



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 06:27 PM UTC

PDB ID : 6WD8 / pdb_00006wd8
EMDB ID : EMD-21627
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure III-A)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.70 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

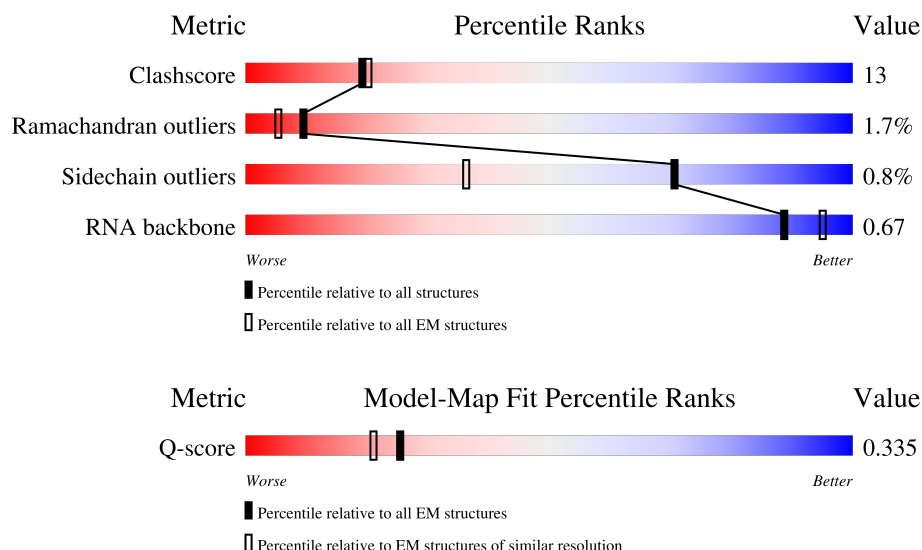
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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.



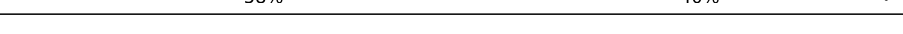
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	58% 37% 5%
2	c	209	65% 33% .
3	d	201	68% 31% .

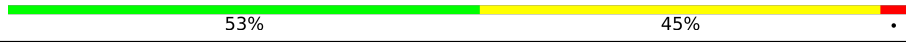
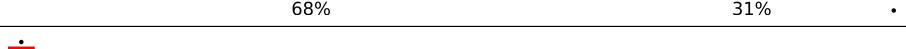
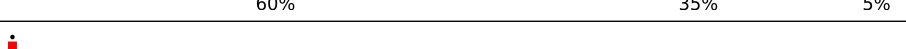
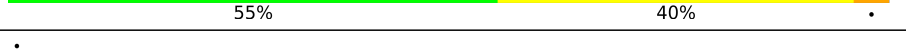
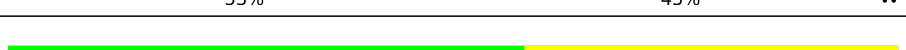
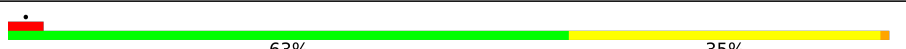
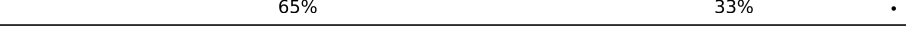
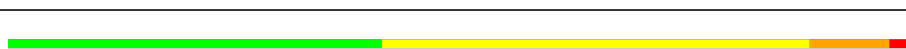
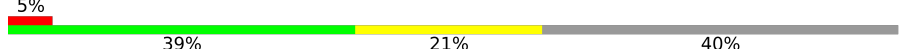
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
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	59%36%5%
55	5	77	65%32%.•
55	6	77	5% 39%61%
56	4	18	6% 67%28%6%
57	7	76	• 43%49%8%
58	8	400	6% 53%40%.•

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 153212 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	conflict	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	384	Total	C	N	O	S	0	0
			2958	1871	509	565	13		

There are 7 discrepancies between the modelled and reference sequences:

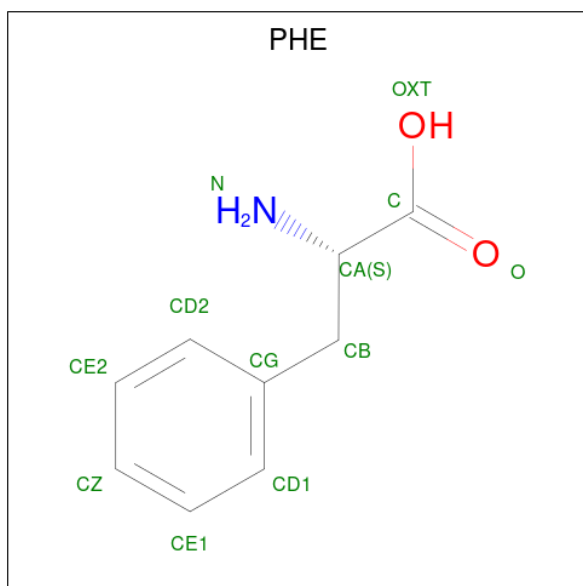
Chain	Residue	Modelled	Actual	Comment	Reference
8	395	SER	-	expression tag	UNP E2QFJ4
8	396	HIS	-	expression tag	UNP E2QFJ4
8	397	HIS	-	expression tag	UNP E2QFJ4
8	398	HIS	-	expression tag	UNP E2QFJ4
8	399	HIS	-	expression tag	UNP E2QFJ4
8	400	HIS	-	expression tag	UNP E2QFJ4
8	401	HIS	-	expression tag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

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



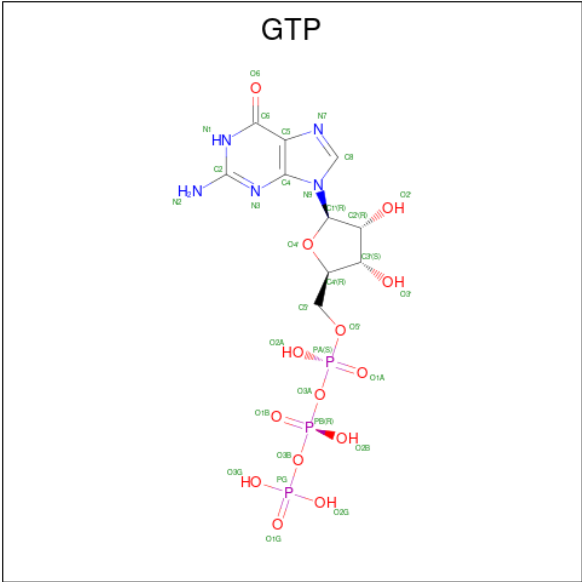
Mol	Chain	Residues	Atoms					AltConf
59	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

- 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'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



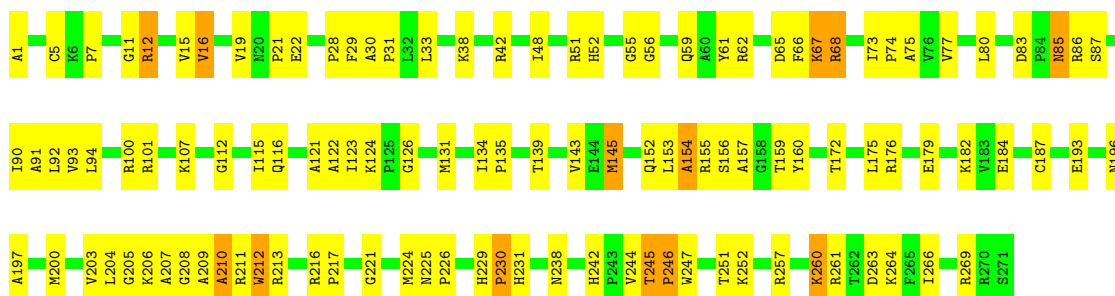
Mol	Chain	Residues	Atoms					AltConf
61	8	1	Total	C	N	O	P	0
			32	10	5	14	3	

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.

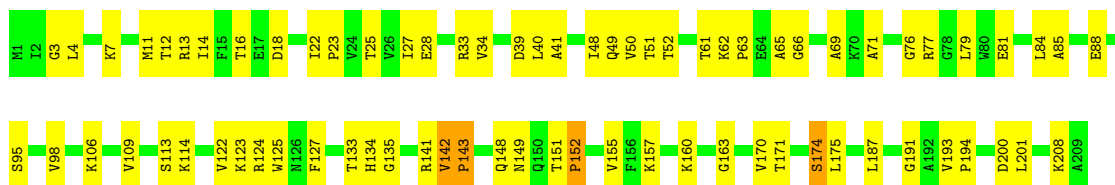
- Molecule 1: 50S ribosomal protein L2

Chain b: 



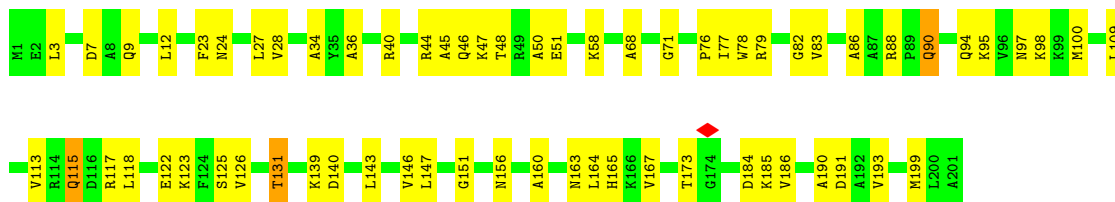
- Molecule 2: 50S ribosomal protein L3

Chain c: 



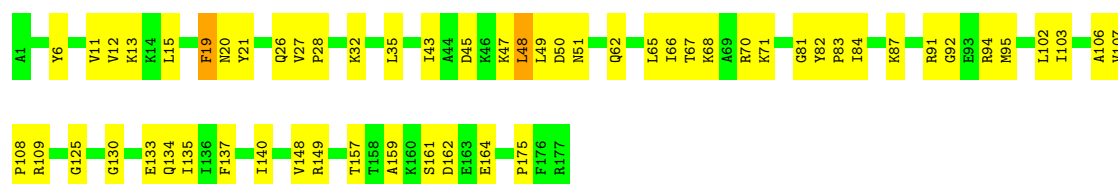
- Molecule 3: 50S ribosomal protein L4

Chain d: 

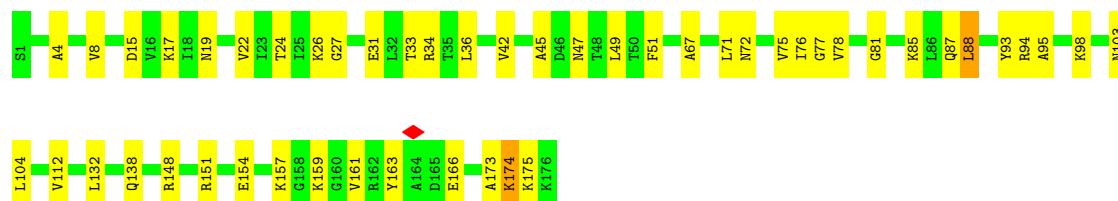


- Molecule 4: 50S ribosomal protein L5

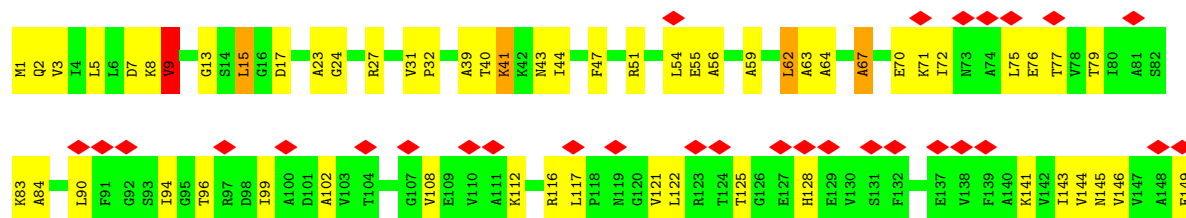
Chain e: 



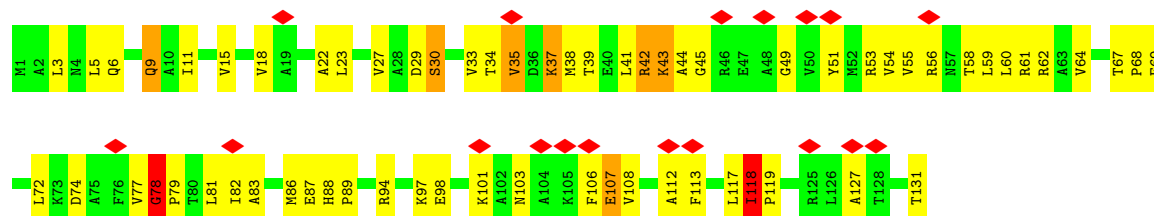
• Molecule 5: 50S ribosomal protein L6



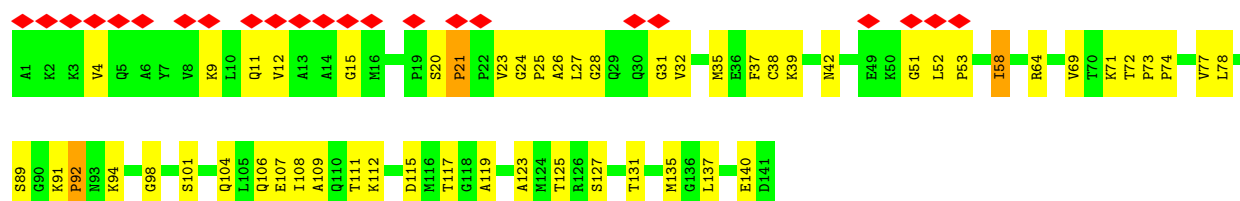
• Molecule 6: 50S ribosomal protein L9



• Molecule 7: 50S ribosomal protein L10

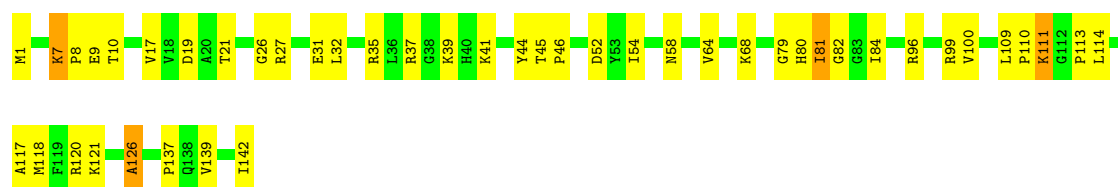


• Molecule 8: 50S ribosomal protein L11



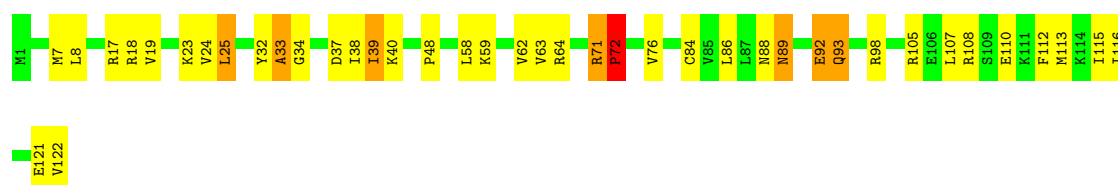
- Molecule 9: 50S ribosomal protein L13

Chain j:  68% 29% .



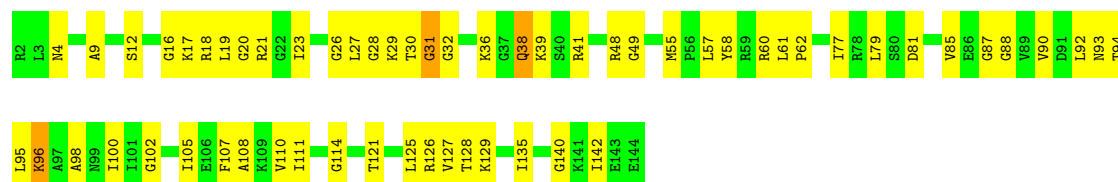
- Molecule 10: 50S ribosomal protein L14

Chain k:  66% 27% 6% .



- Molecule 11: 50S ribosomal protein L15

Chain l:  59% 39% .



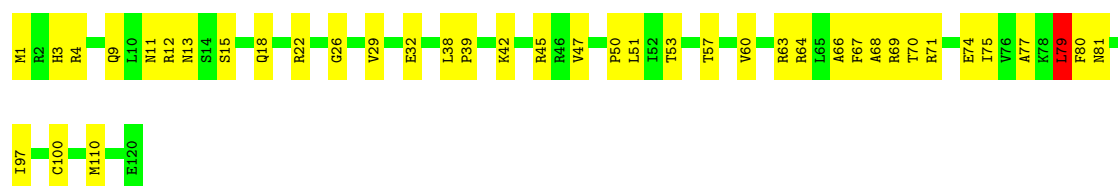
- Molecule 12: 50S ribosomal protein L16

Chain m:  68% 29% .

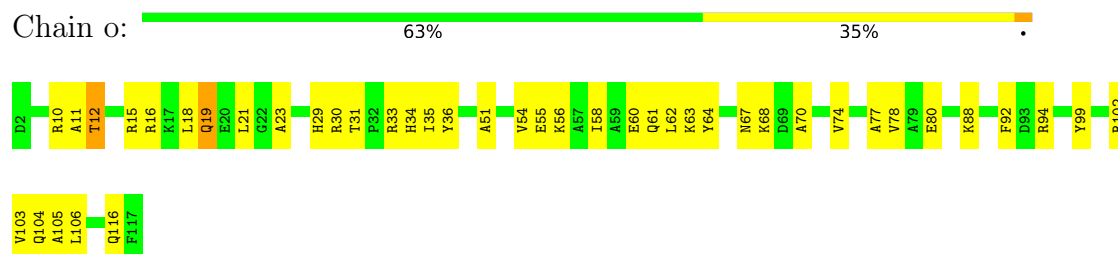


- Molecule 13: 50S ribosomal protein L17

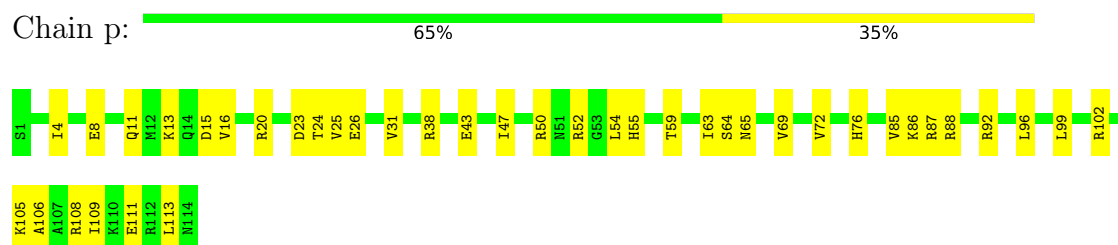
Chain n:  67% 32% .



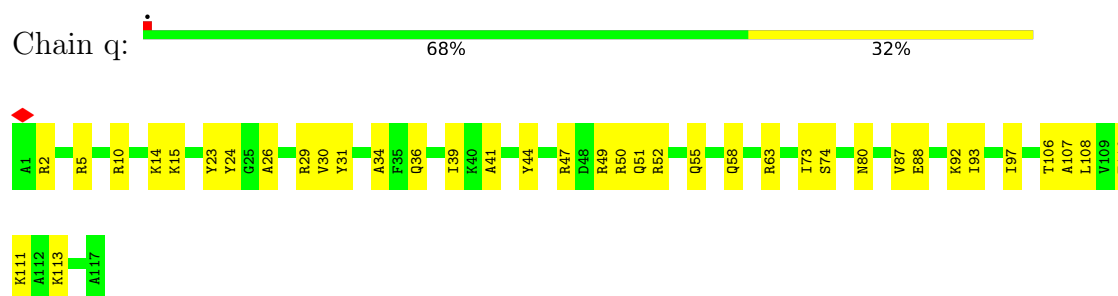
- Molecule 14: 50S ribosomal protein L18



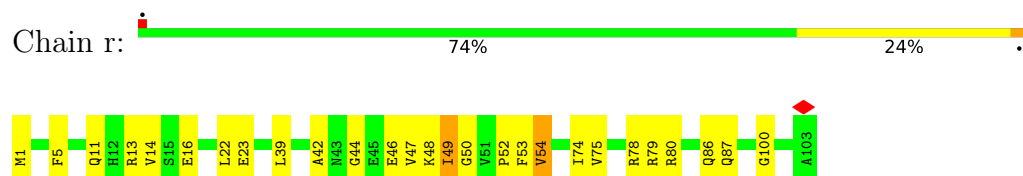
- Molecule 15: 50S ribosomal protein L19



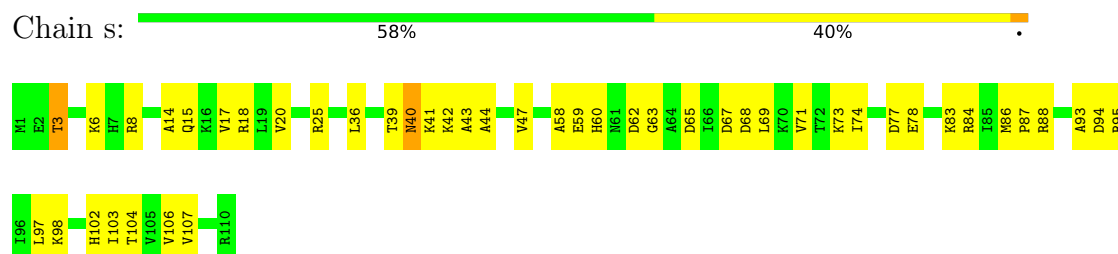
- Molecule 16: 50S ribosomal protein L20



- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23

Chain t:  69% 30%



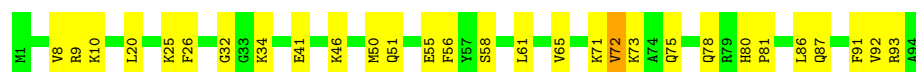
- Molecule 20: 50S ribosomal protein L24

Chain u:  72% 24% 5%



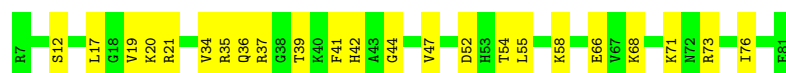
- Molecule 21: 50S ribosomal protein L25

Chain v:  69% 30%



- Molecule 22: 50S ribosomal protein L27

Chain w:  69% 31%



- Molecule 23: 50S ribosomal protein L28

Chain x:  69% 30%



- Molecule 24: 50S ribosomal protein L29

Chain y:  63% 35%



- Molecule 25: 50S ribosomal protein L30

Chain z:  72% 28%



- Molecule 26: 50S ribosomal protein L32

Chain B:  61% 39%



- Molecule 27: 50S ribosomal protein L33

Chain C:  68% 32%



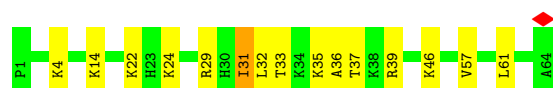
- Molecule 28: 50S ribosomal protein L34

Chain D:  61% 39%



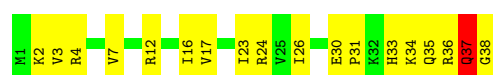
- Molecule 29: 50S ribosomal protein L35

Chain E:  77% 22%



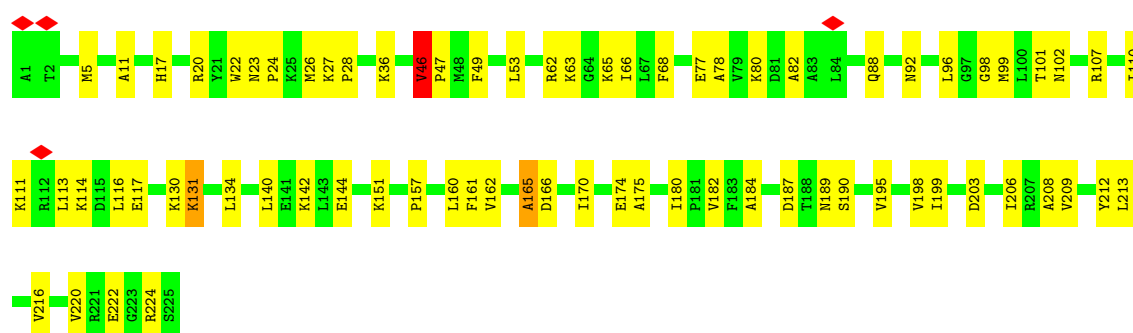
- Molecule 30: 50S ribosomal protein L36

Chain F:  53% 45%

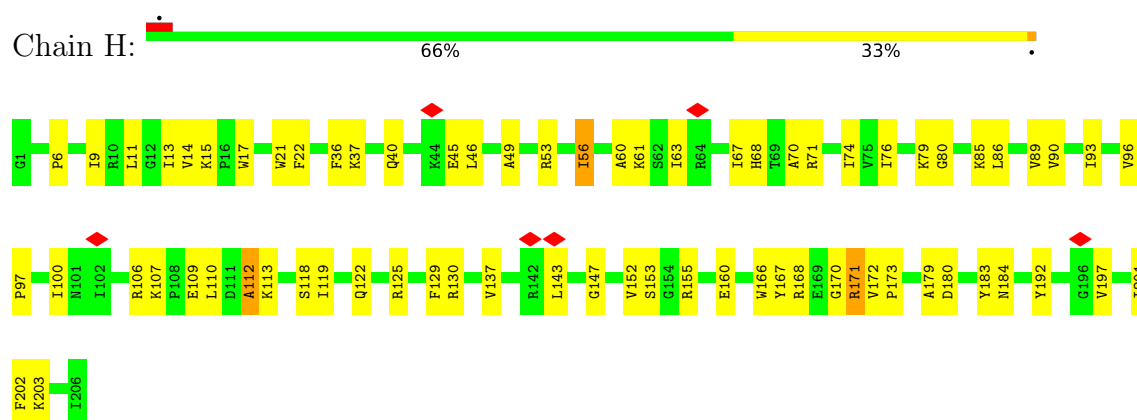


- Molecule 31: 30S ribosomal protein S2

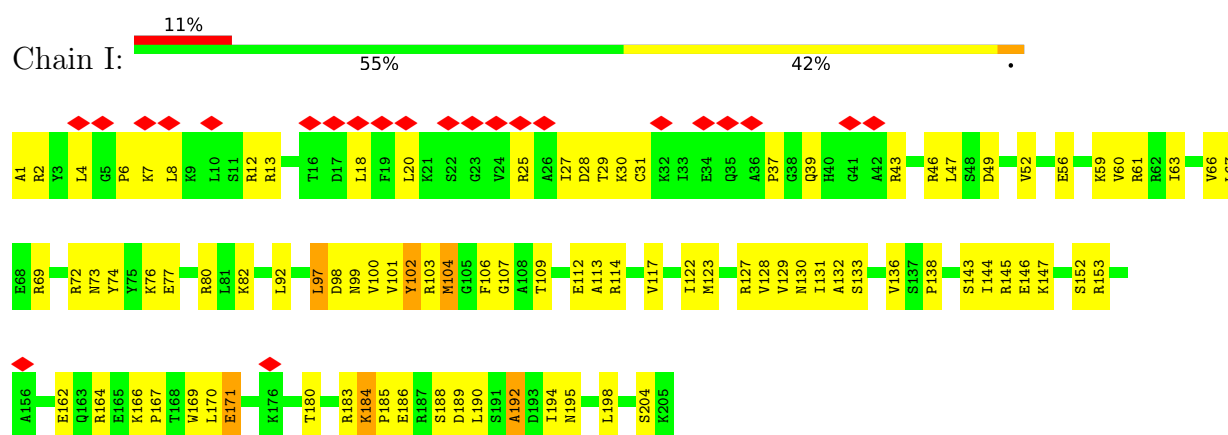
Chain G:  68% 31%



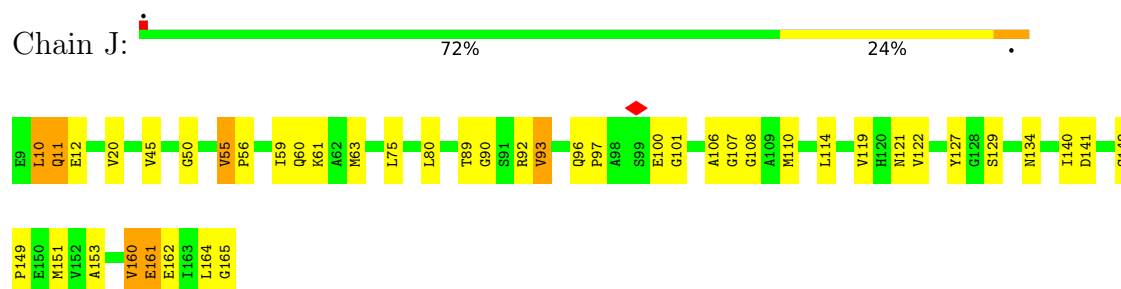
- Molecule 32: 30S ribosomal protein S3



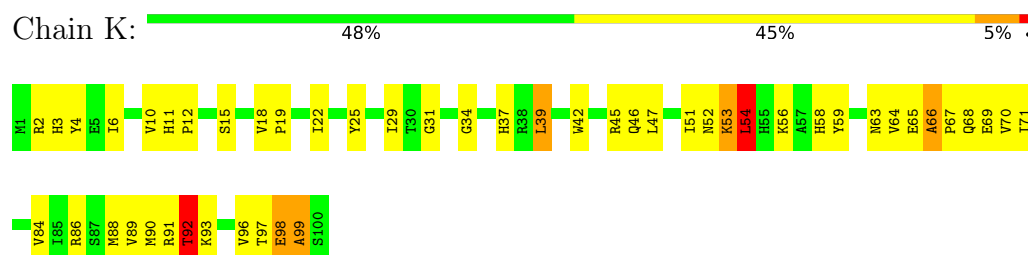
• Molecule 33: 30S ribosomal protein S4



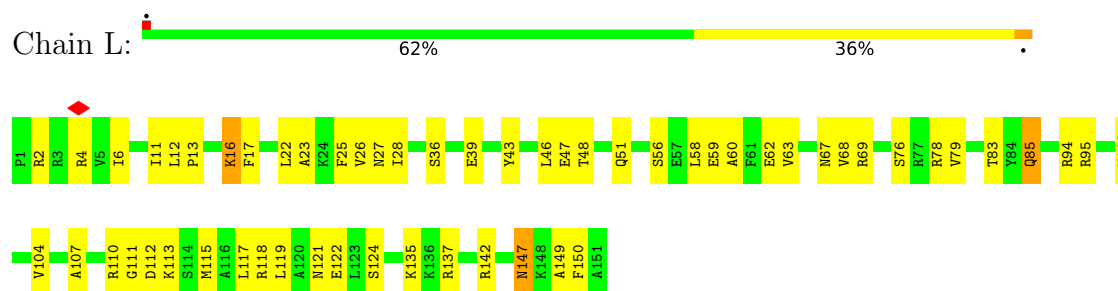
• Molecule 34: 30S ribosomal protein S5



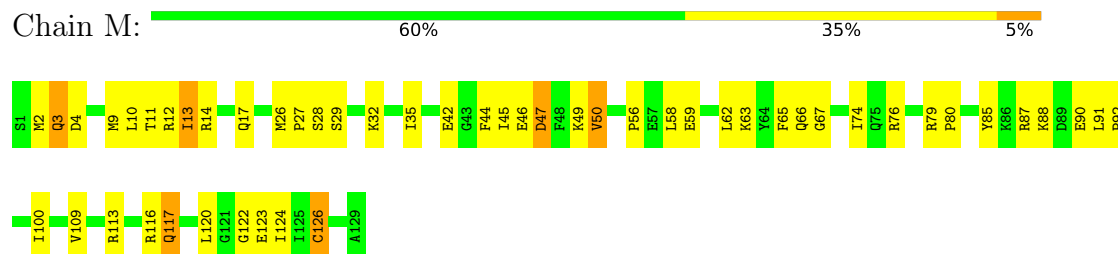
• Molecule 35: 30S ribosomal protein S6



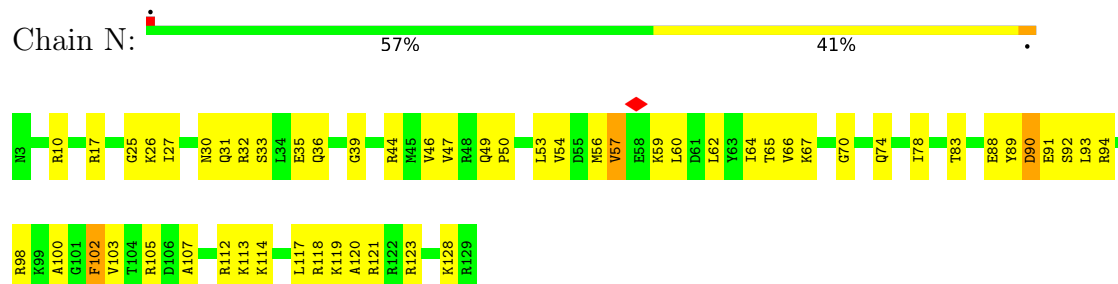
• Molecule 36: 30S ribosomal protein S7



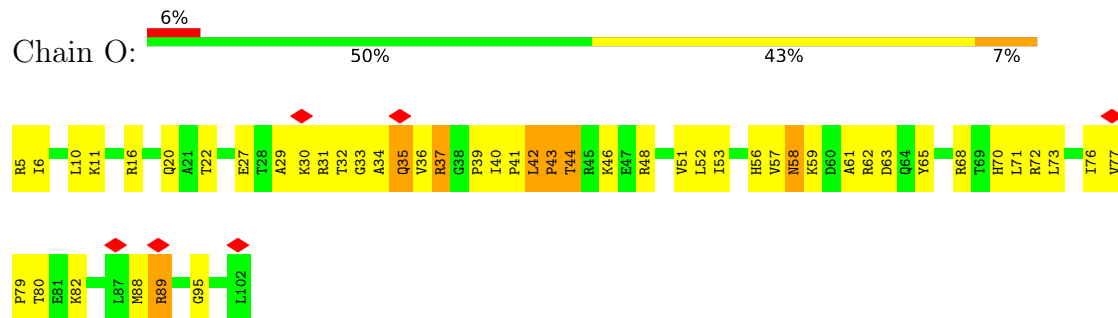
- Molecule 37: 30S ribosomal protein S8



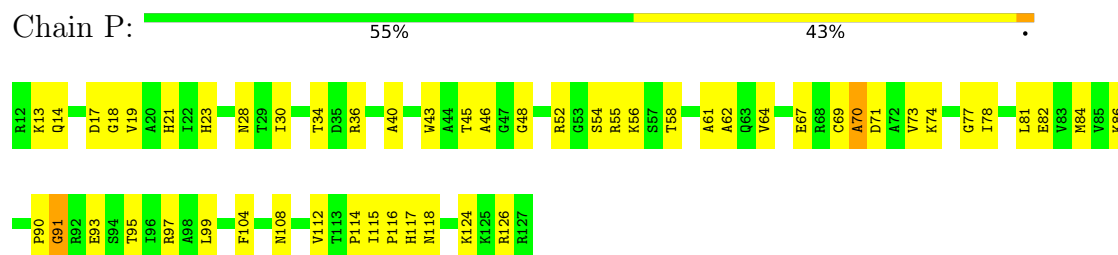
- Molecule 38: 30S ribosomal protein S9



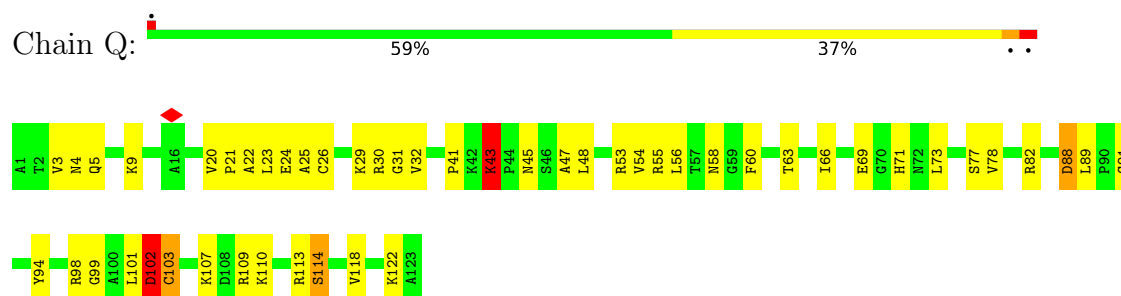
- Molecule 39: 30S ribosomal protein S10



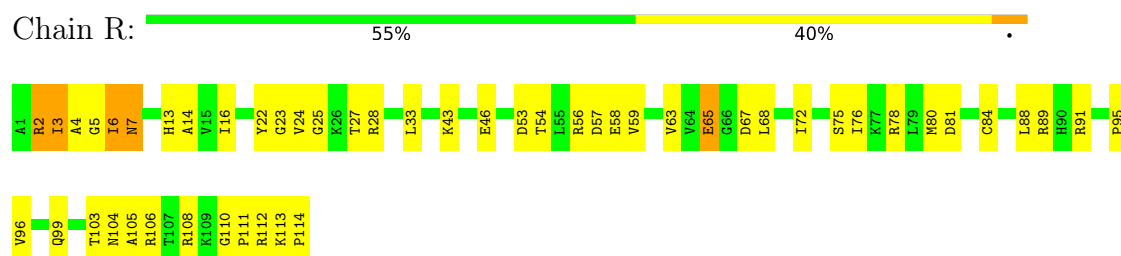
- Molecule 40: 30S ribosomal protein S11



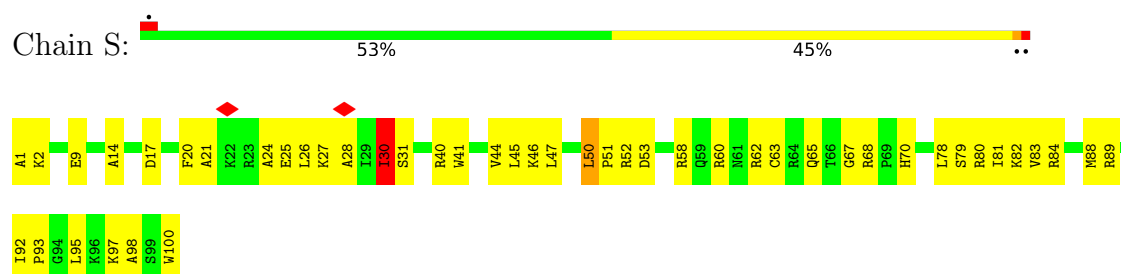
- Molecule 41: 30S ribosomal protein S12



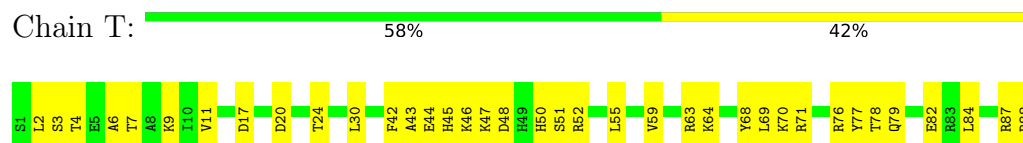
- Molecule 42: 30S ribosomal protein S13



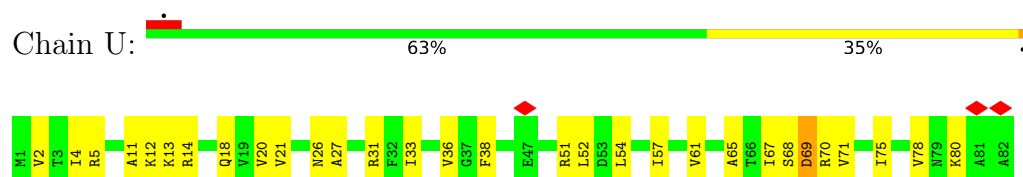
- Molecule 43: 30S ribosomal protein S14



- Molecule 44: 30S ribosomal protein S15



- Molecule 45: 30S ribosomal protein S16

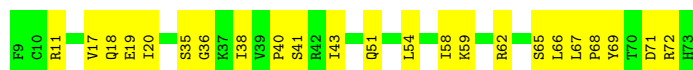


- Molecule 46: 30S ribosomal protein S17





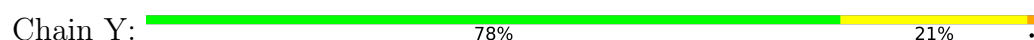
- Molecule 47: 30S ribosomal protein S18



- Molecule 48: 30S ribosomal protein S19



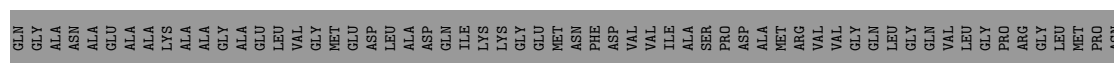
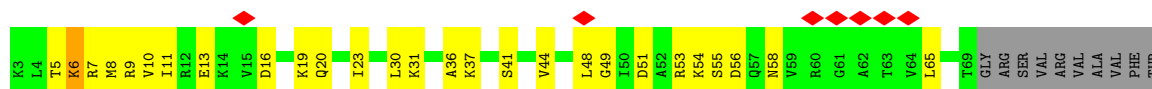
- Molecule 49: 30S ribosomal protein S20



- Molecule 50: 30S ribosomal protein S21



- Molecule 51: 50S ribosomal protein L1



- Molecule 52: 16S ribosomal RNA

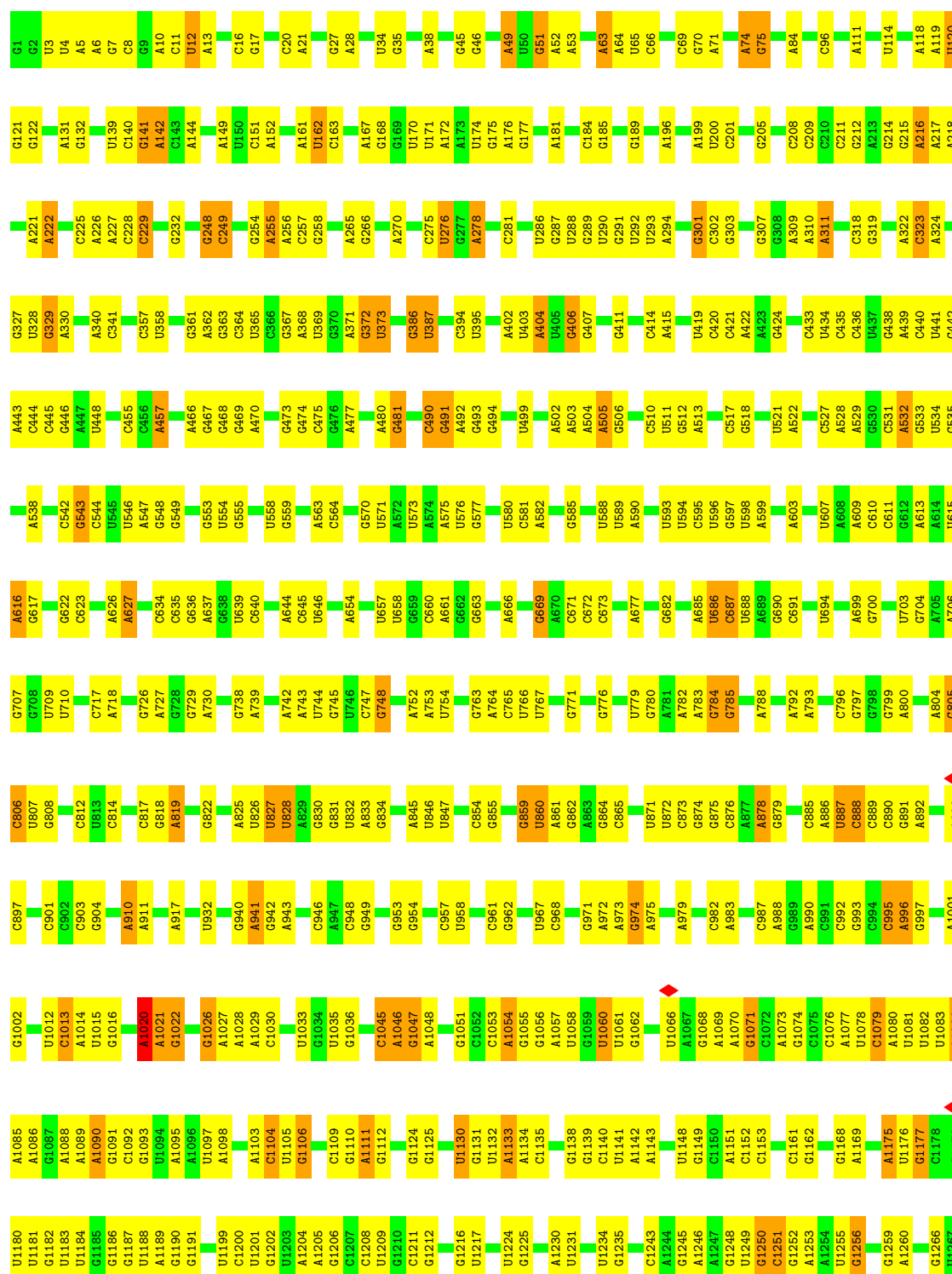
Chain 3:  55% 41% .

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U5	C95	G212	C312	C401	G521	C599	U692	G777	C981	A978	G1088	G1182	G1278	G1371
G6	G100	G213	A321	C403	A523	A600	G693	G778	C982	C979	G1089	G1183	G1279	A1374
G9	C106	U216	A327	U405	C526	G605	A694	C779	C983	U981	G1094	G1184	A1280	A1375
A10	G107	C217	C328	U406	G527	G606	A695	A780	C984	U982	U1095	G1185	C1281	G1379
A16	C110	U224	A329	U407	C528	C613	U701	A784	C987	C985	C1096	G1187	U1286	U1380
U17	C111	C225	C330	U408	G529	C614	A702	G785	C988	U986	C1097	A1188	A1287	U1381
C18	G112	G226	G331	U409	G530	C615	G703	A794	C989	U992	A1101	A1189	A1288	C1384
U20	G113	U229	G332	U410	U531	C616	A706	A815	C990	G993	G1106	A1191	C1296	C1385
G21	U114	U231	U333	A411	A532	C620	A709	A816	C991	C1001	C1107	G1192	U1300	U1390
G22	G115	G232	C334	A412	A533	C621	U710	C817	C992	G1002	G1108	G1193	U1301	U1391
U24	C234	C233	C335	C418	C536	A621	G710	C818	C993	G1003	C1109	G1194	G1302	G1392
C25	U123	G234	G337	C419	G537	A622	G711	C819	C994	A1004	C1110	C1195	C1303	
A26	G128	U236	A338	C422	G538	C623	A712	U820	G902	A1005	U1116	G1196	C1304	
U29	G129	G237	U340	C423	A540	G626	A715	U821	C909	G1006	A1117	U1199	A1306	C1395
U30	A130	A243	C345	C424	G541	G627	A716	C824	C910	C1011	C1120	A1200	G1312	A1396
G31	A131	U244	G346	C425	G542	U628	A717	C825	U911	A1012	C1121	A1201	U1313	C1402
A32	C132	U245	C347	C426	A546	A629	A718	C826	C912	G1013	U1122	U1202	C1314	C1403
A33	U133	A246	G347	A430	A547	A630	A719	C827	U916	A1014	U1123	C1203	U1315	G1405
G34	G142	G247	G350		U552	G633	U723	U828	C917	G1015	G1124	U1211	G1317	
G35	G143		G351	U438	U555	U636	G725	C829	C924	G1020	C1128	U1212	A1318	C1409
C36	U144		C352	U439	U556	C637	G726	A831	G925	G1021	C1129	A1213	A1319	A1410
U37	G145		G353		C556			A832	G926	C1022	A1130	C1218	C1320	A1411
C38			C354	U458	G557	A642	A729	C833	G927	G1023	G1131	C1219	G1323	C1412
G39	A149	G255	C355	A459	G558	G643	G730	U834	G928	U1030	C1136	G1220	A1413	A1413
G45	U150	G259	A356	A467	A559	C651	G731	U835	G933	C1031	C1137	G1221	C1324	U1414
G46	A151		G357		A560	U652	C732	G836	C934	G1032	G1138	A1225	U1325	G1415
C47	A152		U358	U479	U561	C658	G733	U843	A935	G1033	C1139	C1226	C1327	G1422
C48	C156	A262	G359		C564	U659	G734	A844	A936	G1034	C1140	C1227	C1328	U1425
H49	U157	G263	A363	C483	U565	C660	C735	A845	A937		C1141	C1228	A1329	U1426
A50	G163	G265		G484	G566	G661	C736	C846	G939	U1049	A1146	C1229	U1330	
A51	G164	C267	U367	U486		U662	C737	G847	C948	U1052	C1147	C1230	G1331	A1429
C58	C183	G285	U368		G570	U663	G741	C948	C948		U1148	A1238	C1336	A1430
A59	G184	G286	G369	C490	U571	A663	G742	U855	A949	A1055	C1149	U1239	U1337	A1431
G61	U185	A274	A371	G491	A572	G664	A743	C856	U950	U1056	A1150	U1240	C1342	G1432
U62	C186		C372	G497	A573	G665	C744	C857	G951	G1057	A1151	G1241	G1343	A1433
C63	G187	A279		C497	A574	G667	G745	C859	U952	G1058	A1152	A1251	A1346	G1435
U70	A189	G281	U375	A498	G575	G668	C754	A860	C954	C1059	G1156	A1252	G1347	U1436
A71	C194	G289	G376	C501	G576	U673	C755	A861	U955	U1060	A1157	G1253	U1348	A1437
A77	A195	A298	C381	A502	G577	A673	C756	C862	U956	G1061	U1158	A1254	A1349	G1438
A78	G196	G299	A382	C503	G580	A674	C757	A865	A959	C1069	U1159	A1255		A1445
G79	A197	U304	U387	C504	G581	A675	C758	U866	U960	U1070	G1160	A1256	G1353	A1447
A80	A205	U305	G388	C511	G585	A676	G759	C868	U961	C1071	G1161	A1257	U1354	C1448
A81	C206	A306	A393	C512	G586	A677	C760	U870	U962	G1072	A1163	G1258	G1355	C1449
G82	C207	G307	A394	C513	G587	A681	G761	U871	C966	U1073	U1164	C1259	A1363	G1452
C83	U208	C308	C395	C514	U593	U684	A766	A872	A969	G1074	A1167	G1260	U1364	C1453
U84	U209	A397	C396	C515	U594	G685	A767	A873	U969	U1075	U1168		G1365	G1458
U85	C210	U398	C397	C516	U595	G686	A768	C876	C972	G1076	A1169	G1271	C1366	
G86		G399	C399	C518	A596	G688	G769	C976	A975	A1081	A1170	A1272	C1367	
				C519	G597		U772		G976	A1082	C1172	A1274	C1369	U1463

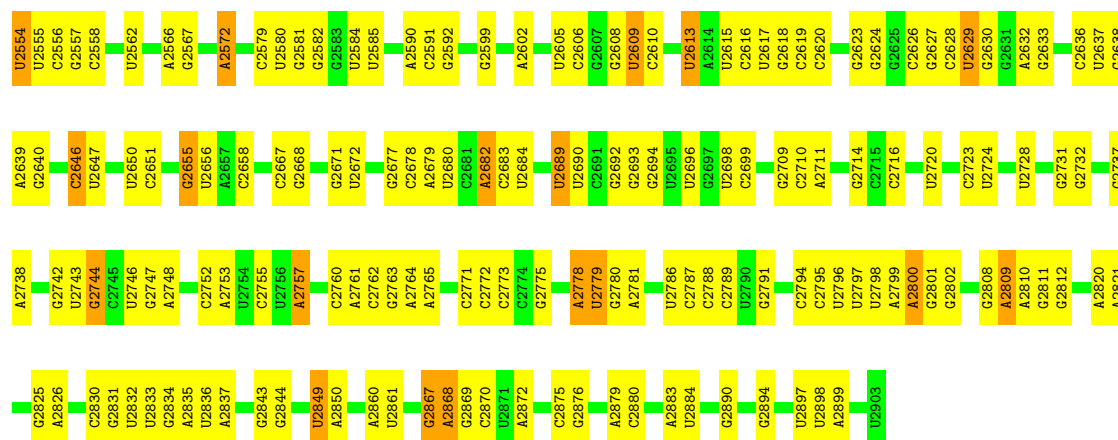


• Molecule 53: 23S ribosomal RNA

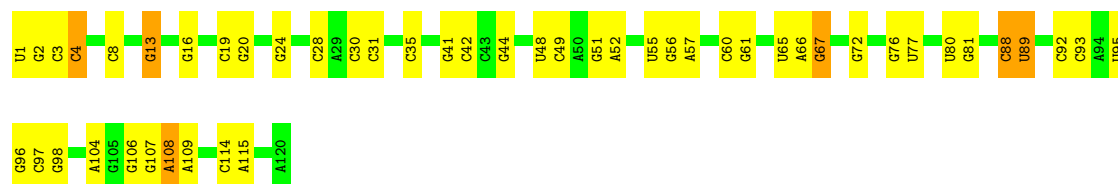
Chain 1: 54% 40% 6%



C2466	G2389	U2299	G2226	U2132	C1958	U1855	A1780	A1664	A1551	G1445	G1357	A1268
C2467	G2390	U2305	A2227	G2133	U1963	U1856	A1783	A1665	G1555	C1446	G1358	A1269
A2468	G2391	C2301	G2230	C2055	G1964	A1857	A1784	G1667	G1555	G1447	G1359	C1270
A2469	A2392	C2309	U2233	G2056	G1965	A1858	A1785	G1667	C1558	G1448	G1360	G1271
G2470	U2393	G2310	G2234	A2060	A1966	U1859	A1786	G1670	U1559	C1454	G1361	A1272
A2471	C2394	A2311	G2234	G2061	C1967	G1860	G1786	U1671	G1560	G1455	C1362	A1275
G2472	G2398	G2312	G2238	A2062	A1970	G1861	C1790	G1674	U1563	U1458	A1365	A1278
C2475	G2399	A2314	G2239	C2066	U1971	C1870	A1791	G1674	A1566	G1459	A1366	G1278
A2476	U2402	G2315	U2240	G2067	G1972	A1871	G1794	A1678	C1564	G1460	G1367	G1279
G2480	C2403	G2318	A2241	U2068	G1973	G1873	A1796	A1679	G1565	C1461	G1368	G1280
G2481	U2404	G2319	G2242	G2069	U1979	G1874	U1796	U1680	A1566	G1462	G1369	G1283
G2485	G2405	A2322	U2245	A2070	G1980	G1875	G1797	G1681	G1567	C1463	C1370	G1283
G2486	U2406	G2323	U2246	C2071	U1981	C1881	U1798	G1682	A1569	G1464	G1371	A1284
G2487	A2407	G2324	A2247	C2072	U1982	U1882	G1799	U1683	A1570	U1372	A1285	A1286
G2488	G2408	G2325	G2248	C2073	U1982	U1883	G1799	U1683	A1571	A1373	A1286	A1286
G2489	G2409	G2326	U2249	U2074	U1991	G1884	A1801	G1684	A1572	U1468	A1378	C1297
G2490	A2412	A2327	G2250	C2078	U1992	A1885	A1805	G1685	G1573	G1475	U1379	C1297
U2491	G2413	G2328	U2251	U2079	U1993	A1885	C1806	G1685	G1581	U1476	U1379	C1298
G2492	G2414	G2329	U2252	A2082	C1996	U1898	G1807	G1709	G1584	G1482	A1383	G1299
G2493	G2415	G2330	G2253	G2083	C1997	A1899	A1808	U1709	C1386	G1490	A1308	A1301
G2494	C2416	G2331	U2254	U2086	A1998	A1900	A1809	A1713	C1386	A1490	G1309	A1308
G2495	C2417	G2332	G2255	A2087	A1999	A1901	G1810	U1714	A1590	G1491	G1387	G1308
C2498	A2418	C2333	U2256	G2088	C2000	G1906	G1811	G1715	A1593	G1498	G1388	G1310
C2499	G2419	U2334	G2257	A2088	C2001	G1907	G1812	G1715	A1597	C1499	U1394	G1311
G2502	G2420	A2335	U2258	G2089	C2002	C1908	G1813	G1720	A1598	G1501	U1395	U1316
G2503	G2421	G2340	C2261	G2093	C2003	G1909	C1816	U1720	A1598	G1501	G1398	G1317
U2504	U2423	G2341	U2262	C2096	C2004	C1909	G1817	U1725	U1609	U1506	U1409	U1326
G2505	C2424	U2343	G2263	U2096	C2005	U1911	U1818	G1726	U1602	C1507	C1320	A1327
G2506	A2425	G2344	U2264	U2105	G2026	A1912	A1819	U1726	U1602	C1507	C1320	A1327
G2507	G2426	U2345	G2265	G2106	A2012	A1913	A1820	U1729	U1603	A1508	A1413	A1326
G2498	C2427	G2345	U2266	U2107	A2013	C1914	G1822	G1730	A1608	A1509	A1416	A1326
G2499	G2428	G2346	U2267	G2108	A2014	A1918	G1823	A1735	A1609	G1510	G1416	A1326
G2500	U2429	U2347	A2273	U2109	A2019	A1919	G1824	U1735	A1610	A1515	G1417	A1328
G2501	A2430	G2348	G2274	U2110	C2022	C1920	U1825	G1738	C1611	A1522	G1418	A1329
G2502	U2431	U2349	A2275	G2111	C2023	U1923	U1826	A1745	A1614	G1524	A1419	A1330
G2503	A2432	G2350	G2276	U2112	G2024	C1924	G1827	A1746	A1615	G1524	A1420	A1331
G2504	G2433	G2351	U2277	U2113	G2025	C1925	A1828	U1747	A1616	A1525	G1423	G1332
G2505	C2434	G2352	A2278	A2114	U2026	G1929	G1829	G1748	C1526	G1526	G1424	G1333
G2506	U2435	G2353	G2279	A2115	G2027	G1930	G1831	C1748	G1645	G1530	G1433	G1334
G2507	G2436	U2354	U2280	U2116	U2028	G1931	C1832	G1757	G1646	G1530	A1434	G1335
G2508	U2437	G2355	G2281	U2117	U2029	A1936	U1834	U1758	U1647	G1530	A1433	G1336
G2509	G2438	G2356	G2282	U2118	A2030	A1937	U1835	G1764	U1648	A1535	A1434	A1337
G2510	A2439	G2357	C2283	U2119	A2031	A1938	G1836	U1765	G1653	C1536	G1435	G1338
G2511	U2440	G2358	G2284	U2120	A2032	U1939	C1837	G1765	G1653	G1537	C1437	G1339
G2512	G2441	U2359	U2285	G2121	G2033	A1940	U1838	G1765	G1653	G1538	U1438	A1341
G2513	C2442	G2360	G2286	U2122	G2034	U1941	A1847	G1773	A1535	A1536	G1438	A1342
G2514	U2443	G2361	C2287	U2123	A2035	U1942	A1848	C1774	A1536	G1537	U1438	A1343
G2515	G2444	G2362	U2288	G2124	G2036	U1943	A1849	U1775	A1537	G1538	G1441	U1344
G2516	C2445	G2363	U2289	G2125	A2037	U1944	G1850	G1776	G1653	G1539	U1442	G1345
G2517	U2446	G2364	G2290	G2126	U2038	U1945	G1851	G1776	G1653	G1540	G1443	U1352
G2518	G2447	G2365	U2291	U2127	G2039	U1946	G1852	G1776	G1653	G1540	U1443	A1353
G2519	A2448	G2366	U2292	G2128	U2040	U1947	G1853	G1776	G1653	G1540	U1443	G1354
G2520	U2449	G2367	U2293	G2129	U2041	U1948	A1854	G1776	G1653	G1540	U1443	G1355
G2521	G2450	G2368	U2294	U2130	A2042	U1949	A1854	G1776	G1653	G1540	U1443	G1356
G2522	C2451	G2369	U2295	U2131	C2043	U1950	A1854	G1776	G1653	G1540	U1443	G1356
G2523	U2452	G2370	U2296	U2132	C2044	U1951	A1854	G1776	G1653	G1540	U1443	G1356
G2524	G2453	G2371	U2297	U2133	C2045	U1952	A1854	G1776	G1653	G1540	U1443	G1356
G2525	C2454	G2372	U2298	U2134	C2046	U1953	A1854	G1776	G1653	G1540	U1443	G1356
G2526	U2455	G2373	U2299	U2135	C2047	U1954	A1854	G1776	G1653	G1540	U1443	G1356
G2527	G2456	G2374	U2300	U2136	C2048	U1955	A1854	G1776	G1653	G1540	U1443	G1356
G2528	C2457	G2375	U2301	U2137	C2049	U1956	A1854	G1776	G1653	G1540	U1443	G1356
G2529	U2458	G2376	U2302	U2138	C2050	U1957	A1854	G1776	G1653	G1540	U1443	G1356
G2530	G2459	G2377	U2303	U2139	C2051	U1958	A1854	G1776	G1653	G1540	U1443	G1356
G2531	U2460	G2378	U2304	U2140	C2052	U1959	A1854	G1776	G1653	G1540	U1443	G1356
G2532	C2461	G2379	U2305	U2141	C2053	U1960	A1854	G1776	G1653	G1540	U1443	G1356
G2533	U2462	G2380	U2306	U2142	C2054	U1961	A1854	G1776	G1653	G1540	U1443	G1356
G2534	G2463	G2381	U2307	U2143	C2055	U1962	A1854	G1776	G1653	G1540	U1443	G1356
G2535	C2464	G2382	U2308	U2144	C2056	U1963	A1854	G1776	G1653	G1540	U1443	G1356
G2536	U2465	G2383	U2309	U2145	C2057	U1964	A1854	G1776	G1653	G1540	U1443	G1356
G2537	G2466	G2384	U2310	U2146	C2058	U1965	A1854	G1776	G1653	G1540	U1443	G1356
G2538	C2467	G2385	U2311	U2147	C2059	U1966	A1854	G1776	G1653	G1540	U1443	G1356
G2539	U2468	G2386	U2312	U2148	C2060	U1967	A1854	G1776	G1653	G1540	U1443	G1356
G2540	G2469	G2387	U2313	U2149	C2061	U1968	A1854	G1776	G1653	G1540	U1443	G1356
G2541	C2470	G2388	U2314	U2150	C2062	U1969	A1854	G1776	G1653	G1540	U1443	G1356
G2542	U2471	G2389	U2315	U2151	C2063	U1970	A1854	G1776	G1653	G1540	U1443	G1356
G2543	G2472	G2390	U2316	U2152	C2064	U1971	A1854	G1776	G1653	G1540	U1443	G1356
G2544	C2473	G2391	U2317	U2153	C2065	U1972	A1854	G1776	G1653	G1540	U1443	G1356
G2545	U2474	G2392	U2318	U2154	C2066	U1973	A1854	G1776	G1653	G1540	U1443	G1356
G2546	G2475	G2393	U2319	U2155	C2067	U1974	A1854	G1776	G1653	G1540	U1443	G1356
G2547	C2476	G2394	U2320	U2156	C2068	U1975	A1854	G1776	G1653	G1540	U1443	G1356
G2548	U2477	G2395	U2321	U2157	C2069	U1976	A1854	G1776	G1653	G1540	U1443	G1356
G2549	G2478	G2396	U2322	U2158	C2070	U1977	A1854	G1776	G1653	G1540	U1443	G1356
G2550	C2479	G2397	U2323	U2159	C2071	U1978	A1854	G1776	G1653	G1540	U1443	G1356
G2551	U2480	G2398	U2324	U2160	C2072	U1979	A1854	G1776	G1653	G1540	U1443	G1356
G2552	G2481	G2399	U2325	U2161	C2073	U1980	A1854	G1776	G1653	G1540	U1443	G1356
G2553	C2482	G2400	U2326	U2162	C2074	U1981	A1854	G1776	G1653	G1540	U1443	G1356
G2554	U2483	G2401	U2327	U2163	C2075	U1982	A1854	G1776	G1653	G1540	U1443	G1356
G2555	G2484	G2402	U2328	U2164	C2076	U1983	A1854	G1776	G1653	G1540	U1443	G1356
G2556	C2485	G2403	U2329	U2165	C2077	U1984	A1854	G1776	G1653	G1540	U1443	G1356
G2557	U2486	G2404	U2330	U2166	C2078	U1985	A1854	G1776	G1653	G1540	U1443	G1356
G2558	G2487	G2405	U2331	U2167	C2079	U1986	A1854	G1776	G1653	G1540	U1443	G1356
G2559	C2488	G2406	U2332	U2168	C2080	U1987	A1854	G1776	G1653	G1540	U1443	G1356
G2560	U2489	G2407	U2333	U2169	C2081	U1988	A1854	G1776	G1653	G1540	U1443	G1356
G2561	G2490	G2408	U2334	U2170	C2082	U1989	A1854	G1776	G1653	G1540	U1443	G1356
G2562	C2491	G2409	U2335	U2171	C2083	U1990	A1854	G1776	G1653	G1540	U1443	G1356
G2563	U2492	G2410	U2336	U2172	C2084	U1991	A1854	G1776	G1653	G1540	U1443	G1356
G2564	G2493	G2411	U2337	U2173	C2085	U1992	A1854	G1776	G1653	G1540	U1443	G1356
G2565	C2494	G2412	U2338	U2174	C2086	U1993	A1854	G1776	G1653	G1540	U1443	G1356
G2566	U2495	G2413	U2339	U217								



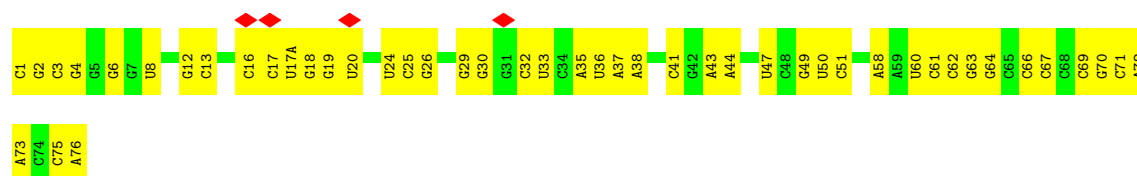
- Molecule 54: 5S ribosomal RNA



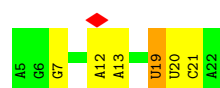
- Molecule 55: tRNA^{fMet}



- Molecule 55: tRNA^{fMet}



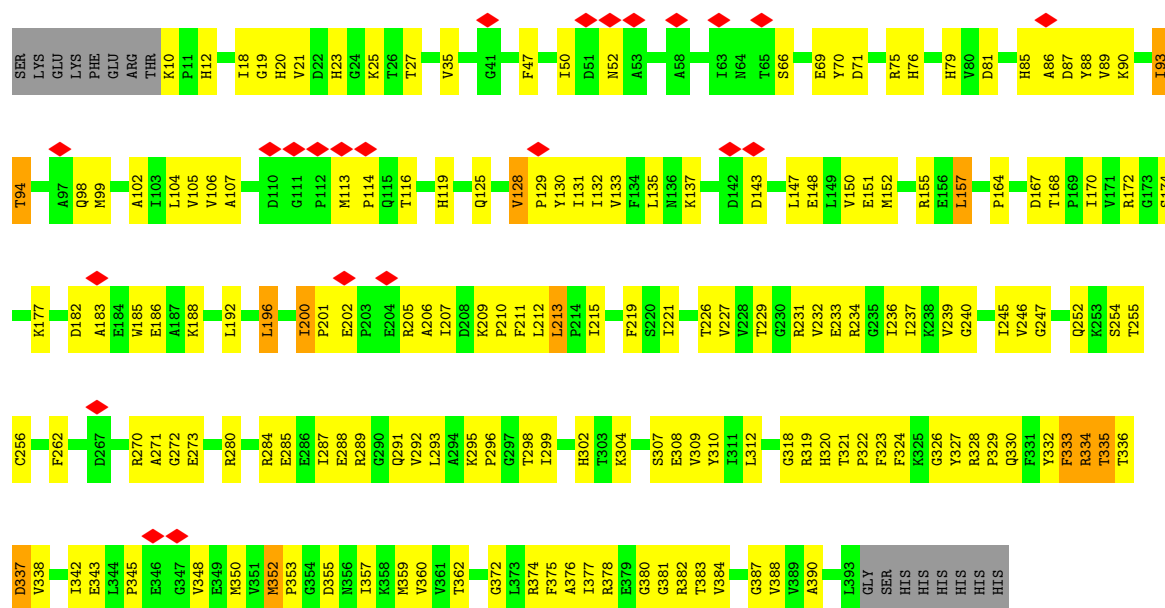
- Molecule 56: mRNA



- Molecule 57: tRNAPhe



• Molecule 58: Elongation factor Tu



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	7269	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	17.471	Depositor
Minimum map value	-9.094	Depositor
Average map value	0.116	Depositor
Map value standard deviation	0.814	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: GTP, FME

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	1.02	12/2852 (0.4%)
2	c	0.30	0/1586	0.86	5/2134 (0.2%)
3	d	0.29	0/1571	0.92	6/2113 (0.3%)
4	e	0.29	0/1435	0.95	4/1926 (0.2%)
5	f	0.31	0/1343	0.90	4/1816 (0.2%)
6	g	0.33	0/1122	0.97	5/1515 (0.3%)
7	h	0.35	0/1002	1.13	14/1350 (1.0%)
8	i	0.36	0/1046	1.01	6/1410 (0.4%)
9	j	0.29	0/1152	0.96	8/1551 (0.5%)
10	k	0.29	0/948	1.00	7/1268 (0.6%)
11	l	0.30	0/1054	0.93	4/1403 (0.3%)
12	m	0.29	0/1093	0.90	3/1460 (0.2%)
13	n	0.30	0/974	0.94	4/1301 (0.3%)
14	o	0.29	0/902	1.03	5/1209 (0.4%)
15	p	0.31	0/929	0.91	1/1242 (0.1%)
16	q	0.29	0/960	0.97	6/1278 (0.5%)
17	r	0.30	0/829	0.89	4/1107 (0.4%)
18	s	0.28	0/864	0.87	2/1156 (0.2%)
19	t	0.29	0/745	0.86	2/994 (0.2%)
20	u	0.28	0/788	1.00	8/1051 (0.8%)
21	v	0.30	0/766	0.90	2/1025 (0.2%)
22	w	0.28	0/582	0.90	0/769
23	x	0.29	0/635	0.88	3/848 (0.4%)
24	y	0.28	0/510	0.88	1/677 (0.1%)
25	z	0.28	0/453	0.85	1/605 (0.2%)
26	B	0.29	0/450	0.93	1/599 (0.2%)
27	C	0.32	0/417	0.78	0/554
28	D	0.29	0/380	0.84	1/498 (0.2%)
29	E	0.30	0/513	0.96	3/676 (0.4%)
30	F	0.31	0/303	0.83	0/397
31	G	0.30	0/1788	0.92	8/2408 (0.3%)
32	H	0.32	0/1652	0.91	4/2225 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.30	0/1665	1.00	14/2227 (0.6%)
34	J	0.32	0/1170	0.90	4/1573 (0.3%)
35	K	0.31	0/836	1.05	5/1128 (0.4%)
36	L	0.29	0/1196	0.94	7/1602 (0.4%)
37	M	0.30	0/989	0.95	5/1326 (0.4%)
38	N	0.29	0/1034	0.94	5/1375 (0.4%)
39	O	0.33	0/797	1.01	5/1077 (0.5%)
40	P	0.33	0/886	1.00	4/1195 (0.3%)
41	Q	0.33	0/969	1.11	10/1300 (0.8%)
42	R	0.32	0/893	0.98	2/1193 (0.2%)
43	S	0.30	0/817	0.93	1/1088 (0.1%)
44	T	0.28	0/722	0.85	2/964 (0.2%)
45	U	0.32	0/659	0.95	3/884 (0.3%)
46	V	0.30	0/658	0.93	0/881
47	W	0.33	0/545	1.02	2/731 (0.3%)
48	X	0.32	0/653	0.92	3/877 (0.3%)
49	Y	0.29	0/671	1.04	4/888 (0.5%)
50	Z	0.34	0/551	1.00	3/728 (0.4%)
51	a	0.32	0/1034	0.83	1/1387 (0.1%)
52	3	0.41	0/36963	0.47	1/57662 (0.0%)
53	1	0.40	0/69796	0.48	1/108888 (0.0%)
54	2	0.41	0/2872	0.47	0/4479
55	5	0.39	0/1832	0.45	0/2855
55	6	0.42	0/1832	0.48	0/2855
56	4	0.42	0/436	0.50	0/679
57	7	0.41	0/1809	0.49	0/2819
58	8	0.32	0/3013	0.97	16/4081 (0.4%)
All	All	0.38	0/166212	0.64	232/248159 (0.1%)

There are no bond length outliers.

All (232) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	Q	20	VAL	N-CA-C	9.69	117.74	108.15
12	m	53	MET	N-CA-C	-9.28	102.47	113.88
1	b	87	SER	N-CA-C	-9.15	101.91	113.43
26	B	53	VAL	N-CA-C	9.13	120.95	111.00
42	R	3	ILE	N-CA-C	8.50	120.06	108.84
8	i	4	VAL	N-CA-C	8.50	119.92	109.30
7	h	30	SER	N-CA-C	-8.40	102.59	113.17
49	Y	83	ASN	N-CA-C	-8.32	103.32	113.97
36	L	79	VAL	N-CA-C	-8.09	105.30	113.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R	2	ARG	N-CA-C	-7.98	102.03	113.21
7	h	117	LEU	N-CA-C	7.87	121.30	107.61
4	e	48	LEU	N-CA-C	-7.84	102.72	111.82
34	J	161	GLU	N-CA-C	7.84	120.92	111.82
1	b	210	ALA	N-CA-C	-7.83	105.69	114.62
33	I	46	ARG	N-CA-C	-7.81	103.21	112.89
47	W	66	LEU	N-CA-C	-7.67	103.53	113.12
7	h	9	GLN	N-CA-C	-7.52	102.76	112.23
44	T	43	ALA	N-CA-C	-7.46	103.16	111.82
58	8	196	LEU	N-CA-C	-7.46	103.64	112.89
58	8	152	MET	N-CA-C	7.40	119.04	110.97
39	O	77	VAL	N-CA-C	7.35	117.44	110.53
37	M	67	GLY	N-CA-C	-7.26	103.73	113.24
19	t	10	VAL	N-CA-C	7.25	118.04	110.72
19	t	13	ALA	N-CA-C	7.21	114.71	108.22
3	d	165	HIS	N-CA-C	7.11	118.68	111.07
16	q	31	TYR	N-CA-C	7.10	118.67	111.07
50	Z	29	ALA	N-CA-C	-7.09	104.52	113.02
41	Q	114	SER	N-CA-C	-7.07	103.50	111.07
5	f	47	ASN	N-CA-C	-7.04	104.49	113.23
13	n	79	LEU	N-CA-C	-7.03	99.52	110.42
58	8	200	ILE	N-CA-C	7.00	115.08	108.15
34	J	160	VAL	N-CA-C	6.96	117.07	110.53
39	O	16	ARG	N-CA-C	6.96	118.86	111.28
33	I	146	GLU	N-CA-C	6.90	118.45	111.07
20	u	96	LYS	N-CA-C	-6.88	100.28	110.46
3	d	140	ASP	N-CA-C	-6.85	104.93	113.28
37	M	13	ILE	N-CA-C	-6.79	104.23	110.82
49	Y	84	LYS	N-CA-C	-6.78	104.49	112.89
18	s	60	HIS	N-CA-C	6.74	118.42	111.14
11	l	96	LYS	N-CA-C	-6.69	104.06	111.82
32	H	112	ALA	N-CA-C	6.67	119.12	111.11
35	K	31	GLY	N-CA-C	-6.64	106.43	114.66
7	h	43	LYS	N-CA-C	-6.63	103.87	112.23
33	I	97	LEU	N-CA-C	6.61	119.31	111.71
16	q	41	ALA	N-CA-C	-6.56	104.75	112.89
7	h	51	TYR	N-CA-C	6.53	118.39	111.28
38	N	88	GLU	N-CA-C	-6.51	104.60	112.54
20	u	10	VAL	N-CA-C	6.45	117.77	108.48
43	S	24	ALA	N-CA-C	-6.42	105.08	113.17
7	h	35	VAL	N-CA-C	-6.35	102.94	111.44
33	I	166	LYS	CA-C-N	6.34	127.77	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	I	166	LYS	C-N-CA	6.34	127.77	119.84
58	8	320	HIS	N-CA-C	-6.34	106.51	114.56
40	P	70	ALA	N-CA-C	-6.32	104.50	111.82
32	H	171	ARG	N-CA-C	6.31	119.23	109.07
1	b	11	GLY	N-CA-C	-6.30	106.84	113.58
58	8	157	LEU	N-CA-C	-6.28	103.96	111.69
7	h	42	ARG	N-CA-C	-6.27	105.12	112.89
40	P	115	ILE	N-CA-C	6.27	114.09	107.76
35	K	25	TYR	N-CA-C	6.23	117.95	111.03
38	N	89	TYR	N-CA-C	-6.21	102.83	110.65
45	U	69	ASP	N-CA-C	6.20	118.55	111.11
2	c	152	PRO	N-CA-C	-6.18	105.11	113.40
36	L	60	ALA	N-CA-C	-6.18	105.22	112.89
49	Y	5	SER	N-CA-C	-6.15	105.53	113.16
5	f	4	ALA	N-CA-C	-6.12	104.51	112.23
41	Q	54	VAL	N-CA-C	6.11	117.38	108.58
14	o	11	ALA	N-CA-C	6.11	118.90	111.82
50	Z	8	ASN	N-CA-C	6.08	123.74	110.80
31	G	175	ALA	N-CA-C	6.04	117.56	110.97
40	P	73	VAL	N-CA-C	-6.02	107.42	113.20
51	a	31	LYS	N-CA-C	-6.00	105.92	113.18
9	j	7	LYS	CA-C-N	5.98	127.32	119.84
9	j	7	LYS	C-N-CA	5.98	127.32	119.84
1	b	197	ALA	N-CA-C	5.96	120.28	113.19
49	Y	28	ARG	N-CA-C	5.94	117.83	111.36
36	L	135	LYS	N-CA-C	-5.94	104.89	111.36
11	l	92	LEU	N-CA-C	-5.93	104.90	111.36
31	G	92	ASN	N-CA-C	5.92	120.52	113.12
12	m	126	ILE	N-CA-C	5.92	117.71	109.55
23	x	6	VAL	N-CA-C	5.90	116.54	110.82
50	Z	55	HIS	N-CA-C	-5.89	105.18	112.90
7	h	37	LYS	N-CA-C	-5.88	105.60	112.89
17	r	44	GLY	N-CA-C	-5.88	105.68	112.73
7	h	79	PRO	N-CA-C	5.88	119.73	111.33
29	E	61	LEU	CA-C-N	5.87	125.55	119.56
29	E	61	LEU	C-N-CA	5.87	125.55	119.56
45	U	20	VAL	N-CA-C	5.87	116.94	108.48
23	x	21	LEU	N-CA-C	5.87	119.78	111.92
5	f	112	VAL	N-CA-C	5.86	115.78	106.88
20	u	29	SER	N-CA-C	5.85	118.44	111.71
32	H	70	ALA	N-CA-C	-5.84	106.78	114.31
4	e	6	TYR	N-CA-C	-5.84	105.05	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	O	20	GLN	N-CA-C	-5.83	104.88	112.23
33	I	184	LYS	CA-C-N	5.82	125.84	119.90
33	I	184	LYS	C-N-CA	5.82	125.84	119.90
7	h	44	ALA	N-CA-C	-5.82	104.90	112.23
1	b	145	MET	N-CA-C	-5.81	104.95	112.68
36	L	16	LYS	N-CA-C	-5.80	108.00	114.62
35	K	66	ALA	N-CA-C	5.80	113.23	108.07
3	d	90	GLN	N-CA-C	5.80	118.85	109.86
6	g	63	ALA	N-CA-C	-5.80	104.93	112.23
31	G	131	LYS	N-CA-C	5.79	117.27	111.07
2	c	174	SER	N-CA-C	5.78	119.22	111.24
41	Q	43	LYS	N-CA-C	5.75	122.53	109.81
3	d	115	GLN	N-CA-C	-5.75	106.27	113.28
44	T	59	VAL	N-CA-C	-5.74	105.25	110.82
1	b	68	ARG	N-CA-C	-5.73	104.00	111.74
20	u	75	ALA	N-CA-C	-5.73	106.21	113.43
9	j	139	VAL	N-CA-C	5.72	116.53	108.36
10	k	25	LEU	N-CA-C	5.71	118.23	110.35
40	P	69	CYS	N-CA-C	-5.70	106.28	113.18
14	o	61	GLN	N-CA-C	-5.70	106.22	112.72
3	d	139	LYS	N-CA-C	-5.68	106.35	113.28
38	N	47	VAL	N-CA-C	-5.68	105.28	113.07
1	b	85	ASN	N-CA-C	5.67	118.98	112.97
7	h	106	PHE	N-CA-C	5.67	117.55	110.91
9	j	79	GLY	N-CA-C	-5.66	107.56	114.92
17	r	49	ILE	N-CA-C	5.66	116.03	108.11
29	E	57	VAL	N-CA-C	5.66	116.30	110.36
33	I	192	ALA	N-CA-C	5.66	120.00	113.38
35	K	98	GLU	N-CA-C	5.64	114.98	108.49
36	L	124	SER	N-CA-C	-5.64	105.22	111.36
8	i	27	LEU	N-CA-C	-5.63	106.25	113.23
11	l	98	ALA	N-CA-C	-5.63	106.46	113.38
9	j	126	ALA	N-CA-C	-5.62	106.55	113.41
6	g	62	LEU	N-CA-C	-5.62	105.92	112.89
10	k	39	ILE	N-CA-C	5.62	116.84	108.46
12	m	107	GLY	N-CA-C	-5.62	107.34	115.27
33	I	102	TYR	N-CA-C	-5.62	105.07	111.14
15	p	15	ASP	N-CA-C	5.62	117.89	108.23
17	r	50	GLY	N-CA-C	-5.62	99.87	113.18
58	8	93	ILE	N-CA-C	-5.62	104.69	112.50
1	b	67	LYS	N-CA-C	5.61	117.39	111.28
33	I	136	VAL	N-CA-C	5.61	116.31	109.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	k	32	TYR	N-CA-C	5.60	118.37	110.14
6	g	67	ALA	N-CA-C	-5.60	105.26	111.36
48	X	69	LYS	N-CA-C	-5.59	101.75	110.42
53	1	1020	A	C2'-C3'-O3'	5.59	117.89	109.50
41	Q	9	LYS	CA-C-N	5.57	126.35	120.11
41	Q	9	LYS	C-N-CA	5.57	126.35	120.11
25	z	42	ALA	N-CA-C	-5.57	104.61	111.40
41	Q	3	VAL	N-CA-C	5.56	118.85	111.17
13	n	66	ALA	N-CA-C	-5.56	106.46	113.18
20	u	76	THR	N-CA-C	-5.56	106.50	113.72
13	n	67	PHE	N-CA-C	-5.53	106.70	113.50
48	X	5	LYS	N-CA-C	5.51	118.00	111.33
20	u	6	ARG	N-CA-C	5.51	117.72	111.11
34	J	141	ASP	N-CA-C	-5.50	105.36	111.36
58	8	183	ALA	N-CA-C	5.50	118.79	111.75
2	c	113	SER	N-CA-C	5.49	117.41	110.33
58	8	237	ILE	N-CA-C	5.48	115.78	108.11
2	c	69	ALA	N-CA-C	-5.48	106.76	113.50
6	g	94	ILE	N-CA-C	5.48	116.47	109.30
10	k	71	ARG	CA-C-N	5.47	126.68	119.84
10	k	71	ARG	C-N-CA	5.47	126.68	119.84
16	q	24	TYR	N-CA-C	5.47	118.16	109.96
39	O	22	THR	N-CA-C	-5.46	105.41	111.36
31	G	222	GLU	N-CA-C	-5.45	105.89	112.54
58	8	372	GLY	N-CA-C	-5.45	108.21	114.69
37	M	117	GLN	N-CA-C	-5.43	105.38	112.23
31	G	46	VAL	CB-CA-C	-5.43	108.59	114.35
58	8	23	HIS	N-CA-C	-5.43	105.39	112.23
52	3	1201	A	C2'-C3'-O3'	5.43	117.64	109.50
28	D	20	ALA	N-CA-C	-5.42	106.51	113.01
9	j	45	THR	CA-C-N	5.41	125.08	119.56
9	j	45	THR	C-N-CA	5.41	125.08	119.56
33	I	104	MET	N-CA-C	-5.41	105.04	111.69
58	8	285	GLU	N-CA-C	5.41	119.72	113.18
5	f	42	VAL	N-CA-C	5.39	116.24	108.48
58	8	221	ILE	N-CA-C	5.37	116.18	108.93
4	e	11	VAL	N-CA-C	5.36	115.57	110.42
8	i	111	THR	N-CA-C	-5.36	105.47	112.23
20	u	100	GLU	N-CA-C	-5.36	101.57	109.18
31	G	165	ALA	N-CA-C	5.35	117.81	111.33
16	q	49	ARG	N-CA-C	-5.33	106.73	113.18
7	h	78	GLY	N-CA-C	5.33	123.22	112.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	k	33	ALA	N-CA-C	-5.33	102.12	110.17
37	M	3	GLN	N-CA-C	-5.33	105.52	112.23
14	o	58	ILE	N-CA-C	5.32	116.14	111.56
38	N	64	ILE	N-CA-C	5.31	116.23	108.53
1	b	12	ARG	N-CA-C	-5.30	105.95	112.90
3	d	131	THR	N-CA-C	5.30	117.81	111.71
36	L	147	ASN	N-CA-C	-5.29	106.59	112.57
14	o	55	GLU	N-CA-C	-5.28	102.04	109.96
41	Q	25	ALA	N-CA-C	5.26	119.53	113.38
33	I	204	SER	N-CA-C	-5.25	105.72	111.82
1	b	16	VAL	N-CA-C	-5.25	100.64	108.46
31	G	184	ALA	N-CA-C	5.24	117.22	108.99
47	W	17	VAL	N-CA-C	5.23	116.99	109.51
6	g	64	ALA	N-CA-C	-5.23	105.64	112.23
58	8	202	GLU	N-CA-C	5.22	116.23	109.65
4	e	19	PHE	N-CA-C	-5.20	106.79	112.72
13	n	68	ALA	N-CA-C	-5.19	106.05	112.38
21	v	26	PHE	CA-C-N	5.18	124.94	119.76
21	v	26	PHE	C-N-CA	5.18	124.94	119.76
34	J	153	ALA	N-CA-C	-5.18	105.70	112.23
33	I	129	VAL	N-CA-C	5.17	116.03	108.53
32	H	125	ARG	N-CA-C	-5.17	106.83	112.72
1	b	207	ALA	N-CA-C	-5.16	105.34	111.69
8	i	21	PRO	N-CA-C	5.16	116.99	110.70
16	q	34	ALA	N-CA-C	-5.15	105.75	111.36
11	l	19	LEU	N-CA-C	5.15	117.17	110.53
45	U	54	LEU	N-CA-C	5.14	117.62	111.71
23	x	57	VAL	N-CA-C	-5.13	104.56	111.44
41	Q	122	LYS	N-CA-C	-5.13	105.87	111.82
14	o	12	THR	N-CA-C	5.11	117.59	111.71
39	O	44	THR	N-CA-C	5.10	118.39	110.17
58	8	94	THR	N-CA-C	-5.10	105.63	111.14
9	j	46	PRO	N-CA-C	5.10	120.47	113.84
7	h	6	GLN	N-CA-C	-5.10	105.91	111.82
7	h	29	ASP	N-CA-C	5.09	116.89	109.71
8	i	37	PHE	N-CA-C	5.09	116.64	111.14
24	y	55	THR	N-CA-C	-5.09	105.43	111.69
58	8	128	VAL	CA-C-N	5.07	126.17	119.84
58	8	128	VAL	C-N-CA	5.07	126.17	119.84
1	b	245	THR	N-CA-C	-5.06	102.69	110.58
20	u	95	PHE	N-CA-C	5.06	118.36	110.32
2	c	71	ALA	N-CA-C	-5.05	106.62	112.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	M	126	CYS	N-CA-C	5.05	117.48	109.50
10	k	72	PRO	N-CA-C	5.05	122.87	112.47
31	G	162	VAL	N-CA-C	5.05	115.85	108.53
38	N	57	VAL	N-CA-C	5.04	115.65	110.36
17	r	14	VAL	N-CA-C	5.04	115.38	108.12
36	L	85	GLN	N-CA-C	5.04	116.48	108.67
41	Q	102	ASP	N-CA-C	5.03	121.52	110.80
16	q	50	ARG	N-CA-C	-5.03	107.70	113.88
8	i	127	SER	N-CA-C	-5.02	106.00	111.82
48	X	19	GLU	N-CA-C	-5.02	106.00	111.82
18	s	59	GLU	N-CA-C	5.01	116.59	111.03
35	K	92	THR	N-CA-C	5.01	121.48	110.80
33	I	77	GLU	N-CA-C	-5.00	105.92	112.23

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	96	0
2	c	1565	0	1616	59	0
3	d	1552	0	1619	50	0
4	e	1411	0	1447	48	0
5	f	1323	0	1374	36	0
6	g	1111	0	1148	42	0
7	h	989	0	1025	57	0
8	i	1032	0	1088	40	0
9	j	1129	0	1162	38	0
10	k	939	0	1012	33	0
11	l	1045	0	1117	47	0
12	m	1074	0	1157	35	0
13	n	961	0	1000	26	0
14	o	892	0	923	30	0
15	p	917	0	965	34	0
16	q	947	0	1022	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	r	816	0	839	23	0
18	s	857	0	922	43	0
19	t	739	0	807	27	0
20	u	780	0	834	18	0
21	v	753	0	780	23	0
22	w	575	0	592	18	0
23	x	625	0	655	16	0
24	y	509	0	543	24	0
25	z	449	0	491	11	0
26	B	444	0	461	20	0
27	C	410	0	440	11	0
28	D	377	0	418	20	0
29	E	504	0	574	12	0
30	F	302	0	343	23	0
31	G	1757	0	1787	62	0
32	H	1625	0	1699	63	0
33	I	1643	0	1710	78	0
34	J	1157	0	1199	35	0
35	K	818	0	808	47	0
36	L	1182	0	1240	43	0
37	M	979	0	1034	40	0
38	N	1022	0	1070	53	0
39	O	787	0	828	46	0
40	P	870	0	878	49	0
41	Q	955	0	1019	39	0
42	R	884	0	944	48	0
43	S	805	0	847	42	0
44	T	714	0	737	28	0
45	U	649	0	666	29	0
46	V	649	0	691	34	0
47	W	536	0	552	17	0
48	X	638	0	665	21	0
49	Y	665	0	714	14	0
50	Z	545	0	579	35	0
51	a	1027	0	1092	39	0
52	3	33012	0	16618	601	0
53	1	62317	0	31346	1008	0
54	2	2568	0	1303	44	0
55	5	1640	0	836	24	0
55	6	1640	0	837	36	0
56	4	388	0	196	4	0
57	7	1619	0	821	57	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	8	2958	0	2972	127	0
59	5	10	0	10	0	0
60	7	11	0	8	3	0
61	8	32	0	12	2	0
All	All	153212	0	104249	3255	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 13.

All (3255) 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)
53:1:1906:G:H2'	53:1:1907:G:H5''	1.26	1.13
38:N:98:ARG:HD2	38:N:103:VAL:HG21	1.30	1.08
1:b:216:ARG:HD3	1:b:217:PRO:HD2	1.40	1.04
53:1:45:G:H5''	53:1:46:G:H5'	1.39	1.02
32:H:171:ARG:HG2	32:H:173:PRO:HD3	1.40	1.01
12:m:45:GLN:HE21	53:1:2485:G:H5''	1.24	1.00
35:K:3:HIS:H	35:K:92:THR:HG22	1.26	0.99
2:c:142:VAL:HG22	2:c:143:PRO:HD2	1.44	0.98
52:3:484:G:H4'	52:3:485:U:H5''	1.43	0.98
42:R:91:ARG:HH12	53:1:887:U:H5'	1.27	0.97
32:H:171:ARG:HG3	52:3:1107:C:OP1	1.67	0.94
57:7:7:A:H3'	57:7:8:U:H5''	1.48	0.93
35:K:18:VAL:HG23	35:K:19:PRO:HD3	1.50	0.93
52:3:1259:C:H3'	52:3:1260:G:H5''	1.48	0.93
53:1:1906:G:C2'	53:1:1907:G:H5''	1.97	0.93
12:m:12:MET:HA	53:1:910:A:H62	1.32	0.93
5:f:75:VAL:HG13	5:f:76:ILE:HD12	1.53	0.91
36:L:110:ARG:HH21	36:L:122:GLU:HG3	1.36	0.90
9:j:7:LYS:HG2	53:1:538:A:H4'	1.53	0.90
38:N:128:LYS:HD2	52:3:966:G:H21	1.33	0.90
34:J:55:VAL:HG13	34:J:56:PRO:HD3	1.53	0.89
38:N:83:THR:HG21	38:N:102:PHE:HB3	1.54	0.89
42:R:23:GLY:HA2	42:R:68:LEU:HD11	1.55	0.89
53:1:1020:A:H1'	53:1:1021:A:OP2	1.72	0.89
38:N:53:LEU:HD12	38:N:54:VAL:HG13	1.54	0.89
51:a:166:ASP:OD1	53:1:2122:U:H5'	1.72	0.89
36:L:111:GLY:HA2	36:L:118:ARG:HD3	1.55	0.88
37:M:13:ILE:O	37:M:17:GLN:HG3	1.73	0.88
16:q:111:LYS:HG3	17:r:48:LYS:HD2	1.54	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:u:73:ASN:HD21	20:u:75:ALA:HB3	1.39	0.87
1:b:251:THR:HG22	1:b:252:LYS:H	1.39	0.87
1:b:216:ARG:HH22	53:1:691:C:H5''	1.39	0.87
53:1:1394:U:H4'	53:1:1603:A:H4'	1.57	0.87
53:1:1645:G:H5''	53:1:1646:C:H5'	1.57	0.86
33:I:195:ASN:HD22	33:I:198:LEU:HG	1.39	0.85
33:I:4:LEU:HD23	52:3:406:G:H5''	1.56	0.85
53:1:1077:A:H2'	53:1:1078:U:H5'	1.58	0.85
31:G:20:ARG:HG2	52:3:831:A:H5'	1.60	0.84
32:H:168:ARG:HH22	52:3:1107:C:H4'	1.42	0.84
36:L:12:LEU:HD12	36:L:13:PRO:HD2	1.60	0.83
7:h:3:LEU:HD12	7:h:5:LEU:H	1.42	0.83
8:i:52:LEU:HD21	8:i:73:PRO:HB3	1.58	0.83
36:L:85:GLN:NE2	55:6:32:C:H4'	1.94	0.83
52:3:405:U:H3'	52:3:406:G:H5'	1.61	0.83
18:s:25:ARG:HE	18:s:74:ILE:HG23	1.43	0.83
41:Q:23:LEU:HD22	41:Q:29:LYS:HE3	1.58	0.83
1:b:16:VAL:HG12	1:b:203:VAL:H	1.43	0.82
46:V:56:ASP:HB3	46:V:81:ALA:HB2	1.62	0.81
52:3:664:G:H22	52:3:741:G:H1	1.27	0.81
2:c:66:GLY:HA3	53:1:2787:C:H5'	1.62	0.81
7:h:55:VAL:HA	53:1:1084:A:H4'	1.61	0.81
53:1:2432:A:H1'	55:6:75:C:H5'	1.61	0.81
9:j:27:ARG:HH22	53:1:1142:A:H4'	1.43	0.81
40:P:118:ASN:OD1	52:3:718:A:H5'	1.80	0.81
1:b:62:ARG:HD3	1:b:90:ILE:HD11	1.63	0.81
53:1:962:G:H21	53:1:2250:G:H1	1.28	0.81
23:x:11:PRO:HG3	23:x:30:PRO:HD2	1.63	0.81
6:g:112:LYS:HE2	53:1:2220:U:H5''	1.61	0.81
13:n:60:VAL:HG22	53:1:1454:C:O2'	1.81	0.80
39:O:88:MET:HG3	39:O:89:ARG:HD3	1.64	0.80
14:o:88:LYS:HG2	14:o:116:GLN:HG2	1.64	0.80
34:J:60:GLN:NE2	34:J:61:LYS:HG3	1.96	0.80
3:d:76:PRO:HA	3:d:82:GLY:HA2	1.64	0.80
10:k:48:PRO:HG3	52:3:1422:G:H5'	1.62	0.80
20:u:85:ARG:HD3	20:u:87:GLU:HG3	1.64	0.79
52:3:1230:C:H5'	55:5:30:G:H5''	1.64	0.79
53:1:2800:A:H3'	53:1:2801:G:H5'	1.62	0.79
37:M:4:ASP:HB2	37:M:80:PRO:HG3	1.63	0.79
43:S:26:LEU:HD11	43:S:46:LYS:HG3	1.64	0.79
53:1:275:C:H2'	53:1:276:U:H4'	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:9:GLU:HB2	50:Z:10:PRO:HD3	1.63	0.79
53:1:2553:G:H3'	53:1:2554:U:H5''	1.65	0.79
58:8:215:ILE:HD13	58:8:287:ILE:HD11	1.62	0.79
39:O:27:GLU:HA	39:O:30:LYS:HE2	1.64	0.79
28:D:12:ARG:HE	28:D:44:VAL:HG11	1.46	0.78
38:N:49:GLN:HG2	38:N:102:PHE:HZ	1.48	0.78
32:H:109:GLU:HB2	32:H:143:LEU:HD22	1.66	0.78
53:1:2277:G:H2'	53:1:2278:A:H5''	1.65	0.78
1:b:16:VAL:HG12	1:b:203:VAL:HG22	1.65	0.78
49:Y:28:ARG:HH12	52:3:1437:A:H5''	1.47	0.78
38:N:65:THR:HG21	52:3:1130:A:OP1	1.84	0.78
28:D:11:LYS:HE3	53:1:686:U:H5''	1.65	0.77
52:3:327:A:O2'	52:3:328:C:H4'	1.84	0.77
42:R:114:PRO:HG2	52:3:1228:C:H5''	1.66	0.77
13:n:38:LEU:HB3	13:n:39:PRO:HD3	1.67	0.77
34:J:107:GLY:HA3	52:3:9:G:H5'	1.66	0.77
7:h:23:LEU:HD13	7:h:118:ILE:HG12	1.65	0.77
52:3:1201:A:H1'	52:3:1202:U:OP2	1.83	0.77
54:2:3:C:H2'	54:2:4:C:H5''	1.64	0.77
1:b:48:ILE:HD11	1:b:51:ARG:HA	1.67	0.76
46:V:65:PRO:HG2	52:3:234:C:H4'	1.68	0.76
52:3:1197:A:H2'	52:3:1198:G:H5''	1.66	0.76
53:1:49:A:H5'	53:1:51:G:O4'	1.86	0.76
52:3:769:G:H4'	52:3:1513:A:H4'	1.67	0.76
57:7:52:G:H2'	57:7:53:G:H8	1.51	0.76
3:d:77:ILE:HG23	3:d:78:TRP:HD1	1.50	0.76
4:e:65:LEU:HD22	54:2:42:C:C4	2.21	0.76
15:p:59:THR:HG22	15:p:72:VAL:HG12	1.68	0.76
26:B:11:LYS:HE3	53:1:2616:C:H5''	1.66	0.76
43:S:30:ILE:H	43:S:30:ILE:HD12	1.50	0.76
1:b:139:THR:HG23	1:b:160:TYR:HB2	1.68	0.76
43:S:50:LEU:HD12	43:S:51:PRO:HD2	1.67	0.76
53:1:1045:C:H5'	53:1:1046:A:H5''	1.66	0.76
32:H:56:ILE:HG22	32:H:63:ILE:HD11	1.67	0.76
3:d:40:ARG:HH22	53:1:1246:A:H4'	1.50	0.76
53:1:917:A:H5''	53:1:2268:A:H61	1.51	0.76
1:b:213:ARG:HH21	53:1:1566:A:H5'	1.49	0.75
44:T:6:ALA:HA	44:T:9:LYS:HD3	1.66	0.75
57:7:6:G:H3'	57:7:7:A:H5''	1.67	0.75
30:F:2:LYS:HG2	30:F:4:ARG:HH21	1.51	0.75
35:K:3:HIS:N	35:K:92:THR:HG22	2.02	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:528:A:C2	53:1:2042:A:H2'	2.22	0.75
51:a:163:TYR:HB2	51:a:171:ILE:HD11	1.69	0.75
53:1:1141:U:H4'	53:1:1142:A:O4'	1.87	0.75
35:K:6:ILE:H	35:K:6:ILE:HD12	1.51	0.75
53:1:2114:A:H61	53:1:2117:A:H62	1.35	0.75
3:d:126:VAL:HG23	3:d:156:ASN:ND2	2.01	0.74
52:3:501:C:H2'	52:3:502:A:H8	1.52	0.74
53:1:1807:G:H2'	53:1:1808:A:H5'	1.68	0.74
20:u:73:ASN:ND2	20:u:75:ALA:HB3	2.03	0.74
2:c:151:THR:HB	2:c:152:PRO:HD3	1.70	0.74
41:Q:109:ARG:HB2	41:Q:118:VAL:HG21	1.69	0.74
7:h:33:VAL:HA	53:1:1055:G:H4'	1.68	0.74
42:R:24:VAL:HG23	42:R:28:ARG:HB3	1.70	0.73
53:1:704:G:H2'	53:1:726:G:H22	1.53	0.73
23:x:4:CYS:HB3	23:x:9:LYS:H	1.53	0.73
45:U:67:ILE:H	45:U:67:ILE:HD12	1.53	0.73
10:k:121:GLU:HG2	10:k:122:VAL:HG23	1.68	0.73
9:j:26:GLY:HA3	53:1:1140:C:H5'	1.69	0.73
17:r:78:ARG:HH12	53:1:990:A:H61	1.36	0.73
57:7:74:C:H4'	58:8:52:ASN:HD22	1.54	0.73
8:i:25:PRO:HG2	57:7:55:U:H3'	1.71	0.73
53:1:1053:C:H2'	53:1:1054:A:H5''	1.69	0.73
52:3:1200:C:H5''	52:3:1201:A:H3'	1.69	0.73
1:b:52:HIS:HA	1:b:216:ARG:HB3	1.69	0.73
15:p:38:ARG:NE	52:3:345:C:H5'	2.04	0.73
30:F:16:ILE:HG22	30:F:23:ILE:HD11	1.71	0.73
32:H:106:ARG:HG2	32:H:107:LYS:HG2	1.69	0.73
54:2:72:G:H21	54:2:104:A:H62	1.35	0.72
31:G:46:VAL:HG23	31:G:47:PRO:HD3	1.72	0.72
43:S:80:ARG:O	43:S:83:VAL:HG12	1.88	0.72
53:1:1801:A:H5''	53:1:2203:U:H2'	1.71	0.72
21:v:80:HIS:HB2	21:v:87:GLN:HE22	1.54	0.72
57:7:64:A:H2	58:8:328:ARG:HH12	1.37	0.72
4:e:109:ARG:HH22	42:R:2:ARG:HH11	1.36	0.72
9:j:7:LYS:HE3	53:1:538:A:H5''	1.71	0.72
11:l:48:ARG:HD3	53:1:666:A:H4'	1.71	0.72
53:1:2391:G:H4'	53:1:2392:A:OP1	1.90	0.72
26:B:30:ASP:HB3	26:B:35:GLU:H	1.54	0.72
53:1:2296:U:H5''	53:1:2297:A:OP1	1.90	0.72
34:J:119:VAL:HG21	34:J:122:VAL:HG13	1.71	0.72
42:R:63:VAL:HG22	42:R:68:LEU:HD23	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:168:ARG:HH12	52:3:1107:C:H5'	1.55	0.72
44:T:78:THR:O	44:T:82:GLU:HG3	1.89	0.72
53:1:546:U:H2'	53:1:547:A:H4'	1.72	0.72
1:b:83:ASP:OD2	1:b:86:ARG:HG2	1.89	0.72
31:G:102:ASN:HD21	52:3:1074:G:H1'	1.53	0.72
37:M:14:ARG:HE	37:M:74:ILE:HG23	1.55	0.72
44:T:4:THR:OG1	52:3:659:U:H5''	1.90	0.72
52:3:730:G:H2'	52:3:731:G:H5'	1.72	0.71
30:F:24:ARG:NH2	30:F:36:ARG:HD3	2.05	0.71
20:u:42:LYS:HD2	53:1:499:U:H5''	1.72	0.71
39:O:65:TYR:HB3	43:S:95:LEU:HD11	1.72	0.71
46:V:12:VAL:HG23	46:V:21:VAL:HG13	1.72	0.71
6:g:128:HIS:HB2	6:g:144:VAL:HG23	1.72	0.71
32:H:118:SER:O	32:H:122:GLN:HG2	1.90	0.71
2:c:142:VAL:CG2	2:c:143:PRO:HD2	2.20	0.71
36:L:23:ALA:O	36:L:26:VAL:HG12	1.91	0.71
3:d:79:ARG:HH21	53:1:448:U:C4'	2.04	0.71
53:1:2286:G:H5''	53:1:2287:A:OP1	1.90	0.71
31:G:130:LYS:HZ1	52:3:1160:G:H4'	1.55	0.71
12:m:12:MET:HA	53:1:910:A:N6	2.04	0.70
57:7:6:G:C3'	57:7:7:A:H5''	2.20	0.70
58:8:133:VAL:HG23	58:8:168:THR:HG21	1.73	0.70
19:t:48:GLN:HE21	19:t:55:VAL:HG12	1.54	0.70
9:j:1:MET:HE1	17:r:13:ARG:HE	1.55	0.70
33:I:67:LEU:HD22	52:3:546:A:OP2	1.90	0.70
42:R:76:ILE:HG13	42:R:80:MET:HE2	1.73	0.70
35:K:37:HIS:HB2	35:K:63:ASN:ND2	2.05	0.70
45:U:31:ARG:HB2	52:3:310:G:H5''	1.74	0.70
54:2:3:C:C2'	54:2:4:C:H5''	2.21	0.70
25:z:29:ARG:HE	53:1:1183:U:H5''	1.57	0.70
1:b:216:ARG:HD3	1:b:217:PRO:CD	2.20	0.70
10:k:86:LEU:H	10:k:86:LEU:HD12	1.57	0.70
11:l:95:LEU:HG	11:l:100:ILE:HD11	1.72	0.70
53:1:310:A:C2'	53:1:311:A:H5''	2.21	0.70
14:o:94:ARG:NH2	53:1:2293:G:H5''	2.06	0.69
7:h:34:THR:O	7:h:37:LYS:HG2	1.91	0.69
52:3:955:U:H3	52:3:1225:A:H61	1.40	0.69
2:c:61:THR:HB	2:c:63:PRO:HD2	1.75	0.69
25:z:29:ARG:NE	53:1:1183:U:H5''	2.08	0.69
39:O:48:ARG:HB2	39:O:48:ARG:NH1	2.07	0.69
52:3:1497:G:O2'	52:3:1498:U:H5'	1.91	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1077:A:C2'	53:1:1078:U:H5'	2.22	0.69
58:8:35:VAL:HG22	58:8:186:GLU:HG3	1.72	0.69
33:I:104:MET:HE1	33:I:170:LEU:HB2	1.74	0.69
42:R:113:LYS:HB2	42:R:114:PRO:HD3	1.75	0.69
54:2:3:C:C3'	54:2:4:C:H5''	2.23	0.69
9:j:96:ARG:NH2	53:1:2639:A:H4'	2.08	0.69
53:1:121:G:H4'	53:1:149:A:H5'	1.73	0.69
7:h:5:LEU:O	7:h:9:GLN:HG3	1.93	0.69
46:V:31:PRO:HB2	46:V:32:ILE:HD12	1.75	0.69
57:7:7:A:H3'	57:7:8:U:C5'	2.23	0.69
52:3:1251:A:O2'	52:3:1370:G:H5'	1.94	0.68
16:q:87:VAL:HA	17:r:49:ILE:HD11	1.75	0.68
33:I:4:LEU:HD23	52:3:406:G:C5'	2.22	0.68
39:O:48:ARG:HB2	39:O:48:ARG:HH11	1.58	0.68
42:R:27:THR:HG21	52:3:1328:C:H5''	1.75	0.68
53:1:1105:U:H2'	53:1:1106:G:H5''	1.74	0.68
58:8:211:PHE:HB3	58:8:295:LYS:HB2	1.75	0.68
33:I:12:ARG:NH2	33:I:31:CYS:SG	2.65	0.68
42:R:91:ARG:NH1	53:1:887:U:H5'	2.07	0.68
41:Q:30:ARG:HG3	52:3:363:A:H5''	1.76	0.68
53:1:45:G:H5''	53:1:46:G:C5'	2.18	0.68
53:1:1837:C:H2'	53:1:1899:A:H61	1.59	0.68
53:1:2743:U:H2'	53:1:2744:G:H5''	1.74	0.68
2:c:48:ILE:HG23	2:c:84:LEU:HD11	1.73	0.68
31:G:110:ILE:HD11	31:G:151:LYS:HA	1.74	0.68
12:m:75:GLU:HB2	12:m:90:GLU:OE2	1.94	0.68
53:1:435:C:H2'	53:1:436:C:H5'	1.76	0.68
3:d:12:LEU:HD21	3:d:193:VAL:HG11	1.76	0.68
10:k:38:ILE:HD11	10:k:59:LYS:HD3	1.76	0.68
6:g:5:LEU:HD13	6:g:13:GLY:HA2	1.76	0.68
3:d:117:ARG:HH21	3:d:184:ASP:HA	1.57	0.67
53:1:2267:A:H5''	53:1:2268:A:H5'	1.75	0.67
8:i:58:ILE:H	8:i:58:ILE:HD12	1.59	0.67
26:B:46:GLY:HA3	26:B:54:ILE:HG22	1.75	0.67
29:E:24:LYS:HE2	29:E:46:LYS:HZ1	1.59	0.67
20:u:42:LYS:HB2	53:1:499:U:H4'	1.74	0.67
53:1:580:U:H2'	53:1:581:C:C6	2.29	0.67
13:n:29:VAL:HB	13:n:75:ILE:HD11	1.76	0.67
31:G:101:THR:HG23	31:G:174:GLU:HG2	1.76	0.67
9:j:81:ILE:HG23	9:j:82:GLY:H	1.58	0.67
31:G:107:ARG:O	31:G:111:LYS:HG3	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:o:21:LEU:HD11	14:o:23:ALA:HB2	1.77	0.67
35:K:18:VAL:CG2	35:K:19:PRO:HD3	2.22	0.67
54:2:13:G:H21	54:2:16:G:H1'	1.60	0.67
58:8:10:LYS:HB3	58:8:76:HIS:HB2	1.77	0.67
8:i:23:VAL:HG13	8:i:26:ALA:HB3	1.75	0.67
53:1:310:A:H2'	53:1:311:A:H5''	1.75	0.67
4:e:15:LEU:HG	4:e:21:TYR:HE2	1.59	0.66
42:R:25:GLY:H	52:3:1329:A:H5''	1.59	0.66
52:3:514:C:H2'	52:3:515:G:H8	1.60	0.66
57:7:25:C:H3'	57:7:26:A:H5''	1.76	0.66
39:O:6:ILE:H	39:O:6:ILE:HD12	1.60	0.66
16:q:55:GLN:O	16:q:58:GLN:HG2	1.95	0.66
23:x:36:ARG:HA	23:x:47:THR:HA	1.78	0.66
35:K:10:VAL:HG12	35:K:58:HIS:HB3	1.75	0.66
52:3:889:A:H5'	52:3:891:U:H1'	1.77	0.66
4:e:134:GLN:HG3	4:e:140:ILE:HG21	1.76	0.66
8:i:119:ALA:HB3	53:1:1082:U:OP1	1.96	0.66
43:S:50:LEU:HD12	43:S:51:PRO:CD	2.26	0.66
45:U:75:ILE:O	45:U:78:VAL:HG12	1.95	0.66
1:b:145:MET:HG2	1:b:152:GLN:HG3	1.77	0.66
53:1:215:G:H4'	53:1:216:A:H4'	1.78	0.66
55:5:75:C:C3'	55:5:76:A:H5''	2.26	0.66
34:J:60:GLN:HE22	34:J:61:LYS:HG3	1.58	0.66
53:1:1796:U:H2'	53:1:1797:G:H8	1.61	0.66
46:V:12:VAL:HG23	46:V:13:SER:H	1.61	0.66
52:3:924:C:H2'	52:3:925:G:H8	1.61	0.66
9:j:37:ARG:HG2	9:j:39:LYS:HG3	1.78	0.66
39:O:80:THR:HG22	39:O:82:LYS:H	1.60	0.66
53:1:2628:C:H3'	53:1:2629:U:H5'	1.78	0.66
30:F:37:GLN:OE1	53:1:1125:G:H5'	1.96	0.65
39:O:52:LEU:HD21	39:O:59:LYS:HD3	1.76	0.65
16:q:10:ARG:HH21	53:1:1216:G:H5''	1.61	0.65
35:K:91:ARG:HG2	52:3:737:C:OP1	1.96	0.65
52:3:501:C:H2'	52:3:502:A:C8	2.30	0.65
1:b:93:VAL:HG11	1:b:115:ILE:HD11	1.79	0.65
38:N:49:GLN:N	38:N:50:PRO:HD2	2.12	0.65
20:u:10:VAL:HG11	20:u:69:VAL:HB	1.77	0.65
48:X:39:ILE:HG23	48:X:66:VAL:HA	1.77	0.65
12:m:13:HIS:HE1	53:1:2265:U:H4'	1.61	0.65
23:x:5:GLN:HG2	23:x:48:LEU:HD22	1.77	0.65
53:1:796:C:H2'	53:1:797:G:H8	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:L:69:ARG:HH11	36:L:95:ARG:HD2	1.60	0.65
53:1:528:A:H2	53:1:2042:A:H2'	1.61	0.65
54:2:3:C:H3'	54:2:4:C:H5''	1.79	0.65
41:Q:5:GLN:HE21	52:3:880:C:H3'	1.61	0.65
41:Q:45:ASN:ND2	52:3:528:C:H41	1.95	0.65
49:Y:28:ARG:NH1	52:3:1437:A:H5''	2.11	0.65
57:7:52:G:H2'	57:7:53:G:C8	2.32	0.65
9:j:35:ARG:HB2	9:j:54:ILE:HD11	1.78	0.65
7:h:45:GLY:HA2	7:h:49:GLY:HA2	1.79	0.65
11:l:55:MET:HE3	53:1:2392:A:N1	2.11	0.65
48:X:30:LEU:HB2	48:X:48:ILE:HG22	1.77	0.65
53:1:807:U:H2'	53:1:808:G:H8	1.61	0.65
53:1:1909:C:H2'	53:1:1910:G:H8	1.62	0.65
12:m:75:GLU:CD	53:1:957:C:H5'	2.21	0.64
47:W:35:SER:HA	47:W:71:ASP:HB3	1.78	0.64
53:1:796:C:H2'	53:1:797:G:C8	2.32	0.64
3:d:34:ALA:HA	3:d:94:GLN:HE21	1.61	0.64
2:c:155:VAL:HG21	53:1:2618:G:H21	1.61	0.64
31:G:36:LYS:HE2	52:3:848:C:OP1	1.97	0.64
52:3:715:A:H2'	52:3:716:A:C8	2.32	0.64
53:1:481:G:H1'	53:1:506:G:N2	2.12	0.64
58:8:151:GLU:HG3	58:8:170:ILE:HG13	1.78	0.64
22:w:36:GLN:NE2	22:w:39:THR:HA	2.12	0.64
34:J:55:VAL:HG13	34:J:56:PRO:CD	2.24	0.64
48:X:69:LYS:HE3	52:3:1319:A:H5''	1.80	0.64
52:3:29:U:O2'	52:3:30:U:H5'	1.97	0.64
1:b:260:LYS:HE2	53:1:2227:A:H5''	1.78	0.64
32:H:71:ARG:O	32:H:74:ILE:HG22	1.98	0.64
40:P:116:PRO:HB3	52:3:676:A:H1'	1.78	0.64
52:3:372:C:N4	52:3:387:U:H2'	2.11	0.64
58:8:345:PRO:HG2	58:8:348:VAL:HB	1.80	0.64
1:b:175:LEU:HD13	53:1:1799:G:C5	2.32	0.64
53:1:1186:G:H2'	53:1:1187:G:O4'	1.97	0.64
41:Q:56:LEU:HD12	41:Q:60:PHE:HB2	1.79	0.64
52:3:539:A:H2'	52:3:540:G:C8	2.33	0.64
52:3:701:U:H4'	52:3:703:G:H1'	1.78	0.64
52:3:1429:A:H2'	52:3:1430:A:H8	1.63	0.64
58:8:377:ILE:HG22	58:8:384:VAL:HG23	1.80	0.64
31:G:20:ARG:CG	52:3:831:A:H5'	2.27	0.64
32:H:171:ARG:CG	32:H:173:PRO:HD3	2.24	0.64
41:Q:23:LEU:HB3	41:Q:26:CYS:SG	2.38	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Q:82:ARG:HH11	52:3:552:U:H5'	1.62	0.64
53:1:2423:U:O2'	53:1:2425:A:H2'	1.97	0.64
7:h:118:ILE:HB	7:h:119:PRO:HD3	1.80	0.64
38:N:113:LYS:HD2	38:N:118:ARG:O	1.98	0.64
46:V:74:LEU:HD23	46:V:75:VAL:N	2.13	0.64
52:3:355:C:H5'	52:3:355:C:H6	1.63	0.64
53:1:1028:A:N6	53:1:1125:G:H2'	2.13	0.64
30:F:7:VAL:HG12	30:F:35:GLN:HG3	1.80	0.64
33:I:12:ARG:HG2	33:I:37:PRO:HG3	1.78	0.64
43:S:30:ILE:HD12	43:S:30:ILE:N	2.12	0.64
58:8:206:ALA:HB1	58:8:209:LYS:HD3	1.80	0.64
5:f:17:LYS:HB3	5:f:24:THR:HB	1.80	0.63
5:f:26:LYS:HD3	5:f:27:GLY:N	2.13	0.63
5:f:72:ASN:O	5:f:75:VAL:HG12	1.97	0.63
22:w:66:GLU:OE1	22:w:68:LYS:HG3	1.98	0.63
36:L:142:ARG:CG	55:6:41:C:H4'	2.28	0.63
2:c:170:VAL:HG12	2:c:171:THR:H	1.61	0.63
52:3:422:C:H4'	52:3:423:G:H5''	1.81	0.63
58:8:147:LEU:O	58:8:150:VAL:HG12	1.97	0.63
35:K:29:ILE:HG22	35:K:34:GLY:HA3	1.80	0.63
43:S:9:GLU:HB2	43:S:62:ARG:HH12	1.62	0.63
9:j:26:GLY:HA3	53:1:1140:C:C5'	2.27	0.63
46:V:46:HIS:ND1	46:V:70:LYS:HD3	2.13	0.63
49:Y:23:ARG:HH22	52:3:1447:A:N6	1.96	0.63
52:3:1506:U:O2'	52:3:1507:A:H5'	1.99	0.63
53:1:2238:G:H2'	53:1:2238:G:N3	2.14	0.63
58:8:215:ILE:HD12	58:8:291:GLN:HB2	1.80	0.63
2:c:12:THR:HG22	2:c:13:ARG:H	1.64	0.63
5:f:85:LYS:HG2	5:f:87:GLN:HE22	1.64	0.63
9:j:27:ARG:H	9:j:27:ARG:HD2	1.64	0.63
44:T:68:TYR:HB2	52:3:754:C:H4'	1.81	0.63
4:e:107:VAL:HB	4:e:108:PRO:HD3	1.80	0.63
31:G:206:ILE:H	31:G:206:ILE:HD12	1.62	0.63
33:I:131:ILE:HG12	52:3:620:C:C2	2.33	0.63
53:1:69:C:H2'	53:1:70:G:C8	2.34	0.63
5:f:93:TYR:OH	5:f:159:LYS:HE3	1.98	0.63
28:D:24:THR:HG23	28:D:27:GLY:H	1.62	0.63
33:I:30:LYS:HE2	52:3:411:A:H2'	1.80	0.63
35:K:78:PHE:HA	35:K:84:VAL:HG11	1.81	0.63
31:G:182:VAL:HG12	31:G:195:VAL:HG13	1.81	0.63
42:R:106:ARG:HH21	42:R:112:ARG:HH21	1.47	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:514:C:H2'	52:3:515:G:C8	2.34	0.63
4:e:84:ILE:HD11	53:1:2311:A:H1'	1.81	0.63
23:x:66:VAL:HG13	23:x:67:LEU:HD22	1.80	0.63
28:D:3:ARG:O	28:D:6:GLN:NE2	2.32	0.63
32:H:21:TRP:HA	39:O:95:GLY:HA2	1.80	0.63
52:3:1414:U:H2'	52:3:1415:G:H8	1.64	0.62
53:1:1089:A:H2	53:1:1090:A:H62	1.46	0.62
39:O:44:THR:HG22	39:O:70:HIS:HA	1.81	0.62
53:1:704:G:H2'	53:1:726:G:N2	2.13	0.62
47:W:40:PRO:HG2	47:W:43:ILE:HG12	1.81	0.62
29:E:14:LYS:HD3	29:E:22:LYS:HE2	1.81	0.62
29:E:32:LEU:HD23	29:E:35:LYS:HD2	1.81	0.62
3:d:147:LEU:HB3	3:d:186:VAL:HG12	1.81	0.62
52:3:1379:G:O2'	52:3:1380:U:H5'	1.99	0.62
36:L:36:SER:O	36:L:39:GLU:HG2	1.98	0.62
52:3:1218:C:H2'	52:3:1219:A:C8	2.33	0.62
35:K:18:VAL:HG11	35:K:58:HIS:CD2	2.35	0.62
53:1:2443:C:H2'	53:1:2444:G:H8	1.64	0.62
2:c:50:VAL:HG22	2:c:51:THR:H	1.65	0.62
15:p:92:ARG:HD3	53:1:1753:G:OP1	1.99	0.62
35:K:96:VAL:HG22	35:K:97:THR:H	1.65	0.62
52:3:358:U:H2'	52:3:359:G:C8	2.35	0.62
53:1:1251:C:O2'	53:1:1252:G:H3'	2.00	0.62
53:1:616:A:H2'	53:1:617:G:O4'	1.99	0.62
53:1:1981:A:H5''	53:1:1982:U:OP2	2.00	0.62
11:l:38:GLN:HG3	53:1:805:G:H5''	1.81	0.62
33:I:145:ARG:HH21	33:I:147:LYS:HG2	1.64	0.62
53:1:554:U:H2'	53:1:555:G:O4'	2.00	0.62
53:1:1071:G:OP1	53:1:1071:G:H3'	1.99	0.62
6:g:84:ALA:HB2	6:g:90:LEU:HD13	1.82	0.61
35:K:3:HIS:H	35:K:92:THR:CG2	2.07	0.61
52:3:673:A:H2'	52:3:674:G:C8	2.35	0.61
58:8:212:LEU:HB3	58:8:234:ARG:HB2	1.81	0.61
1:b:16:VAL:CG1	1:b:203:VAL:HG22	2.30	0.61
18:s:98:LYS:HD2	53:1:2012:G:OP1	2.00	0.61
28:D:12:ARG:NE	28:D:44:VAL:HG11	2.15	0.61
36:L:46:LEU:HD12	36:L:47:GLU:N	2.15	0.61
3:d:143:LEU:HD22	3:d:185:LYS:HG3	1.83	0.61
38:N:114:LYS:HE2	52:3:1187:G:H5'	1.81	0.61
39:O:31:ARG:HD2	39:O:32:THR:HG23	1.82	0.61
47:W:38:ILE:H	47:W:38:ILE:HD12	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1373:A:H4'	53:1:2212:A:H1'	1.81	0.61
57:7:25:C:C3'	57:7:26:A:H5''	2.31	0.61
1:b:59:GLN:HA	53:1:1568:G:H5'	1.83	0.61
13:n:47:VAL:C	13:n:50:PRO:HD2	2.26	0.61
32:H:96:VAL:CG2	32:H:97:PRO:HD2	2.30	0.61
53:1:2800:A:H3'	53:1:2801:G:C5'	2.30	0.61
57:7:62:C:C3'	57:7:63:G:H5''	2.31	0.61
2:c:61:THR:CB	2:c:63:PRO:HD2	2.29	0.61
14:o:77:ALA:O	14:o:80:GLU:HG3	2.00	0.61
15:p:31:VAL:HG12	15:p:38:ARG:O	2.00	0.61
37:M:92:PRO:HD2	37:M:124:ILE:HG12	1.82	0.61
58:8:308:GLU:HG2	58:8:309:VAL:N	2.15	0.61
2:c:11:MET:HE3	2:c:25:THR:HG22	1.81	0.61
22:w:35:ARG:HA	22:w:54:THR:HG23	1.83	0.61
37:M:10:LEU:HD11	37:M:126:CYS:SG	2.40	0.61
53:1:441:U:O2'	53:1:442:G:H5'	2.01	0.61
1:b:30:ALA:HB3	1:b:31:PRO:HD3	1.81	0.61
1:b:251:THR:HG22	1:b:252:LYS:N	2.13	0.61
10:k:108:ARG:HG3	10:k:116:ILE:HD13	1.82	0.61
32:H:112:ALA:HB3	32:H:184:ASN:HD22	1.65	0.61
34:J:60:GLN:HA	34:J:63:MET:HE2	1.82	0.61
43:S:26:LEU:HD13	43:S:47:LEU:HD13	1.81	0.61
53:1:1045:C:P	53:1:1047:G:H5'	2.40	0.61
50:Z:13:VAL:HG13	50:Z:15:LEU:HG	1.81	0.61
52:3:129:A:O2'	52:3:130:A:H5''	2.01	0.61
52:3:1413:A:H2	52:3:1487:G:H22	1.48	0.61
53:1:2291:U:H2'	53:1:2292:U:C6	2.36	0.61
53:1:2799:A:C2'	53:1:2800:A:H5'	2.30	0.61
52:3:372:C:H41	52:3:387:U:H2'	1.65	0.61
53:1:615:U:H5''	53:1:616:A:OP2	2.00	0.61
53:1:1713:A:H61	53:1:1745:A:H61	1.49	0.61
53:1:2682:A:H61	53:1:2728:U:H1'	1.66	0.61
57:7:62:C:H3'	57:7:63:G:H5''	1.83	0.61
5:f:88:LEU:HD21	5:f:95:ALA:HB2	1.82	0.60
35:K:51:ILE:C	35:K:53:LYS:H	2.08	0.60
53:1:329:G:O4'	53:1:477:A:H1'	2.00	0.60
53:1:2698:U:H2'	53:1:2699:C:C6	2.36	0.60
7:h:56:ARG:HD3	53:1:1084:A:O4'	2.01	0.60
8:i:123:ALA:HB1	53:1:1081:U:H4'	1.83	0.60
25:z:27:GLY:HA3	25:z:37:ARG:HH21	1.65	0.60
40:P:126:ARG:NH1	52:3:692:U:H5''	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2266:A:H4'	53:1:2267:A:N3	2.16	0.60
1:b:159:THR:HG21	53:1:1819:A:H5''	1.83	0.60
24:y:41:HIS:CE1	53:1:96:C:H4'	2.37	0.60
35:K:66:ALA:HB1	35:K:67:PRO:HD2	1.83	0.60
58:8:308:GLU:HG2	58:8:309:VAL:H	1.66	0.60
9:j:96:ARG:HH21	53:1:2639:A:H4'	1.66	0.60
18:s:83:LYS:O	18:s:84:ARG:NH2	2.35	0.60
23:x:63:ILE:O	23:x:66:VAL:HG12	2.00	0.60
52:3:1432:G:H1'	52:3:1468:A:N6	2.16	0.60
15:p:105:LYS:HE3	15:p:108:ARG:HH21	1.66	0.60
38:N:10:ARG:HB2	38:N:105:ARG:HH22	1.67	0.60
60:7:101:PHE:CD1	58:8:229:THR:HG21	2.35	0.60
27:C:20:TYR:OH	53:1:2348:U:H5'	2.01	0.60
44:T:88:ARG:H	44:T:88:ARG:NE	1.99	0.60
5:f:49:LEU:HD13	5:f:71:LEU:HD21	1.83	0.60
32:H:49:ALA:HA	32:H:74:ILE:HD13	1.84	0.60
43:S:2:LYS:HD2	52:3:1049:U:H2'	1.83	0.60
51:a:218:MET:HE2	53:1:2174:C:H1'	1.82	0.60
53:1:20:C:H2'	53:1:21:A:H8	1.66	0.60
53:1:864:G:O2'	53:1:865:C:H5'	2.01	0.60
53:1:2286:G:H4'	53:1:2287:A:O5'	2.01	0.60
14:o:18:LEU:HD12	14:o:19:GLN:N	2.16	0.60
28:D:26:ASN:OD1	53:1:682:G:H5'	2.01	0.60
32:H:45:GLU:HG3	32:H:46:LEU:HD22	1.83	0.60
53:1:225:C:H2'	53:1:226:A:O4'	2.01	0.60
53:1:2605:U:H2'	53:1:2606:C:C6	2.37	0.60
58:8:75:ARG:HH22	58:8:201:PRO:HA	1.66	0.60
58:8:374:ARG:HH22	58:8:376:ALA:HB2	1.67	0.60
20:u:42:LYS:HD2	53:1:499:U:C5'	2.32	0.60
21:v:9:ARG:HH22	54:2:76:G:H5'	1.67	0.60
21:v:75:GLN:HB2	21:v:92:VAL:HG13	1.83	0.60
53:1:1539:U:H2'	53:1:1540:G:H8	1.66	0.60
53:1:1919:A:H2'	53:1:1920:C:H5'	1.82	0.60
3:d:79:ARG:HH21	53:1:448:U:H4'	1.67	0.60
10:k:110:GLU:O	10:k:113:MET:HE3	2.02	0.60
37:M:26:MET:HG3	37:M:58:LEU:HB3	1.82	0.60
39:O:53:ILE:HG12	52:3:1060:U:H5''	1.83	0.60
53:1:598:U:H2'	53:1:599:A:H8	1.66	0.60
53:1:2398:U:H2'	53:1:2399:G:C8	2.37	0.60
1:b:29:PHE:CE2	1:b:31:PRO:HB2	2.36	0.59
34:J:92:ARG:HB2	34:J:127:TYR:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:V:46:HIS:HB2	46:V:70:LYS:HD3	1.84	0.59
53:1:2799:A:H2'	53:1:2800:A:H5'	1.83	0.59
2:c:200:ASP:O	2:c:201:LEU:HD22	2.02	0.59
39:O:43:PRO:HA	52:3:1151:A:H5'	1.84	0.59
40:P:54:SER:HB2	52:3:694:A:H5''	1.83	0.59
52:3:1280:A:O2'	52:3:1281:C:H5'	2.03	0.59
5:f:148:ARG:HD2	5:f:161:VAL:HG23	1.83	0.59
7:h:30:SER:O	53:1:1054:A:H4'	2.02	0.59
19:t:13:ALA:HB1	24:y:33:ALA:HB1	1.83	0.59
38:N:59:LYS:O	38:N:60:LEU:HD22	2.02	0.59
42:R:89:ARG:HB2	42:R:96:VAL:HG12	1.84	0.59
43:S:89:ARG:NH1	43:S:89:ARG:O	2.34	0.59
49:Y:28:ARG:HH12	52:3:1437:A:C5'	2.15	0.59
53:1:1842:G:H1	53:1:1898:U:H3	1.48	0.59
6:g:24:GLY:HA3	53:1:2093:G:O5'	2.03	0.59
52:3:1033:G:H2'	52:3:1034:G:H5''	1.85	0.59
55:5:75:C:H3'	55:5:76:A:H5''	1.84	0.59
32:H:13:ILE:HG22	32:H:14:VAL:HG23	1.83	0.59
40:P:23:HIS:HB3	40:P:30:ILE:HG23	1.84	0.59
11:l:41:ARG:HA	53:1:671:C:H41	1.67	0.59
12:m:75:GLU:OE1	53:1:957:C:H5'	2.02	0.59
14:o:88:LYS:HE2	14:o:116:GLN:NE2	2.18	0.59
28:D:31:LEU:HB3	28:D:35:ARG:HH12	1.68	0.59
33:I:43:ARG:HH12	52:3:511:C:H4'	1.68	0.59
53:1:575:A:O2'	53:1:576:U:H5'	2.02	0.59
53:1:942:G:H2'	53:1:943:A:O4'	2.03	0.59
53:1:2156:G:C2'	53:1:2157:G:H5'	2.33	0.59
53:1:2537:U:H2'	53:1:2538:C:C6	2.37	0.59
53:1:2849:U:H4'	53:1:2868:A:C2	2.38	0.59
4:e:137:PHE:HB2	4:e:140:ILE:HD13	1.84	0.59
16:q:5:ARG:NH1	53:1:585:G:N7	2.50	0.59
22:w:35:ARG:NH2	53:1:2355:G:H1'	2.18	0.59
29:E:24:LYS:HE2	29:E:46:LYS:NZ	2.18	0.59
31:G:62:ARG:HG3	31:G:62:ARG:HH11	1.67	0.59
47:W:18:GLN:HG3	47:W:19:GLU:H	1.65	0.59
52:3:1156:G:H21	52:3:1179:A:H61	1.51	0.59
53:1:1856:U:H2'	53:1:1857:G:O4'	2.03	0.59
56:4:20:U:H2'	56:4:21:C:C6	2.37	0.59
1:b:242:HIS:O	1:b:244:VAL:HG13	2.02	0.59
1:b:245:THR:HG23	1:b:247:TRP:H	1.67	0.59
3:d:163:ASN:HB2	53:1:322:A:OP2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:56:ARG:HB2	53:1:1084:A:H1'	1.84	0.59
11:l:17:LYS:HD3	53:1:663:G:H5''	1.85	0.59
40:P:13:LYS:HD2	40:P:13:LYS:N	2.18	0.59
52:3:1540:U:O2	52:3:1540:U:H3'	2.02	0.59
53:1:2480:C:H2'	53:1:2481:G:O4'	2.03	0.59
54:2:30:C:H2'	54:2:31:C:O4'	2.03	0.59
38:N:49:GLN:CG	38:N:102:PHE:HZ	2.15	0.59
52:3:1330:U:H2'	52:3:1331:G:O4'	2.02	0.59
58:8:309:VAL:HG11	58:8:359:MET:HE1	1.84	0.59
10:k:86:LEU:HD12	10:k:86:LEU:N	2.17	0.58
40:P:18:GLY:O	40:P:81:LEU:HA	2.03	0.58
45:U:52:LEU:O	45:U:52:LEU:HD12	2.03	0.58
52:3:952:U:H2'	52:3:953:G:H8	1.68	0.58
52:3:1316:G:H2'	52:3:1317:C:H5''	1.85	0.58
53:1:2743:U:C3'	53:1:2744:G:H5''	2.33	0.58
7:h:33:VAL:HG12	53:1:1055:G:H5''	1.84	0.58
20:u:14:THR:OG1	20:u:15:GLY:N	2.36	0.58
49:Y:43:LYS:HB2	49:Y:86:ALA:HB2	1.84	0.58
52:3:225:C:C3'	52:3:226:G:H5''	2.33	0.58
53:1:2834:G:H2'	53:1:2879:A:H61	1.69	0.58
6:g:1:MET:HB3	6:g:3:VAL:HG13	1.86	0.58
15:p:54:LEU:HA	15:p:76:HIS:HD2	1.68	0.58
53:1:2297:A:H62	53:1:2319:G:H1'	1.68	0.58
6:g:75:LEU:HD23	6:g:75:LEU:H	1.67	0.58
7:h:38:MET:HE1	53:1:1058:U:H5'	1.84	0.58
32:H:96:VAL:HG22	32:H:97:PRO:HD2	1.86	0.58
46:V:14:ASP:HA	46:V:20:ILE:HG13	1.85	0.58
53:1:807:U:H2'	53:1:808:G:C8	2.38	0.58
53:1:2130:U:H4'	53:1:2134:A:H4'	1.85	0.58
1:b:160:TYR:HB3	1:b:193:GLU:HG2	1.85	0.58
19:t:77:ARG:NE	53:1:63:A:H4'	2.19	0.58
27:C:5:ARG:NH1	27:C:25:ASN:OD1	2.36	0.58
51:a:10:VAL:HA	51:a:13:GLU:HG2	1.85	0.58
52:3:78:A:H2'	52:3:79:G:O4'	2.03	0.58
52:3:1170:A:H2'	52:3:1171:A:O4'	2.04	0.58
53:1:779:U:H2'	53:1:780:G:C8	2.38	0.58
53:1:1133:A:H4'	53:1:1134:A:H5''	1.85	0.58
58:8:90:LYS:O	58:8:93:ILE:HG22	2.03	0.58
8:i:12:VAL:HG12	53:1:1061:U:C2	2.39	0.58
28:D:12:ARG:HH11	28:D:44:VAL:HG11	1.68	0.58
45:U:26:ASN:HD21	45:U:31:ARG:N	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1512:U:H2'	52:3:1513:A:C8	2.39	0.58
58:8:333:PHE:O	58:8:334:ARG:HG2	2.03	0.58
3:d:163:ASN:OD1	53:1:323:C:H5''	2.03	0.58
35:K:15:SER:O	35:K:18:VAL:HG22	2.04	0.58
36:L:68:VAL:HA	36:L:137:ARG:HD3	1.85	0.58
39:O:57:VAL:O	39:O:58:ASN:HB2	2.02	0.58
44:T:42:PHE:CD2	44:T:55:LEU:HD22	2.39	0.58
52:3:252:U:O2	52:3:252:U:H2'	2.03	0.58
53:1:974:G:H1'	53:1:975:A:C8	2.38	0.58
53:1:1367:A:H2'	53:1:1368:G:H5'	1.85	0.58
53:1:1664:A:H61	53:1:1996:C:H42	1.49	0.58
53:1:2515:C:H2'	53:1:2516:A:H8	1.69	0.58
53:1:2636:C:H2'	53:1:2637:U:C6	2.39	0.58
55:6:71:C:H2'	55:6:72:A:C8	2.38	0.58
58:8:312:LEU:O	58:8:318:GLY:HA3	2.04	0.58
27:C:45:HIS:ND1	53:1:2372:U:H4'	2.19	0.58
31:G:160:LEU:HD23	31:G:180:ILE:HG21	1.86	0.58
38:N:128:LYS:HD2	52:3:966:G:N2	2.12	0.58
42:R:54:THR:O	42:R:57:ASP:OD1	2.21	0.58
43:S:27:LYS:O	43:S:31:SER:HB2	2.03	0.58
53:1:677:A:O2'	53:1:2071:A:H5'	2.03	0.58
53:1:2398:U:H2'	53:1:2399:G:H8	1.67	0.58
53:1:2515:C:H2'	53:1:2516:A:C8	2.39	0.58
2:c:149:ASN:HB3	53:1:2572:A:OP2	2.04	0.58
6:g:31:VAL:N	6:g:32:PRO:HD2	2.19	0.58
9:j:27:ARG:HD2	9:j:27:ARG:N	2.19	0.58
53:1:45:G:C5'	53:1:46:G:H5'	2.25	0.58
53:1:804:A:H2'	53:1:806:C:C4	2.39	0.58
5:f:93:TYR:CZ	5:f:159:LYS:HE3	2.39	0.58
18:s:15:GLN:HE22	53:1:1266:G:C5'	2.16	0.58
28:D:26:ASN:CG	53:1:682:G:H5'	2.29	0.58
41:Q:29:LYS:NZ	41:Q:58:ASN:HD22	2.01	0.58
45:U:26:ASN:ND2	45:U:31:ARG:O	2.36	0.58
52:3:16:A:O2'	52:3:17:U:H5'	2.04	0.58
52:3:784:A:H4'	53:1:1837:C:OP1	2.03	0.58
53:1:278:A:H2'	53:1:278:A:N3	2.19	0.58
58:8:20:HIS:CE1	58:8:113:MET:HE2	2.39	0.58
43:S:1:ALA:HA	52:3:1203:C:OP1	2.04	0.57
51:a:165:ASN:HD22	51:a:169:GLY:HA2	1.69	0.57
52:3:1366:C:H2'	52:3:1367:C:C6	2.39	0.57
53:1:971:G:H2'	53:1:972:A:O4'	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1105:U:C2'	53:1:1106:G:H5''	2.33	0.57
24:y:24:GLU:HA	24:y:28:LEU:HG	1.86	0.57
38:N:114:LYS:HB2	38:N:117:LEU:HD12	1.85	0.57
53:1:2156:G:H2'	53:1:2157:G:H5'	1.85	0.57
53:1:2427:C:H5''	53:1:2429:G:H5'	1.86	0.57
5:f:75:VAL:CG1	5:f:76:ILE:HD12	2.31	0.57
41:Q:113:ARG:HB2	41:Q:118:VAL:O	2.04	0.57
48:X:30:LEU:H	48:X:30:LEU:HD12	1.70	0.57
52:3:526:C:H2'	52:3:527:G:H4'	1.87	0.57
52:3:1106:G:O2'	52:3:1107:C:H5'	2.05	0.57
58:8:324:PHE:HE1	58:8:350:MET:HG2	1.68	0.57
16:q:80:ASN:CG	53:1:1151:A:H4'	2.29	0.57
22:w:71:LYS:HB3	22:w:73:ARG:HG3	1.85	0.57
31:G:111:LYS:HA	31:G:114:LYS:HD2	1.87	0.57
32:H:171:ARG:HG3	52:3:1107:C:P	2.44	0.57
43:S:63:CYS:HB3	43:S:67:GLY:H	1.70	0.57
50:Z:8:ASN:O	50:Z:9:GLU:HG3	2.05	0.57
4:e:135:ILE:HG12	42:R:6:ILE:HD11	1.87	0.57
14:o:51:ALA:HB3	14:o:78:VAL:CG1	2.34	0.57
14:o:62:LEU:HD21	14:o:70:ALA:HA	1.87	0.57
19:t:50:LEU:HD12	19:t:50:LEU:H	1.70	0.57
24:y:7:ARG:HD3	24:y:8:GLU:OE1	2.03	0.57
34:J:148:SER:OG	34:J:151:MET:HG2	2.04	0.57
50:Z:44:ARG:HH12	50:Z:48:LYS:HG2	1.68	0.57
52:3:59:A:H5''	52:3:387:U:H5''	1.87	0.57
52:3:1071:C:H2'	52:3:1072:G:H8	1.70	0.57
2:c:157:LYS:HG2	9:j:80:HIS:CE1	2.40	0.57
23:x:31:ASN:ND2	53:1:2230:G:H1'	2.20	0.57
23:x:39:VAL:HG22	23:x:41:SER:H	1.70	0.57
32:H:37:LYS:HD2	32:H:93:ILE:HG23	1.86	0.57
38:N:117:LEU:HD22	38:N:123:ARG:HA	1.85	0.57
40:P:81:LEU:HD11	40:P:99:LEU:HD21	1.87	0.57
52:3:86:G:H4'	52:3:87:C:C5	2.39	0.57
52:3:860:A:H2'	52:3:861:G:O4'	2.05	0.57
57:7:68:C:H2'	57:7:69:G:C8	2.39	0.57
38:N:56:MET:HG3	38:N:57:VAL:H	1.70	0.57
45:U:61:VAL:HA	45:U:65:ALA:H	1.70	0.57
51:a:7:ARG:HB3	53:1:2129:C:OP1	2.04	0.57
52:3:662:U:H2'	52:3:663:A:C8	2.39	0.57
53:1:20:C:H2'	53:1:21:A:C8	2.40	0.57
53:1:340:A:H2'	53:1:341:C:O4'	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1278:C:H2'	53:1:1279:G:H8	1.70	0.57
53:1:2743:U:C2'	53:1:2744:G:H5''	2.34	0.57
57:7:68:C:H2'	57:7:69:G:H8	1.69	0.57
1:b:15:VAL:HG12	1:b:205:GLY:HA3	1.86	0.57
1:b:65:ASP:HB2	1:b:101:ARG:HD3	1.86	0.57
2:c:14:ILE:HA	15:p:11:GLN:HE22	1.68	0.57
11:l:93:ASN:O	11:l:94:THR:OG1	2.22	0.57
20:u:24:VAL:HG12	20:u:35:VAL:HG22	1.87	0.57
38:N:119:LYS:HG3	52:3:1349:A:OP1	2.05	0.57
43:S:78:LEU:HD21	43:S:83:VAL:HA	1.85	0.57
7:h:33:VAL:HG23	7:h:35:VAL:H	1.70	0.57
7:h:61:ARG:HB3	53:1:1046:A:H4'	1.87	0.57
7:h:67:THR:CG2	7:h:68:PRO:HD3	2.35	0.57
8:i:20:SER:HB2	8:i:21:PRO:HD3	1.87	0.57
12:m:12:MET:O	12:m:86:LYS:NZ	2.38	0.57
30:F:7:VAL:HA	30:F:35:GLN:NE2	2.19	0.57
31:G:113:LEU:O	31:G:117:GLU:HG3	2.04	0.57
32:H:160:GLU:OE1	52:3:1055:A:H4'	2.05	0.57
35:K:68:GLN:O	35:K:71:ILE:HG22	2.04	0.57
37:M:11:THR:HG21	52:3:876:C:H1'	1.87	0.57
52:3:265:G:H2'	52:3:267:C:H5	1.69	0.57
53:1:466:A:H2'	53:1:467:G:H5'	1.86	0.57
53:1:1111:A:H2'	53:1:1111:A:N3	2.19	0.57
53:1:1447:C:H2'	53:1:1448:G:H8	1.68	0.57
7:h:34:THR:HG21	53:1:1057:A:H1'	1.87	0.57
18:s:62:ASP:N	18:s:62:ASP:OD1	2.37	0.57
25:z:8:GLN:HG2	25:z:31:ILE:HA	1.87	0.57
52:3:245:U:O2'	52:3:246:A:H5'	2.05	0.57
52:3:817:C:H4'	52:3:818:G:H5''	1.87	0.57
53:1:2233:U:H2'	53:1:2234:G:C8	2.39	0.57
1:b:92:LEU:HD11	1:b:100:ARG:HB3	1.86	0.56
11:l:57:LEU:O	11:l:61:LEU:HD23	2.05	0.56
24:y:52:ARG:NH2	24:y:52:ARG:HB2	2.20	0.56
32:H:129:PHE:CE1	32:H:130:ARG:HD3	2.40	0.56
41:Q:30:ARG:HG3	52:3:363:A:C5'	2.36	0.56
42:R:113:LYS:HB2	42:R:114:PRO:CD	2.35	0.56
52:3:666:G:H5'	52:3:726:C:H1'	1.87	0.56
52:3:1120:C:H2'	52:3:1121:U:C6	2.40	0.56
53:1:1775:U:H2'	53:1:1776:G:O4'	2.05	0.56
53:1:2788:C:H2'	53:1:2789:C:C6	2.39	0.56
58:8:47:PHE:O	58:8:50:ILE:HG22	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:99:ILE:HD12	6:g:102:ALA:HB3	1.87	0.56
7:h:3:LEU:HD11	7:h:5:LEU:HB2	1.87	0.56
9:j:114:LEU:HG	9:j:118:MET:HE3	1.87	0.56
11:l:62:PRO:HB2	29:E:29:ARG:HH11	1.70	0.56
31:G:130:LYS:NZ	52:3:1160:G:H4'	2.20	0.56
39:O:40:ILE:HD11	52:3:1124:G:H4'	1.87	0.56
41:Q:82:ARG:NH1	52:3:552:U:H5'	2.20	0.56
52:3:225:C:H3'	52:3:226:G:H5''	1.88	0.56
53:1:310:A:O2'	53:1:311:A:H5''	2.05	0.56
53:1:1857:G:N2	53:1:1884:G:H2'	2.20	0.56
53:1:2487:G:H2'	53:1:2488:G:H8	1.69	0.56
3:d:36:ALA:HB1	53:1:443:A:N6	2.20	0.56
5:f:88:LEU:HB3	5:f:161:VAL:HG12	1.86	0.56
9:j:81:ILE:HD11	53:1:2514:U:H5''	1.86	0.56
9:j:99:ARG:HH12	53:1:2780:G:H1	1.53	0.56
18:s:8:ARG:HG3	53:1:494:G:H5'	1.87	0.56
32:H:45:GLU:OE1	32:H:86:LEU:HD11	2.05	0.56
35:K:18:VAL:HG23	35:K:19:PRO:CD	2.32	0.56
39:O:5:ARG:HG2	39:O:79:PRO:HB3	1.87	0.56
43:S:25:GLU:HA	43:S:28:ALA:HB3	1.86	0.56
49:Y:27:MET:HE1	49:Y:57:VAL:HA	1.86	0.56
51:a:221:GLY:N	53:1:2176:A:H5''	2.20	0.56
52:3:396:C:H2'	52:3:397:A:H5''	1.87	0.56
52:3:399:G:H2'	52:3:400:C:C6	2.40	0.56
52:3:1227:A:H3'	52:3:1227:A:N3	2.20	0.56
52:3:1500:A:H5''	52:3:1508:A:H5''	1.87	0.56
53:1:475:C:H4'	53:1:510:C:H5'	1.86	0.56
53:1:1859:U:H2'	53:1:1860:G:H8	1.70	0.56
53:1:1909:C:H2'	53:1:1910:G:C8	2.40	0.56
53:1:2019:A:H2	53:1:2035:G:H22	1.53	0.56
53:1:2432:A:H1'	55:6:75:C:C5'	2.33	0.56
58:8:247:GLY:CA	58:8:291:GLN:HG2	2.35	0.56
58:8:334:ARG:O	58:8:335:THR:OG1	2.17	0.56
12:m:75:GLU:HB2	12:m:90:GLU:CD	2.31	0.56
13:n:100:CYS:HA	26:B:42:ILE:HG12	1.87	0.56
20:u:10:VAL:HG13	20:u:70:ALA:O	2.05	0.56
32:H:155:ARG:HD3	52:3:1055:A:O2'	2.05	0.56
53:1:2693:G:O2'	53:1:2694:G:H5'	2.05	0.56
7:h:53:ARG:HE	53:1:1084:A:P	2.29	0.56
26:B:11:LYS:HA	26:B:14:MET:HE2	1.86	0.56
37:M:12:ARG:CZ	52:3:826:C:H5'	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:Q:41:PRO:HD2	41:Q:47:ALA:H	1.70	0.56
52:3:1138:G:H3'	52:3:1138:G:N3	2.20	0.56
52:3:1513:A:H2'	52:3:1514:G:C8	2.41	0.56
53:1:613:A:H2'	53:1:613:A:N3	2.20	0.56
53:1:1078:U:H5''	53:1:1079:C:H5''	1.87	0.56
1:b:154:ALA:HB1	1:b:159:THR:O	2.06	0.56
32:H:147:GLY:HA3	32:H:171:ARG:O	2.06	0.56
41:Q:99:GLY:C	52:3:35:G:H5''	2.31	0.56
42:R:111:PRO:HB2	42:R:113:LYS:NZ	2.21	0.56
53:1:2112:G:H2'	53:1:2113:U:H5'	1.86	0.56
37:M:28:SER:HB3	37:M:56:PRO:HB2	1.87	0.56
38:N:10:ARG:HB2	38:N:105:ARG:NH2	2.21	0.56
45:U:12:LYS:HD2	52:3:393:A:OP2	2.05	0.56
53:1:288:U:H2'	53:1:289:G:C8	2.41	0.56
53:1:1051:G:H4'	53:1:2752:C:H1'	1.87	0.56
53:1:1611:C:H6	53:1:1611:C:H5'	1.70	0.56
53:1:1725:U:H3	53:1:1735:A:H61	1.53	0.56
2:c:148:GLN:HB2	2:c:152:PRO:HG2	1.87	0.56
8:i:92:PRO:HD2	53:1:1076:C:H1'	1.87	0.56
42:R:84:CYS:O	42:R:88:LEU:HD13	2.05	0.56
52:3:1488:G:H2'	52:3:1489:G:H8	1.70	0.56
58:8:66:SER:OG	58:8:81:ASP:HB3	2.05	0.56
31:G:63:LYS:NZ	31:G:65:LYS:HE2	2.21	0.56
31:G:131:LYS:HZ3	52:3:1159:U:H5'	1.71	0.56
52:3:1306:A:N6	52:3:1331:G:H1'	2.21	0.56
53:1:7:G:H2'	53:1:8:C:C6	2.41	0.56
53:1:1475:G:HO2'	53:1:1476:U:H6	1.54	0.56
57:7:58:A:H1'	57:7:60:U:H5	1.71	0.56
2:c:98:VAL:HG21	2:c:187:LEU:HB2	1.88	0.56
6:g:72:ILE:HD12	6:g:108:VAL:HG13	1.88	0.56
7:h:23:LEU:HB2	7:h:118:ILE:HD11	1.88	0.56
38:N:114:LYS:HE2	52:3:1187:G:C5'	2.36	0.56
40:P:43:TRP:HE1	52:3:686:U:H4'	1.71	0.56
53:1:2297:A:N6	53:1:2319:G:H1'	2.21	0.56
1:b:153:LEU:HD13	1:b:175:LEU:HD21	1.88	0.55
6:g:51:ARG:HA	6:g:55:GLU:HB2	1.88	0.55
32:H:45:GLU:HG3	32:H:46:LEU:CD2	2.36	0.55
41:Q:88:ASP:HB2	52:3:523:A:N1	2.21	0.55
44:T:50:HIS:CE1	52:3:667:G:H4'	2.42	0.55
46:V:46:HIS:HB2	46:V:70:LYS:CG	2.36	0.55
52:3:1005:A:H2'	52:3:1006:G:O4'	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1514:G:O2'	52:3:1515:G:H5'	2.05	0.55
53:1:854:C:H2'	53:1:855:G:H8	1.70	0.55
53:1:1853:A:H2'	53:1:1854:A:C8	2.41	0.55
53:1:2086:U:H2'	53:1:2087:G:C8	2.42	0.55
53:1:2281:A:O2'	53:1:2282:G:H5'	2.06	0.55
53:1:2795:C:H2'	53:1:2796:U:O4'	2.06	0.55
57:7:51:U:H4'	58:8:326:GLY:O	2.06	0.55
3:d:3:LEU:HB2	3:d:12:LEU:HB3	1.87	0.55
3:d:58:LYS:HG2	3:d:71:GLY:HA2	1.88	0.55
6:g:141:LYS:O	6:g:141:LYS:HD2	2.06	0.55
13:n:9:GLN:HB3	53:1:1653:G:C6	2.42	0.55
32:H:37:LYS:HA	32:H:40:GLN:HE21	1.69	0.55
32:H:37:LYS:CD	32:H:93:ILE:HG23	2.36	0.55
52:3:405:U:C3'	52:3:406:G:H5'	2.36	0.55
53:1:118:A:H2'	53:1:120:U:O4	2.05	0.55
53:1:1073:A:H2'	53:1:1074:G:O4'	2.05	0.55
58:8:70:TYR:HE1	58:8:79:HIS:HB2	1.71	0.55
16:q:73:ILE:HD11	16:q:113:LYS:HG3	1.87	0.55
35:K:47:LEU:HD12	47:W:65:SER:HB3	1.87	0.55
35:K:92:THR:OG1	35:K:93:LYS:N	2.39	0.55
38:N:35:GLU:HA	38:N:39:GLY:HA3	1.88	0.55
39:O:53:ILE:HG22	39:O:61:ALA:O	2.06	0.55
52:3:730:G:C2'	52:3:731:G:H5'	2.37	0.55
52:3:1413:A:O2'	52:3:1414:U:H5'	2.07	0.55
52:3:1493:A:O2'	56:4:19:U:H1'	2.06	0.55
53:1:2055:C:H5'	53:1:2056:G:O5'	2.05	0.55
57:7:62:C:H2'	57:7:63:G:H5''	1.88	0.55
18:s:42:LYS:HB2	53:1:2010:G:H5''	1.88	0.55
37:M:3:GLN:O	52:3:587:G:H4'	2.06	0.55
42:R:6:ILE:HG23	42:R:7:ASN:N	2.22	0.55
52:3:225:C:H2'	52:3:226:G:H5''	1.88	0.55
52:3:309:A:H2'	52:3:310:G:C8	2.41	0.55
52:3:404:G:H2'	52:3:405:U:C6	2.41	0.55
52:3:664:G:H2'	52:3:666:G:OP1	2.07	0.55
53:1:2208:C:H2'	53:1:2209:G:C8	2.41	0.55
55:6:12:G:H2'	55:6:13:C:C6	2.42	0.55
3:d:118:LEU:HD12	3:d:118:LEU:O	2.07	0.55
5:f:98:LYS:NZ	5:f:103:ASN:HB2	2.22	0.55
17:r:78:ARG:HH12	53:1:990:A:N6	2.02	0.55
24:y:41:HIS:NE2	53:1:96:C:H4'	2.21	0.55
31:G:63:LYS:HE2	31:G:224:ARG:HH22	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:H:37:LYS:HD2	32:H:93:ILE:O	2.07	0.55
33:I:25:ARG:HD3	33:I:28:ASP:HA	1.88	0.55
47:W:20:ILE:HG21	47:W:54:LEU:HD13	1.88	0.55
52:3:824:G:H2'	52:3:825:A:H8	1.72	0.55
52:3:1513:A:H2'	52:3:1514:G:H8	1.71	0.55
2:c:50:VAL:HG22	2:c:51:THR:N	2.22	0.55
52:3:211:G:H2'	52:3:212:G:H5'	1.88	0.55
52:3:335:C:H2'	52:3:336:A:C8	2.42	0.55
53:1:255:A:H2'	53:1:256:A:O4'	2.07	0.55
53:1:873:C:H2'	53:1:874:G:C8	2.42	0.55
5:f:93:TYR:OH	5:f:151:ARG:NH1	2.39	0.55
13:n:11:ASN:O	13:n:12:ARG:HG3	2.06	0.55
51:a:37:LYS:HB2	53:1:2127:G:H5'	1.87	0.55
52:3:1258:G:H2'	52:3:1259:C:C6	2.41	0.55
53:1:639:U:H2'	53:1:640:C:C6	2.42	0.55
10:k:24:VAL:HA	10:k:39:ILE:HG22	1.88	0.55
14:o:63:LYS:HZ3	54:2:51:G:H5'	1.72	0.55
27:C:40:PRO:HG3	53:1:2348:U:H4'	1.89	0.55
30:F:2:LYS:HG2	30:F:4:ARG:NH2	2.21	0.55
34:J:96:GLN:HG3	34:J:97:PRO:HD2	1.87	0.55
52:3:766:A:H2'	52:3:767:A:O4'	2.06	0.55
52:3:1256:A:H1'	52:3:1258:G:C8	2.41	0.55
52:3:1527:U:H2'	52:3:1528:U:C6	2.41	0.55
53:1:527:C:H4'	53:1:528:A:O4'	2.06	0.55
53:1:742:A:H2'	53:1:743:A:H8	1.71	0.55
53:1:2285:C:O2'	53:1:2287:A:H1'	2.06	0.55
39:O:40:ILE:CD1	52:3:1124:G:H4'	2.37	0.55
53:1:215:G:C4'	53:1:216:A:H4'	2.37	0.55
53:1:323:C:H2'	53:1:1205:A:H61	1.72	0.55
53:1:580:U:H2'	53:1:581:C:H6	1.72	0.55
53:1:1447:C:H2'	53:1:1448:G:C8	2.42	0.55
58:8:247:GLY:HA3	58:8:291:GLN:HG2	1.89	0.55
30:F:37:GLN:HG2	53:1:1124:G:HO2'	1.72	0.55
33:I:56:GLU:HG2	33:I:198:LEU:HB2	1.88	0.55
52:3:31:G:H21	52:3:46:G:H5''	1.71	0.55
52:3:593:U:H2'	52:3:594:U:C6	2.42	0.55
53:1:598:U:H2'	53:1:599:A:C8	2.42	0.55
53:1:1506:U:H2'	53:1:1507:C:C6	2.43	0.55
53:1:2087:G:H2'	53:1:2088:A:H8	1.72	0.55
53:1:2639:A:H2'	53:1:2640:G:O4'	2.06	0.55
54:2:55:U:H2'	54:2:56:G:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:116:GLN:HE21	1:b:121:ALA:HA	1.71	0.54
8:i:101:SER:OG	8:i:104:GLN:HG3	2.05	0.54
12:m:69:PRO:HA	12:m:94:ALA:HB2	1.89	0.54
16:q:106:THR:O	16:q:110:GLU:HG3	2.06	0.54
39:O:6:ILE:HB	39:O:76:ILE:HB	1.87	0.54
51:a:23:ILE:HG23	51:a:186:LYS:HE2	1.89	0.54
1:b:213:ARG:NH2	53:1:1566:A:H5'	2.20	0.54
33:I:2:ARG:HH22	52:3:407:U:H5''	1.72	0.54
53:1:532:A:H2'	53:1:532:A:N3	2.22	0.54
53:1:1936:A:H2	53:1:1943:U:H3	1.55	0.54
53:1:1979:U:O2'	53:1:1980:G:H5'	2.07	0.54
54:2:3:C:H3'	54:2:4:C:C5'	2.38	0.54
3:d:123:LYS:HE2	3:d:125:SER:HB3	1.89	0.54
14:o:12:THR:OG1	53:1:2334:U:H4'	2.07	0.54
31:G:216:VAL:O	31:G:220:VAL:HG23	2.07	0.54
48:X:77:ARG:HD2	52:3:960:U:H5	1.72	0.54
51:a:44:VAL:HG13	51:a:214:ILE:HG22	1.89	0.54
53:1:511:U:H2'	53:1:512:G:H5'	1.89	0.54
55:6:1:C:H2'	55:6:2:G:H8	1.73	0.54
11:l:135:ILE:HD12	11:l:142:ILE:HD11	1.89	0.54
21:v:10:LYS:H	21:v:10:LYS:HD2	1.72	0.54
24:y:24:GLU:O	24:y:28:LEU:HB2	2.07	0.54
33:I:49:ASP:O	33:I:52:VAL:HG12	2.07	0.54
38:N:113:LYS:HG3	38:N:120:ALA:H	1.71	0.54
52:3:1259:C:H3'	52:3:1260:G:C5'	2.30	0.54
53:1:1035:U:H2'	53:1:1036:G:H8	1.71	0.54
53:1:2277:G:C2'	53:1:2278:A:H5''	2.36	0.54
53:1:2617:U:H2'	53:1:2618:G:O4'	2.07	0.54
55:6:70:G:O2'	55:6:71:C:H5'	2.08	0.54
57:7:51:U:H2'	57:7:52:G:C8	2.42	0.54
12:m:3:GLN:HE21	12:m:92:TRP:CD1	2.25	0.54
12:m:50:ARG:NH2	12:m:54:THR:OG1	2.41	0.54
22:w:17:LEU:HD13	22:w:37:ARG:HB2	1.88	0.54
26:B:27:LEU:HD12	26:B:27:LEU:O	2.08	0.54
51:a:181:ASP:HB2	51:a:184:LYS:HD3	1.89	0.54
53:1:890:C:H2'	53:1:891:G:H5'	1.90	0.54
54:2:2:G:H2'	54:2:3:C:C6	2.42	0.54
55:5:69:C:H2'	55:5:70:G:C8	2.43	0.54
11:l:61:LEU:N	11:l:61:LEU:HD22	2.22	0.54
12:m:45:GLN:NE2	53:1:2485:G:H5''	2.07	0.54
18:s:88:ARG:HG3	18:s:94:ASP:OD2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B:10:SER:OG	53:1:17:G:H5'	2.08	0.54
32:H:107:LYS:HB3	32:H:110:LEU:HD13	1.89	0.54
33:I:131:ILE:H	33:I:131:ILE:HD12	1.72	0.54
36:L:12:LEU:HD21	38:N:46:VAL:HG21	1.89	0.54
43:S:20:PHE:O	43:S:21:ALA:HB3	2.06	0.54
50:Z:5:VAL:C	50:Z:6:ARG:HD2	2.32	0.54
53:1:669:G:H2'	53:1:669:G:N3	2.23	0.54
55:6:72:A:H2'	55:6:73:A:O4'	2.07	0.54
57:7:16:U:H1'	57:7:60:U:O2'	2.08	0.54
32:H:100:ILE:HD12	32:H:100:ILE:N	2.22	0.54
50:Z:65:ARG:NE	52:3:1088:G:H4'	2.23	0.54
52:3:410:G:H2'	52:3:429:U:C4	2.42	0.54
53:1:1060:U:H4'	53:1:1061:U:H5'	1.90	0.54
53:1:2329:U:H2'	53:1:2330:G:H8	1.73	0.54
57:7:51:U:H2'	57:7:52:G:H8	1.73	0.54
57:7:73:A:H61	58:8:284:ARG:HH22	1.54	0.54
8:i:23:VAL:CG1	8:i:26:ALA:HB3	2.37	0.54
14:o:30:ARG:HA	14:o:35:ILE:HG13	1.88	0.54
29:E:31:ILE:HG23	29:E:31:ILE:O	2.08	0.54
31:G:102:ASN:ND2	52:3:1074:G:H1'	2.23	0.54
31:G:131:LYS:NZ	52:3:1159:U:H5'	2.23	0.54
32:H:166:TRP:CD1	32:H:166:TRP:H	2.26	0.54
38:N:49:GLN:HG2	38:N:102:PHE:CZ	2.36	0.54
41:Q:101:LEU:O	41:Q:103:CYS:N	2.41	0.54
44:T:24:THR:HG21	44:T:68:TYR:HE2	1.73	0.54
52:3:77:A:H2'	52:3:78:A:C8	2.42	0.54
52:3:764:C:H2'	52:3:765:G:O4'	2.08	0.54
53:1:1268:A:H2'	53:1:1269:A:O4'	2.07	0.54
53:1:1810:A:H2'	53:1:1811:G:O4'	2.07	0.54
53:1:1825:U:H2'	53:1:1826:G:H8	1.73	0.54
53:1:2487:G:H2'	53:1:2488:G:C8	2.43	0.54
54:2:80:U:H2'	54:2:81:G:H8	1.72	0.54
12:m:66:ARG:NH1	12:m:104:GLU:OE2	2.41	0.54
16:q:92:LYS:HE3	53:1:995:C:O2'	2.07	0.54
18:s:39:THR:HG23	18:s:39:THR:O	2.08	0.54
18:s:103:ILE:HD12	18:s:103:ILE:N	2.23	0.54
20:u:5:ARG:N	20:u:8:ASP:OD2	2.35	0.54
33:I:190:LEU:HD12	33:I:192:ALA:H	1.73	0.54
38:N:26:LYS:C	38:N:27:ILE:HD12	2.33	0.54
40:P:126:ARG:N	40:P:126:ARG:HD2	2.23	0.54
48:X:18:VAL:HG11	48:X:43:MET:HE3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:402:A:H2'	53:1:403:U:O4'	2.08	0.54
53:1:1183:U:H2'	53:1:1184:U:C6	2.43	0.54
53:1:1971:U:H5'	53:1:1972:G:H5''	1.89	0.54
2:c:124:ARG:HD3	2:c:163:GLY:H	1.72	0.54
18:s:8:ARG:HB3	18:s:8:ARG:NH1	2.22	0.54
30:F:38:GLY:OXT	53:1:1124:G:H1'	2.08	0.54
31:G:49:PHE:O	31:G:53:LEU:HD23	2.08	0.54
39:O:56:HIS:ND1	39:O:57:VAL:HG23	2.23	0.54
43:S:97:LYS:HD3	52:3:1188:A:O2'	2.08	0.54
44:T:3:SER:O	44:T:7:THR:HG23	2.07	0.54
52:3:20:U:H2'	52:3:21:G:O4'	2.07	0.54
52:3:1342:C:H2'	52:3:1343:G:C8	2.42	0.54
53:1:2183:A:H2'	53:1:2184:A:C8	2.43	0.54
53:1:2208:C:H2'	53:1:2209:G:H8	1.73	0.54
53:1:2467:C:H2'	53:1:2468:A:O4'	2.08	0.54
6:g:8:LYS:O	6:g:9:VAL:O	2.26	0.53
8:i:28:GLY:HA2	8:i:32:VAL:H	1.73	0.53
12:m:74:THR:OG1	12:m:75:GLU:N	2.41	0.53
31:G:62:ARG:HG3	31:G:62:ARG:NH1	2.24	0.53
37:M:91:LEU:HB2	37:M:116:ARG:NH1	2.24	0.53
46:V:64:ARG:HD2	52:3:264:C:H4'	1.90	0.53
52:3:1128:C:H4'	52:3:1148:U:O2	2.08	0.53
53:1:766:U:H2'	53:1:767:U:C6	2.43	0.53
31:G:170:ILE:H	31:G:170:ILE:HD12	1.72	0.53
52:3:113:G:H1'	52:3:354:G:H5''	1.89	0.53
52:3:483:C:H2'	52:3:484:G:C8	2.43	0.53
52:3:1193:G:O2'	52:3:1194:U:H5'	2.09	0.53
53:1:2093:G:H21	53:1:2198:A:N6	2.06	0.53
1:b:62:ARG:HG3	1:b:62:ARG:HH11	1.72	0.53
18:s:41:LYS:CD	53:1:2009:A:H5''	2.38	0.53
30:F:12:ARG:NH2	53:1:1090:A:N3	2.57	0.53
35:K:69:GLU:O	35:K:72:ASP:OD1	2.26	0.53
40:P:118:ASN:CG	52:3:718:A:H5'	2.32	0.53
53:1:174:U:H2'	53:1:175:G:C8	2.44	0.53
53:1:473:G:O2'	53:1:474:G:H5'	2.08	0.53
53:1:581:C:H2'	53:1:582:A:C8	2.43	0.53
16:q:14:LYS:HE3	53:1:1217:U:OP2	2.09	0.53
20:u:50:ALA:O	20:u:51:LEU:HG	2.09	0.53
31:G:206:ILE:HD12	31:G:206:ILE:N	2.23	0.53
33:I:114:ARG:NH1	33:I:132:ALA:HB3	2.23	0.53
36:L:83:THR:HB	55:6:33:U:H4'	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:W:59:LYS:HD3	52:3:735:C:H5'	1.89	0.53
52:3:70:U:H4'	52:3:71:A:H8	1.73	0.53
52:3:206:C:H2'	52:3:207:C:O4'	2.08	0.53
52:3:580:C:H2'	52:3:581:G:O4'	2.08	0.53
52:3:1405:G:H21	52:3:1518:A:H1'	1.73	0.53
53:1:467:G:O2'	53:1:468:G:H5'	2.07	0.53
53:1:1874:C:H2'	53:1:1875:G:O4'	2.08	0.53
9:j:58:ASN:HA	9:j:126:ALA:O	2.08	0.53
12:m:61:GLY:HA3	12:m:108:VAL:HG13	1.90	0.53
14:o:99:TYR:OH	14:o:104:GLN:HG3	2.09	0.53
19:t:2:ILE:HB	19:t:5:GLU:OE2	2.09	0.53
19:t:50:LEU:HD12	19:t:50:LEU:N	2.23	0.53
33:I:109:THR:HG23	33:I:112:GLU:H	1.74	0.53
36:L:28:ILE:HG22	36:L:104:VAL:HG21	1.90	0.53
50:Z:9:GLU:HB2	50:Z:10:PRO:CD	2.34	0.53
52:3:1524:C:H2'	52:3:1525:G:C8	2.43	0.53
53:1:189:G:H2'	53:1:205:G:N2	2.23	0.53
53:1:1872:A:H2'	53:1:1873:G:O4'	2.08	0.53
53:1:2646:C:H2'	53:1:2647:U:O4'	2.09	0.53
53:1:2737:G:H2'	53:1:2738:A:C8	2.44	0.53
10:k:76:VAL:H	15:p:72:VAL:HG22	1.73	0.53
13:n:45:ARG:HD3	13:n:97:ILE:HD11	1.90	0.53
35:K:4:TYR:O	35:K:63:ASN:HA	2.09	0.53
52:3:742:G:H2'	52:3:743:A:C8	2.44	0.53
52:3:952:U:H2'	52:3:953:G:C8	2.43	0.53
53:1:594:U:H2'	53:1:595:C:C6	2.44	0.53
53:1:1682:G:C4	53:1:1757:A:H1'	2.44	0.53
53:1:1709:U:H2'	53:1:1710:G:C8	2.43	0.53
53:1:1857:G:H1'	53:1:1885:A:N6	2.23	0.53
1:b:12:ARG:O	1:b:15:VAL:HG22	2.09	0.53
46:V:75:VAL:HG23	46:V:76:ARG:H	1.74	0.53
52:3:1287:A:H2	52:3:1353:G:H1'	1.73	0.53
53:1:1013:C:H2'	53:1:1014:A:H8	1.74	0.53
53:1:2798:U:H4'	53:1:2799:A:C4	2.43	0.53
53:1:2808:G:H2'	53:1:2890:G:C6	2.43	0.53
57:7:32:U:H3	57:7:38:A:H61	1.55	0.53
7:h:42:ARG:HH12	53:1:1082:U:H4'	1.72	0.53
15:p:88:ARG:HD3	15:p:113:LEU:HD23	1.90	0.53
31:G:166:ASP:HB3	31:G:190:SER:HA	1.91	0.53
33:I:39:GLN:NE2	52:3:540:G:H21	2.06	0.53
33:I:102:TYR:O	33:I:164:ARG:NH1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:J:107:GLY:CA	52:3:9:G:H5'	2.38	0.53
39:O:6:ILE:HD12	39:O:6:ILE:N	2.23	0.53
43:S:68:ARG:NH1	43:S:70:HIS:HB2	2.24	0.53
50:Z:17:ARG:HA	50:Z:20:ARG:HH11	1.73	0.53
51:a:175:ILE:HB	51:a:188:ASN:HB3	1.90	0.53
52:3:358:U:H2'	52:3:359:G:H8	1.74	0.53
52:3:570:G:H5'	52:3:820:U:O4'	2.08	0.53
52:3:622:A:H2'	52:3:623:C:H5'	1.90	0.53
53:1:322:A:H5'	53:1:340:A:H1'	1.91	0.53
55:5:6:G:O2'	55:5:7:G:H5'	2.08	0.53
52:3:304:U:O2'	52:3:305:G:H5'	2.08	0.53
53:1:742:A:H2'	53:1:743:A:C8	2.43	0.53
53:1:2747:G:O6	53:1:2755:C:H5''	2.09	0.53
7:h:34:THR:HG22	53:1:1085:A:H61	1.75	0.53
14:o:64:TYR:HB3	14:o:67:ASN:ND2	2.23	0.53
32:H:153:SER:HB3	52:3:1057:G:H5''	1.91	0.53
34:J:45:VAL:HG21	34:J:140:ILE:HD12	1.91	0.53
37:M:14:ARG:HH12	52:3:876:C:H4'	1.74	0.53
41:Q:31:GLY:O	41:Q:78:VAL:HG13	2.08	0.53
50:Z:11:PHE:C	50:Z:13:VAL:H	2.17	0.53
52:3:354:G:H2'	52:3:355:C:H5'	1.91	0.53
52:3:886:G:H2'	52:3:887:G:O4'	2.09	0.53
53:1:1201:U:H2'	53:1:1202:G:H8	1.73	0.53
53:1:2350:C:H2'	53:1:2351:G:O4'	2.09	0.53
54:2:66:A:H5''	54:2:67:G:OP1	2.09	0.53
55:6:16:C:O2'	55:6:17:C:H5'	2.09	0.53
58:8:102:ALA:HB3	58:8:131:ILE:HG12	1.90	0.53
4:e:65:LEU:HD22	54:2:42:C:C5	2.44	0.52
6:g:23:ALA:HB1	6:g:27:ARG:HH12	1.74	0.52
6:g:47:PHE:HA	6:g:51:ARG:HB2	1.90	0.52
7:h:64:VAL:O	7:h:67:THR:HG22	2.09	0.52
11:l:55:MET:HE3	53:1:2392:A:C2	2.43	0.52
30:F:24:ARG:HG2	30:F:36:ARG:HB2	1.91	0.52
38:N:17:ARG:HD2	52:3:1147:C:O2'	2.09	0.52
38:N:92:SER:OG	38:N:93:LEU:HD12	2.09	0.52
53:1:141:G:H3'	53:1:142:A:O4'	2.08	0.52
53:1:290:U:H2'	53:1:291:G:H8	1.73	0.52
53:1:1783:A:H5'	53:1:2608:G:H4'	1.90	0.52
54:2:48:U:H2'	54:2:49:C:C6	2.44	0.52
57:7:26:A:H2'	57:7:27:G:O4'	2.08	0.52
58:8:116:THR:HA	58:8:119:HIS:CD2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:8:378:ARG:HG2	58:8:383:THR:HA	1.90	0.52
4:e:49:LEU:HD21	4:e:66:ILE:HG21	1.91	0.52
9:j:117:ALA:HA	9:j:120:ARG:HH21	1.73	0.52
10:k:25:LEU:CD2	53:1:2562:U:H4'	2.39	0.52
15:p:52:ARG:NH2	53:1:2720:U:OP1	2.40	0.52
36:L:17:PHE:HE2	36:L:22:LEU:HD12	1.74	0.52
46:V:17:GLU:O	46:V:18:LYS:HG2	2.09	0.52
52:3:163:C:H2'	52:3:164:G:O4'	2.09	0.52
52:3:211:G:C2'	52:3:212:G:H5'	2.40	0.52
52:3:309:A:H2'	52:3:310:G:H8	1.74	0.52
53:1:814:C:H1'	53:1:1225:G:H21	1.74	0.52
53:1:1509:A:H2'	53:1:1510:G:C8	2.45	0.52
58:8:107:ALA:HB1	58:8:137:LYS:HD2	1.90	0.52
1:b:73:ILE:HG12	53:1:1490:A:C6	2.44	0.52
1:b:229:HIS:CD2	1:b:230:PRO:HD2	2.44	0.52
9:j:31:GLU:HG2	9:j:142:ILE:HG12	1.91	0.52
14:o:51:ALA:HB3	14:o:78:VAL:HG12	1.90	0.52
32:H:15:LYS:HE2	32:H:180:ASP:OD1	2.10	0.52
53:1:2293:G:H2'	53:1:2294:G:C8	2.45	0.52
53:1:2591:C:H2'	53:1:2592:G:C8	2.44	0.52
54:2:106:G:H2'	54:2:107:G:O4'	2.09	0.52
18:s:14:ALA:O	18:s:18:ARG:HG3	2.10	0.52
34:J:134:ASN:ND2	52:3:19:A:OP1	2.43	0.52
35:K:3:HIS:HB2	35:K:92:THR:HA	1.90	0.52
37:M:12:ARG:NH2	52:3:826:C:H5'	2.25	0.52
46:V:43:LEU:HD21	52:3:236:A:H5'	1.89	0.52
53:1:1316:U:H2'	53:1:1317:G:C8	2.44	0.52
53:1:1720:U:H2'	53:1:1721:G:O4'	2.10	0.52
58:8:245:ILE:N	58:8:245:ILE:HD12	2.24	0.52
5:f:98:LYS:HZ1	5:f:103:ASN:HB2	1.74	0.52
5:f:154:GLU:HG2	5:f:159:LYS:H	1.74	0.52
18:s:95:ARG:HH11	18:s:97:LEU:HD21	1.74	0.52
31:G:82:ALA:HB2	31:G:213:LEU:HD22	1.91	0.52
40:P:118:ASN:OD1	52:3:718:A:C5'	2.54	0.52
42:R:68:LEU:O	42:R:72:ILE:HG12	2.10	0.52
46:V:45:VAL:CG1	46:V:74:LEU:HB2	2.39	0.52
52:3:1228:C:H2'	52:3:1229:A:C8	2.44	0.52
53:1:967:U:H2'	53:1:968:C:C6	2.45	0.52
53:1:1110:G:H2'	53:1:1111:A:H8	1.75	0.52
53:1:1825:U:H2'	53:1:1826:G:C8	2.45	0.52
53:1:2287:A:O2'	53:1:2288:A:H2'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:8:86:ALA:O	58:8:89:VAL:HG23	2.09	0.52
18:s:8:ARG:HB3	18:s:8:ARG:HH11	1.73	0.52
30:F:37:GLN:HG2	53:1:1124:G:O2'	2.08	0.52
31:G:77:GLU:HA	31:G:80:LYS:HE2	1.92	0.52
40:P:19:VAL:HG23	40:P:82:GLU:HB2	1.92	0.52
41:Q:69:GLU:HG2	52:3:521:G:H4'	1.90	0.52
52:3:45:G:H5''	52:3:307:C:O2'	2.09	0.52
52:3:868:C:H2'	52:3:869:G:O4'	2.10	0.52
52:3:1346:A:O2'	52:3:1347:G:H4'	2.10	0.52
52:3:1499:A:O2'	52:3:1520:C:H5'	2.08	0.52
53:1:161:A:H3'	53:1:162:U:H5''	1.91	0.52
53:1:2108:A:H2'	53:1:2109:U:H5'	1.90	0.52
53:1:2679:A:O2'	53:1:2680:U:H5'	2.09	0.52
35:K:96:VAL:HG22	35:K:97:THR:N	2.25	0.52
37:M:91:LEU:HB2	37:M:116:ARG:HH12	1.75	0.52
39:O:71:LEU:HD23	39:O:72:ARG:N	2.25	0.52
50:Z:6:ARG:C	50:Z:8:ASN:H	2.17	0.52
52:3:352:C:H4'	52:3:354:G:OP1	2.10	0.52
52:3:1201:A:C1'	52:3:1202:U:OP2	2.54	0.52
53:1:634:C:H2'	53:1:635:C:C6	2.45	0.52
53:1:1278:C:H2'	53:1:1279:G:C8	2.44	0.52
53:1:1344:U:H3'	53:1:1345:C:H5'	1.92	0.52
53:1:1434:A:H2'	53:1:1435:G:C8	2.44	0.52
53:1:1539:U:H2'	53:1:1540:G:C8	2.45	0.52
53:1:2073:C:O2'	53:1:2074:U:H5'	2.10	0.52
53:1:2457:U:O2'	53:1:2458:G:H5'	2.10	0.52
58:8:135:LEU:HD12	58:8:172:ARG:HD3	1.91	0.52
2:c:49:GLN:NE2	2:c:79:LEU:HD13	2.25	0.52
2:c:81:GLU:OE2	53:1:2636:C:H4'	2.10	0.52
3:d:95:LYS:HZ1	53:1:607:U:P	2.33	0.52
11:l:77:ILE:HG23	11:l:110:VAL:HA	1.92	0.52
15:p:102:ARG:HD3	15:p:106:ALA:O	2.09	0.52
19:t:2:ILE:O	19:t:5:GLU:HG2	2.10	0.52
33:I:107:GLY:HA3	33:I:113:ALA:HB2	1.90	0.52
40:P:46:ALA:HB1	40:P:61:ALA:HB1	1.92	0.52
41:Q:4:ASN:HD21	52:3:585:G:H4'	1.75	0.52
46:V:32:ILE:HD12	46:V:32:ILE:N	2.24	0.52
52:3:1463:U:H2'	52:3:1464:U:C6	2.45	0.52
53:1:833:A:H2'	53:1:834:G:C8	2.45	0.52
53:1:2293:G:H2'	53:1:2294:G:H8	1.74	0.52
53:1:2427:C:C5'	53:1:2429:G:H5'	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2475:C:C2'	53:1:2476:A:H5'	2.40	0.52
58:8:71:ASP:OD1	58:8:71:ASP:N	2.43	0.52
6:g:96:THR:HG23	6:g:112:LYS:HZ2	1.75	0.52
28:D:12:ARG:HE	28:D:44:VAL:CG1	2.20	0.52
32:H:11:LEU:HD21	32:H:17:TRP:HE1	1.75	0.52
37:M:44:PHE:C	37:M:63:LYS:HZ3	2.18	0.52
53:1:1319:C:O2'	53:1:1320:C:H5'	2.10	0.52
2:c:106:LYS:HD3	2:c:174:SER:HB2	1.92	0.52
7:h:68:PRO:HA	7:h:72:LEU:HG	1.91	0.52
11:l:23:ILE:H	11:l:23:ILE:HD12	1.75	0.52
15:p:43:GLU:HG3	15:p:86:LYS:NZ	2.25	0.52
18:s:77:ASP:HB2	18:s:102:HIS:HB2	1.90	0.52
21:v:72:VAL:HG11	21:v:91:PHE:HB3	1.92	0.52
26:B:12:ARG:NH2	53:1:517:C:OP1	2.43	0.52
33:I:190:LEU:HD12	33:I:192:ALA:N	2.25	0.52
39:O:29:ALA:O	39:O:33:GLY:HA3	2.10	0.52
41:Q:99:GLY:O	52:3:35:G:H5''	2.10	0.52
43:S:40:ARG:HE	48:X:6:LYS:HB3	1.75	0.52
44:T:30:LEU:CD2	52:3:658:C:H5'	2.40	0.52
51:a:166:ASP:OD1	53:1:2121:G:O2'	2.21	0.52
52:3:79:G:O2'	52:3:80:A:H5'	2.10	0.52
53:1:1999:C:O2'	53:1:2000:C:H5'	2.10	0.52
53:1:2027:G:O2'	53:1:2028:U:H5'	2.09	0.52
55:6:16:C:H4'	55:6:60:U:H1'	1.92	0.52
58:8:295:LYS:O	58:8:298:THR:HG23	2.10	0.52
58:8:355:ASP:HB3	58:8:357:ILE:HG23	1.91	0.52
8:i:9:LYS:HD2	53:1:1061:U:H5''	1.92	0.51
33:I:127:ARG:NH2	52:3:619:U:O3'	2.43	0.51
45:U:4:ILE:HG22	45:U:71:VAL:HG11	1.92	0.51
53:1:5:A:H2'	53:1:6:A:C8	2.45	0.51
53:1:2329:U:H2'	53:1:2330:G:C8	2.46	0.51
6:g:59:ALA:O	6:g:62:LEU:HG	2.10	0.51
7:h:37:LYS:O	7:h:41:LEU:HB2	2.10	0.51
9:j:9:GLU:HG2	9:j:10:THR:HG23	1.92	0.51
11:l:60:ARG:O	53:1:2393:U:H5'	2.11	0.51
18:s:15:GLN:HE22	53:1:1266:G:H5''	1.75	0.51
32:H:22:PHE:CE2	39:O:11:LYS:HE3	2.45	0.51
35:K:6:ILE:HG13	35:K:89:VAL:HG22	1.92	0.51
37:M:124:ILE:HD12	37:M:124:ILE:N	2.25	0.51
40:P:117:HIS:CD2	52:3:675:A:H1'	2.45	0.51
52:3:70:U:H5''	52:3:71:A:OP1	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:834:U:H2'	52:3:835:U:C6	2.45	0.51
52:3:909:A:H2'	52:3:910:C:H5'	1.92	0.51
53:1:825:A:H2'	53:1:826:U:C6	2.45	0.51
53:1:2421:G:H2'	55:6:76:A:N6	2.25	0.51
54:2:19:C:H2'	54:2:20:G:C8	2.44	0.51
58:8:18:ILE:HD12	58:8:18:ILE:N	2.24	0.51
58:8:211:PHE:CZ	58:8:213:LEU:HB2	2.45	0.51
58:8:288:GLU:H	58:8:291:GLN:HE22	1.58	0.51
1:b:261:ARG:NH2	53:1:1801:A:C4	2.78	0.51
18:s:86:MET:HE3	18:s:87:PRO:HD2	1.93	0.51
32:H:60:ALA:O	32:H:61:LYS:HG2	2.10	0.51
39:O:63:ASP:OD2	43:S:84:ARG:NH1	2.43	0.51
50:Z:19:LYS:HB3	50:Z:24:LYS:HD3	1.92	0.51
52:3:692:U:H2'	52:3:694:A:OP2	2.11	0.51
53:1:940:G:H2'	53:1:941:A:C4'	2.40	0.51
54:2:19:C:H2'	54:2:20:G:H8	1.75	0.51
58:8:75:ARG:NH1	58:8:200:ILE:O	2.43	0.51
58:8:130:TYR:CE2	58:8:201:PRO:HD2	2.46	0.51
11:l:27:LEU:O	11:l:31:GLY:HA2	2.10	0.51
18:s:3:THR:HG23	18:s:107:VAL:HG13	1.92	0.51
19:t:15:HIS:CE1	19:t:17:SER:HB3	2.46	0.51
42:R:89:ARG:HH21	42:R:95:PRO:HG2	1.76	0.51
43:S:52:ARG:HD2	52:3:1317:C:N3	2.25	0.51
51:a:8:MET:HE2	53:1:2174:C:H5''	1.91	0.51
52:3:106:C:H2'	52:3:107:G:C8	2.45	0.51
53:1:176:A:O2'	53:1:177:G:H5'	2.09	0.51
53:1:873:C:H2'	53:1:874:G:H8	1.75	0.51
53:1:2243:U:H2'	53:1:2244:U:C6	2.45	0.51
53:1:2475:C:H2'	53:1:2476:A:H5'	1.91	0.51
53:1:2538:C:H2'	53:1:2539:C:C6	2.45	0.51
8:i:74:PRO:HG3	53:1:1060:U:OP1	2.10	0.51
34:J:148:SER:HB2	34:J:149:PRO:HD2	1.93	0.51
35:K:45:ARG:O	35:K:56:LYS:HA	2.10	0.51
35:K:67:PRO:HG2	35:K:70:VAL:HG22	1.93	0.51
42:R:63:VAL:HG23	42:R:67:ASP:HB3	1.92	0.51
46:V:30:HIS:HD2	46:V:33:TYR:H	1.57	0.51
53:1:974:G:N3	53:1:974:G:H2'	2.25	0.51
53:1:2710:C:H2'	53:1:2711:A:C8	2.46	0.51
54:2:88:C:H4'	54:2:89:U:OP1	2.09	0.51
58:8:25:LYS:HG3	58:8:105:VAL:HG11	1.93	0.51
58:8:240:GLY:H	58:8:256:CYS:HB3	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:58:THR:HG21	7:h:82:ILE:H	1.76	0.51
15:p:20:ARG:N	15:p:23:ASP:OD2	2.39	0.51
16:q:93:ILE:HD12	17:r:13:ARG:HB2	1.92	0.51
47:W:38:ILE:HD12	47:W:38:ILE:N	2.26	0.51
52:3:736:C:H2'	52:3:737:C:C6	2.45	0.51
52:3:1432:G:H1'	52:3:1468:A:H61	1.76	0.51
53:1:744:U:H2'	53:1:745:G:O4'	2.10	0.51
53:1:1858:A:H1'	53:1:1885:A:C2	2.46	0.51
5:f:173:ALA:C	5:f:174:LYS:HG3	2.35	0.51
13:n:97:ILE:HD12	13:n:97:ILE:N	2.25	0.51
14:o:29:HIS:HB3	14:o:36:TYR:HD2	1.75	0.51
18:s:36:LEU:HA	18:s:39:THR:HG22	1.93	0.51
26:B:1:ALA:HB3	53:1:2056:G:N2	2.25	0.51
30:F:4:ARG:HB2	53:1:2466:C:OP1	2.10	0.51
31:G:27:LYS:N	31:G:28:PRO:CD	2.73	0.51
33:I:97:LEU:HD12	33:I:100:VAL:HB	1.93	0.51
34:J:100:GLU:H	34:J:121:ASN:ND2	2.08	0.51
52:3:335:C:H2'	52:3:336:A:H8	1.76	0.51
52:3:521:G:H21	52:3:536:C:H5'	1.75	0.51
52:3:1014:A:H2'	52:3:1015:G:O4'	2.11	0.51
52:3:1271:A:H5'	52:3:1314:C:H5''	1.92	0.51
52:3:1488:G:H2'	52:3:1489:G:C8	2.46	0.51
53:1:288:U:H2'	53:1:289:G:H8	1.74	0.51
53:1:690:G:O2'	53:1:691:C:H5'	2.11	0.51
53:1:1429:G:H2'	53:1:1430:G:C8	2.46	0.51
53:1:1444:G:H2'	53:1:1445:G:H8	1.76	0.51
4:e:87:LYS:HD2	53:1:2313:C:H5''	1.92	0.51
7:h:39:THR:O	7:h:43:LYS:HB2	2.11	0.51
7:h:88:HIS:HB2	7:h:89:PRO:HD3	1.93	0.51
10:k:98:ARG:NH2	52:3:340:U:OP2	2.44	0.51
16:q:80:ASN:OD1	53:1:1151:A:H4'	2.11	0.51
52:3:231:U:H2'	52:3:232:G:H8	1.76	0.51
52:3:243:A:H4'	52:3:244:U:H3'	1.92	0.51
52:3:916:U:H2'	52:3:917:G:H8	1.76	0.51
52:3:1516:G:H2'	52:3:1518:A:OP2	2.10	0.51
53:1:729:G:H4'	53:1:763:G:H5'	1.92	0.51
53:1:1026:G:H2'	53:1:1027:A:H8	1.74	0.51
53:1:2318:G:H2'	53:1:2319:G:O4'	2.10	0.51
57:7:74:C:C4'	58:8:52:ASN:HD22	2.23	0.51
58:8:343:GLU:HB3	58:8:360:VAL:HB	1.92	0.51
25:z:40:THR:HG23	25:z:43:ILE:H	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:I:80:ARG:HE	52:3:613:C:P	2.33	0.51
52:3:355:C:H1'	52:3:388:G:N3	2.26	0.51
52:3:458:U:H2'	52:3:459:A:C8	2.46	0.51
53:1:2345:G:N3	53:1:2381:A:H2'	2.26	0.51
57:7:64:A:H2'	57:7:65:G:C8	2.46	0.51
4:e:51:ASN:HB3	4:e:149:ARG:HH12	1.75	0.51
11:l:79:LEU:HD12	11:l:114:GLY:H	1.76	0.51
16:q:26:ALA:HB1	16:q:30:VAL:CG2	2.41	0.51
20:u:95:PHE:HB2	20:u:100:GLU:H	1.76	0.51
33:I:74:TYR:CD2	33:I:92:LEU:HG	2.45	0.51
38:N:32:ARG:HD3	38:N:36:GLN:HE21	1.75	0.51
52:3:350:G:H2'	52:3:351:G:C8	2.46	0.51
52:3:418:C:H2'	52:3:419:C:C6	2.46	0.51
52:3:695:A:H2'	52:3:696:A:C8	2.46	0.51
52:3:779:C:H2'	52:3:780:A:O4'	2.11	0.51
53:1:75:G:H2'	53:1:75:G:N3	2.26	0.51
53:1:2443:C:H2'	53:1:2444:G:C8	2.45	0.51
5:f:138:GLN:NE2	53:1:2746:U:H1'	2.26	0.50
14:o:16:ARG:HH11	14:o:19:GLN:NE2	2.09	0.50
32:H:86:LEU:HA	32:H:89:VAL:HG22	1.93	0.50
51:a:55:SER:HA	51:a:58:ASN:ND2	2.26	0.50
52:3:128:G:O2'	52:3:129:A:H5'	2.11	0.50
52:3:663:A:H5'	52:3:836:G:OP1	2.11	0.50
52:3:981:U:H2'	52:3:982:U:C5	2.45	0.50
53:1:466:A:C2'	53:1:467:G:H5'	2.41	0.50
53:1:2106:U:H2'	53:1:2107:G:C8	2.46	0.50
53:1:2139:U:H2'	53:1:2140:G:C8	2.46	0.50
53:1:2286:G:H4'	53:1:2287:A:O4'	2.10	0.50
54:2:66:A:H4'	54:2:67:G:C8	2.46	0.50
54:2:92:C:H2'	54:2:93:C:C6	2.46	0.50
1:b:21:PRO:HG2	1:b:22:GLU:OE2	2.11	0.50
1:b:28:PRO:HG2	1:b:33:LEU:HD11	1.93	0.50
1:b:269:ARG:NH1	53:1:1799:G:OP2	2.42	0.50
2:c:7:LYS:HB3	2:c:28:GLU:OE2	2.11	0.50
4:e:133:GLU:HG3	4:e:135:ILE:HG22	1.93	0.50
7:h:55:VAL:HA	53:1:1084:A:C4'	2.37	0.50
15:p:38:ARG:CZ	52:3:345:C:H5'	2.39	0.50
16:q:55:GLN:HA	16:q:58:GLN:HG2	1.93	0.50
32:H:201:ILE:HG22	32:H:203:LYS:HG2	1.92	0.50
33:I:144:ILE:N	33:I:144:ILE:HD12	2.26	0.50
36:L:110:ARG:NH1	36:L:112:ASP:OD2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:T:2:LEU:HG	44:T:7:THR:HG22	1.93	0.50
51:a:172:HIS:HB3	53:1:2123:G:H4'	1.92	0.50
52:3:405:U:H1'	52:3:498:A:H2'	1.93	0.50
52:3:1033:G:H2'	52:3:1034:G:C5'	2.41	0.50
52:3:1254:A:H2'	52:3:1255:G:C8	2.46	0.50
53:1:445:C:O2'	53:1:446:G:H5'	2.10	0.50
53:1:738:G:O2'	53:1:739:A:H5'	2.11	0.50
53:1:832:U:H2'	53:1:833:A:C8	2.47	0.50
53:1:2389:G:H5''	53:1:2390:U:O4'	2.10	0.50
12:m:42:THR:OG1	12:m:45:GLN:HG3	2.11	0.50
36:L:16:LYS:HG2	36:L:17:PHE:CD1	2.47	0.50
51:a:53:ARG:HG3	55:6:61:C:O2'	2.11	0.50
53:1:435:C:C2'	53:1:436:C:H5'	2.41	0.50
53:1:859:G:H1'	53:1:860:U:H5	1.75	0.50
53:1:1805:A:H2'	53:1:1806:C:C6	2.47	0.50
55:5:47:U:H3'	55:5:48:C:H5'	1.94	0.50
1:b:74:PRO:HA	1:b:116:GLN:HB3	1.94	0.50
8:i:72:THR:OG1	8:i:115:ASP:OD1	2.30	0.50
8:i:74:PRO:O	8:i:77:VAL:HG22	2.12	0.50
10:k:112:PHE:HB3	10:k:115:ILE:HD12	1.92	0.50
13:n:100:CYS:SG	13:n:110:MET:HB3	2.52	0.50
36:L:94:ARG:NH2	52:3:938:A:O2'	2.43	0.50
41:Q:29:LYS:HD2	52:3:363:A:OP1	2.10	0.50
52:3:82:G:H2'	52:3:83:C:O4'	2.11	0.50
52:3:229:U:H2'	52:3:230:G:C8	2.47	0.50
52:3:729:A:H2'	52:3:730:G:H8	1.76	0.50
53:1:745:G:O2'	53:1:748:G:H1'	2.10	0.50
53:1:948:C:H2'	53:1:949:G:C8	2.47	0.50
53:1:1078:U:C5'	53:1:1079:C:H5''	2.42	0.50
53:1:1859:U:H2'	53:1:1860:G:C8	2.47	0.50
58:8:18:ILE:HD11	58:8:99:MET:HE3	1.94	0.50
58:8:104:LEU:N	58:8:132:ILE:O	2.43	0.50
5:f:88:LEU:HA	5:f:161:VAL:HA	1.92	0.50
39:O:39:PRO:HD2	52:3:1123:U:H4'	1.94	0.50
52:3:346:G:H2'	52:3:347:G:H5'	1.93	0.50
53:1:1181:U:H2'	53:1:1182:G:C8	2.47	0.50
53:1:2529:G:OP2	53:1:2530:A:H5''	2.12	0.50
53:1:2638:G:H1'	53:1:2778:A:H61	1.77	0.50
54:2:56:G:H4'	54:2:57:A:H8	1.76	0.50
58:8:130:TYR:CZ	58:8:201:PRO:HD2	2.47	0.50
1:b:62:ARG:HD3	1:b:90:ILE:CD1	2.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:67:LYS:N	1:b:67:LYS:HD2	2.27	0.50
3:d:45:ALA:HB2	53:1:38:A:H4'	1.94	0.50
4:e:21:TYR:HB3	4:e:26:GLN:HB3	1.94	0.50
4:e:62:GLN:OE1	4:e:94:ARG:NH2	2.45	0.50
12:m:127:LYS:NZ	53:1:1030:C:OP2	2.44	0.50
28:D:11:LYS:CE	53:1:686:U:H5''	2.37	0.50
33:I:131:ILE:HD12	33:I:131:ILE:N	2.27	0.50
38:N:10:ARG:C	38:N:105:ARG:HH12	2.19	0.50
52:3:620:C:H2'	52:3:621:A:O4'	2.11	0.50
53:1:833:A:H2'	53:1:834:G:H8	1.76	0.50
53:1:1357:C:H2'	53:1:1358:G:O4'	2.12	0.50
53:1:1386:C:H2'	53:1:1387:A:C8	2.45	0.50
53:1:1570:A:H2'	53:1:1571:A:C8	2.47	0.50
55:5:47:U:H3'	55:5:48:C:C5'	2.42	0.50
58:8:174:SER:HB3	58:8:185:TRP:CD1	2.47	0.50
2:c:62:LYS:N	2:c:63:PRO:CD	2.75	0.50
14:o:10:ARG:HD2	53:1:2294:G:OP1	2.12	0.50
22:w:73:ARG:HH21	53:1:2332:C:H5''	1.77	0.50
46:V:76:ARG:HG2	46:V:76:ARG:HH11	1.77	0.50
53:1:69:C:H2'	53:1:70:G:H8	1.75	0.50
53:1:270:A:C2	53:1:369:U:H4'	2.46	0.50
53:1:1182:G:H2'	53:1:1183:U:O4'	2.12	0.50
53:1:1563:U:H2'	53:1:1564:C:C6	2.46	0.50
58:8:137:LYS:HE2	61:8:501:GTP:C8	2.47	0.50
5:f:19:ASN:HB2	5:f:22:VAL:HG13	1.93	0.50
11:l:93:ASN:HA	11:l:96:LYS:HZ3	1.77	0.50
31:G:5:MET:SD	31:G:5:MET:N	2.84	0.50
36:L:110:ARG:HH22	36:L:121:ASN:HB2	1.77	0.50
38:N:49:GLN:N	38:N:50:PRO:CD	2.75	0.50
39:O:57:VAL:O	39:O:58:ASN:CB	2.60	0.50
44:T:7:THR:O	44:T:11:VAL:HG23	2.10	0.50
52:3:32:A:H2'	52:3:33:A:C8	2.46	0.50
52:3:337:G:H2'	52:3:338:A:C8	2.47	0.50
52:3:411:A:H1'	52:3:413:G:H1'	1.94	0.50
52:3:911:U:H2'	52:3:912:C:C6	2.46	0.50
53:1:27:G:N2	53:1:512:G:H1'	2.27	0.50
53:1:1790:C:H2'	53:1:1791:A:C8	2.46	0.50
53:1:2122:U:H2'	53:1:2123:G:O4'	2.12	0.50
53:1:2636:C:H2'	53:1:2637:U:H6	1.76	0.50
58:8:93:ILE:HD11	58:8:374:ARG:HH21	1.76	0.50
1:b:229:HIS:C	1:b:231:HIS:H	2.19	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:q:36:GLN:O	16:q:39:ILE:HG22	2.12	0.50
33:I:1:ALA:HA	33:I:67:LEU:HD11	1.94	0.50
43:S:79:SER:HB2	43:S:82:LYS:HB2	1.92	0.50
52:3:273:U:C2'	52:3:274:A:H5'	2.42	0.50
52:3:1071:C:H2'	52:3:1072:G:C8	2.47	0.50
53:1:558:U:H2'	53:1:559:G:C8	2.47	0.50
53:1:948:C:H2'	53:1:949:G:H8	1.76	0.50
53:1:1812:U:H2'	53:1:1813:G:H8	1.77	0.50
58:8:329:PRO:HB2	58:8:377:ILE:HG23	1.94	0.50
3:d:79:ARG:NH2	53:1:448:U:H4'	2.26	0.49
15:p:13:LYS:HE3	15:p:76:HIS:HA	1.93	0.49
36:L:28:ILE:N	36:L:28:ILE:HD12	2.27	0.49
51:a:53:ARG:NH1	55:6:58:A:H61	2.09	0.49
52:3:273:U:H2'	52:3:274:A:H5'	1.94	0.49
52:3:1255:G:O2'	52:3:1258:G:H1'	2.11	0.49
53:1:503:A:H4'	53:1:505:A:H5''	1.94	0.49
53:1:687:C:H6	53:1:687:C:H5'	1.77	0.49
53:1:1678:A:H2'	53:1:1679:A:O4'	2.12	0.49
53:1:1725:U:H2'	53:1:1726:C:C6	2.47	0.49
53:1:2030:A:H4'	53:1:2031:A:C8	2.47	0.49
58:8:148:GLU:OE2	58:8:172:ARG:NH2	2.44	0.49
58:8:289:ARG:NH1	58:8:337:ASP:OD1	2.44	0.49
2:c:16:THR:OG1	2:c:18:ASP:OD1	2.24	0.49
5:f:173:ALA:O	5:f:174:LYS:HG3	2.13	0.49
33:I:43:ARG:HH22	52:3:511:C:H4'	1.76	0.49
33:I:101:VAL:HA	33:I:104:MET:HG2	1.94	0.49
36:L:150:PHE:CZ	40:P:55:ARG:HD2	2.47	0.49
38:N:107:ALA:CB	52:3:1117:A:H4'	2.42	0.49
44:T:44:GLU:HG3	44:T:45:HIS:H	1.77	0.49
46:V:67:SER:HB3	46:V:70:LYS:HB3	1.95	0.49
52:3:406:G:O2'	52:3:407:U:H5'	2.12	0.49
52:3:536:C:H2'	52:3:537:G:H8	1.76	0.49
53:1:502:A:H2'	53:1:503:A:H5'	1.93	0.49
53:1:1138:G:H2'	53:1:1139:G:O4'	2.12	0.49
1:b:123:ILE:HG13	35:K:80:PHE:CG	2.47	0.49
6:g:32:PRO:HA	23:x:38:TRP:CD1	2.47	0.49
7:h:58:THR:OG1	7:h:78:GLY:O	2.29	0.49
31:G:63:LYS:HZ2	31:G:65:LYS:HE2	1.75	0.49
34:J:80:LEU:HB2	34:J:97:PRO:HB3	1.94	0.49
34:J:160:VAL:HG13	34:J:161:GLU:N	2.27	0.49
36:L:63:VAL:O	36:L:67:ASN:ND2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:227:A:H1'	53:1:229:C:N4	2.28	0.49
1:b:208:GLY:HA2	1:b:211:ARG:HB2	1.95	0.49
4:e:70:ARG:HG2	4:e:71:LYS:HG2	1.94	0.49
50:Z:8:ASN:C	50:Z:9:GLU:HG3	2.37	0.49
53:1:2328:A:H2'	53:1:2329:U:C6	2.47	0.49
53:1:2590:A:H2'	53:1:2591:C:C6	2.47	0.49
2:c:13:ARG:NH2	53:1:2683:C:H4'	2.28	0.49
8:i:72:THR:HG21	8:i:112:LYS:HG2	1.94	0.49
8:i:98:GLY:HA3	8:i:137:LEU:HG	1.94	0.49
19:t:48:GLN:NE2	19:t:53:VAL:O	2.46	0.49
26:B:11:LYS:HE3	53:1:2616:C:C5'	2.38	0.49
33:I:104:MET:HE2	33:I:170:LEU:HD22	1.94	0.49
34:J:114:LEU:HD13	34:J:122:VAL:HG21	1.94	0.49
38:N:112:ARG:HH12	38:N:114:LYS:HD3	1.77	0.49
51:a:30:LEU:HD21	51:a:185:LEU:HD13	1.95	0.49
52:3:784:A:H2'	52:3:785:G:C8	2.47	0.49
53:1:817:C:H2'	53:1:818:G:O4'	2.13	0.49
53:1:1812:U:H2'	53:1:1813:G:C8	2.47	0.49
53:1:2185:U:H2'	53:1:2186:G:C8	2.47	0.49
1:b:42:ARG:N	1:b:42:ARG:HD2	2.27	0.49
11:l:129:LYS:HG2	53:1:636:G:OP1	2.13	0.49
15:p:63:ILE:HG23	15:p:63:ILE:O	2.11	0.49
16:q:88:GLU:OE1	17:r:52:PRO:HB3	2.13	0.49
22:w:20:LYS:O	22:w:21:ARG:NH1	2.44	0.49
26:B:54:ILE:HG23	26:B:56:LYS:H	1.78	0.49
36:L:85:GLN:HB2	36:L:147:ASN:HD21	1.77	0.49
45:U:68:SER:OG	45:U:71:VAL:HG12	2.13	0.49
52:3:691:G:H2'	52:3:692:U:C6	2.48	0.49
52:3:1171:A:H2'	52:3:1172:C:C6	2.48	0.49
52:3:1259:C:C3'	52:3:1260:G:H5''	2.33	0.49
53:1:1536:C:H4'	53:1:1537:G:C2	2.48	0.49
53:1:2849:U:H3	53:1:2867:G:H5''	1.77	0.49
55:6:29:G:O2'	55:6:30:G:H5'	2.12	0.49
57:7:62:C:C2'	57:7:63:G:H5''	2.43	0.49
18:s:8:ARG:HG3	53:1:494:G:C5'	2.43	0.49
23:x:16:ASN:HB2	23:x:26:ARG:HD2	1.95	0.49
32:H:172:VAL:O	32:H:172:VAL:HG13	2.12	0.49
37:M:14:ARG:HE	37:M:74:ILE:CG2	2.25	0.49
41:Q:88:ASP:HB3	41:Q:89:LEU:HD12	1.93	0.49
42:R:25:GLY:N	52:3:1329:A:H5''	2.25	0.49
51:a:9:ARG:O	51:a:13:GLU:HG2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:530:G:H3'	52:3:531:U:H5''	1.95	0.49
52:3:1033:G:H2'	52:3:1034:G:C4'	2.41	0.49
53:1:249:C:H2'	53:1:2394:C:O2'	2.13	0.49
53:1:861:A:H2'	53:1:862:G:O4'	2.13	0.49
53:1:1020:A:C1'	53:1:1021:A:OP2	2.51	0.49
53:1:1326:U:H2'	53:1:1327:A:H8	1.77	0.49
53:1:2638:G:H22	53:1:2775:G:H2'	1.77	0.49
54:2:65:U:H3'	54:2:108:A:N6	2.27	0.49
55:5:36:U:H2'	55:5:37:A:C8	2.47	0.49
1:b:264:LYS:HE3	53:1:2223:G:O3'	2.13	0.49
2:c:133:THR:HG23	2:c:134:HIS:CD2	2.48	0.49
3:d:77:ILE:HG23	3:d:78:TRP:CD1	2.40	0.49
5:f:8:VAL:HG23	5:f:49:LEU:HD12	1.94	0.49
6:g:47:PHE:HA	6:g:51:ARG:HD2	1.94	0.49
9:j:109:LEU:O	9:j:111:LYS:HD2	2.12	0.49
16:q:29:ARG:HH12	26:B:9:ARG:NE	2.11	0.49
16:q:55:GLN:HA	16:q:58:GLN:CD	2.38	0.49
31:G:198:VAL:C	31:G:199:ILE:HD12	2.38	0.49
34:J:119:VAL:HG21	34:J:122:VAL:CG1	2.42	0.49
36:L:56:SER:OG	36:L:59:GLU:HG2	2.12	0.49
36:L:142:ARG:HG3	55:6:41:C:H4'	1.94	0.49
40:P:124:LYS:O	50:Z:34:ARG:NH2	2.45	0.49
50:Z:23:GLU:OE2	50:Z:24:LYS:N	2.46	0.49
52:3:346:G:C2'	52:3:347:G:H5'	2.43	0.49
52:3:950:U:H2'	52:3:951:G:C8	2.48	0.49
52:3:1502:A:C8	52:3:1505:G:N2	2.80	0.49
53:1:367:G:H2'	53:1:368:A:O4'	2.13	0.49
53:1:1709:U:H2'	53:1:1710:G:H8	1.78	0.49
53:1:2066:C:O2'	53:1:2067:G:H5'	2.12	0.49
53:1:2579:C:O2'	53:1:2580:U:H5'	2.12	0.49
1:b:143:VAL:HB	1:b:153:LEU:HB2	1.94	0.49
3:d:36:ALA:HB1	53:1:443:A:H61	1.78	0.49
4:e:43:ILE:HA	4:e:82:TYR:HE2	1.77	0.49
11:l:26:GLY:C	11:l:27:LEU:HD22	2.38	0.49
19:t:61:LEU:HB3	53:1:1341:G:H4'	1.95	0.49
31:G:24:PRO:HB3	52:3:828:U:H2'	1.95	0.49
32:H:79:LYS:O	32:H:79:LYS:HD3	2.11	0.49
32:H:153:SER:CB	52:3:1057:G:H5''	2.43	0.49
37:M:35:ILE:HG22	37:M:109:VAL:HG11	1.93	0.49
41:Q:21:PRO:HD2	41:Q:94:TYR:OH	2.13	0.49
41:Q:48:LEU:HB2	52:3:520:A:OP1	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:24:U:H2'	52:3:25:C:C6	2.48	0.49
52:3:560:A:H5'	52:3:566:G:N2	2.28	0.49
53:1:2494:G:H2'	53:1:2495:G:H8	1.78	0.49
11:l:90:VAL:HG13	11:l:95:LEU:HD11	1.94	0.49
11:l:111:ILE:HD11	53:1:636:G:C6	2.48	0.49
21:v:20:LEU:HD23	21:v:25:LYS:O	2.13	0.49
33:I:7:LYS:HE2	52:3:408:A:P	2.52	0.49
38:N:105:ARG:NE	52:3:1117:A:O3'	2.40	0.49
45:U:38:PHE:CE1	45:U:51:ARG:HB2	2.48	0.49
46:V:17:GLU:OE2	52:3:255:G:H1'	2.13	0.49
50:Z:11:PHE:O	50:Z:13:VAL:N	2.46	0.49
52:3:1219:A:H2'	52:3:1220:G:C8	2.47	0.49
52:3:1448:C:H2'	52:3:1449:C:C6	2.48	0.49
53:1:521:U:H2'	53:1:522:A:H8	1.76	0.49
53:1:1475:G:O2'	53:1:1476:U:H6	1.96	0.49
53:1:2710:C:H2'	53:1:2711:A:H8	1.78	0.49
1:b:94:LEU:HD21	53:1:1501:G:H4'	1.94	0.48
1:b:208:GLY:C	1:b:210:ALA:H	2.21	0.48
2:c:3:GLY:C	2:c:4:LEU:HD12	2.38	0.48
3:d:98:LYS:HB2	53:1:607:U:OP2	2.13	0.48
9:j:81:ILE:HG23	9:j:82:GLY:N	2.27	0.48
12:m:104:GLU:O	12:m:105:MET:HE2	2.12	0.48
30:F:31:PRO:HA	30:F:34:LYS:NZ	2.28	0.48
45:U:14:ARG:NH1	52:3:618:C:H1'	2.28	0.48
45:U:67:ILE:HD12	45:U:67:ILE:N	2.25	0.48
53:1:1013:C:H2'	53:1:1014:A:C8	2.47	0.48
53:1:1279:G:H2'	53:1:1280:G:C8	2.48	0.48
57:7:74:C:O2'	58:8:52:ASN:ND2	2.46	0.48
58:8:245:ILE:HD12	58:8:245:ILE:H	1.78	0.48
2:c:114:LYS:HD3	53:1:2723:C:OP1	2.13	0.48
13:n:15:SER:HB2	53:1:2710:C:OP1	2.13	0.48
18:s:17:VAL:HG11	18:s:103:ILE:HG12	1.95	0.48
18:s:78:GLU:CD	18:s:78:GLU:H	2.21	0.48
30:F:36:ARG:O	30:F:37:GLN:HB2	2.11	0.48
32:H:86:LEU:O	32:H:90:VAL:HG22	2.13	0.48
33:I:6:PRO:HA	52:3:430:A:O5'	2.12	0.48
33:I:101:VAL:HG22	33:I:106:PHE:HB2	1.96	0.48
38:N:107:ALA:HB2	52:3:1117:A:H4'	1.95	0.48
52:3:1060:U:H2'	52:3:1061:G:H8	1.78	0.48
53:1:1001:A:H2'	53:1:1002:G:O4'	2.13	0.48
53:1:1796:U:H2'	53:1:1797:G:C8	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2001:C:H4'	53:1:2689:U:O2'	2.13	0.48
53:1:2623:G:H2'	53:1:2624:G:H8	1.77	0.48
57:7:6:G:H2'	57:7:7:A:H5''	1.96	0.48
3:d:44:ARG:NH1	53:1:1248:G:OP1	2.45	0.48
5:f:103:ASN:C	5:f:104:LEU:HD22	2.37	0.48
32:H:36:PHE:CD2	43:S:65:GLN:HG2	2.48	0.48
49:Y:79:THR:HA	49:Y:82:ILE:HG12	1.94	0.48
52:3:205:A:H2'	52:3:206:C:O4'	2.11	0.48
53:1:657:U:H2'	53:1:658:U:C6	2.48	0.48
53:1:962:G:N2	53:1:2250:G:H1	2.05	0.48
53:1:1161:C:H2'	53:1:1162:G:H8	1.77	0.48
53:1:1310:G:H3'	53:1:1311:G:C8	2.49	0.48
53:1:1498:C:H2'	53:1:1499:C:C6	2.49	0.48
53:1:2629:U:O2'	53:1:2630:G:H5''	2.13	0.48
53:1:2809:A:H2'	53:1:2810:A:C8	2.47	0.48
55:6:24:U:H2'	55:6:25:C:C6	2.48	0.48
58:8:288:GLU:HB2	58:8:291:GLN:NE2	2.29	0.48
4:e:140:ILE:N	4:e:140:ILE:HD12	2.29	0.48
14:o:88:LYS:HE2	14:o:116:GLN:HE21	1.77	0.48
32:H:110:LEU:O	32:H:201:ILE:HG21	2.13	0.48
32:H:152:VAL:HG12	32:H:197:VAL:HG22	1.94	0.48
37:M:10:LEU:HD22	37:M:74:ILE:HD11	1.94	0.48
42:R:22:TYR:HB3	42:R:65:GLU:OE1	2.14	0.48
51:a:7:ARG:O	51:a:11:ILE:HG13	2.13	0.48
52:3:149:A:H1'	52:3:1446:A:C2	2.48	0.48
52:3:1436:U:H2'	52:3:1437:A:H8	1.78	0.48
53:1:593:U:H2'	53:1:594:U:C6	2.49	0.48
53:1:1279:G:H2'	53:1:1280:G:H8	1.78	0.48
53:1:1432:G:H2'	53:1:1433:A:C8	2.49	0.48
53:1:1794:A:H2'	53:1:1795:C:C6	2.49	0.48
53:1:2557:G:H2'	53:1:2558:C:C6	2.49	0.48
53:1:2743:U:H2'	53:1:2744:G:C5'	2.42	0.48
53:1:2811:G:H2'	53:1:2812:G:H8	1.78	0.48
1:b:65:ASP:OD2	1:b:66:PHE:N	2.46	0.48
2:c:122:VAL:HA	2:c:127:PHE:HB2	1.95	0.48
6:g:116:ARG:C	6:g:117:LEU:HD12	2.38	0.48
7:h:42:ARG:NH1	53:1:1082:U:H4'	2.29	0.48
8:i:52:LEU:HD21	8:i:73:PRO:CB	2.34	0.48
14:o:99:TYR:CZ	14:o:104:GLN:HG3	2.48	0.48
42:R:78:ARG:O	42:R:81:ASP:OD1	2.32	0.48
45:U:2:VAL:HG13	45:U:21:VAL:HG13	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Z:65:ARG:NH2	52:3:1088:G:O3'	2.46	0.48
52:3:1060:U:H3	52:3:1197:A:H61	1.60	0.48
52:3:1453:G:H3'	52:3:1453:G:N3	2.27	0.48
53:1:2193:G:H2'	53:1:2194:U:C6	2.49	0.48
53:1:2538:C:H2'	53:1:2539:C:H6	1.79	0.48
53:1:2667:C:H2'	53:1:2668:G:O4'	2.13	0.48
53:1:2760:C:O2'	53:1:2761:A:H5'	2.14	0.48
1:b:5:CYS:SG	1:b:12:ARG:NH1	2.87	0.48
24:y:28:LEU:HD22	24:y:37:LEU:HD11	1.96	0.48
31:G:68:PHE:HA	31:G:161:PHE:HB3	1.95	0.48
33:I:101:VAL:HA	33:I:104:MET:CG	2.43	0.48
36:L:113:LYS:HB2	36:L:117:LEU:HD12	1.94	0.48
38:N:113:LYS:HA	38:N:120:ALA:HA	1.96	0.48
42:R:104:ASN:O	42:R:105:ALA:HB3	2.14	0.48
52:3:1192:C:H2'	52:3:1193:G:O4'	2.14	0.48
53:1:2039:U:H2'	53:1:2040:G:C8	2.49	0.48
53:1:2533:U:H2'	53:1:2534:A:O4'	2.13	0.48
2:c:66:GLY:HA3	53:1:2786:U:O2'	2.14	0.48
28:D:12:ARG:NH1	28:D:44:VAL:HG11	2.29	0.48
30:F:17:VAL:HG21	30:F:26:ILE:HD12	1.95	0.48
35:K:42:TRP:HB2	35:K:59:TYR:HB2	1.96	0.48
42:R:6:ILE:O	42:R:7:ASN:C	2.56	0.48
46:V:16:MET:HG3	46:V:19:SER:O	2.14	0.48
52:3:216:U:H2'	52:3:217:C:C6	2.48	0.48
52:3:539:A:H2'	52:3:540:G:H8	1.77	0.48
52:3:952:U:H5'	52:3:972:C:H41	1.77	0.48
52:3:1273:C:H2'	52:3:1274:A:O4'	2.14	0.48
52:3:1391:U:H2'	52:3:1392:G:C8	2.48	0.48
53:1:1181:U:H2'	53:1:1182:G:H8	1.77	0.48
53:1:1343:G:N3	53:1:1343:G:H2'	2.28	0.48
53:1:2123:G:H2'	53:1:2124:G:C8	2.47	0.48
53:1:2743:U:H3'	53:1:2744:G:H5''	1.94	0.48
55:6:3:C:H2'	55:6:4:G:H8	1.79	0.48
11:l:39:LYS:HD2	53:1:833:A:P	2.54	0.48
13:n:79:LEU:O	13:n:80:PHE:HB2	2.14	0.48
17:r:74:ILE:N	17:r:74:ILE:HD12	2.29	0.48
21:v:10:LYS:HD2	21:v:10:LYS:N	2.28	0.48
31:G:212:TYR:O	31:G:216:VAL:HG23	2.13	0.48
33:I:130:ASN:HB3	52:3:619:U:H3	1.78	0.48
35:K:37:HIS:NE2	35:K:65:GLU:HB2	2.29	0.48
47:W:54:LEU:O	47:W:58:ILE:HG12	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:114:U:O2'	52:3:115:G:H5'	2.13	0.48
52:3:225:C:C2'	52:3:226:G:H5''	2.44	0.48
52:3:621:A:H2'	52:3:622:A:C8	2.49	0.48
52:3:1429:A:H2'	52:3:1430:A:C8	2.45	0.48
53:1:1331:G:H2'	53:1:1332:G:H5'	1.96	0.48
53:1:1444:G:H2'	53:1:1445:G:C8	2.48	0.48
53:1:2266:A:H4'	53:1:2267:A:C2	2.48	0.48
53:1:2508:G:H1	53:1:2580:U:H3	1.62	0.48
53:1:2836:U:H2'	53:1:2837:A:C8	2.48	0.48
57:7:62:C:H2'	57:7:63:G:C4'	2.43	0.48
3:d:199:MET:HE2	53:1:616:A:O2'	2.14	0.48
18:s:42:LYS:CB	53:1:2010:G:H5''	2.44	0.48
29:E:37:THR:HG21	53:1:2348:U:OP2	2.13	0.48
33:I:73:ASN:HA	33:I:76:LYS:HG2	1.96	0.48
52:3:1522:U:H2'	52:3:1523:G:C8	2.49	0.48
53:1:12:U:H2'	53:1:13:A:H5'	1.96	0.48
53:1:200:U:H2'	53:1:201:C:H5'	1.96	0.48
53:1:1053:C:C2'	53:1:1054:A:H5''	2.41	0.48
53:1:1437:C:H2'	53:1:1438:U:C6	2.49	0.48
53:1:1936:A:H3'	53:1:1937:A:H5'	1.95	0.48
58:8:85:HIS:HB2	58:8:88:TYR:HB2	1.95	0.48
3:d:47:LYS:HG2	3:d:51:GLU:HB3	1.95	0.48
6:g:79:THR:HG23	6:g:145:ASN:HB2	1.95	0.48
9:j:19:ASP:OD2	9:j:21:THR:HG22	2.14	0.48
15:p:4:ILE:O	15:p:8:GLU:HG3	2.14	0.48
16:q:51:GLN:O	16:q:55:GLN:HG3	2.13	0.48
35:K:10:VAL:HG22	35:K:11:HIS:N	2.29	0.48
43:S:81:ILE:HG21	52:3:1202:U:N3	2.28	0.48
45:U:12:LYS:O	45:U:13:LYS:HB2	2.13	0.48
52:3:31:G:N2	52:3:47:C:H5''	2.29	0.48
52:3:715:A:H2'	52:3:716:A:H8	1.78	0.48
53:1:394:C:O2'	53:1:395:U:H5'	2.14	0.48
53:1:570:G:H2'	53:1:2030:A:N7	2.28	0.48
53:1:953:G:O2'	53:1:954:G:H5'	2.13	0.48
53:1:1758:U:C5	53:1:2696:U:H5'	2.49	0.48
53:1:2628:C:O2'	53:1:2781:A:H2'	2.14	0.48
58:8:307:SER:HA	58:8:390:ALA:H	1.79	0.48
7:h:38:MET:HE1	53:1:1058:U:C4'	2.44	0.47
25:z:9:THR:HG23	25:z:10:ARG:H	1.79	0.47
36:L:58:LEU:O	36:L:62:GLU:HG2	2.14	0.47
42:R:53:ASP:HA	42:R:56:ARG:NH1	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:396:C:C3'	52:3:397:A:H5''	2.44	0.47
52:3:1524:C:H2'	52:3:1525:G:H8	1.77	0.47
53:1:414:C:H2'	53:1:415:A:C8	2.48	0.47
53:1:1168:G:H2'	53:1:1169:A:O4'	2.14	0.47
53:1:2415:G:H2'	53:1:2416:C:C6	2.49	0.47
54:2:95:U:H2'	54:2:96:G:C8	2.49	0.47
57:7:74:C:H5''	58:8:52:ASN:O	2.13	0.47
58:8:236:ILE:HG13	58:8:270:ARG:HA	1.96	0.47
2:c:13:ARG:HH11	15:p:55:HIS:HA	1.79	0.47
3:d:173:THR:HA	3:d:199:MET:HE1	1.95	0.47
7:h:67:THR:HG23	7:h:68:PRO:HD3	1.96	0.47
8:i:89:SER:HB3	8:i:135:MET:HA	1.95	0.47
10:k:58:LEU:HD11	10:k:86:LEU:HD23	1.96	0.47
10:k:92:GLU:CD	10:k:92:GLU:H	2.22	0.47
15:p:87:ARG:NH1	15:p:111:GLU:OE2	2.47	0.47
16:q:23:TYR:CE1	53:1:533:G:H5'	2.49	0.47
18:s:73:LYS:HB2	18:s:106:VAL:HB	1.96	0.47
27:C:39:ASP:OD2	27:C:42:VAL:HG22	2.14	0.47
34:J:106:ALA:HB1	34:J:110:MET:HB3	1.96	0.47
38:N:91:GLU:OE2	38:N:94:ARG:NH1	2.47	0.47
40:P:48:GLY:HA2	52:3:688:G:H5'	1.97	0.47
46:V:45:VAL:HG11	46:V:74:LEU:HB2	1.96	0.47
51:a:36:ALA:HA	53:1:2128:G:OP1	2.15	0.47
53:1:576:U:H2'	53:1:577:G:H8	1.78	0.47
53:1:1830:C:H2'	53:1:1831:G:H8	1.78	0.47
57:7:6:G:C2'	57:7:7:A:H5''	2.44	0.47
1:b:61:TYR:OH	1:b:86:ARG:NH2	2.46	0.47
7:h:60:LEU:HA	7:h:64:VAL:HG21	1.95	0.47
8:i:107:GLU:OE2	8:i:108:ILE:HG13	2.14	0.47
12:m:74:THR:HB	12:m:89:VAL:HA	1.96	0.47
24:y:50:VAL:O	24:y:54:LYS:HG3	2.14	0.47
39:O:36:VAL:HG13	39:O:76:ILE:HA	1.96	0.47
48:X:54:ARG:HG3	48:X:55:GLN:CD	2.39	0.47
52:3:423:G:H2'	52:3:424:G:H5'	1.96	0.47
53:1:394:C:H2'	53:1:395:U:O4'	2.14	0.47
53:1:1161:C:H2'	53:1:1162:G:C8	2.49	0.47
53:1:1245:G:H2'	53:1:1246:A:C8	2.49	0.47
53:1:1373:A:C5'	53:1:2212:A:H1'	2.44	0.47
53:1:1965:C:H5''	53:1:1966:A:H2'	1.97	0.47
53:1:2282:G:H4'	53:1:2389:G:O2'	2.14	0.47
55:6:63:G:H2'	55:6:64:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:47:LYS:HA	4:e:50:ASP:OD2	2.14	0.47
6:g:83:LYS:HD3	6:g:84:ALA:N	2.30	0.47
8:i:11:GLN:OE1	8:i:58:ILE:HD11	2.15	0.47
11:l:93:ASN:C	11:l:95:LEU:H	2.20	0.47
13:n:26:GLY:HA2	13:n:75:ILE:HG12	1.96	0.47
16:q:10:ARG:NH2	53:1:1216:G:H5'	2.27	0.47
18:s:41:LYS:HD2	53:1:2009:A:H5'	1.96	0.47
31:G:46:VAL:HG23	31:G:47:PRO:CD	2.42	0.47
31:G:98:GLY:O	31:G:102:ASN:HB2	2.13	0.47
31:G:140:LEU:O	31:G:144:GLU:HG2	2.14	0.47
34:J:10:LEU:HD12	34:J:11:GLN:N	2.30	0.47
36:L:78:ARG:HG2	36:L:83:THR:OG1	2.14	0.47
45:U:11:ALA:HB3	45:U:14:ARG:HB2	1.97	0.47
51:a:51:ASP:OD1	51:a:53:ARG:HB2	2.13	0.47
52:3:59:A:N6	52:3:331:G:H1'	2.29	0.47
52:3:130:A:H1'	52:3:264:C:H5'	1.96	0.47
52:3:367:U:H5'	58:8:280:ARG:HD2	1.95	0.47
52:3:855:U:H2'	52:3:856:C:C6	2.49	0.47
52:3:1128:C:O2'	52:3:1129:C:H5'	2.14	0.47
53:1:996:A:H2'	53:1:997:G:H8	1.80	0.47
53:1:1847:A:H2	53:1:1848:A:H62	1.63	0.47
53:1:2082:A:H2'	53:1:2083:G:O4'	2.15	0.47
53:1:2581:G:H2'	53:1:2581:G:N3	2.29	0.47
6:g:2:GLN:HB2	6:g:39:ALA:HB3	1.95	0.47
14:o:56:LYS:O	14:o:60:GLU:OE1	2.33	0.47
20:u:17:ASP:HB3	20:u:20:LYS:HD2	1.97	0.47
27:C:11:VAL:HA	27:C:19:PHE:HB3	1.97	0.47
37:M:122:GLY:O	37:M:124:ILE:HD12	2.13	0.47
41:Q:66:ILE:HD13	41:Q:73:LEU:HD12	1.96	0.47
51:a:6:LYS:HG3	51:a:7:ARG:H	1.79	0.47
52:3:1323:G:H2'	52:3:1324:A:C8	2.49	0.47
52:3:1346:A:H2'	52:3:1346:A:N3	2.29	0.47
53:1:372:G:H1'	53:1:373:U:H5	1.79	0.47
53:1:546:U:H2'	53:1:547:A:C4'	2.43	0.47
53:1:2834:G:O2'	53:1:2835:A:H5'	2.15	0.47
53:1:2836:U:H2'	53:1:2837:A:H8	1.80	0.47
53:1:2860:A:H2'	53:1:2861:U:H5'	1.96	0.47
1:b:155:ARG:CZ	53:1:1818:U:H5	2.26	0.47
3:d:190:ALA:O	3:d:193:VAL:HG12	2.14	0.47
4:e:157:THR:HG23	4:e:159:ALA:H	1.80	0.47
5:f:27:GLY:HA3	5:f:78:VAL:HB	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:g:96:THR:HG23	6:g:112:LYS:NZ	2.29	0.47
7:h:74:ASP:O	7:h:77:VAL:HG12	2.15	0.47
18:s:74:ILE:HG23	18:s:74:ILE:O	2.15	0.47
31:G:17:HIS:NE2	31:G:187:ASP:OD2	2.47	0.47
50:Z:9:GLU:CB	50:Z:10:PRO:HD3	2.40	0.47
52:3:1287:A:C2	52:3:1353:G:H1'	2.50	0.47
53:1:596:U:H2'	53:1:597:G:H8	1.80	0.47
53:1:1109:C:H2'	53:1:1110:G:O4'	2.14	0.47
53:1:1924:C:H2'	53:1:1925:C:C6	2.49	0.47
53:1:2233:U:H2'	53:1:2234:G:H8	1.79	0.47
58:8:164:PRO:HB2	58:8:167:ASP:HB2	1.95	0.47
58:8:322:PRO:HB3	58:8:352:MET:HA	1.95	0.47
2:c:39:ASP:OD2	2:c:41:ALA:HB3	2.13	0.47
3:d:88:ARG:O	3:d:90:GLN:N	2.48	0.47
7:h:23:LEU:HD13	7:h:118:ILE:CG1	2.38	0.47
7:h:27:VAL:HB	7:h:83:ALA:HB3	1.96	0.47
11:l:57:LEU:N	11:l:60:ARG:HH11	2.13	0.47
16:q:23:TYR:CD1	53:1:533:G:H5'	2.50	0.47
33:I:2:ARG:HB2	33:I:4:LEU:CD1	2.45	0.47
34:J:129:SER:HB3	52:3:20:U:OP2	2.14	0.47
37:M:44:PHE:HE2	37:M:100:ILE:HD11	1.79	0.47
37:M:46:GLU:O	37:M:47:ASP:O	2.33	0.47
37:M:50:VAL:HG22	37:M:50:VAL:O	2.14	0.47
39:O:10:LEU:HD23	39:O:10:LEU:H	1.80	0.47
41:Q:101:LEU:HD23	41:Q:101:LEU:H	1.80	0.47
42:R:114:PRO:HG2	52:3:1228:C:C5'	2.39	0.47
43:S:14:ALA:O	43:S:17:ASP:OD2	2.33	0.47
48:X:27:LYS:HG2	48:X:28:LYS:HG3	1.97	0.47
52:3:321:A:H2	52:3:332:G:H22	1.61	0.47
52:3:328:C:H5'	52:3:329:A:H5'	1.96	0.47
52:3:604:G:H2'	52:3:605:U:O4'	2.15	0.47
52:3:667:G:H2'	52:3:668:G:H8	1.80	0.47
52:3:1527:U:O2'	52:3:1528:U:H5'	2.14	0.47
53:1:211:C:H2'	53:1:212:G:C8	2.49	0.47
53:1:290:U:H2'	53:1:291:G:C8	2.49	0.47
53:1:626:A:H3'	53:1:627:A:C5'	2.45	0.47
53:1:1090:A:H2'	53:1:1091:G:C8	2.49	0.47
53:1:1683:U:H2'	53:1:1684:G:C8	2.50	0.47
53:1:2200:C:H2'	53:1:2201:G:H8	1.79	0.47
57:7:25:C:H2'	57:7:26:A:H5''	1.96	0.47
58:8:12:HIS:CD2	58:8:273:GLU:HA	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:8:172:ARG:HB2	58:8:188:LYS:HE2	1.96	0.47
8:i:74:PRO:O	8:i:78:LEU:HG	2.15	0.47
11:l:26:GLY:O	11:l:27:LEU:HD22	2.15	0.47
16:q:88:GLU:O	17:r:11:GLN:NE2	2.47	0.47
24:y:4:LYS:O	24:y:7:ARG:NH1	2.48	0.47
38:N:33:SER:OG	38:N:36:GLN:HG2	2.14	0.47
40:P:58:THR:HG23	40:P:61:ALA:H	1.80	0.47
44:T:64:LYS:HD3	52:3:755:G:OP2	2.15	0.47
47:W:41:SER:HB3	47:W:51:GLN:HE21	1.80	0.47
52:3:948:C:H2'	52:3:949:A:H8	1.79	0.47
52:3:1004:A:H2'	52:3:1005:A:O4'	2.14	0.47
52:3:1069:C:H42	52:3:1106:G:H1	1.62	0.47
52:3:1096:C:H2'	52:3:1097:C:C6	2.50	0.47
53:1:534:U:H2'	53:1:535:G:C8	2.50	0.47
53:1:995:C:H6	53:1:995:C:H5'	1.80	0.47
53:1:1095:A:H1'	57:7:56:C:N4	2.30	0.47
53:1:1230:A:H2'	53:1:1231:U:C6	2.50	0.47
53:1:1386:C:H2'	53:1:1387:A:H8	1.80	0.47
57:7:76:A:O2'	60:7:101:PHE:C	2.57	0.47
58:8:219:PHE:O	58:8:226:THR:HA	2.15	0.47
12:m:34:LYS:HD2	21:v:81:PRO:O	2.15	0.47
30:F:37:GLN:OE1	53:1:1125:G:C5'	2.63	0.47
33:l:13:ARG:NH2	52:3:542:G:O3'	2.48	0.47
34:J:92:ARG:O	34:J:93:VAL:O	2.32	0.47
37:M:76:ARG:HE	37:M:79:ARG:HA	1.80	0.47
51:a:5:THR:OG1	51:a:6:LYS:N	2.44	0.47
52:3:149:A:H1'	52:3:1446:A:H2	1.80	0.47
52:3:1123:U:O2'	52:3:1124:G:H5'	2.15	0.47
52:3:1497:G:C2'	52:3:1498:U:H5'	2.45	0.47
53:1:74:A:H4'	53:1:75:G:O5'	2.14	0.47
53:1:362:A:H3'	53:1:363:G:H8	1.80	0.47
55:5:69:C:H2'	55:5:70:G:H8	1.80	0.47
3:d:77:ILE:HD11	53:1:1256:G:N3	2.30	0.47
6:g:2:GLN:O	6:g:39:ALA:HB2	2.14	0.47
22:w:42:HIS:HD2	22:w:73:ARG:HB3	1.78	0.47
26:B:49:ARG:HG2	53:1:2884:U:C6	2.48	0.47
30:F:3:VAL:HG21	53:1:2539:C:H4'	1.97	0.47
41:Q:110:LYS:HA	41:Q:110:LYS:HD3	1.82	0.47
50:Z:17:ARG:HA	50:Z:20:ARG:HG2	1.97	0.47
50:Z:23:GLU:C	50:Z:25:ALA:H	2.22	0.47
51:a:54:LYS:HD2	55:6:63:G:H5'	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:893:C:H2'	52:3:894:G:C8	2.50	0.47
53:1:301:G:H1'	53:1:302:C:C6	2.50	0.47
53:1:1468:U:H2'	53:1:1522:A:H61	1.80	0.47
53:1:2257:U:O2'	53:1:2258:C:H5'	2.15	0.47
10:k:25:LEU:HD11	10:k:40:LYS:HB2	1.96	0.46
31:G:22:TRP:HE1	52:3:830:G:C5'	2.28	0.46
33:I:25:ARG:HH21	52:3:410:G:P	2.37	0.46
37:M:74:ILE:HG23	37:M:74:ILE:O	2.15	0.46
44:T:30:LEU:HD21	52:3:658:C:H5'	1.98	0.46
51:a:205:LYS:HD2	53:1:1861:G:H5'	1.97	0.46
52:3:298:A:H2'	52:3:299:G:O4'	2.15	0.46
52:3:742:G:H2'	52:3:743:A:H8	1.79	0.46
52:3:1211:U:H4'	52:3:1213:A:N3	2.30	0.46
53:1:576:U:H2'	53:1:577:G:C8	2.50	0.46
53:1:827:U:H4'	53:1:828:U:C5	2.50	0.46
53:1:1454:C:H2'	53:1:1455:G:H8	1.80	0.46
55:6:3:C:H2'	55:6:4:G:C8	2.50	0.46
1:b:216:ARG:NH2	53:1:691:C:OP1	2.48	0.46
4:e:12:VAL:HG13	4:e:13:LYS:N	2.31	0.46
4:e:92:GLY:O	4:e:95:MET:HG3	2.15	0.46
5:f:77:GLY:HA2	5:f:81:GLY:HA2	1.97	0.46
7:h:118:ILE:CB	7:h:119:PRO:HD3	2.44	0.46
11:l:127:VAL:HG22	11:l:128:THR:N	2.30	0.46
19:t:39:THR:O	19:t:43:ILE:HG12	2.15	0.46
22:w:52:ASP:HA	53:1:2386:A:H4'	1.97	0.46
25:z:4:ILE:HD11	25:z:56:VAL:HG23	1.98	0.46
26:B:11:LYS:HA	26:B:14:MET:CE	2.45	0.46
32:H:76:ILE:HB	32:H:80:GLY:HA2	1.97	0.46
41:Q:53:ARG:HD2	41:Q:53:ARG:HA	1.62	0.46
52:3:663:A:H2'	52:3:664:G:O4'	2.15	0.46
53:1:1458:U:H4'	53:1:1459:G:C4	2.50	0.46
53:1:2041:U:H2'	53:1:2042:A:C8	2.50	0.46
55:5:36:U:H2'	55:5:37:A:H8	1.80	0.46
58:8:20:HIS:CD2	58:8:21:VAL:H	2.33	0.46
58:8:295:LYS:HG2	58:8:296:PRO:HD2	1.98	0.46
2:c:133:THR:OG1	2:c:134:HIS:N	2.44	0.46
13:n:38:LEU:HG	13:n:42:LYS:HE2	1.96	0.46
21:v:32:GLY:O	21:v:93:ARG:NH1	2.45	0.46
27:C:36:LYS:O	27:C:45:HIS:NE2	2.48	0.46
40:P:93:GLU:O	40:P:97:ARG:NH1	2.49	0.46
41:Q:32:VAL:HB	41:Q:55:ARG:HB3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:91:ARG:HD2	53:1:888:C:C5	2.51	0.46
46:V:46:HIS:HB2	46:V:70:LYS:CD	2.45	0.46
52:3:70:U:H4'	52:3:71:A:C8	2.51	0.46
52:3:112:G:H21	52:3:354:G:H5'	1.80	0.46
52:3:133:U:H3	52:3:229:U:H3	1.62	0.46
52:3:195:A:H2'	52:3:196:A:C8	2.51	0.46
52:3:882:C:O2'	52:3:883:C:H5'	2.14	0.46
52:3:1191:A:H2'	52:3:1191:A:N3	2.30	0.46
52:3:1225:A:H2'	52:3:1225:A:N3	2.31	0.46
52:3:1270:G:H2'	52:3:1271:A:H8	1.79	0.46
53:1:521:U:H2'	53:1:522:A:C8	2.50	0.46
53:1:581:C:H2'	53:1:582:A:H8	1.80	0.46
53:1:1597:A:H5''	53:1:1598:A:H5'	1.98	0.46
3:d:109:LEU:O	3:d:113:VAL:HG23	2.16	0.46
12:m:30:SER:HA	12:m:133:LYS:HB2	1.96	0.46
17:r:87:GLN:HG3	53:1:1224:U:O2'	2.15	0.46
23:x:6:VAL:HG13	23:x:7:THR:HG23	1.97	0.46
31:G:20:ARG:HD2	31:G:20:ARG:O	2.15	0.46
36:L:25:PHE:CD1	36:L:100:MET:HG3	2.50	0.46
42:R:13:HIS:CD2	52:3:1296:C:H5'	2.51	0.46
52:3:1481:U:H2'	52:3:1482:G:C8	2.50	0.46
53:1:52:A:H2'	53:1:53:A:C8	2.50	0.46
53:1:799:G:H5''	53:1:800:A:H2'	1.97	0.46
53:1:1045:C:OP1	53:1:1047:G:H5'	2.16	0.46
53:1:1060:U:H4'	53:1:1061:U:C5'	2.46	0.46
53:1:1367:A:C2'	53:1:1368:G:H5'	2.46	0.46
53:1:1589:U:H2'	53:1:1590:A:C8	2.50	0.46
53:1:2360:G:H2'	53:1:2361:G:H5'	1.97	0.46
1:b:216:ARG:HH22	53:1:691:C:C5'	2.19	0.46
4:e:67:THR:OG1	4:e:68:LYS:N	2.48	0.46
8:i:131:THR:O	8:i:135:MET:HG2	2.16	0.46
28:D:34:ARG:NH1	53:1:467:G:OP2	2.48	0.46
36:L:47:GLU:OE2	36:L:48:THR:HG23	2.16	0.46
39:O:44:THR:HG21	39:O:70:HIS:CD2	2.50	0.46
43:S:100:TRP:CZ2	52:3:1368:A:H5''	2.51	0.46
48:X:14:LEU:C	48:X:14:LEU:HD23	2.40	0.46
52:3:536:C:H2'	52:3:537:G:C8	2.51	0.46
53:1:69:C:O2'	53:1:70:G:H5'	2.16	0.46
53:1:828:U:H4'	53:1:831:G:N1	2.31	0.46
53:1:1786:A:H1'	53:1:1938:A:N6	2.30	0.46
53:1:2224:G:H4'	53:1:2226:C:C2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2494:G:H2'	53:1:2495:G:C8	2.50	0.46
53:1:2801:G:H2'	53:1:2802:G:C8	2.50	0.46
4:e:68:LYS:HD2	4:e:81:GLY:C	2.40	0.46
5:f:51:PHE:HZ	5:f:71:LEU:HD13	1.79	0.46
22:w:55:LEU:HD22	22:w:76:ILE:HD12	1.96	0.46
29:E:4:LYS:NZ	53:1:254:G:N7	2.56	0.46
31:G:22:TRP:HE1	52:3:830:G:H5'	1.80	0.46
33:I:61:ARG:NE	33:I:66:VAL:O	2.49	0.46
33:I:72:ARG:HG2	33:I:76:LYS:NZ	2.30	0.46
34:J:119:VAL:CG2	34:J:122:VAL:HG13	2.43	0.46
38:N:113:LYS:HD2	38:N:118:ARG:C	2.39	0.46
39:O:76:ILE:N	39:O:76:ILE:HD12	2.30	0.46
40:P:19:VAL:HA	40:P:82:GLU:H	1.81	0.46
50:Z:19:LYS:HB3	50:Z:24:LYS:CD	2.46	0.46
52:3:9:G:H2'	52:3:10:A:C8	2.50	0.46
52:3:1070:U:H2'	52:3:1071:C:H6	1.81	0.46
53:1:211:C:H2'	53:1:212:G:H8	1.80	0.46
53:1:357:C:H2'	53:1:358:U:C6	2.50	0.46
53:1:1550:C:H2'	53:1:1551:A:C8	2.50	0.46
53:1:1764:C:H2'	53:1:1765:U:C6	2.51	0.46
53:1:2104:C:H2'	53:1:2105:U:C6	2.50	0.46
55:5:51:C:H2'	55:5:52:G:C8	2.51	0.46
57:7:54:U:OP1	58:8:321:THR:OG1	2.34	0.46
58:8:70:TYR:CE1	58:8:79:HIS:HB2	2.51	0.46
1:b:200:MET:SD	52:3:773:G:O3'	2.74	0.46
1:b:216:ARG:CD	1:b:217:PRO:HD2	2.28	0.46
6:g:125:THR:HG23	6:g:146:VAL:HG12	1.96	0.46
12:m:96:ILE:HD13	12:m:126:ILE:HD11	1.97	0.46
13:n:69:ARG:C	13:n:71:ARG:H	2.23	0.46
15:p:43:GLU:HG3	15:p:86:LYS:HZ3	1.81	0.46
31:G:170:ILE:HG23	52:3:1101:A:N7	2.30	0.46
32:H:155:ARG:HH21	32:H:192:TYR:HD1	1.64	0.46
32:H:168:ARG:HH12	52:3:1107:C:C5'	2.26	0.46
42:R:106:ARG:O	42:R:110:GLY:N	2.49	0.46
44:T:52:ARG:HD3	44:T:52:ARG:HA	1.83	0.46
52:3:151:A:H2'	52:3:152:A:O4'	2.16	0.46
52:3:1395:C:H6	52:3:1395:C:H5'	1.81	0.46
53:1:131:A:H2'	53:1:132:G:C8	2.50	0.46
53:1:864:G:HO2'	53:1:865:C:H5'	1.80	0.46
53:1:1139:G:O2'	53:1:1140:C:H5'	2.15	0.46
53:1:1234:U:H2'	53:1:1235:G:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2013:A:H61	53:1:2613:U:H3	1.64	0.46
53:1:2412:A:H2'	53:1:2413:G:O4'	2.15	0.46
58:8:155:ARG:HH21	58:8:170:ILE:HG12	1.81	0.46
1:b:257:ARG:NH2	1:b:266:ILE:HD12	2.31	0.46
10:k:88:ASN:ND2	10:k:93:GLN:O	2.47	0.46
11:l:102:GLY:H	11:l:105:ILE:HG13	1.80	0.46
15:p:87:ARG:HH12	15:p:109:ILE:HD11	1.81	0.46
21:v:72:VAL:CG1	21:v:91:PHE:HB3	2.46	0.46
23:x:71:ARG:NH2	23:x:77:TYR:OH	2.49	0.46
26:B:18:HIS:HD2	53:1:2046:G:H1'	1.80	0.46
38:N:66:VAL:HG22	38:N:67:LYS:N	2.31	0.46
40:P:17:ASP:OD1	40:P:36:ARG:NH1	2.49	0.46
40:P:112:VAL:O	40:P:112:VAL:HG13	2.16	0.46
45:U:4:ILE:HD13	45:U:67:ILE:HG13	1.96	0.46
52:3:50:A:H4'	52:3:51:A:H5'	1.97	0.46
53:1:257:C:H2'	53:1:258:G:O4'	2.15	0.46
53:1:457:A:H61	53:1:470:A:H5''	1.79	0.46
53:1:685:A:H5''	53:1:788:A:H62	1.81	0.46
53:1:729:G:H4'	53:1:763:G:C5'	2.46	0.46
53:1:753:A:H2'	53:1:754:U:C6	2.51	0.46
53:1:818:G:O2'	53:1:819:A:H5''	2.15	0.46
53:1:979:A:H2'	53:1:982:C:N4	2.31	0.46
3:d:146:VAL:HG12	3:d:185:LYS:HB2	1.98	0.46
7:h:18:VAL:HA	7:h:86:MET:HE2	1.97	0.46
7:h:59:LEU:HB3	7:h:62:ARG:CB	2.45	0.46
9:j:32:LEU:HD22	9:j:54:ILE:HG21	1.97	0.46
11:l:135:ILE:HG22	11:l:140:GLY:O	2.16	0.46
17:r:75:VAL:HG22	17:r:86:GLN:HG3	1.97	0.46
17:r:80:ARG:HH12	53:1:571:U:P	2.39	0.46
31:G:170:ILE:HD12	31:G:170:ILE:N	2.31	0.46
53:1:687:C:H2'	53:1:688:U:O4'	2.15	0.46
53:1:1266:G:H22	53:1:2012:G:H2'	1.81	0.46
53:1:1387:A:H2'	53:1:1388:G:C8	2.51	0.46
53:1:1565:C:O2'	53:1:1566:A:H2'	2.16	0.46
53:1:1906:G:C3'	53:1:1907:G:H5''	2.43	0.46
1:b:213:ARG:HH21	53:1:1566:A:C5'	2.24	0.46
6:g:15:LEU:HD21	6:g:56:ALA:HB1	1.97	0.46
10:k:71:ARG:HB3	10:k:72:PRO:HD2	1.98	0.46
32:H:6:PRO:HD2	32:H:183:TYR:CD2	2.51	0.46
40:P:43:TRP:HE1	52:3:686:U:C4'	2.29	0.46
52:3:194:C:O2'	52:3:195:A:H5'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1228:C:H2'	52:3:1229:A:H8	1.81	0.46
52:3:1302:C:O2'	52:3:1303:C:H5'	2.16	0.46
53:1:871:U:H2'	53:1:872:U:C6	2.51	0.46
53:1:2196:C:O2'	53:1:2197:U:H5'	2.15	0.46
53:1:2248:C:C2'	53:1:2249:U:H5'	2.45	0.46
53:1:2537:U:H2'	53:1:2538:C:H6	1.81	0.46
1:b:7:PRO:O	53:1:1695:G:H1'	2.16	0.45
2:c:98:VAL:HG22	2:c:98:VAL:O	2.15	0.45
3:d:115:GLN:HG2	3:d:117:ARG:HD2	1.97	0.45
3:d:115:GLN:CG	3:d:117:ARG:HD2	2.45	0.45
3:d:151:GLY:HA3	3:d:191:ASP:OD2	2.17	0.45
6:g:5:LEU:HD12	6:g:17:ASP:HB2	1.98	0.45
7:h:112:ALA:O	7:h:113:PHE:C	2.59	0.45
28:D:42:LEU:HD12	28:D:42:LEU:N	2.31	0.45
31:G:23:ASN:HB2	31:G:189:ASN:HA	1.97	0.45
38:N:56:MET:HG3	38:N:57:VAL:N	2.30	0.45
44:T:24:THR:HG21	44:T:68:TYR:CE2	2.51	0.45
45:U:31:ARG:HB2	52:3:310:G:C5'	2.45	0.45
47:W:36:GLY:O	47:W:62:ARG:NH2	2.49	0.45
47:W:71:ASP:OD2	47:W:72:ARG:NH1	2.49	0.45
51:a:49:GLY:HA2	51:a:210:LYS:HD2	1.98	0.45
52:3:79:G:H2'	52:3:80:A:O4'	2.16	0.45
52:3:332:G:O2'	52:3:333:U:H5'	2.16	0.45
52:3:541:G:H2'	52:3:542:G:C8	2.51	0.45
52:3:729:A:H2'	52:3:730:G:C8	2.52	0.45
52:3:1346:A:H2'	52:3:1347:G:H4'	1.97	0.45
53:1:548:G:H2'	53:1:549:G:O4'	2.16	0.45
53:1:878:A:H3'	53:1:879:G:H8	1.82	0.45
53:1:1550:C:H2'	53:1:1551:A:H8	1.81	0.45
53:1:2345:G:H21	53:1:2381:A:H3'	1.81	0.45
53:1:2811:G:H2'	53:1:2812:G:C8	2.52	0.45
54:2:97:C:H2'	54:2:98:G:O4'	2.15	0.45
12:m:41:LEU:O	12:m:94:ALA:N	2.48	0.45
31:G:77:GLU:HG2	31:G:78:ALA:N	2.30	0.45
34:J:75:LEU:C	34:J:75:LEU:HD12	2.42	0.45
42:R:3:ILE:O	42:R:5:GLY:N	2.46	0.45
51:a:205:LYS:NZ	53:1:1861:G:H4'	2.31	0.45
52:3:952:U:H5'	52:3:972:C:N4	2.31	0.45
52:3:1477:U:H2'	52:3:1478:U:C6	2.52	0.45
53:1:275:C:H2'	53:1:276:U:C4'	2.39	0.45
53:1:419:U:H2'	53:1:420:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:792:A:H5''	53:1:793:A:H5'	1.97	0.45
53:1:1387:A:H2'	53:1:1388:G:H8	1.81	0.45
53:1:1900:A:H1'	53:1:1970:A:H2'	1.97	0.45
53:1:2221:G:O2'	53:1:2222:C:H5'	2.16	0.45
53:1:2417:C:H2'	53:1:2418:A:H8	1.80	0.45
53:1:2443:C:O2'	53:1:2444:G:H5'	2.17	0.45
53:1:2553:G:H1'	53:1:2582:G:H21	1.81	0.45
58:8:381:GLY:C	58:8:382:ARG:HD3	2.41	0.45
3:d:97:ASN:HB2	3:d:100:MET:HB2	1.98	0.45
9:j:41:LYS:HE3	9:j:52:ASP:OD2	2.16	0.45
14:o:68:LYS:HE3	54:2:49:C:O3'	2.15	0.45
18:s:3:THR:HG23	18:s:3:THR:O	2.16	0.45
24:y:52:ARG:HB2	24:y:52:ARG:CZ	2.46	0.45
32:H:85:LYS:NZ	32:H:89:VAL:HG11	2.31	0.45
35:K:10:VAL:HG22	35:K:11:HIS:H	1.80	0.45
50:Z:49:ALA:O	50:Z:52:VAL:HG12	2.15	0.45
52:3:212:G:H2'	52:3:213:G:H8	1.81	0.45
52:3:763:G:H2'	52:3:764:C:C6	2.51	0.45
52:3:1522:U:H2'	52:3:1523:G:H8	1.80	0.45
53:1:706:A:H2'	53:1:707:G:O4'	2.16	0.45
53:1:1549:A:H2'	53:1:1550:C:C6	2.52	0.45
53:1:2241:A:H2'	53:1:2242:G:C8	2.51	0.45
53:1:2263:C:H2'	53:1:2264:C:C6	2.52	0.45
53:1:2459:A:H2'	53:1:2459:A:N3	2.32	0.45
53:1:2498:C:O2'	53:1:2499:C:H5'	2.16	0.45
53:1:2626:C:O2'	53:1:2627:G:H5'	2.16	0.45
57:7:62:C:H2'	57:7:63:G:C5'	2.45	0.45
1:b:135:PRO:HG2	35:K:80:PHE:HD1	1.82	0.45
1:b:172:THR:OG1	1:b:182:LYS:HE2	2.16	0.45
1:b:204:LEU:HD22	1:b:213:ARG:HH12	1.81	0.45
5:f:163:TYR:H	5:f:166:GLU:HB2	1.80	0.45
7:h:94:ARG:HD3	7:h:131:THR:HG22	1.98	0.45
12:m:2:LEU:O	12:m:69:PRO:HG2	2.16	0.45
13:n:18:GLN:HE21	13:n:22:ARG:NH1	2.14	0.45
16:q:44:TYR:HD1	16:q:47:ARG:HE	1.64	0.45
33:I:131:ILE:HG22	33:I:133:SER:H	1.81	0.45
34:J:108:GLY:H	52:3:9:G:C5'	2.29	0.45
41:Q:71:HIS:HA	41:Q:98:ARG:HH22	1.80	0.45
43:S:41:TRP:O	43:S:45:LEU:HG	2.16	0.45
52:3:86:G:H4'	52:3:87:C:C6	2.51	0.45
52:3:815:A:H4'	52:3:817:C:C5	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1058:G:H1	52:3:1199:U:H3	1.63	0.45
52:3:1137:C:H4'	52:3:1138:G:C2	2.51	0.45
53:1:208:C:H2'	53:1:209:C:C6	2.51	0.45
53:1:372:G:HO2'	53:1:373:U:P	2.39	0.45
53:1:1152:C:O2'	53:1:1153:C:H5'	2.15	0.45
53:1:2114:A:H2'	53:1:2114:A:N3	2.32	0.45
58:8:135:LEU:HB2	58:8:172:ARG:HA	1.99	0.45
5:f:157:LYS:HD3	53:1:2658:C:H5''	1.98	0.45
6:g:8:LYS:O	6:g:8:LYS:HG3	2.16	0.45
8:i:35:MET:O	8:i:39:LYS:HG2	2.16	0.45
11:l:88:GLY:O	11:l:121:THR:N	2.49	0.45
21:v:51:GLN:OE1	21:v:86:LEU:HD11	2.17	0.45
31:G:96:LEU:HB2	31:G:99:MET:HG2	1.98	0.45
33:I:27:ILE:HG13	33:I:29:THR:HG23	1.98	0.45
33:I:104:MET:CE	33:I:170:LEU:HD22	2.46	0.45
34:J:59:ILE:O	34:J:63:MET:HG3	2.17	0.45
34:J:162:GLU:O	37:M:113:ARG:NH2	2.49	0.45
35:K:3:HIS:HD2	35:K:92:THR:HB	1.81	0.45
37:M:49:LYS:HB2	37:M:59:GLU:HB3	1.98	0.45
52:3:503:C:O2'	52:3:504:C:H5'	2.17	0.45
52:3:555:U:H2'	52:3:556:C:C6	2.51	0.45
52:3:925:G:H1'	52:3:1502:A:C4	2.51	0.45
52:3:939:G:H21	52:3:1375:A:H2	1.64	0.45
53:1:558:U:H2'	53:1:559:G:H8	1.82	0.45
53:1:2322:A:H2'	53:1:2323:G:O4'	2.16	0.45
57:7:74:C:C2'	57:7:75:C:H5'	2.46	0.45
58:8:130:TYR:HB3	58:8:200:ILE:HG12	1.99	0.45
2:c:109:VAL:HG11	2:c:193:VAL:HG23	1.97	0.45
11:l:30:THR:O	11:l:32:GLY:N	2.49	0.45
17:r:79:ARG:HD2	53:1:564:C:OP2	2.17	0.45
26:B:28:SER:HB3	26:B:39:ARG:HD2	1.97	0.45
33:I:98:ASP:HA	33:I:101:VAL:HG12	1.98	0.45
36:L:6:ILE:HD12	36:L:6:ILE:N	2.31	0.45
40:P:62:ALA:HB1	40:P:95:THR:HB	1.98	0.45
52:3:142:G:H2'	52:3:143:A:O4'	2.17	0.45
52:3:236:A:H2'	52:3:237:G:H8	1.82	0.45
52:3:665:A:O4'	52:3:733:G:H1'	2.17	0.45
52:3:784:A:H2'	52:3:785:G:H8	1.82	0.45
52:3:869:G:H4'	52:3:872:A:C8	2.52	0.45
53:1:16:C:H2'	53:1:17:G:C8	2.52	0.45
53:1:1266:G:N2	53:1:2012:G:H2'	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2875:C:H2'	53:1:2876:G:H8	1.80	0.45
57:7:6:G:H3'	57:7:7:A:C5'	2.40	0.45
58:8:69:GLU:HB3	58:8:262:PHE:CE2	2.51	0.45
58:8:332:TYR:HB2	58:8:376:ALA:HB3	1.98	0.45
1:b:77:VAL:HB	1:b:112:GLY:H	1.81	0.45
1:b:93:VAL:HG11	1:b:115:ILE:CD1	2.45	0.45
1:b:157:ALA:HB1	1:b:196:ASN:O	2.16	0.45
7:h:11:ILE:O	7:h:15:VAL:HG23	2.17	0.45
8:i:31:GLY:O	8:i:64:ARG:NH1	2.45	0.45
10:k:7:MET:HG3	10:k:18:ARG:HD2	1.99	0.45
10:k:63:VAL:HG23	10:k:64:ARG:N	2.32	0.45
16:q:47:ARG:NH2	16:q:51:GLN:HE21	2.15	0.45
27:C:4:ILE:HG23	27:C:27:ARG:CZ	2.47	0.45
29:E:46:LYS:HD3	29:E:46:LYS:N	2.32	0.45
32:H:179:ALA:HB1	32:H:202:PHE:HE1	1.82	0.45
33:I:99:ASN:O	33:I:102:TYR:HB3	2.16	0.45
36:L:27:ASN:HB3	52:3:1374:A:O2'	2.17	0.45
36:L:149:ALA:HB1	40:P:58:THR:HG21	1.98	0.45
37:M:42:GLU:HG2	37:M:100:ILE:HD13	1.97	0.45
40:P:112:VAL:O	40:P:114:PRO:HD3	2.17	0.45
41:Q:99:GLY:HA3	52:3:35:G:H4'	1.98	0.45
52:3:232:G:H1'	52:3:262:A:H61	1.82	0.45
52:3:396:C:C2'	52:3:397:A:H5''	2.46	0.45
52:3:1346:A:C2'	52:3:1347:G:H4'	2.47	0.45
52:3:1390:U:H2'	52:3:1391:U:C6	2.52	0.45
52:3:1403:C:H1'	52:3:1500:A:N1	2.32	0.45
52:3:1499:A:O2'	52:3:1500:A:H5'	2.16	0.45
53:1:889:C:H2'	53:1:890:C:O4'	2.16	0.45
53:1:1190:G:H2'	53:1:1191:G:H8	1.81	0.45
53:1:1316:U:H2'	53:1:1317:G:H8	1.81	0.45
53:1:1601:G:O2'	53:1:1602:U:H5'	2.17	0.45
53:1:2036:C:H2'	53:1:2037:A:C8	2.52	0.45
53:1:2041:U:H2'	53:1:2042:A:H8	1.81	0.45
53:1:2340:A:H2'	53:1:2341:G:C8	2.51	0.45
54:2:95:U:H2'	54:2:96:G:H8	1.82	0.45
2:c:14:ILE:HA	15:p:11:GLN:NE2	2.32	0.45
8:i:101:SER:HA	8:i:140:GLU:O	2.16	0.45
20:u:25:LYS:HD3	20:u:36:GLU:HG2	1.97	0.45
25:z:31:ILE:HG13	25:z:31:ILE:O	2.17	0.45
33:I:117:VAL:HG22	33:I:122:ILE:HG13	1.99	0.45
33:I:190:LEU:CD1	33:I:192:ALA:H	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:70:GLY:HA3	52:3:1371:G:O3'	2.17	0.45
39:O:31:ARG:CD	39:O:32:THR:HG23	2.47	0.45
39:O:76:ILE:HD12	39:O:76:ILE:H	1.82	0.45
50:Z:33:ARG:O	50:Z:34:ARG:HB2	2.17	0.45
52:3:357:G:OP1	52:3:367:U:H5''	2.17	0.45
53:1:694:U:OP1	53:1:1569:A:H1'	2.17	0.45
53:1:854:C:H2'	53:1:855:G:C8	2.51	0.45
53:1:1935:G:H1'	53:1:1964:G:N2	2.32	0.45
53:1:2364:C:H2'	53:1:2365:G:O4'	2.17	0.45
53:1:2391:G:H2'	53:1:2424:C:N4	2.31	0.45
53:1:2469:A:H2'	53:1:2470:G:O4'	2.16	0.45
53:1:2898:U:H2'	53:1:2899:A:C8	2.52	0.45
55:5:57:A:H2'	55:5:58:A:H5'	1.99	0.45
58:8:207:ILE:HG23	58:8:236:ILE:HB	1.98	0.45
1:b:75:ALA:HB3	1:b:115:ILE:HG13	1.99	0.45
13:n:51:LEU:HD21	13:n:69:ARG:HD2	1.98	0.45
15:p:16:VAL:O	15:p:16:VAL:HG13	2.16	0.45
18:s:65:ASP:OD1	18:s:68:ASP:HB3	2.17	0.45
29:E:39:ARG:NH1	53:1:2362:C:H5''	2.32	0.45
33:I:28:ASP:OD2	33:I:28:ASP:N	2.50	0.45
38:N:33:SER:H	38:N:36:GLN:HG2	1.82	0.45
52:3:1354:U:H2'	52:3:1355:G:H8	1.82	0.45
53:1:167:A:H2'	53:1:168:G:O4'	2.17	0.45
53:1:440:C:H2'	53:1:441:U:C6	2.51	0.45
53:1:610:C:H2'	53:1:611:C:H6	1.82	0.45
55:6:66:C:H2'	55:6:67:C:C6	2.52	0.45
57:7:52:G:H5'	58:8:327:TYR:HB2	1.98	0.45
58:8:304:LYS:HD2	58:8:362:THR:HG22	1.98	0.45
1:b:206:LYS:HB2	1:b:209:ALA:HB2	1.99	0.45
2:c:125:TRP:CD1	2:c:160:LYS:HB3	2.52	0.45
8:i:94:LYS:NZ	53:1:1076:C:H4'	2.33	0.45
9:j:118:MET:HA	9:j:121:LYS:HZ2	1.81	0.45
11:l:9:ALA:HB3	11:l:12:SER:OG	2.16	0.45
14:o:15:ARG:HH22	54:2:8:C:H5''	1.82	0.45
21:v:9:ARG:HB3	21:v:41:GLU:HB3	1.98	0.45
26:B:37:HIS:HB3	26:B:43:THR:HG22	1.99	0.45
30:F:17:VAL:O	30:F:23:ILE:HD12	2.17	0.45
31:G:107:ARG:O	31:G:110:ILE:HG22	2.16	0.45
32:H:53:ARG:O	32:H:68:HIS:ND1	2.44	0.45
36:L:150:PHE:HZ	40:P:55:ARG:HD2	1.81	0.45
39:O:5:ARG:HB3	39:O:6:ILE:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:P:28:ASN:HD22	40:P:56:LYS:HD2	1.82	0.45
45:U:26:ASN:HD21	45:U:31:ARG:H	1.64	0.45
47:W:11:ARG:HD2	52:3:845:A:N3	2.32	0.45
52:3:9:G:H2'	52:3:10:A:H8	1.81	0.45
52:3:212:G:H2'	52:3:213:G:C8	2.52	0.45
52:3:423:G:C2'	52:3:424:G:H5'	2.47	0.45
52:3:1478:U:H2'	52:3:1479:C:C6	2.52	0.45
53:1:2514:U:H2'	53:1:2515:C:C6	2.52	0.45
57:7:25:C:C2'	57:7:26:A:H5''	2.47	0.45
57:7:76:A:HO2'	60:7:101:PHE:C	2.24	0.45
58:8:87:ASP:O	58:8:90:LYS:NZ	2.50	0.45
1:b:122:ALA:HB3	1:b:124:LYS:NZ	2.32	0.44
2:c:200:ASP:C	2:c:201:LEU:HD22	2.41	0.44
5:f:163:TYR:HB2	5:f:166:GLU:HB2	1.99	0.44
8:i:91:LYS:N	8:i:92:PRO:HD3	2.32	0.44
12:m:4:PRO:HG3	12:m:68:PHE:HE2	1.82	0.44
15:p:50:ARG:HE	15:p:52:ARG:HG3	1.81	0.44
19:t:48:GLN:HE21	19:t:55:VAL:H	1.64	0.44
30:F:30:GLU:HG2	30:F:33:HIS:CD2	2.52	0.44
31:G:20:ARG:HD2	31:G:20:ARG:C	2.42	0.44
43:S:2:LYS:HD2	52:3:1049:U:C2'	2.46	0.44
50:Z:59:LEU:C	50:Z:59:LEU:HD12	2.42	0.44
52:3:893:C:H2'	52:3:894:G:H8	1.82	0.44
52:3:985:C:H2'	52:3:986:U:C6	2.52	0.44
52:3:1324:A:H2'	52:3:1325:C:O4'	2.18	0.44
53:1:1021:A:H3'	53:1:1021:A:N3	2.32	0.44
53:1:1923:U:H2'	53:1:1924:C:C6	2.51	0.44
53:1:2277:G:H2'	53:1:2278:A:C5'	2.42	0.44
53:1:2609:U:H5'	53:1:2610:C:OP2	2.17	0.44
57:7:48:C:H5'	57:7:50:U:OP2	2.16	0.44
57:7:53:G:H5''	58:8:321:THR:CG2	2.47	0.44
4:e:65:LEU:HD12	54:2:41:G:H21	1.82	0.44
4:e:161:SER:HB3	4:e:164:GLU:HB3	1.98	0.44
7:h:38:MET:HE1	53:1:1058:U:C5'	2.47	0.44
10:k:34:GLY:H	10:k:37:ASP:HB2	1.82	0.44
24:y:25:GLN:HE21	24:y:29:ARG:NH2	2.15	0.44
31:G:65:LYS:HB2	31:G:157:PRO:HA	1.99	0.44
31:G:209:VAL:HA	31:G:212:TYR:CD2	2.52	0.44
32:H:113:LYS:HB2	32:H:113:LYS:HE3	1.78	0.44
35:K:12:PRO:O	35:K:15:SER:OG	2.20	0.44
38:N:62:LEU:HD12	38:N:62:LEU:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:95:PRO:N	42:R:108:ARG:HG2	2.32	0.44
45:U:33:ILE:N	45:U:33:ILE:HD12	2.32	0.44
52:3:1342:C:H2'	52:3:1343:G:H8	1.82	0.44
52:3:1436:U:H2'	52:3:1437:A:C8	2.52	0.44
53:1:1849:G:H2'	53:1:1850:G:H8	1.82	0.44
53:1:2850:A:C2	53:1:2869:G:H4'	2.52	0.44
58:8:128:VAL:CG2	58:8:131:ILE:HD11	2.48	0.44
58:8:205:ARG:O	58:8:207:ILE:HD12	2.17	0.44
3:d:131:THR:HG22	3:d:160:ALA:O	2.17	0.44
4:e:45:ASP:O	4:e:48:LEU:HB3	2.16	0.44
4:e:102:LEU:O	4:e:107:VAL:HG23	2.17	0.44
12:m:40:ARG:NH2	53:1:958:U:H5	2.15	0.44
13:n:50:PRO:O	13:n:53:THR:HB	2.17	0.44
13:n:63:ARG:NH1	53:1:1454:C:O5'	2.51	0.44
14:o:31:THR:HG21	54:2:28:C:OP1	2.18	0.44
19:t:54:GLU:HB3	19:t:88:LYS:HD2	2.00	0.44
21:v:46:LYS:O	21:v:50:MET:HG2	2.18	0.44
31:G:142:LYS:HD3	52:3:1098:C:OP1	2.17	0.44
39:O:34:ALA:C	39:O:35:GLN:HG3	2.42	0.44
40:P:30:ILE:HG13	40:P:45:THR:HG22	1.99	0.44
40:P:78:ILE:HD12	40:P:78:ILE:N	2.32	0.44
44:T:70:LYS:HD2	44:T:71:ARG:HH12	1.82	0.44
52:3:1114:C:H2'	52:3:1115:U:O4'	2.17	0.44
52:3:1251:A:H2'	52:3:1252:A:O4'	2.17	0.44
52:3:1409:C:H2'	52:3:1410:A:H8	1.81	0.44
52:3:1464:U:H2'	52:3:1465:A:C8	2.53	0.44
53:1:214:G:O2'	53:1:215:G:H5'	2.18	0.44
53:1:1308:A:H2'	53:1:1309:G:O4'	2.17	0.44
53:1:1883:U:H2'	53:1:1884:G:O4'	2.17	0.44
53:1:2008:C:H2'	53:1:2009:A:C8	2.53	0.44
53:1:2163:A:H2'	53:1:2164:C:H5'	1.98	0.44
53:1:2553:G:H3'	53:1:2554:U:C5'	2.43	0.44
55:5:29:G:H2'	55:5:30:G:H8	1.83	0.44
58:8:232:VAL:HB	58:8:271:ALA:HA	1.98	0.44
3:d:164:LEU:HB3	3:d:167:VAL:HG22	2.00	0.44
14:o:102:ARG:O	14:o:106:LEU:N	2.50	0.44
28:D:34:ARG:NH2	28:D:39:ARG:HD3	2.33	0.44
40:P:108:ASN:HB2	50:Z:6:ARG:HG3	1.98	0.44
44:T:69:LEU:HD23	44:T:77:TYR:HD1	1.82	0.44
48:X:5:LYS:HG2	52:3:1314:C:OP2	2.17	0.44
52:3:541:G:H2'	52:3:542:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:64:A:H2'	53:1:65:U:C6	2.52	0.44
53:1:433:C:O2'	53:1:434:U:H5'	2.17	0.44
53:1:1055:G:H2'	53:1:1056:G:O4'	2.17	0.44
53:1:1300:G:H4'	53:1:1301:A:H5'	1.98	0.44
53:1:1373:A:C4'	53:1:2212:A:H1'	2.47	0.44
53:1:1773:A:H2'	53:1:1774:C:O4'	2.17	0.44
53:1:1981:A:C5'	53:1:1982:U:OP2	2.65	0.44
58:8:125:GLN:HB3	58:8:374:ARG:HD2	1.99	0.44
2:c:48:ILE:HD13	2:c:84:LEU:HD21	1.98	0.44
7:h:98:GLU:HA	7:h:101:LYS:HE2	2.00	0.44
8:i:106:GLN:HG3	8:i:125:THR:HG21	1.98	0.44
14:o:63:LYS:NZ	54:2:51:G:H5'	2.32	0.44
21:v:56:PHE:CE1	21:v:61:LEU:HD21	2.53	0.44
32:H:46:LEU:HD12	32:H:49:ALA:HB2	1.98	0.44
33:I:30:LYS:CE	52:3:411:A:H2'	2.46	0.44
48:X:79:TYR:CE1	48:X:80:ARG:HG3	2.53	0.44
52:3:355:C:H2'	52:3:356:A:O4'	2.18	0.44
52:3:375:U:H2'	52:3:376:G:H8	1.82	0.44
52:3:613:C:H2'	52:3:614:C:C6	2.52	0.44
52:3:909:A:C2'	52:3:910:C:H5'	2.48	0.44
52:3:916:U:H2'	52:3:917:G:C8	2.51	0.44
52:3:1434:A:H2'	52:3:1435:G:O4'	2.17	0.44
53:1:12:U:C2'	53:1:13:A:H5'	2.47	0.44
53:1:443:A:H5''	53:1:444:C:C5'	2.48	0.44
53:1:1086:A:H3'	53:1:1086:A:N3	2.33	0.44
53:1:1911:U:H2'	53:1:1918:A:N1	2.33	0.44
53:1:2314:A:H2'	53:1:2315:G:C8	2.53	0.44
55:5:43:A:O2'	55:5:44:A:H5'	2.18	0.44
55:5:76:A:H5'	55:5:76:A:C8	2.53	0.44
58:8:252:GLN:OE1	58:8:252:GLN:N	2.48	0.44
58:8:318:GLY:HA2	58:8:384:VAL:HA	1.98	0.44
58:8:374:ARG:HA	58:8:388:VAL:HA	1.98	0.44
2:c:170:VAL:HG12	2:c:171:THR:N	2.28	0.44
4:e:15:LEU:HD11	4:e:19:PHE:HD2	1.82	0.44
6:g:51:ARG:HA	6:g:55:GLU:OE2	2.18	0.44
9:j:114:LEU:O	9:j:118:MET:HG2	2.17	0.44
31:G:23:ASN:O	31:G:26:MET:HG2	2.18	0.44
32:H:112:ALA:HB3	32:H:184:ASN:ND2	2.32	0.44
41:Q:63:THR:OG1	41:Q:91:GLY:O	2.34	0.44
52:3:651:C:H2'	52:3:652:U:C6	2.53	0.44
52:3:661:G:O2'	52:3:662:U:H5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:861:G:H2'	52:3:862:C:O4'	2.18	0.44
52:3:1088:G:H21	52:3:1167:A:H61	1.65	0.44
52:3:1120:C:H2'	52:3:1121:U:H6	1.83	0.44
52:3:1128:C:H2'	52:3:1129:C:C6	2.52	0.44
52:3:1306:A:H61	52:3:1331:G:H1'	1.81	0.44
53:1:1111:A:O2'	53:1:1112:G:H4'	2.17	0.44
53:1:1417:C:H2'	53:1:1418:G:O4'	2.18	0.44
53:1:1572:A:O2'	53:1:1573:G:H5'	2.18	0.44
53:1:1972:G:H2'	53:1:1973:G:H8	1.82	0.44
54:2:56:G:H4'	54:2:57:A:C8	2.52	0.44
55:6:26:G:H1	55:6:44:A:H61	1.65	0.44
58:8:319:ARG:HB2	58:8:353:PRO:HG3	1.99	0.44
58:8:333:PHE:HB3	58:8:375:PHE:HB3	1.98	0.44
1:b:264:LYS:HD2	53:1:2224:G:OP1	2.18	0.44
2:c:85:ALA:N	2:c:88:GLU:OE1	2.49	0.44
10:k:23:LYS:HE2	10:k:23:LYS:HB2	1.87	0.44
10:k:40:LYS:HE2	10:k:89:ASN:HD21	1.81	0.44
17:r:46:GLU:CD	17:r:47:VAL:N	2.75	0.44
18:s:20:VAL:HG21	18:s:43:ALA:HB3	2.00	0.44
21:v:58:SER:O	21:v:73:LYS:NZ	2.50	0.44
22:w:58:LYS:HE3	53:1:2366:A:H4'	1.99	0.44
32:H:96:VAL:HG22	32:H:97:PRO:CD	2.48	0.44
33:I:59:LYS:O	33:I:63:ILE:HG13	2.17	0.44
33:I:153:ARG:HH12	52:3:406:G:H21	1.66	0.44
36:L:76:SER:HB3	36:L:85:GLN:HE22	1.83	0.44
38:N:91:GLU:HA	38:N:94:ARG:HB2	2.00	0.44
44:T:50:HIS:CG	52:3:667:G:H4'	2.53	0.44
47:W:67:LEU:HA	47:W:68:PRO:HD3	1.87	0.44
50:Z:20:ARG:N	50:Z:24:LYS:HE2	2.32	0.44
52:3:950:U:H2'	52:3:951:G:H8	1.82	0.44
52:3:979:C:H2'	52:3:980:C:H5'	2.00	0.44
52:3:1325:C:O2'	52:3:1326:U:H5'	2.18	0.44
52:3:1409:C:H2'	52:3:1410:A:C8	2.52	0.44
52:3:1412:C:H2'	52:3:1413:A:C8	2.53	0.44
53:1:543:G:H2'	53:1:544:C:O4'	2.18	0.44
53:1:1026:G:H2'	53:1:1027:A:C8	2.52	0.44
53:1:2554:U:H2'	53:1:2555:U:C6	2.52	0.44
55:6:43:A:H2'	55:6:44:A:C8	2.53	0.44
58:8:239:VAL:HA	58:8:256:CYS:SG	2.58	0.44
1:b:184:GLU:HB3	1:b:187:CYS:SG	2.57	0.44
3:d:68:ALA:HA	53:1:1255:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:32:LYS:HD3	4:e:91:ARG:HH22	1.82	0.44
11:l:110:VAL:HB	11:l:127:VAL:HG23	1.99	0.44
13:n:79:LEU:C	13:n:81:ASN:H	2.26	0.44
17:r:22:LEU:HD12	17:r:23:GLU:O	2.18	0.44
33:I:123:MET:HA	33:I:128:VAL:HA	1.99	0.44
34:J:101:GLY:H	34:J:121:ASN:HB2	1.83	0.44
45:U:69:ASP:OD2	45:U:70:ARG:N	2.48	0.44
53:1:553:G:H2'	53:1:554:U:C6	2.53	0.44
53:1:596:U:H2'	53:1:597:G:C8	2.53	0.44
53:1:1468:U:H2'	53:1:1522:A:N6	2.32	0.44
53:1:2180:U:H4'	55:6:17(A):U:O4'	2.18	0.44
53:1:2752:C:H2'	53:1:2753:A:O4'	2.18	0.44
54:2:88:C:C4'	54:2:89:U:OP1	2.66	0.44
55:5:42:G:H2'	55:5:43:A:C8	2.52	0.44
55:5:51:C:H2'	55:5:52:G:H8	1.83	0.44
57:7:25:C:H2'	57:7:26:A:C5'	2.47	0.44
58:8:106:VAL:O	58:8:106:VAL:HG13	2.18	0.44
58:8:246:VAL:HB	58:8:292:VAL:HG13	2.00	0.44
58:8:299:ILE:HD11	58:8:302:HIS:HE1	1.83	0.44
3:d:122:GLU:HG2	3:d:123:LYS:N	2.33	0.44
6:g:7:ASP:C	6:g:9:VAL:H	2.26	0.44
6:g:121:VAL:HG22	6:g:121:VAL:O	2.18	0.44
7:h:54:VAL:O	7:h:56:ARG:HD2	2.17	0.44
12:m:29:GLY:HA2	12:m:106:ASP:HB2	2.00	0.44
17:r:53:PHE:O	17:r:54:VAL:C	2.59	0.44
23:x:11:PRO:HB3	23:x:29:LEU:HD23	2.00	0.44
31:G:116:LEU:HB3	31:G:140:LEU:HD13	1.99	0.44
33:I:183:ARG:HD2	33:I:184:LYS:O	2.18	0.44
38:N:17:ARG:HH11	52:3:1147:C:H1'	1.83	0.44
38:N:30:ASN:O	38:N:31:GLN:HB2	2.17	0.44
41:Q:77:SER:HB2	41:Q:102:ASP:HB3	1.99	0.44
41:Q:107:LYS:HE2	41:Q:107:LYS:HB3	1.80	0.44
46:V:46:HIS:CB	46:V:70:LYS:HD3	2.46	0.44
52:3:871:U:H5''	52:3:872:A:OP2	2.18	0.44
52:3:884:U:H4'	52:3:885:G:H5''	2.00	0.44
52:3:959:A:H2'	52:3:960:U:H4'	2.00	0.44
52:3:1256:A:H1'	52:3:1258:G:C4	2.53	0.44
52:3:1301:U:O2	52:3:1301:U:H2'	2.17	0.44
53:1:372:G:O2'	53:1:373:U:P	2.76	0.44
53:1:481:G:H1'	53:1:506:G:H21	1.81	0.44
53:1:1355:G:H2'	53:1:1356:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1360:G:H2'	53:1:1361:G:H5'	2.00	0.44
53:1:1412:U:H2'	53:1:1413:A:C8	2.53	0.44
53:1:1423:G:H2'	53:1:1424:G:C8	2.53	0.44
53:1:2011:U:H2'	53:1:2012:G:O4'	2.16	0.44
53:1:2078:C:O2'	53:1:2079:U:H5'	2.18	0.44
53:1:2584:U:H2'	53:1:2585:U:H2'	1.98	0.44
54:2:76:G:H2'	54:2:77:U:O4'	2.17	0.44
58:8:333:PHE:CD1	58:8:333:PHE:N	2.85	0.44
4:e:162:ASP:OD1	4:e:162:ASP:N	2.50	0.43
12:m:41:LEU:HD21	12:m:46:ILE:HG12	2.00	0.43
18:s:67:ASP:O	18:s:69:LEU:N	2.51	0.43
19:t:2:ILE:HD11	53:1:144:A:H4'	1.99	0.43
26:B:39:ARG:O	26:B:40:HIS:HB2	2.19	0.43
33:I:61:ARG:HH21	33:I:67:LEU:HA	1.83	0.43
33:I:72:ARG:HG2	33:I:76:LYS:HZ1	1.83	0.43
33:I:138:PRO:HB3	33:I:183:ARG:HA	2.00	0.43
33:I:171:GLU:HB2	33:I:180:THR:HB	2.00	0.43
50:Z:13:VAL:O	50:Z:14:ALA:C	2.61	0.43
52:3:224:U:H2'	52:3:225:C:C6	2.52	0.43
52:3:744:C:H2'	52:3:745:G:H8	1.83	0.43
52:3:772:U:H2'	52:3:773:G:C8	2.53	0.43
53:1:2786:U:H2'	53:1:2787:C:C6	2.53	0.43
58:8:19:GLY:N	58:8:25:LYS:HD3	2.32	0.43
1:b:156:SER:OG	1:b:159:THR:HG21	2.19	0.43
1:b:245:THR:OG1	1:b:246:PRO:HD2	2.18	0.43
7:h:56:ARG:HD3	53:1:1084:A:C1'	2.48	0.43
8:i:12:VAL:HG12	53:1:1061:U:O2	2.18	0.43
11:l:20:GLY:O	11:l:21:ARG:NH2	2.51	0.43
11:l:108:ALA:HB3	11:l:125:LEU:HD11	2.00	0.43
15:p:64:SER:OG	15:p:65:ASN:N	2.48	0.43
19:t:48:GLN:NE2	19:t:55:VAL:H	2.16	0.43
24:y:25:GLN:HE21	24:y:29:ARG:HH22	1.66	0.43
32:H:166:TRP:H	32:H:166:TRP:HD1	1.66	0.43
52:3:636:U:H2'	52:3:637:C:C6	2.53	0.43
52:3:680:C:H2'	52:3:681:A:H8	1.81	0.43
52:3:924:C:H2'	52:3:925:G:C8	2.47	0.43
52:3:1070:U:H2'	52:3:1071:C:C6	2.53	0.43
52:3:1256:A:H1'	52:3:1258:G:N9	2.33	0.43
52:3:1402:C:H2'	52:3:1403:C:O4'	2.18	0.43
53:1:28:A:H1'	53:1:513:A:C2	2.53	0.43
53:1:171:U:H2'	53:1:172:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:174:U:H2'	53:1:175:G:H8	1.83	0.43
53:1:709:U:H2'	53:1:710:U:C6	2.53	0.43
53:1:1078:U:H4'	53:1:1079:C:H5''	1.99	0.43
53:1:1370:C:H2'	53:1:1371:G:O4'	2.17	0.43
53:1:1998:A:H2'	53:1:1999:C:C6	2.53	0.43
53:1:2110:G:C5'	53:1:2118:U:H2'	2.48	0.43
53:1:2830:C:H2'	53:1:2831:G:H8	1.83	0.43
54:2:114:C:H2'	54:2:115:A:C8	2.53	0.43
55:6:69:C:H2'	55:6:70:G:H8	1.81	0.43
1:b:145:MET:CG	1:b:152:GLN:HG3	2.45	0.43
2:c:33:ARG:O	2:c:51:THR:HG22	2.19	0.43
6:g:9:VAL:HB	6:g:13:GLY:HA3	2.00	0.43
16:q:26:ALA:HB1	16:q:30:VAL:HG22	2.01	0.43
17:r:16:GLU:OE1	17:r:100:GLY:HA2	2.18	0.43
18:s:58:ALA:O	18:s:62:ASP:OD1	2.36	0.43
19:t:48:GLN:HE22	19:t:54:GLU:HA	1.84	0.43
33:I:186:GLU:HG3	33:I:188:SER:H	1.83	0.43
35:K:98:GLU:HB3	35:K:99:ALA:H	1.49	0.43
39:O:65:TYR:C	43:S:98:ALA:HB2	2.43	0.43
42:R:57:ASP:OD1	42:R:57:ASP:N	2.51	0.43
47:W:59:LYS:HD3	52:3:734:G:O2'	2.17	0.43
52:3:927:G:H2'	52:3:928:G:H8	1.84	0.43
52:3:1060:U:H2'	52:3:1061:G:C8	2.53	0.43
53:1:610:C:H2'	53:1:611:C:C6	2.54	0.43
53:1:1054:A:H2'	53:1:1055:G:C8	2.53	0.43
53:1:1148:U:H2'	53:1:1149:G:C8	2.53	0.43
53:1:2772:C:H2'	53:1:2773:C:C6	2.53	0.43
57:7:76:A:H4'	58:8:219:PHE:CE2	2.53	0.43
58:8:231:ARG:NH2	58:8:272:GLY:HA2	2.33	0.43
1:b:80:LEU:HD23	1:b:91:ALA:HB2	2.01	0.43
1:b:260:LYS:HA	1:b:263:ASP:CG	2.43	0.43
2:c:62:LYS:HA	2:c:65:ALA:HB3	1.99	0.43
7:h:97:LYS:HG3	7:h:101:LYS:NZ	2.33	0.43
8:i:25:PRO:HD2	57:7:56:C:OP2	2.19	0.43
9:j:99:ARG:NH1	53:1:2780:G:H1	2.15	0.43
33:I:43:ARG:NH1	52:3:511:C:H4'	2.31	0.43
33:I:169:TRP:CG	33:I:185:PRO:HG3	2.53	0.43
34:J:108:GLY:N	52:3:9:G:H4'	2.34	0.43
35:K:88:MET:HE2	35:K:90:MET:SD	2.59	0.43
36:L:28:ILE:CG2	36:L:104:VAL:HG21	2.48	0.43
37:M:65:PHE:CD2	37:M:66:GLN:HG2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:N:25:GLY:N	38:N:57:VAL:O	2.50	0.43
38:N:59:LYS:C	38:N:60:LEU:HD22	2.43	0.43
39:O:51:VAL:O	39:O:62:ARG:HB3	2.19	0.43
40:P:67:GLU:O	40:P:70:ALA:HB3	2.19	0.43
43:S:60:ARG:O	43:S:60:ARG:NH1	2.49	0.43
47:W:62:ARG:HB3	47:W:69:TYR:CE1	2.52	0.43
51:a:65:LEU:HD13	51:a:175:ILE:O	2.18	0.43
52:3:156:C:H2'	52:3:157:U:O4'	2.19	0.43
52:3:208:U:H2'	52:3:210:C:H1'	2.00	0.43
52:3:1082:A:H2'	52:3:1083:U:O4'	2.18	0.43
53:1:1103:A:H2'	53:1:1104:C:OP1	2.19	0.43
53:1:1609:A:H1'	53:1:1616:A:C1'	2.48	0.43
53:1:1991:U:H2'	53:1:1992:G:C5'	2.48	0.43
53:1:2340:A:H2'	53:1:2341:G:H8	1.83	0.43
58:8:330:GLN:NE2	58:8:380:GLY:H	2.17	0.43
2:c:33:ARG:HA	2:c:95:SER:HA	2.00	0.43
4:e:49:LEU:HD13	4:e:83:PRO:HB2	2.00	0.43
7:h:59:LEU:HB3	7:h:62:ARG:HB2	2.00	0.43
15:p:25:VAL:HG22	15:p:26:GLU:N	2.34	0.43
16:q:52:ARG:HH11	53:1:995:C:P	2.40	0.43
19:t:77:ARG:CZ	53:1:63:A:H4'	2.48	0.43
22:w:12:SER:HB2	53:1:2261:C:OP2	2.18	0.43
22:w:19:VAL:HG22	22:w:34:VAL:HG22	2.00	0.43
25:z:15:ARG:HE	25:z:52:PHE:HE2	1.66	0.43
34:J:92:ARG:O	34:J:93:VAL:C	2.61	0.43
34:J:164:LEU:HD12	34:J:165:GLY:N	2.34	0.43
46:V:7:LEU:HD12	46:V:7:LEU:N	2.34	0.43
52:3:594:U:C2'	52:3:595:A:H5'	2.49	0.43
52:3:1001:C:H2'	52:3:1002:G:C8	2.54	0.43
53:1:517:C:H2'	53:1:518:G:O4'	2.18	0.43
53:1:527:C:C4	53:1:2779:U:H2'	2.53	0.43
53:1:534:U:H2'	53:1:535:G:H8	1.83	0.43
53:1:660:C:H2'	53:1:661:A:C8	2.54	0.43
53:1:1204:A:H4'	53:1:1205:A:H5''	2.00	0.43
53:1:1666:G:H2'	53:1:1667:G:O4'	2.19	0.43
53:1:2875:C:H2'	53:1:2876:G:C8	2.53	0.43
2:c:7:LYS:O	2:c:27:ILE:HG13	2.19	0.43
4:e:21:TYR:CD1	4:e:26:GLN:HG2	2.54	0.43
5:f:85:LYS:HG2	5:f:87:GLN:NE2	2.32	0.43
6:g:39:ALA:O	6:g:44:ILE:HD11	2.19	0.43
6:g:40:THR:HB	6:g:43:ASN:ND2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:k:76:VAL:HG12	15:p:72:VAL:HG22	2.01	0.43
12:m:74:THR:OG1	12:m:88:ASN:O	2.28	0.43
14:o:92:PHE:HZ	14:o:103:VAL:HB	1.84	0.43
15:p:50:ARG:NH1	53:1:2684:U:OP2	2.52	0.43
19:t:38:ALA:O	19:t:81:LYS:NZ	2.52	0.43
32:H:67:ILE:O	32:H:67:ILE:HG13	2.19	0.43
38:N:90:ASP:N	38:N:90:ASP:OD1	2.52	0.43
44:T:50:HIS:ND1	52:3:667:G:H4'	2.32	0.43
46:V:43:LEU:HD21	52:3:236:A:C5'	2.49	0.43
49:Y:70:LYS:HA	49:Y:73:ARG:NH1	2.33	0.43
50:Z:61:ARG:H	50:Z:61:ARG:HD3	1.83	0.43
52:3:512:U:H2'	52:3:513:C:C6	2.53	0.43
53:1:542:C:H2'	53:1:543:G:H5''	2.00	0.43
53:1:1015:U:H2'	53:1:1016:G:C8	2.52	0.43
53:1:1048:A:H2	53:1:1112:G:H1'	1.83	0.43
53:1:2544:G:H2'	53:1:2545:G:H8	1.84	0.43
55:6:62:C:H2'	55:6:63:G:C8	2.54	0.43
57:7:7:A:H61	57:7:66:U:H3	1.66	0.43
57:7:15:G:H22	57:7:48:C:H42	1.66	0.43
58:8:323:PHE:HE2	58:8:342:ILE:HG21	1.84	0.43
8:i:52:LEU:HA	8:i:53:PRO:HD3	1.85	0.43
19:t:14:PRO:HA	19:t:32:LEU:HD13	2.00	0.43
22:w:39:THR:HG22	22:w:41:PHE:O	2.19	0.43
42:R:6:ILE:CG2	42:R:7:ASN:N	2.81	0.43
42:R:22:TYR:CE1	52:3:1330:U:H4'	2.54	0.43
42:R:54:THR:O	42:R:58:GLU:HG2	2.18	0.43
43:S:53:ASP:HA	43:S:58:ARG:NE	2.33	0.43
45:U:36:VAL:HG21	45:U:57:ILE:HG13	2.00	0.43
50:Z:39:LYS:O	50:Z:40:PRO:C	2.59	0.43
52:3:77:A:H2'	52:3:78:A:H8	1.82	0.43
52:3:484:G:C5	52:3:486:U:H1'	2.52	0.43
52:3:828:U:N3	52:3:859:G:H1'	2.34	0.43
52:3:955:U:H3	52:3:1225:A:N6	2.13	0.43
53:1:184:C:H2'	53:1:185:G:H8	1.84	0.43
53:1:302:C:H2'	53:1:303:G:H8	1.83	0.43
53:1:890:C:C2'	53:1:891:G:H5'	2.48	0.43
53:1:1833:C:C2'	53:1:1834:U:H5'	2.49	0.43
53:1:1833:C:O2'	53:1:1834:U:H5'	2.18	0.43
53:1:1881:C:H2'	53:1:1882:U:O4'	2.19	0.43
53:1:2404:U:H2'	53:1:2405:G:O4'	2.19	0.43
53:1:2897:U:H2'	53:1:2898:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:6:37:A:H2'	55:6:38:A:O4'	2.19	0.43
57:7:64:A:H2'	57:7:65:G:H8	1.83	0.43
58:8:209:LYS:HB3	58:8:234:ARG:HH21	1.83	0.43
2:c:34:VAL:HA	2:c:50:VAL:HA	2.00	0.43
7:h:22:ALA:HB3	7:h:87:GLU:OE2	2.19	0.43
11:l:18:ARG:HH22	53:1:1249:U:H2'	1.84	0.43
14:o:102:ARG:HA	14:o:105:ALA:HB3	2.00	0.43
17:r:1:MET:N	17:r:42:ALA:O	2.52	0.43
19:t:80:TRP:CZ3	19:t:82:LYS:HB3	2.54	0.43
19:t:80:TRP:HZ3	19:t:82:LYS:HB3	1.84	0.43
28:D:7:PRO:HB2	53:1:1309:G:H4'	2.00	0.43
28:D:31:LEU:O	28:D:35:ARG:HG3	2.18	0.43
33:I:69:ARG:O	33:I:73:ASN:ND2	2.52	0.43
37:M:85:TYR:CE1	37:M:123:GLU:HB2	2.54	0.43
40:P:118:ASN:ND2	52:3:718:A:H5'	2.34	0.43
43:S:53:ASP:HA	43:S:58:ARG:HE	1.83	0.43
43:S:60:ARG:HA	43:S:60:ARG:HD2	1.85	0.43
48:X:41:PRO:O	48:X:44:ILE:HG13	2.18	0.43
52:3:484:G:H4'	52:3:485:U:C5'	2.31	0.43
53:1:248:G:N3	53:1:2431:U:H4'	2.34	0.43
53:1:438:G:H2'	53:1:439:A:C8	2.54	0.43
54:2:51:G:H2'	54:2:52:A:O4'	2.18	0.43
2:c:123:LYS:NZ	53:1:2724:U:H5''	2.34	0.43
21:v:71:LYS:HA	21:v:71:LYS:HD3	1.84	0.43
35:K:18:VAL:O	35:K:22:ILE:HG13	2.18	0.43
35:K:29:ILE:HG21	35:K:64:VAL:HG21	2.00	0.43
38:N:10:ARG:HD3	52:3:1149:C:OP1	2.19	0.43
45:U:36:VAL:O	45:U:36:VAL:HG22	2.18	0.43
46:V:17:GLU:C	46:V:19:SER:H	2.27	0.43
52:3:312:C:H2'	52:3:313:A:C8	2.54	0.43
52:3:825:A:H2'	52:3:826:C:C6	2.54	0.43
52:3:865:A:H5'	52:3:1078:U:O4	2.18	0.43
53:1:368:A:C2'	53:1:369:U:H5'	2.49	0.43
53:1:1028:A:H61	53:1:1125:G:H2'	1.82	0.43
53:1:1526:C:H2'	53:1:1527:G:O4'	2.19	0.43
53:1:1827:U:O2'	53:1:1828:G:H5'	2.19	0.43
53:1:2432:A:H1'	55:6:75:C:C4'	2.49	0.43
53:1:2590:A:H2'	53:1:2591:C:H6	1.83	0.43
53:1:2650:U:H2'	53:1:2651:C:C6	2.54	0.43
58:8:94:THR:O	58:8:98:GLN:HG3	2.19	0.43
5:f:36:LEU:HD13	5:f:67:ALA:HB1	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:h:41:LEU:HD13	53:1:1083:U:O5'	2.18	0.43
13:n:64:ARG:HG3	53:1:1454:C:O2	2.19	0.43
17:r:39:LEU:O	17:r:49:ILE:HG23	2.19	0.43
18:s:6:LYS:HB3	18:s:104:THR:HG23	2.01	0.43
23:x:6:VAL:HG13	23:x:7:THR:N	2.34	0.43
27:C:6:GLU:CD	27:C:6:GLU:H	2.27	0.43
33:I:59:LYS:HE3	33:I:194:ILE:HG22	2.00	0.43
40:P:71:ASP:HA	40:P:74:LYS:HE3	2.00	0.43
48:X:54:ARG:HG3	48:X:55:GLN:OE1	2.18	0.43
51:a:48:LEU:HD23	51:a:49:GLY:N	2.33	0.43
52:3:235:C:H2'	52:3:236:A:C8	2.53	0.43
52:3:680:C:H2'	52:3:681:A:C8	2.54	0.43
52:3:684:U:H2'	52:3:685:G:O4'	2.18	0.43
53:1:622:G:H2'	53:1:623:C:C6	2.54	0.43
53:1:1175:A:H5'	53:1:1176:U:O4'	2.19	0.43
53:1:2220:U:H2'	53:1:2221:G:H8	1.83	0.43
53:1:2619:C:O2'	53:1:2620:C:H5'	2.19	0.43
58:8:20:HIS:O	58:8:25:LYS:NZ	2.52	0.43
1:b:245:THR:C	1:b:247:TRP:H	2.27	0.42
7:h:15:VAL:HG13	7:h:69:PHE:CE2	2.54	0.42
7:h:103:ASN:HA	7:h:107:GLU:HB3	2.01	0.42
9:j:117:ALA:HA	9:j:120:ARG:NH2	2.33	0.42
18:s:62:ASP:HB2	18:s:63:GLY:H	1.63	0.42
31:G:11:ALA:HB1	31:G:208:ALA:HA	2.00	0.42
36:L:115:MET:O	36:L:119:LEU:HG	2.19	0.42
42:R:13:HIS:O	42:R:16:ILE:HG12	2.19	0.42
45:U:18:GLN:HA	45:U:38:PHE:HA	2.01	0.42
51:a:206:GLY:N	53:1:1861:G:OP1	2.52	0.42
52:3:664:G:N2	52:3:741:G:H22	2.16	0.42
52:3:709:U:H2'	52:3:710:G:C8	2.53	0.42
53:1:248:G:H3'	53:1:249:C:C5'	2.50	0.42
53:1:1330:C:H2'	53:1:1331:G:C8	2.54	0.42
53:1:1694:C:H4'	53:1:1695:G:C4	2.54	0.42
53:1:2126:A:H2'	53:1:2162:G:C2	2.53	0.42
58:8:192:LEU:O	58:8:196:LEU:HG	2.19	0.42
1:b:179:GLU:OE1	1:b:179:GLU:N	2.52	0.42
2:c:77:ARG:HG3	2:c:77:ARG:O	2.18	0.42
12:m:27:SER:H	12:m:66:ARG:HH12	1.67	0.42
13:n:3:HIS:O	13:n:4:ARG:HB2	2.18	0.42
13:n:57:THR:HG23	13:n:57:THR:O	2.19	0.42
21:v:41:GLU:HG3	21:v:41:GLU:O	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:y:31:GLN:CG	24:y:37:LEU:HG	2.50	0.42
33:I:82:LYS:HG2	52:3:5:U:O4	2.19	0.42
34:J:20:VAL:HB	52:3:1080:A:O3'	2.18	0.42
36:L:11:ILE:HD11	36:L:27:ASN:HD21	1.83	0.42
39:O:10:LEU:HD23	39:O:10:LEU:N	2.34	0.42
40:P:19:VAL:O	40:P:19:VAL:HG13	2.19	0.42
40:P:91:GLY:O	40:P:93:GLU:N	2.46	0.42
52:3:405:U:O2	52:3:498:A:H2'	2.19	0.42
52:3:597:G:H2'	52:3:598:U:H5'	2.00	0.42
53:1:859:G:C2'	53:1:860:U:OP2	2.67	0.42
53:1:2146:C:H4'	53:1:2147:A:C5	2.54	0.42
53:1:2207:C:H2'	53:1:2208:C:C6	2.54	0.42
53:1:2270:A:H2'	53:1:2271:G:O4'	2.18	0.42
53:1:2810:A:H2'	53:1:2811:G:O4'	2.19	0.42
55:5:75:C:H2'	55:5:76:A:H5''	2.01	0.42
55:6:1:C:H2'	55:6:2:G:C8	2.52	0.42
58:8:27:THR:HG21	61:8:501:GTP:H3'	2.01	0.42
4:e:12:VAL:HG13	4:e:13:LYS:H	1.84	0.42
8:i:69:VAL:HG22	8:i:71:LYS:HG2	2.01	0.42
11:l:18:ARG:HD2	53:1:1249:U:C4	2.55	0.42
11:l:20:GLY:HA2	11:l:28:GLY:HA2	2.01	0.42
12:m:31:PHE:HE2	12:m:108:VAL:O	2.02	0.42
13:n:70:THR:O	13:n:71:ARG:C	2.63	0.42
15:p:96:LEU:HB3	15:p:99:LEU:HD12	2.01	0.42
19:t:57:VAL:HG12	19:t:86:THR:OG1	2.19	0.42
35:K:42:TRP:HE3	35:K:45:ARG:NH1	2.18	0.42
36:L:4:ARG:NH1	52:3:933:G:OP1	2.52	0.42
37:M:2:MET:HE2	37:M:2:MET:HA	2.01	0.42
37:M:26:MET:HA	37:M:27:PRO:HD3	1.93	0.42
42:R:75:SER:O	42:R:78:ARG:HB3	2.20	0.42
42:R:103:THR:O	42:R:106:ARG:NH2	2.51	0.42
43:S:44:VAL:O	43:S:44:VAL:HG12	2.20	0.42
52:3:355:C:H5'	52:3:355:C:C6	2.50	0.42
52:3:832:G:O2'	52:3:833:G:H5'	2.20	0.42
53:1:286:U:H2'	53:1:287:G:C8	2.54	0.42
53:1:364:C:H2'	53:1:365:U:C6	2.55	0.42
53:1:493:G:O2'	53:1:494:G:H5'	2.18	0.42
53:1:1528:A:H2'	53:1:1529:G:O4'	2.19	0.42
53:1:1821:A:H2'	53:1:1822:C:C6	2.54	0.42
53:1:2039:U:H2'	53:1:2040:G:H8	1.82	0.42
53:1:2087:G:H2'	53:1:2088:A:C8	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2489:U:O2'	53:1:2490:G:H5'	2.19	0.42
55:6:17:C:OP1	55:6:61:C:H5'	2.19	0.42
58:8:231:ARG:NE	58:8:233:GLU:OE1	2.52	0.42
58:8:288:GLU:HB2	58:8:291:GLN:HE22	1.84	0.42
3:d:94:GLN:HB2	53:1:660:C:OP1	2.19	0.42
4:e:102:LEU:HA	4:e:106:ALA:HB3	1.99	0.42
5:f:93:TYR:O	5:f:94:ARG:NH1	2.48	0.42
6:g:77:THR:HG23	6:g:143:ILE:HB	2.02	0.42
7:h:67:THR:N	7:h:68:PRO:CD	2.82	0.42
9:j:21:THR:HB	9:j:58:ASN:HD22	1.84	0.42
9:j:68:LYS:HD3	53:1:1022:G:N7	2.34	0.42
10:k:8:LEU:HD13	10:k:84:CYS:SG	2.59	0.42
14:o:74:VAL:HG13	14:o:106:LEU:HD11	2.02	0.42
32:H:170:GLY:C	52:3:1106:G:H4'	2.45	0.42
33:I:8:LEU:HD12	52:3:429:U:H3'	2.02	0.42
33:I:183:ARG:NH1	33:I:184:LYS:O	2.52	0.42
40:P:86:LYS:HB2	40:P:112:VAL:HG13	2.00	0.42
41:Q:22:ALA:O	41:Q:23:LEU:C	2.62	0.42
42:R:63:VAL:CG2	42:R:68:LEU:HD23	2.45	0.42
49:Y:28:ARG:HD3	52:3:1438:G:OP1	2.20	0.42
52:3:188:C:H2'	52:3:189:A:O4'	2.18	0.42
52:3:626:G:H2'	52:3:627:G:C8	2.54	0.42
53:1:226:A:H2'	53:1:227:A:O4'	2.19	0.42
53:1:783:A:C4	53:1:785:G:H1'	2.54	0.42
53:1:910:A:H2'	53:1:911:A:C8	2.54	0.42
53:1:1124:G:H2'	53:1:1125:G:O4'	2.20	0.42
53:1:1779:U:H5	53:1:1784:A:N7	2.18	0.42
53:1:1794:A:H4'	53:1:1900:A:C6	2.54	0.42
53:1:2030:A:H4'	53:1:2031:A:H8	1.83	0.42
58:8:336:THR:HG22	58:8:338:VAL:HG23	2.02	0.42
2:c:22:ILE:HA	2:c:23:PRO:HD3	1.84	0.42
8:i:15:GLY:HA3	8:i:51:GLY:H	1.85	0.42
11:l:17:LYS:HB2	53:1:663:G:OP1	2.19	0.42
11:l:49:GLY:HA3	11:l:58:TYR:CE1	2.53	0.42
19:t:18:GLU:O	19:t:22:THR:HG23	2.18	0.42
19:t:68:LYS:HE2	53:1:1336:A:OP2	2.18	0.42
23:x:6:VAL:HG13	23:x:7:THR:H	1.85	0.42
28:D:39:ARG:NH2	53:1:469:G:O6	2.53	0.42
37:M:87:ARG:H	37:M:90:GLU:HB2	1.85	0.42
40:P:13:LYS:N	40:P:13:LYS:CD	2.82	0.42
51:a:7:ARG:HB3	53:1:2129:C:P	2.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:185:U:H2'	52:3:186:C:C6	2.55	0.42
52:3:1162:C:H2'	52:3:1163:A:C8	2.54	0.42
52:3:1507:A:H2'	52:3:1508:A:C8	2.55	0.42
53:1:941:A:H2'	53:1:942:G:O4'	2.20	0.42
53:1:1429:G:H2'	53:1:1430:G:H8	1.83	0.42
53:1:1849:G:H2'	53:1:1850:G:C8	2.54	0.42
53:1:2762:C:H2'	53:1:2763:G:O4'	2.18	0.42
3:d:23:PHE:CZ	3:d:28:VAL:HG11	2.55	0.42
4:e:32:LYS:HD3	4:e:91:ARG:NH2	2.34	0.42
5:f:15:ASP:OD1	5:f:15:ASP:N	2.53	0.42
6:g:8:LYS:O	6:g:9:VAL:C	2.63	0.42
9:j:17:VAL:HG23	9:j:137:PRO:HB2	2.01	0.42
10:k:8:LEU:HB2	10:k:19:VAL:HG23	2.02	0.42
16:q:2:ARG:HA	53:1:1248:G:O2'	2.18	0.42
19:t:14:PRO:HD2	24:y:33:ALA:HB1	2.02	0.42
21:v:80:HIS:CB	21:v:87:GLN:HE22	2.27	0.42
22:w:71:LYS:NZ	53:1:2333:A:OP2	2.52	0.42
24:y:41:HIS:CD2	53:1:96:C:H4'	2.55	0.42
31:G:180:ILE:H	31:G:180:ILE:HD12	1.83	0.42
37:M:29:SER:OG	37:M:32:LYS:HG2	2.20	0.42
39:O:42:LEU:HA	39:O:43:PRO:HD2	1.81	0.42
48:X:71:GLY:HA3	52:3:1320:C:O2	2.19	0.42
49:Y:77:ASN:ND2	52:3:259:G:OP1	2.53	0.42
51:a:19:LYS:HD3	51:a:20:GLN:N	2.34	0.42
52:3:24:U:H2'	52:3:25:C:H6	1.84	0.42
52:3:123:U:OP1	52:3:312:C:H5'	2.19	0.42
52:3:131:A:H2'	52:3:132:C:C6	2.55	0.42
52:3:428:G:H4'	52:3:429:U:O5'	2.19	0.42
52:3:428:G:O4'	52:3:430:A:C8	2.72	0.42
53:1:406:G:H2'	53:1:407:G:C8	2.54	0.42
53:1:589:U:H2'	53:1:590:A:C8	2.54	0.42
53:1:1097:U:H2'	53:1:1098:A:O4'	2.20	0.42
53:1:1434:A:H2'	53:1:1435:G:H8	1.83	0.42
53:1:1441:G:H2'	53:1:1442:U:C6	2.55	0.42
53:1:1507:C:C2'	53:1:1508:A:H4'	2.49	0.42
53:1:2022:U:O2'	53:1:2617:U:H5'	2.19	0.42
58:8:333:PHE:C	58:8:335:THR:H	2.28	0.42
1:b:225:ASN:HA	1:b:226:PRO:HD3	1.94	0.42
8:i:72:THR:HG23	8:i:73:PRO:HD2	2.02	0.42
13:n:1:MET:SD	53:1:2723:C:H4'	2.59	0.42
15:p:105:LYS:HE3	15:p:108:ARG:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:s:40:ASN:O	18:s:41:LYS:HD2	2.20	0.42
22:w:44:GLY:H	22:w:47:VAL:HB	1.85	0.42
24:y:2:LYS:HG3	24:y:3:ALA:H	1.84	0.42
24:y:58:ASN:ND2	53:1:111:A:O2'	2.53	0.42
26:B:3:GLN:HA	53:1:2615:U:C2	2.55	0.42
31:G:131:LYS:O	31:G:134:LEU:HG	2.20	0.42
33:I:101:VAL:O	33:I:104:MET:HB2	2.20	0.42
40:P:52:ARG:HH12	52:3:688:G:H5'	1.85	0.42
40:P:61:ALA:O	40:P:64:VAL:HG12	2.19	0.42
42:R:14:ALA:HB1	42:R:33:LEU:HD11	2.00	0.42
45:U:4:ILE:HB	45:U:67:ILE:HG23	2.02	0.42
45:U:5:ARG:HB3	52:3:376:G:H5''	2.02	0.42
52:3:1052:U:H2'	52:3:1200:C:H41	1.84	0.42
52:3:1162:C:H2'	52:3:1163:A:H8	1.85	0.42
53:1:217:A:H2'	53:1:218:A:O4'	2.18	0.42
53:1:318:C:O2'	53:1:319:G:H5'	2.19	0.42
53:1:672:C:O2'	53:1:673:C:H5'	2.19	0.42
53:1:1091:G:O2'	53:1:1092:C:H5'	2.20	0.42
53:1:1299:G:H5''	53:1:1300:G:OP1	2.20	0.42
53:1:2692:G:H5''	53:1:2870:C:O2'	2.19	0.42
3:d:48:THR:C	3:d:50:ALA:H	2.28	0.42
3:d:98:LYS:H	53:1:607:U:P	2.42	0.42
4:e:87:LYS:HD2	53:1:2313:C:C5'	2.50	0.42
12:m:6:ARG:HG3	12:m:6:ARG:O	2.20	0.42
18:s:36:LEU:HD13	18:s:47:VAL:HG13	2.01	0.42
23:x:63:ILE:O	23:x:67:LEU:HD23	2.20	0.42
27:C:22:THR:OG1	27:C:23:THR:N	2.52	0.42
35:K:52:ASN:O	35:K:53:LYS:HG3	2.20	0.42
41:Q:114:SER:OG	52:3:501:C:O3'	2.30	0.42
50:Z:27:VAL:O	50:Z:31:VAL:HG22	2.19	0.42
52:3:367:U:O2'	52:3:368:U:H4'	2.19	0.42
53:1:1558:C:H4'	53:1:1560:G:OP2	2.20	0.42
53:1:2709:G:H2'	53:1:2710:C:C6	2.54	0.42
1:b:238:ASN:ND2	53:1:2599:G:O6	2.53	0.42
4:e:84:ILE:HG21	53:1:2312:U:H5'	2.02	0.42
4:e:102:LEU:HD23	4:e:103:ILE:N	2.34	0.42
16:q:73:ILE:HG22	16:q:74:SER:N	2.34	0.42
24:y:10:SER:HA	24:y:13:GLU:HG2	2.01	0.42
33:I:18:LEU:HB3	33:I:20:LEU:CD1	2.50	0.42
33:I:60:VAL:HA	33:I:63:ILE:HD12	2.01	0.42
39:O:52:LEU:HD23	39:O:62:ARG:HG2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:99:GLN:OE1	42:R:99:GLN:N	2.52	0.42
43:S:81:ILE:HG21	52:3:1202:U:C2	2.54	0.42
50:Z:46:ARG:HH11	50:Z:49:ALA:HB3	1.84	0.42
52:3:61:G:O2'	52:3:62:U:H5'	2.18	0.42
52:3:401:C:H2'	52:3:402:G:H8	1.84	0.42
52:3:1329:A:O2'	52:3:1330:U:H5'	2.20	0.42
52:3:1425:U:H2'	52:3:1426:G:H8	1.84	0.42
52:3:1435:G:H2'	52:3:1436:U:C6	2.55	0.42
52:3:1509:C:H2'	52:3:1510:C:C6	2.55	0.42
53:1:1409:U:H3	53:1:1593:A:H61	1.68	0.42
53:1:1923:U:H2'	53:1:1924:C:H6	1.84	0.42
53:1:2472:G:H2'	53:1:2475:C:H42	1.85	0.42
55:5:75:C:C2'	55:5:76:A:H5''	2.49	0.42
57:7:76:A:C1'	58:8:227:VAL:HG11	2.50	0.42
58:8:309:VAL:HG22	58:8:310:TYR:N	2.35	0.42
1:b:155:ARG:CZ	53:1:1818:U:C5	3.02	0.42
4:e:27:VAL:HA	4:e:28:PRO:HD3	1.87	0.42
5:f:34:ARG:HG3	5:f:34:ARG:HH11	1.85	0.42
11:l:4:ASN:O	53:1:1243:C:H1'	2.19	0.42
30:F:24:ARG:NH1	53:1:2742:G:OP2	2.48	0.42
31:G:220:VAL:O	31:G:224:ARG:HG2	2.20	0.42
33:I:143:SER:OG	33:I:144:ILE:N	2.53	0.42
35:K:46:GLN:NE2	35:K:47:LEU:O	2.53	0.42
36:L:2:ARG:HA	52:3:1380:U:C4	2.55	0.42
43:S:84:ARG:NH1	43:S:88:MET:HE2	2.35	0.42
46:V:24:ILE:HB	46:V:41:THR:HB	2.02	0.42
48:X:4:LEU:HD13	52:3:1319:A:OP2	2.20	0.42
52:3:36:C:H2'	52:3:37:U:C6	2.55	0.42
52:3:423:G:H3'	52:3:423:G:N3	2.35	0.42
52:3:730:G:H2'	52:3:731:G:C5'	2.46	0.42
52:3:734:G:H2'	52:3:735:C:C6	2.55	0.42
53:1:45:G:H5''	53:1:46:G:C4'	2.49	0.42
53:1:151:C:H2'	53:1:152:A:H8	1.85	0.42
53:1:327:G:O2'	53:1:328:U:H5'	2.20	0.42
53:1:368:A:H2'	53:1:369:U:H5'	2.01	0.42
53:1:1103:A:H2'	53:1:1103:A:N3	2.34	0.42
53:1:1176:U:H2'	53:1:1177:G:C8	2.55	0.42
53:1:1670:C:H2'	53:1:1671:U:O4'	2.20	0.42
53:1:2200:C:H2'	53:1:2201:G:C8	2.55	0.42
54:2:88:C:H5''	54:2:89:U:OP1	2.20	0.42
55:6:32:C:H2'	55:6:33:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:7:54:U:P	58:8:321:THR:HG1	2.42	0.42
1:b:1:ALA:N	1:b:19:VAL:O	2.51	0.41
1:b:38:LYS:HE3	1:b:55:GLY:O	2.20	0.41
1:b:269:ARG:HH12	53:1:1799:G:P	2.43	0.41
4:e:130:GLY:HA3	53:1:2305:U:H5'	2.02	0.41
7:h:3:LEU:CD1	7:h:5:LEU:HB2	2.50	0.41
8:i:109:ALA:HB3	8:i:125:THR:HG22	2.01	0.41
21:v:8:VAL:HG13	21:v:65:VAL:HG21	2.02	0.41
21:v:80:HIS:ND1	21:v:81:PRO:HD2	2.35	0.41
46:V:50:ASN:ND2	46:V:52:CYS:O	2.53	0.41
51:a:10:VAL:HA	51:a:13:GLU:CG	2.49	0.41
52:3:82:G:H1	52:3:87:C:N4	2.18	0.41
52:3:629:A:H2'	52:3:630:A:O4'	2.19	0.41
52:3:663:A:O2'	52:3:664:G:H5'	2.20	0.41
52:3:1473:G:O2'	52:3:1474:U:H5'	2.20	0.41
52:3:1504:G:OP1	52:3:1507:A:H4'	2.20	0.41
53:1:65:U:H2'	53:1:66:C:C6	2.55	0.41
53:1:386:G:H3'	53:1:387:U:C5'	2.50	0.41
53:1:609:A:H2'	53:1:610:C:O4'	2.19	0.41
53:1:874:G:H2'	53:1:875:G:C8	2.54	0.41
53:1:1463:C:H2'	53:1:1464:G:C8	2.55	0.41
53:1:1837:C:H2'	53:1:1899:A:N6	2.29	0.41
53:1:2544:G:H2'	53:1:2545:G:C8	2.55	0.41
54:2:92:C:H2'	54:2:93:C:H6	1.85	0.41
57:7:49:C:H2'	57:7:50:U:C6	2.55	0.41
4:e:82:TYR:CG	4:e:83:PRO:HD2	2.54	0.41
4:e:84:ILE:CD1	53:1:2311:A:H1'	2.48	0.41
5:f:132:LEU:O	5:f:132:LEU:HD12	2.20	0.41
9:j:7:LYS:HA	9:j:8:PRO:HD3	1.76	0.41
10:k:17:ARG:HD3	10:k:17:ARG:HA	1.86	0.41
16:q:15:LYS:HE2	16:q:15:LYS:HB3	1.84	0.41
20:u:35:VAL:HG12	20:u:38:ILE:HG13	2.01	0.41
21:v:55:GLU:N	21:v:55:GLU:OE2	2.53	0.41
28:D:14:ARG:HD2	53:1:771:G:OP1	2.20	0.41
34:J:165:GLY:HA2	37:M:113:ARG:HD2	2.01	0.41
38:N:10:ARG:CZ	52:3:1149:C:OP2	2.68	0.41
40:P:21:HIS:NE2	40:P:84:MET:SD	2.93	0.41
43:S:30:ILE:H	43:S:30:ILE:CD1	2.28	0.41
52:3:106:C:H2'	52:3:107:G:H8	1.85	0.41
52:3:370:C:H2'	52:3:371:A:H8	1.84	0.41
52:3:605:U:H2'	52:3:606:G:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:676:A:O2'	52:3:677:U:H5'	2.20	0.41
52:3:757:U:H2'	52:3:758:C:C6	2.55	0.41
53:1:3:U:H2'	53:1:4:U:C6	2.54	0.41
53:1:222:A:H61	53:1:232:G:H1'	1.84	0.41
53:1:322:A:H5'	53:1:340:A:C1'	2.50	0.41
53:1:386:G:H3'	53:1:387:U:H5''	2.02	0.41
53:1:703:U:H2'	53:1:704:G:O4'	2.20	0.41
53:1:1190:G:H2'	53:1:1191:G:C8	2.55	0.41
53:1:1657:U:O2'	53:1:1658:C:H5'	2.19	0.41
53:1:1747:U:H2'	53:1:1748:C:C6	2.55	0.41
54:2:1:U:H2'	54:2:2:G:C8	2.55	0.41
54:2:3:C:C3'	54:2:4:C:C5'	2.95	0.41
55:5:5:G:H2'	55:5:6:G:C8	2.55	0.41
2:c:175:LEU:HD22	2:c:191:GLY:HA3	2.03	0.41
8:i:72:THR:CG2	8:i:73:PRO:HD2	2.50	0.41
21:v:34:LYS:HD3	21:v:34:LYS:HA	1.80	0.41
26:B:10:SER:HG	53:1:17:G:H5'	1.85	0.41
39:O:37:ARG:HG3	52:3:1124:G:H5''	2.01	0.41
40:P:126:ARG:HD2	40:P:126:ARG:H	1.84	0.41
43:S:92:ILE:N	43:S:92:ILE:HD12	2.35	0.41
44:T:17:ASP:OD1	44:T:20:ASP:HB2	2.21	0.41
45:U:26:ASN:OD1	45:U:27:ALA:N	2.53	0.41
53:1:443:A:H5''	53:1:444:C:H5''	2.02	0.41
53:1:979:A:H2'	53:1:982:C:H42	1.85	0.41
53:1:1068:G:H2'	53:1:1069:A:O4'	2.20	0.41
53:1:1092:C:H2'	53:1:1093:G:O4'	2.20	0.41
53:1:1333:G:H2'	53:1:1334:G:H8	1.85	0.41
53:1:1423:G:H2'	53:1:1424:G:H8	1.85	0.41
53:1:2008:C:H2'	53:1:2009:A:H8	1.84	0.41
53:1:2343:U:H2'	53:1:2344:U:C6	2.55	0.41
53:1:2462:C:H2'	53:1:2463:C:C6	2.55	0.41
53:1:2492:U:H2'	53:1:2493:U:C6	2.54	0.41
53:1:2556:C:H2'	53:1:2557:G:O4'	2.19	0.41
4:e:125:GLY:O	4:e:157:THR:HG22	2.20	0.41
9:j:64:VAL:HB	9:j:68:LYS:HE3	2.01	0.41
13:n:74:GLU:O	13:n:77:ALA:HB3	2.21	0.41
18:s:41:LYS:O	18:s:44:ALA:HB3	2.20	0.41
25:z:9:THR:HG23	25:z:10:ARG:N	2.35	0.41
29:E:36:ALA:HB3	29:E:39:ARG:HB2	2.02	0.41
33:I:103:ARG:HA	33:I:103:ARG:HD3	1.90	0.41
40:P:40:ALA:O	52:3:685:G:H4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:P:81:LEU:HD22	40:P:104:PHE:HB3	2.02	0.41
41:Q:5:GLN:NE2	52:3:880:C:H3'	2.33	0.41
43:S:20:PHE:O	43:S:21:ALA:CB	2.67	0.41
49:Y:43:LYS:HB3	49:Y:85:LEU:HG	2.01	0.41
49:Y:47:GLN:O	49:Y:51:ASN:ND2	2.53	0.41
52:3:824:G:H2'	52:3:825:A:C8	2.53	0.41
52:3:1328:C:H2'	52:3:1329:A:C8	2.56	0.41
52:3:1384:C:H2'	52:3:1385:G:H8	1.85	0.41
53:1:765:C:H2'	53:1:766:U:C6	2.56	0.41
53:1:891:G:H2'	53:1:892:A:C8	2.56	0.41
53:1:1337:G:H2'	53:1:1338:G:H8	1.85	0.41
53:1:2737:G:H2'	53:1:2738:A:H8	1.86	0.41
53:1:2825:G:H2'	53:1:2826:A:H5'	2.02	0.41
53:1:2832:U:H1'	53:1:2834:G:C2	2.56	0.41
1:b:68:ARG:NH2	1:b:126:GLY:O	2.53	0.41
5:f:31:GLU:OE2	5:f:33:THR:OG1	2.38	0.41
6:g:67:ALA:O	6:g:70:GLU:HG3	2.20	0.41
8:i:38:CYS:SG	8:i:42:ASN:ND2	2.93	0.41
10:k:107:LEU:HD23	10:k:107:LEU:O	2.20	0.41
24:y:18:LEU:HD12	24:y:18:LEU:HA	1.93	0.41
24:y:24:GLU:H	24:y:24:GLU:HG2	1.52	0.41
30:F:36:ARG:O	30:F:37:GLN:CB	2.68	0.41
35:K:53:LYS:C	35:K:54:LEU:HG	2.46	0.41
39:O:46:LYS:HE2	39:O:68:ARG:HG2	2.02	0.41
43:S:82:LYS:HE3	43:S:82:LYS:HB3	1.88	0.41
46:V:64:ARG:HD3	52:3:130:A:O4'	2.21	0.41
52:3:110:C:H2'	52:3:111:G:O4'	2.21	0.41
53:1:11:C:H3'	53:1:12:U:C5'	2.50	0.41
53:1:307:G:N2	53:1:309:A:H3'	2.35	0.41
53:1:987:C:H2'	53:1:988:A:O4'	2.19	0.41
53:1:1297:C:OP1	53:1:2710:C:H4'	2.20	0.41
53:1:2731:G:H2'	53:1:2732:G:C8	2.56	0.41
55:5:29:G:H2'	55:5:30:G:C8	2.55	0.41
58:8:113:MET:SD	58:8:114:PRO:HD2	2.60	0.41
1:b:56:GLY:HA2	1:b:212:TRP:C	2.46	0.41
2:c:187:LEU:HD12	2:c:187:LEU:HA	1.88	0.41
4:e:35:LEU:HD12	4:e:35:LEU:N	2.35	0.41
4:e:134:GLN:HB2	4:e:140:ILE:HG12	2.02	0.41
4:e:148:VAL:O	4:e:148:VAL:HG22	2.21	0.41
9:j:113:PRO:HD2	53:1:558:U:P	2.60	0.41
11:l:49:GLY:HA3	11:l:58:TYR:HE1	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:r:16:GLU:CD	17:r:100:GLY:HA2	2.46	0.41
32:H:6:PRO:O	32:H:9:ILE:HG22	2.20	0.41
36:L:107:ALA:HA	36:L:122:GLU:OE2	2.20	0.41
38:N:74:GLN:O	38:N:78:ILE:HG13	2.21	0.41
39:O:68:ARG:NH2	52:3:1152:A:OP1	2.54	0.41
45:U:75:ILE:HG22	45:U:80:LYS:NZ	2.36	0.41
47:W:58:ILE:O	47:W:62:ARG:HG3	2.20	0.41
50:Z:35:GLU:C	50:Z:37:TYR:H	2.29	0.41
52:3:130:A:O2'	52:3:264:C:H5'	2.21	0.41
52:3:1328:C:H2'	52:3:1329:A:H8	1.86	0.41
53:1:490:C:O2'	53:1:491:G:P	2.77	0.41
53:1:903:C:H2'	53:1:904:G:C8	2.56	0.41
53:1:1285:A:H2'	53:1:1286:A:H5'	2.03	0.41
53:1:1361:G:H2'	53:1:1362:C:C6	2.55	0.41
53:1:1530:G:H2'	53:1:1531:C:O4'	2.20	0.41
53:1:2243:U:H2'	53:1:2244:U:H6	1.83	0.41
53:1:2632:A:O2'	53:1:2633:G:H5'	2.20	0.41
53:1:2671:G:O2'	53:1:2672:U:H5'	2.21	0.41
53:1:2746:U:O4	53:1:2755:C:H4'	2.21	0.41
57:7:13:C:O2'	57:7:14:A:H5'	2.21	0.41
58:8:143:ASP:OD1	58:8:143:ASP:N	2.53	0.41
58:8:213:LEU:O	58:8:293:LEU:N	2.51	0.41
1:b:62:ARG:HG3	1:b:62:ARG:NH1	2.34	0.41
1:b:225:ASN:ND2	53:1:784:G:O4'	2.54	0.41
11:l:93:ASN:HA	11:l:96:LYS:NZ	2.35	0.41
15:p:24:THR:OG1	15:p:87:ARG:NH2	2.54	0.41
15:p:47:ILE:HA	15:p:96:LEU:HD12	2.02	0.41
18:s:71:VAL:O	18:s:71:VAL:HG13	2.20	0.41
18:s:93:ALA:HB2	53:1:1614:A:C2	2.55	0.41
18:s:94:ASP:HB3	53:1:2014:A:H5'	2.02	0.41
22:w:35:ARG:HH22	53:1:2355:G:H1'	1.82	0.41
32:H:137:VAL:HG21	32:H:167:TYR:CD2	2.56	0.41
33:I:30:LYS:HE2	52:3:411:A:C2'	2.47	0.41
33:I:162:GLU:OE1	33:I:162:GLU:N	2.52	0.41
40:P:126:ARG:HH22	52:3:693:G:P	2.43	0.41
42:R:43:LYS:HB2	42:R:46:GLU:OE2	2.20	0.41
46:V:14:ASP:OD2	46:V:54:ILE:HB	2.20	0.41
48:X:2:ARG:HA	52:3:1312:G:N7	2.35	0.41
48:X:30:LEU:O	48:X:49:ALA:N	2.51	0.41
48:X:35:ARG:NH2	48:X:74:ALA:O	2.53	0.41
52:3:490:C:H2'	52:3:491:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:3:1011:C:H2'	52:3:1012:A:H8	1.86	0.41
52:3:1199:U:H2'	52:3:1200:C:H5'	2.01	0.41
52:3:1374:A:H2'	52:3:1375:A:O4'	2.21	0.41
53:1:420:C:H2'	53:1:421:C:C6	2.55	0.41
53:1:992:C:H2'	53:1:993:G:C8	2.55	0.41
53:1:1079:C:H2'	53:1:1080:A:C8	2.56	0.41
53:1:1491:G:H2'	53:1:1492:G:C8	2.55	0.41
53:1:1657:U:H2'	53:1:1658:C:C6	2.56	0.41
53:1:1805:A:H2'	53:1:1806:C:H6	1.84	0.41
53:1:1823:G:O2'	53:1:1824:G:H5'	2.20	0.41
53:1:2655:G:O2'	53:1:2656:U:H5	2.04	0.41
54:2:60:C:H2'	54:2:61:G:H8	1.86	0.41
55:5:5:G:H2'	55:5:6:G:H8	1.85	0.41
57:7:15:G:H2'	57:7:16:U:H5'	2.02	0.41
2:c:194:PRO:HA	53:1:2680:U:H5'	2.03	0.41
3:d:46:GLN:HB2	3:d:86:ALA:HA	2.02	0.41
3:d:126:VAL:O	3:d:156:ASN:ND2	2.54	0.41
6:g:40:THR:O	6:g:41:LYS:C	2.64	0.41
6:g:71:LYS:NZ	6:g:76:GLU:HG3	2.35	0.41
6:g:83:LYS:HA	6:g:149:GLU:OXT	2.21	0.41
10:k:62:VAL:HG22	10:k:84:CYS:SG	2.61	0.41
21:v:72:VAL:HG12	21:v:73:LYS:N	2.36	0.41
24:y:1:MET:HA	24:y:4:LYS:NZ	2.36	0.41
27:C:16:THR:HG21	27:C:39:ASP:OD1	2.21	0.41
29:E:33:THR:HB	53:1:2420:C:OP1	2.20	0.41
37:M:9:MET:SD	37:M:35:ILE:HD11	2.61	0.41
40:P:40:ALA:HB2	52:3:706:A:H2	1.85	0.41
41:Q:43:LYS:NZ	56:4:20:U:O3'	2.52	0.41
52:3:38:G:H22	52:3:397:A:P	2.43	0.41
52:3:1140:C:H2'	52:3:1141:C:C6	2.56	0.41
53:1:421:C:H2'	53:1:422:A:OP2	2.21	0.41
53:1:468:G:O2'	53:1:469:G:H5'	2.21	0.41
53:1:644:A:H2'	53:1:645:C:O4'	2.19	0.41
53:1:973:A:H5'	53:1:1188:U:H1'	2.03	0.41
53:1:1354:A:H2'	53:1:1355:G:O4'	2.21	0.41
57:7:74:C:H2'	57:7:75:C:H5'	2.03	0.41
58:8:210:PRO:HD2	58:8:234:ARG:NH2	2.36	0.41
1:b:83:ASP:CG	1:b:86:ARG:HG2	2.45	0.41
1:b:176:ARG:HA	1:b:176:ARG:HD2	1.84	0.41
1:b:221:GLY:HA2	1:b:224:MET:SD	2.61	0.41
3:d:7:ASP:O	3:d:9:GLN:NE2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:d:164:LEU:HB3	3:d:167:VAL:CG2	2.51	0.41
11:l:18:ARG:NH2	53:1:1250:G:OP2	2.54	0.41
11:l:81:ASP:OD1	11:l:81:ASP:N	2.47	0.41
11:l:107:PHE:HB3	11:l:126:ARG:HH12	1.86	0.41
11:l:125:LEU:HD12	11:l:125:LEU:HA	1.90	0.41
14:o:36:TYR:HE1	14:o:54:VAL:HG21	1.86	0.41
15:p:47:ILE:HG13	15:p:59:THR:OG1	2.20	0.41
16:q:107:ALA:HB1	17:r:48:LYS:NZ	2.35	0.41
18:s:44:ALA:O	18:s:47:VAL:HG12	2.21	0.41
19:t:67:VAL:O	19:t:67:VAL:HG13	2.20	0.41
20:u:5:ARG:NH1	53:1:84:A:OP1	2.54	0.41
24:y:1:MET:HG2	24:y:4:LYS:HD2	2.02	0.41
28:D:1:MET:HG3	28:D:1:MET:O	2.21	0.41
31:G:66:ILE:HB	31:G:88:GLN:HG3	2.03	0.41
31:G:180:ILE:HD12	31:G:180:ILE:N	2.36	0.41
33:I:189:ASP:OD2	33:I:189:ASP:N	2.53	0.41
35:K:89:VAL:O	52:3:737:C:H5'	2.20	0.41
36:L:47:GLU:O	36:L:51:GLN:HG3	2.20	0.41
36:L:58:LEU:HD23	36:L:58:LEU:H	1.84	0.41
38:N:17:ARG:NH1	52:3:1147:C:H1'	2.35	0.41
40:P:19:VAL:HG13	40:P:34:THR:HG23	2.03	0.41
42:R:104:ASN:ND2	52:3:948:C:C5	2.89	0.41
43:S:78:LEU:CD2	43:S:83:VAL:HA	2.50	0.41
44:T:47:LYS:HE2	44:T:47:LYS:HB3	1.94	0.41
46:V:46:HIS:CG	46:V:70:LYS:HD3	2.56	0.41
49:Y:25:SER:HB3	52:3:1458:G:H5''	2.02	0.41
50:Z:54:ARG:NH2	56:4:7:G:OP2	2.54	0.41
52:3:58:C:O2'	52:3:59:A:H5'	2.20	0.41
52:3:710:G:H2'	52:3:711:G:C8	2.56	0.41
52:3:710:G:H2'	52:3:711:G:H8	1.85	0.41
52:3:1197:A:H2'	52:3:1198:G:C5'	2.41	0.41
52:3:1270:G:H2'	52:3:1271:A:C8	2.54	0.41
52:3:1384:C:H2'	52:3:1385:G:C8	2.55	0.41
53:1:403:U:O3'	53:1:404:A:H4'	2.21	0.41
53:1:468:G:C2'	53:1:469:G:H5'	2.50	0.41
53:1:492:A:H2'	53:1:493:G:O4'	2.21	0.41
53:1:542:C:H2'	53:1:543:G:C5'	2.51	0.41
53:1:634:C:H2'	53:1:635:C:H6	1.85	0.41
53:1:699:A:H2'	53:1:700:G:O4'	2.20	0.41
53:1:704:G:H1'	53:1:727:A:H61	1.86	0.41
53:1:1130:U:C2	53:1:2025:C:H5''	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:1199:U:H2'	53:1:1200:C:C6	2.56	0.41
53:1:1208:C:H2'	53:1:1209:U:O4'	2.20	0.41
53:1:1662:U:O2'	53:1:1663:G:H5'	2.20	0.41
53:1:1680:U:H2'	53:1:1681:G:H5'	2.01	0.41
53:1:1680:U:C2'	53:1:1681:G:H5'	2.51	0.41
53:1:2105:U:H2'	53:1:2106:U:O4'	2.21	0.41
55:6:72:A:O2'	55:6:73:A:H5'	2.21	0.41
2:c:141:ARG:NH1	53:1:1998:A:OP2	2.53	0.41
6:g:121:VAL:C	6:g:122:LEU:HD12	2.46	0.41
8:i:24:GLY:HA3	8:i:25:PRO:HD3	1.85	0.41
15:p:25:VAL:HG23	15:p:85:VAL:HA	2.02	0.41
17:r:47:VAL:HG23	17:r:47:VAL:O	2.21	0.41
18:s:15:GLN:NE2	53:1:1266:G:H5''	2.35	0.41
19:t:34:VAL:HG11	19:t:43:ILE:HD12	2.03	0.41
33:I:101:VAL:HG13	33:I:113:ALA:HB1	2.03	0.41
35:K:53:LYS:O	35:K:54:LEU:O	2.39	0.41
37:M:88:LYS:HB2	52:3:600:A:OP1	2.21	0.41
39:O:6:ILE:HD11	39:O:79:PRO:HA	2.03	0.41
42:R:112:ARG:HD3	52:3:1229:A:OP2	2.21	0.41
44:T:63:ARG:HH12	44:T:87:ARG:NE	2.19	0.41
50:Z:9:GLU:CB	50:Z:10:PRO:CD	2.98	0.41
51:a:41:SER:HB3	53:1:2124:G:O2'	2.21	0.41
51:a:177:LYS:NZ	53:1:2125:G:OP1	2.52	0.41
52:3:381:C:H2'	52:3:382:A:O4'	2.21	0.41
52:3:497:G:H2'	52:3:498:A:C8	2.56	0.41
52:3:767:A:H2'	52:3:768:A:O4'	2.21	0.41
52:3:1379:G:H2'	52:3:1380:U:C6	2.56	0.41
52:3:1499:A:H1'	52:3:1520:C:O5'	2.20	0.41
53:1:1076:C:H2'	53:1:1077:A:O4'	2.21	0.41
53:1:1188:U:O2'	53:1:1189:A:H5'	2.20	0.41
53:1:1259:G:H2'	53:1:1260:A:C8	2.56	0.41
53:1:1623:G:O2'	53:1:1624:U:H5'	2.21	0.41
53:1:1795:C:H2'	53:1:1796:U:O4'	2.20	0.41
53:1:2437:G:O2'	53:1:2438:U:H5'	2.21	0.41
58:8:254:SER:OG	58:8:255:THR:N	2.52	0.41
58:8:309:VAL:HA	58:8:387:GLY:HA2	2.03	0.41
7:h:97:LYS:HZ3	7:h:127:ALA:HA	1.86	0.40
10:k:34:GLY:N	10:k:37:ASP:OD2	2.54	0.40
10:k:71:ARG:HH22	10:k:105:ARG:NH1	2.20	0.40
31:G:165:ALA:HB3	31:G:190:SER:HB2	2.03	0.40
32:H:45:GLU:C	32:H:46:LEU:HD22	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:K:2:ARG:HG2	35:K:91:ARG:CZ	2.51	0.40
37:M:45:ILE:HG23	37:M:62:LEU:HA	2.04	0.40
40:P:19:VAL:HG12	40:P:34:THR:O	2.22	0.40
46:V:6:THR:C	46:V:7:LEU:HD12	2.46	0.40
48:X:14:LEU:O	48:X:18:VAL:HG13	2.21	0.40
52:3:438:U:C2'	52:3:439:U:OP2	2.69	0.40
52:3:1411:C:H2'	52:3:1412:C:C6	2.55	0.40
53:1:170:U:H2'	53:1:171:U:C6	2.56	0.40
53:1:292:U:H2'	53:1:293:U:C6	2.56	0.40
53:1:445:C:C2'	53:1:446:G:H5'	2.51	0.40
53:1:818:G:C2'	53:1:819:A:H5''	2.50	0.40
53:1:828:U:H4'	53:1:831:G:C2	2.57	0.40
53:1:1948:G:H1	53:1:1958:C:H42	1.69	0.40
53:1:2323:G:O2'	53:1:2324:U:H5'	2.21	0.40
55:5:62:C:H2'	55:5:63:G:C8	2.55	0.40
1:b:122:ALA:HB3	1:b:124:LYS:HZ3	1.87	0.40
7:h:54:VAL:HG23	53:1:1084:A:H5''	2.02	0.40
9:j:113:PRO:HD2	53:1:558:U:OP1	2.21	0.40
10:k:24:VAL:O	10:k:24:VAL:HG23	2.20	0.40
25:z:16:LEU:O	25:z:20:LYS:HG3	2.20	0.40
32:H:119:ILE:HG21	32:H:197:VAL:HG11	2.03	0.40
34:J:12:GLU:H	34:J:12:GLU:HG2	1.72	0.40
35:K:39:LEU:HD12	35:K:39:LEU:HA	1.84	0.40
37:M:113:ARG:HG2	37:M:117:GLN:HE22	1.86	0.40
39:O:29:ALA:HB1	39:O:36:VAL:HG21	2.04	0.40
44:T:84:LEU:HD12	44:T:84:LEU:HA	1.85	0.40
48:X:57:VAL:HA	48:X:58:PRO:HD3	1.87	0.40
50:Z:65:ARG:O	50:Z:65:ARG:HD3	2.21	0.40
51:a:16:ASP:OD2	51:a:19:LYS:HB2	2.21	0.40
51:a:56:ASP:OD1	51:a:56:ASP:N	2.53	0.40
52:3:62:U:H2'	52:3:63:C:C6	2.56	0.40
52:3:709:U:H2'	52:3:710:G:H8	1.86	0.40
53:1:121:G:H2'	53:1:122:G:H8	1.86	0.40
53:1:1077:A:C3'	53:1:1078:U:H5'	2.52	0.40
53:1:1283:G:H1'	53:1:1329:U:O2	2.21	0.40
53:1:1301:A:N3	53:1:1301:A:H2'	2.36	0.40
53:1:1564:C:H2'	53:1:1565:C:O4'	2.22	0.40
53:1:2134:A:N6	53:1:2157:G:H4'	2.37	0.40
53:1:2161:C:H2'	53:1:2162:G:H5'	2.03	0.40
53:1:2247:A:H2'	53:1:2248:C:C6	2.56	0.40
53:1:2283:C:H2'	53:1:2284:A:H5'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2809:A:OP2	53:1:2809:A:H3'	2.21	0.40
53:1:2834:G:H2'	53:1:2879:A:N6	2.34	0.40
54:2:2:G:H2'	54:2:3:C:H6	1.84	0.40
58:8:177:LYS:HB3	58:8:182:ASP:OD2	2.22	0.40
2:c:208:LYS:NZ	53:1:2732:G:H5'	2.36	0.40
9:j:44:TYR:O	16:q:63:ARG:NE	2.50	0.40
10:k:24:VAL:HG12	10:k:33:ALA:HB2	2.04	0.40
18:s:73:LYS:HE2	18:s:73:LYS:HB3	1.77	0.40
24:y:48:ARG:HA	24:y:48:ARG:HD3	1.78	0.40
44:T:42:PHE:HE2	44:T:55:LEU:HB2	1.86	0.40
45:U:31:ARG:HB3	45:U:31:ARG:NH1	2.35	0.40
46:V:59:GLU:HG3	46:V:76:ARG:NH1	2.35	0.40
49:Y:76:ALA:O	49:Y:79:THR:OG1	2.36	0.40
52:3:1011:C:H2'	52:3:1012:A:C8	2.56	0.40
52:3:1158:C:H3'	52:3:1158:C:O2	2.22	0.40
52:3:1395:C:O2'	52:3:1396:A:H5'	2.21	0.40
53:1:406:G:H2'	53:1:407:G:H8	1.86	0.40
53:1:480:A:H3'	53:1:481:G:H5''	2.04	0.40
53:1:827:U:H1'	53:1:2246:G:O2'	2.21	0.40
53:1:2677:G:H2'	53:1:2678:C:C6	2.57	0.40
53:1:2771:C:H2'	53:1:2772:C:C6	2.57	0.40
55:5:42:G:H2'	55:5:43:A:H8	1.84	0.40
55:6:35:A:H2'	55:6:36:U:C6	2.56	0.40
1:b:131:MET:HG2	1:b:134:ILE:HD12	2.03	0.40
2:c:52:THR:O	2:c:76:GLY:HA3	2.22	0.40
3:d:24:ASN:ND2	3:d:27:LEU:HB2	2.37	0.40
4:e:12:VAL:HG23	4:e:27:VAL:HG11	2.03	0.40
12:m:74:THR:HG22	12:m:86:LYS:HE2	2.03	0.40
14:o:31:THR:C	14:o:33:ARG:N	2.80	0.40
16:q:93:ILE:O	16:q:97:ILE:HG13	2.21	0.40
20:u:31:GLY:O	20:u:66:VAL:HG23	2.21	0.40
37:M:85:TYR:CD1	37:M:123:GLU:HB2	2.55	0.40
39:O:40:ILE:HB	39:O:73:LEU:HB2	2.03	0.40
44:T:48:ASP:OD2	44:T:51:SER:OG	2.34	0.40
52:3:1318:A:H2'	52:3:1319:A:H5'	2.04	0.40
52:3:1353:G:O2'	52:3:1354:U:H5'	2.21	0.40
53:1:717:C:H2'	53:1:718:A:H5'	2.02	0.40
53:1:876:C:H42	53:1:901:C:H42	1.68	0.40
53:1:1029:A:H2'	53:1:1030:C:O4'	2.21	0.40
53:1:1507:C:O2'	53:1:1508:A:H4'	2.21	0.40
53:1:2298:A:H2'	53:1:2299:U:O4'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:1:2485:G:O2'	53:1:2486:C:H5'	2.21	0.40
53:1:2843:G:O2'	53:1:2844:G:H5'	2.21	0.40
57:7:54:U:O5'	57:7:54:U:H6	2.05	0.40
1:b:224:MET:SD	1:b:229:HIS:HB2	2.62	0.40
2:c:39:ASP:OD1	2:c:39:ASP:N	2.54	0.40
2:c:40:LEU:H	2:c:40:LEU:HD12	1.85	0.40
10:k:92:GLU:O	10:k:93:GLN:O	2.39	0.40
12:m:69:PRO:O	12:m:70:ASP:OD1	2.39	0.40
17:r:5:PHE:O	17:r:11:GLN:HA	2.21	0.40
30:F:16:ILE:CG2	30:F:23:ILE:HD11	2.48	0.40
36:L:43:TYR:O	36:L:46:LEU:HG	2.22	0.40
38:N:44:ARG:H	38:N:44:ARG:HD3	1.85	0.40
41:Q:113:ARG:NH2	52:3:501:C:OP2	2.54	0.40
42:R:56:ARG:HA	42:R:59:VAL:HG22	2.03	0.40
44:T:76:ARG:HA	44:T:79:GLN:NE2	2.37	0.40
50:Z:56:ALA:O	50:Z:59:LEU:HG	2.22	0.40
52:3:26:A:H61	52:3:558:G:H1'	1.86	0.40
52:3:409:U:H2'	52:3:410:G:O4'	2.22	0.40
52:3:594:U:H2'	52:3:595:A:O4'	2.22	0.40
52:3:711:G:O2'	52:3:712:A:H5'	2.22	0.40
52:3:891:U:O2'	52:3:892:A:H5'	2.22	0.40
53:1:131:A:H2'	53:1:132:G:H8	1.85	0.40
53:1:1853:A:H1'	53:1:2233:U:O2'	2.21	0.40
53:1:1991:U:H2'	53:1:1992:G:H5''	2.03	0.40
53:1:2273:A:H2'	53:1:2274:A:C8	2.57	0.40
53:1:2408:U:H2'	53:1:2409:G:C8	2.57	0.40
53:1:2757:A:N3	53:1:2757:A:H2'	2.36	0.40
55:6:50:U:H2'	55:6:51:C:C6	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	223 (83%)	41 (15%)	5 (2%)	6	33
2	c	207/209 (99%)	181 (87%)	24 (12%)	2 (1%)	12	43
3	d	199/201 (99%)	175 (88%)	23 (12%)	1 (0%)	24	56
4	e	175/177 (99%)	153 (87%)	20 (11%)	2 (1%)	11	42
5	f	174/176 (99%)	155 (89%)	16 (9%)	3 (2%)	7	34
6	g	147/149 (99%)	127 (86%)	17 (12%)	3 (2%)	6	32
7	h	129/131 (98%)	96 (74%)	28 (22%)	5 (4%)	2	21
8	i	139/141 (99%)	120 (86%)	18 (13%)	1 (1%)	18	50
9	j	140/142 (99%)	128 (91%)	8 (6%)	4 (3%)	3	26
10	k	120/122 (98%)	98 (82%)	18 (15%)	4 (3%)	3	25
11	l	141/143 (99%)	114 (81%)	20 (14%)	7 (5%)	1	17
12	m	134/136 (98%)	113 (84%)	18 (13%)	3 (2%)	5	31
13	n	118/120 (98%)	105 (89%)	12 (10%)	1 (1%)	16	48
14	o	114/116 (98%)	103 (90%)	10 (9%)	1 (1%)	14	45
15	p	112/114 (98%)	98 (88%)	14 (12%)	0	100	100
16	q	115/117 (98%)	111 (96%)	4 (4%)	0	100	100
17	r	101/103 (98%)	85 (84%)	15 (15%)	1 (1%)	12	43
18	s	108/110 (98%)	92 (85%)	14 (13%)	2 (2%)	6	33
19	t	91/93 (98%)	77 (85%)	14 (15%)	0	100	100
20	u	100/102 (98%)	88 (88%)	11 (11%)	1 (1%)	12	43
21	v	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
22	w	73/75 (97%)	68 (93%)	5 (7%)	0	100	100
23	x	75/77 (97%)	70 (93%)	5 (7%)	0	100	100
24	y	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
25	z	56/58 (97%)	50 (89%)	6 (11%)	0	100	100
26	B	54/56 (96%)	47 (87%)	7 (13%)	0	100	100
27	C	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
28	D	44/46 (96%)	36 (82%)	7 (16%)	1 (2%)	5	30
29	E	62/64 (97%)	49 (79%)	12 (19%)	1 (2%)	7	35
30	F	36/38 (95%)	31 (86%)	4 (11%)	1 (3%)	4	27
31	G	223/225 (99%)	210 (94%)	13 (6%)	0	100	100
32	H	204/206 (99%)	186 (91%)	18 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	I	203/205 (99%)	177 (87%)	23 (11%)	3 (2%)	8	36
34	J	155/157 (99%)	128 (83%)	22 (14%)	5 (3%)	3	25
35	K	98/100 (98%)	76 (78%)	16 (16%)	6 (6%)	1	14
36	L	149/151 (99%)	135 (91%)	14 (9%)	0	100	100
37	M	127/129 (98%)	114 (90%)	11 (9%)	2 (2%)	7	35
38	N	125/127 (98%)	106 (85%)	15 (12%)	4 (3%)	3	25
39	O	96/98 (98%)	81 (84%)	9 (9%)	6 (6%)	1	14
40	P	114/116 (98%)	95 (83%)	15 (13%)	4 (4%)	3	24
41	Q	121/123 (98%)	96 (79%)	20 (16%)	5 (4%)	2	20
42	R	112/114 (98%)	97 (87%)	11 (10%)	4 (4%)	2	23
43	S	98/100 (98%)	79 (81%)	17 (17%)	2 (2%)	6	32
44	T	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	10	40
45	U	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
46	V	78/80 (98%)	63 (81%)	9 (12%)	6 (8%)	1	10
47	W	63/65 (97%)	53 (84%)	10 (16%)	0	100	100
48	X	77/79 (98%)	70 (91%)	7 (9%)	0	100	100
49	Y	83/85 (98%)	78 (94%)	5 (6%)	0	100	100
50	Z	63/65 (97%)	43 (68%)	13 (21%)	7 (11%)	0	5
51	a	130/223 (58%)	121 (93%)	7 (5%)	2 (2%)	8	36
58	8	382/400 (96%)	342 (90%)	37 (10%)	3 (1%)	16	48
All	All	6301/6512 (97%)	5475 (87%)	717 (11%)	109 (2%)	9	34

All (109) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	83	VAL
5	f	174	LYS
6	g	9	VAL
6	g	41	LYS
7	h	107	GLU
7	h	108	VAL
10	k	92	GLU
11	l	31	GLY
11	l	38	GLN
17	r	54	VAL

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Mol	Chain	Res	Type
18	s	40	ASN
20	u	51	LEU
29	E	31	ILE
34	J	93	VAL
35	K	53	LYS
35	K	54	LEU
35	K	92	THR
37	M	47	ASP
38	N	90	ASP
39	O	58	ASN
41	Q	24	GLU
41	Q	102	ASP
42	R	4	ALA
42	R	6	ILE
46	V	15	LYS
50	Z	8	ASN
50	Z	14	ALA
50	Z	64	ALA
51	a	208	TYR
58	8	335	THR
1	b	107	LYS
5	f	45	ALA
7	h	81	LEU
9	j	81	ILE
11	l	29	LYS
11	l	85	VAL
12	m	69	PRO
30	F	37	GLN
34	J	50	GLY
35	K	39	LEU
35	K	99	ALA
38	N	100	ALA
40	P	14	GLN
40	P	77	GLY
41	Q	43	LYS
42	R	7	ASN
42	R	65	GLU
46	V	50	ASN
46	V	70	LYS
50	Z	12	ASP
58	8	334	ARG
1	b	154	ALA

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Mol	Chain	Res	Type
1	b	260	LYS
4	e	20	ASN
7	h	118	ILE
11	l	36	LYS
12	m	6	ARG
18	s	3	THR
33	I	47	LEU
34	J	11	GLN
34	J	89	THR
34	J	90	GLY
35	K	86	ARG
39	O	35	GLN
39	O	37	ARG
39	O	43	PRO
44	T	46	LYS
50	Z	9	GLU
5	f	175	LYS
8	i	92	PRO
10	k	72	PRO
33	I	167	PRO
38	N	102	PHE
41	Q	88	ASP
43	S	93	PRO
46	V	17	GLU
51	a	6	LYS
6	g	15	LEU
9	j	111	LYS
10	k	89	ASN
10	k	93	GLN
13	n	32	GLU
14	o	34	HIS
28	D	4	THR
39	O	42	LEU
46	V	18	LYS
46	V	48	GLU
50	Z	24	LYS
50	Z	25	ALA
58	8	129	PRO
33	I	152	SER
38	N	121	ARG
40	P	91	GLY
41	Q	103	CYS

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Mol	Chain	Res	Type
1	b	246	PRO
12	m	125	PRO
1	b	230	PRO
37	M	50	VAL
43	S	30	ILE
2	c	135	GLY
9	j	110	PRO
11	l	16	GLY
2	c	143	PRO
4	e	175	PRO
7	h	78	GLY
9	j	100	VAL
11	l	87	GLY
39	O	41	PRO
40	P	90	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	75
2	c	164/164 (100%)	163 (99%)	1 (1%)	78	79
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	148 (100%)	0	100	100
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	77
6	g	114/114 (100%)	112 (98%)	2 (2%)	51	67
7	h	100/100 (100%)	99 (99%)	1 (1%)	68	74
8	i	109/109 (100%)	107 (98%)	2 (2%)	51	67
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	75
10	k	103/103 (100%)	103 (100%)	0	100	100
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	107 (98%)	2 (2%)	51	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	n	100/100 (100%)	98 (98%)	2 (2%)	48	64
14	o	86/86 (100%)	85 (99%)	1 (1%)	63	72
15	p	99/99 (100%)	98 (99%)	1 (1%)	68	74
16	q	89/89 (100%)	88 (99%)	1 (1%)	65	73
17	r	84/84 (100%)	84 (100%)	0	100	100
18	s	93/93 (100%)	93 (100%)	0	100	100
19	t	80/80 (100%)	80 (100%)	0	100	100
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	76 (97%)	2 (3%)	40	60
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	67 (100%)	0	100	100
24	y	55/55 (100%)	54 (98%)	1 (2%)	51	67
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	47 (100%)	0	100	100
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	38 (100%)	0	100	100
29	E	51/51 (100%)	51 (100%)	0	100	100
30	F	34/34 (100%)	33 (97%)	1 (3%)	37	57
31	G	186/186 (100%)	184 (99%)	2 (1%)	65	73
32	H	170/170 (100%)	169 (99%)	1 (1%)	78	79
33	I	172/172 (100%)	171 (99%)	1 (1%)	78	79
34	J	119/119 (100%)	117 (98%)	2 (2%)	53	67
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	73
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	74
38	N	105/105 (100%)	105 (100%)	0	100	100
39	O	86/86 (100%)	85 (99%)	1 (1%)	63	72
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	103 (100%)	0	100	100
42	R	92/92 (100%)	92 (100%)	0	100	100
43	S	83/83 (100%)	81 (98%)	2 (2%)	43	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	65 (100%)	0	100	100
46	V	74/74 (100%)	73 (99%)	1 (1%)	59	70
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	70 (100%)	0	100	100
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	52 (94%)	3 (6%)	19	46
51	a	110/174 (63%)	109 (99%)	1 (1%)	70	75
58	8	317/332 (96%)	312 (98%)	5 (2%)	55	68
All	All	5225/5304 (98%)	5183 (99%)	42 (1%)	70	76

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	85	ASN
1	b	212	TRP
2	c	142	VAL
5	f	88	LEU
6	g	9	VAL
6	g	54	LEU
7	h	118	ILE
8	i	58	ILE
8	i	117	THR
9	j	84	ILE
12	m	70	ASP
12	m	119	LEU
13	n	13	ASN
13	n	79	LEU
14	o	19	GLN
15	p	69	VAL
16	q	108	LEU
21	v	72	VAL
21	v	78	GLN
24	y	24	GLU
30	F	37	GLN
31	G	46	VAL
31	G	203	ASP
32	H	56	ILE
33	I	171	GLU

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Mol	Chain	Res	Type
34	J	10	LEU
34	J	55	VAL
35	K	54	LEU
37	M	120	LEU
39	O	89	ARG
43	S	30	ILE
43	S	50	LEU
46	V	54	ILE
50	Z	10	PRO
50	Z	28	LEU
50	Z	40	PRO
51	a	164	ARG
58	8	157	LEU
58	8	213	LEU
58	8	333	PHE
58	8	337	ASP
58	8	352	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (123) such sidechains are listed below:

Mol	Chain	Res	Type
1	b	116	GLN
1	b	127	ASN
1	b	225	ASN
1	b	229	HIS
1	b	238	ASN
2	c	42	ASN
2	c	49	GLN
2	c	94	GLN
2	c	136	ASN
2	c	148	GLN
2	c	185	ASN
3	d	9	GLN
3	d	46	GLN
3	d	94	GLN
3	d	97	ASN
3	d	115	GLN
3	d	156	ASN
3	d	195	GLN
4	e	36	ASN
4	e	126	ASN
5	f	21	GLN

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Mol	Chain	Res	Type
5	f	47	ASN
5	f	63	GLN
5	f	110	HIS
6	g	2	GLN
6	g	66	ASN
7	h	88	HIS
8	i	18	ASN
8	i	30	GLN
8	i	42	ASN
9	j	58	ASN
9	j	80	HIS
10	k	9	ASN
10	k	89	ASN
11	l	38	GLN
11	l	99	ASN
12	m	13	HIS
12	m	22	GLN
13	n	3	HIS
13	n	18	GLN
13	n	23	ASN
14	o	19	GLN
14	o	116	GLN
15	p	11	GLN
16	q	55	GLN
16	q	71	ASN
17	r	82	HIS
17	r	87	GLN
17	r	89	HIS
18	s	15	GLN
19	t	48	GLN
20	u	39	ASN
20	u	65	GLN
20	u	73	ASN
20	u	98	ASN
22	w	72	ASN
23	x	5	GLN
24	y	15	ASN
24	y	25	GLN
24	y	41	HIS
24	y	58	ASN
26	B	3	GLN
28	D	29	GLN

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Mol	Chain	Res	Type
29	E	27	ASN
30	F	35	GLN
31	G	50	ASN
31	G	119	GLN
31	G	202	ASN
32	H	2	GLN
32	H	5	HIS
32	H	31	ASN
32	H	40	GLN
32	H	184	ASN
33	I	39	GLN
33	I	88	ASN
33	I	130	ASN
33	I	151	GLN
33	I	195	ASN
34	J	60	GLN
34	J	131	ASN
34	J	145	ASN
35	K	46	GLN
35	K	58	HIS
36	L	27	ASN
36	L	67	ASN
36	L	85	GLN
36	L	129	ASN
37	M	66	GLN
38	N	4	GLN
38	N	36	GLN
39	O	99	GLN
40	P	14	GLN
40	P	39	ASN
40	P	63	GLN
41	Q	4	ASN
41	Q	45	ASN
41	Q	58	ASN
41	Q	74	GLN
42	R	51	GLN
42	R	104	ASN
43	S	3	GLN
43	S	61	ASN
44	T	19	ASN
44	T	34	GLN
44	T	61	GLN

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Mol	Chain	Res	Type
45	U	18	GLN
45	U	59	HIS
45	U	79	ASN
46	V	30	HIS
46	V	50	ASN
47	W	30	ASN
47	W	51	GLN
48	X	13	HIS
49	Y	51	ASN
49	Y	60	GLN
51	a	20	GLN
51	a	58	ASN
51	a	165	ASN
58	8	20	HIS
58	8	52	ASN
58	8	79	HIS
58	8	291	GLN
58	8	330	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	146 (9%)	2 (0%)
53	1	2902/2903 (99%)	327 (11%)	11 (0%)
54	2	119/120 (99%)	9 (7%)	1 (0%)
55	5	76/77 (98%)	7 (9%)	0
55	6	76/77 (98%)	7 (9%)	0
56	4	17/18 (94%)	3 (17%)	0
57	7	75/76 (98%)	15 (20%)	0
All	All	4803/4810 (99%)	514 (10%)	14 (0%)

All (514) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	22	G
52	3	31	G
52	3	32	A
52	3	39	G
52	3	48	C

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Mol	Chain	Res	Type
52	3	50	A
52	3	51	A
52	3	71	A
52	3	85	U
52	3	87	C
52	3	95	C
52	3	100	G
52	3	122	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	279	A
52	3	281	G
52	3	289	G
52	3	345	C
52	3	352	C
52	3	355	C
52	3	367	U
52	3	372	C
52	3	411	A
52	3	412	A
52	3	413	G
52	3	429	U
52	3	439	U
52	3	467	U
52	3	479	U
52	3	485	U
52	3	486	U
52	3	497	G
52	3	518	C
52	3	527	G
52	3	531	U
52	3	533	A

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Mol	Chain	Res	Type
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	642	A
52	3	665	A
52	3	688	G
52	3	702	A
52	3	703	G
52	3	723	U
52	3	724	G
52	3	755	G
52	3	777	A
52	3	794	A
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	873	A
52	3	890	G
52	3	902	G
52	3	934	C
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

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Mol	Chain	Res	Type
52	3	1004	A
52	3	1020	G
52	3	1028	C
52	3	1030	U
52	3	1031	C
52	3	1033	G
52	3	1034	G
52	3	1094	G
52	3	1101	A
52	3	1136	C
52	3	1137	C
52	3	1138	G
52	3	1139	G
52	3	1146	A
52	3	1159	U
52	3	1168	U
52	3	1182	G
52	3	1184	G
52	3	1196	A
52	3	1198	G
52	3	1201	A
52	3	1202	U
52	3	1213	A
52	3	1225	A
52	3	1238	A
52	3	1240	U
52	3	1241	G
52	3	1258	G
52	3	1260	G
52	3	1275	A
52	3	1278	G
52	3	1280	A
52	3	1286	U
52	3	1287	A
52	3	1300	G
52	3	1317	C
52	3	1336	C
52	3	1346	A
52	3	1347	G
52	3	1363	A
52	3	1364	U
52	3	1381	U

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Mol	Chain	Res	Type
52	3	1395	C
52	3	1446	A
52	3	1448	C
52	3	1452	C
52	3	1492	A
52	3	1503	A
52	3	1506	U
52	3	1517	G
52	3	1519	A
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	139	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
53	1	199	A
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

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Mol	Chain	Res	Type
53	1	255	A
53	1	265	A
53	1	266	G
53	1	276	U
53	1	278	A
53	1	281	C
53	1	294	A
53	1	301	G
53	1	311	A
53	1	323	C
53	1	324	A
53	1	329	G
53	1	330	A
53	1	361	G
53	1	371	A
53	1	372	G
53	1	373	U
53	1	386	G
53	1	387	U
53	1	404	A
53	1	406	G
53	1	411	G
53	1	424	G
53	1	455	C
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	531	C
53	1	532	A
53	1	543	G
53	1	563	A
53	1	573	U
53	1	588	U
53	1	603	A
53	1	616	A
53	1	627	A
53	1	637	A
53	1	646	U
53	1	654	A

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Mol	Chain	Res	Type
53	1	669	G
53	1	686	U
53	1	687	C
53	1	730	A
53	1	747	C
53	1	748	G
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	806	C
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	885	C
53	1	886	A
53	1	887	U
53	1	888	C
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	983	A
53	1	995	C
53	1	996	A
53	1	1012	U
53	1	1013	C

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Mol	Chain	Res	Type
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	1175	A
53	1	1177	G
53	1	1180	U
53	1	1206	G
53	1	1211	C
53	1	1212	G
53	1	1250	G
53	1	1251	C
53	1	1253	A
53	1	1256	G
53	1	1271	G
53	1	1272	A
53	1	1275	A
53	1	1301	A
53	1	1321	A
53	1	1329	U
53	1	1330	C

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Mol	Chain	Res	Type
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	1398	C
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	1491	G
53	1	1498	C
53	1	1515	A
53	1	1524	G
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	1581	G
53	1	1584	U
53	1	1608	A
53	1	1611	C
53	1	1616	A
53	1	1647	U
53	1	1648	U
53	1	1674	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

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Mol	Chain	Res	Type
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	1847	A
53	1	1871	A
53	1	1901	A
53	1	1906	G
53	1	1907	G
53	1	1913	A
53	1	1914	C
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	1972	G
53	1	1991	U
53	1	1992	G
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	2036	C
53	1	2043	C
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	2096	C
53	1	2110	G

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Mol	Chain	Res	Type
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	2172	U
53	1	2173	A
53	1	2189	U
53	1	2198	A
53	1	2204	G
53	1	2211	A
53	1	2213	U
53	1	2225	A
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	2335	A
53	1	2350	C
53	1	2383	G
53	1	2385	C
53	1	2392	A
53	1	2402	U
53	1	2406	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	2448	A

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Mol	Chain	Res	Type
53	1	2476	A
53	1	2491	U
53	1	2498	C
53	1	2502	G
53	1	2503	A
53	1	2505	G
53	1	2513	A
53	1	2518	A
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	2609	U
53	1	2613	U
53	1	2629	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	2716	C
53	1	2744	G
53	1	2748	A
53	1	2757	A
53	1	2764	A
53	1	2765	A
53	1	2778	A
53	1	2779	U
53	1	2791	G
53	1	2794	C
53	1	2797	U
53	1	2800	A
53	1	2809	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

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Mol	Chain	Res	Type
53	1	2872	A
53	1	2880	C
53	1	2883	A
53	1	2894	G
54	2	4	C
54	2	13	G
54	2	24	G
54	2	35	C
54	2	44	G
54	2	67	G
54	2	89	U
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	8	U
55	6	18	G
55	6	19	G
55	6	20	U
55	6	47	U
55	6	49	G
56	4	12	A
56	4	13	A
56	4	19	U
57	7	8	U
57	7	9	A
57	7	10	G
57	7	18	G
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	56	C

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Mol	Chain	Res	Type
57	7	59	U
57	7	61	C
57	7	63	G

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	438	U
52	3	1201	A
53	1	372	G
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

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
60	PHE	7	101	57	10,11,12	0.66	0	8,13,15	0.28	0
61	GTP	8	501	-	33,34,34	0.91	1 (3%)	50,54,54	1.53	9 (18%)
59	FME	5	101	55	8,9,10	0.50	0	8,9,11	0.90	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
60	PHE	7	101	57	-	0/5/6/8	0/1/1/1
61	GTP	8	501	-	-	5/22/38/38	0/3/3/3
59	FME	5	101	55	-	2/7/9/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	8	501	GTP	C2-N3	2.00	1.38	1.33

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	8	501	GTP	C5-C4-N3	-4.76	120.81	128.39
61	8	501	GTP	C2-N3-C4	4.20	119.53	112.30
61	8	501	GTP	C2-N1-C6	-2.99	119.69	125.11
61	8	501	GTP	N9-C4-N3	2.97	131.90	125.95
61	8	501	GTP	N9-C8-N7	-2.56	108.65	113.40
61	8	501	GTP	O6-C6-C5	-2.43	120.12	126.53
61	8	501	GTP	C5-C6-N1	2.41	119.39	113.25
61	8	501	GTP	C8-N7-C5	2.38	108.49	104.26
61	8	501	GTP	C3'-C2'-C1'	2.05	105.34	101.46

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	5	101	FME	O1-CN-N-CA
59	5	101	FME	O-C-CA-CB
61	8	501	GTP	O4'-C4'-C5'-O5'
61	8	501	GTP	C3'-C4'-C5'-O5'

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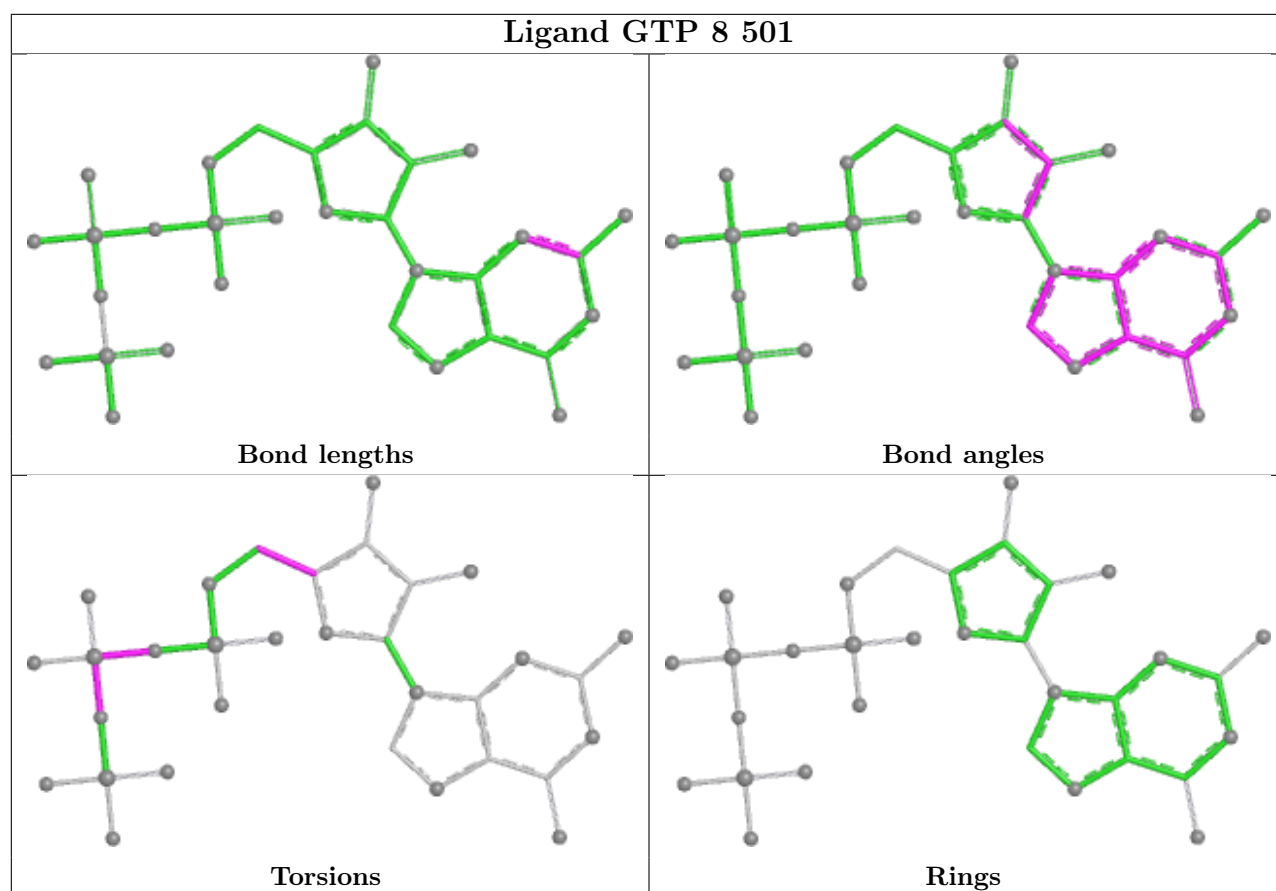
Mol	Chain	Res	Type	Atoms
61	8	501	GTP	PG-O3B-PB-O2B
61	8	501	GTP	PA-O3A-PB-O2B
61	8	501	GTP	PA-O3A-PB-O1B

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	7	101	PHE	3	0
61	8	501	GTP	2	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.

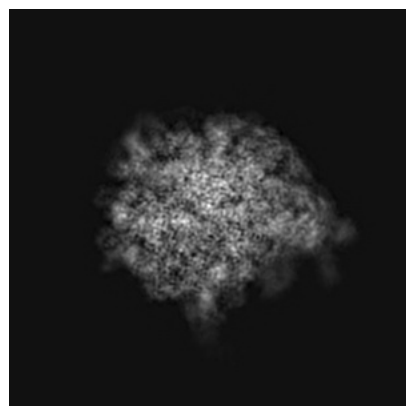
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21627. These allow visual inspection of the internal detail of the map and identification of artifacts.

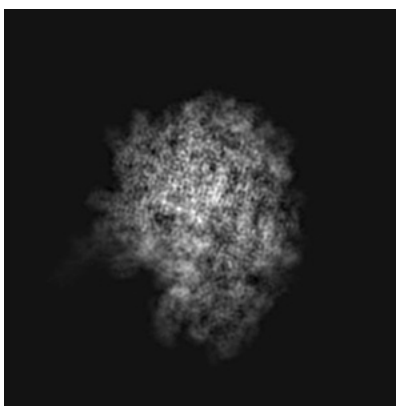
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

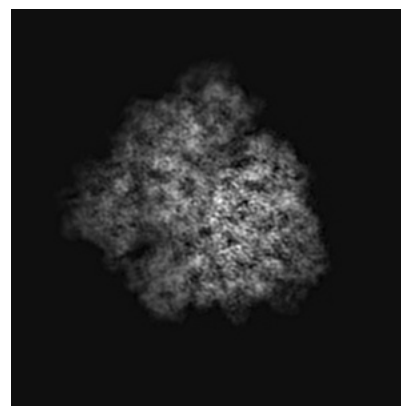
6.1.1 Primary map



X

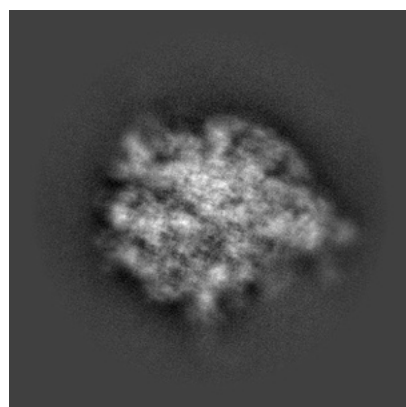


Y

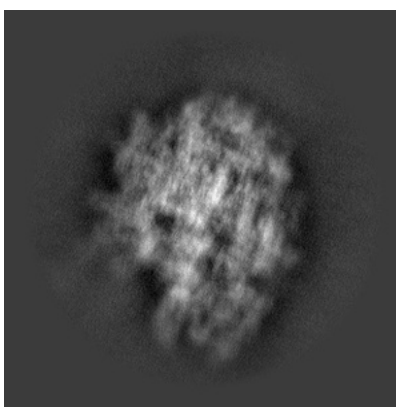


Z

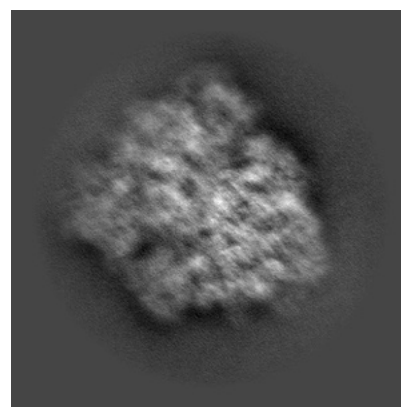
6.1.2 Raw map



X



Y

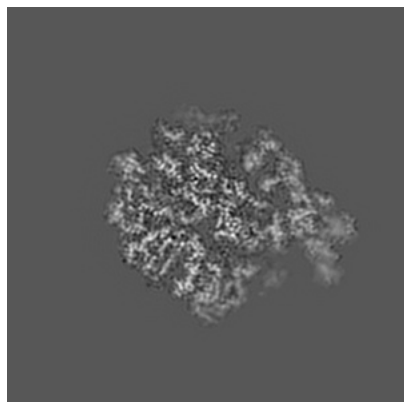


Z

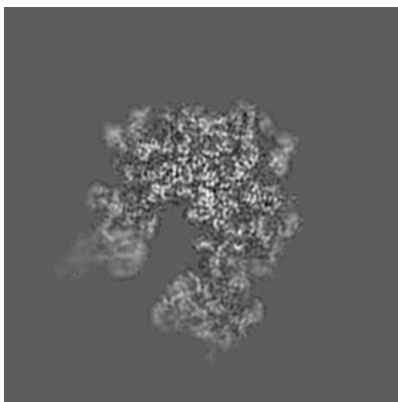
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

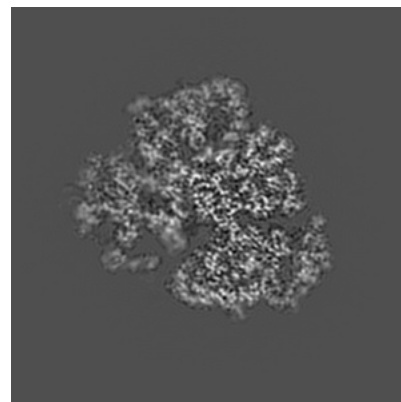
6.2.1 Primary map



X Index: 144

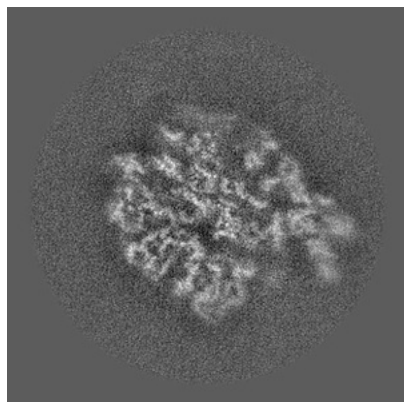


Y Index: 144

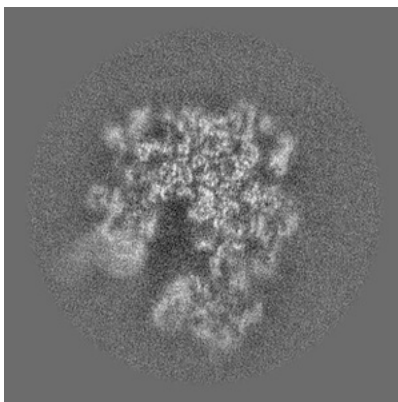


Z Index: 144

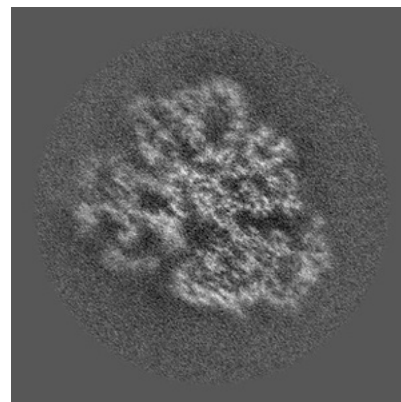
6.2.2 Raw map



X Index: 144



Y Index: 144

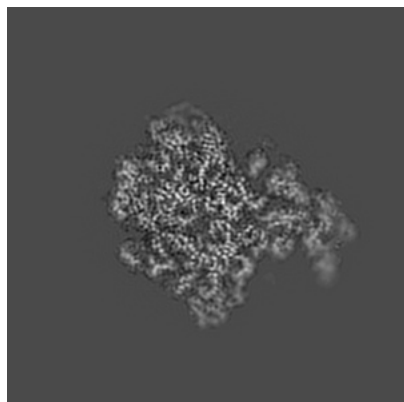


Z Index: 144

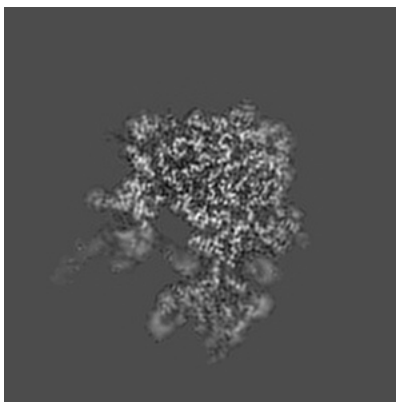
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

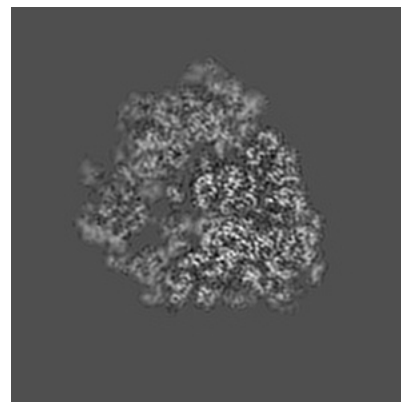
6.3.1 Primary map



X Index: 149

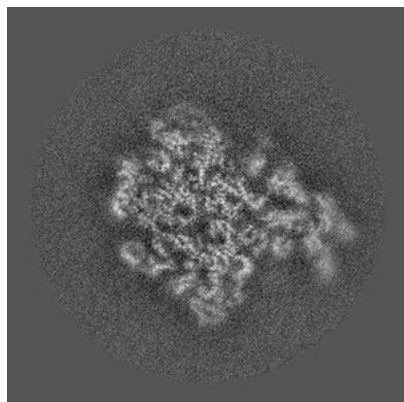


Y Index: 151

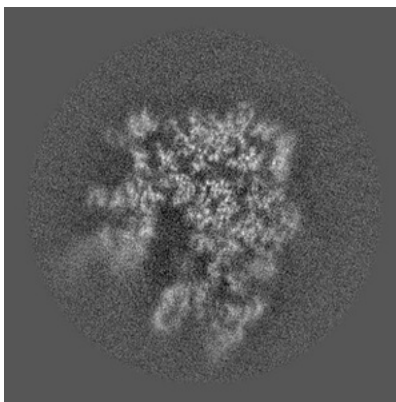


Z Index: 135

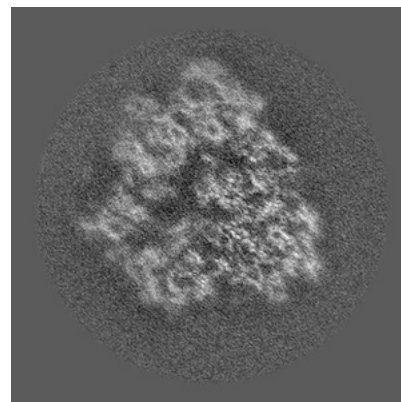
6.3.2 Raw map



X Index: 149



Y Index: 148

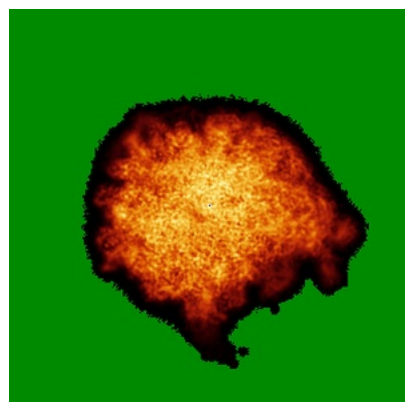


Z Index: 132

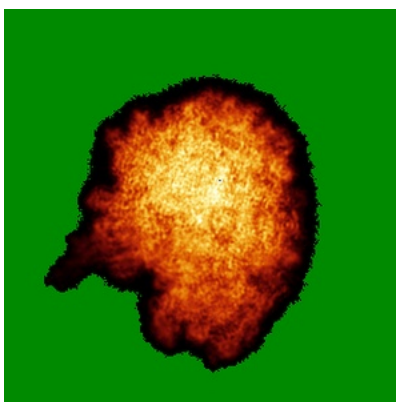
The images above show the largest variance slices of the map in three orthogonal directions.

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

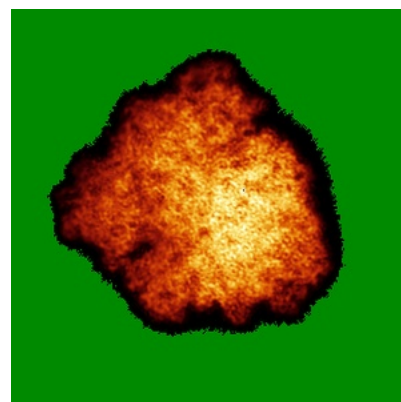
6.4.1 Primary map



X

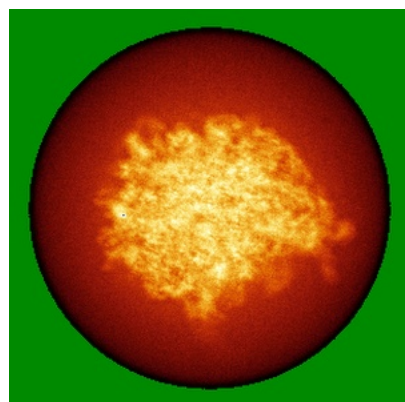


Y

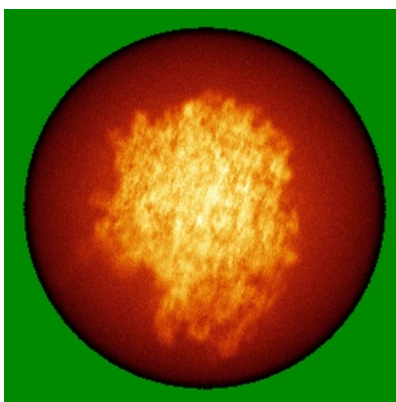


Z

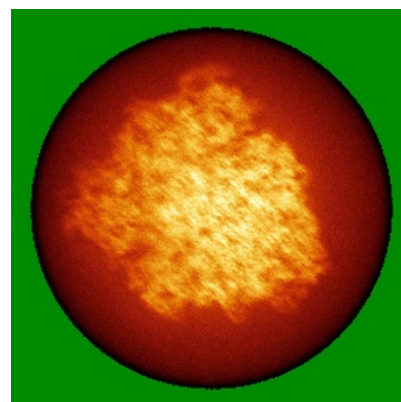
6.4.2 Raw map



X



Y



Z

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

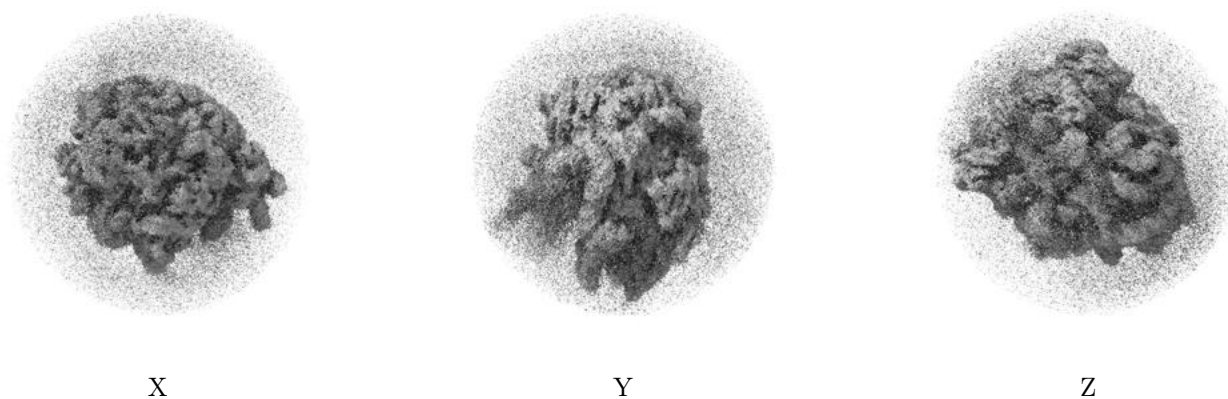
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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



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.

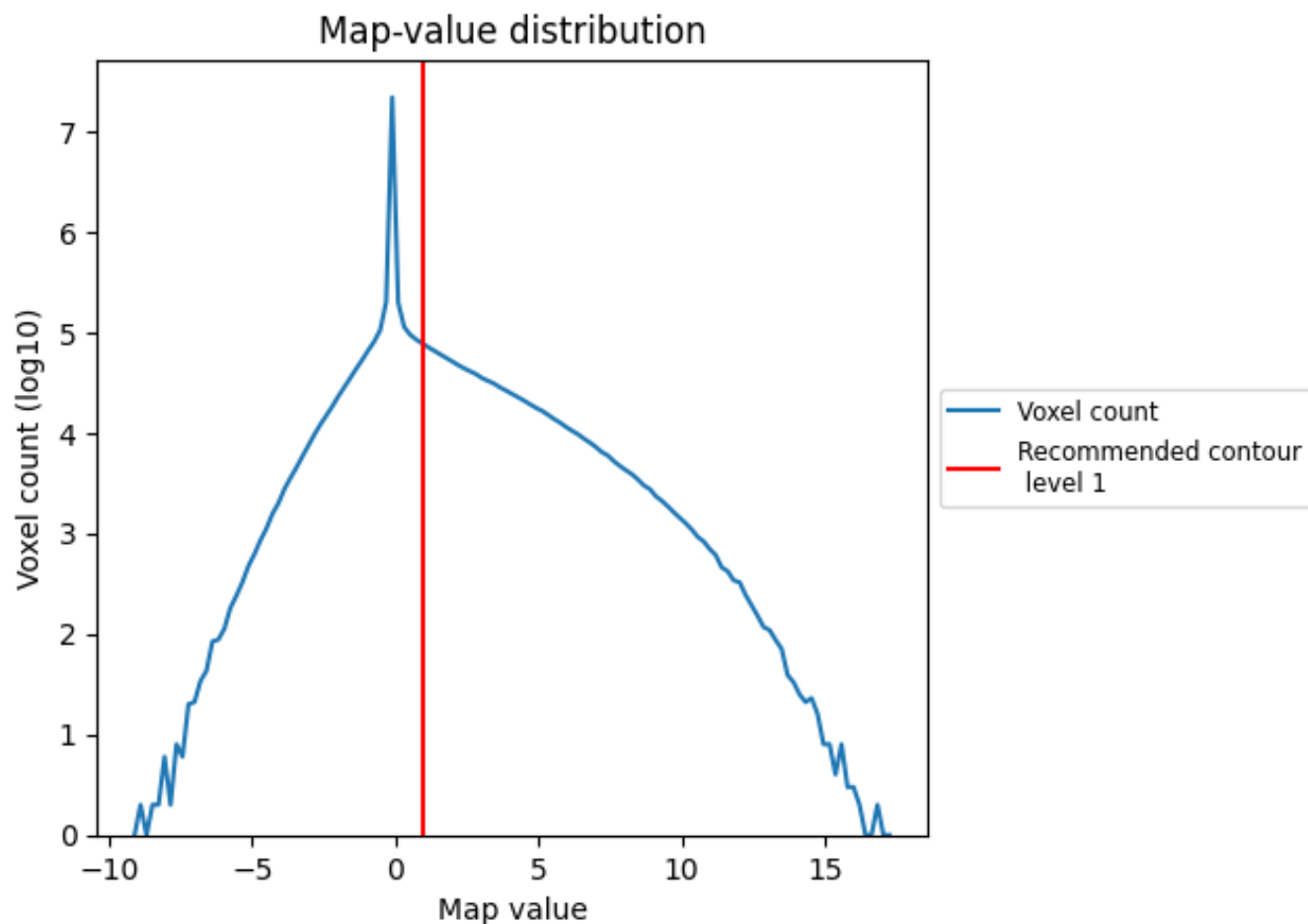
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

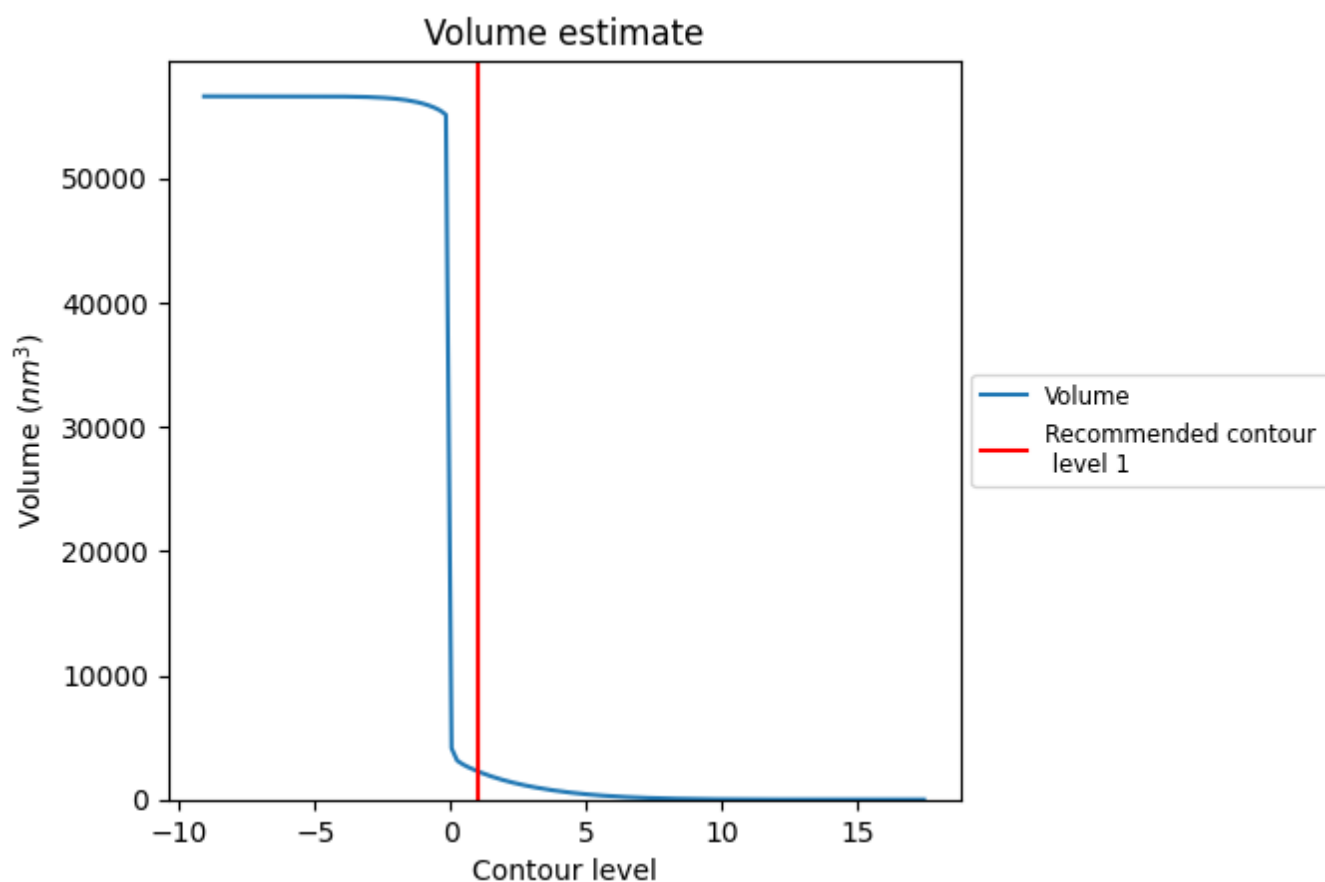
This section contains the results of statistical analysis of the map.

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.

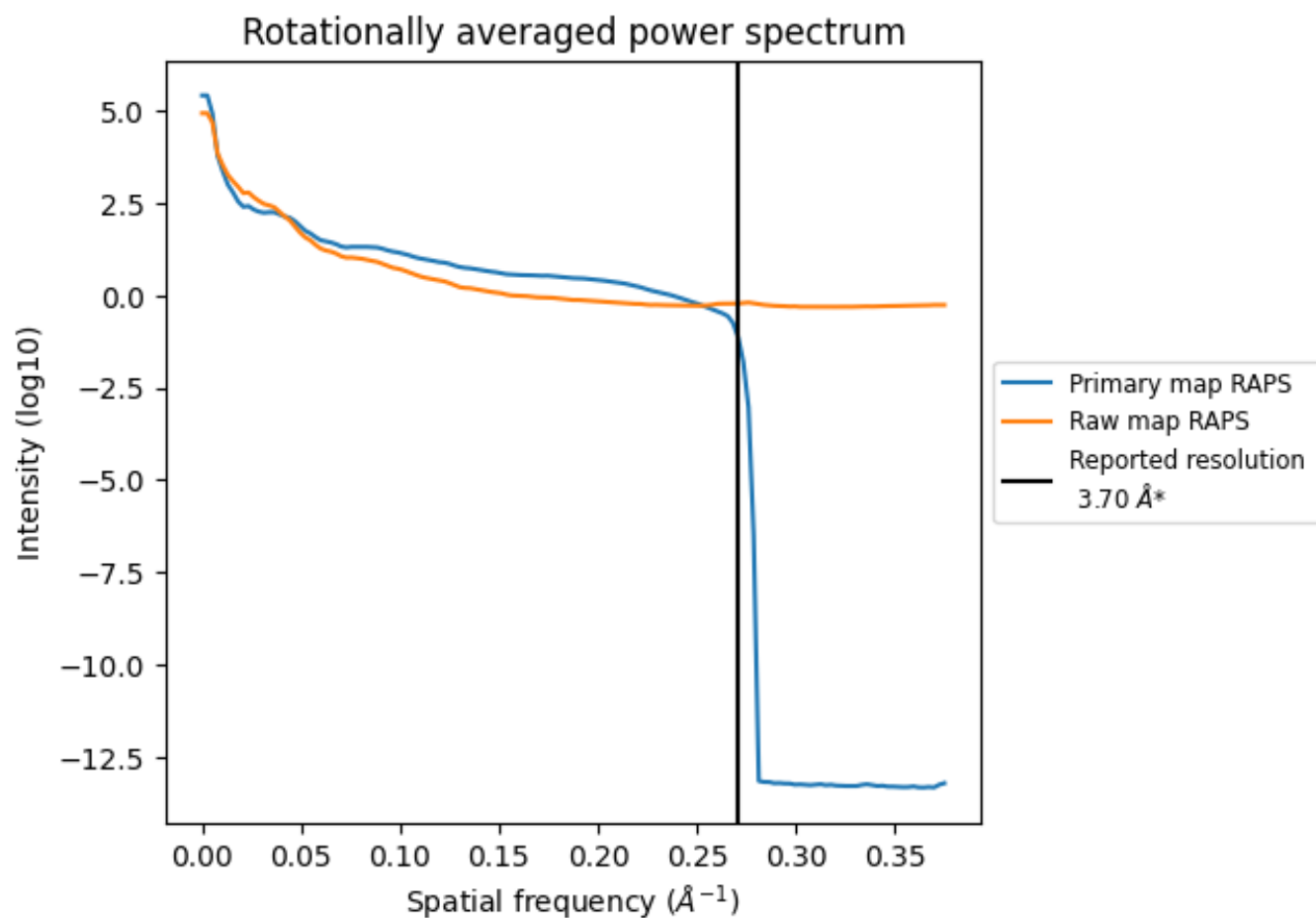
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2276 nm³; this corresponds to an approximate mass of 2056 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 ⓘ

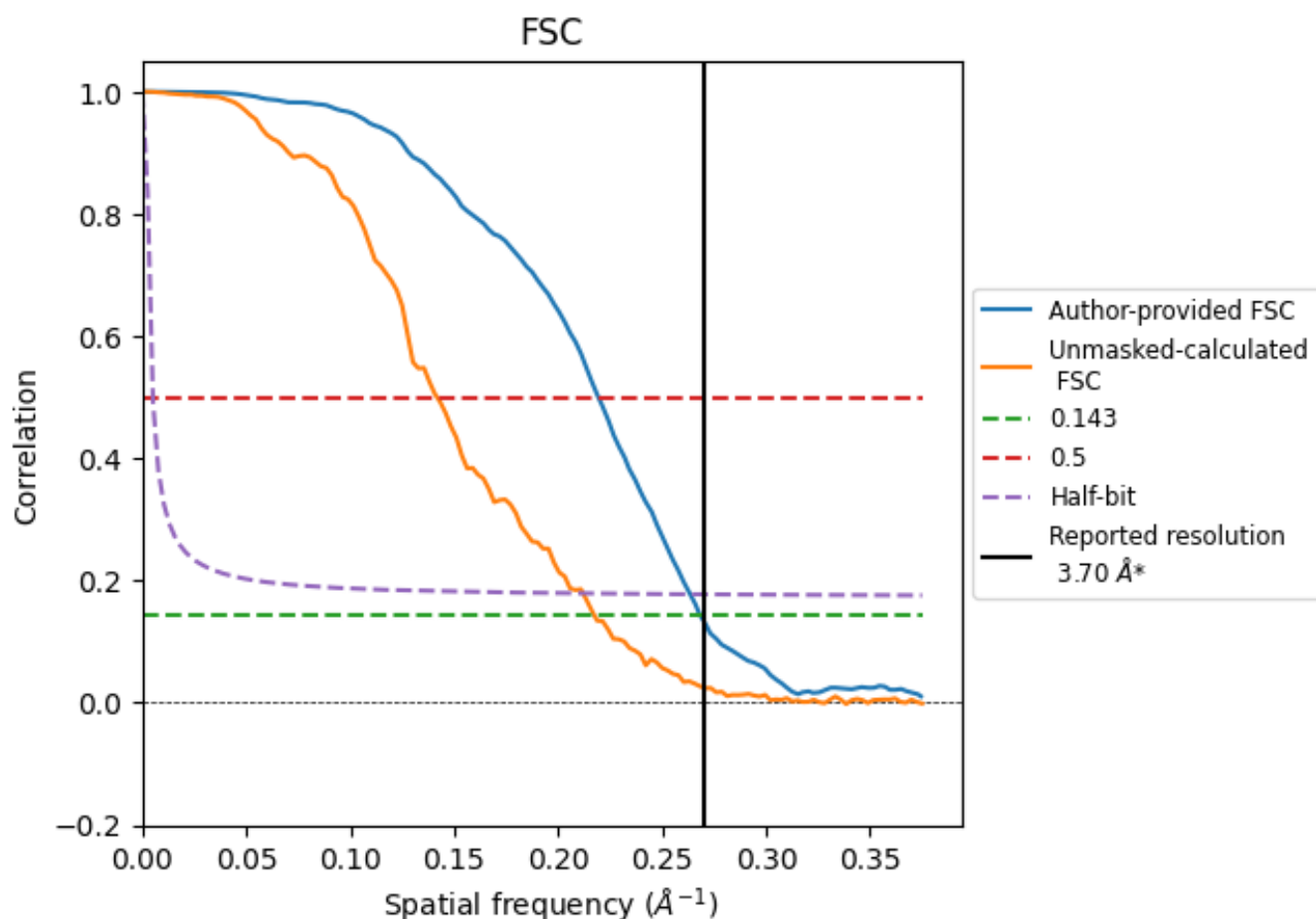


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

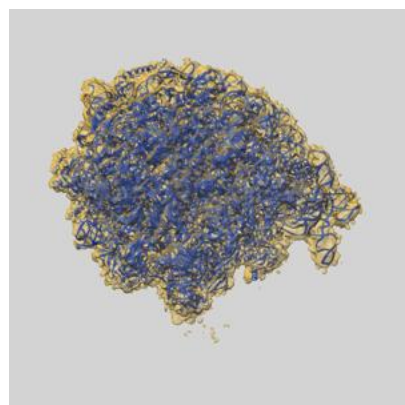
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.73	4.56	3.80
Unmasked-calculated*	4.60	7.06	4.72

*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 4.60 differs from the reported value 3.7 by more than 10 %

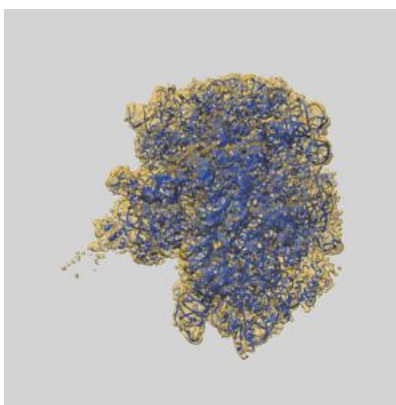
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21627 and PDB model 6WD8. Per-residue inclusion information can be found in section [3](#) on page [17](#).

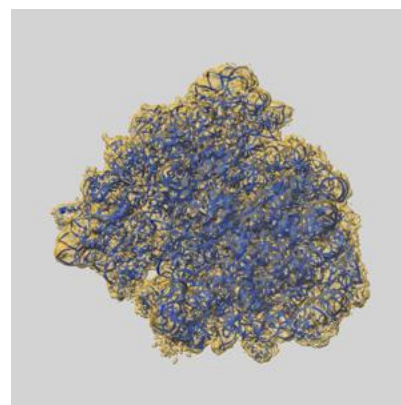
9.1 Map-model overlay [i](#)



X



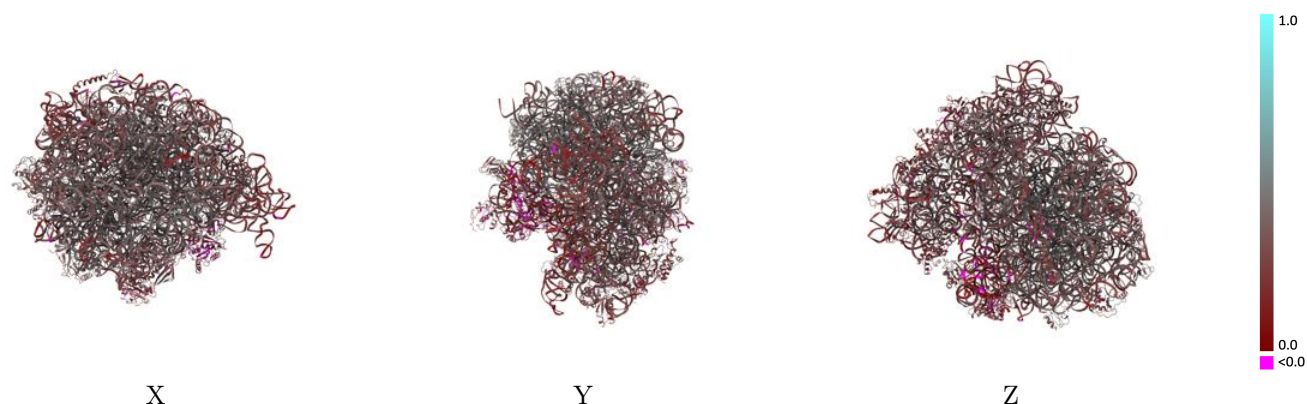
Y



Z

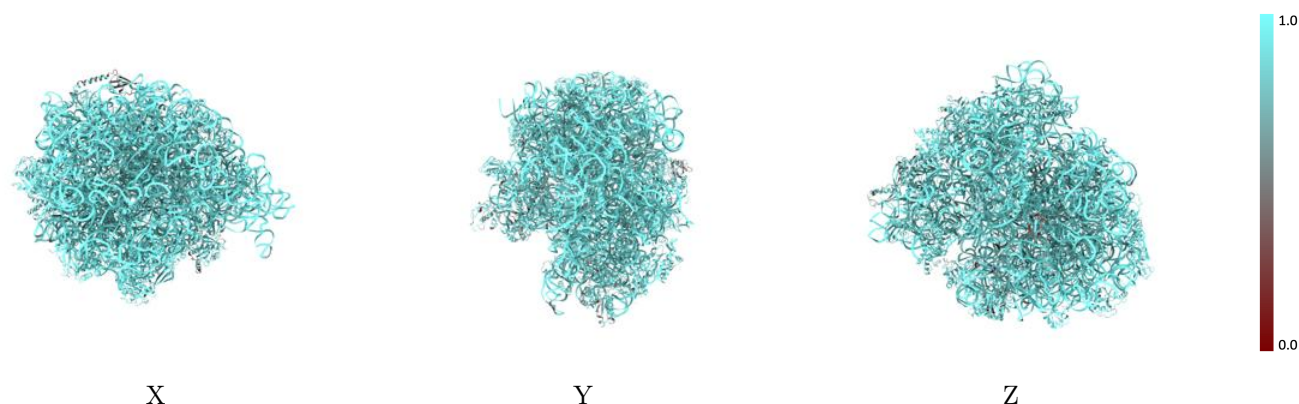
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



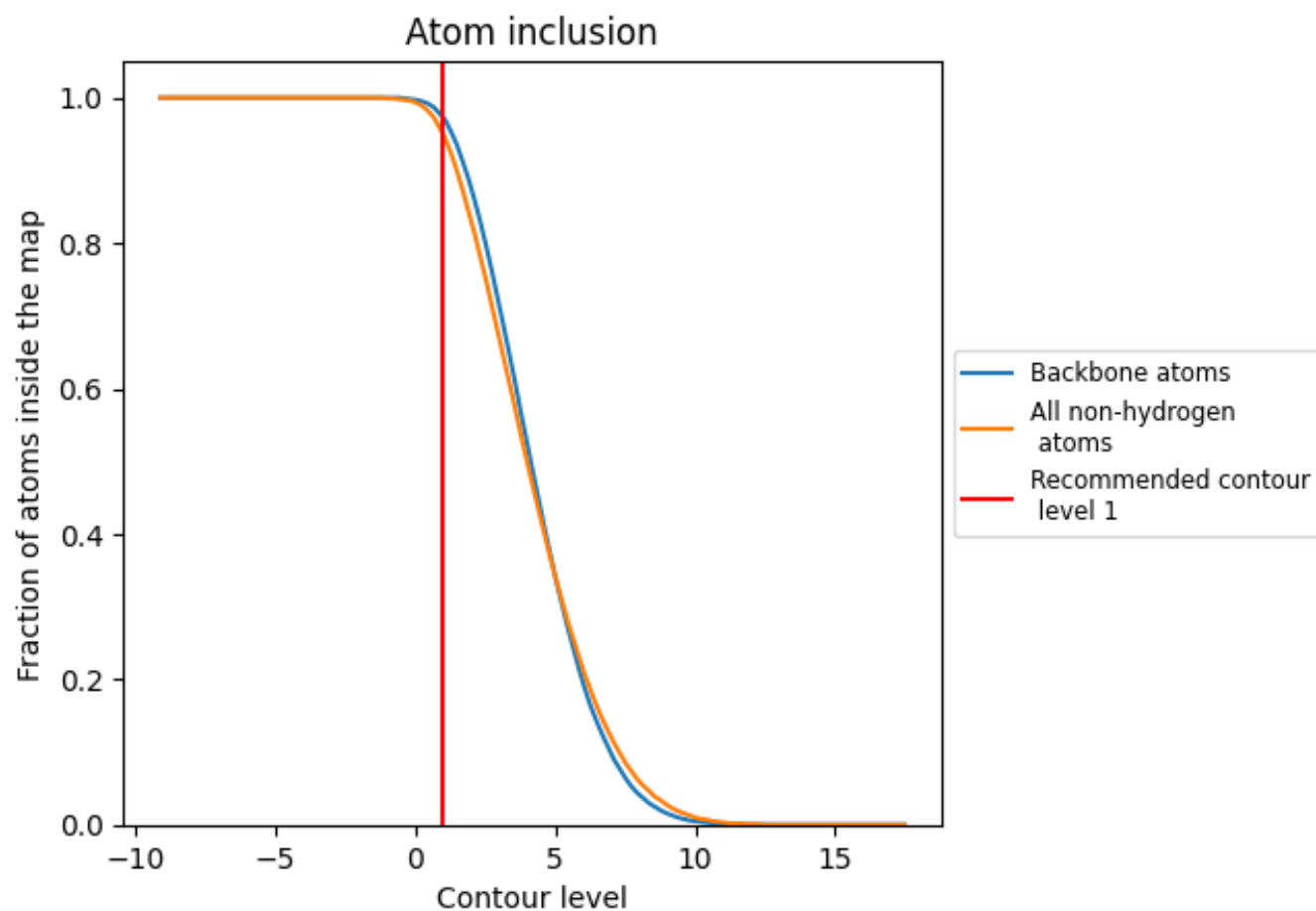
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 97% of all backbone atoms, 95% 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	 0.9500	 0.3350
1	 0.9800	 0.3620
2	 0.9810	 0.3170
3	 0.9770	 0.3110
4	 0.8810	 0.2270
5	 0.9680	 0.2730
6	 0.7770	 0.1260
7	 0.9130	 0.1430
8	 0.8720	 0.1580
B	 0.9510	 0.4160
C	 0.8210	 0.3360
D	 0.9320	 0.4410
E	 0.9330	 0.4430
F	 0.8290	 0.3810
G	 0.8820	 0.2930
H	 0.8140	 0.3320
I	 0.7990	 0.2390
J	 0.9260	 0.3660
K	 0.9540	 0.3420
L	 0.9180	 0.2950
M	 0.9410	 0.3800
N	 0.8850	 0.2940
O	 0.7240	 0.2800
P	 0.9400	 0.3620
Q	 0.9480	 0.3670
R	 0.9140	 0.2720
S	 0.8200	 0.3020
T	 0.9620	 0.3600
U	 0.8880	 0.3100
V	 0.9420	 0.3510
W	 0.9300	 0.3330
X	 0.9370	 0.2790
Y	 0.9480	 0.3100
Z	 0.8760	 0.2960
a	 0.7900	 0.1530



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Chain	Atom inclusion	Q-score
b	 0.9550	 0.4510
c	 0.9490	 0.4300
d	 0.9310	 0.3780
e	 0.9380	 0.2970
f	 0.9520	 0.2980
g	 0.6740	 0.2550
h	 0.7540	 0.1810
i	 0.7470	 0.1620
j	 0.9430	 0.4310
k	 0.9420	 0.4310
l	 0.9370	 0.4060
m	 0.9130	 0.4080
n	 0.9480	 0.4300
o	 0.9400	 0.3320
p	 0.9490	 0.4160
q	 0.9460	 0.4180
r	 0.9540	 0.3910
s	 0.9290	 0.4170
t	 0.9410	 0.4070
u	 0.9310	 0.3630
v	 0.9420	 0.3620
w	 0.9410	 0.4170
x	 0.9470	 0.4260
y	 0.9190	 0.3210
z	 0.9290	 0.4070