	1.83	0.43
32:H:127:VAL:HG22	32:H:128:MET:N	2.33	0.43
32:H:137:VAL:HG21	32:H:167:TYR:CE2	2.54	0.43
37:M:8:ASP:O	37:M:12:ARG:HG3	2.19	0.43
37:M:73:SER:HB3	37:M:75:GLN:HE22	1.84	0.43
38:N:49:GLN:N	38:N:50:PRO:HD2	2.33	0.43
40:P:92:ARG:NH2	40:P:111:ASP:OD1	2.52	0.43
41:Q:47:ALA:C	41:Q:48:LEU:HD22	2.44	0.43
41:Q:112:ALA:HB2	52:3:503:C:OP2	2.18	0.43
42:R:74:MET:SD	42:R:75:SER:N	2.92	0.43
46:V:15:LYS:HD2	46:V:15:LYS:HA	1.86	0.43
50:Z:64:ALA:C	50:Z:66:ARG:H	2.27	0.43
53:1:306:U:H2'	53:1:307:G:O4'	2.19	0.43
53:1:445:C:O2'	53:1:446:G:H5'	2.19	0.43
53:1:1775:U:H2'	53:1:1776:G:H5'	2.01	0.43
53:1:2685:G:H2'	53:1:2686:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2704:C:H2'	53:1:2705:A:O4'	2.19	0.43
53:1:2853:C:H2'	53:1:2854:G:H8	1.83	0.43
1:b:180:MET:HB2	1:b:267:VAL:HB	2.00	0.43
2:c:62:LYS:NZ	53:1:2810:A:H5''	2.34	0.43
4:e:51:ASN:HB3	4:e:149:ARG:HH21	1.83	0.43
5:f:102:ILE:HG22	5:f:104:LEU:HD21	1.99	0.43
6:g:4:ILE:HG12	6:g:16:GLY:HA2	2.00	0.43
7:h:97:LYS:HE2	7:h:97:LYS:HB3	1.91	0.43
11:l:110:VAL:HB	11:l:127:VAL:HG13	2.01	0.43
11:l:132:ARG:HG3	11:l:142:ILE:HD12	2.00	0.43
12:m:75:GLU:OE1	53:1:957:C:H5'	2.19	0.43
17:r:34:GLU:HB3	17:r:58:VAL:HG13	2.00	0.43
18:s:18:ARG:NH1	53:1:518:G:O5'	2.52	0.43
18:s:21:ALA:O	18:s:25:ARG:NH1	2.52	0.43
35:K:6:ILE:N	35:K:6:ILE:HD12	2.34	0.43
36:L:142:ARG:HG2	55:6:41:C:C4'	2.43	0.43
45:U:33:ILE:HG21	45:U:60:TRP:CZ2	2.53	0.43
45:U:40:ASN:CG	45:U:43:ALA:HB2	2.44	0.43
50:Z:3:ILE:HA	50:Z:19:LYS:HE3	2.01	0.43
51:a:173:THR:CG2	51:a:192:LEU:HD11	2.49	0.43
52:3:123:U:H2'	52:3:124:C:C6	2.53	0.43
52:3:782:A:H4'	52:3:1514:G:O2'	2.19	0.43
52:3:1342:C:H2'	52:3:1343:G:C8	2.54	0.43
53:1:248:G:C5'	53:1:249:C:H5'	2.49	0.43
53:1:471:A:H2'	53:1:472:A:O4'	2.18	0.43
53:1:1435:G:H2'	53:1:1436:G:H8	1.83	0.43
54:2:13:G:O2'	54:2:15:A:H2'	2.19	0.43
55:5:47:U:H3'	55:5:48:C:H5'	2.01	0.43
58:8:325:LYS:HG3	58:8:344:LEU:H	1.84	0.43
1:b:120:ASP:O	1:b:120:ASP:OD2	2.37	0.42
5:f:2:ARG:HH12	53:1:1113:U:C5'	2.29	0.42
7:h:118:ILE:HG22	7:h:119:PRO:N	2.34	0.42
34:J:14:LEU:C	34:J:15:ILE:HD12	2.44	0.42
36:L:32:ASP:OD1	52:3:1351:U:H5'	2.18	0.42
36:L:137:ARG:HH11	36:L:141:HIS:CE1	2.37	0.42
51:a:200:LYS:HA	51:a:201:PRO:HD3	1.88	0.42
52:3:332:G:O2'	52:3:333:U:H5'	2.19	0.42
52:3:354:G:H2'	52:3:355:C:H5'	2.01	0.42
52:3:355:C:H2'	52:3:356:A:O4'	2.19	0.42
52:3:1368:A:O2'	52:3:1369:C:H5'	2.18	0.42
52:3:1527:U:H2'	52:3:1528:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:367:G:H3'	53:1:368:A:H8	1.84	0.42
53:1:1111:A:O2'	53:1:1112:G:H4'	2.19	0.42
53:1:2302:U:H2'	53:1:2303:G:H8	1.83	0.42
53:1:2897:U:H2'	53:1:2898:U:C6	2.54	0.42
55:5:24:U:H2'	55:5:25:C:C6	2.54	0.42
58:8:23:HIS:O	58:8:136:ASN:ND2	2.51	0.42
58:8:209:LYS:HE3	58:8:210:PRO:HD2	2.01	0.42
58:8:244:GLU:HA	58:8:253:LYS:HA	2.00	0.42
2:c:46:ARG:HB2	2:c:84:LEU:HD12	2.01	0.42
4:e:159:ALA:HB1	4:e:164:GLU:HB3	2.00	0.42
7:h:59:LEU:HD12	53:1:1108:U:OP2	2.19	0.42
7:h:97:LYS:HE3	7:h:129:LEU:HD12	2.01	0.42
10:k:104:THR:HG23	10:k:107:LEU:HB2	2.01	0.42
12:m:31:PHE:HB3	12:m:130:PHE:HE1	1.83	0.42
19:t:50:LEU:HD12	19:t:50:LEU:H	1.83	0.42
31:G:84:LEU:HD12	31:G:84:LEU:C	2.44	0.42
36:L:142:ARG:HG2	55:6:41:C:C5'	2.49	0.42
39:O:40:ILE:CB	39:O:73:LEU:HB2	2.49	0.42
39:O:89:ARG:HG2	39:O:89:ARG:HH11	1.84	0.42
42:R:92:ARG:HB3	42:R:94:LEU:HD23	2.01	0.42
52:3:123:U:OP1	52:3:312:C:H5'	2.19	0.42
52:3:948:C:H5'	52:3:1306:A:O2'	2.19	0.42
52:3:1011:C:H2'	52:3:1012:A:C8	2.54	0.42
52:3:1287:A:H2'	52:3:1288:A:C8	2.54	0.42
53:1:704:G:H1'	53:1:727:A:N6	2.34	0.42
53:1:1199:U:H2'	53:1:1200:C:C6	2.54	0.42
53:1:1287:A:H2'	53:1:1288:G:H5'	2.00	0.42
53:1:1424:G:H2'	53:1:1425:G:O4'	2.20	0.42
53:1:2163:A:C2'	53:1:2164:C:H5'	2.47	0.42
53:1:2361:G:O2'	53:1:2362:C:H5'	2.19	0.42
53:1:2707:U:H2'	53:1:2708:G:H8	1.83	0.42
54:2:39:A:H2'	54:2:40:U:C6	2.54	0.42
57:7:65:G:H2'	57:7:66:U:C6	2.54	0.42
58:8:216:GLU:HG3	58:8:217:ASP:H	1.83	0.42
58:8:304:LYS:HE3	58:8:360:VAL:HG11	2.00	0.42
58:8:332:TYR:HA	58:8:336:THR:O	2.19	0.42
4:e:135:ILE:HD12	4:e:135:ILE:N	2.31	0.42
15:p:25:VAL:HG22	15:p:26:GLU:N	2.34	0.42
19:t:92:ASN:OD1	19:t:93:LEU:N	2.52	0.42
20:u:43:LYS:O	20:u:58:VAL:HG22	2.20	0.42
25:z:29:ARG:NH2	25:z:29:ARG:HG2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:G:4:SER:O	31:G:7:ASP:OD1	2.37	0.42
32:H:9:ILE:HG23	32:H:10:ARG:HG3	2.01	0.42
32:H:128:MET:HB3	32:H:131:ARG:HB2	2.01	0.42
36:L:68:VAL:HA	36:L:137:ARG:HD3	2.01	0.42
40:P:63:GLN:HG3	40:P:98:ALA:HB2	2.01	0.42
41:Q:49:ARG:HH21	52:3:522:C:N4	2.18	0.42
41:Q:74:GLN:HG2	41:Q:74:GLN:O	2.19	0.42
46:V:56:ASP:HB3	46:V:81:ALA:N	2.33	0.42
49:Y:79:THR:O	49:Y:83:ASN:ND2	2.52	0.42
50:Z:23:GLU:O	50:Z:25:ALA:N	2.41	0.42
52:3:593:U:H2'	52:3:594:U:C6	2.54	0.42
52:3:886:G:H2'	52:3:887:G:H8	1.82	0.42
52:3:908:A:H2'	52:3:909:A:C8	2.55	0.42
52:3:1459:G:H2'	52:3:1460:C:C6	2.54	0.42
53:1:370:G:H2'	53:1:423:A:N7	2.34	0.42
53:1:657:U:H2'	53:1:658:U:C6	2.55	0.42
53:1:813:U:O2'	53:1:1225:G:H1'	2.19	0.42
53:1:871:U:H2'	53:1:872:U:C6	2.54	0.42
53:1:894:U:O2'	53:1:895:U:H5'	2.20	0.42
53:1:1337:G:H2'	53:1:1338:G:H8	1.84	0.42
53:1:2106:U:H2'	53:1:2107:G:H8	1.84	0.42
53:1:2257:U:O2'	53:1:2258:C:H5'	2.19	0.42
57:7:62:C:H2'	57:7:63:G:C5'	2.49	0.42
1:b:13:ARG:HH22	53:1:1693:U:H1'	1.84	0.42
1:b:141:HIS:CD2	1:b:194:VAL:HG22	2.55	0.42
7:h:23:LEU:CD1	7:h:118:ILE:HB	2.49	0.42
10:k:9:ASN:O	10:k:83:ALA:HA	2.19	0.42
11:l:141:LYS:NZ	11:l:143:GLU:OE1	2.49	0.42
18:s:33:LEU:O	18:s:37:THR:HG23	2.19	0.42
24:y:39:GLN:HE21	24:y:42:LEU:HD11	1.84	0.42
33:I:187:ARG:HD2	33:I:190:LEU:HD21	2.01	0.42
34:J:97:PRO:HA	34:J:122:VAL:HG12	2.01	0.42
37:M:21:LYS:HE3	52:3:827:U:H5''	2.01	0.42
41:Q:64:SER:OG	41:Q:96:THR:HG23	2.19	0.42
51:a:211:LYS:HZ2	53:1:2177:C:H5''	1.83	0.42
52:3:45:G:H5''	52:3:307:C:O2'	2.19	0.42
52:3:216:U:H2'	52:3:217:C:C6	2.54	0.42
53:1:705:A:C2	53:1:727:A:H1'	2.54	0.42
53:1:1259:G:H2'	53:1:1260:A:C8	2.55	0.42
53:1:2391:G:H1'	53:1:2429:G:N2	2.34	0.42
53:1:2623:G:H2'	53:1:2624:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:8:20:HIS:ND1	58:8:21:VAL:HG12	2.35	0.42
5:f:42:VAL:HG22	5:f:51:PHE:HD1	1.85	0.42
15:p:96:LEU:HB3	15:p:99:LEU:HD13	2.02	0.42
23:x:54:GLY:O	23:x:57:VAL:HG12	2.20	0.42
24:y:24:GLU:O	24:y:25:GLN:C	2.62	0.42
30:F:32:LYS:HE3	53:1:2478:A:H5'	2.02	0.42
32:H:69:THR:OG1	32:H:70:ALA:N	2.53	0.42
33:I:75:TYR:HD1	33:I:89:LEU:HD11	1.84	0.42
45:U:33:ILE:N	45:U:33:ILE:HD12	2.35	0.42
46:V:10:ARG:HB3	46:V:10:ARG:CZ	2.50	0.42
46:V:22:VAL:HG12	46:V:43:LEU:O	2.20	0.42
46:V:56:ASP:HB3	46:V:81:ALA:CA	2.49	0.42
52:3:160:A:H2'	52:3:161:A:O4'	2.19	0.42
52:3:321:A:H2'	52:3:322:C:C6	2.54	0.42
52:3:1342:C:H2'	52:3:1343:G:H8	1.84	0.42
52:3:1512:U:H2'	52:3:1513:A:H8	1.84	0.42
53:1:11:C:H3'	53:1:12:U:H5''	2.01	0.42
53:1:426:C:H2'	53:1:427:U:C6	2.54	0.42
53:1:834:G:H1'	53:1:2358:A:N3	2.34	0.42
53:1:984:A:H5''	53:1:985:C:OP2	2.19	0.42
53:1:1278:C:H2'	53:1:1279:G:C8	2.54	0.42
53:1:1300:G:H4'	53:1:1301:A:H5''	2.01	0.42
53:1:1430:G:H2'	53:1:1431:A:O4'	2.20	0.42
53:1:1668:A:N6	53:1:1676:A:H61	2.16	0.42
53:1:2347:C:H2'	53:1:2348:U:C6	2.54	0.42
58:8:231:ARG:NH1	58:8:233:GLU:OE2	2.53	0.42
2:c:170:VAL:HG23	2:c:194:PRO:HG2	2.01	0.42
3:d:40:ARG:HD2	53:1:443:A:C4	2.55	0.42
8:i:57:VAL:HG12	8:i:71:LYS:NZ	2.32	0.42
10:k:1:MET:HE3	10:k:67:LYS:HG2	2.01	0.42
18:s:57:ASN:OD1	18:s:61:ASN:ND2	2.52	0.42
24:y:43:LEU:O	24:y:46:VAL:HG12	2.19	0.42
31:G:93:HIS:CG	31:G:94:ARG:H	2.37	0.42
32:H:21:TRP:HB3	32:H:58:ARG:HD2	2.01	0.42
33:I:126:GLY:C	33:I:127:ARG:HD2	2.45	0.42
34:J:137:ARG:NH2	52:3:1078:U:H4'	2.34	0.42
45:U:8:ARG:O	45:U:28:ARG:NH1	2.52	0.42
53:1:259:G:H2'	53:1:260:G:H8	1.84	0.42
53:1:783:A:H2'	53:1:784:G:C5'	2.49	0.42
53:1:1779:U:OP1	53:1:1780:A:H5'	2.20	0.42
53:1:2580:U:H2'	53:1:2581:G:H5'	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2:51:G:H2'	54:2:52:A:O4'	2.20	0.42
54:2:55:U:O2'	54:2:56:G:H5'	2.19	0.42
58:8:115:GLN:HG3	58:8:119:HIS:HE1	1.85	0.42
58:8:301:PRO:HB2	58:8:366:PRO:HB2	2.02	0.42
9:j:21:THR:OG1	9:j:61:LYS:HD2	2.20	0.42
11:l:23:ILE:HD12	11:l:23:ILE:N	2.35	0.42
11:l:36:LYS:NZ	53:1:567:U:O3'	2.52	0.42
12:m:40:ARG:NH1	53:1:958:U:C5	2.88	0.42
13:n:4:ARG:HD2	53:1:2874:C:OP1	2.19	0.42
26:B:8:THR:OG1	26:B:9:ARG:N	2.53	0.42
31:G:23:ASN:HA	31:G:24:PRO:HD3	1.89	0.42
31:G:112:ARG:O	31:G:116:LEU:HD23	2.19	0.42
33:I:89:LEU:O	33:I:93:LEU:HD23	2.19	0.42
37:M:12:ARG:NH2	52:3:826:C:H5'	2.34	0.42
43:S:25:GLU:O	43:S:29:ILE:HG12	2.19	0.42
44:T:55:LEU:HD21	53:1:715:A:C2	2.54	0.42
44:T:63:ARG:HA	44:T:63:ARG:HD2	1.83	0.42
51:a:189:LEU:O	51:a:193:LEU:HG	2.20	0.42
52:3:31:G:H21	52:3:47:C:H5''	1.85	0.42
52:3:744:C:H2'	52:3:745:G:H8	1.85	0.42
52:3:994:A:C8	52:3:1216:A:H4'	2.55	0.42
52:3:1251:A:H2'	52:3:1252:A:C8	2.54	0.42
53:1:722:A:H2'	53:1:723:C:C6	2.55	0.42
53:1:1801:A:H5''	53:1:2203:U:C2'	2.49	0.42
53:1:1859:U:H2'	53:1:1860:G:H8	1.84	0.42
53:1:2577:A:H2'	53:1:2614:A:N6	2.34	0.42
53:1:2773:C:H2'	53:1:2774:C:H6	1.85	0.42
53:1:2789:C:H2'	53:1:2790:U:H5'	2.02	0.42
53:1:2818:U:H4'	53:1:2837:A:H4'	2.02	0.42
58:8:328:ARG:HG2	58:8:341:THR:HA	2.02	0.42
9:j:35:ARG:HA	9:j:40:HIS:CD2	2.55	0.42
11:l:94:THR:O	11:l:97:ALA:HB3	2.19	0.42
12:m:6:ARG:HH12	55:5:52:G:H4'	1.83	0.42
15:p:12:MET:O	15:p:14:GLN:NE2	2.51	0.42
35:K:18:VAL:N	35:K:19:PRO:HD3	2.34	0.42
36:L:146:ALA:HB1	55:6:40:C:H4'	2.01	0.42
40:P:59:PRO:HB3	40:P:91:GLY:HA2	2.00	0.42
45:U:46:LYS:NZ	45:U:48:GLU:O	2.53	0.42
46:V:22:VAL:HG22	46:V:23:ALA:N	2.33	0.42
46:V:39:ARG:HH11	46:V:39:ARG:HG3	1.85	0.42
48:X:37:SER:O	48:X:70:LEU:HG	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:303:A:H2'	52:3:304:U:O4'	2.20	0.42
52:3:448:A:H3'	52:3:449:G:C8	2.54	0.42
52:3:537:G:H2'	52:3:538:G:H8	1.85	0.42
52:3:539:A:H2'	52:3:540:G:H8	1.84	0.42
52:3:1315:U:H2'	52:3:1316:G:O4'	2.20	0.42
52:3:1433:A:H2'	52:3:1434:A:O4'	2.19	0.42
53:1:368:A:H2'	53:1:369:U:O4'	2.19	0.42
53:1:879:G:H2'	53:1:880:G:H8	1.84	0.42
53:1:2128:G:H1'	53:1:2173:A:N3	2.34	0.42
53:1:2183:A:H2'	53:1:2184:A:C8	2.54	0.42
53:1:2619:C:H2'	53:1:2620:C:H6	1.85	0.42
53:1:2642:G:O2'	53:1:2643:G:H5'	2.20	0.42
53:1:2662:A:H2'	53:1:2663:G:O4'	2.20	0.42
2:c:4:LEU:HB3	2:c:32:ASN:ND2	2.35	0.42
3:d:154:ASP:OD1	3:d:154:ASP:N	2.48	0.42
31:G:27:LYS:N	31:G:28:PRO:CD	2.83	0.42
36:L:24:LYS:HA	36:L:27:ASN:HD22	1.85	0.42
36:L:90:VAL:HG22	36:L:91:ARG:N	2.35	0.42
40:P:86:LYS:NZ	40:P:112:VAL:O	2.53	0.42
49:Y:67:HIS:C	49:Y:69:ASN:H	2.27	0.42
49:Y:75:LYS:O	49:Y:79:THR:OG1	2.32	0.42
52:3:629:A:H2'	52:3:630:A:O4'	2.20	0.42
52:3:822:U:H2'	52:3:823:C:C6	2.55	0.42
52:3:1391:U:H2'	52:3:1392:G:H8	1.84	0.42
53:1:14:A:C6	53:1:526:A:C2	3.08	0.42
53:1:646:U:C4	53:1:2368:C:H1'	2.55	0.42
53:1:1550:C:H2'	53:1:1551:A:C8	2.55	0.42
53:1:1657:U:H2'	53:1:1658:C:H6	1.79	0.42
53:1:2345:G:N3	53:1:2381:A:H2'	2.34	0.42
53:1:2545:G:H2'	53:1:2546:U:C5'	2.50	0.42
1:b:89:ASN:HD22	1:b:89:ASN:HA	1.70	0.42
4:e:62:GLN:NE2	54:2:43:C:O4'	2.53	0.42
13:n:83:LEU:HD23	13:n:83:LEU:HA	1.86	0.42
32:H:52:SER:HG	32:H:68:HIS:C	2.27	0.42
33:I:55:ARG:HA	33:I:55:ARG:HD3	1.61	0.42
34:J:104:ILE:HG13	34:J:104:ILE:O	2.20	0.42
34:J:113:VAL:HG13	34:J:114:LEU:HD22	2.01	0.42
36:L:122:GLU:O	36:L:125:ASP:OD1	2.37	0.42
38:N:90:ASP:HB2	38:N:91:GLU:H	1.75	0.42
41:Q:111:GLN:HB2	52:3:538:G:OP2	2.20	0.42
47:W:31:TYR:CD2	47:W:54:LEU:HD11	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:244:U:O4	52:3:906:A:H1'	2.19	0.42
52:3:434:U:H2'	52:3:435:A:C8	2.55	0.42
52:3:603:U:H2'	52:3:604:G:C8	2.55	0.42
53:1:1366:A:H2'	53:1:1367:A:O4'	2.20	0.42
53:1:1441:G:H2'	53:1:1442:U:C6	2.55	0.42
53:1:2024:G:OP2	53:1:2034:U:H4'	2.19	0.42
53:1:2036:C:H2'	53:1:2037:A:C8	2.54	0.42
53:1:2062:A:C2	59:5:101:FME:HE1	2.54	0.42
53:1:2318:G:H2'	53:1:2319:G:O4'	2.19	0.42
55:6:17(A):U:O2'	55:6:18:G:OP1	2.36	0.42
4:e:30:VAL:HA	4:e:157:THR:HA	2.01	0.41
4:e:137:PHE:HA	4:e:138:PRO:HD3	1.84	0.41
13:n:64:ARG:HG3	53:1:1454:C:O2	2.20	0.41
15:p:2:ASN:HA	15:p:5:LYS:HB3	2.00	0.41
19:t:68:LYS:HG3	19:t:77:ARG:HH22	1.85	0.41
20:u:10:VAL:HB	20:u:69:VAL:HG22	2.02	0.41
22:w:74:LYS:HZ3	53:1:857:G:H5''	1.84	0.41
34:J:92:ARG:O	34:J:93:VAL:O	2.37	0.41
34:J:114:LEU:O	34:J:117:ALA:HB3	2.20	0.41
38:N:6:TYR:CE2	52:3:1147:C:H4'	2.54	0.41
38:N:59:LYS:HD2	38:N:59:LYS:HA	1.90	0.41
40:P:107:THR:OG1	40:P:108:ASN:N	2.53	0.41
49:Y:29:THR:HG21	52:3:1457:G:O3'	2.19	0.41
52:3:337:G:H2'	52:3:338:A:H8	1.85	0.41
52:3:419:C:O2'	52:3:420:U:H5'	2.20	0.41
52:3:1255:G:H2'	52:3:1279:G:H1	1.85	0.41
53:1:460:A:H2'	53:1:461:C:O4'	2.20	0.41
53:1:543:G:H2'	53:1:544:C:O4'	2.19	0.41
53:1:969:G:H2'	53:1:970:U:C6	2.55	0.41
53:1:1601:G:O2'	53:1:1602:U:H5'	2.20	0.41
53:1:1701:A:H2'	53:1:1702:G:H5'	2.02	0.41
53:1:2078:C:O2'	53:1:2079:U:H5'	2.20	0.41
53:1:2637:U:H2'	53:1:2638:G:O4'	2.19	0.41
53:1:2888:C:H2'	53:1:2889:C:C6	2.54	0.41
54:2:66:A:N1	54:2:107:G:H2'	2.35	0.41
1:b:13:ARG:NH2	53:1:1693:U:O2	2.53	0.41
1:b:59:GLN:HA	53:1:1568:G:H5'	2.03	0.41
5:f:1:SER:OG	5:f:2:ARG:N	2.52	0.41
11:l:57:LEU:HA	11:l:60:ARG:HE	1.85	0.41
12:m:44:ARG:HG2	12:m:44:ARG:HH21	1.85	0.41
33:I:77:GLU:O	33:I:81:LEU:HG	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:K:42:TRP:HB2	35:K:59:TYR:HB2	2.02	0.41
36:L:4:ARG:HB3	36:L:6:ILE:HG23	2.02	0.41
36:L:150:PHE:HZ	40:P:55:ARG:HG2	1.85	0.41
43:S:26:LEU:HA	43:S:30:ILE:HD11	2.02	0.41
45:U:5:ARG:HD3	52:3:377:G:OP1	2.20	0.41
46:V:11:VAL:CG1	46:V:20:ILE:HD11	2.50	0.41
47:W:17:VAL:C	47:W:18:GLN:HG3	2.45	0.41
52:3:510:A:N3	52:3:543:U:H1'	2.36	0.41
52:3:1067:A:N6	52:3:1109:C:H5'	2.35	0.41
53:1:1755:A:H2'	53:1:1756:G:H5'	2.01	0.41
53:1:1853:A:H2'	53:1:1854:A:C8	2.55	0.41
53:1:2462:C:H2'	53:1:2463:C:C6	2.55	0.41
53:1:2747:G:O6	53:1:2755:C:H5''	2.20	0.41
55:6:16:C:H4'	55:6:60:U:O2	2.20	0.41
57:7:62:C:C2'	57:7:63:G:H5''	2.49	0.41
58:8:45:ARG:NH1	58:8:69:GLU:OE2	2.52	0.41
1:b:88:ALA:HB1	1:b:194:VAL:HG11	2.02	0.41
1:b:242:HIS:HA	1:b:243:PRO:HD3	1.93	0.41
3:d:29:HIS:CD2	11:l:8:PRO:HD3	2.56	0.41
3:d:63:LYS:NZ	53:1:2444:G:OP2	2.53	0.41
3:d:105:LEU:O	3:d:109:LEU:HD13	2.21	0.41
5:f:44:HIS:NE2	5:f:46:ASP:O	2.53	0.41
5:f:129:GLU:HG2	5:f:130:ILE:N	2.35	0.41
5:f:146:ASP:O	5:f:149:ALA:HB3	2.20	0.41
8:i:21:PRO:CB	8:i:22:PRO:HD3	2.48	0.41
12:m:13:HIS:HB3	53:1:954:G:OP1	2.19	0.41
14:o:3:LYS:HD2	54:2:47:C:OP2	2.20	0.41
19:t:61:LEU:O	19:t:81:LYS:HG3	2.20	0.41
25:z:37:ARG:HH21	53:1:929:U:H4'	1.82	0.41
32:H:58:ARG:HE	32:H:63:ILE:HG12	1.85	0.41
39:O:42:LEU:HD11	39:O:73:LEU:HG	2.03	0.41
39:O:52:LEU:HD11	39:O:59:LYS:HE3	2.03	0.41
40:P:80:ASN:OD1	40:P:80:ASN:N	2.48	0.41
40:P:124:LYS:HD2	40:P:124:LYS:C	2.44	0.41
53:1:466:A:H2'	53:1:467:G:H5'	2.02	0.41
53:1:1201:U:H2'	53:1:1202:G:H8	1.85	0.41
53:1:1736:U:H2'	53:1:1737:G:O4'	2.21	0.41
53:1:2248:C:H2'	53:1:2249:U:C5'	2.49	0.41
53:1:2283:C:H2'	53:1:2284:A:O4'	2.19	0.41
53:1:2452:C:H42	53:1:2504:U:H3	1.68	0.41
58:8:14:ASN:ND2	58:8:100:ASP:OD2	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:8:336:THR:HG22	58:8:338:VAL:HG23	2.02	0.41
3:d:186:VAL:O	3:d:186:VAL:HG13	2.20	0.41
7:h:94:ARG:HD3	7:h:94:ARG:N	2.35	0.41
12:m:53:MET:HE1	12:m:103:TYR:HB3	2.03	0.41
18:s:77:ASP:OD1	18:s:77:ASP:N	2.54	0.41
31:G:20:ARG:HA	52:3:830:G:H4'	2.01	0.41
31:G:103:TRP:HA	31:G:106:VAL:HG12	2.02	0.41
34:J:108:GLY:O	34:J:109:ALA:HB3	2.20	0.41
36:L:20:GLU:H	36:L:20:GLU:CD	2.28	0.41
36:L:52:ARG:HH22	36:L:121:ASN:HD22	1.68	0.41
42:R:22:TYR:HB3	42:R:65:GLU:CG	2.51	0.41
46:V:43:LEU:HD23	46:V:43:LEU:C	2.45	0.41
49:Y:2:ASN:ND2	52:3:351:G:OP1	2.53	0.41
49:Y:23:ARG:NH1	52:3:176:C:H5''	2.36	0.41
51:a:175:ILE:HB	51:a:188:ASN:HB3	2.01	0.41
53:1:167:A:H2'	53:1:168:G:O4'	2.21	0.41
53:1:198:C:O2'	53:1:199:A:H5'	2.21	0.41
53:1:558:U:H2'	53:1:559:G:H8	1.84	0.41
53:1:640:C:H2'	53:1:641:U:C6	2.56	0.41
53:1:818:G:C2'	53:1:819:A:H5''	2.50	0.41
53:1:2340:A:H2'	53:1:2341:G:H8	1.85	0.41
53:1:2391:G:H2'	53:1:2424:C:N4	2.35	0.41
53:1:2777:G:H1'	53:1:2779:U:H5	1.85	0.41
53:1:2855:C:H2'	53:1:2856:A:C8	2.55	0.41
55:6:51:C:H2'	55:6:52:G:C8	2.55	0.41
4:e:4:HIS:CD2	4:e:8:LYS:HE3	2.55	0.41
5:f:131:VAL:O	5:f:131:VAL:HG23	2.20	0.41
12:m:44:ARG:HG2	12:m:44:ARG:NH2	2.35	0.41
14:o:11:ALA:HB2	14:o:96:GLY:N	2.35	0.41
21:v:1:MET:SD	21:v:1:MET:C	3.03	0.41
26:B:16:ARG:HA	26:B:19:ASP:OD2	2.21	0.41
26:B:21:LEU:HD12	26:B:21:LEU:H	1.85	0.41
32:H:113:LYS:HG3	32:H:184:ASN:HD21	1.86	0.41
36:L:15:PRO:HG2	38:N:44:ARG:NH2	2.36	0.41
38:N:17:ARG:HH21	38:N:65:THR:HG21	1.84	0.41
43:S:92:ILE:N	43:S:92:ILE:HD12	2.34	0.41
45:U:5:ARG:NH2	45:U:23:ASP:O	2.54	0.41
50:Z:39:LYS:HB2	50:Z:40:PRO:HD3	2.03	0.41
50:Z:66:ARG:HG2	52:3:1099:G:H5'	2.03	0.41
52:3:410:G:H2'	52:3:429:U:C4	2.55	0.41
52:3:744:C:H2'	52:3:745:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1318:A:C2'	52:3:1319:A:H5'	2.46	0.41
53:1:383:C:H5''	53:1:385:C:OP2	2.20	0.41
53:1:548:G:H2'	53:1:549:G:O4'	2.20	0.41
53:1:1098:A:H2'	53:1:1099:G:O4'	2.19	0.41
53:1:2417:C:H2'	53:1:2418:A:H8	1.86	0.41
53:1:2739:U:O2'	53:1:2740:A:H5'	2.20	0.41
54:2:66:A:H4'	54:2:67:G:C8	2.55	0.41
57:7:49:C:H2'	57:7:50:U:C6	2.56	0.41
58:8:247:GLY:HA3	58:8:291:GLN:HG2	2.03	0.41
3:d:30:GLN:HG3	53:1:659:G:H21	1.85	0.41
3:d:61:ARG:HE	3:d:61:ARG:HB2	1.70	0.41
7:h:34:THR:HB	7:h:38:MET:HE2	2.02	0.41
10:k:48:PRO:HB3	52:3:1422:G:H4'	2.02	0.41
13:n:8:ARG:N	13:n:43:GLU:OE2	2.52	0.41
15:p:13:LYS:HG3	15:p:16:VAL:CG2	2.51	0.41
28:D:24:THR:HG23	28:D:27:GLY:H	1.85	0.41
38:N:34:LEU:HD11	38:N:47:VAL:HG21	2.02	0.41
41:Q:43:LYS:HD2	41:Q:44:PRO:N	2.35	0.41
43:S:33:VAL:O	43:S:33:VAL:HG22	2.20	0.41
44:T:68:TYR:CD2	52:3:754:C:H1'	2.56	0.41
45:U:17:TYR:O	45:U:39:PHE:N	2.50	0.41
52:3:202:G:H2'	52:3:203:G:C8	2.55	0.41
52:3:1192:C:H6	52:3:1192:C:O5'	2.03	0.41
52:3:1436:U:H2'	52:3:1437:A:H8	1.85	0.41
52:3:1539:C:O2'	52:3:1540:U:H5'	2.20	0.41
53:1:576:U:H2'	53:1:577:G:C8	2.54	0.41
53:1:1463:C:H2'	53:1:1464:G:C8	2.55	0.41
53:1:1873:G:O2'	53:1:1874:C:H5'	2.21	0.41
53:1:2024:G:H2'	53:1:2025:C:C6	2.56	0.41
53:1:2417:C:H2'	53:1:2418:A:C8	2.56	0.41
53:1:2665:A:O2'	53:1:2666:C:H5'	2.20	0.41
53:1:2699:C:H2'	53:1:2700:A:C8	2.56	0.41
53:1:2743:U:H3'	53:1:2744:G:H5''	2.01	0.41
55:6:66:C:H2'	55:6:67:C:C6	2.55	0.41
19:t:58:VAL:HG22	19:t:85:VAL:HG22	2.03	0.41
23:x:65:THR:O	23:x:68:ALA:HB3	2.21	0.41
32:H:155:ARG:NE	32:H:159:ALA:O	2.47	0.41
37:M:83:ARG:NH2	52:3:587:G:OP1	2.53	0.41
37:M:91:LEU:HD23	37:M:91:LEU:HA	1.90	0.41
38:N:44:ARG:H	38:N:44:ARG:HD3	1.84	0.41
38:N:74:GLN:O	38:N:78:ILE:HG12	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:V:30:HIS:HB2	46:V:37:ILE:HD11	2.03	0.41
50:Z:36:PHE:O	50:Z:37:TYR:HB3	2.20	0.41
53:1:765:C:H2'	53:1:766:U:H6	1.85	0.41
53:1:826:U:H5''	53:1:2429:G:P	2.61	0.41
53:1:1417:C:H2'	53:1:1418:G:O4'	2.21	0.41
53:1:1859:U:H2'	53:1:1860:G:C8	2.55	0.41
53:1:2655:G:O2'	53:1:2656:U:H5	2.03	0.41
58:8:132:ILE:HG13	58:8:196:LEU:HD22	2.01	0.41
58:8:358:LYS:HD2	58:8:358:LYS:C	2.45	0.41
58:8:370:ASP:OD1	58:8:370:ASP:N	2.53	0.41
3:d:119:ILE:O	3:d:187:VAL:HG23	2.20	0.41
3:d:144:GLU:OE1	3:d:144:GLU:N	2.53	0.41
3:d:164:LEU:HD12	3:d:164:LEU:N	2.34	0.41
5:f:116:LEU:HA	5:f:117:PRO:HD3	1.94	0.41
6:g:37:VAL:HA	6:g:38:PRO:HD3	1.97	0.41
6:g:66:ASN:HD22	6:g:135:HIS:CD2	2.38	0.41
7:h:112:ALA:O	7:h:113:PHE:C	2.63	0.41
8:i:21:PRO:HD2	8:i:22:PRO:HD3	2.03	0.41
8:i:33:ASN:CB	8:i:36:GLU:HG2	2.43	0.41
12:m:105:MET:HE1	12:m:116:ALA:HB3	2.02	0.41
22:w:28:LEU:HD12	53:1:2354:C:OP1	2.20	0.41
31:G:36:LYS:HA	31:G:36:LYS:HE2	2.03	0.41
34:J:53:ARG:HG2	34:J:53:ARG:HH11	1.86	0.41
39:O:9:ARG:CZ	52:3:1279:G:H5''	2.50	0.41
40:P:49:SER:HB3	40:P:68:ARG:HH11	1.86	0.41
41:Q:49:ARG:HH21	52:3:522:C:H41	1.68	0.41
46:V:46:HIS:HA	46:V:70:LYS:HD2	2.01	0.41
52:3:234:C:O2'	52:3:235:C:H5'	2.21	0.41
52:3:273:U:O2'	52:3:274:A:H5'	2.21	0.41
52:3:291:U:O2'	52:3:292:G:H5'	2.19	0.41
52:3:390:U:H2'	52:3:391:G:C8	2.56	0.41
52:3:830:G:O2'	52:3:831:A:H5'	2.21	0.41
52:3:1016:A:H4'	52:3:1218:C:H4'	2.02	0.41
52:3:1171:A:H2'	52:3:1172:C:C6	2.55	0.41
53:1:889:C:H2'	53:1:890:C:O4'	2.20	0.41
53:1:1251:C:O2'	53:1:1252:G:H3'	2.19	0.41
53:1:1367:A:H2'	53:1:1368:G:C5'	2.50	0.41
53:1:1464:G:H2'	53:1:1465:G:C8	2.56	0.41
53:1:1685:C:H2'	53:1:1686:C:C6	2.56	0.41
53:1:1911:U:H2'	53:1:1918:A:N1	2.36	0.41
53:1:2083:G:H2'	53:1:2084:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2196:C:H2'	53:1:2197:U:C6	2.55	0.41
53:1:2329:U:H2'	53:1:2330:G:H8	1.84	0.41
54:2:49:C:H2'	54:2:50:A:H8	1.84	0.41
55:5:10:G:C2	55:5:26:G:H1'	2.56	0.41
57:7:23:A:H2'	57:7:24:G:C8	2.56	0.41
57:7:52:G:H2'	57:7:53:G:H8	1.86	0.41
58:8:18:ILE:HB	58:8:92:MET:HE1	2.03	0.41
1:b:24:HIS:CD2	1:b:79:ARG:HH11	2.38	0.41
1:b:109:LEU:HD12	1:b:109:LEU:HA	1.92	0.41
1:b:149:LYS:HE2	53:1:2204:G:O5'	2.21	0.41
1:b:257:ARG:HD3	53:1:1799:G:OP1	2.21	0.41
3:d:1:MET:HB3	3:d:14:VAL:HG23	2.02	0.41
3:d:128:ALA:O	3:d:130:LYS:N	2.53	0.41
9:j:40:HIS:CE1	9:j:41:LYS:HG3	2.56	0.41
10:k:98:ARG:HD3	10:k:98:ARG:HA	1.77	0.41
15:p:38:ARG:HH12	52:3:345:C:C5'	2.23	0.41
16:q:61:ILE:HG21	53:1:1009:A:O2'	2.20	0.41
17:r:7:SER:OG	17:r:8:GLY:N	2.54	0.41
17:r:35:PHE:HB2	17:r:59:ILE:HB	2.03	0.41
17:r:71:LYS:HA	17:r:90:ARG:HG2	2.02	0.41
18:s:15:GLN:OE1	26:B:16:ARG:NH2	2.54	0.41
18:s:86:MET:HA	18:s:87:PRO:HD3	1.88	0.41
20:u:27:VAL:HB	20:u:33:VAL:HG12	2.03	0.41
23:x:5:GLN:O	23:x:73:ARG:NH1	2.53	0.41
31:G:162:VAL:C	31:G:163:ILE:HD12	2.46	0.41
33:I:66:VAL:C	33:I:67:LEU:HD22	2.46	0.41
41:Q:107:LYS:HD3	41:Q:107:LYS:N	2.36	0.41
42:R:23:GLY:O	52:3:1329:A:H4'	2.21	0.41
42:R:79:LEU:HA	42:R:82:LEU:HD12	2.02	0.41
43:S:81:ILE:HD12	52:3:1202:U:H1'	2.02	0.41
46:V:4:ILE:O	46:V:6:THR:HG23	2.21	0.41
47:W:52:ARG:NH2	52:3:835:U:OP1	2.53	0.41
48:X:51:HIS:ND1	48:X:55:GLN:O	2.53	0.41
51:a:204:ALA:O	51:a:205:LYS:HD3	2.21	0.41
52:3:319:G:H2'	52:3:320:A:C8	2.56	0.41
52:3:355:C:H5'	52:3:355:C:C6	2.50	0.41
52:3:823:C:H2'	52:3:824:G:C8	2.56	0.41
52:3:1162:C:H2'	52:3:1163:A:C8	2.56	0.41
52:3:1329:A:O2'	52:3:1330:U:H5'	2.21	0.41
52:3:1432:G:H1'	52:3:1468:A:H62	1.84	0.41
52:3:1488:G:H2'	52:3:1489:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1491:G:N2	52:3:1492:A:H62	2.18	0.41
53:1:18:U:H2'	53:1:19:A:C8	2.56	0.41
53:1:36:G:O2'	53:1:37:C:H5'	2.20	0.41
53:1:108:G:H2'	53:1:109:C:C6	2.56	0.41
53:1:151:C:H2'	53:1:152:A:H8	1.86	0.41
53:1:326:G:H2'	53:1:327:G:C8	2.56	0.41
53:1:879:G:H2'	53:1:880:G:C8	2.56	0.41
53:1:905:A:O2'	53:1:906:U:H5'	2.21	0.41
53:1:1026:G:H2'	53:1:1027:A:C8	2.54	0.41
53:1:1078:U:C4'	53:1:1079:C:H5''	2.50	0.41
53:1:1099:G:O2'	53:1:1100:C:H5'	2.21	0.41
53:1:1169:A:O2'	53:1:1170:C:H5'	2.20	0.41
53:1:1857:G:H1'	53:1:1885:A:N6	2.35	0.41
53:1:1900:A:C2	53:1:1970:A:C6	3.09	0.41
53:1:1930:G:O2'	53:1:1931:U:C6	2.74	0.41
53:1:2065:C:H1'	53:1:2449:U:O2	2.21	0.41
53:1:2220:U:H2'	53:1:2221:G:H8	1.86	0.41
53:1:2484:G:O2'	53:1:2485:G:H5'	2.21	0.41
55:5:47:U:H3'	55:5:48:C:C5'	2.50	0.41
55:5:51:C:H2'	55:5:52:G:H8	1.86	0.41
58:8:117:ARG:HG3	58:8:161:TYR:HE2	1.86	0.41
58:8:124:ARG:HD3	58:8:163:PHE:CE2	2.56	0.41
58:8:373:LEU:HB3	58:8:389:VAL:HB	2.03	0.41
7:h:60:LEU:HA	7:h:64:VAL:CG2	2.50	0.41
17:r:24:LYS:HD2	17:r:24:LYS:C	2.46	0.41
21:v:83:LYS:HA	21:v:84:PRO:HD3	1.93	0.41
33:I:168:THR:O	33:I:182:LYS:HE3	2.20	0.41
37:M:95:MET:HE3	37:M:98:LEU:O	2.21	0.41
39:O:42:LEU:HA	39:O:43:PRO:HD2	1.88	0.41
42:R:27:THR:OG1	42:R:28:ARG:N	2.53	0.41
46:V:62:GLU:HG2	46:V:72:TRP:CZ2	2.56	0.41
50:Z:66:ARG:HG2	52:3:1099:G:C4'	2.51	0.41
52:3:867:G:H21	52:3:873:A:H2	1.68	0.41
52:3:1140:C:H2'	52:3:1141:C:C6	2.56	0.41
53:1:609:A:H2'	53:1:610:C:O4'	2.21	0.41
53:1:796:C:H2'	53:1:797:G:C8	2.55	0.41
53:1:1073:A:H4'	53:1:2475:C:OP1	2.20	0.41
53:1:1110:G:H2'	53:1:1111:A:H8	1.86	0.41
53:1:1775:U:H2'	53:1:1776:G:O4'	2.20	0.41
53:1:1934:C:O2'	53:1:1935:G:H5'	2.21	0.41
53:1:2156:G:C2'	53:1:2157:G:H5'	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2590:A:O2'	53:1:2591:C:H5'	2.21	0.41
58:8:72:THR:HG22	58:8:73:PRO:CD	2.50	0.41
58:8:192:LEU:O	58:8:196:LEU:HD23	2.20	0.41
1:b:215:VAL:HG12	1:b:216:ARG:N	2.35	0.40
2:c:208:LYS:HG3	53:1:2733:A:N1	2.36	0.40
3:d:68:ALA:HA	53:1:1255:U:C5	2.56	0.40
6:g:65:ALA:HB1	6:g:68:ARG:HH21	1.85	0.40
9:j:136:GLN:N	9:j:137:PRO:HD3	2.36	0.40
11:l:19:LEU:HD11	11:l:31:GLY:O	2.20	0.40
11:l:55:MET:HA	11:l:56:PRO:HD3	1.82	0.40
12:m:64:TRP:CZ3	12:m:106:ASP:HB3	2.44	0.40
14:o:7:ARG:HD2	14:o:97:PHE:CZ	2.56	0.40
28:D:10:LEU:HD23	53:1:770:G:H5''	2.03	0.40
33:I:59:LYS:O	33:I:63:ILE:HG13	2.20	0.40
34:J:114:LEU:HD12	34:J:119:VAL:HG21	2.03	0.40
39:O:34:ALA:C	39:O:35:GLN:HG3	2.46	0.40
52:3:556:C:O2'	52:3:557:G:H5'	2.21	0.40
52:3:1173:U:H2'	52:3:1174:G:H8	1.84	0.40
53:1:2520:C:O2'	53:1:2521:C:H5'	2.21	0.40
53:1:2557:G:H2'	53:1:2558:C:C6	2.56	0.40
53:1:2834:G:H2'	53:1:2879:A:N6	2.36	0.40
55:6:52:G:H2'	55:6:53:G:C8	2.56	0.40
2:c:116:LYS:HD2	2:c:165:MET:SD	2.62	0.40
3:d:44:ARG:NH2	3:d:87:ALA:HB3	2.36	0.40
4:e:46:LYS:NZ	4:e:83:PRO:HG2	2.36	0.40
4:e:109:ARG:O	4:e:109:ARG:HG3	2.22	0.40
9:j:93:ILE:HD12	9:j:97:PRO:HA	2.04	0.40
15:p:52:ARG:HA	15:p:52:ARG:HD2	1.94	0.40
34:J:84:VAL:HG22	34:J:85:LYS:N	2.36	0.40
34:J:146:MET:HG2	34:J:147:ASN:N	2.37	0.40
39:O:78:GLU:CD	39:O:78:GLU:H	2.29	0.40
40:P:19:VAL:HG13	40:P:84:MET:HE3	2.02	0.40
43:S:53:ASP:HB3	43:S:54:SER:H	1.72	0.40
52:3:119:A:H4'	52:3:120:A:C4	2.55	0.40
52:3:621:A:H2'	52:3:622:A:C8	2.56	0.40
52:3:1472:U:H2'	52:3:1473:G:C8	2.56	0.40
53:1:162:U:C2'	53:1:163:C:H5'	2.50	0.40
53:1:1817:G:C2	53:1:1818:U:H1'	2.55	0.40
53:1:2724:U:H2'	53:1:2725:A:C8	2.56	0.40
55:6:5:G:O2'	55:6:6:G:O5'	2.36	0.40
58:8:322:PRO:HA	58:8:351:VAL:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:259:ASN:O	1:b:261:ARG:N	2.53	0.40
4:e:37:MET:HE2	4:e:56:LEU:CD2	2.51	0.40
8:i:92:PRO:HD2	53:1:1076:C:H1'	2.02	0.40
11:l:19:LEU:HD11	11:l:31:GLY:C	2.47	0.40
12:m:5:LYS:HE2	12:m:5:LYS:HB3	1.79	0.40
12:m:42:THR:N	12:m:45:GLN:OE1	2.47	0.40
16:q:61:ILE:HG21	53:1:1010:A:H5'	2.02	0.40
17:r:53:PHE:O	17:r:54:VAL:C	2.64	0.40
19:t:74:ILE:H	19:t:74:ILE:HG12	1.71	0.40
32:H:149:LYS:HE3	32:H:200:TRP:CZ3	2.57	0.40
33:I:205:LYS:HB3	52:3:8:A:N7	2.36	0.40
35:K:89:VAL:HG23	52:3:737:C:H5'	2.04	0.40
37:M:45:ILE:HD12	37:M:45:ILE:N	2.37	0.40
42:R:28:ARG:HH22	42:R:61:LYS:NZ	2.19	0.40
42:R:95:PRO:HB2	42:R:99:GLN:HE21	1.86	0.40
43:S:91:GLU:C	43:S:92:ILE:HD12	2.46	0.40
45:U:5:ARG:HD2	52:3:376:G:O3'	2.22	0.40
52:3:37:U:O2'	52:3:38:G:H5'	2.22	0.40
52:3:925:G:C6	52:3:927:G:N7	2.89	0.40
53:1:368:A:C2'	53:1:369:U:H5'	2.52	0.40
53:1:1091:G:O2'	53:1:1092:C:H5'	2.20	0.40
53:1:1299:G:O6	53:1:1639:C:H5''	2.22	0.40
53:1:1479:G:O2'	53:1:1480:C:H5'	2.22	0.40
53:1:1664:A:C6	53:1:2726:A:N7	2.90	0.40
53:1:1689:A:H2'	53:1:1690:A:C8	2.57	0.40
58:8:216:GLU:HG3	58:8:217:ASP:N	2.36	0.40
58:8:370:ASP:O	58:8:373:LEU:HB2	2.20	0.40
5:f:5:LYS:HA	5:f:5:LYS:HD3	1.84	0.40
5:f:132:LEU:O	5:f:132:LEU:HD12	2.21	0.40
7:h:58:THR:HG21	7:h:82:ILE:HB	2.02	0.40
10:k:20:MET:HE2	10:k:44:LYS:HD3	2.03	0.40
15:p:38:ARG:HH22	52:3:345:C:H5''	1.83	0.40
19:t:11:LEU:H	19:t:11:LEU:HD12	1.87	0.40
23:x:50:VAL:HG22	23:x:51:SER:N	2.35	0.40
24:y:21:LEU:HA	24:y:25:GLN:CB	2.49	0.40
34:J:75:LEU:HD23	34:J:75:LEU:H	1.85	0.40
39:O:10:LEU:O	39:O:71:LEU:HD12	2.21	0.40
39:O:69:THR:O	39:O:69:THR:HG23	2.22	0.40
42:R:62:PHE:O	42:R:63:VAL:C	2.64	0.40
50:Z:28:LEU:HD13	50:Z:28:LEU:HA	1.96	0.40
52:3:229:U:H2'	52:3:230:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:636:U:O2'	52:3:637:C:H5'	2.21	0.40
52:3:1237:C:O2'	52:3:1300:G:N2	2.55	0.40
53:1:64:A:H2'	53:1:65:U:C6	2.56	0.40
53:1:357:C:H2'	53:1:358:U:C6	2.56	0.40
53:1:859:G:H1'	53:1:860:U:H5	1.86	0.40
53:1:1093:G:H21	53:1:1098:A:H62	1.68	0.40
53:1:1989:G:H2'	53:1:1990:C:O4'	2.20	0.40
53:1:2041:U:H2'	53:1:2042:A:H8	1.86	0.40
53:1:2609:U:H5'	53:1:2610:C:OP2	2.21	0.40
1:b:44:ASN:ND2	53:1:1812:U:H1'	2.36	0.40
1:b:224:MET:SD	1:b:229:HIS:HB2	2.62	0.40
4:e:110:ILE:HB	4:e:113:PHE:HB2	2.04	0.40
7:h:41:LEU:CD1	53:1:1082:U:H2'	2.51	0.40
9:j:2:LYS:HA	53:1:995:C:N3	2.37	0.40
17:r:78:ARG:HH12	53:1:990:A:N6	2.11	0.40
19:t:75:GLY:HA3	53:1:64:A:H4'	2.04	0.40
19:t:76:ARG:HH12	19:t:79:ASP:CG	2.30	0.40
21:v:55:GLU:HB2	21:v:59:GLU:OE1	2.21	0.40
21:v:63:ILE:HD12	21:v:72:VAL:HG21	2.02	0.40
33:I:32:LYS:HB3	33:I:35:GLN:HE22	1.86	0.40
34:J:71:ILE:HD13	34:J:140:ILE:HG23	2.04	0.40
38:N:27:ILE:HD12	38:N:27:ILE:N	2.35	0.40
39:O:53:ILE:HG23	52:3:1060:U:H4'	2.02	0.40
40:P:112:VAL:HG12	47:W:72:ARG:HD2	2.04	0.40
46:V:16:MET:SD	46:V:16:MET:N	2.95	0.40
52:3:110:C:H2'	52:3:111:G:O4'	2.21	0.40
52:3:424:G:O2'	52:3:425:G:H5'	2.21	0.40
52:3:502:A:H61	52:3:543:U:H3	1.69	0.40
52:3:513:C:H2'	52:3:514:C:C6	2.57	0.40
52:3:828:U:H3	52:3:859:G:H1'	1.86	0.40
52:3:1143:G:H2'	52:3:1144:G:H8	1.87	0.40
52:3:1304:G:H2'	52:3:1305:G:N9	2.37	0.40
53:1:184:C:H2'	53:1:185:G:C8	2.57	0.40
53:1:538:A:H2'	53:1:539:G:O4'	2.22	0.40
53:1:877:A:H1'	53:1:900:A:N6	2.36	0.40
53:1:1067:A:H2'	53:1:1067:A:N3	2.37	0.40
53:1:1165:A:O2'	53:1:1166:G:H5'	2.21	0.40
53:1:1300:G:C4'	53:1:1301:A:H5''	2.51	0.40
53:1:1465:G:H2'	53:1:1466:U:O4'	2.22	0.40
53:1:1727:C:H2'	53:1:1728:C:O4'	2.22	0.40
53:1:1746:A:H2'	53:1:1747:U:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1955:U:C4	53:1:2552:U:H1'	2.56	0.40
53:1:2451:A:H1'	55:5:76:A:H1'	2.03	0.40
53:1:2860:A:H2'	53:1:2861:U:H5'	2.02	0.40
57:7:26:A:H2'	57:7:27:G:O4'	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	224 (83%)	41 (15%)	4 (2%)	8	37
2	c	207/209 (99%)	185 (89%)	20 (10%)	2 (1%)	12	45
3	d	199/201 (99%)	178 (89%)	18 (9%)	3 (2%)	8	37
4	e	175/177 (99%)	147 (84%)	25 (14%)	3 (2%)	7	35
5	f	174/176 (99%)	156 (90%)	16 (9%)	2 (1%)	11	43
6	g	147/149 (99%)	123 (84%)	20 (14%)	4 (3%)	4	27
7	h	129/131 (98%)	92 (71%)	33 (26%)	4 (3%)	3	25
8	i	139/141 (99%)	119 (86%)	14 (10%)	6 (4%)	2	18
9	j	140/142 (99%)	125 (89%)	14 (10%)	1 (1%)	18	51
10	k	120/122 (98%)	100 (83%)	18 (15%)	2 (2%)	7	35
11	l	141/143 (99%)	117 (83%)	21 (15%)	3 (2%)	5	31
12	m	134/136 (98%)	117 (87%)	15 (11%)	2 (2%)	8	37
13	n	118/120 (98%)	99 (84%)	19 (16%)	0	100	100
14	o	114/116 (98%)	104 (91%)	7 (6%)	3 (3%)	4	27
15	p	112/114 (98%)	93 (83%)	19 (17%)	0	100	100
16	q	115/117 (98%)	110 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	r	101/103 (98%)	85 (84%)	14 (14%)	2 (2%)	6	32
18	s	108/110 (98%)	96 (89%)	11 (10%)	1 (1%)	14	46
19	t	91/93 (98%)	79 (87%)	11 (12%)	1 (1%)	11	43
20	u	100/102 (98%)	84 (84%)	14 (14%)	2 (2%)	6	32
21	v	92/94 (98%)	83 (90%)	9 (10%)	0	100	100
22	w	73/75 (97%)	65 (89%)	8 (11%)	0	100	100
23	x	75/77 (97%)	69 (92%)	5 (7%)	1 (1%)	9	39
24	y	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	7	36
25	z	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
26	B	54/56 (96%)	47 (87%)	7 (13%)	0	100	100
27	C	48/50 (96%)	42 (88%)	6 (12%)	0	100	100
28	D	44/46 (96%)	37 (84%)	7 (16%)	0	100	100
29	E	62/64 (97%)	55 (89%)	6 (10%)	1 (2%)	7	36
30	F	36/38 (95%)	28 (78%)	7 (19%)	1 (3%)	4	26
31	G	223/225 (99%)	203 (91%)	18 (8%)	2 (1%)	14	46
32	H	204/206 (99%)	192 (94%)	11 (5%)	1 (0%)	24	57
33	I	203/205 (99%)	181 (89%)	21 (10%)	1 (0%)	24	57
34	J	155/157 (99%)	130 (84%)	21 (14%)	4 (3%)	4	27
35	K	98/100 (98%)	81 (83%)	13 (13%)	4 (4%)	2	19
36	L	149/151 (99%)	128 (86%)	19 (13%)	2 (1%)	9	39
37	M	127/129 (98%)	113 (89%)	13 (10%)	1 (1%)	16	49
38	N	125/127 (98%)	102 (82%)	17 (14%)	6 (5%)	2	16
39	O	96/98 (98%)	72 (75%)	15 (16%)	9 (9%)	0	6
40	P	114/116 (98%)	94 (82%)	16 (14%)	4 (4%)	3	23
41	Q	121/123 (98%)	94 (78%)	21 (17%)	6 (5%)	1	16
42	R	112/114 (98%)	95 (85%)	12 (11%)	5 (4%)	2	17
43	S	98/100 (98%)	80 (82%)	18 (18%)	0	100	100
44	T	86/88 (98%)	79 (92%)	7 (8%)	0	100	100
45	U	80/82 (98%)	67 (84%)	12 (15%)	1 (1%)	9	39
46	V	78/80 (98%)	60 (77%)	14 (18%)	4 (5%)	1	15
47	W	63/65 (97%)	57 (90%)	5 (8%)	1 (2%)	7	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	X	77/79 (98%)	62 (80%)	14 (18%)	1 (1%)	9	39
49	Y	83/85 (98%)	76 (92%)	7 (8%)	0	100	100
50	Z	63/65 (97%)	44 (70%)	14 (22%)	5 (8%)	1	8
51	a	130/223 (58%)	125 (96%)	5 (4%)	0	100	100
58	8	379/400 (95%)	333 (88%)	41 (11%)	5 (1%)	9	39
All	All	6298/6512 (97%)	5433 (86%)	754 (12%)	111 (2%)	9	34

All (111) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	232	GLY
2	c	86	GLU
3	d	83	VAL
5	f	45	ALA
5	f	174	LYS
6	g	9	VAL
7	h	108	VAL
7	h	118	ILE
17	r	54	VAL
23	x	2	ARG
29	E	31	ILE
34	J	122	VAL
37	M	47	ASP
38	N	57	VAL
41	Q	24	GLU
41	Q	43	LYS
42	R	65	GLU
46	V	49	ASN
46	V	50	ASN
50	Z	34	ARG
1	b	260	LYS
3	d	93	SER
6	g	11	ASN
10	k	110	GLU
24	y	24	GLU
30	F	37	GLN
34	J	11	GLN
34	J	49	TYR
34	J	93	VAL
35	K	40	GLU

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Mol	Chain	Res	Type
35	K	92	THR
35	K	94	HIS
36	L	6	ILE
38	N	90	ASP
38	N	107	ALA
38	N	125	GLN
40	P	89	GLY
42	R	7	ASN
42	R	63	VAL
46	V	17	GLU
47	W	13	THR
50	Z	14	ALA
50	Z	66	ARG
58	8	335	THR
7	h	107	GLU
7	h	113	PHE
10	k	35	VAL
11	l	29	LYS
12	m	59	ARG
14	o	34	HIS
20	u	97	SER
32	H	126	ARG
35	K	56	LYS
38	N	42	THR
39	O	35	GLN
39	O	56	HIS
41	Q	35	ARG
41	Q	75	GLU
42	R	6	ILE
45	U	79	ASN
46	V	70	LYS
58	8	222	SER
2	c	58	ASN
4	e	40	GLY
6	g	15	LEU
6	g	41	LYS
8	i	11	GLN
8	i	22	PRO
19	t	72	GLN
20	u	6	ARG
36	L	57	GLU
38	N	71	ILE

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Mol	Chain	Res	Type
39	O	34	ALA
39	O	41	PRO
40	P	14	GLN
41	Q	2	THR
41	Q	87	LYS
48	X	4	LEU
50	Z	24	LYS
1	b	226	PRO
1	b	246	PRO
3	d	49	ARG
4	e	175	PRO
8	i	92	PRO
12	m	69	PRO
42	R	5	GLY
50	Z	9	GLU
58	8	334	ARG
4	e	20	ASN
8	i	13	ALA
18	s	3	THR
31	G	154	GLY
39	O	30	LYS
39	O	42	LEU
39	O	58	ASN
40	P	88	PRO
58	8	4	GLU
31	G	148	GLY
58	8	73	PRO
9	j	82	GLY
33	I	167	PRO
39	O	77	VAL
8	i	21	PRO
8	i	31	GLY
11	l	52	GLY
11	l	65	GLY
14	o	101	GLY
17	r	47	VAL
40	P	90	PRO
39	O	33	GLY
14	o	32	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	b	216/216 (100%)	214 (99%)	2 (1%)	70	76
2	c	164/164 (100%)	163 (99%)	1 (1%)	78	79
3	d	165/165 (100%)	164 (99%)	1 (1%)	78	79
4	e	148/148 (100%)	146 (99%)	2 (1%)	59	71
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	78
6	g	114/114 (100%)	113 (99%)	1 (1%)	70	76
7	h	100/100 (100%)	96 (96%)	4 (4%)	28	54
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	116 (100%)	0	100	100
10	k	103/103 (100%)	101 (98%)	2 (2%)	50	67
11	l	102/102 (100%)	99 (97%)	3 (3%)	37	60
12	m	109/109 (100%)	109 (100%)	0	100	100
13	n	100/100 (100%)	99 (99%)	1 (1%)	68	75
14	o	86/86 (100%)	85 (99%)	1 (1%)	63	73
15	p	99/99 (100%)	99 (100%)	0	100	100
16	q	89/89 (100%)	89 (100%)	0	100	100
17	r	84/84 (100%)	83 (99%)	1 (1%)	63	73
18	s	93/93 (100%)	91 (98%)	2 (2%)	45	65
19	t	80/80 (100%)	79 (99%)	1 (1%)	61	72
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	76 (97%)	2 (3%)	40	62
22	w	57/57 (100%)	56 (98%)	1 (2%)	51	68
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	54 (98%)	1 (2%)	51	68
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	C	45/45 (100%)	44 (98%)	1 (2%)	45	65
28	D	38/38 (100%)	37 (97%)	1 (3%)	40	62
29	E	51/51 (100%)	49 (96%)	2 (4%)	28	54
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	186 (100%)	0	100	100
32	H	170/170 (100%)	167 (98%)	3 (2%)	51	68
33	I	172/172 (100%)	172 (100%)	0	100	100
34	J	119/119 (100%)	117 (98%)	2 (2%)	53	69
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	74
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	75
38	N	105/105 (100%)	104 (99%)	1 (1%)	68	75
39	O	86/86 (100%)	84 (98%)	2 (2%)	44	64
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	101 (98%)	2 (2%)	50	67
42	R	92/92 (100%)	91 (99%)	1 (1%)	65	74
43	S	83/83 (100%)	83 (100%)	0	100	100
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	62 (95%)	3 (5%)	24	51
46	V	74/74 (100%)	74 (100%)	0	100	100
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	69 (99%)	1 (1%)	59	71
49	Y	65/65 (100%)	64 (98%)	1 (2%)	57	70
50	Z	55/55 (100%)	55 (100%)	0	100	100
51	a	110/174 (63%)	109 (99%)	1 (1%)	70	76
58	8	318/332 (96%)	318 (100%)	0	100	100
All	All	5226/5304 (98%)	5176 (99%)	50 (1%)	65	75

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	34	GLU
1	b	119	VAL

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Mol	Chain	Res	Type
2	c	18	ASP
3	d	84	THR
4	e	135	ILE
4	e	143	ASP
5	f	113	ASP
6	g	6	LEU
7	h	33	VAL
7	h	51	TYR
7	h	81	LEU
7	h	118	ILE
10	k	69	VAL
10	k	86	LEU
11	l	46	VAL
11	l	54	GLN
11	l	94	THR
13	n	43	GLU
14	o	32	PRO
17	r	32	THR
18	s	77	ASP
18	s	109	ASP
19	t	32	LEU
21	v	20	LEU
21	v	90	ASP
22	w	39	THR
24	y	36	GLN
27	C	22	THR
28	D	44	VAL
29	E	6	VAL
29	E	53	ASP
32	H	84	GLU
32	H	93	ILE
32	H	123	LEU
34	J	42	ASN
34	J	159	SER
35	K	94	HIS
37	M	60	LEU
38	N	93	LEU
39	O	10	LEU
39	O	14	ASP
41	Q	54	VAL
41	Q	86	VAL
42	R	65	GLU

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Mol	Chain	Res	Type
45	U	19	VAL
45	U	36	VAL
45	U	69	ASP
48	X	78	THR
49	Y	54	GLN
51	a	189	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (108) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	24	HIS
1	b	36	ASN
1	b	52	HIS
1	b	59	GLN
1	b	85	ASN
1	b	89	ASN
1	b	127	ASN
1	b	133	ASN
1	b	199	HIS
1	b	225	ASN
1	b	238	ASN
2	c	32	ASN
2	c	36	GLN
2	c	134	HIS
2	c	150	GLN
2	c	164	GLN
2	c	173	GLN
3	d	29	HIS
3	d	90	GLN
3	d	97	ASN
4	e	22	ASN
4	e	126	ASN
5	f	72	ASN
5	f	114	HIS
5	f	138	GLN
6	g	28	ASN
6	g	33	GLN
6	g	66	ASN
6	g	73	ASN
6	g	145	ASN
7	h	6	GLN
7	h	103	ASN

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Mol	Chain	Res	Type
9	j	40	HIS
9	j	135	GLN
10	k	3	GLN
10	k	5	GLN
11	l	54	GLN
11	l	99	ASN
12	m	3	GLN
12	m	13	HIS
12	m	88	ASN
12	m	97	GLN
13	n	9	GLN
13	n	62	ASN
14	o	38	GLN
14	o	98	GLN
16	q	36	GLN
16	q	71	ASN
18	s	9	HIS
19	t	15	HIS
19	t	59	ASN
20	u	68	ASN
20	u	73	ASN
21	v	75	GLN
21	v	78	GLN
22	w	8	ASN
23	x	15	ASN
23	x	16	ASN
24	y	20	ASN
24	y	39	GLN
25	z	8	GLN
26	B	3	GLN
26	B	5	ASN
26	B	18	HIS
26	B	41	HIS
27	C	25	ASN
27	C	44	GLN
30	F	37	GLN
31	G	17	HIS
31	G	50	ASN
31	G	121	GLN
31	G	176	ASN
32	H	5	HIS
32	H	7	ASN

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Mol	Chain	Res	Type
32	H	24	ASN
32	H	99	GLN
32	H	139	ASN
34	J	81	GLN
34	J	134	ASN
35	K	11	HIS
35	K	55	HIS
36	L	8	GLN
36	L	27	ASN
36	L	121	ASN
37	M	75	GLN
39	O	70	HIS
39	O	99	GLN
40	P	14	GLN
40	P	21	HIS
40	P	37	GLN
40	P	100	ASN
40	P	118	ASN
41	Q	45	ASN
41	Q	95	HIS
41	Q	111	GLN
42	R	99	GLN
43	S	65	GLN
44	T	34	GLN
45	U	26	ASN
46	V	30	HIS
46	V	50	ASN
49	Y	51	ASN
49	Y	83	ASN
51	a	58	ASN
51	a	188	ASN
58	8	91	ASN
58	8	160	GLN
58	8	291	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	139 (9%)	4 (0%)
53	1	2902/2903 (99%)	327 (11%)	12 (0%)
54	2	119/120 (99%)	9 (7%)	1 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
55	5	76/77 (98%)	7 (9%)	0
55	6	76/77 (98%)	6 (7%)	1 (1%)
56	4	17/18 (94%)	3 (17%)	0
57	7	75/76 (98%)	14 (18%)	0
All	All	4803/4810 (99%)	505 (10%)	18 (0%)

All (505) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	7	A
52	3	9	G
52	3	22	G
52	3	31	G
52	3	32	A
52	3	39	G
52	3	48	C
52	3	51	A
52	3	71	A
52	3	87	C
52	3	95	C
52	3	100	G
52	3	130	A
52	3	144	G
52	3	183	C
52	3	184	G
52	3	197	A
52	3	209	U
52	3	210	C
52	3	226	G
52	3	247	G
52	3	251	G
52	3	266	G
52	3	267	C
52	3	281	G
52	3	289	G
52	3	345	C
52	3	346	G
52	3	352	C
52	3	355	C
52	3	367	U
52	3	372	C

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Mol	Chain	Res	Type
52	3	411	A
52	3	412	A
52	3	413	G
52	3	422	C
52	3	429	U
52	3	467	U
52	3	479	U
52	3	484	G
52	3	485	U
52	3	486	U
52	3	497	G
52	3	518	C
52	3	532	A
52	3	547	A
52	3	561	U
52	3	564	C
52	3	572	A
52	3	573	A
52	3	575	G
52	3	576	C
52	3	577	G
52	3	633	G
52	3	665	A
52	3	688	G
52	3	703	G
52	3	724	G
52	3	755	G
52	3	777	A
52	3	793	U
52	3	815	A
52	3	817	C
52	3	818	G
52	3	819	A
52	3	821	G
52	3	843	U
52	3	844	G
52	3	846	G
52	3	871	U
52	3	872	A
52	3	902	G
52	3	926	G
52	3	934	C

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Mol	Chain	Res	Type
52	3	935	A
52	3	960	U
52	3	961	U
52	3	966	G
52	3	969	A
52	3	975	A
52	3	976	G
52	3	977	A
52	3	992	U
52	3	993	G
52	3	1004	A
52	3	1028	C
52	3	1031	C
52	3	1033	G
52	3	1034	G
52	3	1085	U
52	3	1094	G
52	3	1101	A
52	3	1137	C
52	3	1138	G
52	3	1139	G
52	3	1159	U
52	3	1168	U
52	3	1182	G
52	3	1184	G
52	3	1191	A
52	3	1196	A
52	3	1197	A
52	3	1198	G
52	3	1201	A
52	3	1202	U
52	3	1225	A
52	3	1238	A
52	3	1240	U
52	3	1241	G
52	3	1257	A
52	3	1258	G
52	3	1260	G
52	3	1275	A
52	3	1278	G
52	3	1280	A
52	3	1282	C

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Mol	Chain	Res	Type
52	3	1286	U
52	3	1287	A
52	3	1300	G
52	3	1317	C
52	3	1346	A
52	3	1347	G
52	3	1363	A
52	3	1364	U
52	3	1395	C
52	3	1433	A
52	3	1446	A
52	3	1448	C
52	3	1452	C
52	3	1492	A
52	3	1493	A
52	3	1503	A
52	3	1506	U
52	3	1517	G
52	3	1529	G
52	3	1530	G
52	3	1533	C
52	3	1540	U
53	1	10	A
53	1	12	U
53	1	34	U
53	1	35	G
53	1	49	A
53	1	51	G
53	1	63	A
53	1	71	A
53	1	74	A
53	1	75	G
53	1	114	U
53	1	119	A
53	1	120	U
53	1	140	C
53	1	141	G
53	1	142	A
53	1	162	U
53	1	163	C
53	1	181	A
53	1	196	A

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Mol	Chain	Res	Type
53	1	216	A
53	1	221	A
53	1	222	A
53	1	228	C
53	1	229	C
53	1	248	G
53	1	249	C
53	1	255	A
53	1	265	A
53	1	266	G
53	1	276	U
53	1	281	C
53	1	294	A
53	1	301	G
53	1	311	A
53	1	323	C
53	1	329	G
53	1	330	A
53	1	371	A
53	1	372	G
53	1	386	G
53	1	387	U
53	1	404	A
53	1	406	G
53	1	411	G
53	1	422	A
53	1	424	G
53	1	451	U
53	1	457	A
53	1	481	G
53	1	491	G
53	1	504	A
53	1	505	A
53	1	529	A
53	1	530	G
53	1	531	C
53	1	532	A
53	1	543	G
53	1	563	A
53	1	573	U
53	1	575	A
53	1	588	U

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Mol	Chain	Res	Type
53	1	603	A
53	1	616	A
53	1	627	A
53	1	637	A
53	1	646	U
53	1	654	A
53	1	669	G
53	1	686	U
53	1	687	C
53	1	695	G
53	1	730	A
53	1	747	C
53	1	752	A
53	1	764	A
53	1	776	G
53	1	782	A
53	1	784	G
53	1	785	G
53	1	805	G
53	1	812	C
53	1	819	A
53	1	822	G
53	1	827	U
53	1	828	U
53	1	830	G
53	1	845	A
53	1	846	U
53	1	847	U
53	1	860	U
53	1	878	A
53	1	886	A
53	1	887	U
53	1	896	A
53	1	897	C
53	1	910	A
53	1	932	U
53	1	941	A
53	1	946	C
53	1	961	C
53	1	974	G
53	1	975	A
53	1	983	A

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Mol	Chain	Res	Type
53	1	995	C
53	1	996	A
53	1	1012	U
53	1	1013	C
53	1	1021	A
53	1	1022	G
53	1	1026	G
53	1	1033	U
53	1	1045	C
53	1	1046	A
53	1	1047	G
53	1	1054	A
53	1	1060	U
53	1	1062	G
53	1	1066	U
53	1	1070	A
53	1	1071	G
53	1	1079	C
53	1	1084	A
53	1	1088	A
53	1	1090	A
53	1	1104	C
53	1	1106	G
53	1	1111	A
53	1	1131	G
53	1	1132	U
53	1	1133	A
53	1	1135	C
53	1	1143	A
53	1	1157	G
53	1	1174	U
53	1	1175	A
53	1	1177	G
53	1	1180	U
53	1	1206	G
53	1	1212	G
53	1	1238	G
53	1	1250	G
53	1	1251	C
53	1	1253	A
53	1	1256	G
53	1	1271	G

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Mol	Chain	Res	Type
53	1	1272	A
53	1	1275	A
53	1	1301	A
53	1	1321	A
53	1	1329	U
53	1	1330	C
53	1	1332	G
53	1	1345	C
53	1	1352	U
53	1	1365	A
53	1	1378	A
53	1	1379	U
53	1	1383	A
53	1	1395	A
53	1	1416	G
53	1	1419	A
53	1	1420	A
53	1	1454	C
53	1	1461	C
53	1	1476	U
53	1	1482	G
53	1	1490	A
53	1	1498	C
53	1	1515	A
53	1	1524	G
53	1	1533	C
53	1	1535	A
53	1	1536	C
53	1	1537	G
53	1	1555	G
53	1	1560	G
53	1	1569	A
53	1	1578	U
53	1	1581	G
53	1	1584	U
53	1	1585	C
53	1	1608	A
53	1	1611	C
53	1	1616	A
53	1	1647	U
53	1	1648	U
53	1	1674	G

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Mol	Chain	Res	Type
53	1	1699	G
53	1	1715	G
53	1	1729	U
53	1	1730	C
53	1	1738	G
53	1	1758	U
53	1	1764	C
53	1	1773	A
53	1	1780	A
53	1	1800	C
53	1	1801	A
53	1	1808	A
53	1	1816	C
53	1	1829	A
53	1	1871	A
53	1	1901	A
53	1	1906	G
53	1	1907	G
53	1	1913	A
53	1	1919	A
53	1	1929	G
53	1	1930	G
53	1	1931	U
53	1	1937	A
53	1	1938	A
53	1	1944	U
53	1	1955	U
53	1	1963	U
53	1	1967	C
53	1	1970	A
53	1	1971	U
53	1	1972	G
53	1	1991	U
53	1	1993	U
53	1	1997	C
53	1	2022	U
53	1	2023	C
53	1	2030	A
53	1	2031	A
53	1	2043	C
53	1	2049	G
53	1	2052	A

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Mol	Chain	Res	Type
53	1	2055	C
53	1	2056	G
53	1	2060	A
53	1	2061	G
53	1	2062	A
53	1	2069	G
53	1	2072	C
53	1	2096	C
53	1	2110	G
53	1	2111	U
53	1	2112	G
53	1	2113	U
53	1	2118	U
53	1	2119	A
53	1	2132	U
53	1	2133	G
53	1	2147	A
53	1	2162	G
53	1	2171	A
53	1	2172	U
53	1	2173	A
53	1	2198	A
53	1	2203	U
53	1	2204	G
53	1	2211	A
53	1	2213	U
53	1	2225	A
53	1	2238	G
53	1	2239	G
53	1	2278	A
53	1	2283	C
53	1	2287	A
53	1	2297	A
53	1	2305	U
53	1	2309	A
53	1	2325	G
53	1	2327	A
53	1	2334	U
53	1	2350	C
53	1	2383	G
53	1	2385	C
53	1	2392	A

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Mol	Chain	Res	Type
53	1	2402	U
53	1	2406	A
53	1	2407	A
53	1	2423	U
53	1	2424	C
53	1	2427	C
53	1	2429	G
53	1	2430	A
53	1	2435	A
53	1	2441	U
53	1	2447	G
53	1	2448	A
53	1	2476	A
53	1	2498	C
53	1	2502	G
53	1	2503	A
53	1	2504	U
53	1	2505	G
53	1	2518	A
53	1	2520	C
53	1	2529	G
53	1	2547	A
53	1	2554	U
53	1	2566	A
53	1	2567	G
53	1	2572	A
53	1	2602	A
53	1	2603	G
53	1	2609	U
53	1	2613	U
53	1	2646	C
53	1	2655	G
53	1	2682	A
53	1	2689	U
53	1	2690	U
53	1	2714	G
53	1	2744	G
53	1	2748	A
53	1	2764	A
53	1	2765	A
53	1	2778	A
53	1	2779	U

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Mol	Chain	Res	Type
53	1	2791	G
53	1	2794	C
53	1	2797	U
53	1	2800	A
53	1	2820	A
53	1	2821	A
53	1	2833	U
53	1	2849	U
53	1	2867	G
53	1	2868	A
53	1	2872	A
53	1	2880	C
53	1	2883	A
54	2	4	C
54	2	13	G
54	2	35	C
54	2	44	G
54	2	67	G
54	2	89	U
54	2	90	C
54	2	108	A
54	2	109	A
55	5	9	G
55	5	19	G
55	5	20	U
55	5	47	U
55	5	48	C
55	5	59	A
55	5	61	C
55	6	6	G
55	6	18	G
55	6	19	G
55	6	20	U
55	6	47	U
55	6	48	C
56	4	12	A
56	4	13	A
56	4	16	A
57	7	8	U
57	7	9	A
57	7	10	G
57	7	18	G

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Mol	Chain	Res	Type
57	7	21	A
57	7	26	A
57	7	44	G
57	7	45	U
57	7	46	G
57	7	48	C
57	7	55	U
57	7	59	U
57	7	61	C
57	7	63	G

All (18) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	421	U
52	3	1190	G
52	3	1201	A
52	3	1432	G
53	1	227	A
53	1	421	C
53	1	490	C
53	1	859	G
53	1	1020	A
53	1	1130	U
53	1	1475	G
53	1	1930	G
53	1	2286	G
53	1	2296	U
53	1	2326	C
53	1	2391	G
54	2	88	C
55	6	17(A)	U

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
61	GDP	8	501	-	29,30,30	1.28	3 (10%)	45,47,47	2.24	17 (37%)
59	FME	5	101	55	8,9,10	0.48	0	8,9,11	0.86	0
60	PHE	7	101	57	10,11,12	0.70	0	8,13,15	0.25	0

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
61	GDP	8	501	-	-	2/16/32/32	0/3/3/3
59	FME	5	101	55	-	1/7/9/11	-
60	PHE	7	101	57	-	0/5/6/8	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	8	501	GDP	PB-O1B	2.97	1.59	1.50
61	8	501	GDP	PA-O3A	2.91	1.62	1.59
61	8	501	GDP	PB-O2B	2.35	1.63	1.54

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	8	501	GDP	C2-N3-C4	5.55	121.86	112.30
61	8	501	GDP	C5-C4-N3	-5.34	119.89	128.39
61	8	501	GDP	O2B-PB-O1B	-4.47	93.41	110.83
61	8	501	GDP	O3B-PB-O1B	4.29	127.56	110.83
61	8	501	GDP	N9-C4-N3	4.02	133.99	125.95
61	8	501	GDP	O3B-PB-O2B	3.75	121.87	107.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	8	501	GDP	O3A-PB-O1B	-3.32	93.58	111.04
61	8	501	GDP	O4'-C4'-C3'	3.16	111.42	105.15
61	8	501	GDP	C8-N7-C5	2.85	109.33	104.26
61	8	501	GDP	C3'-C2'-C1'	2.52	106.24	101.46
61	8	501	GDP	C6-C5-N7	2.51	134.85	130.29
61	8	501	GDP	C2-N1-C6	-2.48	120.62	125.11
61	8	501	GDP	O3B-PB-O3A	2.28	112.27	104.64
61	8	501	GDP	O5'-PA-O1A	-2.27	99.93	108.94
61	8	501	GDP	O6-C6-C5	-2.27	120.54	126.53
61	8	501	GDP	C5-C6-N1	2.20	118.86	113.25
61	8	501	GDP	C4-C5-N7	-2.14	107.27	110.67

There are no chirality outliers.

All (3) torsion outliers are listed below:

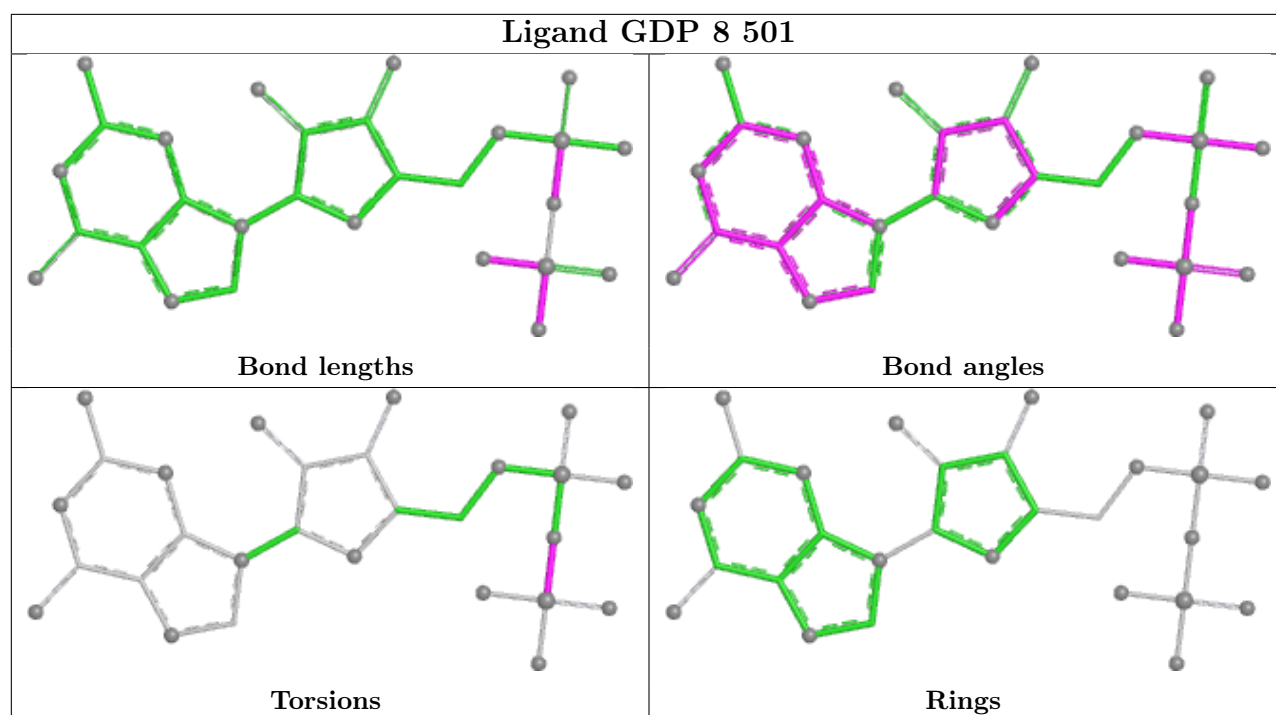
Mol	Chain	Res	Type	Atoms
59	5	101	FME	O1-CN-N-CA
61	8	501	GDP	PA-O3A-PB-O2B
61	8	501	GDP	PA-O3A-PB-O3B

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	5	101	FME	3	0
60	7	101	PHE	3	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

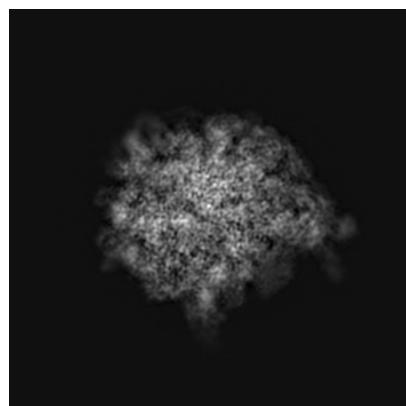
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21622. These allow visual inspection of the internal detail of the map and identification of artifacts.

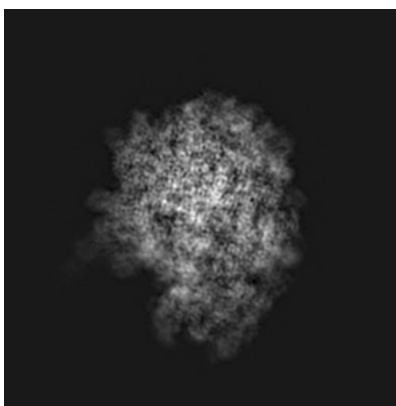
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

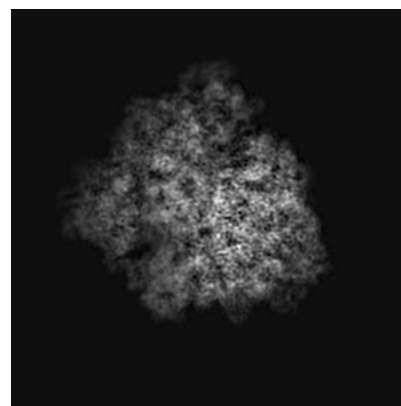
6.1.1 Primary map



X

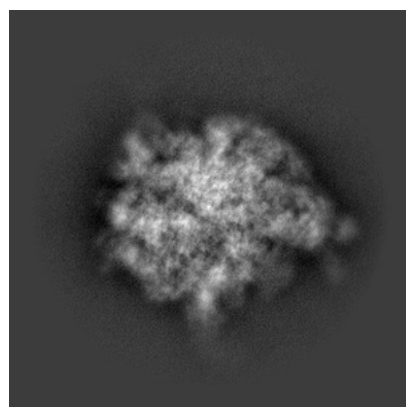


Y

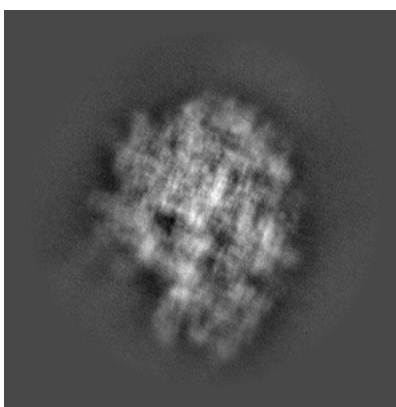


Z

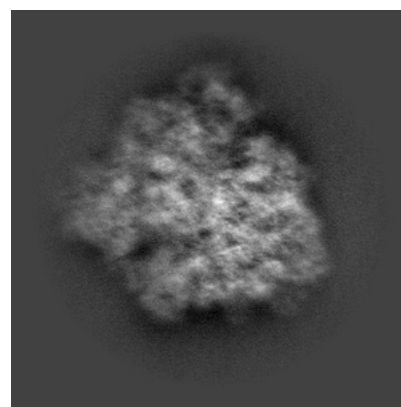
6.1.2 Raw map



X



Y

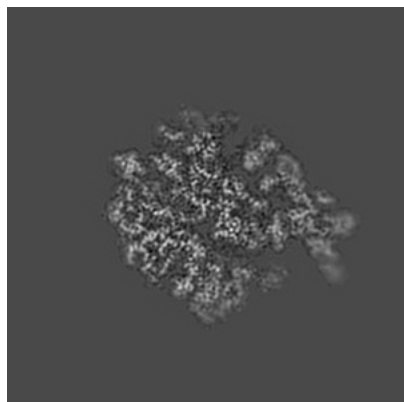


Z

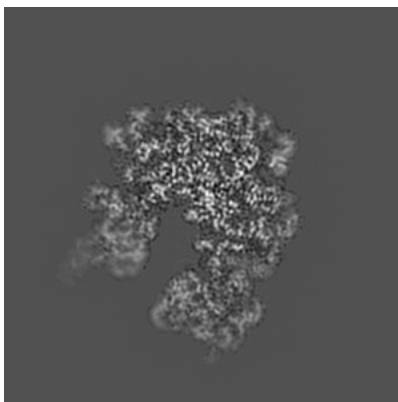
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

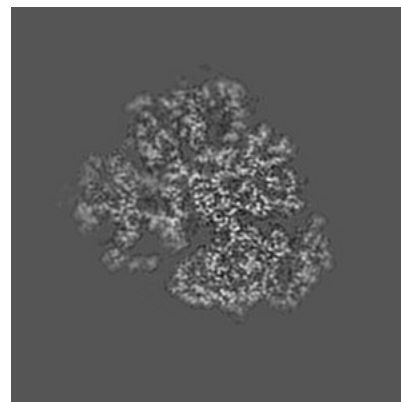
6.2.1 Primary map



X Index: 144

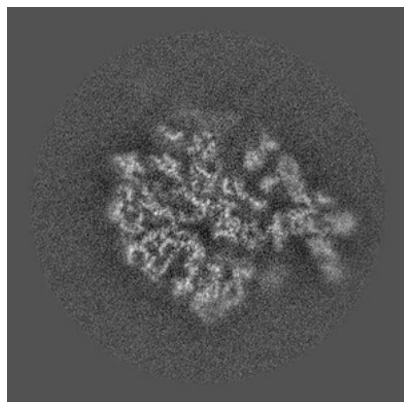


Y Index: 144

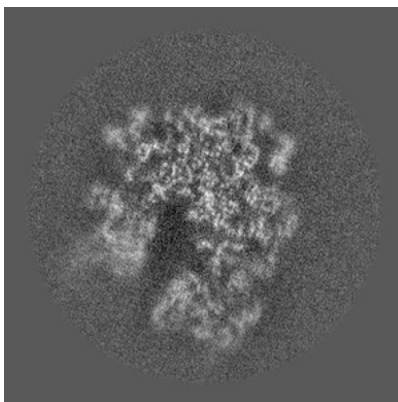


Z Index: 144

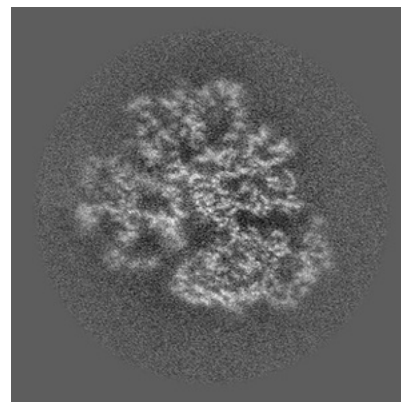
6.2.2 Raw map



X Index: 144



Y Index: 144

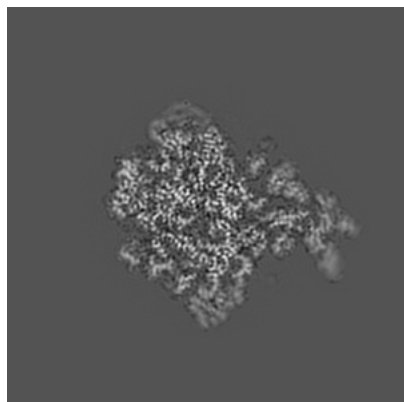


Z Index: 144

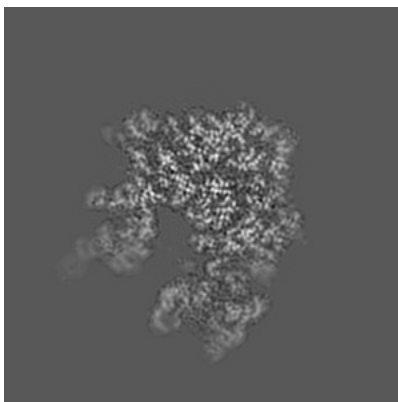
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

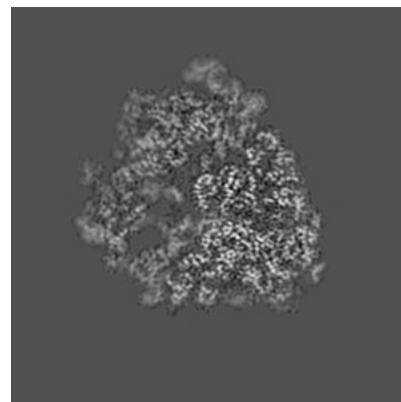
6.3.1 Primary map



X Index: 149

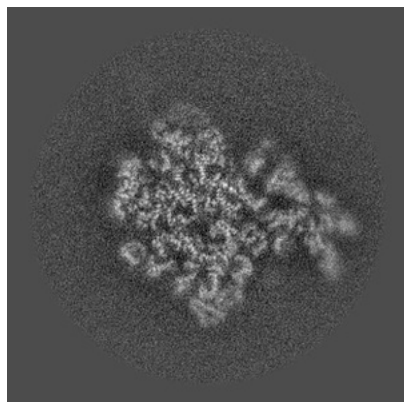


Y Index: 148

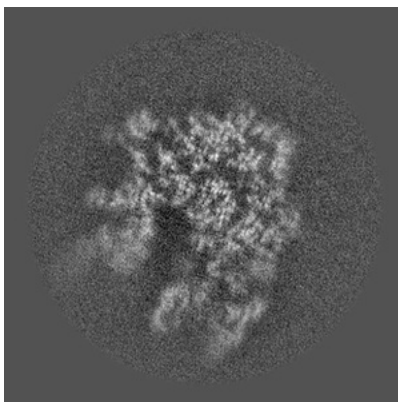


Z Index: 135

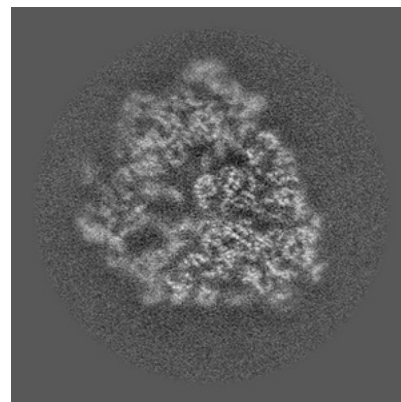
6.3.2 Raw map



X Index: 148



Y Index: 148

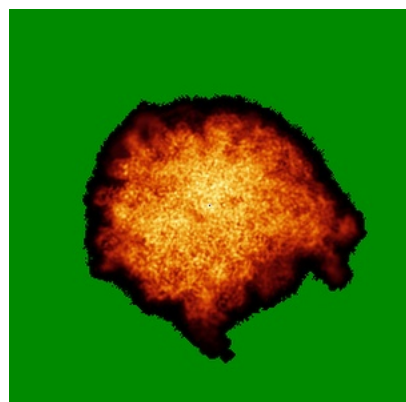


Z Index: 135

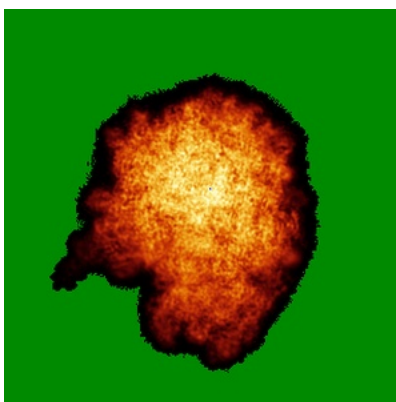
The images above show the largest variance slices of the map in three orthogonal directions.

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

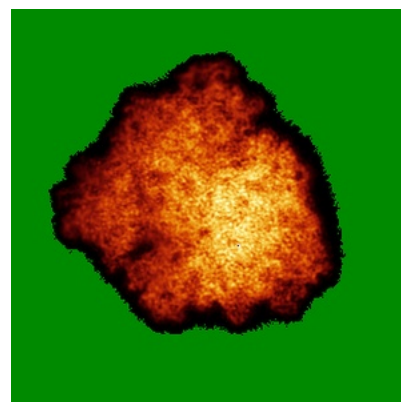
6.4.1 Primary map



X

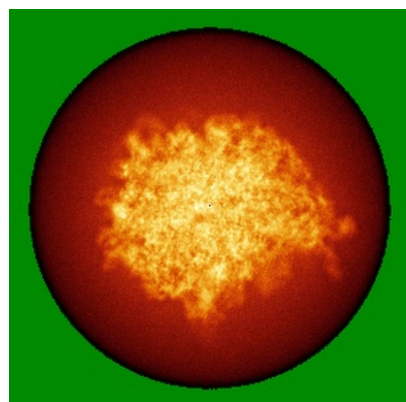


Y

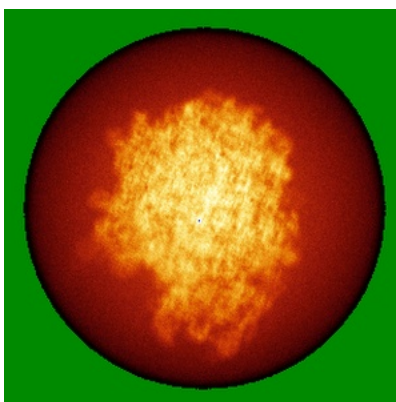


Z

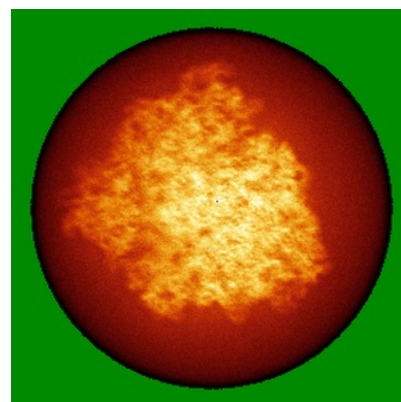
6.4.2 Raw map



X



Y



Z

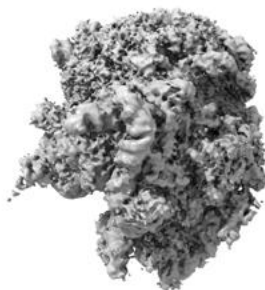
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



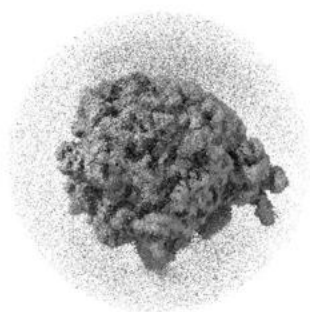
Y



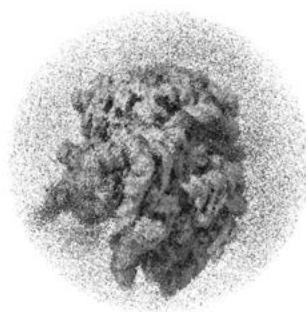
Z

The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

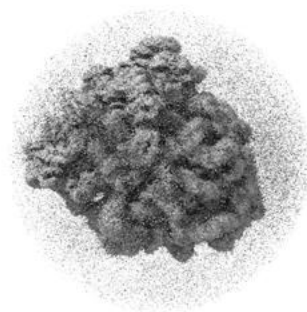
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

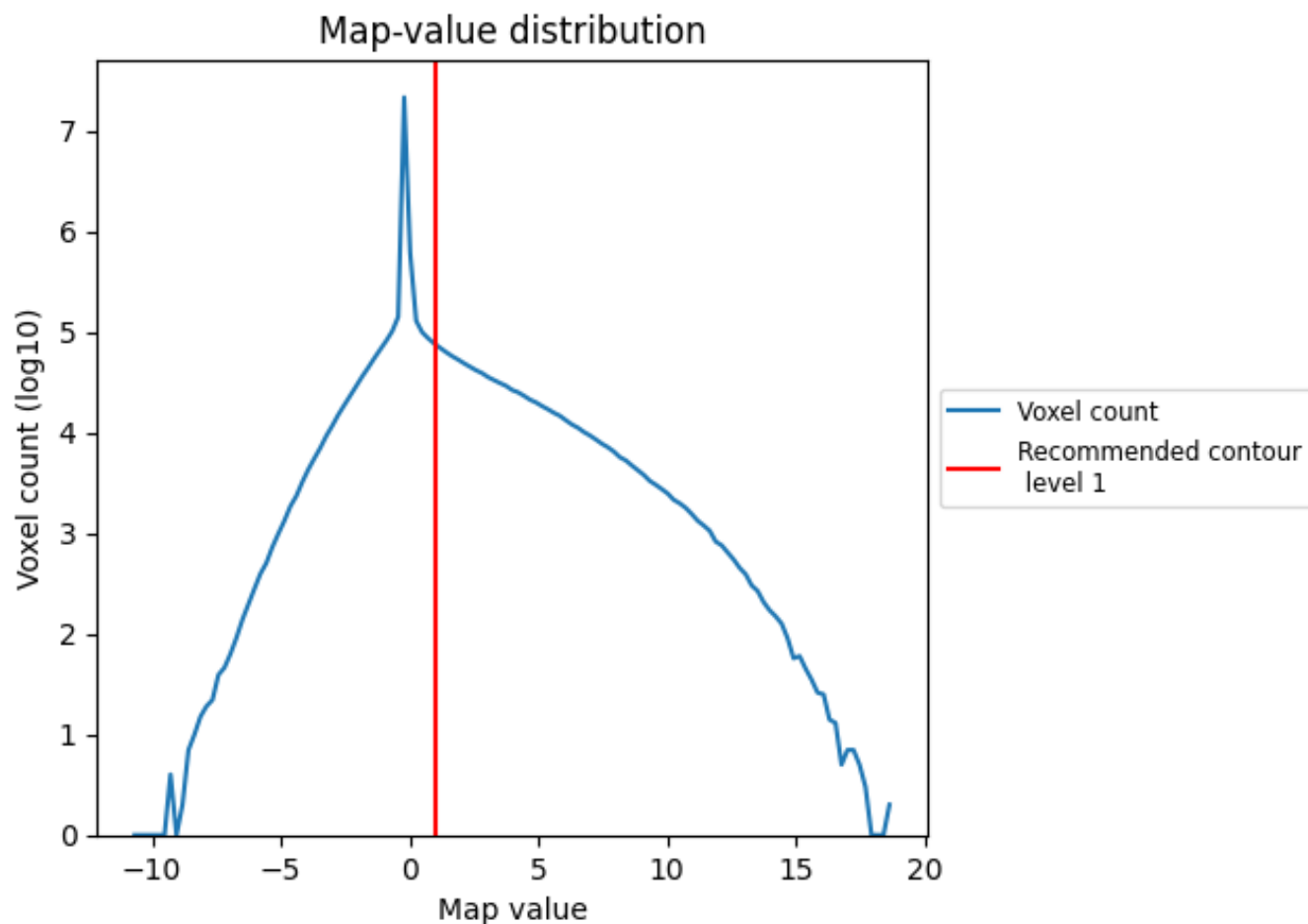
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

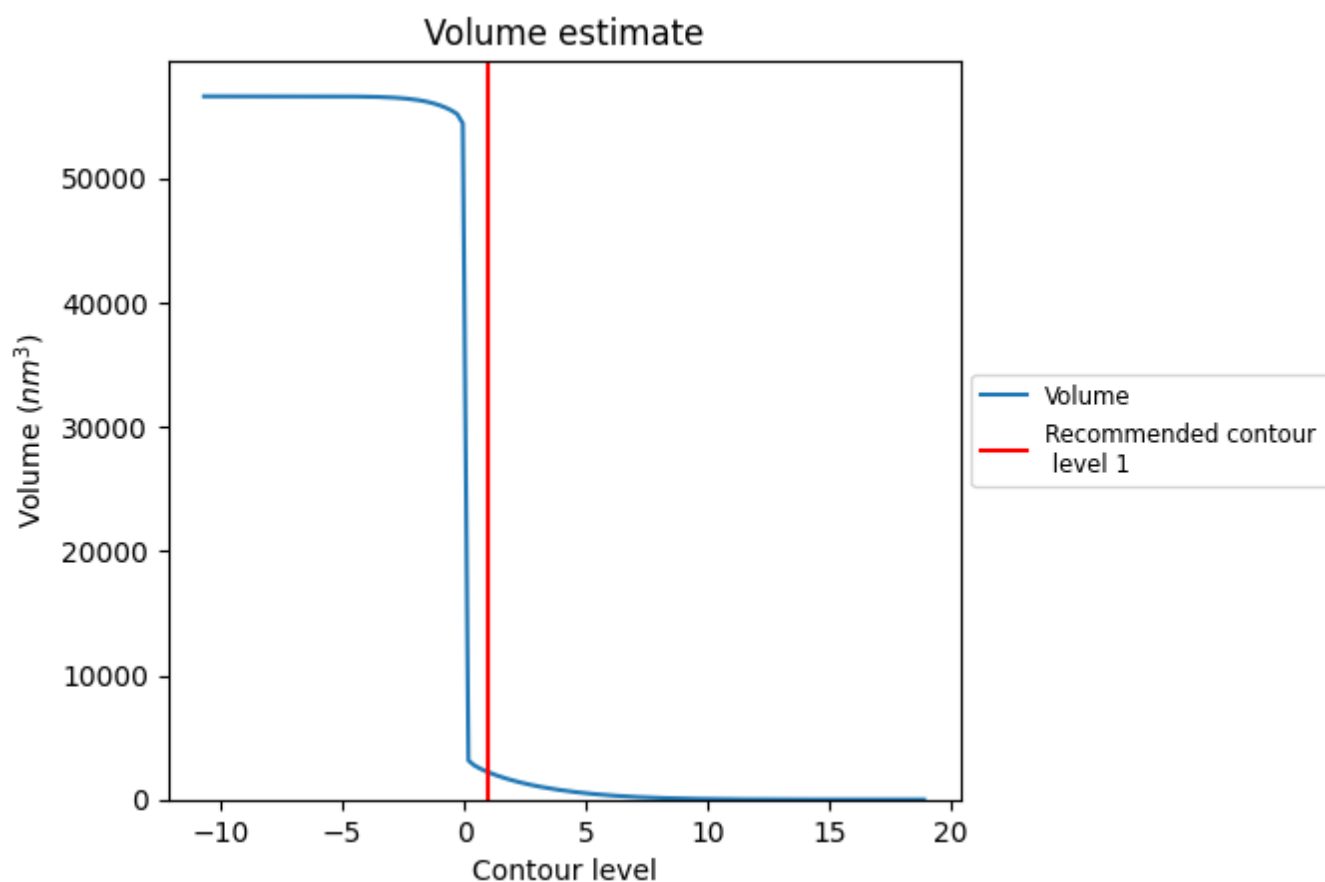
This section contains the results of statistical analysis of the map.

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.

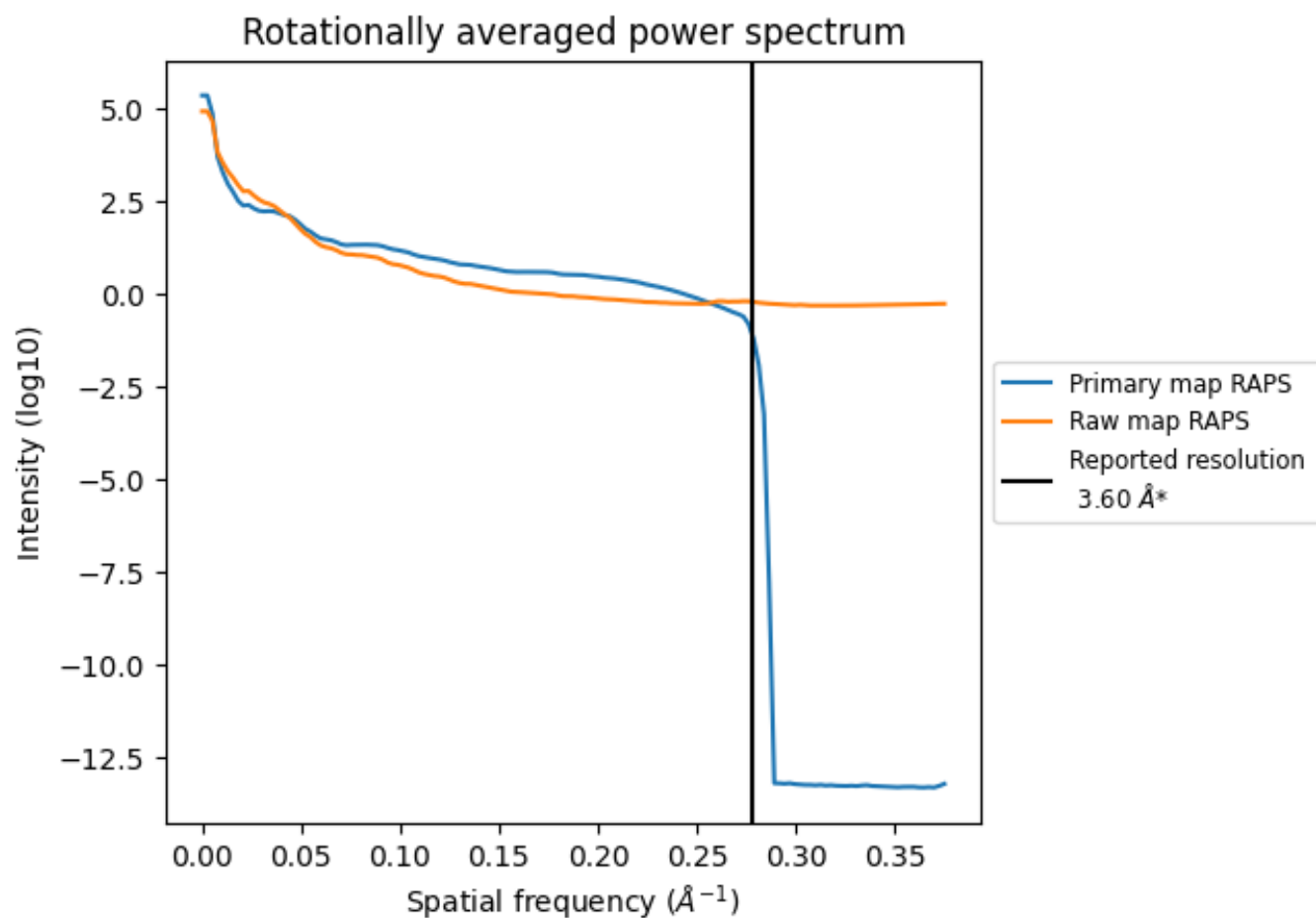
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2191 nm³; this corresponds to an approximate mass of 1979 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

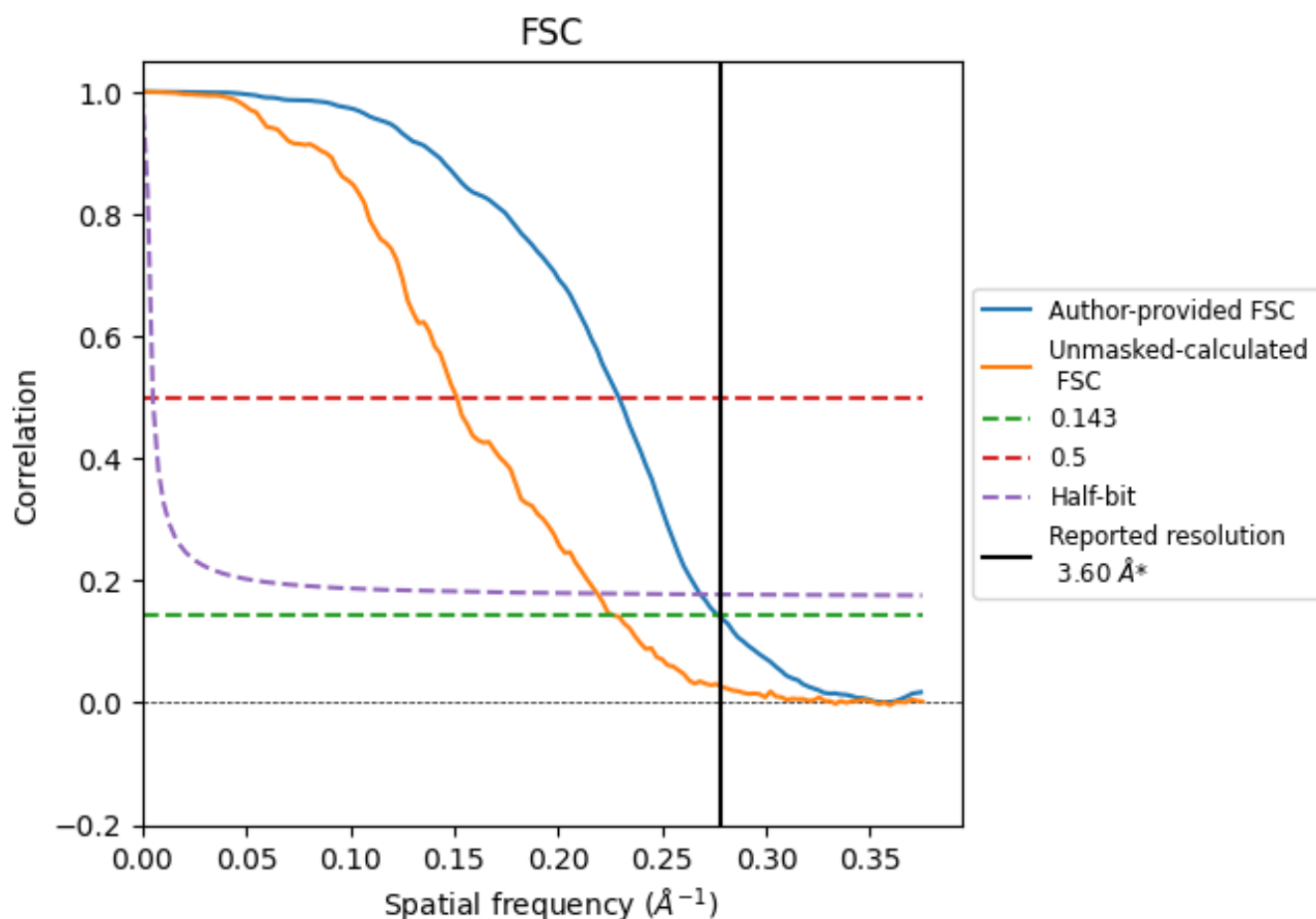


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

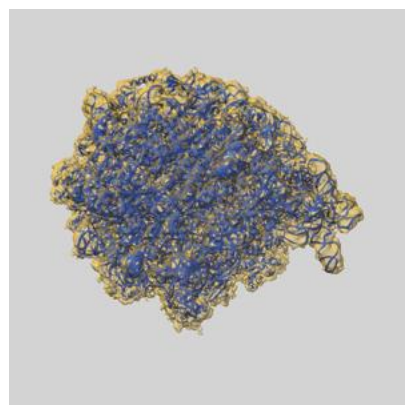
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.61	4.36	3.73
Unmasked-calculated*	4.42	6.61	4.57

*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 4.42 differs from the reported value 3.6 by more than 10 %

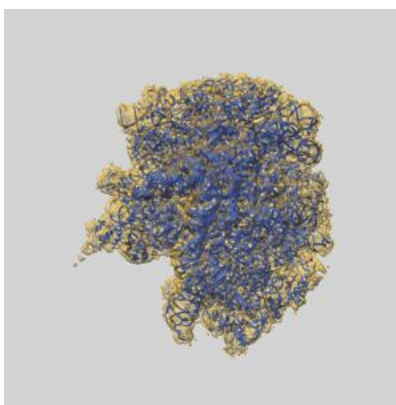
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21622 and PDB model 6WD3. Per-residue inclusion information can be found in section [3](#) on page [17](#).

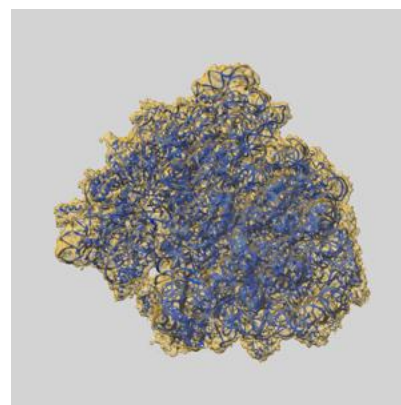
9.1 Map-model overlay [i](#)



X



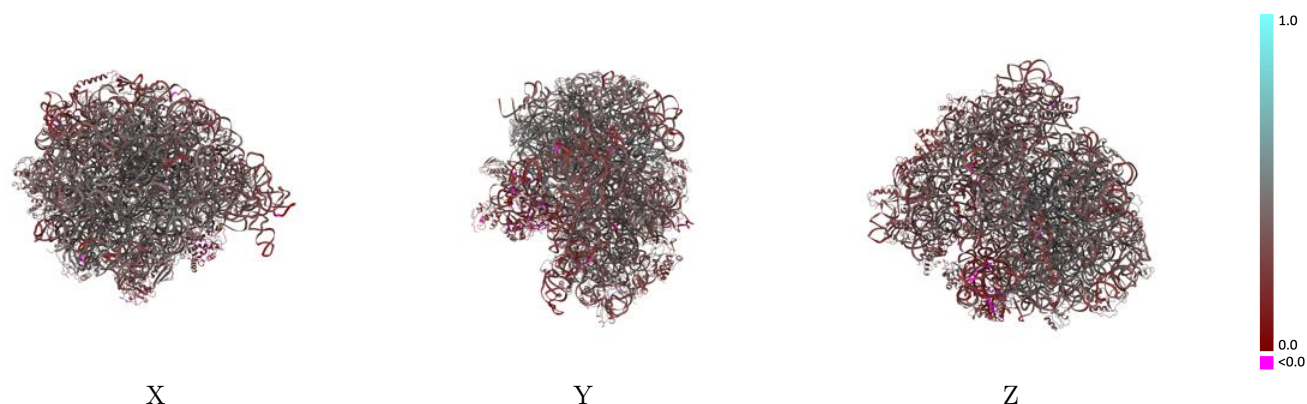
Y



Z

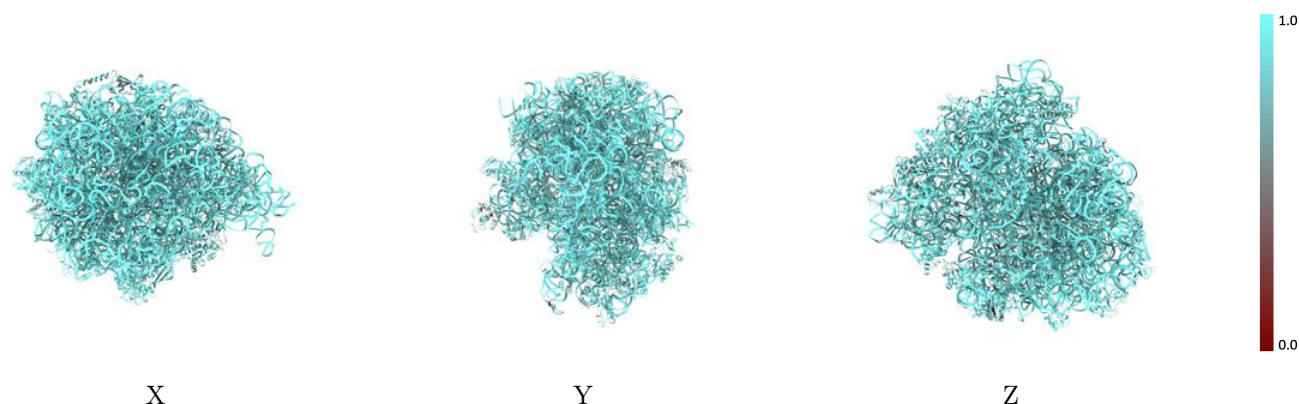
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



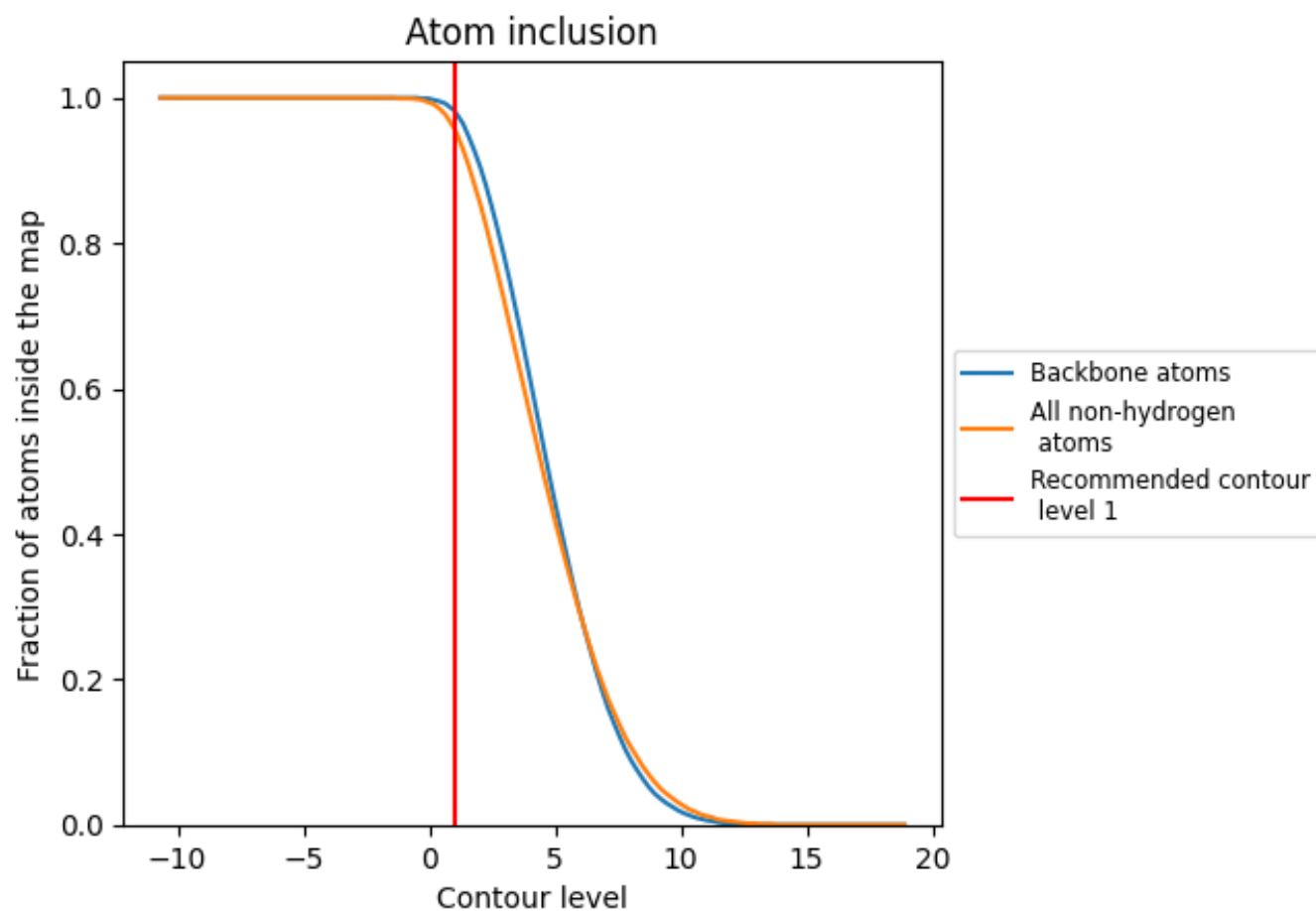
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9570	 0.3630
1	 0.9840	 0.3850
2	 0.9880	 0.3360
3	 0.9800	 0.3470
4	 0.8350	 0.2100
5	 0.9680	 0.3190
6	 0.8110	 0.1460
7	 0.9320	 0.1770
8	 0.8990	 0.2070
B	 0.9440	 0.4370
C	 0.8480	 0.3910
D	 0.9240	 0.4510
E	 0.9670	 0.4760
F	 0.9010	 0.4220
G	 0.9000	 0.3150
H	 0.8140	 0.3500
I	 0.8820	 0.3080
J	 0.9370	 0.4040
K	 0.9510	 0.3740
L	 0.9370	 0.3380
M	 0.9280	 0.4100
N	 0.8790	 0.3320
O	 0.7820	 0.3150
P	 0.9480	 0.3810
Q	 0.9110	 0.4120
R	 0.9430	 0.3320
S	 0.8370	 0.3270
T	 0.9610	 0.3860
U	 0.9030	 0.3690
V	 0.9230	 0.3630
W	 0.9240	 0.3720
X	 0.9680	 0.3250
Y	 0.8980	 0.3390
Z	 0.8730	 0.2940
a	 0.7970	 0.1520



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Chain	Atom inclusion	Q-score
b	 0.9590	 0.4600
c	 0.9560	 0.4610
d	 0.9520	 0.4080
e	 0.9480	 0.3330
f	 0.9490	 0.3340
g	 0.7740	 0.2590
h	 0.7580	 0.1650
i	 0.8240	 0.1870
j	 0.9540	 0.4500
k	 0.9220	 0.4480
l	 0.9500	 0.4270
m	 0.9460	 0.4490
n	 0.9440	 0.4420
o	 0.9530	 0.3510
p	 0.9490	 0.4470
q	 0.9540	 0.4400
r	 0.9620	 0.4170
s	 0.9410	 0.4460
t	 0.9410	 0.4210
u	 0.9410	 0.3990
v	 0.9510	 0.4050
w	 0.9500	 0.4640
x	 0.9630	 0.4480
y	 0.9300	 0.3440
z	 0.9430	 0.4170