



Full wwPDB EM Validation Report ⓘ

Jun 18, 2026 – 01:15 pm BST

PDB ID : 7PJY / pdb_00007pjy
EMDB ID : EMD-13464
Title : Structure of the 70S-EF-G-GDP ribosome complex with tRNAs in chimeric state 1 (CHI1-EF-G-GDP)
Authors : Petrychenko, V.; Peng, B.Z.; Schwarzer, A.C.; Peske, F.; Rodnina, M.V.; Fischer, N.
Deposited on : 2021-08-24
Resolution : 3.10 Å (reported)
Based on initial models : 5J9Z, 4AQY, 5LZD, 6YSS

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:

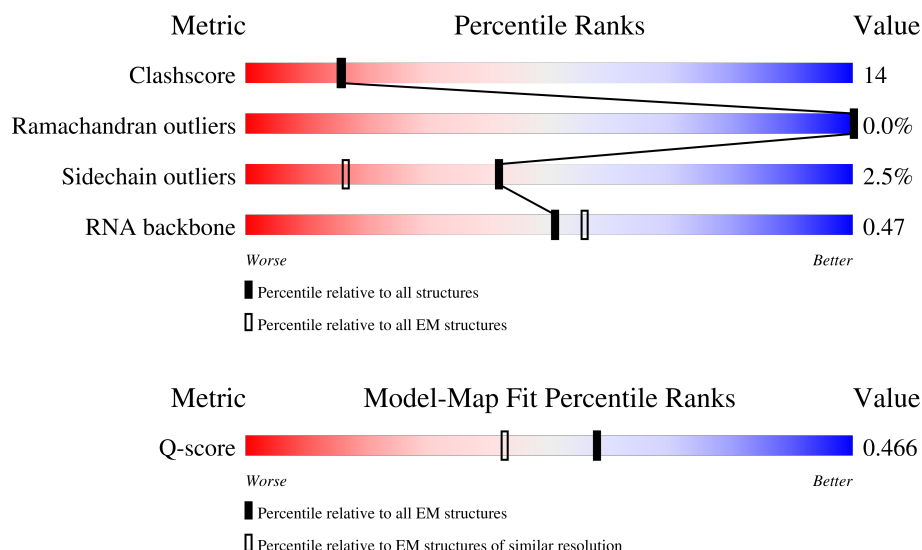
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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	0	57	 65% 33%
2	1	55	 56% 35% 9%

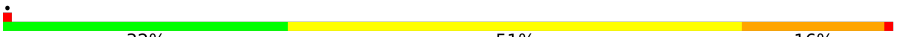
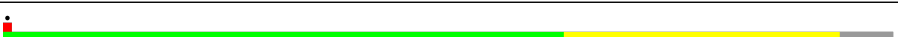
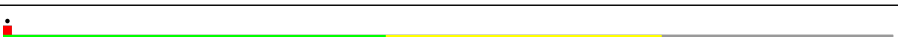
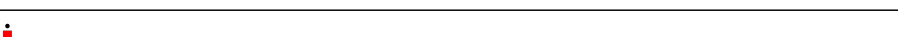
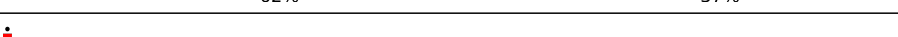
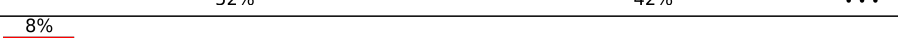
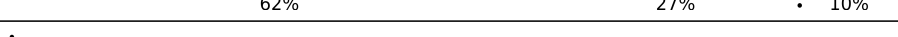
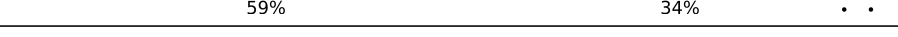
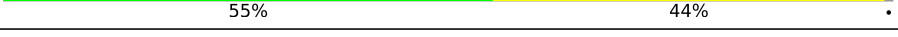
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Mol	Chain	Length	Quality of chain
3	2	46	
4	3	65	
5	4	38	
6	5	165	
7	6	70	
8	A	2903	
9	B	120	
10	C	273	
11	D	209	
12	E	201	
13	F	179	
14	G	177	
15	H	149	
16	I	142	
17	J	142	
18	K	123	
19	L	144	
20	M	136	
21	N	127	
22	O	117	
23	P	115	
24	Q	118	
25	R	103	
26	S	110	
27	T	100	

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Mol	Chain	Length	Quality of chain
28	U	104	
29	V	94	
30	W	85	
31	X	78	
32	Y	63	
33	Z	59	
34	a	1542	
35	b	240	
36	c	233	
37	d	206	
38	e	167	
39	f	135	
40	g	179	
41	h	130	
42	i	130	
43	j	103	
44	k	129	
45	l	124	
46	m	118	
47	n	102	
48	o	89	
49	p	82	
50	q	84	
51	r	75	
52	s	92	

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Mol	Chain	Length	Quality of chain
53	t	87	60% 38%
54	u	71	68% 20% 8%
55	v	77	43% 36% 19%
56	w	76	37% 49% 12%
57	x	704	7% 50% 44% 5%
58	y	2	50% 50%
59	z	33	21% 6% 70%

2 Entry composition

There are 64 unique types of molecules in this entry. The entry contains 153095 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 L32.

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

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	5	131	Total	C	N	O	0	0
			647	385	131	131		

- Molecule 7 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 8 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	2903	Total	C	N	O	P	0	0
			62338	27816	11471	20148	2903		

- Molecule 9 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	120	Total	C	N	O	P	0	0
			2570	1144	468	838	120		

- Molecule 10 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 11 is a protein called 50S ribosomal protein L3.

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

- Molecule 12 is a protein called 50S ribosomal protein L4.

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

- Molecule 13 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 14 is a protein called 50S ribosomal protein L6.

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

- Molecule 15 is a protein called 50S ribosomal protein L9.

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

- Molecule 16 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	141	Total	C	N	O	S	0	0
			693	411	141	141			

- Molecule 17 is a protein called 50S ribosomal protein L13.

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

- Molecule 18 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 19 is a protein called 50S ribosomal protein L15.

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

- Molecule 20 is a protein called 50S ribosomal protein L16.

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

- Molecule 21 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 22 is a protein called 50S ribosomal protein L18.

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

- Molecule 23 is a protein called 50S ribosomal protein L19.

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

- Molecule 24 is a protein called 50S ribosomal protein L20.

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

- Molecule 25 is a protein called 50S ribosomal protein L21.

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

- Molecule 26 is a protein called 50S ribosomal protein L22.

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

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	U	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 29 is a protein called 50S ribosomal protein L25.

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

- Molecule 30 is a protein called 50S ribosomal protein L27.

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

- Molecule 31 is a protein called 50S ribosomal protein L28.

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

- Molecule 32 is a protein called 50S ribosomal protein L29.

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

- Molecule 33 is a protein called 50S ribosomal protein L30.

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

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	1540	Total	C	N	O	P	0	0
			33050	14748	6057	10705	1540		

- Molecule 35 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 36 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 37 is a protein called 30S ribosomal protein S4.

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

- Molecule 38 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

- Molecule 39 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	f	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 40 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	g	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 41 is a protein called 30S ribosomal protein S8.

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

- Molecule 42 is a protein called 30S ribosomal protein S9.

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

- Molecule 43 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	j	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 44 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	k	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 45 is a protein called 30S ribosomal protein S12.

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

- Molecule 46 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	m	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 47 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	n	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP P0AG59

- Molecule 48 is a protein called 30S ribosomal protein S15.

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

- Molecule 49 is a protein called 30S ribosomal protein S16.

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

- Molecule 50 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 51 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 52 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s	82	Total	C	N	O	S	0	0
			658	421	125	110	2		

- Molecule 53 is a protein called 30S ribosomal protein S20.

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

- Molecule 54 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	65	Total	C	N	O	S	0	0
			506	313	105	87	1		

- Molecule 55 is a RNA chain called P-site tRNA(fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
55	v	77	Total	C	N	O	P	S	0	0
			1642	733	297	534	77	1		

- Molecule 56 is a RNA chain called P-site fMet-Phe-tRNA(Phe).

Mol	Chain	Residues	Atoms						AltConf	Trace
56	w	76	Total	C	N	O	P	S	0	0
			1631	731	291	531	76	2		

- Molecule 57 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	x	697	Total	C	N	O	S	1	0
			5416	3413	938	1040	25		

- Molecule 58 is a protein called Dipeptide (FME-PHE).

Mol	Chain	Residues	Atoms					AltConf	Trace
58	y	2	Total	C	N	O	S	0	0
			21	15	2	3	1		

- Molecule 59 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	z	10	Total	C	N	O	P	0	0
			208	93	29	76	10		

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	0	1	Total	Mg	0
			1	1	
60	1	1	Total	Mg	0
			1	1	
60	6	1	Total	Mg	0
			1	1	
60	A	267	Total	Mg	0
			267	267	
60	B	6	Total	Mg	0
			6	6	
60	C	3	Total	Mg	0
			3	3	

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Mol	Chain	Residues	Atoms		AltConf
60	D	1	Total 1	Mg 1	0
60	M	1	Total 1	Mg 1	0
60	O	1	Total 1	Mg 1	0
60	P	1	Total 1	Mg 1	0
60	a	34	Total 34	Mg 34	0
60	w	1	Total 1	Mg 1	0

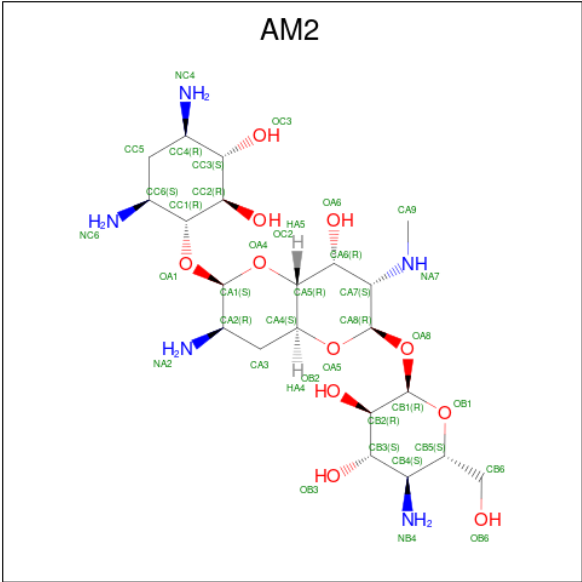
- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
61	4	1	Total 1	Zn 1	0
61	6	1	Total 1	Zn 1	0

- Molecule 62 is SODIUM ION (CCD ID: NA) (formula: Na).

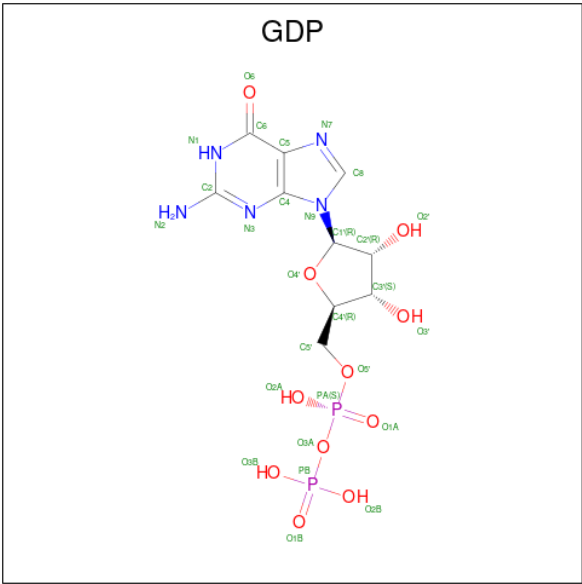
Mol	Chain	Residues	Atoms		AltConf
62	B	1	Total 1	Na 1	0

- Molecule 63 is APRAMYCIN (CCD ID: AM2) (formula: C₂₁H₄₁N₅O₁₁).



Mol	Chain	Residues	Atoms				AltConf
63	a	1	Total	C	N	O	0
			37	21	5	11	
63	a	1	Total	C	N	O	0
			37	21	5	11	
63	a	1	Total	C	N	O	0
			37	21	5	11	
63	a	1	Total	C	N	O	0
			37	21	5	11	

- Molecule 64 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

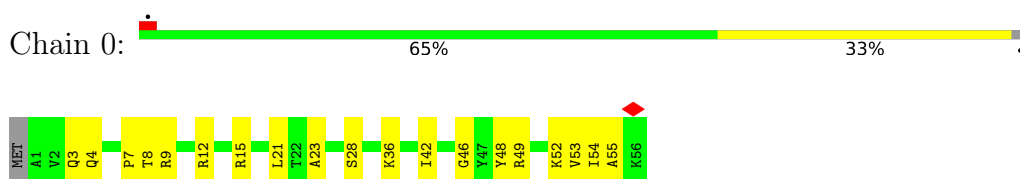


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
64	x	1	28	10	5	11	2	0

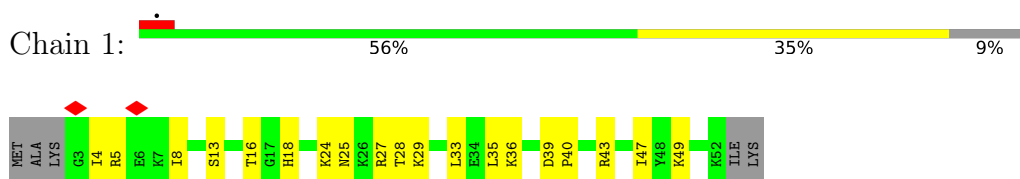
3 Residue-property plots

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.

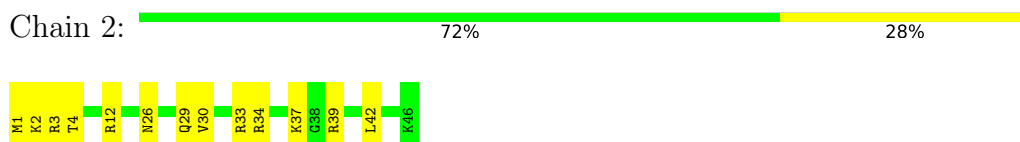
- Molecule 1: 50S ribosomal protein L32



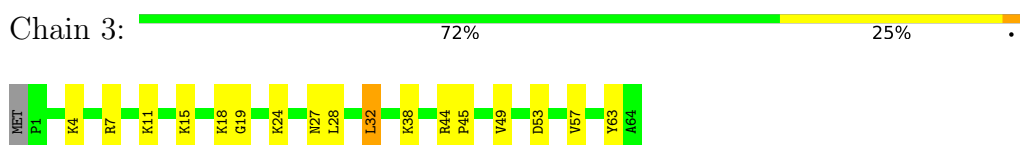
- Molecule 2: 50S ribosomal protein L33



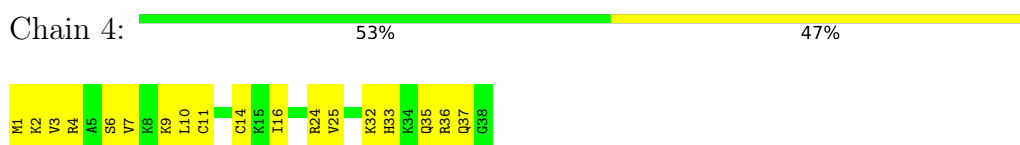
- Molecule 3: 50S ribosomal protein L34



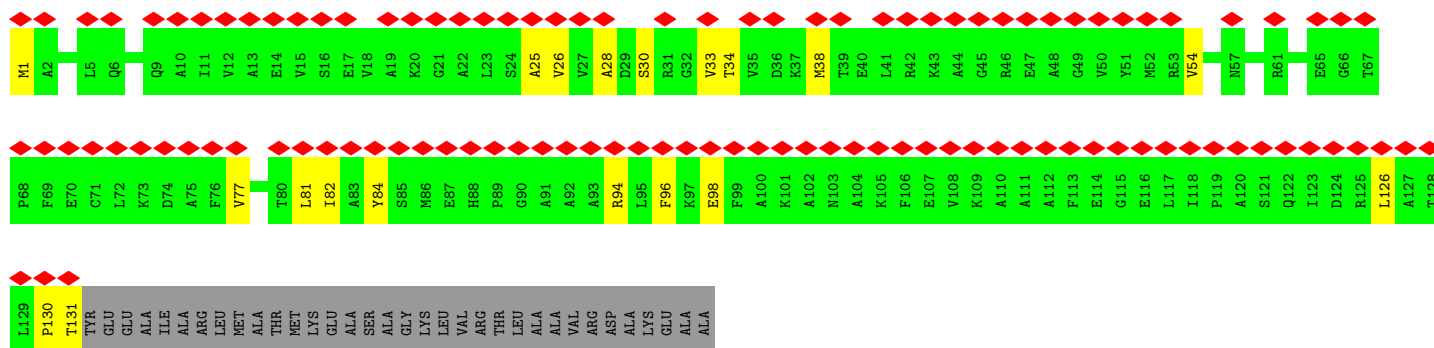
- Molecule 4: 50S ribosomal protein L35



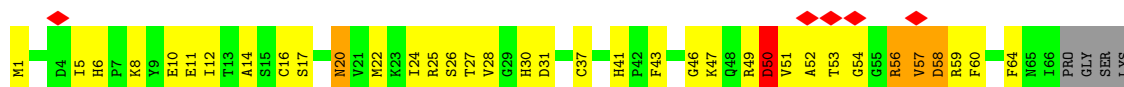
- Molecule 5: 50S ribosomal protein L36



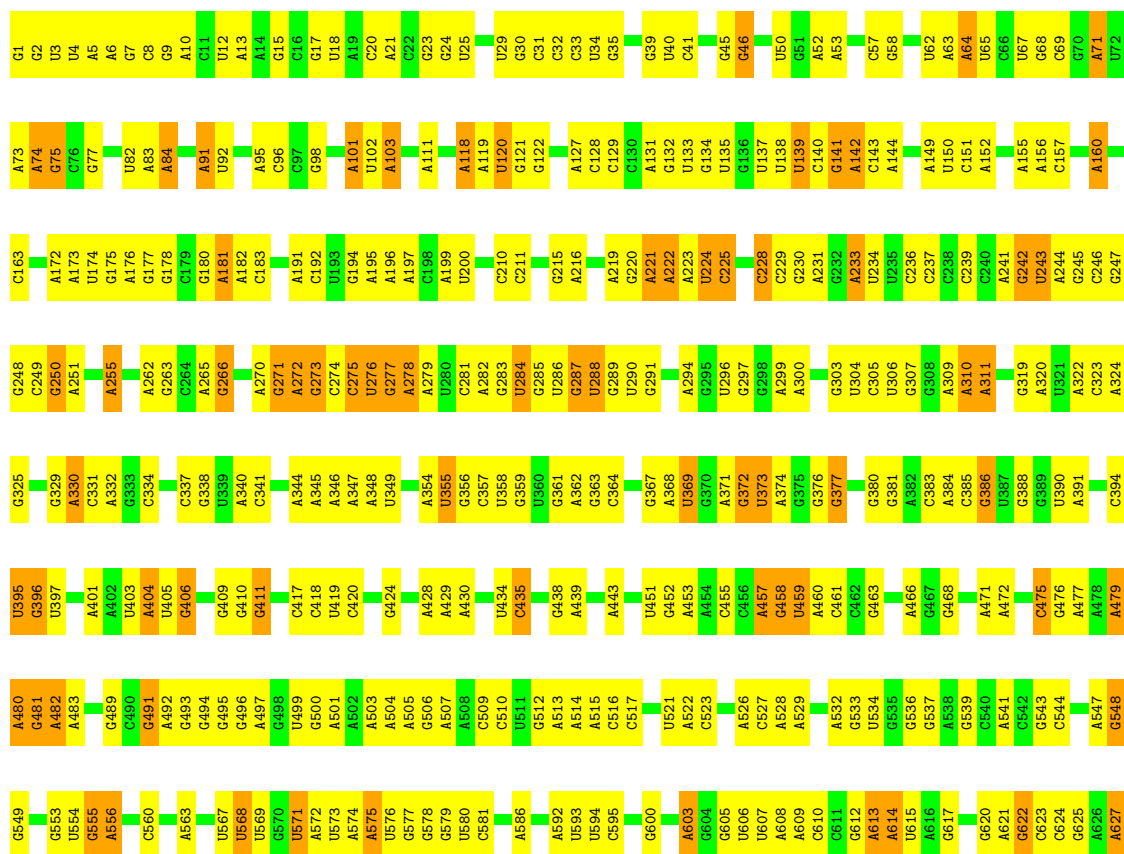
- Molecule 6: 50S ribosomal protein L10



• Molecule 7: 50S ribosomal protein L31



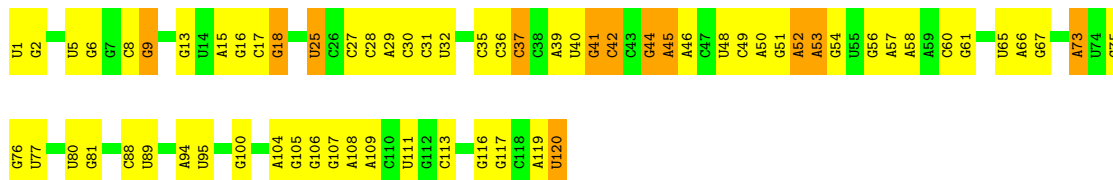
• Molecule 8: 23S ribosomal RNA



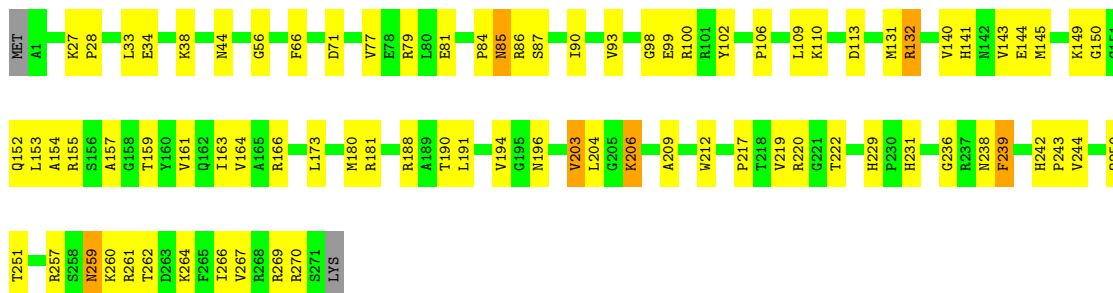




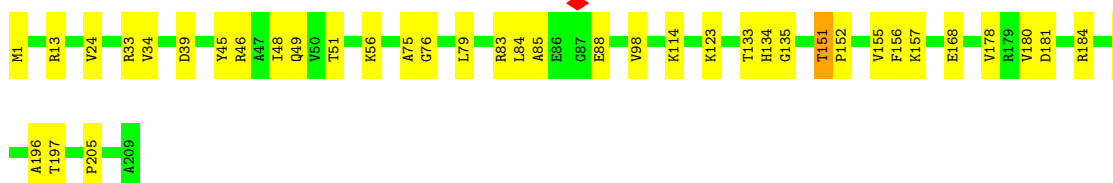
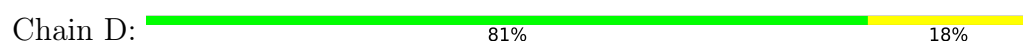
- Molecule 9: 5S ribosomal RNA



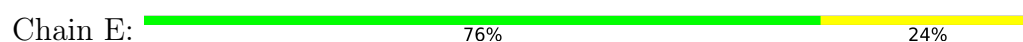
- Molecule 10: 50S ribosomal protein L2



- Molecule 11: 50S ribosomal protein L3

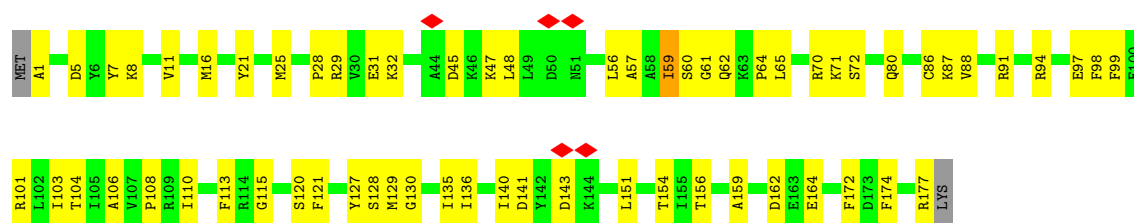


- Molecule 12: 50S ribosomal protein L4



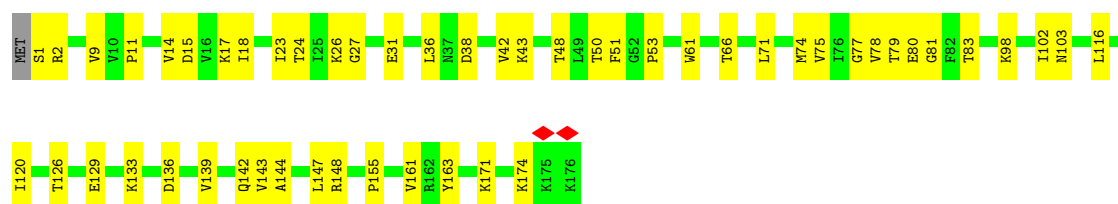
- Molecule 13: 50S ribosomal protein L5

Chain F: 



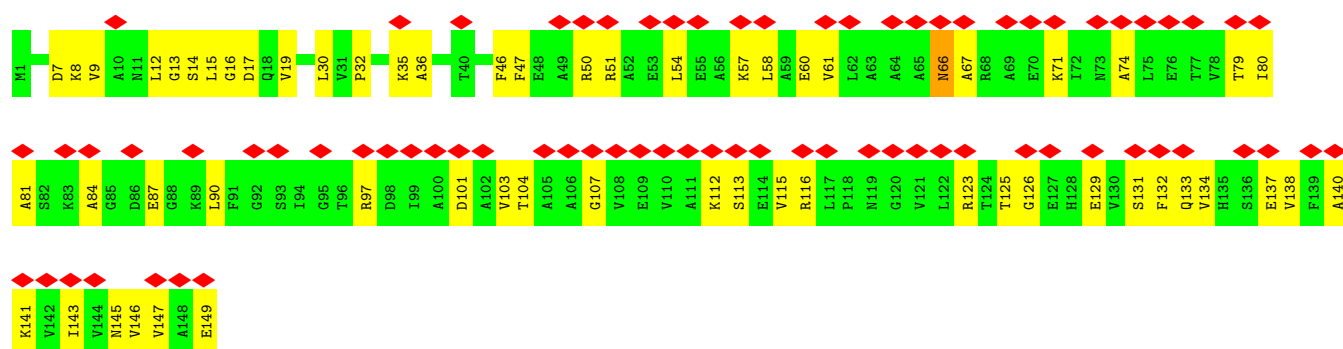
- Molecule 14: 50S ribosomal protein L6

Chain G: 

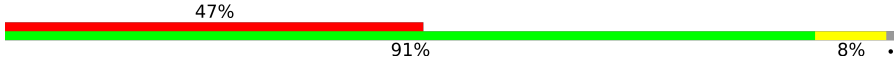


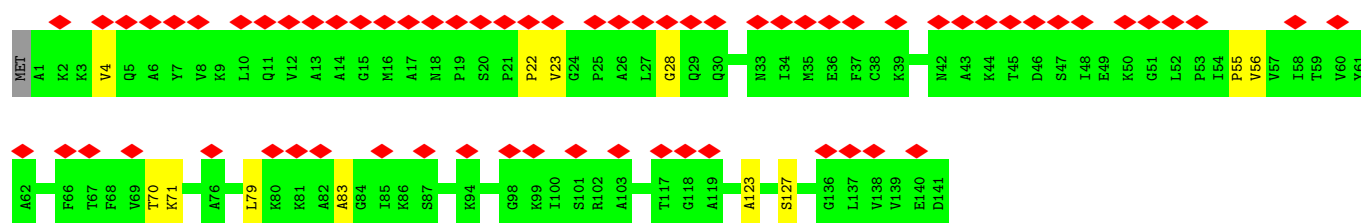
- Molecule 15: 50S ribosomal protein L9

Chain H: 



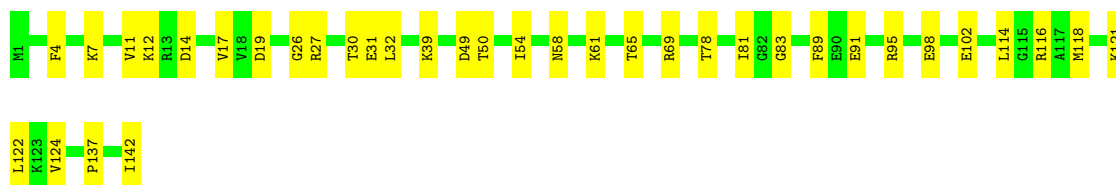
- Molecule 16: 50S ribosomal protein L11

Chain I: 



- Molecule 17: 50S ribosomal protein L13

Chain J: 



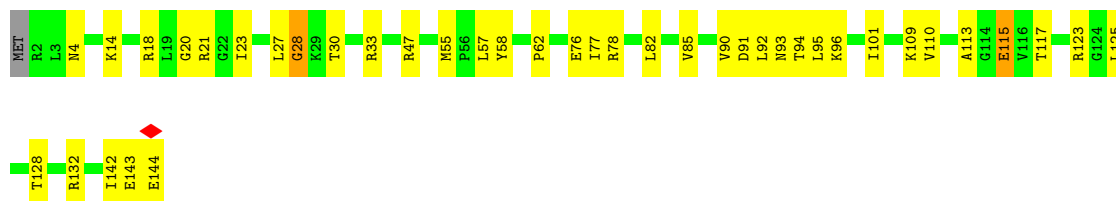
- Molecule 18: 50S ribosomal protein L14

Chain K: 67% 33%



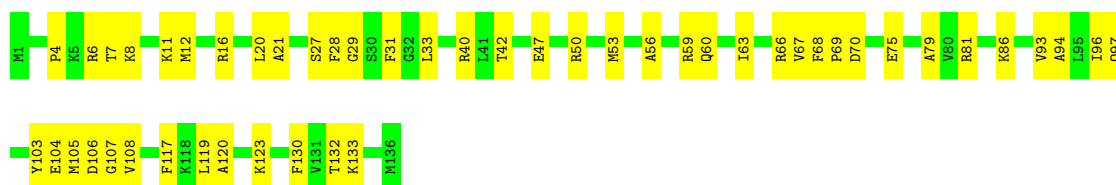
- Molecule 19: 50S ribosomal protein L15

Chain L: 72% 26%



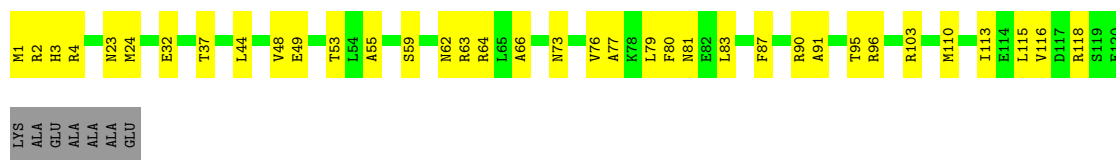
- Molecule 20: 50S ribosomal protein L16

Chain M: 64% 36%



- Molecule 21: 50S ribosomal protein L17

Chain N: 66% 28% 6%



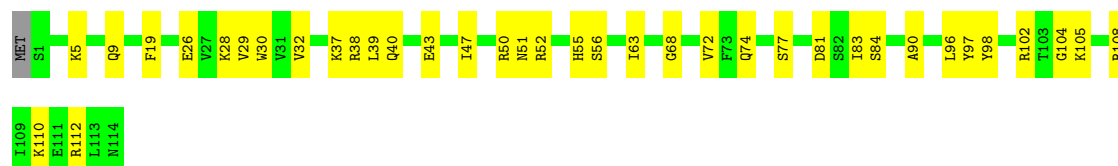
- Molecule 22: 50S ribosomal protein L18

Chain O: 66% 32%



- Molecule 23: 50S ribosomal protein L19

Chain P: 67% 32%



- Molecule 24: 50S ribosomal protein L20

Chain Q: 73% 26%



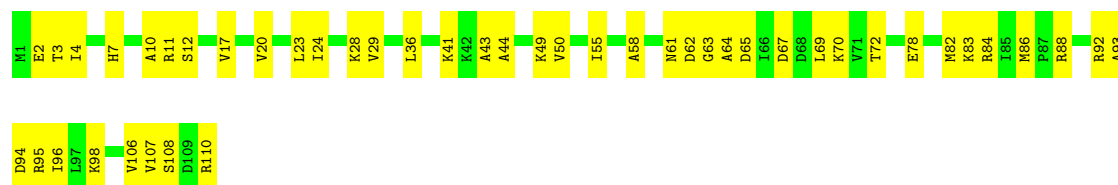
- Molecule 25: 50S ribosomal protein L21

Chain R: 71% 26%



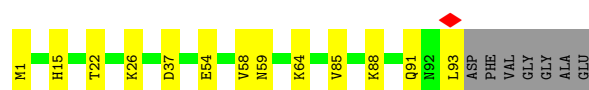
- Molecule 26: 50S ribosomal protein L22

Chain S: 58% 42%



- Molecule 27: 50S ribosomal protein L23

Chain T: 80% 13% 7%



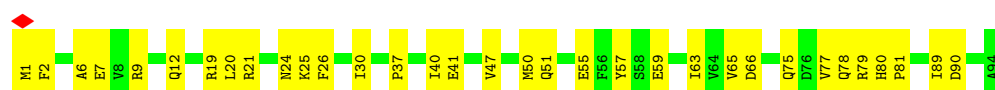
- Molecule 28: 50S ribosomal protein L24

Chain U:  69% 29% .



- Molecule 29: 50S ribosomal protein L25

Chain V:  65% 35%



- Molecule 30: 50S ribosomal protein L27

Chain W:  65% 24% 12%



- Molecule 31: 50S ribosomal protein L28

Chain X:  72% 27%



- Molecule 32: 50S ribosomal protein L29

Chain Y:  70% 27%



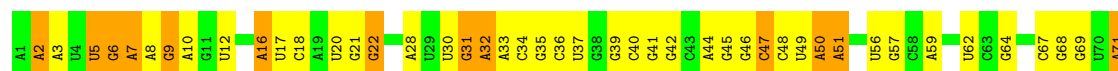
- Molecule 33: 50S ribosomal protein L30

Chain Z:  71% 27%

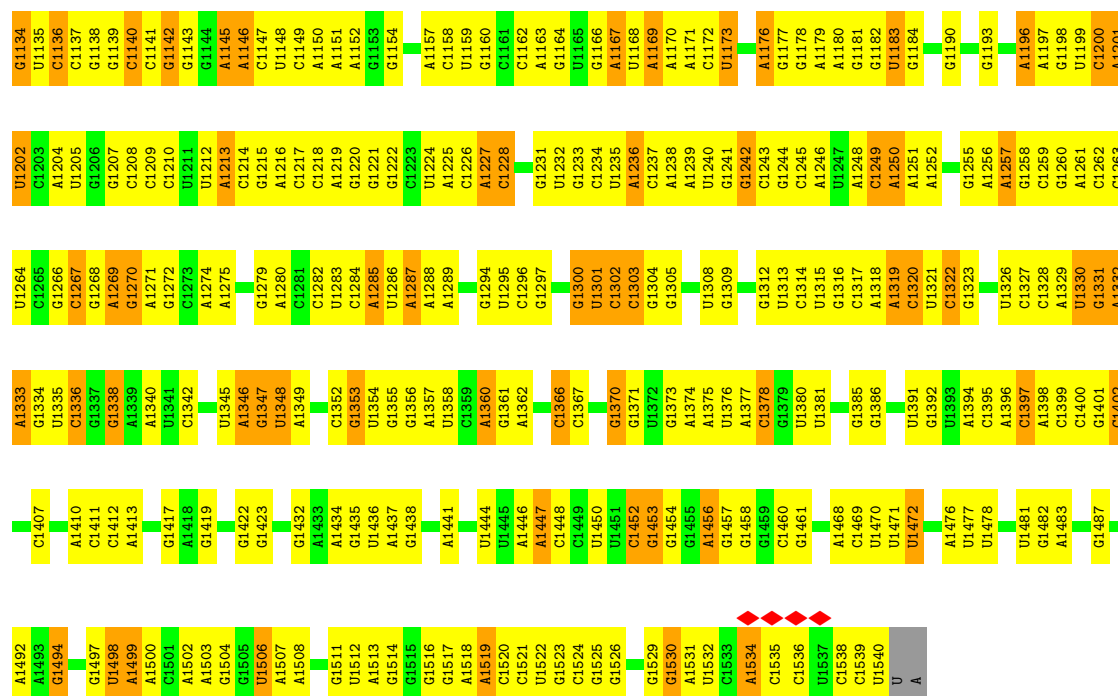


- Molecule 34: 16S ribosomal RNA

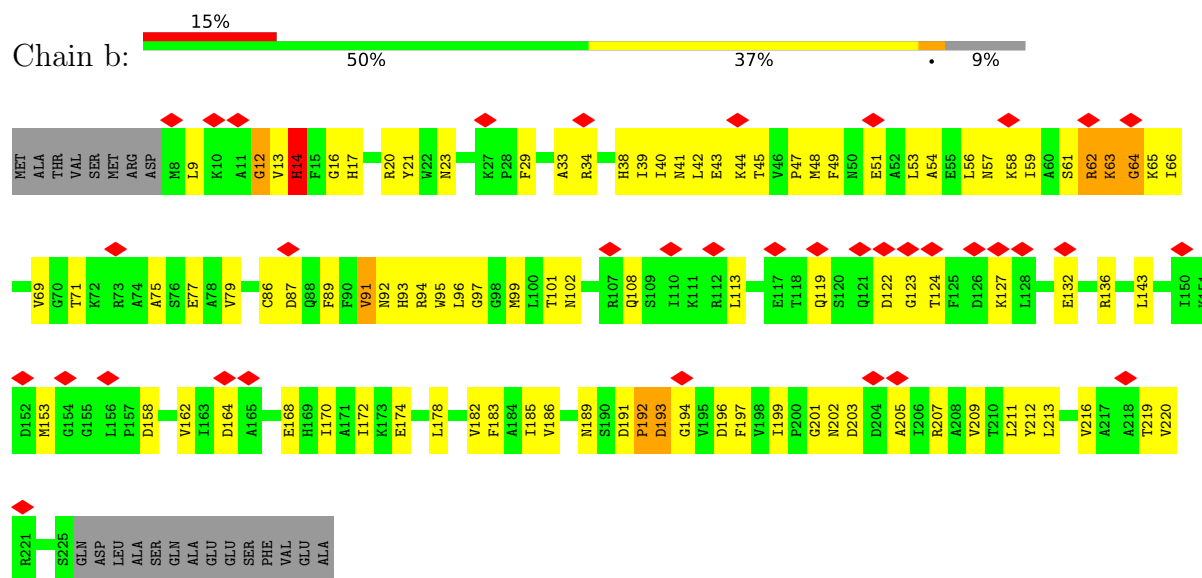
Chain a:  32% 51% 16%



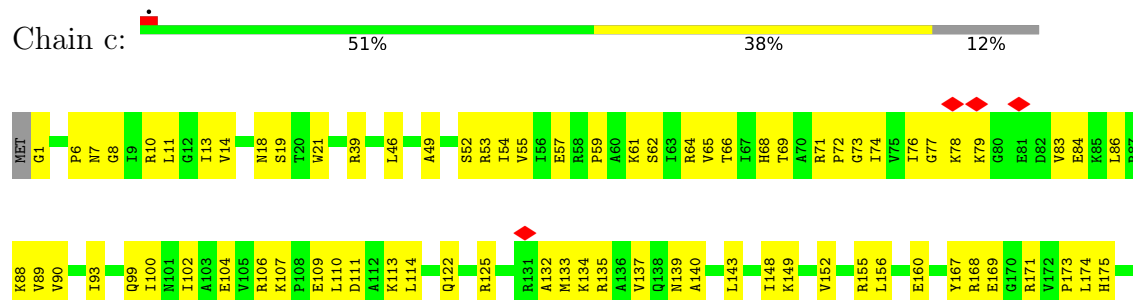
U1062	C998	G926	G844	U757	G691	A622	U555	C489	G428	A356	C284	G211	G146	A72
G1063	C999	G927	A845	C758	U692	C623	C556	C490	U429	G357		G212	G147	C73
U1065	A1000	C931	G846	A759	G693	G624	G557	G491	A430	U358	G289	G213	A74	
	C1001	C932	G847	A766	A694	U625	G558	C492	A431	G359		C214	A149	G75
G1071	G1002	C933	G849	A767	A696	G626	A559	A493	A432	G360	G292	C215	U150	G76
G1072	G1003	C934	U850	A768	A696		A560	G494	G433	G361	G293	C216	A151	A77
U1073	A1004	A935	G851	G769	U697		U561	A495	U434	A152		U216	A151	
G1074	A1005				G700	A630	U562	A496	A435	A152	U296	C217	A152	A78
U1075	G1006	G939	U855	G776	U701	G631	A563	G497	A436			U218		A79
U1076	U1007	C940	C956	A777	A702	U632	C564	A498	U437	G158	G297	U219	G158	A80
G1077	U1008			G778	G703	G633	U565	A499	U438	A81	G298	G220	G159	A81
U1078	U1009	G944	G859	C779		A635	U566	A500	U439	A160	G299	G221	U160	G82
G1079	U1010	G945		A780	A706	U636	G570	C501	C440	A161	A300	C222	A161	C83
A1080	C1011	A946	A864	A781	U707	U637	U571	A502	A441	C372	G302	A223	A162	U84
A1081	A1012	G947	A865	C782	C708	U638	A572		G442	A373	A303	U224	C163	U85
A1082	G1013	C948	C866	A783	U709	U639	A573	G506	C443	A374	U304	G225	G164	G86
U1083	A1014	A949	G867	A784	G710	A640	A574	U375	G444	U376	G305	G226	G165	C87
G1084	G1015		C868	A785	G711	U641	G575	C507	G445	G376	A306	G227	G166	
U1085	A1016	U952	G869	G786	A712		C576	U508	G446	G377		A228	U166	U88
U1086	U1017	G953	U870	A787	G713		G577	A509	G447	C378	A309	U231	C169	C90
G1087	G1018		U871		G714	G645		A510	G448	C379	G310	U231	C169	U91
G1088	A1019	A958	A872	A792	A715	G646	C582	C511	A449	G380	C311	G235	A171	U92
		A959	A873	U793	A716	G647	A583	U512	G450	C381		A236	A172	U93
U1022	U1023	U960	G874	A794	U717	A649	G584	C514	A451	A382	C316	G240	U173	G94
G1094	G1024	U961	U875	C795	A718	G875	G585	G515	A452	A383	U317	G240	A174	C95
U1095	U1025	C962	C876	C796	C719	C651	C586	G516	G453	G384	G318		C175	U96
C1096	G1026	G963	G877	C797	G720	U652	G587	U517	G454	G388	G319	U245	C176	G97
C1097	U1027	A964	A878	U798	G721	U653	U588	C518	G455	A389	A320	A246	C177	A98
C1098	C1028	U965	C880	G799	G722	U653	U589	C519	A456	A321	C322	G247	C178	C99
U1099	G967	C967	G881	U723	U723	G656	U590		G457	U390	U323		C179	G100
C1100	U1030	A968	C882	A802	G724	U657	U591	A523	A459	C392	G324		C180	
A1101	C1031	A969	C883	C811	G727	G661	U593	G524	A460	A397	A326	G251	A181	G105
A1102	G1032		G884	G812	A728	U662	C594	C525	A461	U398	G326	U252	C106	C106
G1034	G1033	C972	G885	A816	A729	A663	U594	G526	G462	U399	A327	G253	C107	G107
		G973	A815	A816	G730	G664	A596	C528	U463	G399	C328	G255	G108	G108
C1037	C1037	A974	G890	C817	G731	A665	C529	G529	U464	C400	A329	G257	A109	A109
		A975	U891	C817	C732	G666	U598	G530	A465	C401	C330	C258	C110	C110
G1106	G1106	C976	A892	G818	G733	G667	C599	U531	A466	G402	G331	G258	G187	
C1107	A976	A977	C893	A819	G734		A600	G532	U467	U405	G332	G259	C188	U114
G1108	A1042	C978	U820	G821	C735	U672	G601	A532	A468	G406	C335	U261	A190	G113
A1111	G1043	C979	U820	G820	C736	A673	A602	A535	C469	U407	A336	A262	G191	U121
	A1044	U822	U822	G821	C736	G674	U603	C536	C470	A407	A336	A262	A192	G122
G1045	C980	U822	G898	U822	C737	A675	G604	C537	U471	A408	G337	C263	A192	U123
A1046	U981	U981	C699	C738	G738	A675	G604	G537	U472	A409	A338	G265	C194	
C1047	U982	U982	A900	C826	C739	A676	U605	G538	U473	A410	C339	G266	A195	G126
G1048	A963	U827	A901	U827	U740	U677	G606	A539	G474	A411	U340	G267	A196	G127
C1049	G902	U828	G902	U828	G741	U678	A607	G540	C475	A412	C341	U268	A197	
U1049		G742	C680	G742	G742	C679	A608	G541	U476	C477	C342	C269	A198	A130
G1050	A908		A909	G833	G745	A681	U610	G544	C477	A415	U343	A270	A199	A131
	A909	U834	A909	U835	A746	G682	U610	C545	A478	A416	C344	C271	G201	C132
G1053	U913	U835	A913	G836	A747	G683	C613	C546	U479	G416	U345	G272	G201	G133
C1054	A914	G837	A914	U837	A747	U684	C614	A546	G481		C346	U273	G202	G134
A1055	U1056	U838	G838	G838	G748	G685		A547	G481	U421	G347	U273	G203	C135
U1057	U991	U991	U1056	U839	G752	U686	C617	G550	C482	C422	G278	G278	G204	C136
G1058	U992	U992	A919	C839	G752	U686	U617	G550	A482	C422	G351	A279	A205	A130
C1059	U993	U993	A919	C840	A753	U686	C618	U551	C483	G423	G352	C279	C206	A130
U1060	A994	A994	U921	C841	G754	G688	U619	U552	G434	G424	G353	G281	C207	A131
	C995	C995	U942	U841	G755	G689	C620	A553	U485	G425	A354	G282	U208	C132
G1133	G1061	A996	U943	U943	C756	G690	A621	A554	U486	U426	G355	U283	G144	G145

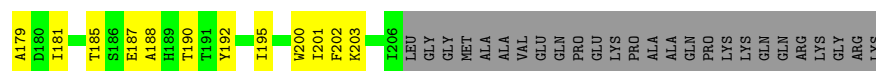


• Molecule 35: 30S ribosomal protein S2



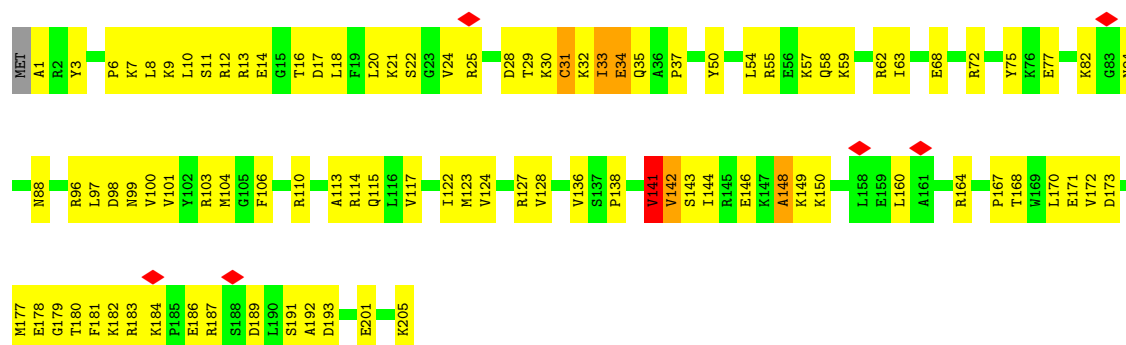
• Molecule 36: 30S ribosomal protein S3





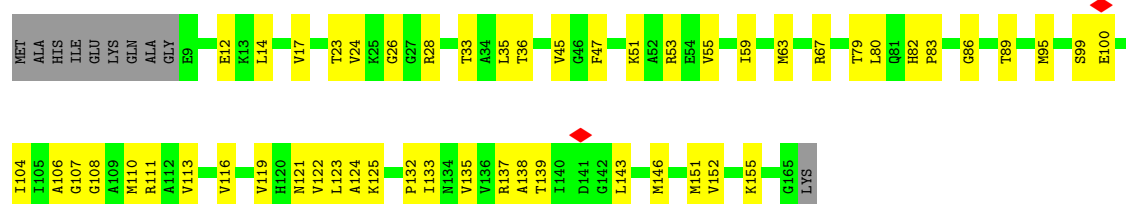
• Molecule 37: 30S ribosomal protein S4

Chain d: 53% 44%



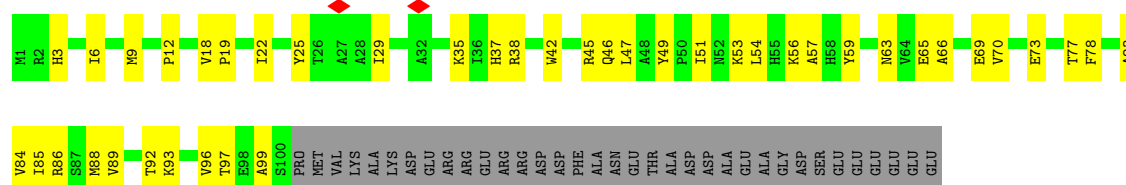
• Molecule 38: 30S ribosomal protein S5

Chain e: 63% 31% 6%



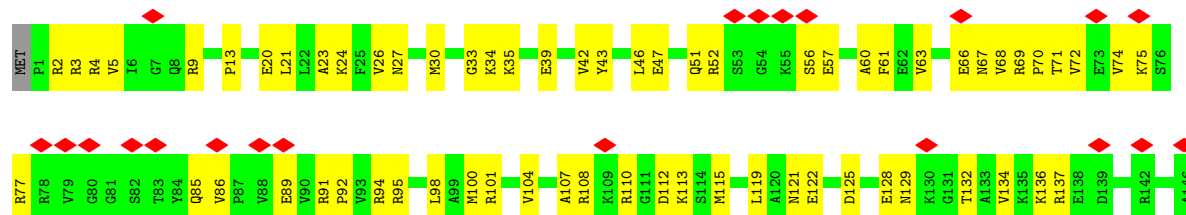
• Molecule 39: 30S ribosomal protein S6, fully modified isoform

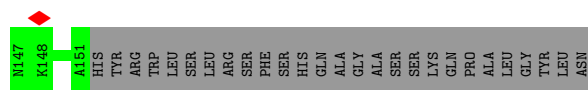
Chain f: 43% 31% 26%



• Molecule 40: 30S ribosomal protein S7

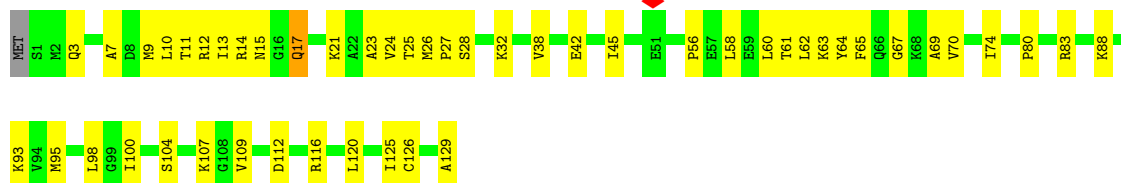
Chain g: 12% 48% 36% 16%





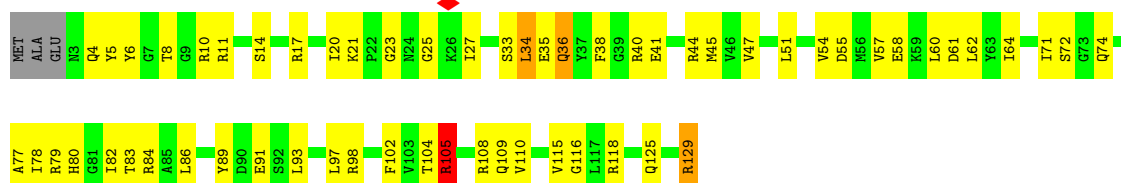
- Molecule 41: 30S ribosomal protein S8

Chain h: 62% 37%



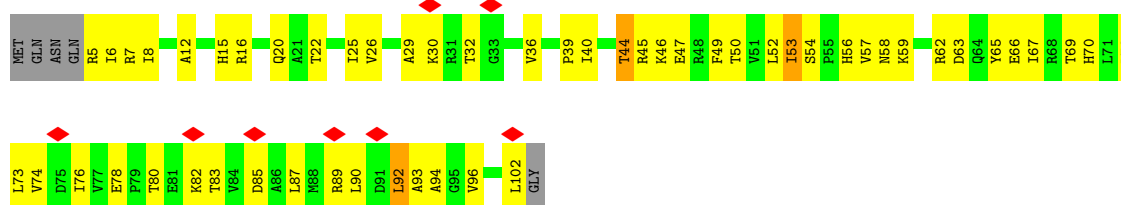
- Molecule 42: 30S ribosomal protein S9

Chain i: 52% 42%



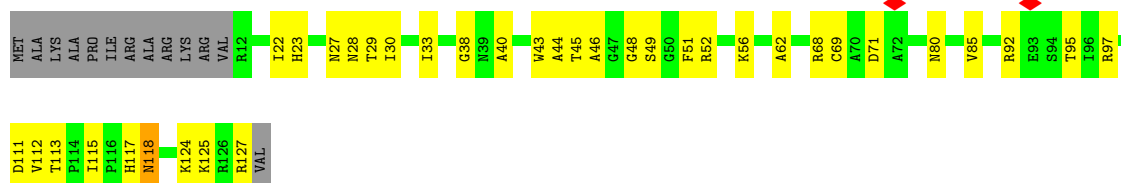
- Molecule 43: 30S ribosomal protein S10

Chain j: 8% 43% 50% 5%



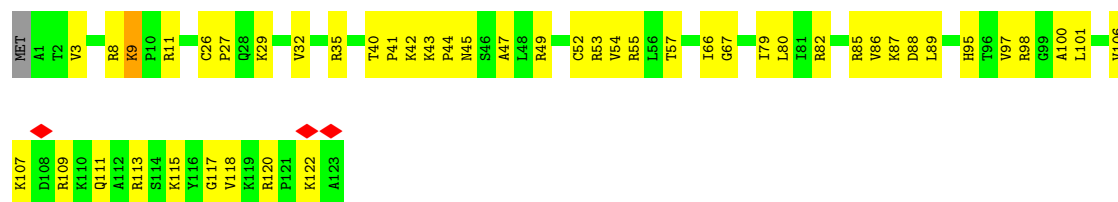
- Molecule 44: 30S ribosomal protein S11

Chain k: 62% 27% 10%

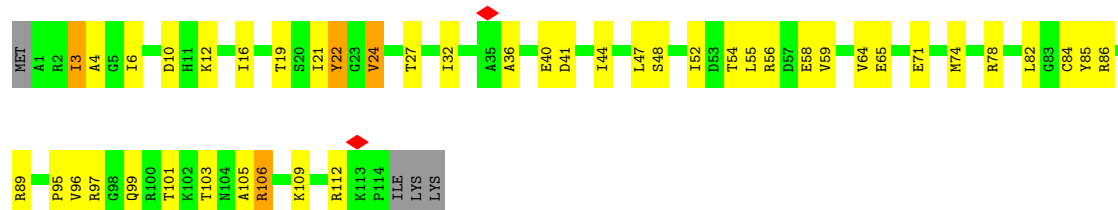


- Molecule 45: 30S ribosomal protein S12

Chain l: 61% 37%



• Molecule 46: 30S ribosomal protein S13



• Molecule 47: 30S ribosomal protein S14



• Molecule 48: 30S ribosomal protein S15



• Molecule 49: 30S ribosomal protein S16



• Molecule 50: 30S ribosomal protein S17





- Molecule 51: 30S ribosomal protein S18

Chain r:



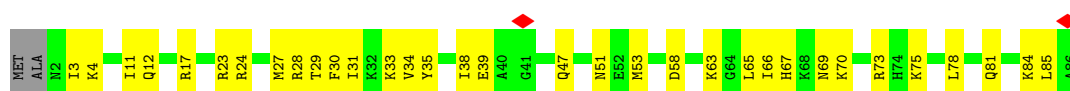
- Molecule 52: 30S ribosomal protein S19

Chain s:



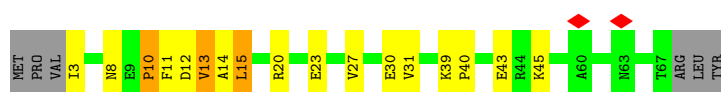
- Molecule 53: 30S ribosomal protein S20

Chain t:



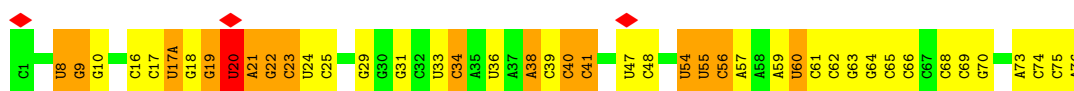
- Molecule 54: 30S ribosomal protein S21

Chain u:



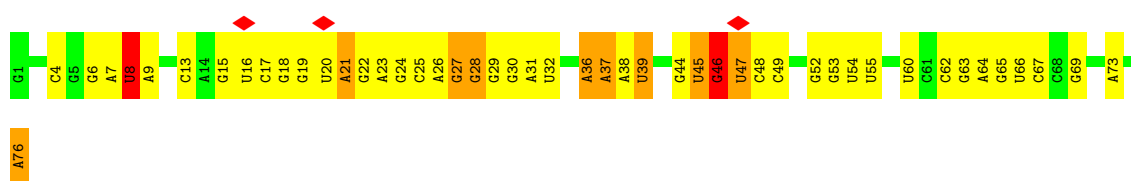
- Molecule 55: P-site tRNA(fMet)

Chain v:

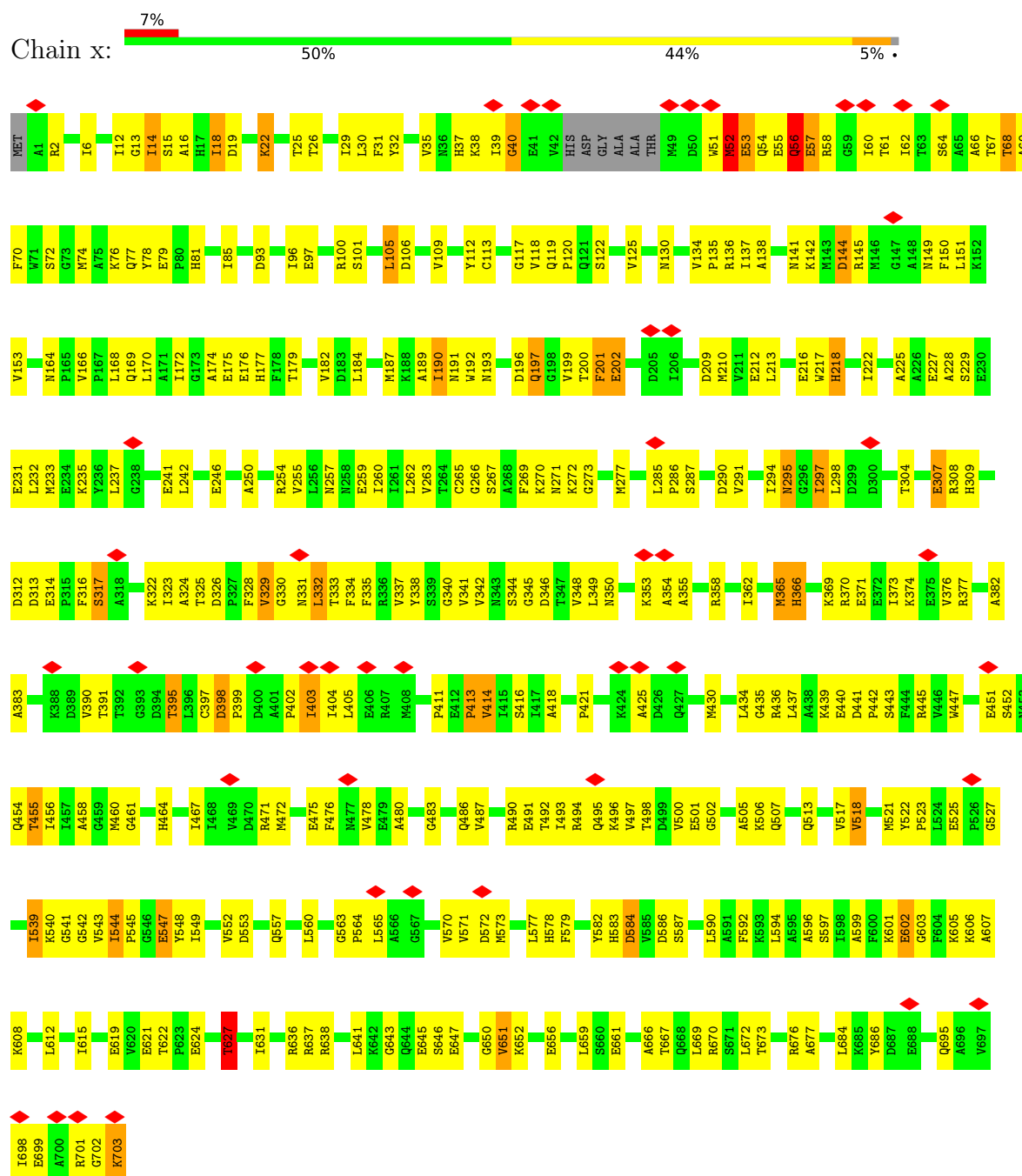


- Molecule 56: P-site fMet-Phe-tRNA(Phe)

Chain w:



- Molecule 57: Elongation factor G



- Molecule 58: Dipeptide (FME-PHE)



- Molecule 59: mRNA





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23737	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	15.892	Depositor
Minimum map value	-8.596	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.5	Depositor
Map size ($\text{\AA}$)	334.08, 334.08, 334.08	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.6525, 0.6525, 0.6525	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, AM2, MA6, 2MA, FME, 2MG, PSU, OMU, G7M, 5MC, UR3, 3TD, 4OC, OMC, 6MZ, 5MU, MIA, 4SU, OMG, MG, 1MG, GDP, NA

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	0	0.31	0/450	0.47	0/599
2	1	0.24	0/416	0.43	0/554
3	2	0.33	0/380	0.47	0/498
4	3	0.41	0/513	0.66	1/676 (0.1%)
5	4	0.30	0/303	0.54	0/397
6	5	0.33	0/646	0.78	3/898 (0.3%)
7	6	0.47	0/531	1.10	8/709 (1.1%)
8	A	0.33	1/69266 (0.0%)	0.38	8/108055 (0.0%)
9	B	0.25	0/2873	0.32	0/4478
10	C	0.46	0/2121	0.69	6/2852 (0.2%)
11	D	0.38	0/1586	0.54	2/2134 (0.1%)
12	E	0.39	0/1571	0.54	0/2113
13	F	0.30	0/1434	0.49	0/1926
14	G	0.28	0/1343	0.51	0/1816
15	H	0.35	0/1122	0.76	2/1515 (0.1%)
16	I	1.06	0/692	1.29	2/960 (0.2%)
17	J	0.30	0/1152	0.43	0/1551
18	K	0.42	0/947	0.52	1/1268 (0.1%)
19	L	0.49	0/1054	0.71	2/1403 (0.1%)
20	M	0.36	0/1093	0.53	0/1460
21	N	0.33	0/973	0.56	1/1301 (0.1%)
22	O	0.36	0/902	0.73	4/1209 (0.3%)
23	P	0.37	0/929	0.55	0/1242
24	Q	0.34	0/960	0.41	0/1278
25	R	0.67	3/829 (0.4%)	0.89	6/1107 (0.5%)
26	S	0.38	0/864	0.71	5/1156 (0.4%)
27	T	0.44	0/744	0.60	1/994 (0.1%)
28	U	0.34	0/787	0.52	0/1051
29	V	0.27	0/766	0.42	0/1025
30	W	0.31	0/582	0.45	0/769
31	X	0.37	0/635	0.53	0/848

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	0.40	0/510	0.54	1/677 (0.1%)
33	Z	0.28	0/453	0.42	0/605
34	a	0.29	6/36725 (0.0%)	0.41	24/57285 (0.0%)
35	b	0.44	0/1735	0.86	8/2338 (0.3%)
36	c	0.23	0/1651	0.46	0/2225
37	d	0.42	0/1665	0.75	7/2227 (0.3%)
38	e	0.35	0/1154	0.60	0/1554
39	f	0.21	0/835	0.49	0/1128
40	g	0.25	0/1195	0.49	0/1602
41	h	0.36	0/989	0.70	3/1326 (0.2%)
42	i	0.47	0/1034	0.77	2/1375 (0.1%)
43	j	0.40	0/796	0.75	2/1077 (0.2%)
44	k	0.23	0/885	0.47	0/1195
45	l	0.46	0/969	0.83	7/1300 (0.5%)
46	m	0.45	0/892	0.76	2/1193 (0.2%)
47	n	0.49	0/811	0.78	2/1081 (0.2%)
48	o	0.23	0/722	0.44	0/964
49	p	0.46	0/659	0.82	4/884 (0.5%)
50	q	0.45	0/657	0.80	3/881 (0.3%)
51	r	0.54	0/544	0.91	7/731 (1.0%)
52	s	0.48	0/675	0.88	4/908 (0.4%)
53	t	0.23	0/671	0.43	0/888
54	u	0.36	0/512	1.13	6/683 (0.9%)
55	v	0.41	3/1767 (0.2%)	0.42	0/2750
56	w	0.37	1/1650 (0.1%)	0.55	0/2569
57	x	0.79	2/5516 (0.0%)	1.20	31/7460 (0.4%)
58	y	0.12	0/11	0.73	0/13
59	z	0.47	0/230	0.65	0/355
All	All	0.37	16/164377 (0.0%)	0.52	165/245116 (0.1%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	a	1081	A	O3'-P	8.21	1.73	1.61
55	v	20	U	C5-C6	7.56	1.49	1.34
25	R	49	ILE	CA-C	-7.54	1.44	1.52
34	a	921	U	C5'-C4'	6.68	1.61	1.51
25	R	57	GLY	CA-C	-6.12	1.43	1.52
34	a	1081	A	C3'-O3'	6.08	1.51	1.42
55	v	20	U	C2-N3	5.77	1.49	1.37
8	A	887	A	C1'-N9	-5.70	1.39	1.48
57	x	425	ALA	C-N	-5.58	1.26	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	x	144	ASP	C-O	-5.54	1.16	1.24
34	a	1011	C	C5'-C4'	5.53	1.59	1.51
34	a	921	U	P-O5'	5.45	1.68	1.59
25	R	54	VAL	CA-C	-5.33	1.47	1.52
34	a	920	U	O3'-P	5.32	1.69	1.61
56	w	46	G7M	O3'-P	5.23	1.61	1.56
55	v	20	U	N1-C2	5.20	1.49	1.38

All (165) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	903	C	P-O3'-C3'	26.12	159.38	120.20
54	u	13	VAL	N-CA-C	-16.13	96.84	112.17
10	C	238	ASN	N-CA-C	14.34	127.00	111.36
57	x	304	THR	N-CA-C	-13.74	92.33	109.65
57	x	56	GLN	N-CA-C	-12.14	98.10	113.16
34	a	920	U	OP2-P-O3'	-11.76	72.73	108.00
22	O	34	HIS	N-CA-C	11.65	127.01	111.28
37	d	148	ALA	N-CA-C	-11.61	97.90	112.88
52	s	28	LYS	N-CA-C	-11.56	92.31	109.42
35	b	14	HIS	N-CA-C	-11.35	98.23	112.88
45	l	120	ARG	N-CA-C	11.21	124.20	110.07
54	u	15	LEU	N-CA-C	-11.18	98.89	112.54
34	a	1081	A	O3'-P-O5'	10.85	120.27	104.00
47	n	35	ALA	N-CA-C	-10.73	94.11	110.10
34	a	1081	A	P-O3'-C3'	10.70	136.24	120.20
8	A	903	C	OP1-P-O3'	10.69	140.07	108.00
22	O	31	THR	N-CA-C	-10.63	95.92	108.25
47	n	38	ASP	N-CA-C	-10.57	99.76	111.28
41	h	67	GLY	N-CA-C	-10.43	100.93	115.32
49	p	48	GLU	N-CA-C	-10.03	101.28	112.72
25	R	51	VAL	CA-C-N	-9.93	108.02	118.85
25	R	51	VAL	C-N-CA	-9.93	108.02	118.85
16	I	4	VAL	N-CA-C	9.41	120.22	110.62
25	R	55	ASP	N-CA-C	9.27	122.37	111.71
7	6	58	ASP	N-CA-C	9.15	120.86	111.07
57	x	547	GLU	N-CA-C	-8.98	101.85	113.17
35	b	64	GLY	N-CA-C	8.87	123.22	112.49
34	a	920	U	OP1-P-O3'	8.77	134.31	108.00
51	r	44	THR	N-CA-C	-8.61	94.48	108.52
54	u	14	ALA	N-CA-C	-8.61	102.49	113.16
10	C	236	GLY	N-CA-C	-8.52	99.38	110.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	903	C	O3'-P-O5'	-8.45	91.32	104.00
6	5	82	ILE	N-CA-C	8.27	119.26	108.35
35	b	61	SER	N-CA-C	-8.23	102.39	111.36
34	a	921	U	OP1-P-OP2	-8.22	94.94	119.60
57	x	602	GLU	N-CA-C	-8.15	104.48	114.75
25	R	50	GLY	N-CA-C	-8.04	100.60	111.54
7	6	57	VAL	N-CA-C	-8.02	102.58	112.76
26	S	63	GLY	N-CA-C	8.00	120.85	110.45
46	m	106	ARG	N-CA-C	7.93	119.92	111.28
42	i	36	GLN	N-CA-C	-7.80	101.88	111.40
25	R	51	VAL	CB-CA-C	7.74	125.44	111.36
10	C	231	HIS	CA-C-N	-7.58	112.31	122.54
10	C	231	HIS	C-N-CA	-7.58	112.31	122.54
26	S	64	ALA	N-CA-C	7.54	123.39	114.04
50	q	51	GLU	N-CA-C	7.53	119.56	111.36
32	Y	16	THR	N-CA-C	-7.48	102.80	112.23
57	x	637	ARG	N-CA-C	-7.46	100.68	110.53
34	a	920	U	O3'-P-O5'	7.43	115.15	104.00
57	x	76	LYS	N-CA-C	-7.40	96.20	108.34
45	l	117	GLY	N-CA-C	7.34	124.20	113.48
51	r	20	ILE	N-CA-C	-7.33	97.04	107.75
34	a	920	U	P-O3'-C3'	7.30	131.16	120.20
34	a	921	U	O5'-C5'-C4'	7.29	122.44	111.50
45	l	115	LYS	N-CA-C	-7.29	100.22	110.50
8	A	903	C	OP2-P-O3'	-7.26	86.23	108.00
37	d	82	LYS	N-CA-C	7.25	119.93	110.43
15	H	67	ALA	N-CA-C	-7.19	103.45	111.28
35	b	192	PRO	N-CA-C	-7.07	103.70	113.53
37	d	31	CYS	N-CA-C	7.06	119.65	109.14
18	K	37	ASP	N-CA-C	7.04	120.69	110.28
57	x	627	THR	CB-CA-C	-7.02	100.15	110.96
57	x	544	ILE	N-CA-C	-6.99	93.78	108.88
57	x	451	GLU	N-CA-C	-6.85	103.81	111.28
57	x	651	VAL	N-CA-C	-6.82	98.35	108.45
10	C	132	ARG	N-CA-C	-6.77	105.97	114.56
34	a	1010	U	C2'-C3'-O3'	6.76	123.84	113.70
34	a	1081	A	N9-C1'-C2'	6.75	122.12	112.00
42	i	105	ARG	N-CA-C	-6.74	100.06	110.10
54	u	11	PHE	N-CA-C	6.72	119.86	108.90
11	D	151	THR	CA-C-N	-6.70	111.47	119.84
11	D	151	THR	C-N-CA	-6.70	111.47	119.84
37	d	33	ILE	N-CA-C	6.68	117.47	110.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	r	47	ARG	N-CA-C	-6.67	101.10	110.50
41	h	69	ALA	N-CA-C	6.66	119.89	110.23
50	q	52	CYS	N-CA-C	6.66	119.32	110.53
35	b	193	ASP	CB-CA-C	-6.66	108.91	116.63
26	S	62	ASP	N-CA-C	6.57	120.95	112.41
52	s	26	ASP	N-CA-C	-6.56	97.67	108.49
19	L	28	GLY	N-CA-C	6.49	127.20	112.01
8	A	1078	U	C4'-C3'-O3'	6.43	119.04	109.40
19	L	27	LEU	N-CA-C	-6.42	104.36	111.36
57	x	313	ASP	N-CA-C	-6.41	105.76	113.97
57	x	518	VAL	N-CA-CB	6.36	119.85	112.15
16	I	23	VAL	N-CA-C	6.35	116.52	110.74
4	3	32	LEU	N-CA-C	6.34	119.18	111.82
35	b	97	GLY	N-CA-C	-6.33	103.95	111.36
34	a	921	U	C5'-C4'-C3'	6.33	125.49	116.00
22	O	33	ARG	N-CA-C	-6.29	99.91	109.85
7	6	49	ARG	N-CA-C	-6.25	105.30	113.17
34	a	921	U	P-O5'-C5'	6.23	130.24	120.90
34	a	921	U	O5'-P-OP2	6.22	126.67	108.00
8	A	1062	G	C4'-C3'-O3'	-6.22	103.67	113.00
34	a	1082	A	O5'-P-OP2	-6.21	89.37	108.00
15	H	66	ASN	N-CA-C	-6.20	105.84	113.41
25	R	52	PRO	N-CA-C	-6.14	105.18	113.40
37	d	68	GLU	N-CA-C	6.09	119.18	111.69
50	q	58	VAL	N-CA-C	6.07	116.86	108.12
41	h	65	PHE	N-CA-C	6.07	117.56	111.07
52	s	35	ARG	N-CA-C	-6.04	105.87	113.72
6	5	126	LEU	N-CA-C	6.03	117.86	111.28
57	x	286	PRO	N-CA-C	5.96	120.86	111.38
7	6	56	ARG	CB-CA-C	5.96	121.39	110.36
34	a	1196	A	C2'-C3'-O3'	-5.93	100.61	109.50
35	b	62	ARG	N-CA-C	-5.92	102.71	110.53
57	x	202	GLU	N-CA-C	5.92	119.13	108.48
34	a	1081	A	C5'-C4'-C3'	5.91	124.87	116.00
21	N	118	ARG	N-CA-C	5.88	117.69	111.28
52	s	33	TRP	N-CA-C	-5.84	106.16	113.28
57	x	40	GLY	N-CA-C	5.83	121.53	112.60
34	a	1196	A	C4'-C3'-O3'	5.82	118.12	109.40
6	5	77	VAL	N-CA-C	5.77	117.77	111.77
43	j	94	ALA	CB-CA-C	-5.75	109.41	117.23
27	T	91	GLN	N-CA-C	5.74	117.91	109.24
34	a	1011	C	C5'-C4'-C3'	5.72	124.58	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	S	65	ASP	N-CA-C	5.66	118.00	107.99
57	x	650	GLY	N-CA-C	-5.64	102.51	110.75
54	u	31	VAL	N-CA-C	-5.62	107.27	112.83
43	j	93	ALA	N-CA-C	5.60	119.37	111.52
7	6	46	GLY	N-CA-C	5.59	121.15	113.99
8	A	902	C	C4'-C3'-O3'	-5.58	104.62	113.00
51	r	45	GLY	N-CA-C	-5.54	100.06	113.18
37	d	141	VAL	N-CA-C	5.52	115.60	107.15
34	a	1081	A	OP2-P-O3'	5.50	124.51	108.00
34	a	1011	C	N1-C1'-C2'	-5.49	103.76	112.00
57	x	57	GLU	N-CA-C	-5.47	106.45	113.02
10	C	203	VAL	N-CA-C	-5.45	100.47	108.11
51	r	13	THR	N-CA-C	-5.45	106.47	113.01
49	p	11	ALA	N-CA-C	5.44	117.86	110.35
57	x	307	GLU	N-CA-C	-5.43	100.94	109.25
57	x	29	ILE	N-CA-C	-5.41	105.10	110.62
49	p	43	ALA	N-CA-C	5.40	117.25	111.36
34	a	921	U	O4'-C1'-N1	5.40	116.60	108.50
7	6	60	PHE	N-CA-C	-5.37	105.42	111.28
46	m	22	TYR	N-CA-C	-5.37	102.45	110.23
57	x	647	GLU	N-CA-C	-5.33	103.35	110.55
7	6	51	VAL	N-CA-C	-5.33	100.17	108.86
57	x	413	PRO	CB-CA-C	-5.31	104.95	111.64
57	x	79	GLU	N-CA-C	5.28	121.47	109.81
51	r	46	THR	N-CA-C	-5.27	99.36	108.69
37	d	142	VAL	N-CA-C	-5.25	102.74	109.30
26	S	67	ASP	N-CA-C	5.24	117.07	111.36
22	O	34	HIS	CB-CA-C	-5.22	104.48	112.11
57	x	67	THR	N-CA-C	5.22	117.46	110.35
57	x	72	SER	N-CA-C	5.19	117.02	111.36
57	x	38	LYS	N-CA-C	-5.19	102.37	110.10
57	x	333	THR	CB-CA-C	-5.18	102.79	110.67
8	A	1062	G	C2'-C3'-O3'	5.18	121.47	113.70
57	x	79	GLU	CA-C-N	-5.17	114.40	119.93
57	x	79	GLU	C-N-CA	-5.17	114.40	119.93
57	x	52	MET	N-CA-C	-5.16	107.04	113.19
7	6	50	ASP	CB-CA-C	-5.15	110.62	116.54
45	l	9	LYS	CA-C-N	-5.14	115.06	120.66
45	l	9	LYS	C-N-CA	-5.14	115.06	120.66
45	l	117	GLY	CA-C-N	-5.14	116.81	123.19
45	l	117	GLY	C-N-CA	-5.14	116.81	123.19
34	a	1011	C	P-O5'-C5'	5.13	128.60	120.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	158	G	C4'-C3'-C2'	-5.13	97.47	102.60
57	x	584	ASP	N-CA-C	5.12	116.54	111.07
35	b	12	GLY	N-CA-C	-5.10	103.08	112.62
57	x	467	ILE	N-CA-C	-5.08	107.39	111.91
34	a	1196	A	C3'-C2'-O2'	-5.07	107.00	114.60
51	r	22	TYR	N-CA-C	-5.05	106.21	112.38
54	u	10	PRO	N-CA-C	-5.04	103.27	111.03
49	p	12	LYS	N-CA-C	5.00	117.68	110.28

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	444	0	461	18	0
2	1	409	0	440	12	0
3	2	377	0	418	14	0
4	3	504	0	574	17	0
5	4	302	0	340	14	0
6	5	647	0	336	11	0
7	6	522	0	521	33	0
8	A	62338	0	31367	1254	0
9	B	2570	0	1301	54	0
10	C	2082	0	2157	62	0
11	D	1565	0	1616	30	0
12	E	1552	0	1619	37	0
13	F	1410	0	1447	46	0
14	G	1323	0	1374	36	0
15	H	1111	0	1148	47	0
16	I	693	0	347	7	0
17	J	1129	0	1162	27	0
18	K	938	0	1012	36	0
19	L	1045	0	1117	31	0
20	M	1074	0	1157	40	0
21	N	960	0	1000	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	O	892	0	923	31	0
23	P	917	0	965	27	0
24	Q	947	0	1022	27	0
25	R	816	0	839	20	0
26	S	857	0	922	41	0
27	T	738	0	807	11	0
28	U	779	0	834	20	0
29	V	753	0	780	25	0
30	W	575	0	592	15	0
31	X	625	0	655	19	0
32	Y	509	0	543	11	0
33	Z	449	0	491	12	0
34	a	33050	0	16653	910	0
35	b	1704	0	1732	65	0
36	c	1624	0	1699	65	0
37	d	1643	0	1710	77	0
38	e	1141	0	1170	47	0
39	f	817	0	808	35	0
40	g	1181	0	1240	58	0
41	h	979	0	1034	41	0
42	i	1022	0	1070	45	0
43	j	786	0	828	51	0
44	k	869	0	878	36	0
45	l	955	0	1019	32	0
46	m	883	0	944	36	0
47	n	799	0	841	34	0
48	o	714	0	737	24	0
49	p	649	0	666	28	0
50	q	648	0	691	24	0
51	r	535	0	552	18	0
52	s	658	0	685	24	0
53	t	665	0	714	25	0
54	u	506	0	502	9	0
55	v	1642	0	837	27	0
56	w	1631	0	838	40	0
57	x	5416	0	5398	218	0
58	y	21	0	19	1	0
59	z	208	0	104	3	0
60	0	1	0	0	0	0
60	1	1	0	0	0	0
60	6	1	0	0	0	0
60	A	267	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	B	6	0	0	0	0
60	C	3	0	0	0	0
60	D	1	0	0	0	0
60	M	1	0	0	0	0
60	O	1	0	0	1	0
60	P	1	0	0	0	0
60	a	34	0	0	0	0
60	w	1	0	0	0	0
61	4	1	0	0	0	0
61	6	1	0	0	0	0
62	B	1	0	0	0	0
63	a	148	0	164	2	0
64	x	28	0	12	1	0
All	All	153095	0	103832	3620	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 14.

All (3620) 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)
8:A:1915:3TD:C1'	8:A:1915:3TD:O4'	1.68	1.16
34:a:438:U:C2	34:a:496:A:N6	2.30	0.99
8:A:2100:G:H1	8:A:2189:U:H3	1.10	0.97
34:a:409:U:H3	34:a:433:G:H1	1.15	0.93
34:a:1498:UR3:O2'	34:a:1499:A:OP2	1.88	0.92
34:a:920:U:H3'	34:a:1082:A:P	2.12	0.90
8:A:1051:G:H1	8:A:1108:U:H3	1.18	0.89
8:A:1068:G:H21	8:A:1070:A:H62	1.20	0.88
57:x:316:PHE:HA	57:x:340:GLY:HA3	1.54	0.88
8:A:1081:U:H1'	16:I:123:ALA:HB1	1.55	0.87
8:A:1936:A:H2	8:A:1943:U:H3	1.23	0.87
34:a:210:C:H5'	34:a:211:G:H5'	1.57	0.87
57:x:14:ILE:HG22	57:x:109:VAL:HB	1.53	0.87
8:A:1062:G:H5'	8:A:1063:G:OP2	1.74	0.87
57:x:138:ALA:HB3	57:x:263:VAL:HG12	1.57	0.87
57:x:353:LYS:HZ1	57:x:391:THR:H	1.22	0.86
37:d:138:PRO:HA	37:d:181:PHE:HB3	1.57	0.85
34:a:673:A:H2'	34:a:674:G:C8	2.11	0.85
34:a:674:G:H2'	34:a:675:A:H8	1.41	0.85
56:w:22:G:O6	56:w:46:G7M:N2	2.10	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:920:U:O2	34:a:1081:A:O2'	1.96	0.84
34:a:686:U:H1'	44:k:43:TRP:HE1	1.42	0.84
3:2:39:ARG:NH2	8:A:468:G:N7	2.26	0.83
34:a:458:U:O2	34:a:474:G:N2	2.12	0.83
36:c:72:PRO:HB3	36:c:102:ILE:HG21	1.61	0.83
34:a:920:U:H2'	34:a:1081:A:C2'	2.08	0.83
34:a:984:C:N3	34:a:1222:G:N2	2.27	0.83
8:A:1779:U:OP2	8:A:1784:A:N6	2.11	0.83
57:x:184:LEU:HD13	57:x:218:HIS:HA	1.61	0.82
34:a:921:U:H6	34:a:1082:A:OP2	1.63	0.81
34:a:1259:C:O2'	34:a:1283:U:O2	1.99	0.81
56:w:52:G:N2	56:w:62:C:O2	2.11	0.81
43:j:16:ARG:O	43:j:20:GLN:NE2	2.14	0.81
8:A:1601:G:OP1	27:T:64:LYS:NZ	2.14	0.81
8:A:976:G:HO2'	8:A:1155:A:HO2'	1.24	0.80
7:6:16:CYS:CB	7:6:37:CYS:SG	2.70	0.80
9:B:31:C:O2	9:B:53:A:N6	2.14	0.80
8:A:698:C:O2'	8:A:734:A:N6	2.15	0.79
13:F:25:MET:O	13:F:29:ARG:NH1	2.14	0.79
8:A:1664:A:N3	18:K:67:LYS:NZ	2.31	0.79
8:A:1093:G:O2'	8:A:1095:A:N7	2.15	0.79
34:a:1077:G:N2	34:a:1080:A:OP2	2.14	0.79
34:a:202:G:HO2'	34:a:468:A:HO2'	1.22	0.78
34:a:846:G:H2'	34:a:847:G:C8	2.18	0.78
34:a:202:G:O2'	34:a:468:A:O2'	1.96	0.78
36:c:10:ARG:NH2	36:c:174:LEU:O	2.17	0.78
57:x:97:GLU:HG3	57:x:100:ARG:NH2	1.98	0.78
8:A:1660:G:N2	8:A:2689:U:O4	2.16	0.78
34:a:1309:G:N7	46:m:97:ARG:NH2	2.32	0.78
8:A:481:G:O2'	8:A:506:G:N2	2.17	0.77
34:a:490:C:H2'	34:a:491:G:H8	1.47	0.77
8:A:2117:A:N6	8:A:2163:A:OP1	2.17	0.77
35:b:119:GLN:HA	35:b:123:GLY:HA3	1.67	0.77
34:a:1284:C:H3'	34:a:1285:A:H2'	1.65	0.77
8:A:1100:C:H3'	8:A:1101:U:H5''	1.66	0.77
21:N:77:ALA:O	21:N:81:ASN:HB2	1.83	0.77
44:k:111:ASP:H	54:u:3:ILE:HG23	1.50	0.77
34:a:920:U:H3'	34:a:1082:A:O5'	1.85	0.76
36:c:190:THR:HG23	36:c:192:TYR:H	1.49	0.76
8:A:1826:G:O2'	8:A:1971:U:OP2	2.04	0.76
34:a:1178:G:N7	42:i:98:ARG:NH1	2.33	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:C:56:GLY:HA2	10:C:212:TRP:HA	1.67	0.76
37:d:99:ASN:OD1	37:d:110:ARG:NH2	2.18	0.76
8:A:200:U:O2	8:A:386:G:N2	2.19	0.76
8:A:1539:U:H2'	8:A:1540:G:H8	1.48	0.76
10:C:206:LYS:HG3	10:C:209:ALA:HB2	1.67	0.76
8:A:500:G:N1	8:A:503:A:OP2	2.16	0.76
8:A:1141:U:H2'	17:J:65:THR:HG21	1.68	0.76
34:a:1297:G:N2	40:g:113:LYS:O	2.19	0.76
55:v:20:U:H3'	55:v:20:U:OP2	1.85	0.75
37:d:103:ARG:HH12	37:d:110:ARG:HH12	1.33	0.75
34:a:674:G:H21	44:k:117:HIS:HB2	1.49	0.75
35:b:45:THR:O	35:b:49:PHE:HB2	1.86	0.75
34:a:946:A:OP1	46:m:112:ARG:NH2	2.19	0.75
34:a:1266:G:N2	34:a:1269:A:OP2	2.18	0.75
8:A:84:A:H62	8:A:101:A:H2	1.32	0.75
8:A:715:A:OP2	48:o:88:ARG:NH2	2.18	0.75
57:x:97:GLU:HG3	57:x:100:ARG:HH21	1.50	0.75
8:A:2109:U:N3	8:A:2120:G:N7	2.35	0.74
57:x:335:PHE:CE2	57:x:376:VAL:HG11	2.22	0.74
34:a:1151:A:H5''	43:j:44:THR:HG22	1.66	0.74
34:a:1377:A:OP1	40:g:91:ARG:NH2	2.20	0.74
39:f:38:ARG:HB3	39:f:63:ASN:HB2	1.69	0.74
8:A:1816:C:N4	10:C:34:GLU:OE2	2.18	0.74
34:a:216:U:H4'	34:a:464:U:H1'	1.69	0.74
34:a:689:C:OP2	44:k:52:ARG:NH1	2.19	0.74
8:A:25:U:O2	8:A:515:A:N6	2.20	0.74
34:a:920:U:H2'	34:a:1081:A:O2'	1.87	0.74
8:A:242:G:N2	8:A:255:A:OP2	2.18	0.74
8:A:1568:G:N7	10:C:27:LYS:NZ	2.36	0.74
42:i:83:THR:HG21	42:i:102:PHE:HB3	1.70	0.74
15:H:116:ARG:HB2	15:H:131:SER:HB2	1.70	0.73
38:e:35:LEU:HD22	38:e:133:ILE:HD13	1.70	0.73
9:B:30:C:H1'	9:B:57:A:H61	1.52	0.73
43:j:6:ILE:HD12	43:j:102:LEU:HG	1.69	0.73
34:a:776:G:N2	34:a:802:A:OP2	2.20	0.73
34:a:1330:U:H3'	34:a:1331:G:H4'	1.69	0.73
46:m:6:ILE:HD11	46:m:21:ILE:HG12	1.69	0.73
47:n:15:LEU:HG	47:n:55:SER:HB3	1.69	0.73
34:a:933:G:O6	40:g:2:ARG:NH2	2.20	0.73
45:l:35:ARG:HB2	45:l:53:ARG:HB3	1.69	0.73
8:A:499:U:H5''	28:U:42:LYS:HE2	1.68	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:x:612:LEU:HB3	57:x:686:TYR:HB3	1.70	0.73
8:A:1059:G:N7	8:A:1088:A:N6	2.37	0.73
8:A:2661:G:H5''	57:x:18:ILE:HG12	1.69	0.73
8:A:848:C:H2'	8:A:849:A:H8	1.52	0.73
8:A:1597:A:H5''	8:A:1598:A:H5'	1.70	0.73
34:a:826:C:O2	41:h:15:ASN:ND2	2.22	0.73
8:A:2391:G:O2'	8:A:2429:G:N2	2.22	0.72
34:a:769:G:H4'	34:a:1513:A:H4'	1.71	0.72
57:x:317:SER:HA	57:x:397:CYS:HA	1.70	0.72
5:4:2:LYS:NZ	5:4:32:LYS:O	2.23	0.72
8:A:270:A:N1	8:A:369:U:O2'	2.22	0.72
8:A:569:U:O2'	8:A:983:A:N1	2.21	0.72
34:a:8:A:N6	37:d:201:GLU:O	2.22	0.72
57:x:335:PHE:HE2	57:x:376:VAL:HG11	1.54	0.72
35:b:101:THR:HB	35:b:178:LEU:HD21	1.72	0.72
38:e:106:ALA:O	38:e:111:ARG:NH2	2.22	0.72
41:h:17:GLN:HG2	41:h:62:LEU:HD13	1.71	0.72
43:j:12:ALA:HB2	43:j:96:VAL:HG22	1.69	0.72
8:A:627:A:OP1	19:L:78:ARG:NH1	2.23	0.72
34:a:875:U:O2'	41:h:14:ARG:NH1	2.23	0.72
8:A:859:G:O2'	8:A:916:G:O6	2.06	0.72
15:H:125:THR:HA	15:H:146:VAL:HB	1.71	0.72
40:g:26:VAL:HG22	40:g:42:VAL:HG11	1.70	0.72
8:A:1478:G:H1	8:A:1513:U:H3	1.37	0.72
8:A:2636:C:O2'	11:D:45:TYR:OH	2.06	0.72
8:A:2788:C:O2'	8:A:2809:A:N3	2.22	0.72
35:b:12:GLY:HA2	35:b:207:ARG:HE	1.55	0.72
46:m:32:ILE:HG21	46:m:59:VAL:HG12	1.71	0.72
8:A:1858:A:N6	8:A:1884:G:O2'	2.22	0.72
15:H:113:SER:O	15:H:116:ARG:NH2	2.23	0.72
28:U:85:ARG:NH2	28:U:87:GLU:OE2	2.23	0.72
34:a:1522:U:H2'	34:a:1523:G:H8	1.54	0.72
8:A:1087:G:N3	8:A:1102:C:N4	2.38	0.72
8:A:2163:A:OP1	8:A:2165:C:N4	2.23	0.71
57:x:334:PHE:HA	57:x:383:ALA:HA	1.72	0.71
34:a:795:C:O2'	44:k:127:ARG:O	2.09	0.71
63:a:1620:AM2:HB2	45:l:40:THR:HG21	1.70	0.71
8:A:1900:A:H1'	8:A:1970:A:H2'	1.72	0.71
20:M:63:ILE:HG12	20:M:105:MET:HG2	1.73	0.71
24:Q:49:ARG:O	24:Q:53:LYS:NZ	2.24	0.71
34:a:921:U:O5'	34:a:1082:A:O5'	2.07	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1328:C:H2'	34:a:1329:A:H8	1.56	0.71
8:A:1386:C:H2'	8:A:1387:A:H8	1.54	0.71
8:A:2328:A:H2'	8:A:2329:U:C6	2.25	0.71
34:a:1360:A:OP2	47:n:75:ARG:NH2	2.24	0.71
34:a:587:G:OP1	41:h:83:ARG:NH2	2.23	0.71
20:M:66:ARG:NH1	20:M:104:GLU:OE2	2.24	0.71
41:h:11:THR:HG22	41:h:14:ARG:HH12	1.56	0.71
34:a:456:A:H2	34:a:476:U:H3	1.39	0.71
23:P:63:ILE:HA	23:P:68:GLY:HA2	1.71	0.71
8:A:2618:G:H21	11:D:155:VAL:HG21	1.56	0.70
2:1:25:ASN:ND2	8:A:2285:C:OP1	2.24	0.70
8:A:1802:A:H2'	8:A:1803:A:C8	2.26	0.70
34:a:601:G:H2'	34:a:602:A:H8	1.56	0.70
35:b:124:THR:HG23	35:b:127:LYS:HE2	1.72	0.70
8:A:495:G:N3	26:S:61:ASN:ND2	2.38	0.70
8:A:2102:G:H1	8:A:2187:U:H3	1.39	0.70
34:a:1397:C:OP2	38:e:28:ARG:NH2	2.23	0.70
57:x:447:TRP:HB2	57:x:456:ILE:HB	1.73	0.70
8:A:1607:C:N4	8:A:1622:G:OP2	2.25	0.70
8:A:2006:C:O2'	8:A:2823:A:N3	2.24	0.70
50:q:75:VAL:HG12	50:q:76:ARG:HG2	1.72	0.70
57:x:492:THR:HG22	57:x:612:LEU:HD11	1.73	0.70
8:A:1040:A:H61	8:A:1115:G:H1	1.39	0.70
15:H:90:LEU:O	15:H:123:ARG:NH1	2.24	0.70
34:a:1432:G:O2'	34:a:1468:A:N6	2.25	0.70
9:B:5:U:OP1	9:B:61:G:O2'	2.10	0.70
57:x:168:LEU:HD13	57:x:262:LEU:HD13	1.73	0.70
8:A:2291:U:H2'	8:A:2292:U:C6	2.27	0.70
34:a:411:A:H4'	34:a:412:A:H5'	1.73	0.69
46:m:105:ALA:HB3	46:m:109:LYS:HD3	1.74	0.69
8:A:483:A:H5''	28:U:46:LYS:HD2	1.74	0.69
15:H:51:ARG:HB2	15:H:54:LEU:HB3	1.72	0.69
34:a:920:U:H2'	34:a:1081:A:H2'	1.74	0.69
8:A:746:PSU:HO2'	8:A:2611:C:HO2'	1.36	0.69
34:a:458:U:H3	34:a:474:G:H1	1.39	0.69
36:c:65:VAL:HB	36:c:100:ILE:HG22	1.73	0.69
41:h:28:SER:HB3	41:h:56:PRO:HB2	1.72	0.69
10:C:106:PRO:HD2	10:C:109:LEU:HD22	1.75	0.69
34:a:601:G:H2'	34:a:602:A:C8	2.27	0.69
34:a:921:U:C5'	34:a:1081:A:H3'	2.21	0.69
57:x:190:ILE:HD11	57:x:201:PHE:HB2	1.72	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1799:G:OP1	10:C:257:ARG:NH1	2.24	0.69
15:H:9:VAL:H	15:H:13:GLY:HA3	1.57	0.69
17:J:58:ASN:OD1	17:J:61:LYS:NZ	2.23	0.69
34:a:451:A:H61	34:a:481:G:H5'	1.58	0.69
35:b:33:ALA:HA	35:b:39:ILE:HG22	1.74	0.69
8:A:1248:G:OP1	12:E:44:ARG:NH2	2.21	0.69
8:A:1857:G:O2'	8:A:1885:A:N6	2.25	0.69
29:V:6:ALA:HB3	29:V:65:VAL:HG22	1.73	0.69
34:a:1356:G:H2'	34:a:1357:A:C8	2.28	0.69
57:x:64:SER:HB3	57:x:365:MET:HG3	1.75	0.69
8:A:659:G:N2	12:E:30:GLN:OE1	2.24	0.69
8:A:1417:C:HO2'	8:A:1587:G:HO2'	1.28	0.69
21:N:59:SER:OG	21:N:62:ASN:OD1	2.11	0.69
37:d:57:LYS:NZ	37:d:58:GLN:OE1	2.22	0.69
42:i:115:VAL:HG11	43:j:62:ARG:HB2	1.74	0.69
8:A:2683:C:OP1	23:P:50:ARG:NH2	2.24	0.69
13:F:135:ILE:HA	13:F:140:ILE:HG21	1.75	0.69
19:L:132:ARG:HG3	19:L:142:ILE:HD12	1.75	0.69
8:A:1386:C:H2'	8:A:1387:A:C8	2.28	0.68
8:A:2120:G:OP1	8:A:2120:G:N2	2.25	0.68
14:G:120:ILE:HD11	14:G:139:VAL:HG13	1.75	0.68
40:g:39:GLU:OE2	42:i:40:ARG:NH1	2.25	0.68
42:i:20:ILE:HB	42:i:60:LEU:HD21	1.76	0.68
17:J:19:ASP:OD1	17:J:58:ASN:ND2	2.25	0.68
8:A:2881:U:O2'	21:N:95:THR:O	2.12	0.68
34:a:674:G:H2'	34:a:675:A:C8	2.26	0.68
34:a:846:G:H2'	34:a:847:G:H8	1.58	0.68
8:A:630:G:N2	8:A:633:A:OP2	2.23	0.68
15:H:101:ASP:HA	15:H:107:GLY:HA2	1.74	0.68
56:w:62:C:H2'	56:w:63:G:H8	1.58	0.68
8:A:84:A:N1	8:A:98:G:O2'	2.24	0.68
8:A:319:G:H1	8:A:323:C:H5	1.40	0.68
8:A:560:C:O2'	24:Q:47:ARG:NH2	2.26	0.68
8:A:1980:G:O2'	8:A:1982:U:OP2	2.11	0.68
26:S:83:LYS:HG2	26:S:95:ARG:HH11	1.58	0.68
34:a:1200:C:O2'	34:a:1201:A:OP2	2.11	0.68
51:r:70:THR:HG23	51:r:72:ARG:H	1.58	0.68
8:A:1223:G:N2	8:A:1226:A:OP2	2.25	0.68
34:a:1305:G:N2	34:a:1332:A:OP2	2.26	0.68
37:d:100:VAL:HG22	37:d:104:MET:HE2	1.76	0.68
39:f:59:TYR:OH	51:r:65:SER:OG	2.11	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:24:ARG:NH1	8:A:2742:G:OP2	2.27	0.68
8:A:288:U:H2'	8:A:289:G:H8	1.57	0.68
8:A:310:A:O2'	8:A:311:A:O5'	2.11	0.68
8:A:1385:A:O2'	8:A:1396:U:O2	2.11	0.68
8:A:2637:U:OP1	11:D:83:ARG:NH2	2.27	0.68
13:F:106:ALA:HB1	13:F:136:ILE:HG13	1.75	0.68
34:a:1267:C:H2'	34:a:1268:G:C4	2.28	0.68
8:A:617:G:OP1	12:E:102:ARG:NH2	2.27	0.68
35:b:89:PHE:CD2	35:b:153:MET:HG3	2.28	0.68
36:c:134:LYS:NZ	36:c:169:GLU:OE1	2.26	0.68
34:a:925:G:O2'	34:a:927:G:OP1	2.12	0.68
34:a:1125:U:H2'	34:a:1126:U:H2'	1.74	0.68
34:a:179:A:H61	34:a:196:A:H62	1.40	0.67
34:a:673:A:O3'	39:f:86:ARG:NH2	2.26	0.67
1:0:12:ARG:NH1	8:A:1263:U:OP1	2.27	0.67
4:3:38:LYS:NZ	8:A:2365:G:N7	2.34	0.67
56:w:15:G:N2	56:w:21:A:N3	2.42	0.67
34:a:1125:U:OP2	34:a:1145:A:N6	2.27	0.67
37:d:146:GLU:C	37:d:148:ALA:H	2.01	0.67
18:K:98:ARG:NH1	34:a:339:C:OP2	2.27	0.67
34:a:836:G:O6	34:a:850:U:O2	2.12	0.67
14:G:136:ASP:HB3	14:G:139:VAL:HG12	1.75	0.67
17:J:12:LYS:NZ	17:J:14:ASP:OD1	2.27	0.67
35:b:183:PHE:HB3	35:b:197:PHE:HB2	1.74	0.67
8:A:286:U:H2'	8:A:287:G:C8	2.30	0.67
18:K:98:ARG:NH2	34:a:338:A:OP2	2.27	0.67
34:a:1178:G:O6	42:i:98:ARG:NH2	2.27	0.67
36:c:104:GLU:O	36:c:106:ARG:NH2	2.24	0.67
39:f:49:TYR:OH	51:r:62:ARG:O	2.09	0.67
8:A:931:U:OP1	33:Z:29:ARG:NH1	2.26	0.67
9:B:94:A:OP1	29:V:19:ARG:NH1	2.26	0.67
25:R:69:GLY:O	25:R:90:ARG:NH1	2.28	0.67
35:b:43:GLU:OE1	35:b:43:GLU:N	2.28	0.67
44:k:49:SER:HB3	44:k:68:ARG:HH11	1.60	0.67
8:A:476:G:N1	8:A:479:A:OP2	2.27	0.67
34:a:713:G:H2'	34:a:714:G:C8	2.30	0.67
40:g:52:ARG:NH1	40:g:121:ASN:OD1	2.23	0.67
8:A:704:G:H2'	8:A:726:G:H22	1.57	0.67
8:A:1332:G:N7	8:A:1609:A:O2'	2.25	0.67
16:I:55:PRO:O	16:I:71:LYS:N	2.28	0.67
8:A:1799:G:OP2	10:C:269:ARG:NH2	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:i:11:ARG:HH22	42:i:108:ARG:HH21	1.42	0.66
57:x:501:GLU:HG3	57:x:518:VAL:HG12	1.76	0.66
24:Q:99:VAL:O	24:Q:102:LYS:NZ	2.28	0.66
8:A:1178:C:O2	8:A:1179:G:N1	2.28	0.66
8:A:1454:C:O2'	8:A:1455:G:N7	2.27	0.66
34:a:246:A:N1	34:a:278:G:O2'	2.29	0.66
34:a:673:A:H2'	34:a:674:G:H8	1.59	0.66
44:k:23:HIS:HB3	44:k:30:ILE:HB	1.78	0.66
1:O:48:TYR:OH	8:A:2883:A:OP1	2.13	0.66
57:x:68:THR:HG23	57:x:366:HIS:HB2	1.77	0.66
8:A:2146:C:O2'	8:A:2147:A:N7	2.29	0.66
34:a:292:G:H21	34:a:608:A:H61	1.42	0.66
8:A:574:A:N6	8:A:2034:U:OP1	2.29	0.66
34:a:296:U:O2'	34:a:556:C:O2	2.14	0.66
34:a:1224:U:O2'	34:a:1322:C:OP1	2.12	0.66
8:A:320:A:OP1	12:E:130:LYS:NZ	2.29	0.66
34:a:1080:A:C8	34:a:1081:A:H1'	2.31	0.66
23:P:105:LYS:O	23:P:108:ARG:NH2	2.28	0.66
34:a:202:G:N2	34:a:203:G:H1'	2.10	0.66
57:x:144:ASP:O	57:x:175:GLU:HA	1.95	0.66
8:A:58:G:O2'	8:A:73:A:N1	2.27	0.65
8:A:2343:U:HO2'	8:A:2373:G:HO2'	1.44	0.65
34:a:1506:U:O2	44:k:127:ARG:NH1	2.29	0.65
35:b:89:PHE:CG	35:b:153:MET:HG3	2.31	0.65
7:6:56:ARG:HH11	7:6:59:ARG:HB2	1.62	0.65
8:A:172:A:H2'	8:A:173:A:H8	1.61	0.65
8:A:1509:A:H2'	8:A:1510:G:H8	1.60	0.65
13:F:45:ASP:HB2	13:F:48:LEU:HD23	1.77	0.65
15:H:71:LYS:HA	15:H:74:ALA:HB2	1.77	0.65
26:S:82:MET:HB3	26:S:84:ARG:HH22	1.61	0.65
47:n:30:ILE:HD13	47:n:45:VAL:HG22	1.78	0.65
8:A:320:A:N3	12:E:163:ASN:ND2	2.41	0.65
35:b:162:VAL:HG12	35:b:164:ASP:H	1.62	0.65
18:K:121:GLU:HG2	18:K:122:VAL:HG23	1.79	0.65
36:c:109:GLU:HB2	36:c:143:LEU:HD22	1.78	0.65
48:o:78:THR:O	48:o:82:GLU:HG2	1.97	0.65
34:a:944:G:N1	34:a:1338:G:OP2	2.29	0.65
34:a:946:A:H2'	34:a:947:G:H8	1.61	0.65
35:b:119:GLN:HG3	35:b:124:THR:H	1.62	0.65
8:A:463:G:N2	8:A:466:A:OP2	2.28	0.65
8:A:1798:U:OP2	10:C:270:ARG:NH2	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:F:7:TYR:OH	13:F:28:PRO:O	2.14	0.65
28:U:47:PRO:HB2	28:U:53:GLN:HB2	1.79	0.65
39:f:38:ARG:NH2	39:f:99:ALA:O	2.29	0.65
42:i:23:GLY:H	42:i:60:LEU:HA	1.61	0.65
43:j:66:GLU:HB2	47:n:99:ALA:HB2	1.77	0.65
52:s:47:THR:HB	52:s:60:PHE:HD1	1.61	0.65
34:a:539:A:OP2	45:l:111:GLN:NE2	2.24	0.65
34:a:1071:C:H2'	34:a:1072:G:H8	1.62	0.65
53:t:34:VAL:HG21	53:t:53:MET:HG2	1.79	0.65
57:x:130:ASN:OD1	57:x:136:ARG:NH2	2.30	0.65
10:C:164:VAL:HG21	10:C:180:MET:HE1	1.79	0.65
17:J:17:VAL:HG23	17:J:137:PRO:HB2	1.79	0.65
34:a:188:C:O2'	34:a:189:A:O4'	2.14	0.65
18:K:49:ARG:NH1	34:a:1423:G:OP1	2.28	0.65
3:2:12:ARG:NH2	8:A:686:U:O4	2.30	0.64
34:a:876:C:H1'	41:h:11:THR:HG21	1.78	0.64
55:v:40:C:O2'	55:v:41:C:O5'	2.14	0.64
56:w:62:C:H2'	56:w:63:G:C8	2.33	0.64
36:c:137:VAL:HG13	36:c:148:ILE:HG23	1.79	0.64
46:m:97:ARG:HB2	46:m:99:GLN:HE22	1.61	0.64
8:A:1532:A:N6	8:A:1540:G:O6	2.31	0.64
8:A:2839:G:N2	21:N:91:ALA:O	2.21	0.64
34:a:1498:UR3:H6	34:a:1499:A:N7	2.12	0.64
8:A:1432:G:H2'	8:A:1433:A:C8	2.32	0.64
11:D:48:ILE:HG23	11:D:84:LEU:HD21	1.80	0.64
23:P:32:VAL:HG22	23:P:37:LYS:HG3	1.79	0.64
25:R:77:PHE:HD1	25:R:84:ARG:HB3	1.62	0.64
29:V:20:LEU:HD21	29:V:41:GLU:HG2	1.78	0.64
8:A:281:C:H2'	8:A:282:A:H8	1.62	0.64
34:a:691:G:O6	44:k:52:ARG:NH2	2.31	0.64
41:h:10:LEU:HD22	41:h:74:ILE:HD11	1.79	0.64
8:A:629:G:N3	8:A:639:U:O2'	2.31	0.64
8:A:1063:G:H2'	8:A:1064:C:H5'	1.80	0.64
8:A:1788:C:OP1	10:C:220:ARG:NH2	2.31	0.64
8:A:1827:U:OP1	8:A:1971:U:O2'	2.16	0.64
12:E:170:ARG:NH2	12:E:179:SER:OG	2.30	0.64
26:S:2:GLU:HG2	26:S:108:SER:HB2	1.79	0.64
37:d:123:MET:HA	37:d:128:VAL:HA	1.80	0.64
37:d:173:ASP:HB2	37:d:178:GLU:HB2	1.78	0.64
50:q:10:ARG:H	50:q:22:VAL:HG13	1.61	0.64
17:J:31:GLU:HG2	17:J:142:ILE:HB	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:P:90:ALA:HB2	23:P:112:ARG:HA	1.80	0.64
34:a:1287:A:H2	34:a:1353:G:H1'	1.63	0.64
45:l:67:GLY:O	45:l:98:ARG:NH1	2.31	0.64
57:x:673:THR:HG21	57:x:677:ALA:HB3	1.80	0.64
8:A:1808:A:H3'	8:A:1809:A:C8	2.33	0.64
8:A:2076:U:OP2	8:A:2238:G:N2	2.27	0.64
8:A:2676:C:OP1	18:K:31:ARG:NH2	2.31	0.64
34:a:179:A:H3'	34:a:180:U:H6	1.62	0.64
34:a:1084:G:OP2	34:a:1086:U:C6	2.51	0.64
34:a:1218:C:H2'	34:a:1219:A:C8	2.31	0.64
8:A:265:A:O2'	8:A:428:A:N6	2.30	0.64
10:C:71:ASP:OD2	10:C:188:ARG:NH2	2.30	0.64
34:a:864:A:H2'	34:a:865:A:C8	2.33	0.64
36:c:110:LEU:HG	36:c:143:LEU:HD23	1.78	0.64
41:h:23:ALA:HA	41:h:61:THR:HA	1.80	0.64
4:3:7:ARG:NH2	8:A:245:G:N7	2.45	0.63
8:A:221:A:H1'	8:A:233:A:H1'	1.78	0.63
8:A:512:G:OP1	8:A:1234:U:O2'	2.13	0.63
8:A:1081:U:H5'	8:A:1082:U:C4	2.33	0.63
34:a:1243:C:H2'	34:a:1244:G:H8	1.63	0.63
42:i:83:THR:HB	42:i:97:LEU:HD13	1.80	0.63
8:A:1509:A:H2'	8:A:1510:G:C8	2.33	0.63
8:A:1724:G:O6	8:A:1737:G:N2	2.29	0.63
8:A:2638:G:H1'	8:A:2778:A:H61	1.63	0.63
57:x:259:GLU:HG3	57:x:260:ILE:H	1.63	0.63
12:E:146:VAL:HG12	12:E:167:VAL:HG22	1.80	0.63
14:G:26:LYS:HG2	14:G:31:GLU:HG2	1.81	0.63
34:a:270:A:H2'	34:a:271:C:C6	2.33	0.63
34:a:1157:A:H61	34:a:1178:G:H1'	1.64	0.63
34:a:1301:U:OP2	34:a:1303:C:N4	2.20	0.63
56:w:63:G:H2'	56:w:64:A:H8	1.64	0.63
57:x:40:GLY:HA3	57:x:51:TRP:CD1	2.33	0.63
5:4:7:VAL:HG12	5:4:35:GLN:HB3	1.81	0.63
8:A:676:A:O2'	8:A:2442:C:O2'	2.17	0.63
8:A:1800:C:OP2	10:C:181:ARG:NH2	2.32	0.63
10:C:244:VAL:HG12	10:C:250:GLN:HA	1.81	0.63
34:a:585:G:OP1	50:q:38:LYS:NZ	2.30	0.63
53:t:47:GLN:NE2	53:t:51:ASN:OD1	2.30	0.63
8:A:263:G:O2'	8:A:429:A:N3	2.30	0.63
8:A:2144:G:O2'	8:A:2147:A:N6	2.31	0.63
20:M:53:MET:HG3	20:M:120:ALA:HB2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:691:G:OP2	44:k:27:ASN:ND2	2.29	0.63
46:m:52:ILE:O	46:m:56:ARG:HG2	1.99	0.63
8:A:1042:G:H1	8:A:1113:U:H3	1.45	0.63
15:H:30:LEU:HB3	15:H:36:ALA:HB3	1.79	0.63
53:t:28:ARG:HA	53:t:31:ILE:HD12	1.81	0.63
8:A:2851:A:O2'	21:N:64:ARG:NH2	2.31	0.63
56:w:22:G:H2'	56:w:23:A:H8	1.64	0.63
8:A:1058:U:H2'	8:A:1059:G:H5''	1.81	0.63
8:A:1405:U:H2'	8:A:1406:U:C6	2.34	0.63
34:a:216:U:H2'	34:a:217:C:C6	2.34	0.63
34:a:575:G:O2'	34:a:821:G:H5'	1.98	0.63
8:A:288:U:H2'	8:A:289:G:C8	2.33	0.63
26:S:84:ARG:HB2	26:S:96:ILE:HB	1.80	0.63
34:a:201:G:H21	34:a:468:A:H2	1.47	0.63
34:a:460:A:H2	34:a:473:U:H3	1.46	0.63
34:a:921:U:P	34:a:1082:A:C8	2.92	0.63
52:s:46:LEU:HD13	52:s:48:ILE:HD11	1.81	0.63
56:w:15:G:N2	56:w:48:C:N4	2.47	0.63
8:A:704:G:O2'	8:A:727:A:N6	2.32	0.62
8:A:2233:U:H2'	8:A:2234:G:C8	2.33	0.62
34:a:253:A:OP1	50:q:68:LYS:NZ	2.17	0.62
37:d:63:ILE:O	37:d:110:ARG:NE	2.32	0.62
45:l:52:CYS:HB3	45:l:66:ILE:HD11	1.80	0.62
48:o:3:SER:OG	48:o:5:GLU:OE2	2.12	0.62
7:6:16:CYS:HB2	7:6:37:CYS:SG	2.39	0.62
8:A:32:C:H2'	8:A:33:C:C6	2.34	0.62
34:a:1355:G:H2'	34:a:1356:G:H8	1.64	0.62
47:n:26:LEU:HD21	47:n:47:LYS:HG3	1.81	0.62
8:A:230:G:H2'	8:A:231:A:H8	1.63	0.62
8:A:577:G:O2'	8:A:1254:A:OP1	2.17	0.62
8:A:989:G:OP2	33:Z:11:SER:OG	2.14	0.62
20:M:42:THR:HG22	20:M:93:VAL:HG12	1.82	0.62
34:a:321:A:H2'	34:a:322:C:C6	2.34	0.62
34:a:501:C:OP1	45:l:113:ARG:NH2	2.33	0.62
34:a:511:C:O2'	34:a:512:U:O5'	2.18	0.62
8:A:396:G:OP2	31:X:9:LYS:NZ	2.32	0.62
34:a:8:A:H1'	38:e:107:GLY:HA2	1.81	0.62
34:a:1149:C:H2'	34:a:1150:A:H8	1.64	0.62
36:c:53:ARG:HB3	36:c:68:HIS:HB2	1.80	0.62
7:6:14:ALA:HB3	7:6:22:MET:HB2	1.81	0.62
8:A:2246:G:H2'	8:A:2247:A:H8	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:202:G:C2	34:a:216:U:C2	2.87	0.62
36:c:122:GLN:OE1	36:c:125:ARG:NH2	2.32	0.62
8:A:307:G:N1	8:A:310:A:OP2	2.30	0.62
8:A:1047:G:N2	8:A:1110:G:O2'	2.33	0.62
34:a:28:A:O2'	34:a:296:U:OP1	2.16	0.62
36:c:18:ASN:HB3	36:c:39:ARG:HH12	1.63	0.62
8:A:1231:U:H2'	8:A:1232:G:H8	1.65	0.62
8:A:2278:A:OP2	30:W:8:ASN:ND2	2.28	0.62
8:A:2646:C:OP2	8:A:2732:G:O2'	2.18	0.62
10:C:250:GLN:NE2	10:C:251:THR:O	2.33	0.62
34:a:12:U:O2'	34:a:914:A:OP2	2.17	0.62
34:a:34:C:H2'	34:a:35:G:H8	1.64	0.62
34:a:170:U:H3'	34:a:171:A:O4'	2.00	0.62
34:a:430:A:H5''	37:d:6:PRO:HB3	1.79	0.62
34:a:459:A:N6	34:a:460:A:N1	2.47	0.62
34:a:693:G:N2	55:v:38:A:O2'	2.33	0.62
34:a:757:U:OP1	34:a:822:U:O2'	2.18	0.62
44:k:44:ALA:HB3	44:k:69:CYS:HB2	1.81	0.62
57:x:498:THR:HG21	57:x:606:LYS:HG3	1.82	0.62
8:A:239:C:O2'	8:A:622:G:O2'	2.18	0.62
34:a:169:C:H2'	34:a:170:U:H4'	1.81	0.62
40:g:68:VAL:HA	40:g:137:ARG:HD3	1.82	0.62
4:3:11:LYS:NZ	8:A:249:C:O2	2.33	0.61
8:A:1152:C:H2'	8:A:1153:C:H6	1.65	0.61
13:F:7:TYR:HB2	13:F:172:PHE:HZ	1.64	0.61
23:P:28:LYS:HE2	23:P:39:LEU:HG	1.81	0.61
39:f:12:PRO:HD2	39:f:54:LEU:HD11	1.81	0.61
56:w:25:C:H2'	56:w:26:A:H8	1.64	0.61
8:A:572:A:OP2	25:R:80:ARG:NH1	2.29	0.61
9:B:37:C:O2	22:O:100:HIS:NE2	2.32	0.61
9:B:75:G:OP1	29:V:12:GLN:NE2	2.25	0.61
34:a:1526:G:N7	54:u:39:LYS:NZ	2.42	0.61
46:m:78:ARG:NE	52:s:64:GLU:OE1	2.32	0.61
8:A:692:C:H5''	10:C:38:LYS:HB2	1.81	0.61
8:A:1631:G:N1	8:A:1634:A:OP2	2.32	0.61
34:a:694:A:N6	34:a:787:A:O2'	2.33	0.61
8:A:155:A:H2'	8:A:156:A:C8	2.35	0.61
34:a:582:C:O2	34:a:759:A:N6	2.33	0.61
34:a:980:C:H4'	47:n:59:ARG:HH21	1.64	0.61
34:a:1347:G:H1'	34:a:1348:U:H5	1.66	0.61
8:A:1266:G:O2'	8:A:2012:G:O6	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2320:U:O2'	8:A:2322:A:N7	2.30	0.61
34:a:144:G:N2	34:a:196:A:N7	2.48	0.61
44:k:29:THR:HG22	44:k:46:ALA:HB2	1.83	0.61
44:k:62:ALA:HB1	44:k:95:THR:HG23	1.81	0.61
46:m:21:ILE:HB	46:m:24:VAL:HG13	1.81	0.61
57:x:254:ARG:NH1	57:x:259:GLU:OE1	2.32	0.61
8:A:990:A:OP2	8:A:991:C:OP2	2.18	0.61
8:A:1198:U:H2'	8:A:1199:U:C6	2.35	0.61
34:a:622:A:H2'	34:a:623:C:H5'	1.83	0.61
34:a:662:U:H2'	34:a:663:A:C8	2.35	0.61
34:a:921:U:P	34:a:1081:A:H3'	2.41	0.61
7:6:16:CYS:HB3	7:6:37:CYS:SG	2.37	0.61
44:k:124:LYS:HG3	44:k:125:LYS:H	1.65	0.61
8:A:275:C:O2'	8:A:362:A:N6	2.33	0.61
8:A:2279:G:N7	30:W:10:ARG:NH2	2.49	0.61
26:S:28:LYS:HE3	26:S:70:LYS:HZ3	1.66	0.61
34:a:202:G:N1	34:a:216:U:C2	2.69	0.61
7:6:54:GLY:HA3	52:s:63:ASP:OD2	2.00	0.61
8:A:1818:U:O2'	10:C:152:GLN:O	2.15	0.61
8:A:2483:C:N3	20:M:123:LYS:NZ	2.48	0.61
34:a:292:G:N2	34:a:608:A:H61	1.99	0.61
34:a:363:A:N6	45:l:26:CYS:SG	2.72	0.61
34:a:1213:A:O2'	34:a:1215:G:N7	2.26	0.61
49:p:4:ILE:HG12	49:p:21:VAL:HG22	1.83	0.61
1:0:4:GLN:OE1	8:A:2056:G:O2'	2.19	0.60
8:A:1441:G:H2'	8:A:1442:U:C6	2.36	0.60
22:O:64:TYR:O	22:O:67:ASN:ND2	2.33	0.60
34:a:205:A:H5'	34:a:206:C:C6	2.36	0.60
34:a:380:G:N2	34:a:383:A:OP2	2.33	0.60
8:A:272:A:H2'	8:A:273:G:H8	1.67	0.60
8:A:354:A:H2'	8:A:355:U:O4'	2.00	0.60
8:A:1536:C:H4'	8:A:1537:G:C2	2.36	0.60
8:A:2637:U:H2'	8:A:2638:G:O4'	2.01	0.60
8:A:2650:U:H2'	8:A:2651:C:H6	1.66	0.60
9:B:77:U:P	29:V:21:ARG:HH22	2.24	0.60
34:a:413:G:O6	37:d:31:CYS:HA	2.01	0.60
34:a:429:U:H4'	34:a:430:A:H5'	1.83	0.60
34:a:1355:G:H2'	34:a:1356:G:C8	2.35	0.60
34:a:1377:A:H5'	34:a:1378:C:H5'	1.81	0.60
41:h:28:SER:HB2	41:h:58:LEU:HB2	1.82	0.60
9:B:76:G:O3'	29:V:21:ARG:NH2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:c:19:SER:OG	36:c:21:TRP:NE1	2.34	0.60
56:w:37:MIA:H2'	56:w:38:A:C8	2.36	0.60
57:x:344:SER:HB3	57:x:374:LYS:HB3	1.83	0.60
8:A:1125:G:OP2	8:A:1126:A:O2'	2.19	0.60
8:A:1415:U:H3	8:A:1587:G:H1	1.49	0.60
8:A:2071:A:H2'	8:A:2072:C:C6	2.36	0.60
8:A:2165:C:N4	8:A:2171:A:N7	2.49	0.60
8:A:2657:A:OP1	57:x:145:ARG:NH2	2.34	0.60
34:a:1152:A:OP1	43:j:70:HIS:ND1	2.34	0.60
34:a:1236:A:H4'	34:a:1304:G:H4'	1.83	0.60
57:x:294:ILE:HG13	57:x:338:TYR:CD2	2.36	0.60
8:A:1090:A:H4'	8:A:1091:G:OP1	2.00	0.60
34:a:56:U:H2'	34:a:57:G:C8	2.37	0.60
34:a:263:A:OP1	53:t:73:ARG:NE	2.34	0.60
34:a:792:A:O2'	34:a:794:A:N7	2.31	0.60
34:a:1340:A:HO2'	55:v:31:G:HO2'	1.46	0.60
44:k:97:ARG:HD3	54:u:15:LEU:HD22	1.82	0.60
4:3:53:ASP:HB3	19:L:57:LEU:HD22	1.83	0.60
8:A:281:C:H2'	8:A:282:A:C8	2.37	0.60
8:A:475:C:O2	8:A:479:A:N6	2.35	0.60
8:A:843:G:H2'	8:A:844:A:C8	2.36	0.60
8:A:1664:A:H2	18:K:1:MET:HE1	1.67	0.60
34:a:946:A:H2'	34:a:947:G:C8	2.36	0.60
34:a:1237:C:H3'	34:a:1238:A:H5'	1.83	0.60
7:6:56:ARG:C	7:6:58:ASP:H	2.09	0.60
8:A:1539:U:H2'	8:A:1540:G:C8	2.32	0.60
34:a:310:G:H5''	49:p:31:ARG:HB2	1.84	0.60
34:a:429:U:P	37:d:12:ARG:HH22	2.24	0.60
34:a:1375:A:N7	40:g:9:ARG:NH2	2.49	0.60
34:a:1500:A:H5''	34:a:1508:A:H5''	1.83	0.60
34:a:835:U:H3	34:a:851:G:H1	1.48	0.60
56:w:15:G:N2	56:w:48:C:H42	1.99	0.60
11:D:24:VAL:HG12	11:D:178:VAL:HG21	1.84	0.60
14:G:102:ILE:HD11	14:G:116:LEU:HD21	1.83	0.60
30:W:55:LEU:HD12	30:W:76:ILE:HD12	1.82	0.60
34:a:180:U:H2'	34:a:181:A:C8	2.37	0.60
34:a:652:U:O2'	34:a:653:U:H6	1.84	0.60
34:a:1287:A:N6	34:a:1371:G:O4'	2.34	0.60
56:w:63:G:H2'	56:w:64:A:C8	2.37	0.60
9:B:8:C:O3'	22:O:25:ARG:NH1	2.35	0.60
15:H:14:SER:HB2	15:H:17:ASP:HB2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:U:93:ARG:HB3	28:U:102:ILE:HD12	1.84	0.60
34:a:640:A:O2'	41:h:107:LYS:NZ	2.35	0.60
48:o:28:VAL:O	48:o:32:THR:HG23	2.02	0.60
24:Q:25:GLY:O	24:Q:29:ARG:NH1	2.35	0.59
39:f:86:ARG:NH1	51:r:63:TYR:O	2.35	0.59
8:A:1026:G:H2'	8:A:1027:A:H8	1.66	0.59
34:a:452:A:H1'	49:p:70:ARG:HD3	1.84	0.59
34:a:547:A:OP2	37:d:1:ALA:N	2.34	0.59
34:a:718:A:H5'	44:k:118:ASN:HB2	1.84	0.59
40:g:26:VAL:O	40:g:30:MET:N	2.35	0.59
42:i:57:VAL:HG13	42:i:58:GLU:H	1.66	0.59
48:o:28:VAL:HG11	48:o:66:LEU:HD21	1.83	0.59
7:6:56:ARG:C	7:6:58:ASP:N	2.58	0.59
8:A:644:A:H2'	8:A:645:C:O4'	2.02	0.59
8:A:693:A:O2'	8:A:1353:A:N3	2.35	0.59
8:A:1086:A:H4'	8:A:1087:G:C4	2.37	0.59
8:A:1203:U:H1'	19:L:4:ASN:HB3	1.85	0.59
8:A:1283:G:N1	8:A:1286:A:OP2	2.33	0.59
14:G:53:PRO:HG3	14:G:61:TRP:CE2	2.38	0.59
34:a:1283:U:H2'	34:a:1284:C:C6	2.38	0.59
37:d:201:GLU:OE1	38:e:111:ARG:NH1	2.35	0.59
57:x:172:ILE:HA	57:x:210:MET:HE3	1.85	0.59
34:a:41:G:H2'	34:a:42:G:H8	1.67	0.59
34:a:213:G:H1'	34:a:214:C:H2'	1.83	0.59
34:a:683:G:N2	44:k:38:GLY:O	2.36	0.59
43:j:22:THR:HA	43:j:25:ILE:HG22	1.84	0.59
8:A:2014:A:H2'	8:A:2015:A:C8	2.38	0.59
34:a:1401:G:O6	34:a:1504:G:N2	2.35	0.59
49:p:16:PHE:HE1	49:p:18:GLN:HE21	1.49	0.59
8:A:2514:U:H2'	8:A:2515:C:C6	2.37	0.59
34:a:227:G:N2	49:p:63:GLN:O	2.33	0.59
34:a:1006:G:N1	34:a:1023:U:O2'	2.29	0.59
47:n:88:ALA:HB1	47:n:96:LEU:HD22	1.83	0.59
56:w:7:A:H5''	56:w:8:4SU:H5	1.84	0.59
57:x:229:SER:HB3	57:x:232:LEU:HB2	1.83	0.59
57:x:254:ARG:HB2	57:x:259:GLU:CD	2.28	0.59
8:A:245:G:O2'	8:A:384:A:N1	2.32	0.59
8:A:1754:A:N1	8:A:2716:C:O2'	2.32	0.59
8:A:2144:G:H3'	8:A:2144:G:N3	2.18	0.59
8:A:2530:A:N7	14:G:171:LYS:NZ	2.35	0.59
34:a:31:G:N2	34:a:47:C:OP1	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:c:39:ARG:NH1	36:c:54:ILE:O	2.36	0.59
38:e:132:PRO:HA	38:e:135:VAL:HG12	1.84	0.59
8:A:2305:U:H5''	13:F:130:GLY:HA3	1.83	0.59
9:B:18:G:O6	9:B:65:U:O2	2.21	0.59
46:m:36:ALA:HB2	46:m:58:GLU:HG2	1.85	0.59
5:4:1:MET:SD	5:4:36:ARG:HB2	2.42	0.59
8:A:191:A:H2'	8:A:192:C:C6	2.38	0.59
8:A:547:A:O2'	8:A:548:G:N7	2.35	0.59
8:A:1710:G:H2'	8:A:1711:A:C8	2.38	0.59
8:A:2120:G:H4'	8:A:2169:A:N7	2.18	0.59
34:a:113:G:H1'	34:a:354:G:H5'	1.85	0.59
40:g:91:ARG:O	40:g:95:ARG:N	2.33	0.59
42:i:74:GLN:O	42:i:78:ILE:HG12	2.02	0.59
3:2:29:GLN:NE2	8:A:210:C:OP1	2.29	0.59
8:A:1447:C:O2'	8:A:1544:A:N3	2.32	0.59
34:a:175:C:O2'	34:a:1447:A:N1	2.34	0.59
40:g:92:PRO:HA	40:g:95:ARG:HD2	1.85	0.59
43:j:46:LYS:HB3	43:j:66:GLU:OE2	2.03	0.59
57:x:15:SER:HB2	57:x:125:VAL:HG21	1.85	0.59
57:x:172:ILE:HD11	57:x:189:ALA:HB1	1.85	0.59
57:x:527:GLY:N	57:x:572:ASP:OD1	2.36	0.59
12:E:118:LEU:HD11	12:E:188:MET:HG3	1.84	0.58
34:a:321:A:N7	34:a:328:C:O2'	2.35	0.58
34:a:1216:A:OP1	47:n:2:LYS:NZ	2.35	0.58
36:c:13:ILE:HG22	36:c:14:VAL:HG13	1.85	0.58
34:a:56:U:H2'	34:a:57:G:H8	1.68	0.58
34:a:1354:U:H2'	34:a:1355:G:H8	1.68	0.58
48:o:6:ALA:O	48:o:10:ILE:HG12	2.02	0.58
21:N:103:ARG:HD3	21:N:110:MET:HE2	1.84	0.58
34:a:17:U:H2'	34:a:18:C:C6	2.39	0.58
39:f:47:LEU:HD21	39:f:57:ALA:HB3	1.85	0.58
45:l:54:VAL:HG11	45:l:79:ILE:HD11	1.84	0.58
57:x:164:ASN:HB3	57:x:260:ILE:HG22	1.85	0.58
8:A:1080:A:H1'	16:I:127:SER:HA	1.85	0.58
8:A:1527:G:N1	8:A:1544:A:OP2	2.28	0.58
34:a:207:C:H2'	34:a:208:U:H4'	1.85	0.58
36:c:188:ALA:HB3	36:c:195:ILE:HB	1.85	0.58
1:0:12:ARG:NH2	8:A:517:C:OP1	2.25	0.58
8:A:2547:A:H2'	8:A:2548:U:C6	2.39	0.58
21:N:83:LEU:HD22	21:N:87:PHE:HE2	1.67	0.58
34:a:1003:G:N1	34:a:1033:G:O6	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:534:U:O2'	24:Q:48:ASP:OD2	2.12	0.58
8:A:742:A:H2'	8:A:743:A:C8	2.38	0.58
8:A:1428:C:N4	8:A:1570:A:OP2	2.34	0.58
34:a:1279:G:O2'	34:a:1282:C:N4	2.36	0.58
42:i:54:VAL:HG22	42:i:55:ASP:H	1.68	0.58
44:k:92:ARG:NH2	44:k:111:ASP:OD2	2.37	0.58
57:x:192:TRP:CD1	57:x:201:PHE:HB3	2.39	0.58
57:x:235:LYS:NZ	57:x:241:GLU:O	2.36	0.58
10:C:143:VAL:HB	10:C:153:LEU:HB2	1.85	0.58
8:A:303:G:H2'	8:A:304:U:C6	2.39	0.58
8:A:555:G:O2'	8:A:556:A:O5'	2.20	0.58
14:G:126:THR:HB	14:G:129:GLU:HG2	1.86	0.58
34:a:684:U:O2'	44:k:40:ALA:O	2.20	0.58
40:g:129:ASN:HA	40:g:134:VAL:HG11	1.85	0.58
8:A:451:U:OP1	12:E:47:LYS:NZ	2.36	0.58
8:A:2795:C:H2'	8:A:2796:U:C6	2.39	0.58
14:G:17:LYS:HE2	14:G:24:THR:HB	1.86	0.58
15:H:80:ILE:HB	15:H:146:VAL:HG22	1.85	0.58
33:Z:10:ARG:NH2	33:Z:52:PHE:O	2.36	0.58
34:a:462:G:H22	34:a:468:A:H61	1.51	0.58
40:g:74:VAL:HB	40:g:85:GLN:HB3	1.86	0.58
8:A:1184:U:OP2	33:Z:30:ARG:NH1	2.37	0.58
12:E:158:PHE:HA	12:E:169:VAL:HG21	1.86	0.58
22:O:2:ASP:OD1	22:O:3:LYS:N	2.37	0.58
34:a:202:G:N1	34:a:216:U:N3	2.52	0.58
51:r:37:LYS:NZ	54:u:30:GLU:OE2	2.31	0.58
14:G:139:VAL:O	14:G:143:VAL:HG23	2.03	0.57
34:a:193:C:H2'	34:a:194:C:C6	2.39	0.57
34:a:337:G:H2'	34:a:338:A:C8	2.39	0.57
34:a:461:A:N7	34:a:470:C:N4	2.51	0.57
34:a:736:C:H2'	34:a:737:C:H6	1.69	0.57
34:a:859:G:OP2	34:a:869:G:N1	2.25	0.57
34:a:1296:C:H4'	34:a:1302:C:C4	2.38	0.57
34:a:1354:U:H2'	34:a:1355:G:C8	2.40	0.57
8:A:1131:G:N2	8:A:1132:U:O4	2.26	0.57
8:A:1437:C:O2'	8:A:1516:G:O2'	2.16	0.57
8:A:2650:U:H2'	8:A:2651:C:C6	2.40	0.57
8:A:2768:U:O2'	17:J:95:ARG:NH1	2.38	0.57
8:A:2821:A:OP2	21:N:3:HIS:CE1	2.56	0.57
11:D:1:MET:HG2	11:D:205:PRO:HG2	1.85	0.57
22:O:83:LEU:HD11	22:O:114:GLY:HA3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:X:4:CYS:HA	31:X:32:LEU:HD21	1.85	0.57
34:a:269:C:H2'	34:a:270:A:C8	2.38	0.57
34:a:1432:G:N2	34:a:1468:A:OP2	2.37	0.57
8:A:141:G:H4'	8:A:142:A:OP1	2.03	0.57
8:A:819:A:OP2	8:A:1187:G:N2	2.22	0.57
8:A:1127:A:N7	8:A:2488:G:O2'	2.37	0.57
18:K:2:ILE:HB	18:K:33:ALA:HB3	1.87	0.57
34:a:1012:A:OP2	34:a:1012:A:H8	1.87	0.57
36:c:46:LEU:HD21	36:c:86:LEU:HD21	1.87	0.57
6:5:54:VAL:O	8:A:1084:A:N6	2.37	0.57
8:A:155:A:H2'	8:A:156:A:H8	1.69	0.57
8:A:177:G:H3'	8:A:178:G:H8	1.68	0.57
8:A:514:A:N3	8:A:581:C:O2'	2.31	0.57
8:A:1528:A:N6	8:A:1543:G:O2'	2.36	0.57
8:A:1716:U:H2'	8:A:1717:A:H8	1.70	0.57
8:A:1744:A:H3'	8:A:1745:A:H8	1.68	0.57
17:J:26:GLY:O	17:J:30:THR:HG23	2.04	0.57
34:a:324:G:N1	34:a:327:A:OP2	2.37	0.57
40:g:94:ARG:O	40:g:98:LEU:HG	2.05	0.57
40:g:98:LEU:HD23	40:g:101:ARG:HH12	1.69	0.57
57:x:32:TYR:CE2	57:x:69:ALA:HB1	2.40	0.57
57:x:353:LYS:HZ1	57:x:391:THR:N	1.98	0.57
8:A:2773:C:O2'	11:D:168:GLU:OE2	2.22	0.57
34:a:868:C:H2'	34:a:869:G:O4'	2.05	0.57
47:n:52:PRO:O	47:n:55:SER:OG	2.20	0.57
50:q:20:ILE:HG13	50:q:45:VAL:HB	1.87	0.57
8:A:1087:G:H3'	8:A:1088:A:H4'	1.87	0.57
8:A:1288:G:OP1	8:A:1289:C:N4	2.22	0.57
31:X:11:PRO:HB3	31:X:29:LEU:HD23	1.87	0.57
38:e:152:VAL:HG11	41:h:98:LEU:HB2	1.86	0.57
8:A:805:G:N2	8:A:829:A:OP1	2.37	0.57
8:A:1182:G:H2'	8:A:1183:U:O4'	2.05	0.57
30:W:33:ILE:HD11	30:W:78:ILE:HD11	1.87	0.57
34:a:62:U:H3	34:a:105:G:H1	1.52	0.57
37:d:14:GLU:HG2	37:d:59:LYS:HB2	1.87	0.57
7:6:25:ARG:O	13:F:101:ARG:NH2	2.38	0.57
8:A:1062:G:H2'	8:A:1063:G:N7	2.19	0.57
9:B:76:G:N3	29:V:78:GLN:NE2	2.47	0.57
34:a:179:A:H3'	34:a:180:U:C6	2.40	0.57
34:a:555:U:H2'	34:a:556:C:C6	2.39	0.57
34:a:714:G:H2'	34:a:715:A:C8	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:x:502:GLY:HA3	57:x:599:ALA:HB2	1.87	0.57
1:0:9:ARG:NH1	8:A:516:C:OP1	2.38	0.57
8:A:813:U:H2'	8:A:814:C:H6	1.70	0.57
8:A:1529:G:O6	8:A:1542:U:O2	2.23	0.57
34:a:1402:4OC:O5'	34:a:1402:4OC:H6	2.05	0.57
37:d:100:VAL:HG11	37:d:136:VAL:HG21	1.85	0.57
39:f:38:ARG:HD2	39:f:97:THR:HA	1.86	0.57
57:x:168:LEU:HD22	57:x:262:LEU:HB3	1.86	0.57
8:A:1800:C:H5'	10:C:145:MET:HE1	1.86	0.57
34:a:321:A:N1	34:a:332:G:O6	2.38	0.57
34:a:382:A:H2'	34:a:383:A:H8	1.70	0.57
34:a:490:C:H2'	34:a:491:G:C8	2.35	0.57
34:a:593:U:H2'	34:a:594:U:C6	2.40	0.57
34:a:1055:A:N3	36:c:155:ARG:NH1	2.53	0.57
34:a:1097:C:H2'	34:a:1098:C:C6	2.40	0.57
8:A:539:G:H1	8:A:554:U:H3	1.52	0.56
8:A:1288:G:OP2	8:A:1288:G:N2	2.37	0.56
8:A:1730:C:H1'	8:A:1731:G:C2	2.40	0.56
8:A:1996:C:N4	18:K:32:TYR:OH	2.37	0.56
8:A:2184:A:N6	8:A:2185:U:O2	2.38	0.56
30:W:46:ASN:HB2	30:W:78:ILE:HB	1.87	0.56
36:c:107:LYS:HD3	36:c:110:LEU:HD12	1.86	0.56
47:n:46:LEU:O	47:n:50:THR:HG23	2.05	0.56
56:w:15:G:H21	56:w:21:A:H1'	1.70	0.56
8:A:2229:U:H2'	8:A:2230:G:H8	1.70	0.56
8:A:2287:A:O2'	8:A:2288:A:O5'	2.19	0.56
8:A:2498:OMC:HM22	8:A:2499:C:H5'	1.87	0.56
34:a:79:G:H2'	34:a:80:A:H5''	1.87	0.56
34:a:429:U:OP1	37:d:12:ARG:NH2	2.37	0.56
34:a:1135:U:H2'	34:a:1136:C:H3'	1.87	0.56
34:a:1166:G:N1	34:a:1169:A:OP1	2.38	0.56
40:g:98:LEU:HD22	40:g:101:ARG:HH22	1.69	0.56
8:A:284:U:O2	8:A:356:G:N2	2.34	0.56
8:A:526:A:O2'	8:A:2043:C:O2	2.21	0.56
8:A:528:A:C2	8:A:2043:C:H4'	2.39	0.56
8:A:2116:G:N2	8:A:2163:A:OP2	2.32	0.56
10:C:144:GLU:HG2	10:C:150:GLY:H	1.71	0.56
10:C:154:ALA:HB2	10:C:161:VAL:HG23	1.88	0.56
15:H:81:ALA:HB1	15:H:149:GLU:HB3	1.88	0.56
15:H:125:THR:OG1	15:H:146:VAL:O	2.21	0.56
20:M:47:GLU:OE2	20:M:50:ARG:NH1	2.32	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:S:72:THR:OG1	26:S:106:VAL:O	2.22	0.56
33:Z:10:ARG:HB2	33:Z:53:MET:HB2	1.87	0.56
34:a:373:A:H1'	34:a:481:G:C8	2.41	0.56
34:a:451:A:N6	34:a:481:G:H5'	2.21	0.56
34:a:472:U:H2'	34:a:473:U:C6	2.40	0.56
34:a:966:2MG:HM23	34:a:967:5MC:H1'	1.87	0.56
34:a:1014:A:H5''	52:s:13:HIS:CG	2.41	0.56
34:a:1222:G:OP1	52:s:77:ARG:NH1	2.38	0.56
34:a:1233:G:H2'	34:a:1234:C:C6	2.40	0.56
34:a:1333:A:H3'	34:a:1334:G:H8	1.70	0.56
34:a:1376:U:OP2	40:g:24:LYS:NZ	2.34	0.56
41:h:13:ILE:HD12	41:h:60:LEU:HD11	1.87	0.56
56:w:46:G7M:H3'	56:w:47:U:H4'	1.86	0.56
57:x:699:GLU:HA	57:x:703:LYS:HA	1.87	0.56
57:x:702:GLY:O	57:x:703:LYS:C	2.48	0.56
8:A:272:A:H2'	8:A:273:G:C8	2.41	0.56
8:A:482:A:OP2	8:A:507:A:N6	2.38	0.56
8:A:1721:G:O2'	8:A:1739:A:N6	2.38	0.56
8:A:2199:A:N1	8:A:2226:C:N4	2.52	0.56
8:A:2698:U:H2'	8:A:2699:C:C6	2.40	0.56
14:G:98:LYS:NZ	14:G:103:ASN:HB2	2.21	0.56
20:M:21:ALA:HB2	20:M:97:GLN:HB2	1.86	0.56
34:a:401:C:O2'	34:a:621:A:N3	2.35	0.56
38:e:33:THR:HG22	38:e:51:LYS:HG3	1.88	0.56
39:f:12:PRO:HB3	39:f:56:LYS:O	2.05	0.56
8:A:2243:U:H2'	8:A:2244:U:C6	2.40	0.56
9:B:1:U:H2'	9:B:2:G:H8	1.70	0.56
29:V:24:ASN:ND2	29:V:24:ASN:O	2.39	0.56
34:a:2:A:N6	34:a:3:A:N1	2.54	0.56
36:c:148:ILE:HG13	36:c:200:TRP:O	2.06	0.56
57:x:269:PHE:CE2	57:x:270:LYS:HE3	2.41	0.56
7:6:16:CYS:HB3	7:6:20:ASN:HD21	1.70	0.56
8:A:1013:C:H2'	8:A:1014:A:H8	1.71	0.56
8:A:1794:A:H2'	8:A:1795:C:C6	2.40	0.56
8:A:2809:A:OP2	8:A:2890:G:N1	2.29	0.56
34:a:598:U:H2'	34:a:599:C:C6	2.41	0.56
34:a:1163:A:H2'	34:a:1164:G:C8	2.40	0.56
1:0:15:ARG:HG3	8:A:2046:G:H5'	1.87	0.56
8:A:45:G:H5'	8:A:46:G:OP1	2.05	0.56
8:A:606:U:O2	8:A:622:G:O6	2.24	0.56
8:A:1009:A:N3	8:A:1153:C:O2'	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1684:G:H2'	8:A:1685:C:C6	2.41	0.56
33:Z:3:THR:OG1	33:Z:37:ARG:O	2.17	0.56
8:A:685:A:N1	8:A:787:C:H1'	2.21	0.56
12:E:48:THR:HG23	12:E:86:ALA:HB3	1.88	0.56
34:a:462:G:H1	34:a:468:A:H62	1.54	0.56
34:a:1004:A:N1	34:a:1026:G:H1'	2.21	0.56
35:b:56:LEU:HD23	35:b:59:ILE:HD11	1.88	0.56
37:d:10:LEU:HB3	37:d:62:ARG:HD3	1.88	0.56
8:A:2134:A:H2'	8:A:2135:A:H5''	1.88	0.56
34:a:919:A:H2'	34:a:920:U:C6	2.41	0.56
34:a:921:U:P	34:a:1081:A:H2'	2.45	0.56
34:a:991:U:O2	34:a:1213:A:N7	2.38	0.56
34:a:1241:G:OP1	40:g:34:LYS:NZ	2.38	0.56
40:g:77:ARG:HE	40:g:86:VAL:HG21	1.71	0.56
47:n:50:THR:HG22	52:s:12:LEU:HD22	1.88	0.56
53:t:24:ARG:HG3	53:t:65:LEU:HD11	1.87	0.56
57:x:666:ALA:HA	57:x:669:LEU:HB3	1.88	0.56
8:A:1508:A:H2'	8:A:1509:A:O4'	2.06	0.56
8:A:2328:A:H2'	8:A:2329:U:H6	1.70	0.56
12:E:194:LYS:O	12:E:198:GLU:HG2	2.05	0.56
20:M:53:MET:HE2	20:M:117:PHE:HD1	1.70	0.56
34:a:201:G:N1	34:a:217:C:N3	2.54	0.56
34:a:1352:C:H2'	34:a:1353:G:C8	2.41	0.56
40:g:104:VAL:O	40:g:108:ARG:HG3	2.06	0.56
8:A:24:G:O2'	26:S:78:GLU:O	2.24	0.55
8:A:1219:U:H2'	8:A:1220:G:C8	2.41	0.55
34:a:10:A:HO2'	34:a:507:C:HO2'	1.54	0.55
34:a:257:G:H2'	34:a:258:G:H8	1.71	0.55
34:a:413:G:H1'	34:a:428:G:H21	1.71	0.55
34:a:527:G7M:O2'	34:a:535:A:N1	2.36	0.55
34:a:538:G:H2'	34:a:539:A:H8	1.70	0.55
34:a:921:U:OP2	34:a:1082:A:C8	2.60	0.55
39:f:37:HIS:HE2	39:f:65:GLU:HB2	1.71	0.55
43:j:6:ILE:HB	43:j:76:ILE:HG23	1.88	0.55
43:j:30:LYS:HE2	43:j:36:VAL:HB	1.88	0.55
55:v:9:G:O2'	55:v:10:G:N7	2.39	0.55
3:2:26:ASN:CG	8:A:682:G:H5'	2.31	0.55
8:A:2474:U:H5''	8:A:2475:C:H5	1.71	0.55
8:A:2688:G:N1	8:A:2720:U:OP2	2.21	0.55
13:F:110:ILE:HB	13:F:113:PHE:HB2	1.88	0.55
14:G:11:PRO:HD2	14:G:14:VAL:HG21	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:260:G:H2'	34:a:261:U:C6	2.40	0.55
34:a:261:U:O4	53:t:73:ARG:NH1	2.40	0.55
34:a:623:C:H2'	34:a:624:C:C6	2.41	0.55
34:a:975:A:N1	43:j:62:ARG:NH1	2.55	0.55
34:a:1302:C:C4	46:m:16:ILE:HG13	2.41	0.55
57:x:490:ARG:NH2	57:x:571:VAL:O	2.39	0.55
2:1:39:ASP:O	2:1:43:ARG:N	2.38	0.55
5:4:9:LYS:HG2	5:4:14:CYS:HB2	1.87	0.55
8:A:1569:A:H2'	8:A:1570:A:C8	2.42	0.55
8:A:2543:G:H2'	8:A:2544:G:C8	2.41	0.55
11:D:49:GLN:HE21	11:D:79:LEU:HB3	1.70	0.55
34:a:76:G:N2	34:a:93:U:O2	2.34	0.55
34:a:80:A:N6	34:a:91:U:O2	2.38	0.55
34:a:707:U:H2'	34:a:708:C:C6	2.41	0.55
36:c:133:MET:HE2	36:c:167:TYR:HD2	1.71	0.55
38:e:110:MET:HG2	38:e:139:THR:HG21	1.87	0.55
46:m:22:TYR:HB3	46:m:65:GLU:HA	1.88	0.55
56:w:27:G:H2'	56:w:28:G:C8	2.41	0.55
57:x:254:ARG:C	57:x:259:GLU:HG2	2.32	0.55
57:x:326:ASP:HB3	57:x:330:GLY:H	1.70	0.55
8:A:700:G:O2'	8:A:1632:A:N3	2.30	0.55
8:A:971:G:OP2	8:A:974:G:N2	2.39	0.55
8:A:1058:U:N3	8:A:1060:U:O4	2.39	0.55
8:A:1070:A:N7	8:A:1095:A:O2'	2.38	0.55
8:A:2795:C:H2'	8:A:2796:U:H6	1.70	0.55
18:K:87:LEU:HD13	18:K:92:GLU:HB3	1.89	0.55
34:a:501:C:H2'	34:a:502:A:C8	2.42	0.55
44:k:28:ASN:OD1	44:k:29:THR:N	2.39	0.55
55:v:22:G:H2'	55:v:23:C:H6	1.71	0.55
8:A:172:A:H2'	8:A:173:A:C8	2.41	0.55
8:A:251:A:N6	8:A:386:G:O6	2.26	0.55
8:A:1170:C:H42	8:A:1178:C:H41	1.54	0.55
8:A:1672:A:C2	8:A:2582:G:H5'	2.42	0.55
8:A:1992:G:N2	8:A:1996:C:O2'	2.39	0.55
8:A:2455:G:H2'	8:A:2456:C:C6	2.41	0.55
8:A:2638:G:H1'	8:A:2778:A:N6	2.21	0.55
34:a:49:U:H3	34:a:362:G:H1'	1.71	0.55
34:a:921:U:H5'	34:a:1081:A:H3'	1.89	0.55
39:f:73:GLU:O	39:f:77:THR:HG23	2.06	0.55
59:z:4:U:H2'	59:z:5:U:C6	2.42	0.55
8:A:869:G:H1'	20:M:8:LYS:HE3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:J:114:LEU:HG	17:J:118:MET:HE3	1.87	0.55
19:L:85:VAL:HG22	19:L:94:THR:HG22	1.89	0.55
22:O:39:VAL:HB	22:O:49:VAL:HG22	1.88	0.55
34:a:1032:G:H3'	34:a:1034:G:H22	1.72	0.55
34:a:1376:U:O3'	40:g:94:ARG:NH1	2.40	0.55
35:b:186:VAL:HG11	35:b:192:PRO:HA	1.88	0.55
37:d:84:ASN:O	37:d:88:ASN:ND2	2.40	0.55
8:A:139:U:C2	27:T:1:MET:HE1	2.41	0.55
8:A:813:U:H2'	8:A:814:C:C6	2.42	0.55
8:A:1120:G:H2'	8:A:1121:C:C6	2.41	0.55
8:A:2196:C:O2'	8:A:2197:U:H5'	2.07	0.55
26:S:24:ILE:HD13	26:S:36:LEU:HD11	1.87	0.55
34:a:179:A:N6	34:a:196:A:H62	2.04	0.55
34:a:921:U:H6	34:a:1082:A:P	2.30	0.55
34:a:1256:A:H4'	34:a:1257:A:H5'	1.88	0.55
34:a:1356:G:H2'	34:a:1357:A:H8	1.71	0.55
39:f:3:HIS:CE1	39:f:65:GLU:OE1	2.60	0.55
57:x:16:ALA:N	57:x:22:LYS:HD3	2.22	0.55
57:x:421:PRO:HA	57:x:480:ALA:HA	1.88	0.55
13:F:120:SER:OG	13:F:128:SER:O	2.18	0.55
35:b:48:MET:HA	35:b:51:GLU:HG2	1.89	0.55
7:6:1:MET:HE1	13:F:62:GLN:HG2	1.88	0.55
8:A:1093:G:H2'	8:A:1094:U:H1'	1.88	0.55
8:A:1219:U:H2'	8:A:1220:G:H8	1.71	0.55
8:A:1842:G:H2'	8:A:1843:C:H6	1.71	0.55
8:A:2530:A:N6	14:G:155:PRO:HG3	2.22	0.55
25:R:51:VAL:HB	25:R:52:PRO:HD3	1.89	0.55
34:a:757:U:O2'	34:a:879:C:O2	2.24	0.55
41:h:45:ILE:HD13	41:h:60:LEU:HD13	1.88	0.55
57:x:119:GLN:O	57:x:120:PRO:C	2.50	0.55
7:6:30:HIS:ND1	7:6:31:ASP:O	2.39	0.55
8:A:310:A:O2'	8:A:311:A:H2'	2.07	0.55
8:A:2086:U:H2'	8:A:2087:G:C8	2.42	0.55
8:A:2339:C:O3'	9:B:41:G:N2	2.40	0.55
34:a:908:A:H2'	34:a:909:A:H8	1.72	0.55
46:m:4:ALA:C	46:m:6:ILE:H	2.13	0.55
57:x:294:ILE:O	57:x:307:GLU:HA	2.07	0.55
8:A:1386:C:H1'	8:A:1470:A:H1'	1.88	0.54
34:a:255:G:H2'	34:a:256:U:C6	2.42	0.54
34:a:746:A:H2'	34:a:747:A:C8	2.42	0.54
34:a:913:A:OP1	45:l:42:LYS:NZ	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:b:29:PHE:HE2	35:b:48:MET:HE1	1.71	0.54
39:f:59:TYR:OH	51:r:64:LEU:O	2.25	0.54
57:x:416:SER:HA	57:x:458:ALA:HA	1.89	0.54
8:A:475:C:H4'	8:A:510:C:H5'	1.89	0.54
8:A:1366:A:OP1	31:X:1:SER:OG	2.18	0.54
8:A:1735:A:H2'	8:A:1736:U:C6	2.42	0.54
11:D:180:VAL:HG22	11:D:187:LEU:HD12	1.89	0.54
34:a:618:C:H42	34:a:623:C:N4	2.05	0.54
40:g:125:ASP:HA	40:g:128:GLU:HG2	1.89	0.54
43:j:12:ALA:CB	43:j:96:VAL:HG22	2.37	0.54
57:x:496:LYS:HD2	57:x:608:LYS:HG2	1.90	0.54
8:A:438:G:H2'	8:A:439:A:C8	2.43	0.54
8:A:1028:A:H2'	8:A:1029:A:C8	2.41	0.54
8:A:1747:U:H2'	8:A:1748:C:C6	2.42	0.54
34:a:656:G:H2'	34:a:657:U:H6	1.73	0.54
34:a:900:A:H2'	34:a:901:A:C8	2.42	0.54
43:j:65:TYR:CG	47:n:96:LEU:HD21	2.43	0.54
55:v:22:G:H2'	55:v:23:C:C6	2.42	0.54
5:4:7:VAL:HG13	5:4:37:GLN:O	2.07	0.54
8:A:197:A:H62	8:A:2430:A:H2'	1.71	0.54
8:A:394:C:H2'	8:A:395:U:O4'	2.07	0.54
8:A:492:A:H2'	8:A:493:G:O4'	2.07	0.54
8:A:729:G:O2'	8:A:763:G:H4'	2.08	0.54
8:A:1451:C:O2'	8:A:1452:G:N2	2.41	0.54
12:E:22:ASP:OD1	12:E:22:ASP:N	2.39	0.54
20:M:117:PHE:HD2	20:M:130:PHE:HD1	1.55	0.54
34:a:375:U:OP1	49:p:70:ARG:NH1	2.41	0.54
36:c:11:LEU:HD11	47:n:91:GLY:HA2	1.88	0.54
8:A:1503:A:H2'	8:A:1504:A:H8	1.72	0.54
8:A:1666:G:H4'	18:K:6:THR:HG23	1.89	0.54
8:A:2306:C:H3'	8:A:2307:G:H2'	1.89	0.54
8:A:2515:C:H2'	8:A:2516:A:H8	1.72	0.54
13:F:59:ILE:HG12	13:F:98:PHE:HE2	1.73	0.54
13:F:72:SER:HB3	13:F:80:GLN:H	1.73	0.54
34:a:985:C:H2'	34:a:986:U:C6	2.43	0.54
34:a:1199:U:H4'	43:j:56:HIS:CD2	2.43	0.54
34:a:1233:G:H2'	34:a:1234:C:H6	1.73	0.54
34:a:1288:A:N1	34:a:1371:G:H1'	2.23	0.54
37:d:122:ILE:HD11	37:d:142:VAL:HG12	1.89	0.54
42:i:34:LEU:O	42:i:38:PHE:HB2	2.07	0.54
49:p:69:ASP:OD1	49:p:69:ASP:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:33:VAL:HA	8:A:1055:G:H4'	1.90	0.54
8:A:1059:G:N2	8:A:1080:A:N3	2.56	0.54
8:A:2202:U:O2'	8:A:2204:G:OP1	2.15	0.54
26:S:4:ILE:HG13	26:S:106:VAL:HG22	1.90	0.54
30:W:33:ILE:HG21	30:W:76:ILE:HG21	1.89	0.54
34:a:427:U:O2'	34:a:541:G:OP1	2.25	0.54
34:a:921:U:O4'	34:a:1081:A:H5'	2.08	0.54
36:c:140:ALA:HB3	36:c:148:ILE:HG21	1.89	0.54
48:o:2:LEU:HD12	48:o:34:GLN:HB2	1.90	0.54
57:x:590:LEU:HD23	57:x:590:LEU:H	1.72	0.54
8:A:1060:U:H4'	8:A:1061:U:H5''	1.90	0.54
8:A:1726:C:H2'	8:A:1727:C:H6	1.72	0.54
8:A:1853:A:H2'	8:A:1854:A:C8	2.42	0.54
13:F:57:ALA:HB2	13:F:64:PRO:HD3	1.89	0.54
27:T:54:GLU:HB2	27:T:88:LYS:HE2	1.89	0.54
34:a:1001:C:H2'	34:a:1002:G:C8	2.43	0.54
34:a:1163:A:H2'	34:a:1164:G:H8	1.71	0.54
42:i:5:TYR:CD2	42:i:89:TYR:HB2	2.43	0.54
57:x:287:SER:H	57:x:290:ASP:HB2	1.71	0.54
8:A:774:G:O2'	8:A:775:G:H5''	2.08	0.54
14:G:23:ILE:HD13	14:G:71:LEU:HD21	1.90	0.54
25:R:16:GLU:HG2	25:R:100:GLY:HA2	1.88	0.54
34:a:181:A:H61	34:a:194:C:H3'	1.72	0.54
34:a:920:U:O2'	34:a:1080:A:N6	2.41	0.54
34:a:985:C:H2'	34:a:986:U:H6	1.73	0.54
34:a:1151:A:HO2'	34:a:1152:A:H8	1.55	0.54
57:x:487:VAL:HG13	57:x:659:LEU:HD22	1.90	0.54
15:H:129:GLU:HA	15:H:143:ILE:HG22	1.90	0.54
34:a:150:U:O4	34:a:170:U:H5''	2.08	0.54
34:a:222:C:H2'	34:a:223:A:H8	1.72	0.54
35:b:96:LEU:HB2	35:b:99:MET:HG3	1.89	0.54
42:i:6:TYR:HE1	42:i:17:ARG:HB3	1.72	0.54
50:q:12:VAL:HB	50:q:21:VAL:HG23	1.90	0.54
7:6:16:CYS:SG	7:6:17:SER:N	2.81	0.54
8:A:828:U:H2'	8:A:829:A:C8	2.42	0.54
8:A:833:A:H2'	8:A:834:G:C8	2.43	0.54
8:A:1873:G:H2'	8:A:1874:C:C6	2.43	0.54
8:A:2845:U:O3'	23:P:52:ARG:NH1	2.41	0.54
34:a:130:A:O2'	34:a:131:A:O5'	2.25	0.54
34:a:715:A:H2'	34:a:716:A:C8	2.43	0.54
34:a:966:2MG:HM22	55:v:34:C:H5'	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1119:C:H2'	34:a:1120:C:C6	2.43	0.54
34:a:1315:U:O2'	34:a:1360:A:N3	2.37	0.54
34:a:1397:C:O2'	59:z:9:U:O4	2.16	0.54
34:a:1507:A:H2'	34:a:1508:A:C8	2.43	0.54
36:c:78:LYS:HG2	36:c:79:LYS:HG2	1.90	0.54
40:g:60:ALA:HA	40:g:63:VAL:HG22	1.90	0.54
43:j:50:THR:HG22	43:j:62:ARG:HD2	1.90	0.54
8:A:17:G:H4'	24:Q:24:TYR:CE1	2.43	0.53
8:A:931:U:O2	8:A:1167:C:O2'	2.22	0.53
8:A:1341:G:O2'	27:T:59:ASN:OD1	2.26	0.53
8:A:1746:A:H2'	8:A:1747:U:C6	2.43	0.53
8:A:2123:G:H1	8:A:2170:A:H5'	1.73	0.53
8:A:2728:U:H2'	8:A:2729:G:C8	2.43	0.53
24:Q:88:GLU:O	25:R:11:GLN:NE2	2.33	0.53
32:Y:39:GLN:HB3	32:Y:41:HIS:CE1	2.42	0.53
34:a:377:G:H2'	34:a:378:G:H8	1.73	0.53
34:a:1366:C:HO2'	43:j:62:ARG:HH12	1.55	0.53
40:g:115:MET:HE3	40:g:119:LEU:HD12	1.90	0.53
57:x:670:ARG:HA	57:x:673:THR:HG22	1.91	0.53
4:3:15:LYS:HE2	4:3:19:GLY:HA2	1.90	0.53
8:A:380:G:H5'	31:X:17:ARG:HG3	1.90	0.53
8:A:419:U:H2'	8:A:420:C:C6	2.44	0.53
14:G:38:ASP:N	14:G:38:ASP:OD1	2.40	0.53
30:W:66:GLU:OE2	30:W:77:SER:OG	2.26	0.53
34:a:30:U:H3	34:a:553:A:H62	1.57	0.53
34:a:415:A:H2'	34:a:416:G:C8	2.42	0.53
34:a:677:U:H3	34:a:713:G:H22	1.56	0.53
37:d:54:LEU:O	37:d:58:GLN:HG2	2.07	0.53
43:j:54:SER:OG	43:j:58:ASN:HB2	2.07	0.53
48:o:73:ASP:OD2	48:o:76:ARG:NE	2.40	0.53
57:x:518:VAL:HG23	57:x:578:HIS:HB3	1.89	0.53
8:A:191:A:H2'	8:A:192:C:H6	1.72	0.53
8:A:2185:U:H2'	8:A:2186:G:C8	2.44	0.53
8:A:2376:A:N6	22:O:94:ARG:HD3	2.22	0.53
17:J:32:LEU:HD22	17:J:54:ILE:HG21	1.89	0.53
34:a:776:G:H22	34:a:802:A:P	2.30	0.53
38:e:106:ALA:H	38:e:111:ARG:NH2	2.07	0.53
38:e:135:VAL:O	38:e:139:THR:HG23	2.09	0.53
41:h:17:GLN:NE2	41:h:64:TYR:CZ	2.76	0.53
41:h:42:GLU:HG2	41:h:100:ILE:HD13	1.90	0.53
57:x:495:GLN:H	57:x:523:PRO:HG3	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:53:ASP:OD2	8:A:2359:C:O2'	2.20	0.53
8:A:251:A:OP1	19:L:58:TYR:OH	2.15	0.53
8:A:276:U:H4'	8:A:278:A:H2	1.72	0.53
8:A:641:U:H3	8:A:647:G:H1	1.56	0.53
8:A:1047:G:O2'	8:A:1110:G:N1	2.39	0.53
8:A:1638:C:H4'	8:A:2710:C:O2	2.08	0.53
8:A:2250:G:O2'	8:A:2496:C:OP1	2.12	0.53
8:A:2467:C:H2'	8:A:2468:A:O4'	2.09	0.53
15:H:12:LEU:HD22	15:H:19:VAL:HG21	1.90	0.53
34:a:524:G:H2'	34:a:525:C:C6	2.42	0.53
34:a:975:A:N1	34:a:1366:C:O2'	2.32	0.53
34:a:1139:G:H4'	34:a:1140:C:H5'	1.90	0.53
35:b:16:GLY:H	35:b:40:ILE:HG13	1.72	0.53
35:b:202:ASN:OD1	35:b:203:ASP:N	2.41	0.53
36:c:65:VAL:N	36:c:99:GLN:O	2.42	0.53
46:m:84:CYS:HB2	52:s:72:GLU:HG3	1.90	0.53
53:t:35:TYR:O	53:t:39:GLU:HG2	2.09	0.53
34:a:629:A:H2'	34:a:630:A:O4'	2.08	0.53
34:a:1346:A:H61	34:a:1374:A:H5''	1.73	0.53
40:g:56:SER:OG	40:g:57:GLU:N	2.39	0.53
8:A:309:A:H4'	28:U:15:GLY:HA2	1.90	0.53
8:A:395:U:H2'	8:A:396:G:N7	2.24	0.53
8:A:396:G:H21	8:A:2231:U:HO2'	1.54	0.53
8:A:1923:U:H2'	8:A:1924:C:C6	2.43	0.53
8:A:2134:A:C4	8:A:2159:G:H4'	2.43	0.53
34:a:1270:G:HO2'	34:a:1313:U:HO2'	1.54	0.53
56:w:30:G:H2'	56:w:31:A:H8	1.74	0.53
8:A:134:G:H2'	8:A:135:U:C6	2.43	0.53
8:A:974:G:O2'	8:A:989:G:N2	2.41	0.53
8:A:1094:U:O2'	8:A:1095:A:H3'	2.08	0.53
8:A:1794:A:H2'	8:A:1795:C:H6	1.73	0.53
8:A:2292:U:H2'	8:A:2293:G:H8	1.73	0.53
8:A:2696:U:H2'	8:A:2697:G:C8	2.44	0.53
8:A:2857:G:N2	8:A:2860:A:OP2	2.35	0.53
31:X:2:ARG:HD2	31:X:29:LEU:HD22	1.91	0.53
32:Y:19:LEU:O	32:Y:23:ARG:HG3	2.09	0.53
34:a:424:G:H2'	34:a:425:G:C8	2.43	0.53
34:a:500:G:H2'	34:a:501:C:C6	2.43	0.53
34:a:745:G:H2'	34:a:746:A:H8	1.73	0.53
34:a:1108:G:OP1	36:c:174:LEU:N	2.40	0.53
40:g:39:GLU:HA	40:g:42:VAL:HG12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:i:64:ILE:HG21	42:i:78:ILE:HD12	1.91	0.53
4:3:63:TYR:HH	8:A:592:A:HO2'	1.57	0.53
8:A:2169:A:H2	55:v:19:G:H1	1.56	0.53
8:A:2728:U:H2'	8:A:2729:G:H8	1.74	0.53
34:a:33:A:H2'	34:a:34:C:C6	2.44	0.53
34:a:538:G:H2'	34:a:539:A:C8	2.44	0.53
34:a:1060:U:H5	36:c:1:GLY:HA2	1.74	0.53
38:e:17:VAL:HG11	38:e:55:VAL:HG13	1.91	0.53
57:x:106:ASP:O	57:x:135:PRO:HD2	2.09	0.53
26:S:69:LEU:HD22	26:S:107:VAL:HB	1.90	0.53
33:Z:36:GLU:O	33:Z:37:ARG:NH1	2.42	0.53
34:a:9:G:OP2	38:e:125:LYS:NZ	2.26	0.53
34:a:10:A:O2'	34:a:507:C:O2'	2.24	0.53
35:b:79:VAL:HG22	35:b:213:LEU:HD11	1.89	0.53
49:p:58:ALA:HA	49:p:61:VAL:HG22	1.89	0.53
8:A:1059:G:N2	16:I:127:SER:O	2.42	0.53
8:A:1313:U:H4'	8:A:1332:G:H4'	1.91	0.53
8:A:1475:G:H1'	8:A:1732:C:H41	1.74	0.53
8:A:2064:C:H2'	8:A:2065:C:C6	2.43	0.53
8:A:2251:OMG:OP1	20:M:81:ARG:NH1	2.42	0.53
18:K:9:ASN:OD1	18:K:18:ARG:NH1	2.42	0.53
22:O:24:THR:HG23	22:O:90:VAL:HG12	1.90	0.53
34:a:34:C:H2'	34:a:35:G:C8	2.43	0.53
34:a:501:C:H2'	34:a:502:A:H8	1.73	0.53
35:b:14:HIS:O	35:b:201:GLY:HA2	2.08	0.53
37:d:11:SER:OG	37:d:16:THR:O	2.26	0.53
42:i:25:GLY:HA2	42:i:61:ASP:HA	1.91	0.53
49:p:8:ARG:HG2	49:p:17:TYR:CE2	2.44	0.53
52:s:19:GLU:HA	52:s:22:VAL:HG22	1.91	0.53
57:x:13:GLY:HA3	57:x:105:LEU:HD21	1.91	0.53
8:A:284:U:H2'	8:A:285:G:C8	2.44	0.52
8:A:639:U:H2'	8:A:640:C:C6	2.43	0.52
8:A:998:C:OP1	24:Q:83:LYS:NZ	2.29	0.52
8:A:2100:G:N2	8:A:2189:U:O2	2.35	0.52
19:L:78:ARG:HB3	19:L:113:ALA:HB3	1.90	0.52
24:Q:105:PHE:HA	24:Q:108:LEU:HD12	1.89	0.52
27:T:22:THR:O	27:T:26:LYS:HG3	2.09	0.52
40:g:23:ALA:O	40:g:27:ASN:ND2	2.43	0.52
1:0:23:ALA:HB2	26:S:23:LEU:HD22	1.92	0.52
2:1:13:SER:HB3	2:1:49:LYS:HE3	1.90	0.52
7:6:12:ILE:HD13	7:6:28:VAL:HB	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:247:G:OP2	8:A:249:C:N4	2.39	0.52
8:A:947:A:H2'	8:A:948:C:C6	2.44	0.52
8:A:2314:A:OP1	13:F:87:LYS:NZ	2.42	0.52
8:A:2327:A:H2'	8:A:2328:A:C8	2.44	0.52
13:F:28:PRO:HB3	13:F:159:ALA:HB2	1.90	0.52
34:a:921:U:OP2	34:a:1082:A:N9	2.42	0.52
34:a:1171:A:H2'	34:a:1172:C:C6	2.45	0.52
48:o:35:ILE:HG23	48:o:55:LEU:HD11	1.91	0.52
8:A:593:U:H2'	8:A:594:U:C6	2.44	0.52
8:A:671:C:P	19:L:33:ARG:HH12	2.32	0.52
8:A:2139:U:H3	8:A:2152:G:H1	1.57	0.52
12:E:149:ILE:HD12	12:E:188:MET:HG2	1.91	0.52
34:a:652:U:O4	34:a:752:G:O2'	2.24	0.52
34:a:1235:U:O2'	34:a:1305:G:OP1	2.20	0.52
38:e:143:LEU:HD23	38:e:146:MET:HE3	1.92	0.52
57:x:350:ASN:HB2	57:x:355:ALA:HB3	1.91	0.52
2:1:4:ILE:HG21	2:1:27:ARG:HH21	1.74	0.52
8:A:493:G:H2'	8:A:494:G:O4'	2.09	0.52
22:O:64:TYR:HB3	22:O:67:ASN:HD22	1.75	0.52
34:a:9:G:H5'	38:e:107:GLY:HA3	1.92	0.52
34:a:30:U:H3	34:a:553:A:N6	2.07	0.52
34:a:672:U:H2'	34:a:673:A:C8	2.45	0.52
34:a:828:U:OP1	41:h:21:LYS:NZ	2.41	0.52
34:a:976:G:OP2	34:a:1358:U:O2'	2.27	0.52
34:a:1119:C:H2'	34:a:1120:C:H6	1.75	0.52
34:a:1233:G:OP1	42:i:118:ARG:NH1	2.42	0.52
34:a:1314:C:H2'	34:a:1315:U:C6	2.44	0.52
56:w:23:A:H2'	56:w:24:G:C8	2.44	0.52
57:x:170:LEU:HB3	57:x:182:VAL:HB	1.92	0.52
57:x:543:VAL:HG21	57:x:579:PHE:CE1	2.45	0.52
8:A:3:U:H2'	8:A:4:U:C6	2.45	0.52
8:A:1010:A:OP1	24:Q:65:ASN:ND2	2.38	0.52
8:A:1281:G:H2'	8:A:1282:U:C6	2.44	0.52
15:H:46:PHE:HD1	15:H:50:ARG:HG3	1.74	0.52
26:S:20:VAL:HG11	26:S:44:ALA:HA	1.90	0.52
26:S:29:VAL:HB	26:S:55:ILE:HD11	1.91	0.52
26:S:88:ARG:NH2	26:S:94:ASP:OD2	2.42	0.52
34:a:222:C:H2'	34:a:223:A:C8	2.44	0.52
34:a:445:G:H2'	34:a:446:G:C8	2.44	0.52
34:a:661:G:O2'	34:a:662:U:OP1	2.26	0.52
35:b:9:LEU:HB2	35:b:42:LEU:HD22	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:x:619:GLU:HB3	57:x:652:LYS:HE3	1.92	0.52
8:A:527:C:C2	8:A:2779:U:H2'	2.44	0.52
8:A:1582:C:O2'	8:A:1585:C:N3	2.35	0.52
8:A:2039:U:H2'	8:A:2040:G:C8	2.44	0.52
8:A:2246:G:H2'	8:A:2247:A:C8	2.43	0.52
8:A:2391:G:H2'	8:A:2424:C:H41	1.73	0.52
10:C:131:MET:HG2	10:C:163:ILE:HD11	1.91	0.52
13:F:5:ASP:HA	13:F:8:LYS:HE3	1.92	0.52
15:H:7:ASP:OD1	15:H:8:LYS:N	2.43	0.52
34:a:197:A:H4'	34:a:198:G:H5'	1.92	0.52
34:a:449:G:H2'	34:a:450:G:C8	2.45	0.52
34:a:963:G:N2	43:j:57:VAL:HG11	2.24	0.52
34:a:1481:U:H2'	34:a:1482:G:C8	2.45	0.52
8:A:91:A:H4'	8:A:92:U:H5'	1.92	0.52
8:A:918:A:N3	9:B:80:U:O2'	2.43	0.52
8:A:1040:A:N6	8:A:1115:G:H1	2.07	0.52
8:A:1171:G:H22	8:A:1177:G:H1	1.56	0.52
8:A:1942:C:OP2	8:A:1943:U:O2'	2.22	0.52
8:A:2127:G:H2'	8:A:2128:G:C8	2.45	0.52
34:a:767:A:O2'	34:a:1524:C:O2	2.27	0.52
34:a:1096:C:O2	34:a:1170:A:O2'	2.28	0.52
36:c:18:ASN:O	36:c:39:ARG:NH2	2.28	0.52
50:q:27:PHE:CE2	50:q:36:PHE:HB3	2.45	0.52
1:0:49:ARG:HG2	8:A:2884:U:C6	2.44	0.52
8:A:871:U:H2'	8:A:872:U:C6	2.45	0.52
8:A:934:U:H2'	8:A:935:C:C6	2.44	0.52
8:A:1710:G:H2'	8:A:1711:A:H8	1.74	0.52
8:A:2100:G:N1	8:A:2189:U:N3	2.32	0.52
13:F:99:PHE:HE1	13:F:174:PHE:HE1	1.58	0.52
14:G:1:SER:OG	14:G:2:ARG:N	2.43	0.52
34:a:736:C:H2'	34:a:737:C:C6	2.45	0.52
34:a:908:A:H2'	34:a:909:A:C8	2.45	0.52
34:a:1236:A:H2'	34:a:1237:C:C6	2.45	0.52
41:h:95:MET:SD	41:h:129:ALA:HB1	2.49	0.52
8:A:2705:A:O2'	8:A:2852:G:OP1	2.19	0.52
25:R:27:ILE:HG22	25:R:31:GLU:HB2	1.92	0.52
25:R:58:VAL:O	25:R:102:SER:OG	2.26	0.52
29:V:30:ILE:HD11	29:V:40:ILE:HD13	1.91	0.52
34:a:438:U:O2	34:a:496:A:C6	2.63	0.52
34:a:603:U:H2'	34:a:604:G:C8	2.44	0.52
34:a:939:G:H21	34:a:1375:A:H2	1.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1042:A:H2'	34:a:1043:G:C8	2.45	0.52
43:j:36:VAL:HG22	43:j:76:ILE:HG13	1.91	0.52
57:x:443:SER:HB2	57:x:460:MET:HE3	1.92	0.52
8:A:848:C:H2'	8:A:849:A:C8	2.40	0.52
8:A:1100:C:H3'	8:A:1101:U:C5'	2.37	0.52
8:A:2012:G:P	26:S:11:ARG:HH22	2.33	0.52
8:A:2441:U:OP2	8:A:2586:U:O2'	2.28	0.52
15:H:66:ASN:OD1	15:H:134:VAL:HG13	2.11	0.52
34:a:766:A:H61	34:a:1511:G:H1'	1.75	0.52
34:a:835:U:OP1	51:r:52:ARG:NH2	2.43	0.52
37:d:3:TYR:OH	37:d:6:PRO:O	2.22	0.52
47:n:7:ALA:HA	47:n:10:VAL:HG12	1.91	0.52
3:2:30:VAL:HG22	3:2:33:ARG:HH12	1.75	0.51
8:A:568:U:O4	25:R:81:LYS:NZ	2.43	0.51
8:A:1131:G:O2'	8:A:1133:A:N7	2.37	0.51
8:A:2299:U:OP1	13:F:71:LYS:NZ	2.43	0.51
9:B:9:G:O6	9:B:111:U:O2	2.28	0.51
34:a:559:A:H4'	34:a:560:A:H3'	1.92	0.51
34:a:974:A:OP1	47:n:69:ARG:NH1	2.43	0.51
34:a:1016:A:H3'	34:a:1017:U:C6	2.45	0.51
34:a:1328:C:H5''	46:m:27:THR:HG21	1.91	0.51
34:a:1385:G:H2'	34:a:1386:G:C8	2.46	0.51
40:g:107:ALA:HA	40:g:122:GLU:HG3	1.91	0.51
57:x:472:MET:HB3	57:x:478:VAL:HG13	1.93	0.51
57:x:698:ILE:HG13	57:x:699:GLU:N	2.25	0.51
2:1:5:ARG:NH1	8:A:2285:C:OP2	2.33	0.51
7:6:41:HIS:CD2	13:F:108:PRO:HB3	2.45	0.51
8:A:75:G:H22	8:A:111:A:H2	1.57	0.51
8:A:77:G:O3'	32:Y:7:ARG:NH1	2.44	0.51
8:A:332:A:O2'	8:A:334:C:OP2	2.25	0.51
10:C:110:LYS:N	10:C:113:ASP:OD2	2.38	0.51
10:C:259:ASN:OD1	10:C:262:THR:OG1	2.19	0.51
21:N:2:ARG:O	21:N:2:ARG:HD3	2.10	0.51
34:a:246:A:C2	34:a:282:A:C5	2.97	0.51
34:a:1255:G:O2'	34:a:1258:G:N3	2.35	0.51
34:a:1309:G:O6	34:a:1329:A:N6	2.44	0.51
49:p:19:VAL:HG11	49:p:52:LEU:HD21	1.91	0.51
57:x:66:ALA:HA	57:x:85:ILE:O	2.10	0.51
8:A:1292:G:H2'	8:A:1293:C:C6	2.44	0.51
8:A:2290:G:H2'	8:A:2291:U:C6	2.46	0.51
10:C:106:PRO:HG2	10:C:109:LEU:HB2	1.90	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:P:30:TRP:CE3	23:P:37:LYS:HG2	2.46	0.51
34:a:179:A:H61	34:a:196:A:N6	2.07	0.51
34:a:440:C:H2'	34:a:441:A:H8	1.75	0.51
34:a:471:U:H5''	34:a:472:U:C5	2.46	0.51
34:a:1498:UR3:O2'	34:a:1499:A:P	2.68	0.51
57:x:135:PRO:HB3	57:x:255:VAL:O	2.09	0.51
57:x:193:ASN:HB2	57:x:200:THR:HB	1.91	0.51
8:A:621:A:C5	8:A:622:G:H1'	2.46	0.51
8:A:1067:A:H2'	8:A:1068:G:N7	2.26	0.51
8:A:1494:A:H2'	8:A:1495:A:C8	2.45	0.51
8:A:1503:A:H2'	8:A:1504:A:C8	2.45	0.51
8:A:1589:U:O4	8:A:1590:A:N6	2.44	0.51
8:A:1654:A:N1	8:A:2048:G:O2'	2.43	0.51
8:A:2364:C:OP1	30:W:51:ARG:NH1	2.41	0.51
8:A:2405:G:O2'	8:A:2411:A:N6	2.43	0.51
8:A:2591:C:H2'	8:A:2592:G:C8	2.45	0.51
8:A:2804:U:H2'	8:A:2805:C:C6	2.45	0.51
19:L:91:ASP:OD1	19:L:92:LEU:N	2.43	0.51
34:a:322:C:H4'	53:t:17:ARG:HG3	1.93	0.51
34:a:455:G:H2'	34:a:456:A:C8	2.45	0.51
34:a:598:U:H2'	34:a:599:C:H6	1.75	0.51
34:a:920:U:H1'	34:a:1080:A:C6	2.44	0.51
34:a:1202:U:N3	47:n:82:ILE:HG21	2.26	0.51
49:p:12:LYS:C	49:p:14:ARG:H	2.19	0.51
6:5:1:MET:N	8:A:1105:U:OP1	2.36	0.51
8:A:276:U:H4'	8:A:278:A:C2	2.45	0.51
8:A:300:A:OP2	28:U:81:ARG:NH2	2.43	0.51
8:A:2297:A:N6	8:A:2319:G:O2'	2.43	0.51
8:A:2696:U:H2'	8:A:2697:G:H8	1.75	0.51
8:A:2822:G:H2'	8:A:2823:A:H5''	1.91	0.51
9:B:44:G:H4'	9:B:45:A:OP2	2.09	0.51
11:D:51:THR:OG1	11:D:76:GLY:HA3	2.10	0.51
25:R:41:ILE:HB	25:R:48:LYS:HB2	1.91	0.51
34:a:718:A:H2	51:r:37:LYS:HG2	1.76	0.51
34:a:1244:G:H2'	34:a:1245:C:H6	1.75	0.51
40:g:30:MET:HE3	40:g:33:GLY:H	1.76	0.51
43:j:5:ARG:HH11	43:j:78:GLU:HA	1.75	0.51
46:m:85:TYR:O	46:m:89:ARG:HG2	2.10	0.51
8:A:636:G:N2	19:L:76:GLU:OE1	2.37	0.51
8:A:818:G:N1	8:A:1188:U:OP2	2.28	0.51
8:A:1093:G:H21	8:A:1096:A:H3'	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2298:A:OP1	13:F:70:ARG:NH2	2.39	0.51
8:A:2723:C:OP1	11:D:114:LYS:NZ	2.36	0.51
12:E:138:LEU:HD22	12:E:146:VAL:HG11	1.92	0.51
34:a:377:G:H2'	34:a:378:G:C8	2.46	0.51
34:a:745:G:H2'	34:a:746:A:C8	2.44	0.51
44:k:85:VAL:HG11	44:k:92:ARG:HB2	1.92	0.51
57:x:259:GLU:HG3	57:x:260:ILE:N	2.26	0.51
4:3:49:VAL:HG11	4:3:57:VAL:HG21	1.93	0.51
8:A:1450:G:N2	8:A:1452:G:O6	2.27	0.51
8:A:2308:G:O2'	8:A:2309:A:OP1	2.21	0.51
8:A:2687:U:H2'	8:A:2688:G:O4'	2.11	0.51
10:C:140:VAL:HG12	10:C:191:LEU:HD23	1.92	0.51
12:E:97:ASN:ND2	12:E:100:MET:SD	2.84	0.51
19:L:77:ILE:HD11	19:L:101:ILE:CG2	2.41	0.51
34:a:72:A:H2'	34:a:73:C:C6	2.46	0.51
34:a:985:C:N3	34:a:1221:G:N1	2.59	0.51
34:a:1157:A:N6	34:a:1178:G:H1'	2.25	0.51
35:b:49:PHE:HE2	35:b:212:TYR:HD1	1.59	0.51
56:w:22:G:H2'	56:w:23:A:C8	2.44	0.51
57:x:137:ILE:HG22	57:x:262:LEU:HB2	1.93	0.51
8:A:320:A:H4'	8:A:322:A:C8	2.46	0.51
8:A:555:G:O2'	8:A:556:A:H8	1.94	0.51
8:A:576:U:H2'	8:A:577:G:C8	2.45	0.51
8:A:1019:U:H3	8:A:1142:A:H62	1.58	0.51
8:A:1068:G:H21	8:A:1070:A:N6	2.01	0.51
8:A:1209:U:O2'	8:A:1237:A:N1	2.36	0.51
8:A:1857:G:C6	8:A:1884:G:C6	2.99	0.51
8:A:2304:G:H22	8:A:2312:U:H3	1.58	0.51
8:A:2469:A:N6	8:A:2481:G:O2'	2.40	0.51
8:A:2790:U:H5'	8:A:2791:G:OP1	2.11	0.51
9:B:42:C:C5	13:F:65:LEU:HD22	2.46	0.51
9:B:119:A:H2'	9:B:120:U:O4'	2.10	0.51
20:M:69:PRO:HA	20:M:94:ALA:HB2	1.93	0.51
29:V:77:VAL:HG22	29:V:89:ILE:HG23	1.93	0.51
34:a:51:A:N7	34:a:114:U:O2'	2.41	0.51
34:a:201:G:N2	34:a:468:A:H2	2.08	0.51
34:a:539:A:H2'	34:a:540:G:H8	1.74	0.51
34:a:778:G:H2'	34:a:779:C:H6	1.76	0.51
34:a:1162:C:H2'	34:a:1163:A:C8	2.46	0.51
34:a:1219:A:H2'	34:a:1220:G:H8	1.76	0.51
34:a:1243:C:H2'	34:a:1244:G:C8	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1245:C:H2'	34:a:1246:A:C8	2.46	0.51
34:a:1314:C:H2'	34:a:1315:U:H6	1.76	0.51
41:h:9:MET:O	41:h:13:ILE:HG12	2.11	0.51
43:j:87:LEU:HA	43:j:90:LEU:HD12	1.92	0.51
44:k:112:VAL:HA	51:r:72:ARG:HD3	1.92	0.51
52:s:32:THR:HG21	52:s:70:LEU:HD13	1.92	0.51
57:x:413:PRO:HG3	57:x:445:ARG:HD3	1.93	0.51
8:A:224:U:O4	8:A:419:U:O2'	2.28	0.51
8:A:2340:A:H2'	8:A:2341:G:H8	1.76	0.51
8:A:2356:U:O2	8:A:2361:G:O6	2.28	0.51
19:L:23:ILE:HG12	25:R:82:HIS:CE1	2.46	0.51
23:P:5:LYS:O	23:P:9:GLN:HG2	2.10	0.51
34:a:113:G:H2'	34:a:114:U:C6	2.46	0.51
34:a:544:G:OP1	37:d:55:ARG:NH2	2.44	0.51
34:a:865:A:H2'	34:a:866:C:C6	2.44	0.51
37:d:24:VAL:HG23	37:d:25:ARG:H	1.76	0.51
37:d:146:GLU:C	37:d:148:ALA:N	2.66	0.51
37:d:182:LYS:NZ	37:d:183:ARG:HG2	2.26	0.51
38:e:24:VAL:HG23	38:e:26:GLY:H	1.76	0.51
56:w:9:A:H62	56:w:23:A:H62	1.57	0.51
8:A:623:C:H2'	8:A:624:C:H6	1.75	0.51
8:A:1072:C:H41	8:A:1093:G:H1	1.59	0.51
8:A:1645:G:H5''	8:A:1646:C:H5'	1.91	0.51
8:A:1682:G:H2'	8:A:1683:U:C6	2.44	0.51
8:A:2175:C:N4	8:A:2176:A:N7	2.58	0.51
8:A:2548:U:O2	18:K:23:LYS:NZ	2.38	0.51
16:I:28:GLY:HA3	57:x:646:SER:HB2	1.92	0.51
25:R:77:PHE:CD1	25:R:84:ARG:HB3	2.45	0.51
34:a:73:C:H2'	34:a:74:A:O4'	2.11	0.51
34:a:429:U:H3'	37:d:8:LEU:HD12	1.93	0.51
34:a:1023:U:H2'	34:a:1024:G:H8	1.76	0.51
34:a:1043:G:H2'	34:a:1044:A:H8	1.76	0.51
34:a:1148:U:H2'	34:a:1149:C:O4'	2.10	0.51
34:a:1219:A:H2'	34:a:1220:G:C8	2.46	0.51
35:b:53:LEU:HB3	35:b:219:THR:HG21	1.93	0.51
37:d:16:THR:OG1	37:d:17:ASP:N	2.43	0.51
8:A:2:G:H2'	8:A:3:U:C6	2.46	0.50
8:A:121:G:H4'	8:A:149:A:H5'	1.92	0.50
8:A:623:C:H2'	8:A:624:C:C6	2.46	0.50
8:A:1230:A:H2'	8:A:1231:U:O4'	2.10	0.50
8:A:1360:G:N7	8:A:1361:G:C8	2.80	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2684:U:O4'	18:K:70:ARG:NH1	2.44	0.50
13:F:1:ALA:HB2	13:F:97:GLU:HG3	1.93	0.50
13:F:103:ILE:HG13	13:F:104:THR:HG23	1.92	0.50
19:L:110:VAL:HG23	19:L:125:LEU:HD23	1.93	0.50
26:S:82:MET:HB2	26:S:98:LYS:HB2	1.93	0.50
29:V:2:PHE:HB3	29:V:50:MET:HE3	1.92	0.50
34:a:71:A:N6	34:a:99:C:H1'	2.27	0.50
34:a:113:G:H2'	34:a:114:U:H6	1.76	0.50
34:a:390:U:H2'	34:a:391:G:C8	2.46	0.50
34:a:1125:U:C6	43:j:40:ILE:HG21	2.46	0.50
34:a:1130:A:H3'	34:a:1131:G:C8	2.45	0.50
36:c:171:ARG:HH21	36:c:173:PRO:HG3	1.75	0.50
8:A:30:G:H2'	8:A:31:C:C6	2.46	0.50
8:A:1059:G:C4	8:A:1060:U:H5	2.29	0.50
8:A:2012:G:OP1	26:S:11:ARG:NH2	2.44	0.50
8:A:2099:U:O2	8:A:2190:G:O6	2.28	0.50
8:A:2122:U:C2	8:A:2177:C:C4	2.99	0.50
8:A:2513:A:C6	8:A:2574:G:C6	2.98	0.50
8:A:2847:U:H2'	8:A:2848:G:O4'	2.11	0.50
18:K:113:MET:HA	18:K:116:ILE:HG22	1.91	0.50
34:a:1131:G:H2'	34:a:1132:C:C6	2.46	0.50
37:d:113:ALA:O	37:d:117:VAL:HG23	2.11	0.50
41:h:112:ASP:N	41:h:112:ASP:OD1	2.38	0.50
57:x:150:PHE:CD1	57:x:265:CYS:HB3	2.46	0.50
57:x:505:ALA:HA	57:x:513:GLN:O	2.11	0.50
1:O:7:PRO:HD2	8:A:1263:U:O2'	2.11	0.50
8:A:1071:G:N3	8:A:1089:A:N6	2.59	0.50
8:A:1072:C:O2'	8:A:1089:A:O2'	2.27	0.50
8:A:1294:U:O2	21:N:23:ASN:ND2	2.45	0.50
8:A:1353:A:H2'	8:A:1354:A:C8	2.47	0.50
8:A:2271:G:OP1	30:W:14:ALA:HB1	2.11	0.50
8:A:2305:U:H2'	8:A:2306:C:C6	2.46	0.50
8:A:2461:A:H2'	8:A:2462:C:C6	2.46	0.50
8:A:2898:U:H2'	8:A:2899:A:C8	2.47	0.50
15:H:16:GLY:HA2	15:H:47:PHE:CE2	2.46	0.50
15:H:32:PRO:HA	31:X:38:TRP:CD1	2.46	0.50
34:a:382:A:H2'	34:a:383:A:C8	2.45	0.50
34:a:690:G:O6	44:k:52:ARG:NH2	2.44	0.50
37:d:13:ARG:HD2	37:d:37:PRO:HD2	1.93	0.50
42:i:51:LEU:HA	42:i:54:VAL:HG12	1.93	0.50
57:x:254:ARG:O	57:x:257:ASN:N	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:x:316:PHE:CA	57:x:340:GLY:HA3	2.37	0.50
8:A:4:U:H2'	8:A:5:A:H8	1.77	0.50
8:A:1614:A:N1	26:S:93:ALA:HB2	2.26	0.50
8:A:2333:A:H4'	8:A:2334:U:H5''	1.93	0.50
18:K:110:GLU:CD	18:K:110:GLU:H	2.19	0.50
34:a:256:U:H2'	34:a:257:G:C8	2.46	0.50
34:a:473:U:H2'	34:a:474:G:C8	2.46	0.50
34:a:718:A:C2	51:r:37:LYS:HG2	2.46	0.50
34:a:921:U:C6	34:a:1082:A:OP2	2.53	0.50
37:d:141:VAL:HA	37:d:179:GLY:O	2.10	0.50
57:x:500:VAL:HB	57:x:602:GLU:OE2	2.12	0.50
8:A:1954:G:O2'	8:A:1956:U:O4	2.24	0.50
8:A:2308:G:HO2'	8:A:2309:A:P	2.33	0.50
8:A:2329:U:H2'	8:A:2330:G:C8	2.47	0.50
9:B:29:A:H2'	9:B:30:C:C6	2.46	0.50
23:P:30:TRP:NE1	23:P:81:ASP:OD2	2.45	0.50
34:a:340:U:H2'	34:a:341:C:C6	2.46	0.50
34:a:921:U:P	34:a:1081:A:C3'	2.99	0.50
34:a:1326:U:H2'	34:a:1327:C:C6	2.47	0.50
57:x:62:ILE:HG21	57:x:370:ARG:HE	1.77	0.50
57:x:112:TYR:HE1	57:x:122:SER:HB2	1.76	0.50
57:x:673:THR:HG23	57:x:676:ARG:H	1.76	0.50
3:2:3:ARG:NH2	8:A:752:A:OP1	2.41	0.50
8:A:2298:A:H2'	8:A:2299:U:O4'	2.11	0.50
18:K:76:VAL:HG12	23:P:72:VAL:HB	1.92	0.50
34:a:363:A:OP1	45:l:57:THR:OG1	2.28	0.50
34:a:481:G:O2'	34:a:483:C:N4	2.45	0.50
34:a:552:U:C4	34:a:553:A:C2	2.99	0.50
34:a:604:G:H2'	34:a:605:U:O4'	2.12	0.50
34:a:787:A:N6	34:a:793:U:OP2	2.45	0.50
34:a:821:G:H2'	34:a:822:U:C6	2.46	0.50
57:x:627:THR:CG2	57:x:651:VAL:HG21	2.41	0.50
5:4:11:CYS:HB3	5:4:33:HIS:CE1	2.47	0.50
8:A:289:G:H2'	8:A:290:U:C6	2.46	0.50
8:A:902:C:H2'	8:A:903:C:C6	2.47	0.50
8:A:1667:G:O2'	8:A:1991:U:O4	2.24	0.50
8:A:2025:C:H2'	8:A:2026:U:C6	2.47	0.50
8:A:2357:G:N2	8:A:2360:G:OP2	2.41	0.50
8:A:2874:C:OP1	21:N:4:ARG:NH1	2.32	0.50
34:a:67:C:H2'	34:a:68:G:C8	2.47	0.50
34:a:231:U:P	49:p:31:ARG:HH22	2.34	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:864:A:O2'	34:a:1078:U:O4	2.30	0.50
34:a:1258:G:H2'	34:a:1259:C:H6	1.77	0.50
35:b:20:ARG:O	35:b:21:TYR:C	2.54	0.50
8:A:2292:U:H2'	8:A:2293:G:C8	2.47	0.50
29:V:63:ILE:HG22	29:V:65:VAL:HG23	1.94	0.50
34:a:177:G:H3'	34:a:177:G:N3	2.27	0.50
34:a:374:A:N6	34:a:390:U:O2'	2.44	0.50
34:a:652:U:HO2'	34:a:653:U:P	2.35	0.50
34:a:939:G:O2'	34:a:1375:A:O2'	2.23	0.50
47:n:13:VAL:HG12	47:n:60:GLN:CD	2.37	0.50
57:x:638:ARG:H	57:x:661:GLU:HG3	1.76	0.50
57:x:695:GLN:O	57:x:698:ILE:HG12	2.12	0.50
8:A:381:G:OP1	31:X:15:ASN:ND2	2.44	0.50
8:A:1532:A:H2'	8:A:1533:C:O4'	2.12	0.50
8:A:1716:U:H2'	8:A:1717:A:C8	2.47	0.50
8:A:2177:C:H2'	8:A:2178:C:O4'	2.12	0.50
8:A:2812:G:H2'	8:A:2813:A:C8	2.46	0.50
20:M:20:LEU:HD13	29:V:81:PRO:HG2	1.94	0.50
34:a:539:A:H2'	34:a:540:G:C8	2.47	0.50
34:a:554:A:H2'	34:a:555:U:C6	2.47	0.50
36:c:133:MET:O	36:c:137:VAL:HG23	2.12	0.50
8:A:299:A:N3	8:A:319:G:O2'	2.37	0.49
8:A:2077:A:OP1	8:A:2238:G:N2	2.41	0.49
8:A:2233:U:H2'	8:A:2234:G:H8	1.76	0.49
13:F:127:TYR:HE2	13:F:129:MET:HB3	1.77	0.49
34:a:323:U:H2'	34:a:324:G:O4'	2.12	0.49
34:a:683:G:H2'	34:a:684:U:C6	2.47	0.49
34:a:1045:C:H2'	34:a:1046:A:O4'	2.12	0.49
36:c:55:VAL:HB	36:c:66:THR:HB	1.94	0.49
38:e:80:LEU:HD22	38:e:146:MET:HE1	1.92	0.49
38:e:110:MET:HA	38:e:113:VAL:HG12	1.93	0.49
46:m:48:SER:O	46:m:52:ILE:HG12	2.12	0.49
52:s:47:THR:HA	52:s:60:PHE:HA	1.92	0.49
57:x:539:ILE:HD12	57:x:549:ILE:HD11	1.93	0.49
8:A:586:A:N1	8:A:809:G:O2'	2.40	0.49
8:A:674:G:H5''	12:E:71:GLY:N	2.27	0.49
8:A:1170:C:H42	8:A:1178:C:N4	2.09	0.49
8:A:1361:G:H2'	8:A:1362:C:C6	2.47	0.49
8:A:1433:A:H2'	8:A:1434:A:O4'	2.12	0.49
11:D:123:LYS:HE2	21:N:1:MET:HE1	1.93	0.49
15:H:132:PHE:N	15:H:140:ALA:O	2.34	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:O:6:ALA:O	22:O:10:ARG:HB2	2.11	0.49
23:P:90:ALA:HB3	23:P:110:LYS:HG3	1.93	0.49
34:a:920:U:H3'	34:a:1082:A:OP1	2.12	0.49
36:c:18:ASN:C	36:c:39:ARG:HH22	2.17	0.49
40:g:70:PRO:HG3	40:g:98:LEU:HB2	1.93	0.49
57:x:174:ALA:H	57:x:177:HIS:HB2	1.77	0.49
57:x:491:GLU:O	57:x:570:VAL:HA	2.11	0.49
8:A:686:U:H2'	8:A:788:A:N1	2.26	0.49
8:A:1141:U:H4'	8:A:1142:A:O4'	2.12	0.49
8:A:1197:G:H2'	8:A:1198:U:H6	1.77	0.49
8:A:1426:G:OP2	8:A:1427:A:O2'	2.30	0.49
8:A:1955:U:H5'	8:A:1956:U:H5	1.77	0.49
8:A:2575:C:O2'	8:A:2578:G:N7	2.37	0.49
8:A:2591:C:H2'	8:A:2592:G:H8	1.77	0.49
8:A:2834:G:H2'	8:A:2879:A:H61	1.77	0.49
9:B:29:A:H2'	9:B:30:C:H6	1.77	0.49
12:E:148:ILE:HB	12:E:169:VAL:HG12	1.95	0.49
14:G:9:VAL:HA	14:G:48:THR:HA	1.93	0.49
26:S:82:MET:HB3	26:S:84:ARG:NH2	2.28	0.49
34:a:424:G:H2'	34:a:425:G:H8	1.75	0.49
34:a:1221:G:C6	34:a:1222:G:N2	2.80	0.49
35:b:54:ALA:O	35:b:58:LYS:HB2	2.12	0.49
38:e:86:GLY:O	38:e:138:ALA:HB1	2.12	0.49
57:x:18:ILE:O	57:x:19:ASP:C	2.56	0.49
57:x:169:GLN:HG3	57:x:170:LEU:H	1.77	0.49
8:A:1734:G:H2'	8:A:1735:A:H8	1.77	0.49
8:A:1907:G:O6	8:A:1924:C:N4	2.45	0.49
8:A:2431:U:O2'	8:A:2433:A:N7	2.45	0.49
9:B:73:A:H2	29:V:37:PRO:HG3	1.78	0.49
11:D:13:ARG:HG2	23:P:55:HIS:CE1	2.46	0.49
34:a:202:G:C2	34:a:216:U:O2	2.66	0.49
34:a:1012:A:OP2	34:a:1012:A:C8	2.66	0.49
34:a:1162:C:H2'	34:a:1163:A:H8	1.76	0.49
34:a:1534:A:H3'	34:a:1535:C:H4'	1.93	0.49
37:d:101:VAL:HG13	37:d:106:PHE:HB2	1.93	0.49
8:A:594:U:H2'	8:A:595:C:C6	2.46	0.49
8:A:643:A:N1	8:A:2369:A:O2'	2.37	0.49
8:A:1010:A:H1'	8:A:1153:C:H1'	1.95	0.49
8:A:2801:G:H2'	8:A:2802:G:C8	2.47	0.49
15:H:9:VAL:N	15:H:13:GLY:HA3	2.27	0.49
19:L:132:ARG:NH2	19:L:144:GLU:OE2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:768:A:N3	34:a:1512:U:O2'	2.44	0.49
34:a:1016:A:H3'	34:a:1017:U:H6	1.76	0.49
38:e:100:GLU:H	38:e:100:GLU:CD	2.20	0.49
40:g:46:LEU:HB3	40:g:57:GLU:HG2	1.94	0.49
41:h:12:ARG:NH1	41:h:25:THR:O	2.45	0.49
57:x:312:ASP:OD2	57:x:341:VAL:HB	2.13	0.49
57:x:376:VAL:C	57:x:377:ARG:HD2	2.37	0.49
6:5:25:ALA:HB2	6:5:96:PHE:HA	1.94	0.49
8:A:373:U:H2'	8:A:374:A:H8	1.77	0.49
8:A:458:G:O2'	8:A:459:U:OP2	2.31	0.49
8:A:639:U:H2'	8:A:640:C:H6	1.78	0.49
8:A:1801:A:OP2	10:C:149:LYS:NZ	2.41	0.49
8:A:2127:G:O2'	8:A:2128:G:O4'	2.30	0.49
8:A:2229:U:O2	31:X:33:HIS:HE1	1.96	0.49
8:A:2895:G:H2'	8:A:2896:C:C6	2.48	0.49
19:L:82:LEU:HD22	19:L:90:VAL:HG21	1.95	0.49
28:U:33:VAL:HG13	28:U:66:VAL:HG22	1.94	0.49
34:a:203:G:O2'	34:a:466:A:N6	2.46	0.49
34:a:358:U:H2'	34:a:359:G:H8	1.77	0.49
34:a:709:U:H2'	34:a:710:G:C8	2.47	0.49
34:a:747:A:H2'	34:a:748:G:C8	2.48	0.49
34:a:1004:A:C6	34:a:1026:G:H1'	2.48	0.49
35:b:185:ILE:HA	35:b:199:ILE:O	2.13	0.49
44:k:113:THR:HG21	54:u:27:VAL:HB	1.95	0.49
8:A:132:G:H2'	8:A:133:U:C6	2.48	0.49
8:A:1726:C:H2'	8:A:1727:C:C6	2.46	0.49
8:A:2100:G:O6	8:A:2189:U:O4	2.31	0.49
8:A:2800:A:C2	8:A:2895:G:H1'	2.48	0.49
8:A:2834:G:H1'	8:A:2883:A:N6	2.28	0.49
34:a:144:G:H3'	34:a:145:G:H8	1.77	0.49
34:a:565:U:OP2	34:a:566:G:O2'	2.25	0.49
34:a:625:U:H2'	34:a:626:G:H8	1.78	0.49
47:n:73:PHE:CZ	47:n:78:GLY:HA2	2.47	0.49
8:A:305:C:H2'	8:A:306:U:C6	2.47	0.49
8:A:2043:C:H1'	8:A:2779:U:O4	2.13	0.49
8:A:2455:G:H2'	8:A:2456:C:H6	1.78	0.49
34:a:458:U:H2'	34:a:459:A:C8	2.48	0.49
34:a:1300:G:H4'	34:a:1301:U:O5'	2.13	0.49
39:f:18:VAL:O	39:f:22:ILE:HG13	2.12	0.49
53:t:24:ARG:O	53:t:28:ARG:HG2	2.12	0.49
8:A:5:A:H2'	8:A:6:A:H8	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:868:U:O2	20:M:8:LYS:NZ	2.26	0.49
8:A:1000:A:H2'	8:A:1001:A:C8	2.48	0.49
8:A:1429:G:H2'	8:A:1430:G:H8	1.76	0.49
8:A:1490:A:O2'	8:A:1491:G:OP1	2.26	0.49
34:a:197:A:N1	34:a:220:G:O2'	2.31	0.49
34:a:337:G:H2'	34:a:338:A:H8	1.76	0.49
34:a:430:A:H4'	37:d:6:PRO:HG3	1.94	0.49
34:a:447:G:N1	34:a:486:U:OP1	2.43	0.49
34:a:603:U:H2'	34:a:604:G:H8	1.78	0.49
34:a:680:C:H2'	34:a:681:A:C8	2.48	0.49
34:a:683:G:H2'	34:a:684:U:H6	1.78	0.49
34:a:689:C:HO2'	34:a:690:G:P	2.36	0.49
35:b:113:LEU:HD22	35:b:143:LEU:HB3	1.95	0.49
45:l:97:VAL:HG23	45:l:100:ALA:HB3	1.95	0.49
1:0:8:THR:HG22	8:A:2020:A:H5'	1.94	0.49
8:A:17:G:H4'	24:Q:24:TYR:HE1	1.77	0.49
8:A:981:A:OP2	8:A:982:C:N4	2.29	0.49
8:A:1306:C:N4	8:A:1606:C:H2'	2.28	0.49
8:A:2294:G:H2'	8:A:2295:C:H6	1.78	0.49
9:B:30:C:OP1	22:O:3:LYS:NZ	2.34	0.49
34:a:706:A:H2'	34:a:707:U:O4'	2.12	0.49
34:a:767:A:H2'	34:a:768:A:O4'	2.12	0.49
57:x:627:THR:HG23	57:x:651:VAL:HG21	1.95	0.49
1:0:3:GLN:HA	8:A:2615:U:C2	2.47	0.48
8:A:460:A:H2'	8:A:461:C:O4'	2.13	0.48
8:A:2143:C:O2'	8:A:2145:C:N4	2.35	0.48
8:A:2230:G:H2'	8:A:2231:U:C6	2.48	0.48
8:A:2881:U:H4'	21:N:116:VAL:HG11	1.95	0.48
13:F:21:TYR:OH	13:F:164:GLU:OE2	2.30	0.48
23:P:74:GLN:HB2	23:P:77:SER:OG	2.12	0.48
34:a:82:G:H22	34:a:87:C:H41	1.61	0.48
34:a:445:G:H2'	34:a:446:G:H8	1.77	0.48
34:a:712:A:H2'	34:a:713:G:C8	2.48	0.48
34:a:1169:A:OP2	34:a:1169:A:H8	1.96	0.48
34:a:1319:A:C6	34:a:1323:G:C2	3.00	0.48
34:a:1396:A:C2	38:e:23:THR:HG21	2.47	0.48
37:d:96:ARG:NH1	37:d:98:ASP:OD1	2.46	0.48
37:d:97:LEU:HD23	37:d:117:VAL:HG13	1.95	0.48
37:d:183:ARG:HH22	37:d:189:ASP:CG	2.21	0.48
41:h:17:GLN:HA	41:h:17:GLN:HE21	1.77	0.48
42:i:71:ILE:HG13	42:i:72:SER:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:44:ARG:NH2	8:A:2349:G:OP1	2.46	0.48
6:5:28:ALA:HA	6:5:81:LEU:O	2.13	0.48
8:A:781:A:C8	10:C:217:PRO:HG2	2.47	0.48
8:A:970:U:N3	8:A:971:G:N7	2.62	0.48
8:A:1779:U:O2	8:A:1783:A:N6	2.46	0.48
8:A:2577:A:H2'	8:A:2614:A:N6	2.27	0.48
10:C:159:THR:O	10:C:194:VAL:HG23	2.13	0.48
24:Q:97:ILE:HG22	24:Q:105:PHE:HB2	1.95	0.48
32:Y:10:SER:O	32:Y:14:LEU:HG	2.13	0.48
34:a:409:U:OP1	37:d:22:SER:N	2.46	0.48
34:a:1120:C:H2'	34:a:1121:U:H6	1.78	0.48
40:g:46:LEU:HD23	40:g:57:GLU:HB3	1.95	0.48
42:i:91:GLU:OE1	42:i:91:GLU:N	2.47	0.48
46:m:4:ALA:C	46:m:6:ILE:N	2.68	0.48
49:p:53:ASP:HB3	49:p:56:ARG:HB2	1.95	0.48
7:6:8:LYS:NZ	7:6:10:GLU:HB3	2.28	0.48
8:A:1038:G:H2'	8:A:1039:A:C8	2.48	0.48
8:A:1093:G:H2'	8:A:1094:U:C1'	2.43	0.48
8:A:1352:U:O2'	8:A:1570:A:N3	2.38	0.48
8:A:2552:OMU:H5	8:A:2556:C:H41	1.78	0.48
18:K:13:ASN:OD1	18:K:97:THR:N	2.43	0.48
23:P:47:ILE:HB	23:P:96:LEU:HB2	1.95	0.48
34:a:793:U:H5'	34:a:794:A:H5''	1.94	0.48
34:a:1017:U:H2'	34:a:1018:G:H8	1.78	0.48
50:q:22:VAL:O	50:q:43:LEU:N	2.46	0.48
8:A:376:G:H2'	8:A:377:G:H8	1.78	0.48
8:A:1175:A:H5'	8:A:1176:U:C6	2.49	0.48
8:A:2012:G:OP1	26:S:98:LYS:HA	2.14	0.48
8:A:2186:G:H2'	8:A:2187:U:O4'	2.13	0.48
12:E:66:GLY:O	12:E:67:ARG:C	2.57	0.48
25:R:41:ILE:O	25:R:48:LYS:N	2.42	0.48
34:a:292:G:H21	34:a:608:A:N6	2.09	0.48
34:a:406:G:N3	37:d:115:GLN:NE2	2.59	0.48
34:a:625:U:H2'	34:a:626:G:C8	2.47	0.48
34:a:719:C:OP2	34:a:720:C:N4	2.37	0.48
34:a:921:U:O5'	34:a:1081:A:H3'	2.13	0.48
37:d:124:VAL:HG22	37:d:142:VAL:HG13	1.95	0.48
42:i:27:ILE:HG12	42:i:62:LEU:HD12	1.94	0.48
45:l:86:VAL:C	45:l:88:ASP:H	2.20	0.48
45:l:113:ARG:HG2	45:l:118:VAL:O	2.14	0.48
8:A:4:U:H2'	8:A:5:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1022:G:H1'	8:A:1024:G:O6	2.13	0.48
8:A:1071:G:H2'	8:A:1089:A:H62	1.78	0.48
8:A:1103:A:H2'	8:A:1104:C:O4'	2.13	0.48
8:A:1363:C:O2'	8:A:1809:A:N3	2.34	0.48
8:A:1922:G:H2'	8:A:1923:U:O4'	2.13	0.48
8:A:2522:U:O2'	8:A:2647:U:OP1	2.19	0.48
9:B:42:C:C6	13:F:65:LEU:HB2	2.48	0.48
34:a:99:C:O2'	34:a:100:G:H8	1.97	0.48
34:a:135:C:H2'	34:a:136:C:H5'	1.95	0.48
34:a:406:G:H21	37:d:115:GLN:HE22	1.61	0.48
34:a:407:U:H2'	34:a:408:A:H8	1.77	0.48
34:a:838:G:C5	34:a:849:G:C2	3.01	0.48
36:c:57:GLU:OE1	36:c:64:ARG:NH2	2.47	0.48
57:x:93:ASP:HB3	57:x:464:HIS:HB2	1.95	0.48
57:x:395:THR:HB	57:x:405:LEU:HD23	1.95	0.48
2:1:16:THR:OG1	2:1:39:ASP:OD2	2.30	0.48
8:A:251:A:H5''	19:L:47:ARG:HE	1.79	0.48
8:A:607:U:N3	8:A:608:A:N7	2.62	0.48
8:A:653:U:C4	8:A:654:A:H1'	2.49	0.48
8:A:1062:G:C8	8:A:1088:A:N7	2.81	0.48
8:A:2038:G:H2'	8:A:2039:U:O4'	2.13	0.48
15:H:84:ALA:HA	15:H:90:LEU:HA	1.95	0.48
26:S:10:ALA:O	26:S:12:SER:N	2.46	0.48
32:Y:6:LEU:HB3	32:Y:56:LEU:HD13	1.96	0.48
34:a:22:G:O2'	34:a:913:A:N1	2.45	0.48
34:a:747:A:H2'	34:a:748:G:H8	1.78	0.48
34:a:768:A:H4'	34:a:1523:G:N2	2.28	0.48
34:a:920:U:C2'	34:a:1081:A:H2'	2.40	0.48
34:a:1107:C:C4	34:a:1108:G:C8	3.01	0.48
35:b:16:GLY:HA2	35:b:38:HIS:O	2.14	0.48
36:c:49:ALA:O	36:c:69:THR:OG1	2.31	0.48
39:f:51:ILE:HD11	51:r:65:SER:HB3	1.96	0.48
42:i:34:LEU:HD21	42:i:44:ARG:HD3	1.95	0.48
53:t:69:ASN:O	53:t:73:ARG:HG2	2.13	0.48
54:u:20:ARG:HA	54:u:23:GLU:HG2	1.96	0.48
8:A:300:A:O5'	28:U:81:ARG:NH1	2.47	0.48
8:A:358:U:H2'	8:A:359:G:C8	2.49	0.48
8:A:1098:A:H3'	8:A:1099:G:C8	2.48	0.48
8:A:1184:U:P	33:Z:30:ARG:HH12	2.36	0.48
8:A:1866:A:H2'	8:A:1867:G:O4'	2.13	0.48
8:A:2340:A:H5'	9:B:41:G:H21	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2531:A:OP2	14:G:174:LYS:HG3	2.13	0.48
12:E:165:HIS:CD2	12:E:166:LYS:HG3	2.48	0.48
13:F:61:GLY:HA3	13:F:94:ARG:NH1	2.29	0.48
34:a:110:C:O2'	49:p:25:ARG:O	2.29	0.48
34:a:463:U:H4'	34:a:464:U:OP1	2.14	0.48
34:a:828:U:P	41:h:21:LYS:HZ1	2.37	0.48
34:a:1064:G:H1'	34:a:1190:G:H21	1.79	0.48
35:b:91:VAL:HG21	35:b:95:TRP:CE3	2.48	0.48
38:e:55:VAL:O	38:e:59:ILE:HG13	2.13	0.48
40:g:21:LEU:HD22	40:g:61:PHE:HE2	1.77	0.48
57:x:228:ALA:HB1	57:x:254:ARG:HD2	1.96	0.48
8:A:1341:G:OP1	8:A:1397:U:N3	2.37	0.48
8:A:1432:G:O2'	8:A:1433:A:H5'	2.13	0.48
8:A:2262:U:H2'	8:A:2263:C:H6	1.79	0.48
14:G:36:LEU:HD21	14:G:71:LEU:HD11	1.96	0.48
16:I:56:VAL:HA	16:I:70:THR:HA	1.96	0.48
20:M:4:PRO:HG3	20:M:68:PHE:HE2	1.79	0.48
24:Q:77:LYS:O	24:Q:116:LEU:HD11	2.14	0.48
34:a:430:A:H2'	34:a:431:A:O4'	2.14	0.48
34:a:637:C:H2'	34:a:638:U:C6	2.49	0.48
34:a:1073:U:O2	35:b:102:ASN:ND2	2.47	0.48
34:a:1458:G:OP1	53:t:29:THR:OG1	2.30	0.48
45:l:41:PRO:HB3	45:l:88:ASP:CG	2.38	0.48
46:m:95:PRO:HB3	46:m:99:GLN:HB2	1.95	0.48
8:A:223:A:O2'	8:A:420:C:O2	2.31	0.48
8:A:481:G:H4'	8:A:481:G:OP1	2.13	0.48
8:A:1443:U:H2'	8:A:1444:G:H8	1.79	0.48
8:A:1847:G:O2'	8:A:1848:A:O5'	2.29	0.48
8:A:2273:A:H2'	8:A:2274:A:C8	2.48	0.48
8:A:2703:C:C2	8:A:2704:C:C5	3.01	0.48
12:E:97:ASN:HB2	12:E:100:MET:HG3	1.95	0.48
14:G:27:GLY:HA3	14:G:78:VAL:HB	1.95	0.48
27:T:58:VAL:C	27:T:59:ASN:HD22	2.22	0.48
34:a:459:A:N1	34:a:474:G:C6	2.82	0.48
34:a:836:G:O6	34:a:850:U:C2	2.66	0.48
34:a:1062:U:H2'	34:a:1063:C:C6	2.48	0.48
34:a:1204:A:H2'	34:a:1205:U:O4'	2.14	0.48
35:b:92:ASN:OD1	35:b:93:HIS:ND1	2.47	0.48
42:i:129:ARG:HA	42:i:129:ARG:HD3	1.54	0.48
49:p:39:PHE:HE2	49:p:70:ARG:HH21	1.62	0.48
57:x:553:ASP:O	57:x:557:GLN:HG2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:580:U:O3'	24:Q:30:VAL:HG13	2.14	0.48
8:A:980:A:N3	8:A:2037:A:O2'	2.39	0.48
8:A:2561:U:O2	18:K:23:LYS:HE3	2.13	0.48
9:B:31:C:H1'	9:B:54:G:H1	1.77	0.48
34:a:196:A:O3'	34:a:197:A:H2'	2.14	0.48
34:a:778:G:H2'	34:a:779:C:C6	2.49	0.48
34:a:921:U:C6	34:a:1082:A:P	3.07	0.48
34:a:921:U:H3'	34:a:1082:A:OP2	2.14	0.48
34:a:1133:G:C6	34:a:1142:G:C5	3.02	0.48
53:t:81:GLN:HA	53:t:84:LYS:HE2	1.95	0.48
56:w:36:A:H2'	56:w:37:MIA:C8	2.44	0.48
8:A:228:C:N3	8:A:417:C:O2'	2.42	0.47
8:A:1170:C:H2'	8:A:1171:G:C8	2.49	0.47
8:A:1198:U:H2'	8:A:1199:U:H6	1.79	0.47
8:A:1668:A:N3	8:A:1670:C:N4	2.62	0.47
8:A:2031:A:N3	8:A:2455:G:O2'	2.41	0.47
20:M:67:VAL:HG21	20:M:96:ILE:HD11	1.94	0.47
21:N:73:ASN:HA	21:N:76:VAL:HG12	1.96	0.47
34:a:5:U:O2'	34:a:6:G:OP2	2.25	0.47
34:a:106:C:H2'	34:a:107:G:O4'	2.13	0.47
34:a:550:G:H2'	34:a:551:U:C6	2.49	0.47
34:a:688:G:H5'	44:k:48:GLY:HA2	1.96	0.47
34:a:1101:A:H4'	34:a:1102:A:H5'	1.96	0.47
57:x:414:VAL:HG22	57:x:460:MET:O	2.14	0.47
8:A:279:A:N6	8:A:361:G:O2'	2.47	0.47
8:A:632:A:H2'	8:A:633:A:C8	2.49	0.47
8:A:1083:U:O2'	8:A:1085:A:H5''	2.14	0.47
8:A:1091:G:N1	8:A:1101:U:H1'	2.29	0.47
8:A:2079:U:C2	8:A:2080:A:C8	3.03	0.47
8:A:2220:U:O3'	15:H:112:LYS:NZ	2.47	0.47
8:A:2565:A:N6	18:K:28:SER:OG	2.47	0.47
15:H:58:LEU:HA	15:H:61:VAL:HG12	1.96	0.47
30:W:37:ARG:HA	30:W:37:ARG:HE	1.79	0.47
34:a:409:U:O4	34:a:433:G:O6	2.32	0.47
34:a:448:A:H3'	34:a:449:G:H8	1.79	0.47
34:a:515:G:O2'	34:a:516:PSU:H6	1.98	0.47
34:a:600:A:H2'	34:a:601:G:H8	1.79	0.47
34:a:651:C:H2'	34:a:652:U:C6	2.49	0.47
34:a:741:G:H2'	34:a:742:G:O4'	2.13	0.47
34:a:1086:U:H3	34:a:1099:G:H22	1.61	0.47
57:x:471:ARG:O	57:x:475:GLU:N	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:x:518:VAL:HG22	57:x:579:PHE:N	2.29	0.47
2:1:36:LYS:HA	2:1:47:ILE:HA	1.96	0.47
8:A:396:G:C6	8:A:397:U:C4	3.02	0.47
8:A:594:U:H2'	8:A:595:C:H6	1.80	0.47
8:A:940:G:H2'	8:A:941:A:O4'	2.14	0.47
8:A:1571:A:H2'	8:A:1572:A:C8	2.49	0.47
8:A:1736:U:C4	8:A:1737:G:C2	3.02	0.47
8:A:2243:U:H2'	8:A:2244:U:H6	1.79	0.47
8:A:2373:G:H2'	8:A:2374:C:C6	2.49	0.47
8:A:2552:OMU:H2'	8:A:2554:U:OP2	2.14	0.47
8:A:2747:G:O6	8:A:2755:C:H5''	2.14	0.47
8:A:2848:G:O2'	8:A:2849:U:O5'	2.26	0.47
18:K:105:ARG:HH11	18:K:108:ARG:HD2	1.79	0.47
22:O:77:ALA:O	22:O:81:ARG:HG3	2.14	0.47
34:a:262:A:H2'	34:a:263:A:C8	2.50	0.47
34:a:415:A:H2'	34:a:416:G:H8	1.78	0.47
34:a:921:U:P	34:a:1082:A:O5'	2.72	0.47
34:a:981:U:O3'	47:n:63:ARG:NH2	2.48	0.47
38:e:104:ILE:HD11	38:e:119:VAL:O	2.14	0.47
43:j:32:THR:OG1	43:j:83:THR:HG21	2.14	0.47
56:w:64:A:H2'	56:w:65:G:O4'	2.14	0.47
57:x:19:ASP:HA	64:x:801:GDP:O3A	2.15	0.47
8:A:40:U:H2'	8:A:41:C:C6	2.49	0.47
8:A:174:U:C2	8:A:175:G:C8	3.02	0.47
8:A:372:G:C8	31:X:60:LYS:HD2	2.49	0.47
8:A:656:G:H2'	8:A:657:U:C6	2.49	0.47
8:A:793:A:OP2	8:A:2071:A:O2'	2.29	0.47
8:A:1038:G:H2'	8:A:1039:A:H8	1.80	0.47
8:A:1174:U:H2'	8:A:1175:A:C4	2.48	0.47
8:A:1416:G:H2'	8:A:1417:C:C6	2.50	0.47
8:A:2519:U:H5'	8:A:2567:G:H21	1.79	0.47
10:C:66:PHE:HB3	10:C:150:GLY:O	2.14	0.47
34:a:413:G:N2	34:a:428:G:O3'	2.47	0.47
34:a:999:C:H2'	34:a:1000:A:C8	2.50	0.47
34:a:1092:A:H5''	40:g:3:ARG:NH1	2.29	0.47
34:a:1361:G:H2'	34:a:1362:A:C8	2.49	0.47
35:b:56:LEU:HD21	35:b:183:PHE:HZ	1.79	0.47
35:b:91:VAL:HG21	35:b:95:TRP:HE3	1.79	0.47
44:k:71:ASP:OD1	44:k:71:ASP:N	2.42	0.47
57:x:491:GLU:OE2	57:x:565:LEU:HB3	2.15	0.47
8:A:64:A:H2'	8:A:65:U:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1155:A:H5''	24:Q:54:ARG:HD3	1.96	0.47
8:A:2461:A:H2'	8:A:2462:C:H6	1.79	0.47
8:A:2474:U:O2	8:A:2474:U:H2'	2.15	0.47
8:A:2711:A:OP2	8:A:2714:G:OP2	2.32	0.47
34:a:457:G:N2	34:a:476:U:C2	2.83	0.47
34:a:656:G:H2'	34:a:657:U:C6	2.50	0.47
34:a:1146:A:H2'	34:a:1147:C:O4'	2.14	0.47
34:a:1315:U:C2	34:a:1319:A:N6	2.83	0.47
34:a:1345:U:O2'	34:a:1346:A:OP2	2.28	0.47
34:a:1513:A:H2'	34:a:1514:G:C8	2.49	0.47
36:c:73:GLY:O	36:c:77:GLY:N	2.47	0.47
37:d:167:PRO:HB2	37:d:170:LEU:HD23	1.96	0.47
43:j:22:THR:OG1	43:j:39:PRO:HB3	2.14	0.47
50:q:59:GLU:OE1	50:q:76:ARG:NH1	2.47	0.47
3:2:1:MET:N	8:A:1619:G:O2'	2.48	0.47
8:A:222:A:C2	8:A:233:A:H4'	2.50	0.47
8:A:242:G:O2'	8:A:243:U:P	2.72	0.47
8:A:863:A:O3'	9:B:100:G:N2	2.44	0.47
8:A:1484:U:H2'	8:A:1485:U:C6	2.50	0.47
8:A:1501:G:H2'	8:A:1502:A:C8	2.50	0.47
8:A:1505:A:H2'	8:A:1506:U:H6	1.79	0.47
8:A:1730:C:O2'	8:A:1731:G:O5'	2.32	0.47
8:A:1735:A:C6	8:A:1736:U:C4	3.03	0.47
8:A:1809:A:H2'	8:A:1810:A:C8	2.50	0.47
8:A:2557:G:H2'	8:A:2558:C:C6	2.49	0.47
16:I:79:LEU:HA	16:I:83:ALA:HB3	1.96	0.47
34:a:320:A:H2'	34:a:321:A:O4'	2.15	0.47
34:a:462:G:H3'	34:a:462:G:H8	1.80	0.47
35:b:212:TYR:O	35:b:216:VAL:HG23	2.14	0.47
57:x:74:MET:HE2	57:x:74:MET:HB3	1.68	0.47
57:x:342:VAL:HG23	57:x:346:ASP:HB2	1.96	0.47
8:A:181:A:H1'	8:A:435:C:H5'	1.95	0.47
8:A:242:G:H1'	8:A:243:U:H5	1.80	0.47
8:A:600:G:N2	8:A:605:G:O3'	2.48	0.47
8:A:636:G:O2'	8:A:638:G:O2'	2.26	0.47
8:A:680:C:H2'	8:A:681:G:C8	2.49	0.47
8:A:776:G:N7	8:A:793:A:O2'	2.46	0.47
8:A:877:A:H2	8:A:899:A:H2'	1.80	0.47
8:A:1717:A:N6	8:A:1743:G:O2'	2.45	0.47
8:A:2037:A:H2'	8:A:2038:G:C8	2.49	0.47
8:A:2185:U:H2'	8:A:2186:G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2425:A:H4'	8:A:2426:A:H5''	1.95	0.47
8:A:2512:C:H2'	8:A:2513:A:O4'	2.14	0.47
9:B:15:A:H3'	9:B:16:G:H8	1.80	0.47
9:B:104:A:H2'	9:B:105:G:O4'	2.15	0.47
10:C:85:ASN:HB2	10:C:86:ARG:HD2	1.96	0.47
19:L:95:LEU:HD11	19:L:125:LEU:HD21	1.97	0.47
34:a:21:G:H2'	34:a:22:G:C8	2.50	0.47
34:a:123:U:OP1	34:a:311:C:O2'	2.25	0.47
34:a:146:G:N1	34:a:177:G:C8	2.83	0.47
34:a:455:G:C2	34:a:478:A:C2	3.03	0.47
34:a:466:A:H2'	34:a:468:A:H5'	1.97	0.47
34:a:472:U:O2'	34:a:473:U:O4'	2.28	0.47
34:a:570:G:O3'	34:a:819:A:O2'	2.26	0.47
34:a:664:G:H2'	34:a:666:G:OP1	2.14	0.47
34:a:927:G:H21	34:a:1532:U:H5''	1.78	0.47
34:a:1041:G:H2'	34:a:1042:A:C8	2.49	0.47
34:a:1060:U:C5	36:c:1:GLY:HA2	2.50	0.47
35:b:29:PHE:CE2	35:b:48:MET:HE1	2.49	0.47
40:g:26:VAL:HG11	40:g:39:GLU:HG2	1.95	0.47
48:o:54:GLY:O	48:o:58:MET:HG3	2.14	0.47
5:4:2:LYS:HD2	5:4:4:ARG:HE	1.80	0.47
8:A:12:U:O2	8:A:2626:C:H4'	2.14	0.47
8:A:995:C:O2	24:Q:92:LYS:NZ	2.47	0.47
8:A:1143:A:N7	17:J:27:ARG:NH1	2.62	0.47
8:A:1357:C:H2'	8:A:1358:G:O4'	2.14	0.47
8:A:1703:G:H2'	8:A:1704:C:C6	2.50	0.47
8:A:2074:U:H2'	8:A:2075:U:C6	2.49	0.47
8:A:2627:G:N2	8:A:2777:G:OP2	2.37	0.47
8:A:2849:U:O2'	8:A:2866:U:O2	2.21	0.47
17:J:98:GLU:O	17:J:102:GLU:HG3	2.15	0.47
34:a:204:G:H2'	34:a:205:A:H4'	1.95	0.47
34:a:414:A:N7	34:a:430:A:N1	2.63	0.47
34:a:680:C:H2'	34:a:681:A:H8	1.79	0.47
34:a:985:C:C2	34:a:1221:G:N2	2.83	0.47
34:a:1238:A:H5'	34:a:1336:C:H41	1.80	0.47
35:b:62:ARG:O	35:b:63:LYS:C	2.55	0.47
38:e:14:LEU:HA	38:e:36:THR:HG22	1.97	0.47
38:e:80:LEU:HD11	38:e:95:MET:HB3	1.95	0.47
41:h:38:VAL:HG21	41:h:109:VAL:HG12	1.97	0.47
50:q:27:PHE:CZ	50:q:36:PHE:HB3	2.49	0.47
55:v:69:C:H2'	55:v:70:G:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:x:53:GLU:HA	57:x:56:GLN:HB2	1.95	0.47
57:x:430:MET:HE1	57:x:455:THR:HG21	1.97	0.47
8:A:156:A:H2'	8:A:157:C:C6	2.50	0.47
8:A:224:U:H2'	8:A:225:C:O4'	2.14	0.47
8:A:779:U:O2	8:A:785:G:O6	2.33	0.47
8:A:1028:A:N6	8:A:1125:G:H2'	2.30	0.47
8:A:1086:A:H5''	8:A:1087:G:O4'	2.14	0.47
8:A:1506:U:C2	8:A:1507:C:C5	3.02	0.47
10:C:132:ARG:O	10:C:166:ARG:NH2	2.36	0.47
26:S:92:ARG:HG2	26:S:93:ALA:H	1.80	0.47
34:a:362:G:N2	34:a:365:U:OP2	2.45	0.47
34:a:399:G:H2'	34:a:400:C:C6	2.50	0.47
34:a:509:A:H5'	37:d:50:TYR:HD2	1.80	0.47
34:a:523:A:N1	45:l:88:ASP:HB2	2.29	0.47
34:a:1244:G:H2'	34:a:1245:C:C6	2.49	0.47
35:b:69:VAL:HA	35:b:91:VAL:HG23	1.96	0.47
40:g:92:PRO:HA	40:g:95:ARG:HB2	1.96	0.47
40:g:132:THR:O	40:g:136:LYS:HE2	2.15	0.47
44:k:22:ILE:HD13	44:k:95:THR:OG1	2.14	0.47
46:m:10:ASP:HA	46:m:44:ILE:HB	1.96	0.47
46:m:86:ARG:HG3	52:s:72:GLU:OE2	2.15	0.47
49:p:1:MET:SD	49:p:66:THR:OG1	2.66	0.47
56:w:37:MIA:H163	59:z:4:U:O4	2.14	0.47
57:x:2:ARG:HE	57:x:377:ARG:HG2	1.79	0.47
57:x:557:GLN:HA	57:x:560:LEU:HD13	1.97	0.47
8:A:271:G:H1'	8:A:272:A:C8	2.50	0.47
8:A:555:G:HO2'	8:A:556:A:P	2.38	0.47
8:A:1098:A:C5	8:A:1099:G:C6	3.03	0.47
8:A:1268:A:H2'	8:A:1269:A:O4'	2.14	0.47
8:A:1790:C:H2'	8:A:1791:A:C5	2.49	0.47
8:A:2407:A:H2'	8:A:2408:U:C6	2.50	0.47
8:A:2836:U:H2'	8:A:2837:A:C8	2.50	0.47
8:A:2899:A:H2'	8:A:2900:A:C8	2.50	0.47
11:D:156:PHE:CD1	17:J:81:ILE:HD13	2.50	0.47
18:K:23:LYS:HB2	18:K:23:LYS:HE2	1.76	0.47
20:M:29:GLY:O	20:M:133:LYS:HE3	2.14	0.47
34:a:89:U:H5''	34:a:90:C:H5	1.79	0.47
34:a:176:C:H4'	53:t:23:ARG:HH21	1.80	0.47
34:a:188:C:O2'	34:a:189:A:O5'	2.33	0.47
34:a:1130:A:N3	34:a:1130:A:H2'	2.30	0.47
34:a:1198:G:H2'	34:a:1199:U:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:c:72:PRO:O	36:c:76:ILE:HD12	2.15	0.47
36:c:83:VAL:O	36:c:100:ILE:HD11	2.15	0.47
42:i:80:HIS:CE1	42:i:84:ARG:HD2	2.50	0.47
44:k:124:LYS:HG3	44:k:125:LYS:N	2.30	0.47
53:t:38:ILE:HG23	53:t:85:LEU:HD22	1.95	0.47
4:3:53:ASP:O	4:3:57:VAL:HG23	2.15	0.46
5:4:3:VAL:HG12	5:4:3:VAL:O	2.15	0.46
6:5:130:PRO:O	6:5:131:THR:C	2.57	0.46
8:A:1394:U:H4'	8:A:1603:A:H4'	1.96	0.46
8:A:2242:G:H2'	8:A:2243:U:O4'	2.15	0.46
8:A:2295:C:OP1	22:O:10:ARG:NH1	2.38	0.46
14:G:51:PHE:CZ	14:G:71:LEU:HD22	2.50	0.46
32:Y:46:VAL:O	32:Y:50:VAL:HG23	2.15	0.46
33:Z:6:ILE:HD13	33:Z:26:LEU:HD22	1.96	0.46
34:a:79:G:O2'	34:a:80:A:N3	2.46	0.46
34:a:429:U:O2'	37:d:21:LYS:NZ	2.47	0.46
34:a:784:A:H2'	34:a:785:G:H8	1.80	0.46
34:a:972:C:OP2	43:j:59:LYS:NZ	2.48	0.46
34:a:1284:C:OP2	34:a:1285:A:O2'	2.26	0.46
34:a:1347:G:O2'	34:a:1348:U:P	2.73	0.46
43:j:47:GLU:HG2	43:j:49:PHE:CZ	2.49	0.46
45:l:29:LYS:O	45:l:80:LEU:HD12	2.14	0.46
57:x:25:THR:O	57:x:26:THR:C	2.53	0.46
8:A:417:C:H2'	8:A:418:C:C6	2.49	0.46
8:A:600:G:H1'	12:E:100:MET:HG2	1.96	0.46
8:A:720:U:H2'	8:A:721:A:C8	2.50	0.46
8:A:1042:G:H2'	8:A:1043:C:C6	2.50	0.46
8:A:1260:A:H2'	8:A:1261:C:O4'	2.15	0.46
8:A:1796:U:H2'	8:A:1797:G:C8	2.51	0.46
8:A:2314:A:H2'	8:A:2315:G:H8	1.79	0.46
8:A:2554:U:H2'	8:A:2555:U:H6	1.79	0.46
10:C:180:MET:HB2	10:C:267:VAL:HB	1.98	0.46
10:C:266:ILE:HG21	10:C:269:ARG:HG2	1.98	0.46
34:a:98:A:H2'	34:a:99:C:C6	2.50	0.46
34:a:198:G:H2'	34:a:199:A:H8	1.79	0.46
34:a:551:U:H2'	34:a:552:U:C6	2.50	0.46
34:a:945:G:H21	34:a:1334:G:H4'	1.81	0.46
34:a:1058:G:H2'	34:a:1059:C:O4'	2.14	0.46
35:b:17:HIS:CE1	35:b:203:ASP:HB2	2.50	0.46
42:i:8:THR:O	42:i:84:ARG:HD3	2.15	0.46
55:v:62:C:H2'	55:v:63:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:175:G:H2'	8:A:176:A:C8	2.50	0.46
8:A:219:A:N3	8:A:234:U:O2'	2.33	0.46
8:A:1028:A:N3	8:A:2486:C:O2'	2.35	0.46
8:A:2345:G:N3	8:A:2381:A:H2'	2.31	0.46
20:M:6:ARG:O	20:M:6:ARG:HD3	2.15	0.46
25:R:51:VAL:O	25:R:52:PRO:C	2.54	0.46
34:a:211:G:H3'	34:a:211:G:N3	2.30	0.46
34:a:335:C:H2'	34:a:336:A:H8	1.80	0.46
34:a:920:U:H1'	34:a:1080:A:N1	2.30	0.46
34:a:945:G:C2	34:a:946:A:C8	3.03	0.46
37:d:12:ARG:HG3	37:d:37:PRO:HD3	1.96	0.46
37:d:170:LEU:HB2	37:d:172:VAL:HG23	1.97	0.46
47:n:64:CYS:SG	47:n:80:SER:HB3	2.55	0.46
48:o:35:ILE:HG13	48:o:58:MET:HE2	1.96	0.46
50:q:29:LYS:HB2	50:q:36:PHE:CE1	2.50	0.46
57:x:109:VAL:HG13	57:x:277:MET:HE2	1.97	0.46
5:4:16:ILE:HD13	5:4:25:VAL:HG22	1.96	0.46
7:6:26:SER:OG	7:6:27:THR:N	2.49	0.46
7:6:47:LYS:HB2	7:6:50:ASP:HA	1.97	0.46
8:A:504:A:H2'	8:A:504:A:N3	2.30	0.46
8:A:784:G:H5'	8:A:785:G:OP1	2.16	0.46
8:A:954:G:OP2	20:M:16:ARG:NH1	2.31	0.46
8:A:1000:A:OP2	8:A:1154:G:N1	2.31	0.46
8:A:1087:G:H21	8:A:1102:C:H5	1.64	0.46
8:A:1092:C:N4	8:A:1093:G:O6	2.48	0.46
8:A:2187:U:H2'	8:A:2188:U:C5	2.50	0.46
21:N:59:SER:O	21:N:63:ARG:HG2	2.15	0.46
27:T:58:VAL:HG22	27:T:85:VAL:HG13	1.95	0.46
34:a:196:A:N3	34:a:222:C:H1'	2.31	0.46
34:a:981:U:H2'	34:a:982:U:C5	2.50	0.46
43:j:82:LYS:HG3	43:j:83:THR:HG23	1.98	0.46
53:t:58:ASP:OD1	53:t:75:LYS:NZ	2.32	0.46
57:x:70:PHE:HA	57:x:81:HIS:O	2.15	0.46
57:x:138:ALA:O	57:x:263:VAL:HA	2.14	0.46
57:x:225:ALA:O	57:x:228:ALA:HB3	2.15	0.46
57:x:435:GLY:O	57:x:439:LYS:HG3	2.16	0.46
57:x:436:ARG:O	57:x:440:GLU:HG2	2.15	0.46
1:0:52:LYS:HE2	1:0:55:ALA:HA	1.96	0.46
8:A:571:U:C4	8:A:575:A:C5	3.03	0.46
8:A:579:G:O2'	8:A:2019:A:OP1	2.32	0.46
8:A:641:U:O4	8:A:647:G:O6	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1049:C:C2	8:A:1050:A:C8	3.04	0.46
8:A:1491:G:O2'	10:C:99:GLU:OE1	2.34	0.46
8:A:1545:A:H2'	8:A:1546:G:O4'	2.15	0.46
8:A:1796:U:H2'	8:A:1797:G:H8	1.80	0.46
8:A:2096:C:H2'	8:A:2097:A:H8	1.79	0.46
15:H:116:ARG:HH11	15:H:133:GLN:HB2	1.80	0.46
18:K:71:ARG:HH12	18:K:105:ARG:HB2	1.79	0.46
20:M:40:ARG:HB3	20:M:93:VAL:HB	1.98	0.46
20:M:53:MET:HE1	20:M:103:TYR:HB2	1.97	0.46
34:a:6:G:O2'	34:a:7:A:H8	1.98	0.46
34:a:373:A:H1'	34:a:481:G:H8	1.81	0.46
34:a:731:G:H5'	34:a:766:A:H4'	1.97	0.46
34:a:1258:G:H2'	34:a:1259:C:C6	2.50	0.46
54:u:40:PRO:HA	54:u:43:GLU:HG2	1.97	0.46
56:w:27:G:H2'	56:w:28:G:H8	1.79	0.46
57:x:312:ASP:HA	57:x:340:GLY:H	1.80	0.46
8:A:2117:A:H1'	8:A:2161:C:O3'	2.15	0.46
8:A:2250:G:H21	8:A:2250:G:P	2.39	0.46
8:A:2455:G:C4	8:A:2456:C:C5	3.03	0.46
9:B:8:C:OP1	22:O:15:ARG:NH2	2.47	0.46
9:B:52:A:N6	22:O:64:TYR:OH	2.34	0.46
21:N:96:ARG:O	21:N:113:ILE:HA	2.16	0.46
32:Y:21:LEU:HB3	32:Y:50:VAL:HG22	1.98	0.46
34:a:33:A:H2'	34:a:34:C:H6	1.80	0.46
34:a:258:G:C4	34:a:259:G:C8	3.03	0.46
34:a:594:U:H2'	34:a:595:A:O4'	2.15	0.46
42:i:79:ARG:O	42:i:83:THR:HG23	2.16	0.46
44:k:22:ILE:HD12	44:k:85:VAL:HG22	1.97	0.46
45:l:45:ASN:ND2	45:l:88:ASP:OD1	2.49	0.46
57:x:254:ARG:O	57:x:259:GLU:HG2	2.16	0.46
6:5:34:THR:O	6:5:38:MET:CB	2.64	0.46
8:A:138:U:O2'	8:A:141:G:O6	2.26	0.46
8:A:521:U:O4	8:A:522:A:N6	2.48	0.46
8:A:641:U:O2'	8:A:2350:C:OP1	2.34	0.46
8:A:1118:C:H2'	8:A:1119:U:O4'	2.15	0.46
8:A:1504:A:H2'	8:A:1505:A:C8	2.50	0.46
8:A:2331:G:O2'	8:A:2336:A:N1	2.42	0.46
11:D:46:ARG:HB2	11:D:84:LEU:HB2	1.98	0.46
19:L:109:LYS:HZ3	19:L:128:THR:HG22	1.80	0.46
29:V:55:GLU:HB2	29:V:59:GLU:HG3	1.97	0.46
34:a:676:A:H2'	34:a:677:U:H6	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1140:C:H2'	34:a:1141:C:C6	2.51	0.46
34:a:1176:A:H3'	34:a:1177:G:H8	1.79	0.46
37:d:58:GLN:HE21	37:d:62:ARG:NH2	2.13	0.46
48:o:1:SER:O	48:o:1:SER:OG	2.28	0.46
50:q:46:HIS:HA	50:q:70:LYS:HE3	1.97	0.46
55:v:39:C:C2'	55:v:40:C:H5'	2.46	0.46
1:0:4:GLN:O	8:A:2017:U:H4'	2.16	0.46
2:1:8:ILE:HD13	2:1:24:LYS:HB2	1.98	0.46
8:A:175:G:H2'	8:A:176:A:H8	1.81	0.46
8:A:194:G:H2'	8:A:195:A:O4'	2.16	0.46
8:A:244:A:H2'	8:A:245:G:O4'	2.15	0.46
8:A:368:A:H2'	8:A:369:U:O4'	2.16	0.46
8:A:1360:G:C8	8:A:1361:G:C8	3.04	0.46
8:A:1468:U:H2'	8:A:1522:A:H61	1.80	0.46
8:A:1842:G:H2'	8:A:1843:C:C6	2.50	0.46
8:A:2287:A:C5	8:A:2289:G:C8	3.03	0.46
8:A:2685:G:H2'	8:A:2686:G:H8	1.81	0.46
14:G:148:ARG:HA	14:G:161:VAL:HB	1.98	0.46
15:H:54:LEU:O	15:H:58:LEU:HG	2.15	0.46
23:P:26:GLU:OE2	23:P:84:SER:OG	2.34	0.46
26:S:70:LYS:HD2	26:S:110:ARG:HD2	1.96	0.46
30:W:59:ALA:O	30:W:78:ILE:HG21	2.16	0.46
33:Z:38:GLU:H	33:Z:38:GLU:CD	2.24	0.46
34:a:8:A:N6	37:d:205:LYS:HB2	2.31	0.46
34:a:596:A:N6	34:a:645:G:C6	2.84	0.46
34:a:985:C:C2	34:a:1221:G:C2	3.04	0.46
34:a:1181:G:H1'	34:a:1182:G:C4	2.50	0.46
34:a:1402:4OC:HM23	34:a:1402:4OC:H1'	1.78	0.46
49:p:37:GLY:HA3	49:p:51:ARG:O	2.15	0.46
52:s:27:LYS:HG3	52:s:47:THR:CG2	2.46	0.46
53:t:3:ILE:HG22	53:t:4:LYS:HD2	1.98	0.46
55:v:64:G:H2'	55:v:65:C:H6	1.80	0.46
57:x:187:MET:HE1	57:x:218:HIS:CG	2.51	0.46
8:A:221:A:C4	8:A:266:G:N7	2.84	0.46
8:A:756:A:H2'	8:A:757:G:O4'	2.16	0.46
8:A:1223:G:OP1	25:R:68:ARG:NH2	2.49	0.46
8:A:1501:G:H2'	8:A:1502:A:H8	1.81	0.46
8:A:1532:A:N6	8:A:1540:G:C6	2.83	0.46
8:A:1570:A:H2'	8:A:1571:A:C8	2.51	0.46
34:a:376:G:H4'	49:p:5:ARG:HD2	1.98	0.46
34:a:474:G:H2'	34:a:475:C:H6	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1111:A:N6	36:c:175:HIS:O	2.49	0.46
34:a:1413:A:H2	34:a:1487:G:H22	1.63	0.46
39:f:69:GLU:HG2	39:f:70:VAL:N	2.31	0.46
8:A:674:G:H1'	12:E:69:ARG:HD3	1.98	0.46
8:A:783:A:H2'	8:A:784:G:H4'	1.98	0.46
8:A:1178:C:H2'	8:A:1180:U:C6	2.51	0.46
8:A:1416:G:H2'	8:A:1417:C:H6	1.80	0.46
8:A:1465:G:H2'	8:A:1466:U:O4'	2.17	0.46
8:A:1631:G:N2	8:A:1634:A:OP2	2.49	0.46
8:A:1779:U:H5	8:A:1784:A:N7	2.13	0.46
8:A:2743:U:H2'	8:A:2744:G:O4'	2.16	0.46
18:K:75:SER:OG	23:P:72:VAL:O	2.12	0.46
20:M:59:ARG:HA	20:M:59:ARG:HD3	1.83	0.46
20:M:117:PHE:HD2	20:M:130:PHE:CD1	2.33	0.46
22:O:99:TYR:OH	22:O:111:ARG:NH2	2.49	0.46
33:Z:8:GLN:HB2	33:Z:28:LEU:HD13	1.98	0.46
34:a:264:C:H2'	34:a:265:G:O4'	2.16	0.46
34:a:600:A:H2'	34:a:601:G:C8	2.51	0.46
34:a:689:C:O2'	34:a:690:G:OP1	2.31	0.46
34:a:893:C:C4	34:a:894:G:N7	2.83	0.46
36:c:179:ALA:HB1	36:c:202:PHE:HE1	1.81	0.46
46:m:44:ILE:HD13	46:m:47:LEU:HD12	1.97	0.46
7:6:41:HIS:CE1	7:6:43:PHE:HB3	2.51	0.45
8:A:1196:C:H2'	8:A:1197:G:H8	1.80	0.45
8:A:1196:C:H2'	8:A:1197:G:C8	2.52	0.45
8:A:1889:A:H2'	8:A:1890:A:C8	2.50	0.45
8:A:2297:A:N1	8:A:2321:U:H5	2.14	0.45
8:A:2306:C:OP2	8:A:2307:G:O2'	2.23	0.45
8:A:2473:U:O4'	57:x:636:ARG:HA	2.15	0.45
11:D:98:VAL:HG22	11:D:180:VAL:HG13	1.98	0.45
12:E:145:ASP:OD1	12:E:183:PHE:HD1	1.98	0.45
13:F:127:TYR:CE2	13:F:129:MET:HB3	2.51	0.45
15:H:9:VAL:H	15:H:13:GLY:CA	2.26	0.45
28:U:3:LYS:HD3	28:U:82:VAL:HB	1.97	0.45
34:a:263:A:H2'	34:a:264:C:C5	2.51	0.45
34:a:440:C:H2'	34:a:441:A:C8	2.51	0.45
34:a:470:C:H2'	34:a:471:U:O2	2.16	0.45
34:a:472:U:O2'	34:a:473:U:O5'	2.34	0.45
34:a:1048:G:OP1	47:n:2:LYS:N	2.50	0.45
34:a:1055:A:O2'	36:c:160:GLU:O	2.29	0.45
34:a:1308:U:OP1	46:m:96:VAL:N	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1320:C:H41	52:s:36:ARG:HB3	1.80	0.45
36:c:86:LEU:HA	36:c:89:VAL:HG12	1.98	0.45
48:o:87:ARG:HD2	48:o:87:ARG:HA	1.66	0.45
49:p:3:THR:HG23	49:p:66:THR:HB	1.98	0.45
49:p:56:ARG:HH21	49:p:59:HIS:CG	2.35	0.45
50:q:30:HIS:HE1	50:q:32:ILE:HD12	1.79	0.45
57:x:337:VAL:HG21	57:x:376:VAL:HG13	1.98	0.45
4:3:18:LYS:HB2	8:A:651:G:OP1	2.16	0.45
8:A:141:G:H5''	8:A:1595:C:O2'	2.15	0.45
8:A:376:G:H2'	8:A:377:G:C8	2.52	0.45
8:A:417:C:H2'	8:A:418:C:H6	1.80	0.45
8:A:684:G:C2	8:A:794:A:C2	3.04	0.45
8:A:1249:U:H2'	19:L:18:ARG:HH12	1.82	0.45
8:A:1571:A:H2'	8:A:1572:A:H8	1.81	0.45
13:F:11:VAL:HG21	13:F:172:PHE:CE1	2.51	0.45
34:a:339:C:H2'	34:a:340:U:C6	2.51	0.45
34:a:514:C:C2'	34:a:515:G:H5'	2.47	0.45
34:a:602:A:H2'	34:a:603:U:O2	2.17	0.45
34:a:727:G:N2	34:a:730:G:OP2	2.43	0.45
34:a:733:G:O2'	34:a:734:G:OP1	2.27	0.45
34:a:999:C:O2'	34:a:1000:A:H5'	2.17	0.45
34:a:1232:U:H5'	42:i:125:GLN:HB3	1.98	0.45
35:b:23:ASN:H	35:b:189:ASN:HA	1.82	0.45
35:b:64:GLY:O	35:b:65:LYS:C	2.59	0.45
38:e:59:ILE:O	38:e:63:MET:HG2	2.16	0.45
38:e:79:THR:HG22	38:e:121:ASN:O	2.15	0.45
43:j:8:ILE:HB	43:j:74:VAL:HB	1.98	0.45
43:j:29:ALA:HB1	43:j:36:VAL:HG21	1.98	0.45
46:m:3:ILE:HD12	46:m:55:LEU:HB3	1.98	0.45
57:x:190:ILE:HD11	57:x:201:PHE:CB	2.44	0.45
7:6:17:SER:HB3	7:6:52:ALA:HB1	1.97	0.45
8:A:419:U:H2'	8:A:420:C:H6	1.80	0.45
8:A:1317:G:H2'	8:A:1318:U:C6	2.51	0.45
8:A:1532:A:C6	8:A:1540:G:C6	3.05	0.45
8:A:2628:C:O2'	8:A:2782:G:OP1	2.26	0.45
19:L:20:GLY:HA2	19:L:28:GLY:O	2.17	0.45
34:a:62:U:O2'	34:a:379:C:O2	2.34	0.45
34:a:413:G:H1'	34:a:428:G:N2	2.30	0.45
34:a:429:U:H4'	34:a:430:A:C5'	2.46	0.45
34:a:575:G:HO2'	34:a:821:G:H5'	1.81	0.45
34:a:1122:U:H2'	34:a:1123:U:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1125:U:O2'	43:j:7:ARG:NH1	2.40	0.45
34:a:1447:A:H3'	34:a:1448:C:H6	1.81	0.45
37:d:149:LYS:O	37:d:150:LYS:C	2.60	0.45
46:m:40:GLU:HG2	46:m:41:ASP:N	2.31	0.45
57:x:232:LEU:HA	57:x:232:LEU:HD12	1.66	0.45
3:2:4:THR:HG22	8:A:687:C:H1'	1.98	0.45
7:6:56:ARG:O	7:6:58:ASP:N	2.50	0.45
8:A:30:G:H2'	8:A:31:C:H6	1.82	0.45
8:A:283:G:H2'	8:A:284:U:C6	2.52	0.45
8:A:667:U:H2'	8:A:668:A:O4'	2.16	0.45
8:A:1079:C:H4'	8:A:1080:A:N7	2.31	0.45
8:A:1587:G:H2'	8:A:1588:G:C8	2.52	0.45
8:A:2096:C:H2'	8:A:2097:A:C8	2.51	0.45
8:A:2803:G:H2'	8:A:2804:U:C6	2.52	0.45
25:R:6:GLN:HB3	25:R:11:GLN:HG2	1.98	0.45
29:V:21:ARG:HA	29:V:25:LYS:O	2.16	0.45
34:a:374:A:O2'	34:a:451:A:OP2	2.33	0.45
34:a:592:G:C6	34:a:648:A:C6	3.04	0.45
34:a:618:C:H5'	34:a:619:U:H5''	1.98	0.45
34:a:1240:U:P	40:g:115:MET:HB2	2.56	0.45
36:c:7:ASN:O	36:c:11:LEU:N	2.49	0.45
36:c:84:GLU:O	36:c:88:LYS:HG2	2.16	0.45
37:d:98:ASP:OD1	37:d:99:ASN:N	2.50	0.45
40:g:132:THR:HG23	40:g:136:LYS:HZ1	1.80	0.45
44:k:30:ILE:HG12	44:k:45:THR:HG22	1.98	0.45
57:x:552:VAL:HG22	57:x:592:PHE:HB3	1.98	0.45
1:0:21:LEU:HD11	26:S:41:LYS:HE3	1.98	0.45
8:A:121:G:H2'	8:A:122:G:H8	1.80	0.45
8:A:160:A:N3	8:A:2208:C:O2'	2.42	0.45
8:A:568:U:H1'	8:A:2030:6MZ:H9C1	1.98	0.45
8:A:904:G:H2'	8:A:905:A:C8	2.52	0.45
8:A:1361:G:H2'	8:A:1362:C:H6	1.81	0.45
8:A:1406:U:C2	8:A:1407:G:C8	3.05	0.45
8:A:1434:A:H2'	8:A:1435:G:C8	2.51	0.45
8:A:1484:U:H2'	8:A:1485:U:H6	1.81	0.45
8:A:1490:A:HO2'	8:A:1491:G:P	2.38	0.45
8:A:1709:U:H2'	8:A:1710:G:C8	2.51	0.45
8:A:2295:C:P	22:O:9:ARG:HH22	2.40	0.45
9:B:39:A:H2'	9:B:40:U:C6	2.51	0.45
10:C:77:VAL:HG21	10:C:109:LEU:HD21	1.97	0.45
10:C:261:ARG:O	10:C:264:LYS:NZ	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:G:98:LYS:HZ2	14:G:103:ASN:HB2	1.81	0.45
15:H:8:LYS:NZ	15:H:60:GLU:OE1	2.49	0.45
31:X:31:ASN:OD1	31:X:33:HIS:NE2	2.48	0.45
34:a:855:U:OP2	34:a:871:U:N3	2.29	0.45
34:a:945:G:H2'	34:a:946:A:H5'	1.98	0.45
34:a:1088:G:N2	34:a:1167:A:H61	2.15	0.45
34:a:1099:G:H2'	34:a:1100:C:O4'	2.16	0.45
34:a:1222:G:H5''	52:s:77:ARG:HH11	1.81	0.45
40:g:100:MET:O	40:g:104:VAL:HG22	2.17	0.45
46:m:10:ASP:O	46:m:12:LYS:HG2	2.16	0.45
47:n:66:GLN:HG3	47:n:79:LEU:HD22	1.99	0.45
56:w:36:A:N6	56:w:37:MIA:H122	2.30	0.45
57:x:246:GLU:O	57:x:250:ALA:CB	2.65	0.45
1:0:42:ILE:HG22	1:0:48:TYR:HB2	1.97	0.45
8:A:17:G:H2'	8:A:18:U:C6	2.51	0.45
8:A:150:U:H2'	8:A:151:C:C6	2.51	0.45
8:A:635:C:H2'	8:A:636:G:O4'	2.17	0.45
8:A:657:U:H2'	8:A:658:U:C6	2.51	0.45
8:A:1116:G:O2'	8:A:1117:C:H5'	2.17	0.45
8:A:2022:U:O2'	8:A:2617:U:H5'	2.17	0.45
8:A:2376:A:N3	22:O:111:ARG:NH1	2.52	0.45
34:a:75:G:C6	34:a:76:G:C6	3.04	0.45
34:a:105:G:H2'	34:a:106:C:C6	2.51	0.45
34:a:340:U:H2'	34:a:341:C:H6	1.82	0.45
34:a:1326:U:H2'	34:a:1327:C:H6	1.81	0.45
35:b:14:HIS:CE1	35:b:211:LEU:HD22	2.51	0.45
36:c:52:SER:OG	36:c:111:ASP:OD1	2.33	0.45
36:c:133:MET:HE2	36:c:167:TYR:CD2	2.50	0.45
37:d:12:ARG:HB2	37:d:33:ILE:O	2.17	0.45
37:d:29:THR:HG23	37:d:30:LYS:HG3	1.97	0.45
40:g:43:TYR:O	40:g:47:GLU:HG2	2.17	0.45
56:w:15:G:N2	56:w:21:A:H1'	2.30	0.45
56:w:28:G:H2'	56:w:29:G:H8	1.82	0.45
57:x:521:MET:HE2	57:x:573:MET:HE1	1.99	0.45
57:x:597:SER:O	57:x:601:LYS:HG2	2.17	0.45
57:x:615:ILE:HG22	57:x:656:GLU:HB3	1.99	0.45
8:A:52:A:H2'	8:A:53:A:C8	2.52	0.45
8:A:411:G:OP2	8:A:2406:A:O2'	2.24	0.45
8:A:471:A:H2'	8:A:472:A:O4'	2.17	0.45
8:A:753:A:H2'	8:A:754:U:C6	2.52	0.45
8:A:799:G:OP2	8:A:800:A:O2'	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:851:C:H2'	8:A:852:U:C6	2.52	0.45
8:A:911:A:N6	20:M:11:LYS:O	2.42	0.45
8:A:1028:A:H2'	8:A:1029:A:H8	1.81	0.45
8:A:1847:G:HO2'	8:A:1848:A:P	2.39	0.45
8:A:2081:U:H2'	8:A:2082:A:H8	1.81	0.45
8:A:2102:G:O6	8:A:2187:U:O4	2.35	0.45
8:A:2794:C:H2'	8:A:2795:C:C6	2.52	0.45
9:B:60:C:H2'	9:B:61:G:H8	1.82	0.45
11:D:114:LYS:HE3	11:D:196:ALA:HB2	1.98	0.45
15:H:12:LEU:HB3	15:H:19:VAL:HG11	1.99	0.45
18:K:66:LYS:HB3	18:K:66:LYS:HE2	1.80	0.45
22:O:82:ALA:HB3	22:O:115:LEU:HD11	1.98	0.45
28:U:6:ARG:NH2	28:U:7:ASP:OD1	2.50	0.45
28:U:80:ASP:HB3	28:U:95:PHE:HD2	1.81	0.45
34:a:203:G:H3'	34:a:205:A:OP2	2.16	0.45
34:a:513:C:H2'	34:a:514:C:C6	2.51	0.45
34:a:741:G:OP1	48:o:34:GLN:NE2	2.49	0.45
34:a:921:U:O5'	34:a:1082:A:C5'	2.64	0.45
34:a:1134:G:O2'	34:a:1135:U:O4'	2.24	0.45
34:a:1248:A:H2'	34:a:1249:C:C6	2.52	0.45
34:a:1374:A:O2'	40:g:27:ASN:HB3	2.17	0.45
48:o:77:TYR:O	48:o:81:ILE:HG23	2.16	0.45
52:s:16:LYS:HE2	52:s:20:LYS:HZ1	1.82	0.45
52:s:49:ALA:HB1	52:s:56:HIS:HB3	1.99	0.45
53:t:66:ILE:HB	53:t:70:LYS:HD3	1.99	0.45
8:A:95:A:H2'	8:A:96:C:O4'	2.16	0.45
8:A:118:A:N3	8:A:178:G:H1'	2.31	0.45
8:A:324:A:H2'	8:A:325:G:O4'	2.16	0.45
8:A:388:G:O6	8:A:390:U:O2'	2.22	0.45
8:A:491:G:O6	26:S:49:LYS:NZ	2.42	0.45
8:A:645:C:H2'	8:A:647:G:N7	2.31	0.45
8:A:773:U:O2	8:A:778:G:O2'	2.31	0.45
8:A:941:A:H2'	8:A:942:G:O4'	2.17	0.45
8:A:1720:U:H2'	8:A:1721:G:O4'	2.17	0.45
8:A:2168:G:O6	8:A:2171:A:H2	1.99	0.45
8:A:2804:U:H2'	8:A:2805:C:H6	1.82	0.45
10:C:141:HIS:N	10:C:190:THR:O	2.42	0.45
10:C:204:LEU:HB3	10:C:209:ALA:HB3	1.99	0.45
14:G:102:ILE:HD12	14:G:147:LEU:HD21	1.99	0.45
20:M:56:ALA:HB2	20:M:119:LEU:HD12	1.98	0.45
29:V:51:GLN:OE1	29:V:79:ARG:NH2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:407:U:H2'	34:a:408:A:C8	2.51	0.45
34:a:779:C:H2'	34:a:780:A:O4'	2.17	0.45
34:a:1130:A:OP1	42:i:17:ARG:NH2	2.49	0.45
34:a:1152:A:P	43:j:72:ARG:HH22	2.40	0.45
35:b:44:LYS:O	35:b:47:PRO:HD2	2.17	0.45
43:j:5:ARG:NH1	43:j:78:GLU:HA	2.31	0.45
56:w:44:G:O2'	56:w:45:U:H5'	2.16	0.45
8:A:1341:G:H1'	27:T:59:ASN:HB3	1.99	0.45
8:A:1485:U:H2'	8:A:1486:U:C6	2.52	0.45
8:A:1771:C:H2'	8:A:1772:A:H8	1.81	0.45
8:A:1860:G:H2'	8:A:1861:G:O4'	2.16	0.45
8:A:1927:A:H2'	8:A:1928:A:C8	2.51	0.45
8:A:2062:A:H2	8:A:2063:C:C6	2.34	0.45
8:A:2204:G:H4'	10:C:149:LYS:HD3	1.99	0.45
8:A:2451:A:H1'	56:w:76:A:H2'	1.98	0.45
8:A:2808:G:O2'	8:A:2809:A:H8	1.98	0.45
9:B:13:G:N2	9:B:16:G:N3	2.64	0.45
13:F:32:LYS:HD3	13:F:91:ARG:NH1	2.32	0.45
14:G:83:THR:HG23	14:G:133:LYS:HG2	1.99	0.45
17:J:122:LEU:HG	17:J:124:VAL:HG23	1.98	0.45
22:O:49:VAL:HA	60:O:201:MG:MG	1.40	0.45
26:S:11:ARG:HH21	26:S:98:LYS:HD2	1.82	0.45
26:S:86:MET:HB3	26:S:94:ASP:HB2	1.99	0.45
34:a:6:G:O6	38:e:99:SER:N	2.50	0.45
34:a:986:U:H2'	34:a:987:G:C8	2.52	0.45
34:a:1327:C:H2'	34:a:1328:C:C6	2.52	0.45
34:a:1375:A:H2'	34:a:1376:U:O4'	2.17	0.45
34:a:1477:U:H2'	34:a:1478:U:O4'	2.17	0.45
35:b:99:MET:N	35:b:174:GLU:OE2	2.50	0.45
36:c:71:ARG:HD3	36:c:74:ILE:HD11	1.99	0.45
41:h:7:ALA:O	41:h:11:THR:HG23	2.16	0.45
41:h:42:GLU:HG2	41:h:100:ILE:HG21	1.98	0.45
57:x:2:ARG:NH2	57:x:312:ASP:OD2	2.50	0.45
57:x:179:THR:HA	57:x:272:LYS:HE3	1.97	0.45
57:x:698:ILE:HG13	57:x:699:GLU:H	1.82	0.45
1:0:53:VAL:HG23	1:0:54:ILE:HG12	1.99	0.45
6:5:54:VAL:H	8:A:1083:U:P	2.40	0.45
8:A:468:G:H5''	12:E:55:SER:HB3	1.98	0.45
8:A:675:A:N3	8:A:2443:C:O2'	2.42	0.45
8:A:1359:A:H62	8:A:1372:U:H3	1.65	0.45
8:A:2113:U:O4	55:v:20:U:H5'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2562:U:H4'	18:K:25:LEU:HD22	1.99	0.45
9:B:113:C:H1'	22:O:46:GLU:HA	1.99	0.45
13:F:56:LEU:HA	13:F:59:ILE:HG22	1.99	0.45
13:F:59:ILE:HD12	13:F:151:LEU:HD21	1.98	0.45
15:H:8:LYS:HA	15:H:13:GLY:HA3	1.99	0.45
28:U:52:ASN:C	28:U:54:PRO:HD3	2.42	0.45
34:a:590:U:H2'	34:a:591:U:C6	2.52	0.45
34:a:925:G:C2	34:a:927:G:C8	3.04	0.45
34:a:1531:A:H2'	34:a:1532:U:C6	2.52	0.45
37:d:160:LEU:O	37:d:164:ARG:HD3	2.17	0.45
47:n:25:GLU:O	47:n:29:ILE:HG13	2.17	0.45
55:v:16:C:O2'	55:v:61:C:OP1	2.33	0.45
57:x:14:ILE:HD11	57:x:26:THR:OG1	2.17	0.45
57:x:506:LYS:HB2	57:x:506:LYS:HE3	1.63	0.45
57:x:638:ARG:HE	57:x:638:ARG:HB2	1.43	0.45
3:2:37:LYS:HE3	8:A:458:G:N7	2.32	0.44
5:4:24:ARG:HH12	8:A:2742:G:P	2.38	0.44
8:A:182:A:H2'	8:A:183:C:H6	1.82	0.44
8:A:607:U:O2	8:A:608:A:C8	2.69	0.44
8:A:1093:G:C5	8:A:1094:U:C2	3.06	0.44
8:A:1109:C:H2'	8:A:1110:G:O4'	2.16	0.44
8:A:1295:C:C2	8:A:1296:G:C8	3.05	0.44
8:A:1313:U:O2'	8:A:1332:G:O4'	2.35	0.44
8:A:1628:G:H2'	8:A:1629:U:C6	2.52	0.44
8:A:1841:U:C2	8:A:1842:G:C8	3.05	0.44
8:A:1889:A:H2'	8:A:1890:A:H8	1.82	0.44
8:A:1928:A:H2'	8:A:1929:G:O4'	2.16	0.44
8:A:2690:U:O2'	8:A:2872:A:H1'	2.17	0.44
8:A:2723:C:P	11:D:114:LYS:HZ3	2.38	0.44
8:A:2757:A:N1	14:G:66:THR:OG1	2.46	0.44
34:a:564:C:OP1	45:l:11:ARG:NE	2.50	0.44
34:a:667:G:H4'	48:o:50:HIS:ND1	2.32	0.44
34:a:867:G:O2'	34:a:873:A:N1	2.35	0.44
34:a:1221:G:H5''	34:a:1321:U:O2	2.16	0.44
34:a:1456:A:H2'	34:a:1457:G:O4'	2.16	0.44
35:b:77:GLU:CD	35:b:77:GLU:H	2.25	0.44
38:e:45:VAL:HG23	38:e:116:VAL:HG23	1.99	0.44
41:h:12:ARG:HB3	41:h:24:VAL:HG11	1.98	0.44
44:k:49:SER:HB3	44:k:68:ARG:HD3	1.99	0.44
56:w:36:A:H2'	56:w:37:MIA:H8	1.99	0.44
57:x:117:GLY:HA2	57:x:153:VAL:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:6:5:ILE:HG13	7:6:6:HIS:CD2	2.52	0.44
7:6:10:GLU:H	7:6:10:GLU:CD	2.25	0.44
7:6:11:GLU:HA	7:6:25:ARG:HA	1.98	0.44
8:A:715:A:H2	48:o:39:GLN:HE22	1.65	0.44
8:A:856:G:H2'	8:A:857:G:C8	2.51	0.44
8:A:1437:C:H2'	8:A:1438:U:C6	2.52	0.44
8:A:2050:C:H2'	8:A:2051:A:O4'	2.16	0.44
8:A:2079:U:H2'	8:A:2080:A:O4'	2.17	0.44
8:A:2461:A:H1'	8:A:2492:U:C2	2.52	0.44
8:A:2513:A:H2'	8:A:2514:U:C6	2.52	0.44
15:H:87:GLU:OE2	39:f:83:ALA:HB2	2.17	0.44
15:H:101:ASP:HA	15:H:107:GLY:CA	2.43	0.44
19:L:96:LYS:HG3	19:L:101:ILE:HD11	1.98	0.44
24:Q:46:TYR:O	24:Q:50:ARG:NH1	2.47	0.44
34:a:134:G:H2'	34:a:135:C:O4'	2.17	0.44
34:a:298:A:H2'	34:a:299:G:O4'	2.18	0.44
34:a:299:G:H2'	34:a:300:A:C8	2.52	0.44
34:a:593:U:H2'	34:a:594:U:H6	1.81	0.44
34:a:673:A:H4'	39:f:86:ARG:CZ	2.47	0.44
34:a:985:C:C2	34:a:986:U:C5	3.06	0.44
34:a:1244:G:C6	34:a:1294:G:N1	2.85	0.44
34:a:1251:A:H2'	34:a:1252:A:C8	2.52	0.44
34:a:1282:C:C2	34:a:1283:U:C5	3.05	0.44
34:a:1412:C:H2'	34:a:1413:A:C8	2.52	0.44
39:f:19:PRO:HA	39:f:22:ILE:HD12	1.99	0.44
46:m:21:ILE:HB	46:m:24:VAL:CG1	2.47	0.44
57:x:55:GLU:C	57:x:57:GLU:H	2.22	0.44
6:5:94:ARG:O	6:5:98:GLU:N	2.45	0.44
8:A:132:G:H2'	8:A:133:U:H6	1.82	0.44
8:A:181:A:H2'	8:A:182:A:C8	2.52	0.44
8:A:2314:A:H2'	8:A:2315:G:C8	2.52	0.44
8:A:2392:A:C2	19:L:55:MET:HG2	2.53	0.44
8:A:2655:G:O2'	8:A:2664:G:O6	2.26	0.44
9:B:106:G:H2'	9:B:107:G:O4'	2.17	0.44
18:K:92:GLU:OE2	18:K:111:LYS:HB3	2.17	0.44
21:N:44:LEU:O	21:N:48:VAL:HG22	2.18	0.44
21:N:79:LEU:HD23	21:N:83:LEU:HB2	2.00	0.44
29:V:80:HIS:CD2	29:V:81:PRO:HD2	2.53	0.44
34:a:9:G:H4'	38:e:108:GLY:H	1.83	0.44
34:a:464:U:H2'	34:a:465:A:H8	1.82	0.44
34:a:1007:U:H3	34:a:1023:U:H1'	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1217:C:P	47:n:8:ARG:HE	2.41	0.44
34:a:1269:A:N3	34:a:1326:U:H1'	2.32	0.44
35:b:182:VAL:O	35:b:196:ASP:N	2.44	0.44
39:f:46:GLN:HA	39:f:56:LYS:HA	2.00	0.44
40:g:77:ARG:NE	40:g:86:VAL:HG21	2.31	0.44
46:m:99:GLN:OE1	46:m:99:GLN:N	2.50	0.44
57:x:168:LEU:HB3	57:x:262:LEU:HD22	1.99	0.44
57:x:563:GLY:HA2	57:x:564:PRO:HD3	1.83	0.44
8:A:283:G:H2'	8:A:284:U:H6	1.83	0.44
8:A:429:A:H2'	8:A:430:A:C8	2.52	0.44
8:A:499:U:H2'	8:A:500:G:O4'	2.17	0.44
8:A:655:A:H4'	8:A:656:G:H5'	1.99	0.44
8:A:1427:A:H4'	8:A:1428:C:O4'	2.17	0.44
8:A:1567:G:H3'	10:C:84:PRO:HG3	1.99	0.44
8:A:1965:C:OP1	8:A:1966:A:O2'	2.31	0.44
8:A:2340:A:H2'	8:A:2341:G:C8	2.53	0.44
8:A:2751:G:C4	14:G:2:ARG:HD2	2.53	0.44
8:A:2806:C:H2'	8:A:2807:U:O4'	2.18	0.44
10:C:66:PHE:CE1	10:C:155:ARG:HD2	2.52	0.44
29:V:75:GLN:HB3	29:V:90:ASP:HB2	1.98	0.44
34:a:322:C:O2	34:a:332:G:N2	2.50	0.44
34:a:634:C:H2'	34:a:635:A:C8	2.53	0.44
34:a:1011:C:N4	34:a:1019:A:C6	2.85	0.44
34:a:1027:C:C4	34:a:1028:C:C2	3.05	0.44
34:a:1182:G:O2'	34:a:1183:U:H5''	2.17	0.44
34:a:1225:A:H5''	34:a:1226:C:OP2	2.18	0.44
41:h:104:SER:HB2	41:h:125:ILE:HD11	1.98	0.44
44:k:80:ASN:OD1	44:k:80:ASN:N	2.49	0.44
57:x:403:ILE:HG22	57:x:404:ILE:N	2.33	0.44
57:x:583:HIS:HD2	57:x:586:ASP:H	1.64	0.44
5:4:36:ARG:HG2	5:4:37:GLN:HB3	1.99	0.44
8:A:247:G:N2	8:A:250:G:H3'	2.32	0.44
8:A:320:A:H4'	8:A:322:A:N7	2.32	0.44
8:A:804:A:H2'	8:A:806:C:C4	2.53	0.44
8:A:1317:G:H2'	8:A:1318:U:O4'	2.17	0.44
8:A:1339:G:OP2	27:T:15:HIS:NE2	2.51	0.44
8:A:1370:C:H4'	10:C:44:ASN:HD21	1.82	0.44
8:A:1667:G:N2	8:A:1992:G:OP2	2.35	0.44
8:A:2494:G:O2'	20:M:79:ALA:HA	2.18	0.44
13:F:113:PHE:CZ	13:F:115:GLY:HA2	2.52	0.44
17:J:11:VAL:HG11	17:J:50:THR:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:S:86:MET:HB2	26:S:96:ILE:HG12	2.00	0.44
32:Y:19:LEU:HD12	32:Y:19:LEU:HA	1.66	0.44
34:a:537:G:H2'	34:a:538:G:H8	1.83	0.44
34:a:1249:C:H41	34:a:1287:A:H5'	1.82	0.44
34:a:1316:G:N7	52:s:6:LYS:NZ	2.66	0.44
34:a:1366:C:O2'	43:j:62:ARG:NH1	2.36	0.44
34:a:1366:C:O3'	43:j:62:ARG:NH2	2.50	0.44
34:a:1435:G:H2'	34:a:1436:U:C6	2.53	0.44
35:b:57:ASN:HD22	35:b:219:THR:HG23	1.82	0.44
38:e:53:ARG:H	38:e:53:ARG:HD2	1.82	0.44
39:f:42:TRP:HB3	39:f:45:ARG:HD2	2.00	0.44
39:f:92:THR:O	39:f:93:LYS:HG2	2.16	0.44
42:i:33:SER:H	42:i:36:GLN:HB3	1.82	0.44
42:i:80:HIS:CE1	42:i:84:ARG:HH11	2.35	0.44
46:m:101:THR:C	46:m:103:THR:N	2.74	0.44
49:p:20:VAL:HG23	49:p:35:ARG:HA	1.99	0.44
57:x:151:LEU:HD11	57:x:217:TRP:CZ2	2.52	0.44
57:x:222:ILE:HG23	57:x:242:LEU:HD12	2.00	0.44
8:A:177:G:OP2	8:A:177:G:N2	2.37	0.44
8:A:322:A:OP2	12:E:163:ASN:HB2	2.17	0.44
8:A:541:A:C6	8:A:553:G:C6	3.06	0.44
8:A:857:G:N2	8:A:2269:G:O4'	2.50	0.44
8:A:1592:C:H2'	8:A:1593:A:C8	2.53	0.44
8:A:1939:5MU:O4'	8:A:2591:C:O2'	2.30	0.44
8:A:2647:U:O2	8:A:2673:G:O6	2.35	0.44
8:A:2895:G:H2'	8:A:2896:C:H6	1.81	0.44
9:B:27:C:H2'	9:B:28:C:C6	2.53	0.44
9:B:31:C:H2'	9:B:53:A:H61	1.82	0.44
25:R:4:VAL:HA	25:R:12:HIS:O	2.18	0.44
25:R:25:LEU:HB3	25:R:27:ILE:HG12	2.00	0.44
34:a:32:A:H2'	34:a:33:A:C8	2.53	0.44
34:a:35:G:H2'	34:a:36:C:C6	2.52	0.44
34:a:201:G:N2	34:a:216:U:O2	2.50	0.44
34:a:235:C:H2'	34:a:236:A:C8	2.52	0.44
34:a:604:G:N1	34:a:635:A:C6	2.85	0.44
34:a:1319:A:C5	34:a:1323:G:C6	3.06	0.44
34:a:1319:A:N7	34:a:1323:G:C6	2.85	0.44
34:a:1476:A:H2'	34:a:1477:U:O4'	2.18	0.44
37:d:186:GLU:N	37:d:189:ASP:HB3	2.33	0.44
40:g:46:LEU:HB3	40:g:57:GLU:CG	2.47	0.44
40:g:47:GLU:O	40:g:51:GLN:HG2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:h:27:PRO:O	41:h:32:LYS:HD3	2.18	0.44
43:j:63:ASP:OD1	47:n:98:LYS:NZ	2.40	0.44
52:s:16:LYS:O	52:s:20:LYS:HG2	2.17	0.44
57:x:233:MET:O	57:x:237:LEU:HG	2.16	0.44
57:x:545:PRO:HG2	57:x:548:TYR:HD2	1.82	0.44
3:2:29:GLN:O	3:2:33:ARG:HG3	2.18	0.44
8:A:396:G:H1'	31:X:28:PHE:HB3	1.99	0.44
8:A:852:U:H2'	8:A:853:C:C6	2.53	0.44
8:A:964:C:O2	8:A:2273:A:H2	2.01	0.44
8:A:1093:G:N2	8:A:1097:U:O5'	2.51	0.44
8:A:1341:G:OP2	8:A:1394:U:O2'	2.32	0.44
8:A:1500:G:O2'	10:C:98:GLY:O	2.36	0.44
8:A:1664:A:C2	18:K:1:MET:HE1	2.51	0.44
8:A:2114:A:O4'	8:A:2167:U:O2'	2.32	0.44
8:A:2125:G:H1'	8:A:2173:A:N6	2.32	0.44
8:A:2215:C:H2'	8:A:2216:G:C8	2.52	0.44
8:A:2389:G:H5''	8:A:2390:U:O4'	2.18	0.44
8:A:2898:U:H2'	8:A:2899:A:H8	1.82	0.44
34:a:7:A:H2'	38:e:123:LEU:HD22	2.00	0.44
34:a:59:A:H3'	34:a:331:G:H22	1.83	0.44
34:a:227:G:H2'	34:a:228:A:O4'	2.17	0.44
34:a:358:U:H2'	34:a:359:G:C8	2.52	0.44
34:a:406:G:N2	37:d:115:GLN:HE22	2.16	0.44
34:a:794:A:H2'	34:a:795:C:C6	2.53	0.44
34:a:1271:A:H2'	34:a:1272:G:C8	2.52	0.44
35:b:53:LEU:HD23	35:b:53:LEU:HA	1.84	0.44
39:f:78:PHE:HB3	39:f:84:VAL:HG11	2.00	0.44
43:j:52:LEU:HA	43:j:62:ARG:HG2	2.00	0.44
45:l:32:VAL:HG12	45:l:55:ARG:HB3	1.98	0.44
48:o:32:THR:HG22	48:o:62:ARG:HH11	1.83	0.44
57:x:58:ARG:HA	57:x:369:LYS:HD2	1.99	0.44
8:A:5:A:H2'	8:A:6:A:C8	2.53	0.44
8:A:143:C:H2'	8:A:144:A:C8	2.53	0.44
8:A:1073:A:H2'	8:A:1074:G:H5'	1.99	0.44
8:A:1086:A:H5''	8:A:1087:G:H5'	2.00	0.44
8:A:1426:G:O2'	8:A:1572:A:N6	2.41	0.44
8:A:1469:A:H2'	8:A:1470:A:H8	1.83	0.44
8:A:1857:G:H22	8:A:1884:G:H2'	1.82	0.44
8:A:1942:C:H3'	8:A:1943:U:H2'	2.00	0.44
10:C:87:SER:O	10:C:196:ASN:ND2	2.44	0.44
11:D:39:ASP:N	11:D:39:ASP:OD1	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:15:LEU:O	15:H:15:LEU:HD23	2.17	0.44
15:H:116:ARG:HG3	15:H:133:GLN:HG3	1.99	0.44
20:M:68:PHE:HD2	20:M:70:ASP:HB3	1.83	0.44
26:S:11:ARG:NH2	26:S:98:LYS:HD2	2.33	0.44
28:U:91:LYS:HE3	28:U:91:LYS:HB2	1.66	0.44
29:V:7:GLU:O	29:V:41:GLU:N	2.44	0.44
34:a:203:G:N3	34:a:465:A:N6	2.66	0.44
34:a:381:C:H2'	34:a:382:A:O4'	2.18	0.44
34:a:499:A:H4'	34:a:500:G:H5'	2.00	0.44
34:a:682:G:H2'	34:a:683:G:H8	1.82	0.44
34:a:737:C:C2	34:a:738:C:C5	3.06	0.44
34:a:878:A:H5'	41:h:80:PRO:HG2	1.99	0.44
34:a:913:A:OP1	45:l:87:LYS:NZ	2.41	0.44
34:a:1200:C:HO2'	34:a:1201:A:P	2.38	0.44
35:b:41:ASN:HD21	35:b:43:GLU:HB2	1.83	0.44
36:c:201:ILE:HG22	36:c:203:LYS:HG3	2.00	0.44
40:g:110:ARG:HD3	40:g:122:GLU:HG2	1.99	0.44
42:i:41:GLU:HA	42:i:44:ARG:NH1	2.32	0.44
45:l:122:LYS:HD2	45:l:122:LYS:N	2.33	0.44
57:x:329:VAL:HG13	57:x:331:ASN:H	1.83	0.44
57:x:437:LEU:HD21	57:x:476:PHE:HE2	1.83	0.44
57:x:545:PRO:HD3	57:x:582:TYR:HB3	1.99	0.44
8:A:296:U:H2'	8:A:297:G:H8	1.83	0.44
8:A:409:G:H2'	8:A:410:G:C8	2.53	0.44
8:A:992:C:OP1	24:Q:46:TYR:OH	2.31	0.44
8:A:1614:A:N6	26:S:92:ARG:O	2.37	0.44
8:A:1668:A:N3	8:A:1670:C:C4	2.86	0.44
8:A:2399:G:C6	8:A:2418:A:C6	3.06	0.44
8:A:2456:C:C4	8:A:2457:PSU:N1	2.86	0.44
8:A:2460:U:C2	8:A:2461:A:C8	3.05	0.44
8:A:2839:G:O2'	21:N:49:GLU:OE1	2.26	0.44
9:B:52:A:O2'	9:B:53:A:O5'	2.34	0.44
14:G:42:VAL:HA	14:G:50:THR:O	2.18	0.44
20:M:105:MET:HE3	20:M:108:VAL:HG21	1.99	0.44
26:S:17:VAL:HA	26:S:43:ALA:HB1	2.00	0.44
34:a:184:G:H2'	34:a:185:U:H6	1.83	0.44
34:a:438:U:C2	34:a:494:G:C6	3.06	0.44
34:a:959:A:N6	52:s:77:ARG:HG2	2.32	0.44
34:a:1179:A:H2'	34:a:1180:A:C8	2.53	0.44
34:a:1447:A:H3'	34:a:1448:C:C6	2.53	0.44
34:a:1521:C:H2'	34:a:1522:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:b:65:LYS:HB2	35:b:158:ASP:OD2	2.18	0.44
35:b:168:GLU:O	35:b:172:ILE:HG13	2.18	0.44
40:g:5:VAL:O	40:g:5:VAL:HG13	2.17	0.44
41:h:10:LEU:HD11	41:h:126:CYS:HB2	2.00	0.44
41:h:63:LYS:HG2	41:h:70:VAL:HG21	2.00	0.44
46:m:82:LEU:HG	52:s:73:PHE:HE1	1.83	0.44
57:x:418:ALA:HB3	57:x:483:GLY:O	2.17	0.44
57:x:491:GLU:HA	57:x:612:LEU:HD12	2.00	0.44
7:6:26:SER:OG	7:6:28:VAL:HG23	2.16	0.43
8:A:7:G:H2'	8:A:8:C:C6	2.53	0.43
8:A:39:G:H1'	12:E:43:THR:HG21	2.00	0.43
8:A:1013:C:H2'	8:A:1014:A:C8	2.53	0.43
8:A:1022:G:N2	8:A:1142:A:N1	2.65	0.43
8:A:1869:G:H21	8:A:1872:A:H62	1.65	0.43
14:G:43:LYS:HB3	14:G:43:LYS:HE2	1.80	0.43
15:H:97:ARG:NH1	15:H:112:LYS:HB3	2.32	0.43
17:J:7:LYS:O	17:J:11:VAL:HG23	2.18	0.43
20:M:33:LEU:HD13	20:M:117:PHE:HB3	2.00	0.43
34:a:50:A:O2'	34:a:360:G:N2	2.51	0.43
34:a:438:U:C2	34:a:496:A:C6	3.04	0.43
34:a:565:U:H3'	34:a:566:G:H2'	2.00	0.43
34:a:786:G:C2	34:a:797:C:C2	3.06	0.43
34:a:1171:A:H2'	34:a:1172:C:H6	1.82	0.43
34:a:1353:G:H2'	34:a:1354:U:H6	1.82	0.43
43:j:36:VAL:HG13	43:j:76:ILE:HA	1.99	0.43
43:j:89:ARG:HG3	43:j:89:ARG:O	2.17	0.43
55:v:21:A:H2'	55:v:22:G:C8	2.53	0.43
56:w:28:G:H2'	56:w:29:G:C8	2.53	0.43
57:x:39:ILE:HG12	57:x:51:TRP:CZ2	2.52	0.43
57:x:166:VAL:HG21	57:x:260:ILE:HD12	1.99	0.43
4:3:4:LYS:HE2	8:A:242:G:O6	2.18	0.43
4:3:24:LYS:HD3	19:L:62:PRO:HG2	2.00	0.43
8:A:75:G:N3	8:A:75:G:H2'	2.33	0.43
8:A:479:A:H1'	8:A:480:A:H5''	2.00	0.43
8:A:543:G:C6	8:A:544:C:N4	2.87	0.43
8:A:857:G:H2'	8:A:858:G:O4'	2.18	0.43
8:A:1072:C:N4	8:A:1093:G:H1	2.16	0.43
8:A:2625:G:H2'	8:A:2626:C:O4'	2.17	0.43
8:A:2744:G:N2	14:G:142:GLN:OE1	2.49	0.43
9:B:48:U:H2'	9:B:49:C:C6	2.53	0.43
10:C:209:ALA:HA	10:C:212:TRP:CE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:F:56:LEU:HD12	13:F:86:CYS:SG	2.58	0.43
14:G:75:VAL:O	14:G:79:THR:HG22	2.17	0.43
18:K:69:VAL:HG22	18:K:77:ILE:HB	2.00	0.43
34:a:41:G:H2'	34:a:42:G:C8	2.51	0.43
34:a:183:C:H5''	34:a:184:G:OP2	2.18	0.43
34:a:1332:A:H2'	34:a:1333:A:C8	2.52	0.43
34:a:1342:C:O2'	42:i:125:GLN:HA	2.18	0.43
34:a:1434:A:H2'	34:a:1435:G:O4'	2.19	0.43
35:b:71:THR:HG23	35:b:94:ARG:HA	2.00	0.43
39:f:25:TYR:O	39:f:29:ILE:HG12	2.18	0.43
41:h:107:LYS:HD3	41:h:107:LYS:HA	1.83	0.43
45:l:80:LEU:HB2	45:l:101:LEU:HD22	2.00	0.43
49:p:21:VAL:HG21	49:p:60:TRP:CD1	2.52	0.43
52:s:78:THR:O	52:s:78:THR:OG1	2.30	0.43
57:x:353:LYS:NZ	57:x:390:VAL:HA	2.32	0.43
8:A:82:U:H2'	8:A:83:A:C8	2.53	0.43
8:A:659:G:H21	12:E:30:GLN:CD	2.19	0.43
8:A:1172:C:N4	8:A:1175:A:OP1	2.51	0.43
8:A:1475:G:O2'	8:A:1476:U:H6	2.01	0.43
8:A:1592:C:H2'	8:A:1593:A:H8	1.83	0.43
8:A:1770:G:C6	8:A:1983:G:C6	3.06	0.43
8:A:2113:U:O4	55:v:20:U:C5'	2.66	0.43
8:A:2142:A:H2'	8:A:2143:C:H5'	2.00	0.43
8:A:2303:G:H2'	8:A:2304:G:O4'	2.17	0.43
8:A:2438:U:O2'	8:A:2439:A:H5''	2.19	0.43
8:A:2619:C:H5''	11:D:157:LYS:HA	1.99	0.43
8:A:2840:C:H5''	21:N:53:THR:OG1	2.18	0.43
9:B:60:C:H2'	9:B:61:G:C8	2.53	0.43
17:J:49:ASP:OD1	17:J:121:LYS:NZ	2.27	0.43
25:R:71:LYS:HA	25:R:90:ARG:HG3	1.99	0.43
32:Y:9:LYS:O	32:Y:60:LYS:NZ	2.51	0.43
34:a:145:G:HO2'	34:a:146:G:H8	1.61	0.43
34:a:409:U:H2'	34:a:410:G:O4'	2.17	0.43
34:a:455:G:H2'	34:a:456:A:H8	1.82	0.43
34:a:784:A:H2'	34:a:785:G:C8	2.51	0.43
34:a:984:C:H42	34:a:1222:G:H22	1.66	0.43
34:a:1029:U:H4'	34:a:1030:U:H5	1.82	0.43
34:a:1319:A:N6	34:a:1323:G:C2	2.85	0.43
35:b:56:LEU:HD21	35:b:183:PHE:CZ	2.53	0.43
37:d:191:SER:OG	37:d:193:ASP:OD2	2.35	0.43
57:x:297:ILE:HG23	57:x:404:ILE:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:241:A:N1	8:A:255:A:H5'	2.33	0.43
8:A:329:G:O4'	8:A:477:A:H1'	2.17	0.43
8:A:391:A:O2'	8:A:410:G:OP1	2.25	0.43
8:A:629:G:H1'	8:A:639:U:H1'	2.00	0.43
8:A:1095:A:H2	57:x:631:ILE:HD12	1.83	0.43
8:A:1181:U:H2'	8:A:1182:G:C8	2.54	0.43
8:A:1424:G:H2'	8:A:1425:G:C8	2.54	0.43
8:A:1641:A:H2'	8:A:1642:G:O4'	2.18	0.43
8:A:2492:U:H2'	8:A:2493:U:C6	2.53	0.43
15:H:79:THR:HA	15:H:145:ASN:O	2.19	0.43
20:M:31:PHE:HD1	20:M:132:THR:HG22	1.84	0.43
20:M:53:MET:HE2	20:M:117:PHE:CD1	2.53	0.43
31:X:2:ARG:HB2	31:X:11:PRO:HG3	2.01	0.43
34:a:17:U:O2'	34:a:1079:G:N3	2.49	0.43
34:a:252:U:O4	34:a:253:A:N6	2.49	0.43
34:a:489:C:H2'	34:a:490:C:C6	2.54	0.43
34:a:604:G:O6	34:a:635:A:N6	2.51	0.43
34:a:613:C:H2'	34:a:614:C:C6	2.54	0.43
35:b:205:ALA:O	35:b:209:VAL:HG23	2.17	0.43
37:d:96:ARG:HH22	37:d:114:ARG:NH1	2.17	0.43
39:f:29:ILE:HG23	39:f:66:ALA:HB2	2.00	0.43
57:x:494:ARG:HG2	57:x:495:GLN:HG2	1.99	0.43
57:x:669:LEU:O	57:x:673:THR:HG22	2.18	0.43
8:A:817:C:H2'	8:A:818:G:O4'	2.19	0.43
8:A:1501:G:OP1	10:C:100:ARG:NH2	2.51	0.43
8:A:1959:G:H2'	8:A:1960:A:O4'	2.19	0.43
8:A:2169:A:H1'	55:v:56:C:C6	2.54	0.43
8:A:2590:A:H2'	8:A:2591:C:C6	2.53	0.43
8:A:2650:U:C2	8:A:2651:C:C5	3.06	0.43
8:A:2873:A:O2'	8:A:2874:C:H5'	2.18	0.43
9:B:49:C:H2'	9:B:50:A:C8	2.53	0.43
10:C:28:PRO:HB2	10:C:33:LEU:HD11	2.00	0.43
13:F:115:GLY:O	13:F:177:ARG:NH2	2.51	0.43
34:a:5:U:H4'	34:a:6:G:O5'	2.18	0.43
34:a:269:C:H2'	34:a:270:A:H8	1.80	0.43
34:a:474:G:H2'	34:a:475:C:C6	2.54	0.43
34:a:921:U:P	34:a:1081:A:C2'	3.06	0.43
34:a:958:A:N6	52:s:76:THR:O	2.52	0.43
34:a:1370:G:C2	34:a:1371:G:C8	3.07	0.43
34:a:1452:C:H4'	34:a:1453:G:H5'	2.00	0.43
38:e:104:ILE:HG12	38:e:122:VAL:HG12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:e:106:ALA:H	38:e:111:ARG:HH22	1.65	0.43
42:i:44:ARG:HA	42:i:47:VAL:HG12	2.01	0.43
42:i:57:VAL:HG13	42:i:58:GLU:N	2.32	0.43
46:m:71:GLU:HA	46:m:74:MET:HE2	2.00	0.43
48:o:34:GLN:HB3	48:o:58:MET:HE1	2.01	0.43
57:x:270:LYS:HE2	57:x:270:LYS:HA	2.00	0.43
57:x:441:ASP:OD1	57:x:441:ASP:N	2.51	0.43
8:A:18:U:P	24:Q:29:ARG:HH22	2.41	0.43
8:A:645:C:H2'	8:A:647:G:C8	2.53	0.43
8:A:807:U:H2'	8:A:808:G:C8	2.53	0.43
8:A:910:A:H2'	8:A:911:A:C8	2.54	0.43
8:A:1116:G:C2'	8:A:1117:C:H5'	2.48	0.43
8:A:1670:C:H2'	8:A:1671:U:O4'	2.19	0.43
8:A:1727:C:H2'	8:A:1728:C:H6	1.84	0.43
8:A:2107:G:H3'	8:A:2108:A:H8	1.83	0.43
8:A:2820:A:C6	11:D:197:THR:HB	2.54	0.43
15:H:97:ARG:CZ	15:H:112:LYS:HB3	2.49	0.43
19:L:14:LYS:HA	19:L:14:LYS:HD2	1.77	0.43
26:S:20:VAL:HG21	26:S:43:ALA:HB3	2.00	0.43
34:a:6:G:O6	38:e:99:SER:OG	2.27	0.43
34:a:16:A:N3	34:a:1080:A:O2'	2.39	0.43
34:a:679:C:H2'	34:a:680:C:C6	2.52	0.43
34:a:1015:G:H2'	34:a:1016:A:C8	2.53	0.43
34:a:1022:A:H3'	34:a:1023:U:C6	2.54	0.43
34:a:1221:G:N1	34:a:1222:G:N2	2.67	0.43
34:a:1346:A:C8	34:a:1348:U:C2	3.07	0.43
34:a:1522:U:H2'	34:a:1523:G:C8	2.44	0.43
35:b:49:PHE:HE2	35:b:212:TYR:CD1	2.37	0.43
38:e:155:LYS:O	41:h:63:LYS:NZ	2.51	0.43
40:g:110:ARG:HH21	40:g:121:ASN:ND2	2.17	0.43
45:l:41:PRO:HD3	45:l:47:ALA:O	2.18	0.43
48:o:52:ARG:O	48:o:56:LEU:HG	2.18	0.43
8:A:655:A:O3'	8:A:656:G:H8	2.02	0.43
8:A:1196:C:C2	8:A:1197:G:C8	3.06	0.43
8:A:1220:G:H2'	8:A:1221:C:C6	2.52	0.43
8:A:1287:A:O5'	21:N:103:ARG:HD2	2.18	0.43
8:A:1351:C:H2'	8:A:1352:U:O4'	2.18	0.43
8:A:2623:G:H4'	8:A:2825:G:C8	2.54	0.43
28:U:17:ASP:HA	28:U:20:LYS:HE2	2.00	0.43
34:a:268:U:H2'	34:a:269:C:C6	2.53	0.43
34:a:1367:C:OP1	42:i:116:GLY:N	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:c:109:GLU:HG2	36:c:139:ASN:CG	2.44	0.43
40:g:66:GLU:HG3	40:g:69:ARG:NH2	2.32	0.43
43:j:22:THR:O	43:j:26:VAL:HG22	2.18	0.43
50:q:47:ASP:OD2	50:q:50:ASN:HA	2.18	0.43
8:A:2:G:H2'	8:A:3:U:H6	1.83	0.43
8:A:275:C:H1'	8:A:362:A:H62	1.83	0.43
8:A:289:G:H2'	8:A:290:U:H6	1.84	0.43
8:A:740:C:H5'	8:A:1784:A:H3'	2.01	0.43
8:A:1099:G:C6	8:A:1100:C:C4	3.06	0.43
8:A:1220:G:H2'	8:A:1221:C:H6	1.83	0.43
8:A:2036:C:H2'	8:A:2037:A:H8	1.84	0.43
8:A:2291:U:O2'	8:A:2374:C:O2	2.37	0.43
13:F:64:PRO:HA	13:F:88:VAL:HG12	2.00	0.43
17:J:69:ARG:HD3	17:J:89:PHE:CD1	2.54	0.43
34:a:76:G:C6	34:a:77:A:C5	3.06	0.43
34:a:322:C:H2'	34:a:323:U:C6	2.54	0.43
34:a:617:G:H4'	49:p:44:SER:HB3	2.00	0.43
34:a:618:C:H5	34:a:620:C:H5''	1.83	0.43
34:a:984:C:C4	34:a:1222:G:N2	2.86	0.43
34:a:1288:A:H2'	34:a:1289:A:C8	2.54	0.43
34:a:1437:A:H2'	34:a:1438:G:H8	1.83	0.43
35:b:216:VAL:O	35:b:220:VAL:HG13	2.18	0.43
37:d:168:THR:HG23	37:d:183:ARG:HH11	1.84	0.43
38:e:155:LYS:HG2	41:h:70:VAL:HG22	2.01	0.43
43:j:80:THR:C	43:j:82:LYS:H	2.26	0.43
56:w:46:G7M:O2'	56:w:48:C:H5'	2.19	0.43
57:x:312:ASP:HB2	57:x:340:GLY:C	2.44	0.43
57:x:493:ILE:HG13	57:x:523:PRO:HB3	2.00	0.43
57:x:552:VAL:HG11	57:x:577:LEU:HD22	2.00	0.43
2:1:33:LEU:HD11	8:A:2286:G:C2	2.53	0.43
7:6:20:ASN:ND2	7:6:20:ASN:H	2.17	0.43
8:A:84:A:H5''	28:U:5:ARG:HD2	2.01	0.43
8:A:271:G:C6	8:A:367:G:C6	3.07	0.43
8:A:609:A:H2'	8:A:610:C:O4'	2.19	0.43
8:A:653:U:C5	8:A:654:A:H1'	2.54	0.43
8:A:782:A:N7	10:C:219:VAL:HG21	2.34	0.43
8:A:1316:U:H2'	8:A:1317:G:H8	1.84	0.43
8:A:1709:U:H2'	8:A:1710:G:H8	1.83	0.43
8:A:1932:A:H2'	8:A:1933:G:O4'	2.18	0.43
8:A:2153:C:H42	8:A:2156:G:H1	1.67	0.43
8:A:2247:A:H2'	8:A:2248:C:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2566:A:N1	18:K:28:SER:HB2	2.33	0.43
9:B:81:G:O6	9:B:95:U:O2	2.37	0.43
9:B:116:G:H2'	9:B:117:G:C8	2.53	0.43
22:O:79:ALA:HB3	22:O:113:ALA:HB3	2.00	0.43
29:V:1:MET:N	29:V:59:GLU:OE1	2.51	0.43
34:a:193:C:H2'	34:a:194:C:H6	1.83	0.43
34:a:303:A:H2'	34:a:304:U:O4'	2.18	0.43
34:a:309:A:H2'	34:a:310:G:H8	1.84	0.43
34:a:401:C:H2'	34:a:402:G:C8	2.53	0.43
34:a:939:G:H2'	34:a:940:C:C6	2.53	0.43
34:a:1172:C:O2'	34:a:1173:U:H5'	2.18	0.43
36:c:57:GLU:C	36:c:59:PRO:HD3	2.44	0.43
57:x:2:ARG:H	57:x:2:ARG:HG2	1.71	0.43
57:x:266:GLY:HA3	57:x:273:GLY:HA3	2.01	0.43
8:A:536:G:H4'	24:Q:56:PHE:CZ	2.54	0.43
8:A:849:A:H2'	8:A:850:U:H6	1.84	0.43
8:A:898:C:H2'	8:A:899:A:C8	2.53	0.43
8:A:1731:G:C6	8:A:1733:G:C5	3.06	0.43
8:A:2043:C:C2	8:A:2044:C:C5	3.07	0.43
11:D:151:THR:HB	11:D:152:PRO:HD3	2.01	0.43
23:P:98:TYR:O	23:P:102:ARG:HD2	2.19	0.43
28:U:73:ASN:C	28:U:75:ALA:H	2.27	0.43
29:V:9:ARG:HG2	29:V:41:GLU:HG3	2.00	0.43
30:W:79:GLU:O	30:W:81:GLU:N	2.52	0.43
34:a:271:C:H2'	34:a:272:C:H6	1.83	0.43
34:a:272:C:H2'	34:a:273:U:H6	1.84	0.43
34:a:880:C:H2'	34:a:881:G:H8	1.83	0.43
34:a:1133:G:H2'	34:a:1134:G:C8	2.54	0.43
34:a:1399:C:O2	34:a:1502:A:N6	2.52	0.43
37:d:122:ILE:HD12	37:d:143:SER:O	2.19	0.43
40:g:35:LYS:O	40:g:39:GLU:HG3	2.19	0.43
40:g:72:VAL:HG12	40:g:89:GLU:HA	2.00	0.43
43:j:15:HIS:HB3	43:j:70:HIS:CE1	2.54	0.43
54:u:8:ASN:HB3	54:u:10:PRO:HD2	2.00	0.43
8:A:127:A:H5''	8:A:128:C:C6	2.54	0.42
8:A:140:C:H4'	8:A:141:G:O5'	2.20	0.42
8:A:593:U:H2'	8:A:594:U:H6	1.83	0.42
8:A:699:A:H2'	8:A:700:G:O4'	2.19	0.42
8:A:1387:A:C6	8:A:1401:G:N1	2.86	0.42
8:A:1387:A:H5'	8:A:1469:A:H1'	2.00	0.42
8:A:2329:U:H2'	8:A:2330:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2529:G:H5''	8:A:2530:A:H5''	2.01	0.42
8:A:2836:U:H2'	8:A:2837:A:H8	1.84	0.42
9:B:17:C:H2'	9:B:18:G:O4'	2.18	0.42
15:H:57:LYS:O	15:H:57:LYS:HD3	2.19	0.42
17:J:91:GLU:O	17:J:95:ARG:HD3	2.19	0.42
19:L:77:ILE:HD11	19:L:101:ILE:HG22	2.01	0.42
22:O:27:VAL:HG21	22:O:40:ILE:HD12	2.01	0.42
26:S:70:LYS:HD2	26:S:110:ARG:CD	2.49	0.42
34:a:376:G:H2'	34:a:377:G:H8	1.84	0.42
34:a:406:G:H8	34:a:406:G:OP2	2.01	0.42
34:a:672:U:H2'	34:a:673:A:H8	1.84	0.42
34:a:890:G:H4'	34:a:891:U:O5'	2.19	0.42
34:a:1004:A:O2'	34:a:1005:A:O4'	2.37	0.42
34:a:1225:A:H2'	34:a:1225:A:N3	2.34	0.42
34:a:1396:A:H2	38:e:23:THR:HG21	1.84	0.42
35:b:132:GLU:HB3	35:b:136:ARG:NH1	2.34	0.42
35:b:193:ASP:HB3	35:b:194:GLY:H	1.39	0.42
36:c:152:VAL:HG12	36:c:156:LEU:HD21	2.01	0.42
37:d:18:LEU:HB2	37:d:20:LEU:HG	2.00	0.42
37:d:59:LYS:O	37:d:63:ILE:HG12	2.18	0.42
38:e:80:LEU:HD22	38:e:146:MET:CE	2.48	0.42
47:n:81:ARG:HA	47:n:84:VAL:HG12	2.01	0.42
8:A:704:G:C2	8:A:726:G:C2	3.07	0.42
8:A:910:A:H62	20:M:12:MET:HA	1.84	0.42
8:A:966:G:O4'	8:A:2267:A:N6	2.52	0.42
8:A:1059:G:C5	8:A:1088:A:N6	2.86	0.42
8:A:1198:U:C2	8:A:1199:U:C5	3.08	0.42
8:A:1420:A:H1'	8:A:2211:A:C8	2.53	0.42
8:A:2720:U:H5''	23:P:52:ARG:NH2	2.34	0.42
8:A:2751:G:H3'	8:A:2752:C:H6	1.84	0.42
8:A:2843:G:H2'	8:A:2844:G:O4'	2.19	0.42
8:A:2845:U:H5''	23:P:51:ASN:O	2.19	0.42
12:E:51:GLU:OE1	12:E:88:ARG:NH1	2.52	0.42
19:L:123:ARG:HB2	19:L:143:GLU:OE2	2.19	0.42
33:Z:5:LYS:HE3	33:Z:34:THR:HG21	2.01	0.42
34:a:200:G:O2'	34:a:201:G:OP1	2.29	0.42
34:a:264:C:O2'	50:q:65:PRO:O	2.29	0.42
34:a:356:A:H2'	34:a:357:G:O4'	2.19	0.42
34:a:587:G:N1	34:a:754:C:OP2	2.30	0.42
34:a:720:C:O5'	34:a:720:C:H6	2.02	0.42
34:a:1347:G:HO2'	34:a:1348:U:P	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1530:G:H2'	34:a:1531:A:C8	2.54	0.42
36:c:173:PRO:O	36:c:181:ILE:HD11	2.18	0.42
40:g:3:ARG:HG3	40:g:4:ARG:HE	1.84	0.42
41:h:88:LYS:HG3	41:h:120:LEU:N	2.34	0.42
43:j:53:ILE:H	43:j:53:ILE:HG13	1.67	0.42
48:o:68:TYR:HD1	48:o:71:ARG:NH2	2.17	0.42
57:x:350:ASN:O	57:x:354:ALA:N	2.51	0.42
8:A:20:C:H2'	8:A:21:A:H8	1.84	0.42
8:A:176:A:O2'	8:A:177:G:H5'	2.19	0.42
8:A:220:G:O2'	8:A:233:A:N3	2.39	0.42
8:A:750:A:OP1	8:A:1615:C:N4	2.48	0.42
8:A:1067:A:H2	57:x:643:GLY:H	1.67	0.42
8:A:1490:A:O2'	8:A:1491:G:P	2.78	0.42
8:A:1593:A:H2'	8:A:1594:U:O4'	2.19	0.42
8:A:2245:U:O2'	8:A:2436:G:OP2	2.34	0.42
8:A:2399:G:C6	8:A:2418:A:N1	2.87	0.42
8:A:2788:C:H2'	8:A:2789:C:C6	2.54	0.42
9:B:31:C:C2	9:B:32:U:C5	3.07	0.42
15:H:115:VAL:HG13	15:H:132:PHE:CE1	2.54	0.42
28:U:48:VAL:HG22	28:U:50:ALA:H	1.84	0.42
30:W:37:ARG:O	30:W:53:HIS:ND1	2.44	0.42
34:a:544:G:OP1	37:d:58:GLN:HG3	2.19	0.42
34:a:592:G:H2'	34:a:593:U:C6	2.55	0.42
34:a:637:C:H5''	50:q:3:LYS:HE2	2.01	0.42
34:a:714:G:H1'	34:a:777:A:C8	2.54	0.42
34:a:865:A:H8	34:a:865:A:OP2	2.03	0.42
34:a:1043:G:H2'	34:a:1044:A:C8	2.54	0.42
34:a:1201:A:H4'	34:a:1202:U:H5''	2.02	0.42
34:a:1380:U:C4	40:g:2:ARG:HG2	2.54	0.42
34:a:1524:C:H2'	34:a:1525:G:C8	2.54	0.42
37:d:149:LYS:HE3	37:d:149:LYS:HB3	1.84	0.42
37:d:172:VAL:HG12	37:d:173:ASP:N	2.35	0.42
40:g:75:LYS:O	40:g:86:VAL:HG22	2.19	0.42
43:j:49:PHE:HE2	43:j:67:ILE:HG13	1.84	0.42
45:l:8:ARG:HG2	45:l:9:LYS:HG3	2.02	0.42
56:w:26:A:H61	56:w:44:G:H1	1.67	0.42
57:x:365:MET:HB3	57:x:370:ARG:HA	2.01	0.42
7:6:52:ALA:O	7:6:53:THR:C	2.61	0.42
7:6:56:ARG:HD2	7:6:56:ARG:HA	1.77	0.42
8:A:30:G:O2'	8:A:1214:A:N3	2.45	0.42
8:A:137:U:H2'	8:A:138:U:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1071:G:N3	8:A:1071:G:H2'	2.35	0.42
8:A:1278:C:H2'	8:A:1279:G:H8	1.83	0.42
8:A:1615:C:OP2	8:A:1617:C:N4	2.32	0.42
8:A:2194:U:H2'	8:A:2195:U:C6	2.54	0.42
19:L:20:GLY:O	19:L:21:ARG:HD3	2.20	0.42
34:a:202:G:N2	34:a:216:U:C2	2.87	0.42
34:a:206:C:H5''	34:a:207:C:O5'	2.19	0.42
34:a:262:A:H5'	53:t:67:HIS:HB3	2.02	0.42
34:a:293:G:H5'	34:a:610:U:O2	2.19	0.42
34:a:728:A:H2'	34:a:729:A:C8	2.54	0.42
34:a:811:C:H4'	34:a:901:A:H61	1.84	0.42
34:a:878:A:H1'	41:h:3:GLN:NE2	2.34	0.42
34:a:1157:A:H4'	34:a:1158:C:O4'	2.20	0.42
43:j:5:ARG:NH1	43:j:78:GLU:OE1	2.53	0.42
43:j:45:ARG:HB3	43:j:69:THR:CG2	2.49	0.42
49:p:1:MET:O	49:p:24:SER:OG	2.25	0.42
55:v:18:G:H1	55:v:55:PSU:H1'	1.83	0.42
55:v:62:C:H2'	55:v:63:G:H8	1.84	0.42
56:w:37:MIA:H2'	56:w:38:A:H8	1.82	0.42
57:x:602:GLU:HA	57:x:605:LYS:HD2	2.02	0.42
8:A:74:A:H4'	8:A:75:G:O5'	2.19	0.42
8:A:236:C:C2	8:A:237:C:C5	3.07	0.42
8:A:277:G:H4'	8:A:361:G:O6	2.19	0.42
8:A:306:U:H2'	8:A:307:G:O4'	2.20	0.42
8:A:348:A:H2'	8:A:349:U:O4'	2.20	0.42
8:A:453:A:N3	8:A:457:A:O2'	2.53	0.42
8:A:1683:U:H2'	8:A:1684:G:C8	2.54	0.42
8:A:1727:C:H2'	8:A:1728:C:C6	2.55	0.42
8:A:1826:G:OP1	10:C:222:THR:OG1	2.34	0.42
8:A:2721:A:H1'	8:A:2873:A:O2'	2.20	0.42
8:A:2850:A:N7	8:A:2868:A:O2'	2.37	0.42
8:A:2857:G:O2'	8:A:2859:G:O6	2.35	0.42
15:H:35:LYS:H	15:H:35:LYS:HG2	1.63	0.42
34:a:163:C:H2'	34:a:164:G:O4'	2.20	0.42
34:a:553:A:C5	34:a:554:A:N7	2.87	0.42
34:a:720:C:H2'	34:a:721:G:N7	2.35	0.42
34:a:986:U:C2	34:a:987:G:C8	3.08	0.42
34:a:1118:U:H1'	34:a:1179:A:C4	2.55	0.42
34:a:1172:C:H2'	34:a:1173:U:C6	2.55	0.42
34:a:1320:C:H2'	34:a:1321:U:C6	2.55	0.42
43:j:72:ARG:HD3	43:j:72:ARG:HA	1.76	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:l:49:ARG:HG3	45:l:89:LEU:HD21	2.00	0.42
47:n:53:ARG:O	47:n:59:ARG:NH1	2.44	0.42
50:q:59:GLU:O	50:q:75:VAL:HB	2.20	0.42
51:r:64:LEU:O	51:r:65:SER:OG	2.34	0.42
55:v:56:C:H2'	55:v:57:A:C8	2.53	0.42
57:x:517:VAL:HG21	57:x:596:ALA:HA	2.01	0.42
3:2:2:LYS:HE2	8:A:687:C:H5''	2.01	0.42
8:A:210:C:H2'	8:A:211:C:C6	2.54	0.42
8:A:1179:G:N2	8:A:1180:U:O4'	2.53	0.42
8:A:1808:A:H3'	8:A:1809:A:H8	1.82	0.42
8:A:2286:G:H4'	8:A:2287:A:O4'	2.19	0.42
8:A:2549:G:C2	8:A:2550:G:N7	2.87	0.42
20:M:27:SER:OG	20:M:28:PHE:N	2.51	0.42
22:O:37:ALA:HB2	22:O:106:LEU:HD11	2.01	0.42
27:T:54:GLU:HG3	27:T:88:LYS:HB2	2.02	0.42
30:W:27:VAL:HB	30:W:31:SER:OG	2.20	0.42
34:a:768:A:H4'	34:a:1523:G:H21	1.84	0.42
34:a:1216:A:H5'	47:n:4:SER:HB2	2.02	0.42
39:f:47:LEU:HD13	39:f:51:ILE:HD12	2.02	0.42
42:i:93:LEU:O	42:i:97:LEU:HG	2.20	0.42
44:k:51:PHE:O	44:k:56:LYS:N	2.52	0.42
46:m:19:THR:C	46:m:21:ILE:H	2.28	0.42
50:q:16:MET:H	50:q:16:MET:HG3	1.47	0.42
53:t:78:LEU:HA	53:t:78:LEU:HD23	1.73	0.42
57:x:308:ARG:HD3	57:x:308:ARG:HA	1.59	0.42
3:2:3:ARG:HD3	3:2:3:ARG:HA	1.66	0.42
8:A:151:C:H2'	8:A:152:A:H8	1.84	0.42
8:A:410:G:OP1	8:A:411:G:H5'	2.19	0.42
8:A:522:A:H2'	8:A:523:C:C6	2.55	0.42
8:A:742:A:H2'	8:A:743:A:H8	1.85	0.42
8:A:1007:C:OP1	17:J:39:LYS:HD2	2.20	0.42
8:A:1117:C:H2'	8:A:1118:C:C6	2.55	0.42
8:A:1171:G:N2	8:A:1177:G:H1	2.17	0.42
8:A:1381:G:H1'	8:A:1571:A:N1	2.33	0.42
8:A:1507:C:O2	8:A:1508:A:H1'	2.19	0.42
8:A:1792:G:H5'	10:C:203:VAL:HG13	2.02	0.42
8:A:2607:G:H2'	8:A:2608:G:O4'	2.20	0.42
10:C:77:VAL:HG22	10:C:93:VAL:HG22	2.01	0.42
13:F:16:MET:HE3	13:F:16:MET:HB3	1.92	0.42
20:M:4:PRO:CG	20:M:70:ASP:HA	2.50	0.42
24:Q:39:ILE:O	24:Q:43:GLN:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:S:92:ARG:HG2	26:S:93:ALA:N	2.35	0.42
32:Y:31:GLN:HG2	32:Y:37:LEU:HB2	2.01	0.42
34:a:218:U:H2'	34:a:219:U:O4'	2.20	0.42
34:a:401:C:H2'	34:a:402:G:H8	1.85	0.42
34:a:464:U:H2'	34:a:465:A:C8	2.55	0.42
34:a:515:G:C4	34:a:516:PSU:C6	3.08	0.42
34:a:591:U:H2'	34:a:592:G:H8	1.83	0.42
34:a:606:G:H1'	34:a:633:G:C2	2.54	0.42
34:a:883:C:H2'	34:a:884:U:C6	2.55	0.42
34:a:920:U:OP2	34:a:920:U:H6	2.03	0.42
34:a:1080:A:H3'	34:a:1081:A:O4'	2.19	0.42
34:a:1315:U:C4	34:a:1316:G:C6	3.08	0.42
34:a:1319:A:C4	34:a:1323:G:C5	3.08	0.42
34:a:1417:G:O2'	34:a:1483:A:N6	2.46	0.42
36:c:132:ALA:O	36:c:135:ARG:HG2	2.20	0.42
36:c:137:VAL:HG11	36:c:169:GLU:OE2	2.20	0.42
36:c:187:GLU:OE2	36:c:187:GLU:N	2.53	0.42
40:g:24:LYS:HA	40:g:27:ASN:HD22	1.85	0.42
49:p:12:LYS:C	49:p:14:ARG:N	2.76	0.42
50:q:11:VAL:HG21	50:q:52:CYS:HB3	2.02	0.42
56:w:15:G:N2	56:w:48:C:C4	2.86	0.42
57:x:324:ALA:HB3	57:x:332:LEU:HB3	2.01	0.42
57:x:518:VAL:HG22	57:x:579:PHE:H	1.84	0.42
57:x:590:LEU:O	57:x:594:LEU:HD13	2.19	0.42
7:6:12:ILE:N	7:6:24:ILE:O	2.44	0.42
7:6:20:ASN:ND2	7:6:20:ASN:N	2.68	0.42
8:A:139:U:H5''	8:A:140:C:H5	1.84	0.42
8:A:347:A:H2'	8:A:348:A:C8	2.55	0.42
8:A:636:G:N7	19:L:109:LYS:NZ	2.54	0.42
8:A:666:A:H2'	8:A:667:U:C6	2.54	0.42
8:A:719:C:H2'	8:A:720:U:O4'	2.19	0.42
8:A:1048:A:N7	8:A:1111:A:C6	2.88	0.42
8:A:1593:A:H2'	8:A:1594:U:C6	2.55	0.42
8:A:1744:A:H3'	8:A:1745:A:C8	2.52	0.42
8:A:2033:A:H1'	8:A:2035:G:OP2	2.20	0.42
8:A:2375:G:N2	8:A:2378:A:OP2	2.43	0.42
8:A:2704:C:C4	8:A:2705:A:C5	3.08	0.42
10:C:239:PHE:HD1	10:C:239:PHE:HA	1.69	0.42
11:D:34:VAL:HG22	11:D:48:ILE:HD12	2.01	0.42
11:D:88:GLU:N	11:D:88:GLU:OE1	2.53	0.42
12:E:126:VAL:HG22	12:E:128:ALA:H	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:E:178:VAL:O	12:E:182:ALA:HB2	2.19	0.42
17:J:78:THR:HG23	17:J:83:GLY:O	2.19	0.42
18:K:26:GLY:O	18:K:30:ARG:HD2	2.20	0.42
18:K:98:ARG:HH12	34:a:338:A:H3'	1.85	0.42
20:M:4:PRO:HB2	20:M:7:THR:HG23	2.01	0.42
21:N:55:ALA:HA	21:N:80:PHE:CE1	2.55	0.42
29:V:51:GLN:OE1	29:V:57:TYR:OH	2.21	0.42
38:e:151:MET:HE3	38:e:151:MET:HB3	1.79	0.42
43:j:40:ILE:N	43:j:73:LEU:O	2.42	0.42
45:l:43:LYS:HB3	45:l:44:PRO:HD3	2.02	0.42
53:t:11:ILE:HG13	53:t:12:GLN:N	2.34	0.42
53:t:30:PHE:O	53:t:33:LYS:HB3	2.20	0.42
57:x:112:TYR:CE1	57:x:118:VAL:HG12	2.55	0.42
57:x:134:VAL:O	57:x:136:ARG:NH1	2.45	0.42
4:3:44:ARG:N	4:3:45:PRO:HD2	2.35	0.42
7:6:5:ILE:HG13	7:6:6:HIS:HD2	1.84	0.42
8:A:1232:G:C5	8:A:1233:C:C5	3.08	0.42
8:A:1371:G:N2	8:A:1372:U:O4	2.52	0.42
8:A:1394:U:H2'	8:A:1395:A:O4'	2.19	0.42
8:A:1434:A:H2'	8:A:1435:G:H8	1.85	0.42
8:A:1628:G:H2'	8:A:1629:U:H6	1.84	0.42
8:A:2250:G:OP1	8:A:2275:C:O2'	2.35	0.42
8:A:2718:G:H5'	23:P:97:TYR:HD2	1.85	0.42
11:D:85:ALA:H	11:D:88:GLU:CD	2.27	0.42
17:J:69:ARG:HD3	17:J:89:PHE:HD1	1.85	0.42
18:K:17:ARG:HD3	18:K:17:ARG:HA	1.79	0.42
22:O:88:LYS:HE3	22:O:88:LYS:HB2	1.85	0.42
34:a:390:U:H2'	34:a:391:G:H8	1.83	0.42
34:a:1120:C:H2'	34:a:1121:U:C6	2.55	0.42
37:d:72:ARG:O	37:d:75:TYR:HB3	2.19	0.42
38:e:12:GLU:OE2	38:e:67:ARG:NH2	2.49	0.42
46:m:36:ALA:HB1	46:m:54:THR:HG22	2.02	0.42
57:x:397:CYS:HB2	57:x:402:PRO:HD2	2.02	0.42
57:x:496:LYS:HB3	57:x:607:ALA:O	2.20	0.42
8:A:67:U:C2	8:A:68:G:C8	3.07	0.42
8:A:246:C:O2'	8:A:385:C:H4'	2.19	0.42
8:A:262:A:H2'	8:A:263:G:O4'	2.19	0.42
8:A:608:A:H2'	8:A:609:A:H8	1.84	0.42
8:A:1042:G:N2	8:A:1113:U:O2	2.49	0.42
8:A:1326:U:O2'	8:A:2010:G:O2'	2.34	0.42
8:A:1831:G:H2'	8:A:1832:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1891:G:H2'	8:A:1892:C:H6	1.84	0.42
8:A:2313:C:H2'	8:A:2314:A:H8	1.84	0.42
9:B:5:U:H2'	9:B:6:G:H8	1.85	0.42
9:B:18:G:O6	9:B:65:U:C2	2.73	0.42
9:B:25:U:H5	9:B:117:G:O2'	2.03	0.42
13:F:121:PHE:HB3	13:F:162:ASP:OD1	2.19	0.42
13:F:141:ASP:C	13:F:143:ASP:H	2.28	0.42
14:G:77:GLY:HA2	14:G:81:GLY:HA2	2.02	0.42
15:H:103:VAL:HG13	15:H:104:THR:N	2.34	0.42
15:H:126:GLY:O	15:H:145:ASN:HA	2.20	0.42
20:M:106:ASP:OD1	20:M:107:GLY:N	2.53	0.42
34:a:217:C:H4'	34:a:462:G:N2	2.35	0.42
34:a:363:A:C6	45:l:27:PRO:HD2	2.55	0.42
34:a:794:A:H4'	34:a:1521:C:O2'	2.20	0.42
34:a:818:G:H2'	34:a:820:U:C5	2.55	0.42
34:a:855:U:H2'	34:a:856:C:C6	2.55	0.42
34:a:1245:C:H2'	34:a:1246:A:H8	1.84	0.42
37:d:187:ARG:NH2	37:d:192:ALA:HA	2.35	0.42
39:f:9:MET:HB2	39:f:85:ILE:O	2.20	0.42
44:k:62:ALA:HB1	44:k:95:THR:CG2	2.50	0.42
51:r:33:THR:HG22	51:r:37:LYS:O	2.19	0.42
57:x:96:ILE:HD13	57:x:411:PRO:HD2	2.01	0.42
57:x:213:LEU:O	57:x:216:GLU:HG3	2.20	0.42
3:2:42:LEU:HD12	3:2:42:LEU:HA	1.85	0.41
8:A:671:C:H2'	8:A:672:C:C6	2.54	0.41
8:A:729:G:H5'	8:A:730:A:H5''	2.02	0.41
8:A:935:C:H2'	8:A:936:A:H8	1.85	0.41
8:A:936:A:H2'	8:A:937:C:C6	2.55	0.41
8:A:1037:G:N1	8:A:1119:U:O2	2.53	0.41
8:A:1164:C:C2	8:A:1165:A:C8	3.08	0.41
8:A:1981:A:H5''	8:A:1982:U:OP2	2.20	0.41
8:A:2291:U:H5''	8:A:2380:C:O2'	2.20	0.41
8:A:2296:U:C2	8:A:2333:A:H2	2.38	0.41
8:A:2454:G:C6	8:A:2499:C:N4	2.88	0.41
8:A:2662:A:H8	8:A:2662:A:O5'	2.02	0.41
8:A:2722:G:H2'	8:A:2723:C:C6	2.54	0.41
8:A:2803:G:C2	8:A:2804:U:C4	3.08	0.41
8:A:2901:C:N3	8:A:2902:C:N4	2.68	0.41
10:C:27:LYS:HA	10:C:27:LYS:HD3	1.79	0.41
10:C:157:ALA:HB1	10:C:196:ASN:O	2.20	0.41
12:E:46:GLN:HB3	12:E:83:VAL:HG21	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:J:4:PHE:O	24:Q:63:ARG:NH2	2.52	0.41
23:P:26:GLU:HA	23:P:43:GLU:HA	2.01	0.41
26:S:3:THR:HG21	26:S:58:ALA:N	2.35	0.41
26:S:7:HIS:HB2	26:S:50:VAL:HG21	2.02	0.41
29:V:26:PHE:HZ	29:V:47:VAL:HG11	1.84	0.41
29:V:65:VAL:HG12	29:V:66:ASP:OD2	2.18	0.41
34:a:7:A:H5'	34:a:298:A:O4'	2.20	0.41
34:a:184:G:H2'	34:a:185:U:C6	2.55	0.41
34:a:456:A:H2	34:a:476:U:N3	2.10	0.41
34:a:735:C:H2'	34:a:736:C:C6	2.55	0.41
34:a:981:U:H4'	47:n:61:ARG:HG2	2.02	0.41
34:a:1179:A:H2'	34:a:1180:A:O4'	2.20	0.41
34:a:1213:A:C8	34:a:1215:G:C6	3.08	0.41
34:a:1309:G:C6	34:a:1329:A:C6	3.08	0.41
34:a:1504:G:OP1	34:a:1507:A:H4'	2.20	0.41
36:c:149:LYS:HB2	36:c:168:ARG:HG3	2.01	0.41
39:f:88:MET:HE1	51:r:60:ARG:HB3	2.02	0.41
41:h:95:MET:O	41:h:98:LEU:HG	2.19	0.41
43:j:65:TYR:HE1	47:n:98:LYS:HG2	1.85	0.41
47:n:98:LYS:HE3	47:n:98:LYS:HB3	1.74	0.41
57:x:345:GLY:HA2	57:x:358:ARG:HH21	1.85	0.41
58:y:101:FME:HE3	58:y:101:FME:HB3	1.71	0.41
8:A:39:G:H2'	8:A:40:U:C6	2.54	0.41
8:A:128:C:H2'	8:A:129:C:C6	2.55	0.41
8:A:396:G:N2	8:A:2231:U:O2'	2.44	0.41
8:A:438:G:H2'	8:A:439:A:H8	1.84	0.41
8:A:613:A:H4'	8:A:614:A:C8	2.55	0.41
8:A:799:G:C6	8:A:800:A:C6	3.08	0.41
8:A:1041:G:H2'	8:A:1042:G:H8	1.85	0.41
8:A:2294:G:OP1	22:O:10:ARG:HD3	2.21	0.41
8:A:2341:G:H2'	8:A:2342:C:C6	2.55	0.41
8:A:2373:G:H2'	8:A:2374:C:H6	1.84	0.41
8:A:2830:C:O3'	11:D:56:LYS:NZ	2.53	0.41
11:D:133:THR:O	11:D:134:HIS:HB2	2.21	0.41
14:G:79:THR:HG23	14:G:80:GLU:N	2.35	0.41
15:H:81:ALA:HA	15:H:147:VAL:O	2.21	0.41
34:a:18:C:H4'	34:a:1078:U:O2	2.18	0.41
34:a:355:C:H2'	34:a:356:A:O4'	2.20	0.41
34:a:462:G:H1	34:a:468:A:N6	2.17	0.41
34:a:691:G:H2'	34:a:692:U:C6	2.56	0.41
34:a:1095:U:H5'	34:a:1109:C:O2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1231:G:C6	34:a:1232:U:C4	3.09	0.41
34:a:1302:C:C5	46:m:16:ILE:HG13	2.55	0.41
34:a:1471:U:H2'	34:a:1472:U:O4'	2.20	0.41
37:d:201:GLU:OE1	38:e:111:ARG:HD3	2.20	0.41
52:s:65:MET:HG3	52:s:73:PHE:CZ	2.55	0.41
56:w:9:A:H5'	56:w:46:G7M:H1'	2.02	0.41
57:x:461:GLY:H	57:x:464:HIS:HB3	1.84	0.41
8:A:71:A:H5''	8:A:73:A:C8	2.55	0.41
8:A:607:U:C5	8:A:620:G:C4	3.08	0.41
8:A:962:G:OP1	8:A:963:U:OP2	2.38	0.41
8:A:1752:C:H2'	8:A:1753:G:C8	2.55	0.41
8:A:2663:G:H2'	8:A:2664:G:O4'	2.20	0.41
10:C:173:LEU:O	10:C:180:MET:HA	2.20	0.41
23:P:19:PHE:CE2	23:P:83:ILE:HG21	2.55	0.41
23:P:104:GLY:HA3	34:a:1432:G:OP1	2.20	0.41
34:a:20:U:H2'	34:a:21:G:O4'	2.20	0.41
34:a:126:G:H2'	34:a:127:G:O4'	2.20	0.41
34:a:259:G:OP1	53:t:35:TYR:OH	2.32	0.41
34:a:553:A:C8	34:a:554:A:C8	3.08	0.41
34:a:684:U:H2'	34:a:685:G:O4'	2.20	0.41
36:c:52:SER:HB2	36:c:114:LEU:HG	2.02	0.41
37:d:181:PHE:CZ	37:d:184:LYS:HD2	2.55	0.41
49:p:53:ASP:O	49:p:57:ILE:HG12	2.20	0.41
55:v:59:A:H3'	55:v:60:U:H6	1.84	0.41
55:v:64:G:H2'	55:v:65:C:C6	2.56	0.41
57:x:93:ASP:HB3	57:x:464:HIS:N	2.36	0.41
57:x:267:SER:O	57:x:271:ASN:N	2.53	0.41
57:x:349:LEU:HD23	57:x:349:LEU:H	1.84	0.41
8:A:1:G:H2'	8:A:2:G:C8	2.55	0.41
8:A:271:G:C2	8:A:272:A:C5	3.09	0.41
8:A:310:A:HO2'	8:A:311:A:P	2.43	0.41
8:A:567:U:H2'	8:A:568:U:O4'	2.20	0.41
8:A:851:C:H2'	8:A:852:U:H6	1.85	0.41
8:A:897:C:H2'	8:A:898:C:O4'	2.20	0.41
8:A:1070:A:H2'	8:A:1096:A:OP1	2.19	0.41
8:A:1089:A:N3	8:A:1090:A:N6	2.69	0.41
8:A:1631:G:H1'	8:A:1635:A:H61	1.85	0.41
8:A:1827:U:H5'	8:A:1971:U:H4'	2.02	0.41
8:A:2405:G:O2'	8:A:2406:A:P	2.78	0.41
8:A:2414:G:C4	8:A:2415:G:C8	3.09	0.41
8:A:2649:C:H2'	8:A:2650:U:H6	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2732:G:H3'	8:A:2733:A:O4'	2.20	0.41
14:G:74:MET:O	14:G:78:VAL:HG13	2.20	0.41
26:S:86:MET:HG3	26:S:88:ARG:HD3	2.01	0.41
28:U:23:LYS:HB2	28:U:23:LYS:HE3	1.69	0.41
34:a:44:A:H2'	34:a:45:G:H8	1.85	0.41
34:a:76:G:N2	34:a:95:C:C4	2.88	0.41
34:a:209:U:H4'	34:a:210:C:C5	2.55	0.41
34:a:545:C:H2'	34:a:546:A:O4'	2.19	0.41
34:a:1328:C:H2'	34:a:1329:A:C8	2.45	0.41
34:a:1460:C:C4	34:a:1461:G:N7	2.89	0.41
35:b:201:GLY:HA3	35:b:212:TYR:OH	2.20	0.41
43:j:90:LEU:HB3	43:j:92:LEU:HD23	2.03	0.41
44:k:33:ILE:HG12	44:k:69:CYS:SG	2.60	0.41
55:v:24:U:H2'	55:v:25:C:H6	1.85	0.41
56:w:66:U:H2'	56:w:67:C:C6	2.56	0.41
57:x:525:GLU:O	57:x:527:GLY:N	2.53	0.41
8:A:120:U:H5''	8:A:122:G:OP2	2.21	0.41
8:A:177:G:H3'	8:A:178:G:C8	2.51	0.41
8:A:385:C:O2'	8:A:388:G:N2	2.53	0.41
8:A:603:A:N1	8:A:625:G:O2'	2.49	0.41
8:A:1421:G:H2'	8:A:1422:G:H8	1.85	0.41
8:A:1683:U:H2'	8:A:1684:G:H8	1.85	0.41
8:A:2227:A:H5''	10:C:260:LYS:HB3	2.03	0.41
12:E:145:ASP:HB3	12:E:184:ASP:OD2	2.21	0.41
26:S:7:HIS:HB2	26:S:50:VAL:CG2	2.51	0.41
31:X:32:LEU:HD23	31:X:32:LEU:HA	1.88	0.41
31:X:53:LYS:O	31:X:57:VAL:HG23	2.20	0.41
34:a:458:U:O2	34:a:474:G:C2	2.73	0.41
34:a:519:C:N4	34:a:529:G:O2'	2.45	0.41
34:a:589:U:H2'	34:a:590:U:C6	2.56	0.41
34:a:675:A:H2'	34:a:676:A:O4'	2.20	0.41
34:a:1373:G:P	42:i:72:SER:HG	2.43	0.41
34:a:1410:A:H2'	34:a:1411:C:C6	2.55	0.41
36:c:113:LYS:NZ	36:c:185:THR:O	2.51	0.41
40:g:71:THR:HA	40:g:95:ARG:NH1	2.35	0.41
40:g:112:ASP:OD1	40:g:112:ASP:N	2.54	0.41
50:q:57:VAL:HB	50:q:78:VAL:O	2.20	0.41
50:q:67:SER:HB2	50:q:70:LYS:CB	2.50	0.41
57:x:96:ILE:HG12	57:x:442:PRO:HG2	2.03	0.41
57:x:541:GLY:O	57:x:542:GLY:C	2.63	0.41
5:4:6:SER:OG	8:A:2466:C:H5''	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:8:C:C2	8:A:9:G:C8	3.08	0.41
8:A:13:A:O2'	8:A:15:G:N7	2.53	0.41
8:A:83:A:O2'	8:A:103:A:N6	2.53	0.41
8:A:774:G:HO2'	8:A:775:G:H8	1.63	0.41
8:A:955:PSU:H5'	20:M:86:LYS:HD2	2.03	0.41
8:A:957:C:H5'	20:M:75:GLU:OE2	2.20	0.41
8:A:1165:A:H2'	8:A:1166:G:H8	1.85	0.41
8:A:1197:G:N2	8:A:1249:U:O2'	2.53	0.41
8:A:1587:G:H2'	8:A:1588:G:H8	1.86	0.41
8:A:2480:C:H2'	8:A:2481:G:O4'	2.20	0.41
8:A:2700:A:H2'	8:A:2701:U:C6	2.56	0.41
8:A:2783:U:H2'	8:A:2784:U:C6	2.55	0.41
18:K:4:GLU:O	18:K:5:GLN:HB2	2.21	0.41
23:P:29:VAL:O	23:P:39:LEU:HD12	2.20	0.41
23:P:51:ASN:HA	23:P:56:SER:OG	2.21	0.41
34:a:664:G:H22	34:a:741:G:H1	1.68	0.41
34:a:898:G:N2	34:a:900:A:H3'	2.35	0.41
34:a:1411:C:H2'	34:a:1412:C:C6	2.55	0.41
34:a:1513:A:H2'	34:a:1514:G:H8	1.86	0.41
36:c:6:PRO:HB3	36:c:10:ARG:HH12	1.86	0.41
37:d:7:LYS:HB2	37:d:21:LYS:HD3	2.01	0.41
37:d:171:GLU:O	37:d:180:THR:OG1	2.38	0.41
40:g:13:PRO:HA	40:g:20:GLU:HA	2.01	0.41
41:h:3:GLN:O	41:h:80:PRO:HG3	2.21	0.41
41:h:26:MET:O	41:h:58:LEU:N	2.54	0.41
41:h:93:LYS:HE2	41:h:116:ARG:CZ	2.51	0.41
44:k:113:THR:HG23	44:k:115:ILE:HG13	2.02	0.41
51:r:28:LEU:O	51:r:32:ILE:HG23	2.20	0.41
53:t:30:PHE:O	53:t:34:VAL:HG23	2.20	0.41
57:x:113:CYS:SG	57:x:142:LYS:HD2	2.61	0.41
57:x:149:ASN:N	57:x:149:ASN:OD1	2.53	0.41
57:x:287:SER:O	57:x:291:VAL:HG12	2.20	0.41
57:x:398:ASP:CG	57:x:399:PRO:HD2	2.46	0.41
8:A:330:A:H8	8:A:1210:G:C5	2.38	0.41
8:A:537:G:O2'	8:A:556:A:N6	2.51	0.41
8:A:671:C:H2'	8:A:672:C:H6	1.85	0.41
8:A:774:G:O2'	8:A:775:G:H8	2.04	0.41
8:A:997:G:OP1	24:Q:91:ARG:HD2	2.20	0.41
8:A:1277:G:O2'	21:N:24:MET:HG2	2.21	0.41
8:A:1339:G:H2'	8:A:1340:U:O2	2.20	0.41
8:A:1775:U:O4	8:A:1789:A:H2	2.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1782:U:H1'	8:A:2609:U:H5''	2.02	0.41
8:A:2244:U:H2'	8:A:2245:U:C6	2.56	0.41
8:A:2314:A:H1'	13:F:154:THR:HG21	2.03	0.41
8:A:2577:A:O4'	8:A:2612:C:N4	2.54	0.41
10:C:79:ARG:HD2	10:C:81:GLU:OE2	2.20	0.41
31:X:73:ARG:NH1	31:X:75:GLU:OE2	2.45	0.41
34:a:207:C:H2'	34:a:208:U:C4'	2.49	0.41
34:a:339:C:H2'	34:a:340:U:H6	1.86	0.41
34:a:849:G:H2'	34:a:850:U:O4'	2.20	0.41
34:a:1007:U:H2'	34:a:1008:U:O4'	2.20	0.41
34:a:1118:U:OP1	42:i:10:ARG:HD2	2.20	0.41
35:b:75:ALA:O	35:b:79:VAL:HG23	2.21	0.41
39:f:9:MET:SD	39:f:86:ARG:HB2	2.61	0.41
48:o:31:LEU:HD23	48:o:31:LEU:HA	1.93	0.41
50:q:67:SER:HB2	50:q:70:LYS:HB2	2.02	0.41
56:w:25:C:H2'	56:w:26:A:C8	2.51	0.41
57:x:112:TYR:O	57:x:141:ASN:N	2.54	0.41
57:x:295:ASN:OD1	57:x:295:ASN:N	2.46	0.41
57:x:703:LYS:HB2	57:x:703:LYS:HE2	1.85	0.41
4:3:27:ASN:HD22	8:A:2362:C:P	2.44	0.41
8:A:68:G:H2'	8:A:69:C:O4'	2.21	0.41
8:A:142:A:N3	27:T:1:MET:N	2.67	0.41
8:A:277:G:O2'	8:A:361:G:N1	2.53	0.41
8:A:337:C:H2'	8:A:338:G:O4'	2.21	0.41
8:A:357:C:H2'	8:A:358:U:C6	2.56	0.41
8:A:367:G:C6	8:A:368:A:C2	3.08	0.41
8:A:528:A:H3'	17:J:116:ARG:NH2	2.36	0.41
8:A:743:A:OP1	11:D:135:GLY:HA2	2.20	0.41
8:A:1151:A:H2'	8:A:1152:C:C6	2.56	0.41
8:A:1264:A:OP2	8:A:1265:A:O2'	2.31	0.41
8:A:1409:U:C2	8:A:1410:G:C8	3.09	0.41
8:A:1742:U:H2'	8:A:1743:G:O4'	2.21	0.41
8:A:2454:G:C4	8:A:2455:G:C8	3.08	0.41
8:A:2635:A:H2'	8:A:2636:C:O4'	2.21	0.41
8:A:2813:A:C4	8:A:2814:A:C8	3.09	0.41
8:A:2848:G:H2'	8:A:2867:G:N2	2.36	0.41
13:F:129:MET:HE1	13:F:174:PHE:HZ	1.86	0.41
22:O:52:SER:OG	22:O:54:VAL:HG22	2.21	0.41
25:R:16:GLU:HG3	25:R:101:ILE:HG13	2.01	0.41
34:a:109:A:C6	34:a:326:G:C6	3.09	0.41
34:a:146:G:C2	34:a:177:G:C8	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:191:G:H2'	34:a:192:A:C8	2.56	0.41
34:a:476:U:H6	34:a:476:U:H2'	1.65	0.41
34:a:495:A:H4'	34:a:496:A:H5'	2.02	0.41
34:a:631:C:O5'	34:a:632:U:H5'	2.21	0.41
34:a:948:C:H2'	34:a:949:A:H8	1.85	0.41
34:a:1353:G:H2'	34:a:1354:U:C6	2.56	0.41
36:c:59:PRO:O	36:c:62:SER:OG	2.28	0.41
37:d:34:GLU:H	37:d:34:GLU:HG3	1.52	0.41
37:d:168:THR:HG23	37:d:183:ARG:NH1	2.35	0.41
39:f:35:LYS:NZ	39:f:37:HIS:HA	2.35	0.41
43:j:85:ASP:OD1	43:j:85:ASP:N	2.53	0.41
56:w:38:A:C5	56:w:39:PSU:C4	3.09	0.41
57:x:335:PHE:N	57:x:382:ALA:O	2.47	0.41
57:x:507:GLN:HE21	57:x:507:GLN:HB2	1.66	0.41
2:1:18:HIS:CE1	2:1:40:PRO:HD2	2.56	0.41
4:3:7:ARG:NH2	8:A:244:A:OP2	2.52	0.41
5:4:10:LEU:HD22	8:A:2477:U:O4	2.21	0.41
7:6:47:LYS:CB	7:6:50:ASP:HA	2.50	0.41
8:A:404:A:H1'	8:A:406:G:C4	2.55	0.41
8:A:661:A:H2'	8:A:662:G:O4'	2.21	0.41
8:A:714:U:O5'	48:o:88:ARG:NH2	2.53	0.41
8:A:876:C:H2'	8:A:877:A:O4'	2.20	0.41
8:A:1265:A:H8	8:A:1265:A:OP1	2.04	0.41
8:A:1318:U:H2'	8:A:1319:C:C6	2.56	0.41
8:A:1419:A:O2'	8:A:1421:G:N7	2.38	0.41
8:A:1425:G:H2'	8:A:1426:G:C8	2.55	0.41
8:A:1542:U:H2'	8:A:1543:G:O4'	2.21	0.41
8:A:1668:A:H4'	8:A:1669:A:O5'	2.21	0.41
8:A:1999:C:H4'	8:A:2723:C:O2	2.21	0.41
8:A:2079:U:C4	8:A:2080:A:N7	2.88	0.41
8:A:2521:C:C2	8:A:2545:G:N2	2.89	0.41
8:A:2626:C:C2	8:A:2627:G:C8	3.09	0.41
8:A:2686:G:H2'	8:A:2687:U:C6	2.55	0.41
8:A:2812:G:H2'	8:A:2813:A:H8	1.83	0.41
9:B:40:U:N3	9:B:44:G:OP2	2.41	0.41
10:C:90:ILE:HD12	10:C:102:TYR:CG	2.56	0.41
13:F:31:GLU:HG2	13:F:156:THR:O	2.21	0.41
14:G:18:ILE:HG12	14:G:23:ILE:HD12	2.03	0.41
15:H:97:ARG:HA	15:H:97:ARG:HD3	1.89	0.41
15:H:131:SER:HA	15:H:141:LYS:HA	2.02	0.41
18:K:105:ARG:HD3	18:K:108:ARG:HD2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:P:38:ARG:NH1	23:P:40:GLN:HB3	2.36	0.41
24:Q:65:ASN:OD1	24:Q:69:ARG:NE	2.54	0.41
28:U:38:ILE:HD13	28:U:38:ILE:HA	1.91	0.41
34:a:40:C:H2'	34:a:41:G:H8	1.86	0.41
34:a:74:A:C4	34:a:75:G:C8	3.09	0.41
34:a:96:U:O2'	34:a:97:G:H8	2.03	0.41
34:a:469:C:H3'	34:a:470:C:C5'	2.51	0.41
34:a:558:G:OP2	34:a:559:A:O2'	2.35	0.41
34:a:600:A:C4	34:a:639:G:N2	2.88	0.41
34:a:735:C:H2'	34:a:736:C:H6	1.85	0.41
34:a:921:U:OP1	34:a:1081:A:C4	2.73	0.41
34:a:1081:A:O4'	34:a:1081:A:OP2	2.39	0.41
34:a:1469:C:H2'	34:a:1470:U:O4'	2.21	0.41
35:b:56:LEU:HA	35:b:59:ILE:HG12	2.03	0.41
35:b:122:ASP:N	35:b:122:ASP:OD1	2.53	0.41
37:d:177:MET:N	37:d:177:MET:SD	2.93	0.41
45:l:85:ARG:O	45:l:95:HIS:HE1	2.04	0.41
47:n:18:LYS:HZ2	47:n:19:TYR:HE1	1.69	0.41
49:p:7:ALA:HB3	49:p:18:GLN:HB2	2.01	0.41
53:t:63:LYS:HA	53:t:63:LYS:HD2	1.87	0.41
56:w:52:G:H2'	56:w:53:G:H8	1.86	0.41
57:x:30:LEU:HA	57:x:32:TYR:CE2	2.55	0.41
57:x:309:HIS:CE1	57:x:314:GLU:HG2	2.56	0.41
57:x:316:PHE:CD2	57:x:348:VAL:HG11	2.55	0.41
2:1:35:LEU:HD11	8:A:2286:G:N7	2.37	0.41
7:6:56:ARG:O	7:6:57:VAL:C	2.61	0.41
8:A:57:C:H2'	8:A:58:G:O4'	2.20	0.41
8:A:271:G:C4	8:A:367:G:N2	2.89	0.41
8:A:553:G:C6	8:A:554:U:C4	3.08	0.41
8:A:645:C:H2'	8:A:647:G:C5	2.56	0.41
8:A:813:U:O2'	8:A:1225:G:H1'	2.21	0.41
8:A:1233:C:C2	8:A:1234:U:C5	3.09	0.41
8:A:1710:G:C6	8:A:1749:A:N1	2.89	0.41
8:A:2514:U:H4'	17:J:81:ILE:HG12	2.02	0.41
8:A:2542:A:H5''	8:A:2766:A:O2'	2.21	0.41
8:A:2641:G:H5''	17:J:78:THR:HB	2.02	0.41
8:A:2745:C:H2'	8:A:2746:U:C6	2.56	0.41
8:A:2901:C:C4	8:A:2902:C:N4	2.89	0.41
9:B:29:A:H2'	9:B:30:C:O4'	2.21	0.41
17:J:12:LYS:HE2	17:J:12:LYS:HB2	1.93	0.41
19:L:93:ASN:OD1	19:L:93:ASN:N	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:O:64:TYR:HB3	22:O:67:ASN:ND2	2.34	0.41
26:S:24:ILE:O	26:S:24:ILE:HG13	2.21	0.41
31:X:39:VAL:O	31:X:43:LYS:N	2.53	0.41
34:a:147:G:O2'	34:a:148:G:C8	2.67	0.41
34:a:283:U:H2'	34:a:284:C:O4'	2.21	0.41
34:a:721:G:H4'	34:a:722:G:O5'	2.21	0.41
34:a:864:A:H4'	38:e:89:THR:HG23	2.03	0.41
63:a:1620:AM2:HA5	63:a:1620:AM2:HC61	1.86	0.41
35:b:170:ILE:H	35:b:170:ILE:HD12	1.86	0.41
36:c:8:GLY:HA3	47:n:89:MET:SD	2.62	0.41
36:c:90:VAL:HA	36:c:93:ILE:HG12	2.03	0.41
38:e:106:ALA:HB2	38:e:124:ALA:HB3	2.02	0.41
39:f:6:ILE:HG23	39:f:89:VAL:HG12	2.03	0.41
39:f:53:LYS:HE2	39:f:53:LYS:HB2	1.95	0.41
42:i:4:GLN:HG3	42:i:21:LYS:HB3	2.02	0.41
45:l:80:LEU:O	45:l:97:VAL:HG22	2.21	0.41
45:l:109:ARG:HE	45:l:109:ARG:HB3	1.71	0.41
47:n:86:GLU:HG3	47:n:87:ALA:N	2.35	0.41
51:r:40:PRO:HB2	51:r:42:ARG:HG2	2.02	0.41
51:r:44:THR:O	51:r:45:GLY:C	2.62	0.41
55:v:17:C:H3'	55:v:17(A):U:H2'	2.02	0.41
57:x:101:SER:O	57:x:105:LEU:HD22	2.21	0.41
57:x:172:ILE:HD13	57:x:172:ILE:HG21	1.80	0.41
57:x:495:GLN:N	57:x:523:PRO:HG3	2.36	0.41
4:3:63:TYR:CD2	8:A:242:G:H5''	2.57	0.40
6:5:26:VAL:HA	6:5:84:TYR:HA	2.03	0.40
8:A:23:G:C2	8:A:24:G:C8	3.09	0.40
8:A:141:G:H1'	8:A:142:A:O4'	2.20	0.40
8:A:174:U:H2'	8:A:175:G:H8	1.85	0.40
8:A:608:A:H2'	8:A:609:A:C8	2.56	0.40
8:A:1170:C:H2'	8:A:1171:G:H8	1.84	0.40
8:A:1924:C:H2'	8:A:1925:C:C6	2.57	0.40
10:C:161:VAL:HG11	10:C:173:LEU:HD13	2.03	0.40
10:C:242:HIS:HA	10:C:243:PRO:HD3	1.92	0.40
11:D:33:ARG:NH1	11:D:75:ALA:O	2.54	0.40
12:E:88:ARG:HA	12:E:88:ARG:HD3	1.86	0.40
14:G:144:ALA:HB1	14:G:163:TYR:HE1	1.86	0.40
15:H:137:GLU:OE1	15:H:137:GLU:N	2.54	0.40
18:K:17:ARG:HB3	18:K:45:GLU:CD	2.46	0.40
22:O:35:ILE:HG21	22:O:71:ALA:HA	2.03	0.40
30:W:42:HIS:CE1	30:W:73:ARG:NH1	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Y:44:LYS:O	32:Y:48:ARG:HG2	2.20	0.40
34:a:75:G:N3	34:a:75:G:H2'	2.35	0.40
34:a:219:U:H2'	34:a:220:G:H8	1.86	0.40
34:a:697:U:O2	34:a:798:U:H1'	2.20	0.40
34:a:846:G:C6	34:a:847:G:C6	3.09	0.40
34:a:1436:U:N3	34:a:1437:A:N7	2.69	0.40
34:a:1530:G:O6	54:u:45:LYS:NZ	2.45	0.40
35:b:9:LEU:HD12	35:b:14:HIS:NE2	2.35	0.40
35:b:45:THR:O	35:b:49:PHE:CB	2.61	0.40
36:c:61:LYS:HD3	36:c:61:LYS:HA	1.74	0.40
38:e:47:PHE:CZ	38:e:137:ARG:HG2	2.56	0.40
42:i:44:ARG:HG2	42:i:45:MET:HE2	2.02	0.40
45:l:82:ARG:HD3	45:l:97:VAL:HG12	2.03	0.40
51:r:31:TYR:CG	51:r:54:LEU:HD11	2.56	0.40
57:x:518:VAL:N	57:x:579:PHE:O	2.54	0.40
3:2:34:ARG:NE	3:2:42:LEU:O	2.49	0.40
8:A:29:U:O2	8:A:1215:G:O2'	2.40	0.40
8:A:46:G:C6	8:A:180:G:C2	3.09	0.40
8:A:363:G:H2'	8:A:364:C:H6	1.87	0.40
8:A:537:G:H22	8:A:555:G:H2'	1.86	0.40
8:A:612:G:H2'	8:A:614:A:C8	2.56	0.40
8:A:817:C:O2'	8:A:839:U:H5''	2.21	0.40
8:A:906:U:O2'	20:M:66:ARG:NE	2.54	0.40
8:A:1441:G:H2'	8:A:1442:U:H6	1.84	0.40
8:A:1537:G:N1	8:A:1538:G:C4	2.88	0.40
8:A:1565:C:O2'	8:A:1567:G:N7	2.44	0.40
8:A:1913:A:C6	34:a:1494:G:H5''	2.56	0.40
8:A:2193:G:H2'	8:A:2194:U:C6	2.56	0.40
8:A:2472:G:O6	8:A:2475:C:H2'	2.21	0.40
8:A:2545:G:H2'	8:A:2546:U:O4'	2.21	0.40
9:B:28:C:H5''	22:O:31:THR:HG21	2.02	0.40
10:C:259:ASN:C	10:C:261:ARG:H	2.28	0.40
12:E:123:LYS:HE3	12:E:123:LYS:HB3	1.87	0.40
21:N:66:ALA:HB3	21:N:76:VAL:HG23	2.02	0.40
24:Q:45:ALA:O	24:Q:49:ARG:HG3	2.21	0.40
31:X:53:LYS:HA	31:X:56:ARG:HG3	2.02	0.40
34:a:266:G:H3'	50:q:68:LYS:HB2	2.02	0.40
34:a:1530:G:H2'	34:a:1531:A:H8	1.85	0.40
39:f:38:ARG:HH11	39:f:96:VAL:HG12	1.87	0.40
42:i:14:SER:OG	42:i:77:ALA:HB2	2.21	0.40
50:q:43:LEU:HD23	50:q:43:LEU:HA	1.96	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:t:27:MET:HG2	53:t:31:ILE:HD11	2.03	0.40
55:v:65:C:C2	55:v:66:C:C5	3.09	0.40
57:x:12:ILE:HG21	57:x:285:LEU:HD13	2.03	0.40
57:x:191:ASN:O	57:x:202:GLU:HG3	2.21	0.40
57:x:500:VAL:HG11	57:x:603:GLY:HA2	2.03	0.40
57:x:624:GLU:H	57:x:624:GLU:HG2	1.54	0.40
1:0:46:GLY:O	1:0:53:VAL:HG22	2.21	0.40
8:A:197:A:N6	8:A:2430:A:H2'	2.36	0.40
8:A:242:G:O2'	8:A:243:U:O5'	2.38	0.40
8:A:271:G:C5	8:A:367:G:N1	2.89	0.40
8:A:533:G:H5'	24:Q:23:TYR:CE1	2.57	0.40
8:A:639:U:C2	8:A:640:C:C5	3.09	0.40
8:A:764:A:O2'	8:A:765:C:H5'	2.21	0.40
8:A:1031:G:C6	8:A:1124:G:C6	3.10	0.40
8:A:1085:A:H4'	8:A:1086:A:OP1	2.20	0.40
8:A:1087:G:H8	8:A:1088:A:H4'	1.85	0.40
8:A:1417:C:O2'	8:A:1587:G:O2'	2.10	0.40
8:A:1707:G:C8	8:A:1756:G:C5	3.08	0.40
8:A:1803:A:H2	8:A:1823:G:H1'	1.86	0.40
8:A:2117:A:N3	8:A:2161:C:O2'	2.51	0.40
8:A:2502:G:H4'	8:A:2503:2MA:HM23	2.03	0.40
9:B:57:A:H2'	9:B:58:A:C8	2.56	0.40
11:D:181:ASP:OD2	11:D:184:ARG:HB2	2.22	0.40
13:F:21:TYR:HD1	13:F:21:TYR:HA	1.77	0.40
19:L:115:GLU:H	19:L:115:GLU:HG3	1.76	0.40
22:O:90:VAL:O	22:O:117:PHE:HB3	2.21	0.40
34:a:335:C:H2'	34:a:336:A:C8	2.55	0.40
34:a:821:G:H2'	34:a:822:U:H6	1.84	0.40
34:a:1057:G:C6	34:a:1204:A:N1	2.90	0.40
34:a:1117:A:H5''	42:i:105:ARG:NH2	2.36	0.40
34:a:1208:C:H2'	34:a:1209:C:O4'	2.21	0.40
34:a:1242:G:H1	34:a:1295:U:H3	1.68	0.40
34:a:1250:A:C8	34:a:1287:A:C8	3.09	0.40
34:a:1285:A:H4'	34:a:1286:U:H5''	2.02	0.40
34:a:1338:G:H22	55:v:29:G:H22	1.69	0.40
45:l:106:VAL:HG12	45:l:107:LYS:H	1.86	0.40
46:m:16:ILE:HD13	46:m:16:ILE:HA	1.90	0.40
49:p:10:GLY:HA3	49:p:16:PHE:HB3	2.03	0.40
57:x:430:MET:O	57:x:434:LEU:HD23	2.20	0.40
57:x:454:GLN:HE22	57:x:486:GLN:H	1.70	0.40
57:x:497:VAL:HG23	57:x:522:TYR:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:x:500:VAL:HG11	57:x:603:GLY:CA	2.51	0.40
57:x:656:GLU:OE2	57:x:684:LEU:HD22	2.22	0.40
1:0:28:SER:O	1:0:36:LYS:HA	2.20	0.40
6:5:30:SER:O	8:A:1054:A:H1'	2.21	0.40
8:A:247:G:H4'	8:A:386:G:C5	2.57	0.40
8:A:443:A:N7	12:E:40:ARG:HG2	2.36	0.40
8:A:483:A:N7	8:A:497:A:H2	2.19	0.40
8:A:578:G:O2'	8:A:580:U:OP2	2.32	0.40
8:A:870:U:H2'	8:A:871:U:H5'	2.03	0.40
8:A:930:G:C2	8:A:933:A:N7	2.90	0.40
8:A:1014:A:H2'	8:A:1015:U:C6	2.56	0.40
8:A:1232:G:C6	8:A:1233:C:C4	3.09	0.40
8:A:1422:G:C6	8:A:1577:C:N3	2.89	0.40
8:A:2474:U:H5''	8:A:2475:C:C5	2.55	0.40
8:A:2543:G:C6	8:A:2765:A:C5	3.09	0.40
8:A:2880:C:H4'	21:N:90:ARG:HH11	1.87	0.40
9:B:45:A:C4	9:B:46:A:C8	3.09	0.40
12:E:176:ASP:O	12:E:180:LEU:HG	2.22	0.40
13:F:47:LYS:HB2	13:F:47:LYS:HE3	1.73	0.40
13:F:60:SER:CB	13:F:88:VAL:HG21	2.51	0.40
20:M:119:LEU:HD23	20:M:119:LEU:HA	1.85	0.40
21:N:37:THR:HA	21:N:110:MET:HA	2.03	0.40
34:a:318:G:C6	34:a:336:A:C6	3.08	0.40
34:a:864:A:H5''	38:e:89:THR:HA	2.04	0.40
34:a:882:C:C2	34:a:883:C:C5	3.10	0.40
34:a:952:U:H2'	34:a:953:G:C8	2.56	0.40
34:a:1028:C:H2'	34:a:1029:U:O4'	2.21	0.40
34:a:1057:G:H2'	34:a:1058:G:O4'	2.21	0.40
34:a:1227:A:H5'	34:a:1228:C:OP2	2.21	0.40
36:c:169:GLU:OE2	36:c:169:GLU:N	2.54	0.40
37:d:9:LYS:HB3	37:d:9:LYS:HE2	1.77	0.40
37:d:124:VAL:N	37:d:127:ARG:O	2.54	0.40
48:o:7:THR:O	48:o:11:VAL:HG13	2.20	0.40
57:x:52:MET:N	57:x:52:MET:SD	2.94	0.40
57:x:197:GLN:HG3	57:x:199:VAL:HG22	2.04	0.40
2:1:28:THR:HG22	2:1:29:LYS:HG2	2.04	0.40
8:A:340:A:H2'	8:A:341:C:O4'	2.21	0.40
8:A:685:A:C8	8:A:773:U:C4	3.09	0.40
8:A:1098:A:C6	8:A:1099:G:C6	3.10	0.40
8:A:1152:C:H2'	8:A:1153:C:C6	2.51	0.40
8:A:1169:A:H2'	8:A:1170:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1323:C:OP1	26:S:98:LYS:NZ	2.39	0.40
8:A:1825:U:OP1	10:C:229:HIS:NE2	2.55	0.40
8:A:1827:U:H2'	8:A:1828:G:O4'	2.21	0.40
8:A:2019:A:H4'	24:Q:33:VAL:HG21	2.04	0.40
8:A:2036:C:H2'	8:A:2037:A:C8	2.56	0.40
8:A:2146:C:H4'	8:A:2147:A:C6	2.56	0.40
8:A:2236:U:H2'	8:A:2237:G:O4'	2.22	0.40
8:A:2262:U:OP1	8:A:2387:U:O2'	2.39	0.40
8:A:2474:U:H3'	8:A:2475:C:C6	2.56	0.40
8:A:2531:A:C2	8:A:2532:G:C8	3.10	0.40
8:A:2848:G:O2'	8:A:2868:A:N6	2.55	0.40
9:B:52:A:O2'	9:B:53:A:P	2.79	0.40
14:G:15:ASP:O	14:G:17:LYS:NZ	2.55	0.40
19:L:77:ILE:HA	19:L:77:ILE:HD13	1.75	0.40
21:N:32:GLU:HG2	21:N:115:LEU:HD12	2.04	0.40
31:X:9:LYS:HE3	31:X:53:LYS:HD3	2.04	0.40
34:a:31:G:C8	34:a:306:A:H1'	2.57	0.40
34:a:78:A:H2'	34:a:79:G:O4'	2.22	0.40
34:a:283:U:C4	34:a:284:C:C4	3.08	0.40
34:a:459:A:C2	34:a:474:G:C6	3.10	0.40
34:a:647:C:H2'	34:a:648:A:H8	1.86	0.40
34:a:931:C:H2'	34:a:932:C:C6	2.57	0.40
34:a:1053:G:H4'	34:a:1054:C:H5''	2.04	0.40
34:a:1347:G:N2	34:a:1374:A:OP2	2.52	0.40
34:a:1391:U:H2'	34:a:1392:G:C8	2.57	0.40
36:c:179:ALA:HB1	36:c:202:PHE:CE1	2.55	0.40
37:d:32:LYS:HB3	37:d:32:LYS:HE2	1.78	0.40
38:e:82:HIS:HB2	38:e:83:PRO:HD2	2.03	0.40
39:f:56:LYS:HB2	39:f:56:LYS:HE2	1.89	0.40
42:i:35:GLU:CD	42:i:44:ARG:HH11	2.29	0.40
42:i:82:ILE:O	42:i:86:LEU:HD13	2.21	0.40
46:m:40:GLU:H	46:m:40:GLU:CD	2.29	0.40
57:x:335:PHE:CZ	57:x:362:ILE:HG23	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	54/57 (95%)	53 (98%)	1 (2%)	0	100	100
2	1	48/55 (87%)	46 (96%)	2 (4%)	0	100	100
3	2	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
4	3	62/65 (95%)	56 (90%)	6 (10%)	0	100	100
5	4	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
6	5	129/165 (78%)	112 (87%)	17 (13%)	0	100	100
7	6	64/70 (91%)	57 (89%)	7 (11%)	0	100	100
10	C	269/273 (98%)	249 (93%)	20 (7%)	0	100	100
11	D	207/209 (99%)	192 (93%)	15 (7%)	0	100	100
12	E	199/201 (99%)	195 (98%)	4 (2%)	0	100	100
13	F	175/179 (98%)	157 (90%)	18 (10%)	0	100	100
14	G	174/177 (98%)	165 (95%)	9 (5%)	0	100	100
15	H	147/149 (99%)	125 (85%)	22 (15%)	0	100	100
16	I	139/142 (98%)	126 (91%)	12 (9%)	1 (1%)	18	49
17	J	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
18	K	120/123 (98%)	109 (91%)	11 (9%)	0	100	100
19	L	141/144 (98%)	133 (94%)	8 (6%)	0	100	100
20	M	134/136 (98%)	124 (92%)	10 (8%)	0	100	100
21	N	118/127 (93%)	113 (96%)	5 (4%)	0	100	100
22	O	114/117 (97%)	110 (96%)	4 (4%)	0	100	100
23	P	112/115 (97%)	106 (95%)	6 (5%)	0	100	100
24	Q	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
25	R	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	12	41
26	S	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
27	T	91/100 (91%)	88 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	U	100/104 (96%)	90 (90%)	10 (10%)	0	100	100
29	V	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
30	W	73/85 (86%)	68 (93%)	5 (7%)	0	100	100
31	X	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
32	Y	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
33	Z	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
35	b	216/240 (90%)	193 (89%)	23 (11%)	0	100	100
36	c	204/233 (88%)	196 (96%)	8 (4%)	0	100	100
37	d	203/206 (98%)	188 (93%)	15 (7%)	0	100	100
38	e	155/167 (93%)	143 (92%)	12 (8%)	0	100	100
39	f	98/135 (73%)	91 (93%)	7 (7%)	0	100	100
40	g	149/179 (83%)	133 (89%)	16 (11%)	0	100	100
41	h	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
42	i	125/130 (96%)	114 (91%)	11 (9%)	0	100	100
43	j	96/103 (93%)	80 (83%)	16 (17%)	0	100	100
44	k	114/129 (88%)	103 (90%)	11 (10%)	0	100	100
45	l	121/124 (98%)	105 (87%)	16 (13%)	0	100	100
46	m	112/118 (95%)	104 (93%)	8 (7%)	0	100	100
47	n	99/102 (97%)	93 (94%)	6 (6%)	0	100	100
48	o	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
49	p	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
50	q	78/84 (93%)	73 (94%)	5 (6%)	0	100	100
51	r	63/75 (84%)	59 (94%)	4 (6%)	0	100	100
52	s	80/92 (87%)	75 (94%)	5 (6%)	0	100	100
53	t	83/87 (95%)	81 (98%)	2 (2%)	0	100	100
54	u	63/71 (89%)	55 (87%)	8 (13%)	0	100	100
57	x	694/704 (99%)	632 (91%)	61 (9%)	1 (0%)	48	78
All	All	6544/6924 (94%)	6062 (93%)	479 (7%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	R	51	VAL

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Mol	Chain	Res	Type
57	x	403	ILE
16	I	22	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	0	47/48 (98%)	47 (100%)	0	100	100
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	38 (100%)	0	100	100
4	3	51/52 (98%)	49 (96%)	2 (4%)	28	60
5	4	34/34 (100%)	34 (100%)	0	100	100
7	6	59/62 (95%)	56 (95%)	3 (5%)	21	52
10	C	216/218 (99%)	212 (98%)	4 (2%)	50	73
11	D	164/164 (100%)	164 (100%)	0	100	100
12	E	165/165 (100%)	163 (99%)	2 (1%)	63	78
13	F	148/150 (99%)	147 (99%)	1 (1%)	76	82
14	G	137/138 (99%)	137 (100%)	0	100	100
15	H	114/114 (100%)	113 (99%)	1 (1%)	70	80
17	J	116/116 (100%)	116 (100%)	0	100	100
18	K	103/104 (99%)	103 (100%)	0	100	100
19	L	102/103 (99%)	99 (97%)	3 (3%)	37	66
20	M	109/109 (100%)	108 (99%)	1 (1%)	70	80
21	N	100/103 (97%)	100 (100%)	0	100	100
22	O	86/87 (99%)	85 (99%)	1 (1%)	63	78
23	P	99/100 (99%)	99 (100%)	0	100	100
24	Q	89/90 (99%)	89 (100%)	0	100	100
25	R	84/84 (100%)	82 (98%)	2 (2%)	43	69
26	S	93/93 (100%)	93 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	T	80/84 (95%)	78 (98%)	2 (2%)	42	69
28	U	83/85 (98%)	83 (100%)	0	100	100
29	V	78/78 (100%)	78 (100%)	0	100	100
30	W	57/63 (90%)	57 (100%)	0	100	100
31	X	67/68 (98%)	67 (100%)	0	100	100
32	Y	55/55 (100%)	53 (96%)	2 (4%)	31	62
33	Z	48/49 (98%)	48 (100%)	0	100	100
35	b	180/198 (91%)	170 (94%)	10 (6%)	19	49
36	c	170/190 (90%)	170 (100%)	0	100	100
37	d	172/173 (99%)	166 (96%)	6 (4%)	32	62
38	e	114/126 (90%)	114 (100%)	0	100	100
39	f	87/116 (75%)	87 (100%)	0	100	100
40	g	124/147 (84%)	123 (99%)	1 (1%)	73	81
41	h	104/105 (99%)	103 (99%)	1 (1%)	68	79
42	i	105/107 (98%)	99 (94%)	6 (6%)	18	49
43	j	86/90 (96%)	83 (96%)	3 (4%)	32	62
44	k	89/99 (90%)	88 (99%)	1 (1%)	65	78
45	l	103/104 (99%)	102 (99%)	1 (1%)	68	79
46	m	92/96 (96%)	88 (96%)	4 (4%)	26	57
47	n	79/84 (94%)	79 (100%)	0	100	100
48	o	76/77 (99%)	75 (99%)	1 (1%)	61	77
49	p	65/65 (100%)	62 (95%)	3 (5%)	24	55
50	q	74/78 (95%)	71 (96%)	3 (4%)	27	59
51	r	56/65 (86%)	51 (91%)	5 (9%)	9	33
52	s	72/79 (91%)	72 (100%)	0	100	100
53	t	65/66 (98%)	65 (100%)	0	100	100
54	u	46/61 (75%)	44 (96%)	2 (4%)	26	57
57	x	575/578 (100%)	514 (89%)	61 (11%)	6	26
58	y	1/1 (100%)	1 (100%)	0	100	100
All	All	5202/5408 (96%)	5070 (98%)	132 (2%)	42	69

All (132) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	3	28	LEU
4	3	32	LEU
7	6	20	ASN
7	6	50	ASP
7	6	64	PHE
10	C	85	ASN
10	C	206	LYS
10	C	239	PHE
10	C	259	ASN
12	E	65	THR
12	E	125	SER
13	F	59	ILE
15	H	138	VAL
19	L	30	THR
19	L	115	GLU
19	L	117	THR
20	M	60	GLN
22	O	31	THR
25	R	49	ILE
25	R	51	VAL
27	T	37	ASP
27	T	93	LEU
32	Y	19	LEU
32	Y	21	LEU
35	b	13	VAL
35	b	14	HIS
35	b	34	ARG
35	b	63	LYS
35	b	66	ILE
35	b	86	CYS
35	b	87	ASP
35	b	91	VAL
35	b	108	GLN
35	b	191	ASP
37	d	28	ASP
37	d	34	GLU
37	d	35	GLN
37	d	77	GLU
37	d	141	VAL
37	d	144	ILE
40	g	67	ASN
41	h	17	GLN
42	i	34	LEU

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Mol	Chain	Res	Type
42	i	104	THR
42	i	105	ARG
42	i	109	GLN
42	i	110	VAL
42	i	129	ARG
43	j	44	THR
43	j	53	ILE
43	j	92	LEU
44	k	118	ASN
45	l	3	VAL
46	m	3	ILE
46	m	24	VAL
46	m	64	VAL
46	m	106	ARG
48	o	19	ASN
49	p	9	HIS
49	p	12	LYS
49	p	45	GLU
50	q	16	MET
50	q	48	GLU
50	q	51	GLU
51	r	13	THR
51	r	17	VAL
51	r	20	ILE
51	r	44	THR
51	r	46	THR
54	u	12	ASP
54	u	13	VAL
57	x	6	ILE
57	x	14	ILE
57	x	18	ILE
57	x	22	LYS
57	x	31	PHE
57	x	35	VAL
57	x	37	HIS
57	x	52	MET
57	x	53	GLU
57	x	54	GLN
57	x	56	GLN
57	x	60	ILE
57	x	61	THR
57	x	68	THR

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Mol	Chain	Res	Type
57	x	77	GLN
57	x	78	TYR
57	x	105	LEU
57	x	176	GLU
57	x	190	ILE
57	x	196	ASP
57	x	197	GLN
57	x	201	PHE
57	x	209	ASP
57	x	212	GLU
57	x	218	HIS
57	x	227	GLU
57	x	231	GLU
57	x	295	ASN
57	x	297	ILE
57	x	298	LEU
57	x	317	SER
57	x	322	LYS
57	x	323	ILE
57	x	325	THR
57	x	328	PHE
57	x	329	VAL
57	x	332	LEU
57	x	365	MET
57	x	366	HIS
57	x	371	GLU
57	x	373	ILE
57	x	395	THR
57	x	398	ASP
57	x	414	VAL
57	x	452	SER
57	x	455	THR
57	x	539	ILE
57	x	540	LYS
57	x	544	ILE
57	x	547	GLU
57	x	584	ASP
57	x	587	SER
57	x	621	GLU
57	x	622	THR
57	x	627	THR
57	x	641	LEU

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Mol	Chain	Res	Type
57	x	645	GLU
57	x	667	THR
57	x	672	LEU
57	x	701	ARG
57	x	703	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
5	4	13	ASN
10	C	85	ASN
12	E	136	GLN
13	F	20	ASN
14	G	29	ASN
14	G	72	ASN
14	G	110	HIS
15	H	135	HIS
17	J	86	GLN
18	K	88	ASN
23	P	9	GLN
23	P	65	ASN
27	T	70	HIS
35	b	176	ASN
36	c	2	GLN
36	c	139	ASN
39	f	3	HIS
40	g	67	ASN
40	g	129	ASN
43	j	58	ASN
51	r	51	GLN
57	x	56	GLN
57	x	331	ASN
57	x	350	ASN
57	x	695	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	a	1539/1542 (99%)	442 (28%)	0
55	v	76/77 (98%)	24 (31%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
56	w	75/76 (98%)	21 (28%)	0
59	z	9/33 (27%)	2 (22%)	0
8	A	2902/2903 (99%)	574 (19%)	34 (1%)
9	B	119/120 (99%)	21 (17%)	3 (2%)
All	All	4720/4751 (99%)	1084 (22%)	37 (0%)

All (1084) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	A	10	A
8	A	34	U
8	A	35	G
8	A	46	G
8	A	50	U
8	A	62	U
8	A	63	A
8	A	64	A
8	A	71	A
8	A	74	A
8	A	75	G
8	A	84	A
8	A	91	A
8	A	101	A
8	A	102	U
8	A	103	A
8	A	118	A
8	A	119	A
8	A	120	U
8	A	131	A
8	A	139	U
8	A	141	G
8	A	142	A
8	A	160	A
8	A	163	C
8	A	181	A
8	A	196	A
8	A	199	A
8	A	215	G
8	A	216	A
8	A	221	A
8	A	222	A
8	A	224	U

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Mol	Chain	Res	Type
8	A	225	C
8	A	228	C
8	A	229	C
8	A	233	A
8	A	242	G
8	A	243	U
8	A	248	G
8	A	250	G
8	A	255	A
8	A	266	G
8	A	271	G
8	A	272	A
8	A	273	G
8	A	274	C
8	A	275	C
8	A	276	U
8	A	277	G
8	A	278	A
8	A	284	U
8	A	287	G
8	A	288	U
8	A	291	G
8	A	294	A
8	A	311	A
8	A	330	A
8	A	331	C
8	A	345	A
8	A	346	A
8	A	355	U
8	A	369	U
8	A	371	A
8	A	372	G
8	A	373	U
8	A	377	G
8	A	383	C
8	A	386	G
8	A	395	U
8	A	396	G
8	A	401	A
8	A	403	U
8	A	404	A
8	A	405	U

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Mol	Chain	Res	Type
8	A	406	G
8	A	411	G
8	A	424	G
8	A	434	U
8	A	435	C
8	A	452	G
8	A	455	C
8	A	457	A
8	A	458	G
8	A	459	U
8	A	475	C
8	A	480	A
8	A	481	G
8	A	482	A
8	A	489	G
8	A	491	G
8	A	496	G
8	A	501	A
8	A	505	A
8	A	509	C
8	A	513	A
8	A	529	A
8	A	532	A
8	A	548	G
8	A	549	G
8	A	556	A
8	A	563	A
8	A	568	U
8	A	571	U
8	A	573	U
8	A	575	A
8	A	603	A
8	A	613	A
8	A	614	A
8	A	615	U
8	A	622	G
8	A	627	A
8	A	637	A
8	A	645	C
8	A	646	U
8	A	647	G
8	A	653	U

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Mol	Chain	Res	Type
8	A	654	A
8	A	655	A
8	A	669	G
8	A	670	A
8	A	677	A
8	A	682	G
8	A	685	A
8	A	686	U
8	A	730	A
8	A	740	C
8	A	747	5MC
8	A	762	U
8	A	764	A
8	A	765	C
8	A	774	G
8	A	775	G
8	A	776	G
8	A	782	A
8	A	784	G
8	A	785	G
8	A	791	C
8	A	792	A
8	A	805	G
8	A	812	C
8	A	819	A
8	A	827	U
8	A	828	U
8	A	831	G
8	A	845	A
8	A	846	U
8	A	856	G
8	A	859	G
8	A	866	A
8	A	869	G
8	A	875	G
8	A	876	C
8	A	878	A
8	A	879	G
8	A	881	G
8	A	882	G
8	A	884	U
8	A	887	A

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Mol	Chain	Res	Type
8	A	888	C
8	A	889	C
8	A	890	C
8	A	894	U
8	A	896	A
8	A	897	C
8	A	901	C
8	A	907	G
8	A	910	A
8	A	914	G
8	A	927	A
8	A	931	U
8	A	938	G
8	A	941	A
8	A	945	A
8	A	946	C
8	A	959	A
8	A	961	C
8	A	973	A
8	A	974	G
8	A	983	A
8	A	984	A
8	A	990	A
8	A	995	C
8	A	996	A
8	A	999	U
8	A	1005	C
8	A	1012	U
8	A	1013	C
8	A	1025	G
8	A	1026	G
8	A	1033	U
8	A	1040	A
8	A	1044	C
8	A	1045	C
8	A	1046	A
8	A	1047	G
8	A	1048	A
8	A	1057	A
8	A	1058	U
8	A	1059	G
8	A	1060	U

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Mol	Chain	Res	Type
8	A	1061	U
8	A	1062	G
8	A	1063	G
8	A	1064	C
8	A	1065	U
8	A	1066	U
8	A	1067	A
8	A	1068	G
8	A	1069	A
8	A	1070	A
8	A	1072	C
8	A	1073	A
8	A	1074	G
8	A	1075	C
8	A	1076	C
8	A	1077	A
8	A	1079	C
8	A	1080	A
8	A	1081	U
8	A	1082	U
8	A	1083	U
8	A	1084	A
8	A	1085	A
8	A	1086	A
8	A	1087	G
8	A	1088	A
8	A	1089	A
8	A	1091	G
8	A	1092	C
8	A	1093	G
8	A	1094	U
8	A	1095	A
8	A	1097	U
8	A	1099	G
8	A	1100	C
8	A	1101	U
8	A	1102	C
8	A	1103	A
8	A	1105	U
8	A	1106	G
8	A	1107	G
8	A	1111	A

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Mol	Chain	Res	Type
8	A	1112	G
8	A	1115	G
8	A	1117	C
8	A	1120	G
8	A	1130	U
8	A	1132	U
8	A	1133	A
8	A	1135	C
8	A	1139	G
8	A	1172	C
8	A	1174	U
8	A	1175	A
8	A	1176	U
8	A	1177	G
8	A	1178	C
8	A	1179	G
8	A	1180	U
8	A	1204	A
8	A	1227	G
8	A	1247	A
8	A	1253	A
8	A	1255	U
8	A	1256	G
8	A	1271	G
8	A	1272	A
8	A	1294	U
8	A	1300	G
8	A	1301	A
8	A	1332	G
8	A	1341	G
8	A	1345	C
8	A	1359	A
8	A	1365	A
8	A	1368	G
8	A	1378	A
8	A	1379	U
8	A	1380	G
8	A	1383	A
8	A	1395	A
8	A	1408	G
8	A	1415	U
8	A	1416	G

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Mol	Chain	Res	Type
8	A	1419	A
8	A	1420	A
8	A	1427	A
8	A	1428	C
8	A	1433	A
8	A	1452	G
8	A	1454	C
8	A	1455	G
8	A	1458	U
8	A	1460	U
8	A	1461	C
8	A	1482	G
8	A	1490	A
8	A	1491	G
8	A	1493	C
8	A	1497	U
8	A	1498	C
8	A	1515	A
8	A	1523	U
8	A	1529	G
8	A	1534	U
8	A	1535	A
8	A	1536	C
8	A	1558	C
8	A	1566	A
8	A	1569	A
8	A	1578	U
8	A	1583	A
8	A	1584	U
8	A	1585	C
8	A	1603	A
8	A	1608	A
8	A	1610	A
8	A	1634	A
8	A	1647	U
8	A	1648	U
8	A	1649	G
8	A	1654	A
8	A	1674	G
8	A	1675	C
8	A	1698	A
8	A	1715	G

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Mol	Chain	Res	Type
8	A	1729	U
8	A	1730	C
8	A	1731	G
8	A	1732	C
8	A	1738	G
8	A	1744	A
8	A	1757	A
8	A	1764	C
8	A	1773	A
8	A	1784	A
8	A	1786	A
8	A	1787	A
8	A	1791	A
8	A	1800	C
8	A	1801	A
8	A	1807	G
8	A	1808	A
8	A	1809	A
8	A	1811	G
8	A	1816	C
8	A	1829	A
8	A	1848	A
8	A	1857	G
8	A	1884	G
8	A	1896	G
8	A	1900	A
8	A	1901	A
8	A	1906	G
8	A	1912	A
8	A	1913	A
8	A	1914	C
8	A	1915	3TD
8	A	1927	A
8	A	1929	G
8	A	1930	G
8	A	1931	U
8	A	1937	A
8	A	1938	A
8	A	1939	5MU
8	A	1955	U
8	A	1960	A
8	A	1967	C

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Mol	Chain	Res	Type
8	A	1970	A
8	A	1971	U
8	A	1972	G
8	A	1982	U
8	A	1991	U
8	A	1997	C
8	A	2020	A
8	A	2022	U
8	A	2023	C
8	A	2030	6MZ
8	A	2031	A
8	A	2032	G
8	A	2033	A
8	A	2036	C
8	A	2043	C
8	A	2049	G
8	A	2055	C
8	A	2056	G
8	A	2059	A
8	A	2060	A
8	A	2061	G
8	A	2062	A
8	A	2069	G7M
8	A	2072	C
8	A	2093	G
8	A	2100	G
8	A	2104	C
8	A	2105	U
8	A	2107	G
8	A	2108	A
8	A	2109	U
8	A	2110	G
8	A	2111	U
8	A	2112	G
8	A	2113	U
8	A	2114	A
8	A	2115	G
8	A	2116	G
8	A	2118	U
8	A	2120	G
8	A	2121	G
8	A	2123	G

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Mol	Chain	Res	Type
8	A	2125	G
8	A	2126	A
8	A	2129	C
8	A	2131	U
8	A	2132	U
8	A	2133	G
8	A	2134	A
8	A	2136	G
8	A	2140	G
8	A	2141	G
8	A	2143	C
8	A	2144	G
8	A	2145	C
8	A	2146	C
8	A	2147	A
8	A	2149	U
8	A	2151	U
8	A	2153	C
8	A	2155	U
8	A	2156	G
8	A	2157	G
8	A	2158	A
8	A	2159	G
8	A	2164	C
8	A	2165	C
8	A	2170	A
8	A	2171	A
8	A	2172	U
8	A	2173	A
8	A	2174	C
8	A	2176	A
8	A	2177	C
8	A	2179	C
8	A	2181	U
8	A	2184	A
8	A	2185	U
8	A	2186	G
8	A	2187	U
8	A	2188	U
8	A	2189	U
8	A	2193	G
8	A	2197	U

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Mol	Chain	Res	Type
8	A	2198	A
8	A	2203	U
8	A	2204	G
8	A	2211	A
8	A	2225	A
8	A	2238	G
8	A	2239	G
8	A	2266	A
8	A	2273	A
8	A	2278	A
8	A	2279	G
8	A	2283	C
8	A	2287	A
8	A	2288	A
8	A	2297	A
8	A	2305	U
8	A	2309	A
8	A	2310	C
8	A	2312	U
8	A	2319	G
8	A	2320	U
8	A	2322	A
8	A	2325	G
8	A	2333	A
8	A	2334	U
8	A	2336	A
8	A	2344	U
8	A	2345	G
8	A	2347	C
8	A	2350	C
8	A	2357	G
8	A	2361	G
8	A	2382	G
8	A	2383	G
8	A	2385	C
8	A	2402	U
8	A	2406	A
8	A	2407	A
8	A	2408	U
8	A	2410	G
8	A	2423	U
8	A	2425	A

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Mol	Chain	Res	Type
8	A	2426	A
8	A	2429	G
8	A	2430	A
8	A	2432	A
8	A	2435	A
8	A	2441	U
8	A	2445	2MG
8	A	2447	G
8	A	2448	A
8	A	2475	C
8	A	2476	A
8	A	2478	A
8	A	2487	G
8	A	2494	G
8	A	2502	G
8	A	2503	2MA
8	A	2505	G
8	A	2518	A
8	A	2520	C
8	A	2529	G
8	A	2535	G
8	A	2547	A
8	A	2554	U
8	A	2556	C
8	A	2566	A
8	A	2567	G
8	A	2573	C
8	A	2576	G
8	A	2584	U
8	A	2585	U
8	A	2602	A
8	A	2609	U
8	A	2613	U
8	A	2615	U
8	A	2619	C
8	A	2621	G
8	A	2629	U
8	A	2630	G
8	A	2638	G
8	A	2646	C
8	A	2654	A
8	A	2656	U

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Mol	Chain	Res	Type
8	A	2660	A
8	A	2663	G
8	A	2689	U
8	A	2690	U
8	A	2702	G
8	A	2714	G
8	A	2718	G
8	A	2725	A
8	A	2726	A
8	A	2729	G
8	A	2732	G
8	A	2733	A
8	A	2739	U
8	A	2744	G
8	A	2748	A
8	A	2765	A
8	A	2778	A
8	A	2779	U
8	A	2780	G
8	A	2791	G
8	A	2793	C
8	A	2798	U
8	A	2799	A
8	A	2800	A
8	A	2808	G
8	A	2818	U
8	A	2820	A
8	A	2821	A
8	A	2849	U
8	A	2867	G
8	A	2872	A
8	A	2873	A
8	A	2880	C
8	A	2884	U
8	A	2886	A
8	A	2891	U
8	A	2902	C
9	B	9	G
9	B	18	G
9	B	25	U
9	B	35	C
9	B	36	C

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Mol	Chain	Res	Type
9	B	37	C
9	B	41	G
9	B	42	C
9	B	44	G
9	B	45	A
9	B	51	G
9	B	52	A
9	B	53	A
9	B	56	G
9	B	67	G
9	B	73	A
9	B	88	C
9	B	89	U
9	B	108	A
9	B	109	A
9	B	120	U
34	a	2	A
34	a	5	U
34	a	6	G
34	a	7	A
34	a	9	G
34	a	16	A
34	a	22	G
34	a	31	G
34	a	32	A
34	a	37	U
34	a	39	G
34	a	46	G
34	a	47	C
34	a	48	C
34	a	50	A
34	a	51	A
34	a	64	G
34	a	69	G
34	a	71	A
34	a	73	C
34	a	74	A
34	a	77	A
34	a	78	A
34	a	79	G
34	a	80	A
34	a	81	A

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Mol	Chain	Res	Type
34	a	83	C
34	a	84	U
34	a	85	U
34	a	86	G
34	a	88	U
34	a	89	U
34	a	90	C
34	a	92	U
34	a	94	G
34	a	97	G
34	a	114	U
34	a	121	U
34	a	131	A
34	a	133	U
34	a	140	U
34	a	141	G
34	a	144	G
34	a	145	G
34	a	146	G
34	a	148	G
34	a	152	A
34	a	158	G
34	a	160	A
34	a	163	C
34	a	164	G
34	a	166	U
34	a	169	C
34	a	170	U
34	a	171	A
34	a	173	U
34	a	174	A
34	a	179	A
34	a	180	U
34	a	182	A
34	a	183	C
34	a	186	C
34	a	188	C
34	a	189	A
34	a	197	A
34	a	198	G
34	a	201	G
34	a	202	G

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Mol	Chain	Res	Type
34	a	204	G
34	a	205	A
34	a	206	C
34	a	207	C
34	a	208	U
34	a	209	U
34	a	210	C
34	a	211	G
34	a	212	G
34	a	213	G
34	a	214	C
34	a	216	U
34	a	219	U
34	a	221	C
34	a	224	U
34	a	226	G
34	a	240	G
34	a	245	U
34	a	246	A
34	a	247	G
34	a	251	G
34	a	253	A
34	a	262	A
34	a	266	G
34	a	267	C
34	a	271	C
34	a	279	A
34	a	281	G
34	a	289	G
34	a	298	A
34	a	299	G
34	a	301	G
34	a	316	C
34	a	317	U
34	a	321	A
34	a	322	C
34	a	328	C
34	a	330	C
34	a	342	C
34	a	343	U
34	a	344	A
34	a	345	C

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Mol	Chain	Res	Type
34	a	346	G
34	a	347	G
34	a	351	G
34	a	352	C
34	a	353	A
34	a	354	G
34	a	363	A
34	a	367	U
34	a	372	C
34	a	373	A
34	a	374	A
34	a	375	U
34	a	376	G
34	a	384	G
34	a	388	G
34	a	392	C
34	a	397	A
34	a	405	U
34	a	406	G
34	a	411	A
34	a	414	A
34	a	415	A
34	a	421	U
34	a	422	C
34	a	423	G
34	a	428	G
34	a	429	U
34	a	430	A
34	a	435	A
34	a	436	C
34	a	439	U
34	a	442	G
34	a	443	C
34	a	447	G
34	a	448	A
34	a	454	G
34	a	457	G
34	a	458	U
34	a	460	A
34	a	462	G
34	a	463	U
34	a	464	U

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Mol	Chain	Res	Type
34	a	467	U
34	a	468	A
34	a	469	C
34	a	470	C
34	a	471	U
34	a	472	U
34	a	473	U
34	a	476	U
34	a	477	C
34	a	479	U
34	a	482	A
34	a	484	G
34	a	492	C
34	a	495	A
34	a	496	A
34	a	497	G
34	a	505	G
34	a	509	A
34	a	510	A
34	a	511	C
34	a	512	U
34	a	515	G
34	a	516	PSU
34	a	518	C
34	a	524	G
34	a	530	G
34	a	532	A
34	a	547	A
34	a	560	A
34	a	562	U
34	a	564	C
34	a	570	G
34	a	572	A
34	a	573	A
34	a	574	A
34	a	575	G
34	a	576	C
34	a	577	G
34	a	583	A
34	a	596	A
34	a	607	A
34	a	614	C

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Mol	Chain	Res	Type
34	a	618	C
34	a	620	C
34	a	623	C
34	a	624	C
34	a	633	G
34	a	635	A
34	a	636	U
34	a	639	G
34	a	641	U
34	a	650	G
34	a	661	G
34	a	662	U
34	a	665	A
34	a	676	A
34	a	686	U
34	a	687	A
34	a	690	G
34	a	693	G
34	a	695	A
34	a	700	G
34	a	702	A
34	a	703	G
34	a	710	G
34	a	721	G
34	a	723	U
34	a	724	G
34	a	731	G
34	a	733	G
34	a	734	G
34	a	736	C
34	a	739	C
34	a	753	A
34	a	755	G
34	a	777	A
34	a	781	A
34	a	782	A
34	a	793	U
34	a	794	A
34	a	799	G
34	a	812	G
34	a	815	A
34	a	817	C

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Mol	Chain	Res	Type
34	a	818	G
34	a	819	A
34	a	820	U
34	a	821	G
34	a	833	G
34	a	836	G
34	a	837	U
34	a	840	C
34	a	842	U
34	a	843	U
34	a	845	A
34	a	849	G
34	a	864	A
34	a	865	A
34	a	872	A
34	a	876	C
34	a	885	G
34	a	890	G
34	a	891	U
34	a	902	G
34	a	914	A
34	a	920	U
34	a	921	U
34	a	926	G
34	a	927	G
34	a	934	C
34	a	935	A
34	a	945	G
34	a	946	A
34	a	958	A
34	a	960	U
34	a	961	U
34	a	964	A
34	a	965	U
34	a	966	2MG
34	a	967	5MC
34	a	969	A
34	a	975	A
34	a	976	G
34	a	977	A
34	a	979	C
34	a	980	C

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Mol	Chain	Res	Type
34	a	982	U
34	a	984	C
34	a	989	U
34	a	992	U
34	a	993	G
34	a	994	A
34	a	995	C
34	a	996	A
34	a	997	U
34	a	1000	A
34	a	1002	G
34	a	1004	A
34	a	1008	U
34	a	1011	C
34	a	1012	A
34	a	1022	A
34	a	1023	U
34	a	1026	G
34	a	1027	C
34	a	1028	C
34	a	1029	U
34	a	1030	U
34	a	1031	C
34	a	1032	G
34	a	1033	G
34	a	1034	G
34	a	1037	C
34	a	1041	G
34	a	1045	C
34	a	1049	U
34	a	1050	G
34	a	1064	G
34	a	1065	U
34	a	1075	U
34	a	1080	A
34	a	1081	A
34	a	1082	A
34	a	1083	U
34	a	1084	G
34	a	1085	U
34	a	1086	U
34	a	1094	G

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Mol	Chain	Res	Type
34	a	1100	C
34	a	1101	A
34	a	1102	A
34	a	1105	A
34	a	1108	G
34	a	1120	C
34	a	1124	G
34	a	1126	U
34	a	1127	G
34	a	1130	A
34	a	1131	G
34	a	1133	G
34	a	1134	G
34	a	1136	C
34	a	1137	C
34	a	1138	G
34	a	1140	C
34	a	1142	G
34	a	1143	G
34	a	1145	A
34	a	1146	A
34	a	1154	G
34	a	1159	U
34	a	1160	G
34	a	1167	A
34	a	1168	U
34	a	1169	A
34	a	1173	U
34	a	1176	A
34	a	1183	U
34	a	1184	G
34	a	1193	G
34	a	1196	A
34	a	1197	A
34	a	1200	C
34	a	1201	A
34	a	1202	U
34	a	1210	C
34	a	1212	U
34	a	1213	A
34	a	1214	C
34	a	1227	A

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Mol	Chain	Res	Type
34	a	1228	C
34	a	1236	A
34	a	1239	A
34	a	1242	G
34	a	1249	C
34	a	1250	A
34	a	1257	A
34	a	1260	G
34	a	1261	A
34	a	1262	C
34	a	1263	C
34	a	1264	U
34	a	1267	C
34	a	1269	A
34	a	1270	G
34	a	1274	A
34	a	1275	A
34	a	1280	A
34	a	1285	A
34	a	1287	A
34	a	1300	G
34	a	1301	U
34	a	1302	C
34	a	1303	C
34	a	1312	G
34	a	1317	C
34	a	1318	A
34	a	1319	A
34	a	1320	C
34	a	1322	C
34	a	1330	U
34	a	1331	G
34	a	1332	A
34	a	1333	A
34	a	1335	U
34	a	1336	C
34	a	1338	G
34	a	1346	A
34	a	1347	G
34	a	1348	U
34	a	1349	A
34	a	1353	G

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Mol	Chain	Res	Type
34	a	1360	A
34	a	1366	C
34	a	1370	G
34	a	1378	C
34	a	1381	U
34	a	1394	A
34	a	1395	C
34	a	1397	C
34	a	1398	A
34	a	1400	C
34	a	1419	G
34	a	1422	G
34	a	1441	A
34	a	1444	U
34	a	1446	A
34	a	1447	A
34	a	1450	U
34	a	1452	C
34	a	1453	G
34	a	1454	G
34	a	1456	A
34	a	1472	U
34	a	1492	A
34	a	1494	G
34	a	1497	G
34	a	1499	A
34	a	1503	A
34	a	1506	U
34	a	1517	G
34	a	1519	MA6
34	a	1520	C
34	a	1529	G
34	a	1530	G
34	a	1534	A
34	a	1536	C
34	a	1538	C
34	a	1539	C
34	a	1540	U
55	v	8	4SU
55	v	9	G
55	v	17(A)	U
55	v	19	G

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Mol	Chain	Res	Type
55	v	20	U
55	v	21	A
55	v	22	G
55	v	23	C
55	v	33	U
55	v	34	C
55	v	36	U
55	v	38	A
55	v	40	C
55	v	41	C
55	v	47	U
55	v	48	C
55	v	54	5MU
55	v	56	C
55	v	60	U
55	v	68	C
55	v	73	A
55	v	74	C
55	v	75	C
55	v	76	A
56	w	4	C
56	w	6	G
56	w	8	4SU
56	w	13	C
56	w	16	U
56	w	17	C
56	w	18	G
56	w	19	G
56	w	20	U
56	w	21	A
56	w	27	G
56	w	28	G
56	w	36	A
56	w	45	U
56	w	46	G7M
56	w	47	U
56	w	49	C
56	w	60	U
56	w	69	G
56	w	73	A
56	w	76	A
59	z	4	U

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Mol	Chain	Res	Type
59	z	9	U

All (37) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	A	102	U
8	A	141	G
8	A	242	G
8	A	310	A
8	A	344	A
8	A	479	A
8	A	555	G
8	A	733	G
8	A	784	G
8	A	1076	C
8	A	1078	U
8	A	1085	A
8	A	1090	A
8	A	1091	G
8	A	1173	U
8	A	1178	C
8	A	1182	G
8	A	1200	C
8	A	1300	G
8	A	1358	G
8	A	1454	C
8	A	1490	A
8	A	1730	C
8	A	1847	G
8	A	1913	A
8	A	2192	U
8	A	2287	A
8	A	2308	G
8	A	2324	U
8	A	2405	G
8	A	2406	A
8	A	2728	U
8	A	2779	U
8	A	2820	A
9	B	44	G
9	B	52	A
9	B	66	A

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

45 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
8	PSU	A	2604	8	18,21,22	1.06	1 (5%)	22,30,33	1.72	2 (9%)
8	PSU	A	2504	8	18,21,22	1.14	2 (11%)	22,30,33	1.84	4 (18%)
8	2MG	A	2445	8	23,26,27	1.32	3 (13%)	32,38,41	2.35	10 (31%)
56	G7M	w	46	56	23,26,27	2.62	8 (34%)	35,39,42	2.25	10 (28%)
34	MA6	a	1518	34	23,26,27	1.47	5 (21%)	34,38,41	2.75	12 (35%)
55	PSU	v	55	55	18,21,22	1.36	3 (16%)	22,30,33	1.96	4 (18%)
8	PSU	A	2457	8	18,21,22	0.98	2 (11%)	22,30,33	1.88	6 (27%)
8	5MC	A	1962	8	18,22,23	3.65	7 (38%)	26,32,35	0.97	1 (3%)
8	5MC	A	747	8	18,22,23	3.62	7 (38%)	26,32,35	1.14	1 (3%)
8	2MA	A	2503	8,60	22,25,26	3.72	8 (36%)	33,37,40	2.19	7 (21%)
8	PSU	A	2580	8,60	18,21,22	1.11	3 (16%)	22,30,33	1.89	6 (27%)
34	5MC	a	1407	34	18,22,23	1.03	2 (11%)	26,32,35	1.57	7 (26%)
8	2MG	A	1835	8	23,26,27	2.91	8 (34%)	32,38,41	2.26	10 (31%)
58	FME	y	101	58	8,9,10	0.96	0	7,9,11	1.17	1 (14%)
8	PSU	A	746	8,60	18,21,22	1.09	2 (11%)	22,30,33	1.81	5 (22%)
34	UR3	a	1498	34,60	19,22,23	2.69	6 (31%)	26,32,35	1.57	4 (15%)
8	5MU	A	1939	8	19,22,23	4.68	7 (36%)	28,32,35	3.76	9 (32%)
56	PSU	w	55	56	18,21,22	1.43	2 (11%)	22,30,33	1.98	3 (13%)
34	PSU	a	516	34	18,21,22	0.99	1 (5%)	22,30,33	1.79	5 (22%)
8	OMG	A	2251	56,8,60	23,26,27	2.35	9 (39%)	33,38,41	1.86	8 (24%)
34	2MG	a	1207	34	23,26,27	2.95	8 (34%)	32,38,41	2.23	11 (34%)
8	G7M	A	2069	8	23,26,27	2.56	8 (34%)	35,39,42	2.22	10 (28%)
8	PSU	A	955	8	18,21,22	1.07	2 (11%)	22,30,33	1.75	4 (18%)
55	4SU	v	8	55	18,21,22	3.61	7 (38%)	26,30,33	2.32	5 (19%)
56	MIA	w	37	56	28,31,32	2.53	7 (25%)	40,44,47	3.76	18 (45%)
8	PSU	A	1911	8	18,21,22	1.39	3 (16%)	22,30,33	2.01	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	6MZ	A	1618	8	22,25,26	2.97	5 (22%)	30,36,39	4.28	14 (46%)
8	6MZ	A	2030	8	22,25,26	3.01	6 (27%)	30,36,39	4.47	14 (46%)
8	PSU	A	2605	8	18,21,22	1.02	1 (5%)	22,30,33	1.78	2 (9%)
34	2MG	a	966	34	23,26,27	1.39	4 (17%)	32,38,41	2.31	8 (25%)
34	MA6	a	1519	34	23,26,27	1.43	5 (21%)	34,38,41	2.84	12 (35%)
34	2MG	a	1516	34	23,26,27	2.95	9 (39%)	32,38,41	2.28	12 (37%)
8	PSU	A	1917	8	18,21,22	1.06	1 (5%)	22,30,33	1.73	4 (18%)
56	5MU	w	54	56	19,22,23	1.40	4 (21%)	28,32,35	1.94	6 (21%)
55	5MU	v	54	55	19,22,23	4.85	7 (36%)	28,32,35	3.60	9 (32%)
34	G7M	a	527	34	23,26,27	2.61	8 (34%)	35,39,42	2.28	10 (28%)
8	1MG	A	745	8	22,26,27	2.66	6 (27%)	33,39,42	2.10	8 (24%)
34	5MC	a	967	34	18,22,23	3.73	7 (38%)	26,32,35	1.03	2 (7%)
8	OMC	A	2498	8,60	19,22,23	2.92	7 (36%)	26,31,34	0.83	0
56	PSU	w	32	56	18,21,22	1.03	1 (5%)	22,30,33	1.71	4 (18%)
56	4SU	w	8	56	18,21,22	3.62	7 (38%)	26,30,33	2.22	4 (15%)
8	3TD	A	1915	8	18,22,23	7.37	11 (61%)	22,32,35	1.72	3 (13%)
34	4OC	a	1402	34	20,23,24	3.00	8 (40%)	26,32,35	0.82	1 (3%)
8	OMU	A	2552	8,60	19,22,23	2.94	8 (42%)	26,31,34	1.78	5 (19%)
56	PSU	w	39	56	18,21,22	1.04	1 (5%)	22,30,33	1.72	4 (18%)

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
8	PSU	A	2604	8	-	0/7/25/26	0/2/2/2
8	PSU	A	2504	8	-	0/7/25/26	0/2/2/2
8	2MG	A	2445	8	-	2/9/27/28	0/3/3/3
56	G7M	w	46	56	-	2/7/25/26	0/3/3/3
34	MA6	a	1518	34	-	1/11/29/30	0/3/3/3
55	PSU	v	55	55	-	2/7/25/26	0/2/2/2
8	PSU	A	2457	8	-	0/7/25/26	0/2/2/2
8	5MC	A	1962	8	-	2/7/25/26	0/2/2/2
8	5MC	A	747	8	-	1/7/25/26	0/2/2/2
8	2MA	A	2503	8,60	-	3/7/25/26	0/3/3/3
8	PSU	A	2580	8,60	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	5MC	a	1407	34	-	0/7/25/26	0/2/2/2
8	2MG	A	1835	8	-	2/9/27/28	0/3/3/3
58	FME	y	101	58	-	5/7/9/11	-
8	PSU	A	746	8,60	-	2/7/25/26	0/2/2/2
34	UR3	a	1498	34,60	-	4/7/25/26	0/2/2/2
8	5MU	A	1939	8	-	2/7/25/26	0/2/2/2
56	PSU	w	55	56	-	0/7/25/26	0/2/2/2
34	PSU	a	516	34	-	0/7/25/26	0/2/2/2
8	OMG	A	2251	56,8,60	-	1/9/27/28	0/3/3/3
34	2MG	a	1207	34	-	0/9/27/28	0/3/3/3
8	G7M	A	2069	8	-	1/7/25/26	0/3/3/3
8	PSU	A	955	8	-	0/7/25/26	0/2/2/2
55	4SU	v	8	55	-	0/7/25/26	0/2/2/2
56	MIA	w	37	56	-	3/15/33/34	0/3/3/3
8	PSU	A	1911	8	-	0/7/25/26	0/2/2/2
8	6MZ	A	1618	8	-	0/9/27/28	0/3/3/3
8	6MZ	A	2030	8	-	2/9/27/28	0/3/3/3
8	PSU	A	2605	8	-	0/7/25/26	0/2/2/2
34	2MG	a	966	34	-	2/9/27/28	0/3/3/3
34	MA6	a	1519	34	-	1/11/29/30	0/3/3/3
34	2MG	a	1516	34	-	0/9/27/28	0/3/3/3
8	PSU	A	1917	8	-	0/7/25/26	0/2/2/2
56	5MU	w	54	56	-	0/7/25/26	0/2/2/2
55	5MU	v	54	55	-	2/7/25/26	0/2/2/2
34	G7M	a	527	34	-	0/7/25/26	0/3/3/3
8	1MG	A	745	8	-	0/7/25/26	0/3/3/3
34	5MC	a	967	34	-	2/7/25/26	0/2/2/2
8	OMC	A	2498	8,60	-	0/9/27/28	0/2/2/2
56	PSU	w	32	56	-	2/7/25/26	0/2/2/2
56	4SU	w	8	56	-	0/7/25/26	0/2/2/2
8	3TD	A	1915	8	-	3/7/25/26	0/2/2/2
34	4OC	a	1402	34	-	0/9/29/30	0/2/2/2
8	OMU	A	2552	8,60	-	2/9/27/28	0/2/2/2
56	PSU	w	39	56	-	3/7/25/26	0/2/2/2

All (227) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1915	3TD	O4'-C1'	18.04	1.68	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1915	3TD	C2'-C1'	-15.17	1.34	1.53
8	A	1915	3TD	C6-C5	13.53	1.51	1.35
8	A	2030	6MZ	C6-N6	12.17	1.47	1.34
8	A	1618	6MZ	C6-N6	12.15	1.47	1.34
8	A	2503	2MA	C4-N3	11.72	1.49	1.34
55	v	54	5MU	C2-N1	11.31	1.56	1.38
55	v	54	5MU	C6-N1	10.57	1.56	1.38
8	A	1939	5MU	C6-N1	10.26	1.55	1.38
8	A	1939	5MU	C2-N1	10.03	1.54	1.38
55	v	54	5MU	C4-C5	9.95	1.61	1.44
8	A	1915	3TD	C2-N1	9.60	1.49	1.37
8	A	1939	5MU	C4-C5	9.58	1.60	1.44
34	a	967	5MC	C6-C5	9.37	1.50	1.34
8	A	747	5MC	C6-C5	9.07	1.49	1.34
8	A	1962	5MC	C6-C5	9.05	1.49	1.34
56	w	37	MIA	C2-S10	-8.93	1.68	1.75
56	w	8	4SU	C4-N3	8.21	1.46	1.37
8	A	1939	5MU	C4-N3	-8.17	1.23	1.38
55	v	8	4SU	C4-N3	8.13	1.46	1.37
55	v	54	5MU	C4-N3	-7.74	1.24	1.38
55	v	8	4SU	C2-N1	7.59	1.50	1.38
34	a	1207	2MG	C2-N3	7.55	1.46	1.31
34	a	1516	2MG	C2-N3	7.45	1.46	1.31
56	w	8	4SU	C2-N1	7.32	1.50	1.38
8	A	1835	2MG	C2-N3	7.31	1.45	1.31
8	A	745	1MG	C2-N2	7.28	1.47	1.34
34	a	967	5MC	C4-N3	6.99	1.45	1.34
34	a	1498	UR3	C2-N1	6.96	1.48	1.38
8	A	2503	2MA	C2-N3	6.91	1.46	1.34
8	A	1962	5MC	C4-N3	6.87	1.45	1.34
8	A	2552	OMU	C2-N1	6.82	1.49	1.38
34	a	1402	4OC	C4-N3	6.81	1.44	1.32
8	A	747	5MC	C4-N3	6.79	1.45	1.34
56	w	37	MIA	C13-C14	6.56	1.51	1.32
8	A	2552	OMU	C2-N3	6.52	1.49	1.38
34	a	1207	2MG	C4-N3	6.52	1.49	1.34
34	a	527	G7M	C4-N3	6.37	1.49	1.34
8	A	1835	2MG	C4-N3	6.33	1.49	1.34
8	A	1962	5MC	C2-N3	6.32	1.49	1.36
56	w	46	G7M	C4-N3	6.31	1.49	1.34
34	a	967	5MC	C2-N3	6.26	1.49	1.36
34	a	1516	2MG	C4-N3	6.24	1.49	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	a	1207	2MG	C2-N2	6.23	1.47	1.33
8	A	745	1MG	C4-N3	6.23	1.49	1.34
8	A	2069	G7M	C4-N3	6.22	1.49	1.34
8	A	1915	3TD	O4'-C4'	-6.21	1.31	1.45
8	A	2498	OMC	C6-C5	6.21	1.49	1.35
8	A	747	5MC	C2-N3	6.19	1.48	1.36
8	A	2498	OMC	C2-N3	6.18	1.48	1.36
34	a	1516	2MG	C2-N2	6.16	1.47	1.33
8	A	2251	OMG	C4-N3	6.15	1.48	1.34
8	A	1835	2MG	C2-N2	6.13	1.47	1.33
34	a	1498	UR3	C6-C5	5.98	1.49	1.35
8	A	1915	3TD	C6-N1	5.95	1.46	1.36
34	a	1402	4OC	C6-C5	5.90	1.48	1.35
56	w	8	4SU	C6-C5	5.87	1.48	1.35
56	w	46	G7M	C2-N3	5.86	1.47	1.33
55	v	54	5MU	C6-C5	5.85	1.44	1.34
34	a	1402	4OC	C2-N3	5.83	1.48	1.36
8	A	1939	5MU	C6-C5	5.80	1.44	1.34
56	w	8	4SU	C2-N3	5.76	1.48	1.38
55	v	8	4SU	C6-C5	5.74	1.48	1.35
34	a	527	G7M	C2-N3	5.71	1.46	1.33
8	A	2498	OMC	C4-N3	5.68	1.45	1.34
55	v	8	4SU	C2-N3	5.58	1.47	1.38
8	A	745	1MG	C2-N3	5.55	1.44	1.34
8	A	2503	2MA	C6-N1	5.54	1.42	1.35
8	A	2503	2MA	C2-N1	5.51	1.43	1.34
8	A	2552	OMU	C6-C5	5.51	1.47	1.35
8	A	2069	G7M	C2-N3	5.34	1.46	1.33
8	A	2069	G7M	C5-N7	-5.10	1.33	1.39
8	A	2251	OMG	C2-N3	5.09	1.45	1.33
56	w	8	4SU	C4-S4	-5.09	1.58	1.68
55	v	8	4SU	C4-S4	-5.04	1.58	1.68
8	A	1915	3TD	C2-N3	5.01	1.49	1.38
34	a	527	G7M	C5-N7	-4.93	1.33	1.39
34	a	1498	UR3	C2-N3	4.88	1.48	1.39
34	a	967	5MC	C4-N4	4.86	1.46	1.34
8	A	1962	5MC	C4-N4	4.72	1.46	1.34
8	A	1915	3TD	O3'-C3'	-4.71	1.31	1.43
56	w	46	G7M	C5-N7	-4.68	1.33	1.39
8	A	747	5MC	C4-N4	4.67	1.46	1.34
34	a	1516	2MG	C2-N1	4.60	1.44	1.36
8	A	2251	OMG	C2-N2	4.53	1.45	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	a	967	5MC	C6-N1	4.53	1.45	1.38
8	A	1962	5MC	C6-N1	4.45	1.45	1.38
34	a	527	G7M	C2-N2	4.40	1.44	1.34
34	a	1207	2MG	C2-N1	4.39	1.43	1.36
8	A	1835	2MG	C2-N1	4.37	1.43	1.36
8	A	2503	2MA	C5-C6	4.30	1.53	1.41
8	A	747	5MC	C6-N1	4.29	1.45	1.38
8	A	2069	G7M	C2-N2	4.27	1.44	1.34
56	w	46	G7M	C2-N2	4.25	1.44	1.34
34	a	1402	4OC	C4-N4	4.18	1.44	1.35
34	a	967	5MC	C2-N1	4.12	1.48	1.40
8	A	1962	5MC	C2-N1	3.99	1.48	1.40
8	A	747	5MC	C2-N1	3.97	1.48	1.40
56	w	46	G7M	C5-C6	3.97	1.54	1.43
8	A	2498	OMC	C4-N4	3.93	1.43	1.33
34	a	527	G7M	C5-C6	3.83	1.54	1.43
8	A	2552	OMU	C4-N3	3.80	1.45	1.38
34	a	1402	4OC	C5-C4	3.75	1.48	1.40
34	a	1402	4OC	C2-N1	3.72	1.48	1.40
8	A	1835	2MG	C5-N7	-3.68	1.31	1.39
8	A	2069	G7M	C5-C6	3.59	1.53	1.43
8	A	2503	2MA	C6-N6	-3.56	1.25	1.34
8	A	2030	6MZ	C5-C4	-3.56	1.32	1.39
8	A	2498	OMC	C6-N1	3.55	1.46	1.38
8	A	2498	OMC	C2-N1	3.55	1.47	1.40
34	a	1516	2MG	C5-N7	-3.45	1.32	1.39
34	a	1207	2MG	C5-N7	-3.37	1.32	1.39
34	a	1516	2MG	O6-C6	-3.34	1.17	1.23
34	a	1207	2MG	O6-C6	-3.34	1.17	1.23
8	A	1835	2MG	O6-C6	-3.34	1.17	1.23
8	A	2504	PSU	C6-C5	3.34	1.39	1.35
56	w	39	PSU	C6-C5	3.33	1.39	1.35
56	w	37	MIA	C8-N9	-3.27	1.31	1.37
56	w	55	PSU	C6-C5	3.27	1.39	1.35
8	A	1618	6MZ	C5-C4	-3.26	1.32	1.39
8	A	747	5MC	O2-C2	-3.26	1.17	1.23
34	a	1519	MA6	C6-N6	3.22	1.46	1.36
34	a	967	5MC	O2-C2	-3.22	1.17	1.23
55	v	8	4SU	C5-C4	3.21	1.46	1.42
8	A	2251	OMG	C5-N7	-3.21	1.32	1.39
34	a	1518	MA6	C6-N6	3.20	1.46	1.36
56	w	32	PSU	C6-C5	3.20	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1917	PSU	C6-C5	3.17	1.39	1.35
56	w	8	4SU	C5-C4	3.15	1.46	1.42
8	A	745	1MG	C5-N7	-3.13	1.33	1.39
8	A	2030	6MZ	C8-N9	-3.11	1.31	1.37
8	A	1962	5MC	O2-C2	-3.10	1.18	1.23
8	A	2503	2MA	C5-N7	-3.09	1.33	1.39
8	A	1618	6MZ	C8-N9	-3.04	1.32	1.37
8	A	2552	OMU	O4-C4	-3.03	1.18	1.24
34	a	1518	MA6	C8-N9	-3.02	1.32	1.37
56	w	55	PSU	C4-N3	-3.01	1.33	1.38
34	a	966	2MG	C5-C4	3.01	1.47	1.38
34	a	1402	4OC	C6-N1	3.01	1.45	1.38
8	A	1911	PSU	C6-C5	3.00	1.38	1.35
8	A	1915	3TD	C4-N3	2.99	1.46	1.40
8	A	2498	OMC	O2-C2	-2.98	1.18	1.23
55	v	55	PSU	C4-N3	-2.97	1.33	1.38
34	a	1518	MA6	C5-N7	-2.96	1.33	1.39
34	a	516	PSU	C6-C5	2.96	1.38	1.35
34	a	966	2MG	C6-N1	-2.92	1.33	1.38
8	A	2030	6MZ	C4-N9	-2.92	1.31	1.37
8	A	2445	2MG	C6-N1	-2.91	1.33	1.38
56	w	54	5MU	C4-N3	-2.89	1.33	1.38
8	A	1911	PSU	C4-N3	-2.87	1.33	1.38
34	a	1519	MA6	C8-N9	-2.86	1.32	1.37
34	a	1498	UR3	C6-N1	2.86	1.44	1.38
56	w	37	MIA	C5-N7	-2.84	1.33	1.39
8	A	1939	5MU	O2-C2	-2.84	1.17	1.23
8	A	746	PSU	C6-C5	2.83	1.38	1.35
8	A	2604	PSU	C6-C5	2.83	1.38	1.35
34	a	1519	MA6	C5-N7	-2.82	1.33	1.39
8	A	1939	5MU	O4-C4	-2.81	1.18	1.23
34	a	1402	4OC	O2-C2	-2.80	1.18	1.23
8	A	2605	PSU	C6-C5	2.77	1.38	1.35
8	A	955	PSU	C6-C5	2.76	1.38	1.35
56	w	46	G7M	C2-N1	2.75	1.44	1.37
8	A	2580	PSU	C6-C5	2.74	1.38	1.35
8	A	1618	6MZ	C4-N9	-2.70	1.31	1.37
56	w	37	MIA	O4'-C4'	-2.66	1.39	1.45
56	w	37	MIA	C5-C4	2.66	1.44	1.39
8	A	2445	2MG	C5-C4	2.66	1.46	1.38
34	a	527	G7M	O6-C6	-2.64	1.18	1.23
8	A	745	1MG	C5-C6	2.63	1.52	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	a	1518	MA6	C5-C4	-2.63	1.34	1.39
56	w	46	G7M	C6-N1	2.63	1.43	1.38
34	a	1407	5MC	C6-C5	2.61	1.38	1.34
55	v	54	5MU	O4-C4	-2.60	1.18	1.23
8	A	2552	OMU	O2-C2	-2.60	1.18	1.23
34	a	1519	MA6	C5-C4	-2.60	1.34	1.39
8	A	2552	OMU	C6-N1	2.59	1.44	1.38
8	A	2580	PSU	O4'-C1'	-2.59	1.40	1.43
56	w	46	G7M	O6-C6	-2.58	1.18	1.23
34	a	966	2MG	C2-N3	2.58	1.36	1.31
34	a	966	2MG	C5-N7	-2.57	1.34	1.39
8	A	2069	G7M	C2-N1	2.56	1.44	1.37
8	A	2069	G7M	O6-C6	-2.55	1.18	1.23
8	A	2251	OMG	O6-C6	-2.55	1.18	1.23
8	A	2445	2MG	C5-N7	-2.49	1.34	1.39
34	a	1498	UR3	O2-C2	-2.49	1.18	1.22
34	a	527	G7M	C2-N1	2.48	1.43	1.37
56	w	37	MIA	C4-N9	-2.47	1.32	1.37
34	a	1207	2MG	C5-C6	2.47	1.53	1.44
56	w	54	5MU	C6-C5	2.47	1.38	1.34
56	w	8	4SU	O2-C2	-2.45	1.18	1.23
8	A	2503	2MA	C4-N9	-2.45	1.32	1.37
34	a	1516	2MG	C5-C6	2.44	1.53	1.44
55	v	8	4SU	O2-C2	-2.42	1.18	1.23
55	v	55	PSU	C6-C5	2.42	1.38	1.35
8	A	1915	3TD	C3'-C4'	2.41	1.59	1.53
8	A	2251	OMG	C2-N1	2.38	1.43	1.37
8	A	1618	6MZ	C6-N1	-2.36	1.31	1.35
8	A	2030	6MZ	C6-N1	-2.36	1.31	1.35
34	a	1519	MA6	C8-N7	2.35	1.36	1.31
8	A	2069	G7M	C6-N1	2.34	1.43	1.38
56	w	54	5MU	C2-N3	-2.33	1.33	1.38
8	A	2251	OMG	C5-C6	2.32	1.53	1.44
56	w	54	5MU	C6-N1	-2.31	1.34	1.38
34	a	1516	2MG	C6-N1	2.31	1.43	1.38
34	a	1407	5MC	C6-N1	-2.31	1.34	1.38
34	a	1498	UR3	O4-C4	-2.31	1.18	1.23
8	A	1835	2MG	C5-C6	2.29	1.52	1.44
34	a	527	G7M	C6-N1	2.29	1.43	1.38
55	v	54	5MU	O2-C2	-2.26	1.18	1.23
34	a	1518	MA6	C8-N7	2.23	1.35	1.31
8	A	746	PSU	C4-C5	-2.23	1.37	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	2457	PSU	C6-C5	2.21	1.37	1.35
55	v	55	PSU	C2-N3	-2.21	1.33	1.37
8	A	955	PSU	C4-C5	-2.20	1.37	1.44
8	A	745	1MG	C4-N9	-2.20	1.32	1.38
34	a	1516	2MG	C4-N9	-2.14	1.32	1.38
8	A	2552	OMU	C5-C4	2.14	1.48	1.43
8	A	2251	OMG	C6-N1	2.12	1.42	1.38
34	a	1207	2MG	C6-N1	2.11	1.42	1.38
8	A	1911	PSU	C2-N3	-2.10	1.33	1.37
8	A	2457	PSU	O4'-C1'	-2.09	1.40	1.43
8	A	2580	PSU	C4-C5	-2.07	1.38	1.44
8	A	1835	2MG	C6-N1	2.06	1.42	1.38
8	A	2504	PSU	C4-C5	-2.05	1.38	1.44
8	A	1915	3TD	O5'-C5'	-2.05	1.39	1.44
8	A	2030	6MZ	C8-N7	2.05	1.35	1.31
8	A	2251	OMG	C4-N9	-2.02	1.32	1.38

All (289) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2030	6MZ	C4-N9-C8	14.14	121.05	105.73
8	A	1618	6MZ	C4-N9-C8	13.04	119.86	105.73
56	w	37	MIA	C11-S10-C2	-12.51	92.92	102.27
8	A	1939	5MU	C5-C4-N3	12.43	125.92	115.31
55	v	54	5MU	C5-C4-N3	12.19	125.72	115.31
8	A	2030	6MZ	N9-C8-N7	-11.32	98.43	113.91
8	A	1939	5MU	C5-C6-N1	-10.67	112.36	123.34
8	A	1618	6MZ	N9-C8-N7	-10.41	99.68	113.91
34	a	1519	MA6	N1-C6-N6	-10.02	106.12	117.08
55	v	54	5MU	C5-C6-N1	-9.94	113.12	123.34
56	w	37	MIA	C12-C13-C14	-9.61	108.45	127.14
34	a	1518	MA6	N1-C6-N6	-9.44	106.76	117.08
8	A	1618	6MZ	C5-C6-N1	8.51	127.26	118.20
8	A	2030	6MZ	C5-C6-N1	8.25	126.99	118.20
56	w	37	MIA	C5-C4-N3	-8.22	117.94	127.19
55	v	8	4SU	C4-N3-C2	-8.10	119.47	127.34
56	w	8	4SU	C4-N3-C2	-7.58	119.98	127.34
8	A	2445	2MG	C2-N3-C4	7.22	120.99	112.04
34	a	966	2MG	C2-N3-C4	7.16	120.92	112.04
56	w	37	MIA	N3-C4-N9	7.15	136.91	126.99
34	a	1207	2MG	C2-N3-C4	6.68	120.32	112.04
34	a	966	2MG	C5-C4-N3	-6.66	117.65	128.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1835	2MG	C2-N3-C4	6.55	120.16	112.04
34	a	1516	2MG	C2-N3-C4	6.47	120.06	112.04
8	A	1618	6MZ	N3-C4-N9	6.30	137.46	127.08
8	A	2445	2MG	C5-C4-N3	-6.11	118.54	128.46
8	A	1911	PSU	N1-C2-N3	6.08	122.02	115.13
56	w	55	PSU	N1-C2-N3	6.08	122.02	115.13
8	A	2030	6MZ	N3-C4-N9	5.93	136.85	127.08
8	A	2069	G7M	CN7-N7-C5	5.77	133.94	126.77
8	A	2503	2MA	C5-C4-N3	-5.76	120.72	127.19
34	a	1519	MA6	N1-C2-N3	-5.73	119.64	128.60
8	A	2503	2MA	N9-C8-N7	-5.68	106.14	113.91
55	v	8	4SU	C5-C4-N3	5.65	119.93	114.69
8	A	1835	2MG	C5-C4-N3	-5.56	119.44	128.46
8	A	2030	6MZ	N1-C2-N3	-5.54	119.94	128.60
56	w	8	4SU	C5-C4-N3	5.53	119.82	114.69
34	a	1518	MA6	N1-C2-N3	-5.50	119.99	128.60
34	a	1207	2MG	C5-C4-N3	-5.50	119.55	128.46
8	A	745	1MG	C1'-N9-C4	-5.49	110.19	126.50
34	a	527	G7M	CN7-N7-C5	5.49	133.59	126.77
34	a	966	2MG	N9-C4-N3	5.48	136.93	125.94
8	A	1618	6MZ	C9-N6-C6	-5.47	118.16	122.87
55	v	55	PSU	N1-C2-N3	5.46	121.32	115.13
8	A	2552	OMU	C4-N3-C2	-5.27	119.63	126.58
56	w	46	G7M	CN7-N7-C5	5.25	133.29	126.77
8	A	1939	5MU	C4-N3-C2	-5.24	120.57	127.35
8	A	1939	5MU	O4-C4-C5	-5.23	118.84	124.90
8	A	1618	6MZ	N1-C2-N3	-5.22	120.44	128.60
55	v	54	5MU	O4-C4-C5	-5.21	118.87	124.90
8	A	2251	OMG	C5-C4-N3	-5.09	120.20	128.46
34	a	1516	2MG	C5-C4-N3	-5.04	120.28	128.46
34	a	1518	MA6	C5-C4-N3	-4.98	120.25	126.75
8	A	2605	PSU	C4-N3-C2	-4.96	119.19	126.34
8	A	2030	6MZ	C9-N6-C6	-4.95	118.61	122.87
34	a	1519	MA6	C5-C6-N6	4.92	133.87	125.30
8	A	2504	PSU	N1-C2-N3	4.91	120.70	115.13
8	A	745	1MG	C1'-N9-C8	4.87	140.56	126.70
34	a	1519	MA6	C5-C4-N3	-4.87	120.40	126.75
8	A	745	1MG	C5-C4-N3	-4.79	120.69	128.46
8	A	2030	6MZ	C5-N7-C8	4.79	110.31	103.51
8	A	746	PSU	C4-N3-C2	-4.75	119.49	126.34
8	A	2457	PSU	N1-C2-N3	4.74	120.50	115.13
34	a	527	G7M	C2-N3-C4	4.74	120.74	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1939	5MU	N3-C2-N1	4.71	121.15	114.89
8	A	1835	2MG	C2-N1-C6	-4.70	119.07	124.48
8	A	1915	3TD	C4-N3-C2	-4.69	119.52	124.61
34	a	527	G7M	C5-C4-N3	-4.68	119.17	128.15
8	A	2457	PSU	C4-N3-C2	-4.67	119.61	126.34
8	A	2030	6MZ	C5-C4-N9	-4.66	100.37	105.78
55	v	54	5MU	C4-N3-C2	-4.63	121.35	127.35
34	a	516	PSU	N1-C2-N3	4.63	120.38	115.13
8	A	2604	PSU	C4-N3-C2	-4.61	119.70	126.34
56	w	37	MIA	C4-N9-C8	4.59	110.70	105.73
8	A	2445	2MG	N9-C4-N3	4.58	135.13	125.94
56	w	46	G7M	C2-N3-C4	4.57	120.44	112.30
8	A	2251	OMG	C2-N3-C4	4.56	120.43	112.30
56	w	32	PSU	C4-N3-C2	-4.54	119.80	126.34
8	A	1618	6MZ	C5-C4-N9	-4.53	100.51	105.78
34	a	1518	MA6	N9-C8-N7	-4.51	107.75	113.91
34	a	1516	2MG	C2-N1-C6	-4.50	119.30	124.48
56	w	37	MIA	C2'-C1'-N9	-4.49	101.93	113.30
8	A	2580	PSU	N1-C2-N3	4.48	120.21	115.13
8	A	1917	PSU	N1-C2-N3	4.47	120.19	115.13
8	A	2580	PSU	C4-N3-C2	-4.46	119.91	126.34
34	a	1519	MA6	N9-C8-N7	-4.46	107.82	113.91
56	w	39	PSU	N1-C2-N3	4.45	120.17	115.13
56	w	46	G7M	C5-C4-N3	-4.45	119.61	128.15
56	w	54	5MU	N3-C2-N1	4.45	120.79	114.89
34	a	1518	MA6	C5-C6-N6	4.42	133.01	125.30
8	A	2503	2MA	C4-N9-C8	4.42	110.52	105.73
8	A	955	PSU	C4-N3-C2	-4.42	119.97	126.34
56	w	54	5MU	C4-N3-C2	-4.42	121.64	127.35
8	A	746	PSU	N1-C2-N3	4.40	120.11	115.13
34	a	516	PSU	C4-N3-C2	-4.40	120.00	126.34
56	w	32	PSU	N1-C2-N3	4.39	120.11	115.13
56	w	39	PSU	C4-N3-C2	-4.35	120.07	126.34
8	A	1618	6MZ	C5-N7-C8	4.34	109.67	103.51
56	w	37	MIA	C15-C14-C13	-4.33	110.14	122.65
8	A	2605	PSU	N1-C2-N3	4.32	120.02	115.13
34	a	1207	2MG	C2-N1-C6	-4.30	119.53	124.48
8	A	2069	G7M	CN7-N7-C8	-4.29	118.21	124.84
8	A	1911	PSU	C4-N3-C2	-4.29	120.16	126.34
34	a	527	G7M	CN7-N7-C8	-4.28	118.23	124.84
8	A	2504	PSU	C4-N3-C2	-4.28	120.17	126.34
8	A	2069	G7M	C2-N3-C4	4.27	119.91	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2503	2MA	N3-C4-N9	4.25	132.89	126.99
8	A	955	PSU	N1-C2-N3	4.25	119.95	115.13
8	A	2069	G7M	C1'-N9-C4	-4.24	113.91	126.50
8	A	1917	PSU	C4-N3-C2	-4.23	120.24	126.34
8	A	2604	PSU	N1-C2-N3	4.21	119.90	115.13
56	w	46	G7M	C1'-N9-C4	-4.21	114.01	126.50
55	v	55	PSU	C4-N3-C2	-4.19	120.30	126.34
34	a	527	G7M	C5-C6-N1	4.12	120.39	111.79
56	w	54	5MU	C5-C4-N3	4.12	118.83	115.31
56	w	37	MIA	C16-C14-C13	-4.12	110.75	122.65
8	A	1915	3TD	N1-C2-N3	4.10	119.37	116.14
55	v	54	5MU	N3-C2-N1	4.09	120.32	114.89
56	w	46	G7M	CN7-N7-C8	-4.09	118.53	124.84
34	a	1498	UR3	C4-N3-C2	-4.08	120.72	124.56
56	w	55	PSU	C4-N3-C2	-4.04	120.52	126.34
34	a	1498	UR3	C6-N1-C2	-4.03	118.18	121.79
56	w	46	G7M	C5-C6-N1	4.03	120.20	111.79
8	A	2069	G7M	C5-C4-N3	-4.02	120.44	128.15
8	A	747	5MC	C5-C6-N1	-4.00	119.23	123.34
8	A	2552	OMU	N3-C2-N1	3.90	120.07	114.89
56	w	37	MIA	N6-C6-N1	3.89	123.47	118.50
34	a	527	G7M	C1'-N9-C4	-3.89	114.95	126.50
56	w	8	4SU	C5-C4-S4	-3.84	119.52	124.47
56	w	54	5MU	O4-C4-C5	-3.82	120.47	124.90
55	v	8	4SU	C5-C4-S4	-3.78	119.59	124.47
8	A	2069	G7M	C5-C6-N1	3.78	119.69	111.79
8	A	1618	6MZ	C1'-N9-C8	-3.77	118.62	127.14
34	a	1498	UR3	C1'-N1-C2	3.77	123.36	116.99
55	v	54	5MU	C5M-C5-C6	-3.74	117.85	122.85
55	v	8	4SU	N3-C2-N1	3.74	119.86	114.89
34	a	1519	MA6	C2-N1-C6	3.69	120.48	111.75
56	w	37	MIA	C5-N7-C8	3.68	108.74	103.51
55	v	54	5MU	C5M-C5-C4	3.65	122.78	118.77
8	A	1618	6MZ	C5-C4-N3	-3.62	122.02	126.75
8	A	1835	2MG	N9-C4-N3	3.62	133.21	125.94
34	a	967	5MC	C5-C6-N1	-3.62	119.62	123.34
56	w	37	MIA	C4-C5-N7	-3.61	106.22	110.62
8	A	1939	5MU	C5M-C5-C6	-3.58	118.06	122.85
56	w	8	4SU	N3-C2-N1	3.58	119.64	114.89
8	A	745	1MG	C2-N3-C4	3.58	120.02	111.98
34	a	1519	MA6	C2-N3-C4	3.57	120.18	111.75
8	A	2503	2MA	C5-N7-C8	3.57	108.58	103.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	w	46	G7M	O6-C6-C5	-3.55	120.05	128.06
8	A	1618	6MZ	C2-N3-C4	3.54	120.11	111.75
34	a	1518	MA6	C2-N1-C6	3.52	120.07	111.75
34	a	1207	2MG	N9-C4-N3	3.50	132.98	125.94
8	A	2030	6MZ	C2-N3-C4	3.49	119.98	111.75
8	A	2069	G7M	O6-C6-C5	-3.48	120.21	128.06
56	w	37	MIA	N9-C8-N7	-3.47	109.17	113.91
56	w	55	PSU	O2-C2-N1	-3.45	118.99	122.79
8	A	2030	6MZ	C4-C5-C6	-3.45	114.13	116.81
34	a	1518	MA6	C2-N3-C4	3.44	119.87	111.75
8	A	745	1MG	N9-C8-N7	-3.44	106.92	113.39
56	w	37	MIA	C2-N3-C4	3.43	121.39	112.35
34	a	527	G7M	N9-C4-N3	3.42	132.81	125.94
8	A	2552	OMU	C5-C4-N3	3.39	119.91	114.84
8	A	2030	6MZ	C6-C5-N7	3.37	136.03	132.39
8	A	1939	5MU	O2-C2-N1	-3.36	118.31	122.79
34	a	527	G7M	O6-C6-C5	-3.33	120.54	128.06
56	w	46	G7M	C2-N1-C6	-3.32	119.04	125.10
8	A	2503	2MA	N3-C2-N1	-3.32	119.62	125.72
8	A	2030	6MZ	C4-N9-C1'	-3.31	118.71	126.59
34	a	1518	MA6	C4-C5-C6	3.31	119.58	115.88
56	w	46	G7M	C1'-N9-C8	3.31	137.90	126.74
8	A	1911	PSU	O2-C2-N1	-3.30	119.16	122.79
34	a	527	G7M	C2-N1-C6	-3.28	119.12	125.10
34	a	1516	2MG	C1'-N9-C4	-3.28	116.76	126.50
8	A	2069	G7M	C1'-N9-C8	3.27	137.76	126.74
8	A	1939	5MU	C5M-C5-C4	3.25	122.34	118.77
8	A	2504	PSU	C6-N1-C2	-3.22	119.39	122.68
56	w	46	G7M	N9-C4-N3	3.21	132.39	125.94
8	A	2445	2MG	CM2-N2-C2	-3.18	116.84	123.86
34	a	1519	MA6	C5-N7-C8	3.18	108.02	103.51
8	A	2457	PSU	O2-C2-N1	-3.17	119.30	122.79
8	A	1962	5MC	C5-C6-N1	-3.13	120.12	123.34
34	a	1518	MA6	C5-N7-C8	3.12	107.94	103.51
34	a	516	PSU	O2-C2-N1	-3.12	119.36	122.79
34	a	527	G7M	C1'-N9-C8	3.10	137.22	126.74
8	A	2445	2MG	C6-C5-N7	3.08	135.98	130.25
56	w	37	MIA	C6-C5-N7	3.07	135.71	132.39
8	A	2030	6MZ	C1'-N9-C8	-3.06	120.22	127.14
34	a	1518	MA6	N3-C4-N9	3.06	132.13	127.08
34	a	1519	MA6	C4-C5-C6	3.05	119.29	115.88
8	A	2030	6MZ	C5-C4-N3	-3.04	122.78	126.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2251	OMG	N9-C8-N7	-3.03	107.67	113.39
8	A	2251	OMG	N9-C4-N3	3.02	132.01	125.94
56	w	54	5MU	C5-C6-N1	-3.02	120.23	123.34
8	A	2445	2MG	C2'-C1'-N9	-3.02	104.67	113.22
34	a	1516	2MG	N9-C8-N7	-3.01	107.71	113.39
8	A	2069	G7M	N9-C4-N3	3.00	131.96	125.94
8	A	2251	OMG	C2-N1-C6	-2.98	119.66	125.10
8	A	2552	OMU	O4-C4-C5	-2.98	119.92	125.16
34	a	1407	5MC	C5-C6-N1	-2.96	120.29	123.34
55	v	55	PSU	O2-C2-N1	-2.96	119.54	122.79
8	A	746	PSU	C6-C5-C4	2.92	120.24	118.20
34	a	1516	2MG	N9-C4-N3	2.89	131.74	125.94
8	A	1835	2MG	N9-C8-N7	-2.86	108.00	113.39
34	a	1516	2MG	C1'-N9-C8	2.86	134.84	126.70
8	A	745	1MG	N9-C4-N3	2.85	131.66	125.94
8	A	2069	G7M	C2-N1-C6	-2.83	119.94	125.10
8	A	1618	6MZ	C4-C5-C6	-2.83	114.61	116.81
34	a	1207	2MG	N9-C8-N7	-2.79	108.13	113.39
34	a	1519	MA6	N3-C4-N9	2.78	131.67	127.08
8	A	2251	OMG	C5-C6-N1	2.77	120.23	113.19
34	a	1407	5MC	C5-C4-N3	-2.77	118.68	121.67
34	a	516	PSU	C6-N1-C2	-2.77	119.85	122.68
8	A	745	1MG	C5-C6-N1	2.76	120.24	114.91
8	A	2580	PSU	O4'-C1'-C2'	2.76	109.03	105.14
34	a	1207	2MG	C5-C6-N1	2.73	120.11	113.19
8	A	1835	2MG	O6-C6-C5	-2.72	119.38	126.60
8	A	1835	2MG	C5-C6-N1	2.72	120.09	113.19
34	a	1516	2MG	C5-C6-N1	2.71	120.07	113.19
8	A	1915	3TD	O4'-C4'-C3'	-2.70	99.77	105.11
8	A	1835	2MG	CM2-N2-C2	-2.69	117.92	123.86
8	A	2552	OMU	C1'-N1-C2	2.69	122.44	117.57
8	A	1917	PSU	C6-N1-C2	-2.68	119.94	122.68
34	a	1516	2MG	CM2-N2-C2	-2.65	118.01	123.86
34	a	1518	MA6	C4-N9-C8	2.64	108.59	105.73
8	A	2580	PSU	C6-N1-C2	-2.63	119.99	122.68
34	a	1407	5MC	O3'-C3'-C4'	2.62	118.62	111.05
8	A	955	PSU	O2-C2-N1	-2.61	119.92	122.79
34	a	1407	5MC	O4'-C4'-C3'	-2.61	99.96	105.11
34	a	1407	5MC	O2-C2-N3	-2.58	118.14	122.33
8	A	2251	OMG	O6-C6-C5	-2.57	119.77	126.60
56	w	37	MIA	O4'-C4'-C3'	-2.55	100.07	105.11
34	a	1516	2MG	O6-C6-C5	-2.54	119.86	126.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1939	5MU	O4-C4-N3	-2.54	115.25	120.12
8	A	1618	6MZ	C6-C5-N7	2.53	135.13	132.39
8	A	2504	PSU	O2-C2-N1	-2.51	120.02	122.79
34	a	1207	2MG	N1-C2-N3	-2.50	120.08	123.95
8	A	1911	PSU	C3'-C2'-C1'	2.50	104.55	101.64
34	a	1207	2MG	C1'-N9-C4	-2.50	119.08	126.50
56	w	39	PSU	C6-N1-C2	-2.49	120.14	122.68
8	A	1917	PSU	O2-C2-N1	-2.48	120.06	122.79
34	a	1516	2MG	N1-C2-N3	-2.48	120.12	123.95
56	w	32	PSU	O2-C2-N1	-2.46	120.08	122.79
8	A	2580	PSU	O2-C2-N1	-2.46	120.08	122.79
8	A	955	PSU	C6-N1-C2	-2.46	120.17	122.68
55	v	54	5MU	O4-C4-N3	-2.45	115.42	120.12
34	a	1519	MA6	C4-N9-C8	2.39	108.32	105.73
8	A	2445	2MG	C4-C5-N7	-2.38	106.95	110.72
8	A	746	PSU	O2-C2-N1	-2.38	120.17	122.79
8	A	2445	2MG	C2-N1-C6	-2.37	121.75	124.48
8	A	2445	2MG	O6-C6-C5	-2.36	120.34	126.60
34	a	1498	UR3	O2-C2-N3	-2.35	118.03	121.34
56	w	37	MIA	C5-C6-N6	-2.33	117.83	121.76
34	a	1207	2MG	O6-C6-C5	-2.33	120.41	126.60
8	A	2503	2MA	CM2-C2-N3	2.33	120.79	117.15
8	A	2457	PSU	C6-N1-C2	-2.32	120.31	122.68
56	w	39	PSU	O2-C2-N1	-2.32	120.24	122.79
34	a	966	2MG	O6-C6-C5	-2.30	120.49	126.60
34	a	966	2MG	C6-C5-N7	2.30	134.53	130.25
55	v	55	PSU	C6-C5-C4	-2.29	116.60	118.20
8	A	1835	2MG	N1-C2-N3	-2.27	120.45	123.95
56	w	32	PSU	C6-N1-C2	-2.27	120.37	122.68
34	a	1407	5MC	C2'-C1'-N1	-2.24	106.88	113.22
34	a	1519	MA6	C4-C5-N7	-2.23	107.91	110.62
8	A	2457	PSU	C6-C5-C4	2.23	119.75	118.20
8	A	745	1MG	C8-N7-C5	2.22	108.26	104.24
8	A	1835	2MG	C1'-N9-C4	-2.17	120.06	126.50
8	A	1618	6MZ	C4-N9-C1'	-2.16	121.45	126.59
56	w	37	MIA	O4'-C1'-N9	2.16	112.31	108.06
58	y	101	FME	C-CA-N	2.15	113.61	109.73
34	a	1207	2MG	C1'-N9-C8	2.13	132.77	126.70
8	A	2580	PSU	C6-C5-C4	2.13	119.69	118.20
8	A	2251	OMG	C8-N7-C5	2.13	108.10	104.24
34	a	516	PSU	O4'-C1'-C2'	2.12	108.14	105.14
8	A	2457	PSU	O4'-C1'-C2'	2.12	108.13	105.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	w	54	5MU	O2-C2-N1	-2.09	120.01	122.79
8	A	2445	2MG	C5-C6-N1	2.08	118.47	113.19
34	a	1518	MA6	C4-C5-N7	-2.07	108.10	110.62
8	A	746	PSU	C6-N1-C2	-2.06	120.58	122.68
34	a	966	2MG	C2-N1-C6	-2.04	122.13	124.48
34	a	1516	2MG	C8-N7-C5	2.03	107.91	104.24
34	a	966	2MG	C4-C5-N7	-2.03	107.51	110.72
34	a	967	5MC	CM5-C5-C6	-2.03	120.14	122.85
34	a	1402	4OC	C6-C5-C4	2.02	119.44	116.96
56	w	37	MIA	N3-C2-N1	-2.02	123.25	126.95
55	v	54	5MU	C1'-N1-C2	2.02	121.22	117.57
34	a	966	2MG	C5-C6-N1	2.01	118.31	113.19
34	a	1207	2MG	C8-N7-C5	2.01	107.88	104.24
55	v	8	4SU	C1'-N1-C2	2.01	121.21	117.57
34	a	1407	5MC	C2'-C3'-C4'	2.00	106.53	102.64

There are no chirality outliers.

All (52) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	a	967	5MC	O4'-C4'-C5'-O5'
34	a	967	5MC	C3'-C4'-C5'-O5'
34	a	1498	UR3	O4'-C1'-N1-C6
34	a	1498	UR3	O4'-C1'-N1-C2
55	v	54	5MU	C3'-C4'-C5'-O5'
55	v	54	5MU	O4'-C4'-C5'-O5'
55	v	55	PSU	O4'-C1'-C5-C4
55	v	55	PSU	O4'-C1'-C5-C6
8	A	746	PSU	C2'-C1'-C5-C4
8	A	1915	3TD	O4'-C1'-C5-C4
8	A	1915	3TD	O4'-C1'-C5-C6
8	A	2030	6MZ	O4'-C4'-C5'-O5'
8	A	2030	6MZ	C3'-C4'-C5'-O5'
8	A	2552	OMU	O4'-C1'-N1-C2
8	A	2552	OMU	O4'-C1'-N1-C6
56	w	32	PSU	O4'-C1'-C5-C4
56	w	32	PSU	O4'-C1'-C5-C6
56	w	37	MIA	C5-C6-N6-C12
56	w	37	MIA	C12-C13-C14-C16
56	w	39	PSU	O4'-C1'-C5-C4
56	w	39	PSU	C2'-C1'-C5-C6
56	w	39	PSU	O4'-C1'-C5-C6

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Mol	Chain	Res	Type	Atoms
58	y	101	FME	O1-CN-N-CA
58	y	101	FME	N-CA-CB-CG
58	y	101	FME	C-CA-CB-CG
58	y	101	FME	O-C-CA-CB
34	a	966	2MG	O4'-C4'-C5'-O5'
34	a	966	2MG	C3'-C4'-C5'-O5'
8	A	1939	5MU	O4'-C4'-C5'-O5'
8	A	2445	2MG	C3'-C4'-C5'-O5'
8	A	2503	2MA	O4'-C4'-C5'-O5'
58	y	101	FME	CB-CG-SD-CE
8	A	1939	5MU	C3'-C4'-C5'-O5'
8	A	2503	2MA	C3'-C4'-C5'-O5'
8	A	1835	2MG	O4'-C4'-C5'-O5'
8	A	2445	2MG	O4'-C4'-C5'-O5'
56	w	37	MIA	N1-C6-N6-C12
34	a	1518	MA6	C5-C6-N6-C10
8	A	1835	2MG	C3'-C4'-C5'-O5'
34	a	1498	UR3	O4'-C4'-C5'-O5'
56	w	46	G7M	C4'-C5'-O5'-P
8	A	1915	3TD	C3'-C4'-C5'-O5'
56	w	46	G7M	C3'-C4'-C5'-O5'
34	a	1519	MA6	C4'-C5'-O5'-P
34	a	1498	UR3	C3'-C4'-C5'-O5'
8	A	747	5MC	C4'-C5'-O5'-P
8	A	1962	5MC	C2'-C1'-N1-C6
8	A	1962	5MC	O4'-C1'-N1-C6
8	A	2503	2MA	O4'-C1'-N9-C8
8	A	2251	OMG	O4'-C4'-C5'-O5'
8	A	746	PSU	O4'-C1'-C5-C6
8	A	2069	G7M	O4'-C4'-C5'-O5'

There are no ring outliers.

22 monomers are involved in 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	w	46	G7M	4	0
55	v	55	PSU	1	0
8	A	2457	PSU	1	0
8	A	2503	2MA	1	0
58	y	101	FME	1	0
8	A	746	PSU	1	0
34	a	1498	UR3	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	1939	5MU	1	0
34	a	516	PSU	2	0
8	A	2251	OMG	1	0
8	A	955	PSU	1	0
56	w	37	MIA	6	0
8	A	2030	6MZ	1	0
34	a	966	2MG	2	0
34	a	527	G7M	1	0
34	a	967	5MC	1	0
8	A	2498	OMC	1	0
56	w	8	4SU	1	0
8	A	1915	3TD	1	0
34	a	1402	4OC	2	0
8	A	2552	OMU	2	0
56	w	39	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 326 ligands modelled in this entry, 321 are monoatomic - leaving 5 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
64	GDP	x	801	-	28,30,30	1.44	5 (17%)	44,47,47	2.20	16 (36%)
63	AM2	a	1628	-	40,40,40	0.18	0	53,60,60	0.57	0
63	AM2	a	1620	-	40,40,40	0.50	0	53,60,60	0.92	2 (3%)
63	AM2	a	1626	-	40,40,40	0.20	0	53,60,60	0.83	1 (1%)
63	AM2	a	1636	-	40,40,40	0.15	0	53,60,60	0.64	1 (1%)

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
64	GDP	x	801	-	-	2/16/32/32	0/3/3/3
63	AM2	a	1628	-	-	4/12/84/84	1/4/4/4
63	AM2	a	1620	-	-	5/12/84/84	0/4/4/4
63	AM2	a	1626	-	-	3/12/84/84	1/4/4/4
63	AM2	a	1636	-	-	7/12/84/84	1/4/4/4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
64	x	801	GDP	C6-N1	-3.76	1.31	1.38
64	x	801	GDP	C4-N9	-3.16	1.29	1.38
64	x	801	GDP	C5-N7	-2.35	1.34	1.39
64	x	801	GDP	C5-C4	2.12	1.44	1.38
64	x	801	GDP	C2-N1	-2.07	1.32	1.37

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	x	801	GDP	C6-C5-N7	5.04	139.63	130.25
64	x	801	GDP	C5-C4-N3	-4.74	120.77	128.46
64	x	801	GDP	C2-N3-C4	4.66	120.60	112.30
64	x	801	GDP	PA-O3A-PB	-4.02	119.04	132.83
63	a	1626	AM2	CA5-CA6-CA7	-3.50	102.47	110.62
64	x	801	GDP	C4-C5-N7	-3.34	105.43	110.72
64	x	801	GDP	O4'-C1'-N9	3.04	115.32	108.36
64	x	801	GDP	O2B-PB-O3A	2.96	114.56	104.64
64	x	801	GDP	O3A-PB-O1B	-2.89	95.17	111.19
63	a	1620	AM2	CC2-CC3-CC4	-2.89	106.49	111.37
64	x	801	GDP	N9-C4-N3	2.83	131.63	125.94
63	a	1620	AM2	CA8-CA7-NA7	2.63	115.72	111.00
64	x	801	GDP	C2'-C1'-N9	-2.54	106.03	113.22
64	x	801	GDP	C6-C5-C4	-2.50	114.94	118.77
64	x	801	GDP	C1'-N9-C4	-2.38	119.44	126.50
63	a	1636	AM2	OA1-CC1-CC2	2.28	113.34	107.28
64	x	801	GDP	N9-C8-N7	-2.20	109.24	113.39
64	x	801	GDP	C8-N7-C5	2.17	108.17	104.24
64	x	801	GDP	O3'-C3'-C2'	-2.12	104.96	111.82
64	x	801	GDP	C5-C6-N1	2.06	118.41	113.19

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
63	a	1620	AM2	CA8-CA7-NA7-CA9
63	a	1626	AM2	CA2-CA1-OA1-CC1
63	a	1628	AM2	CA2-CA1-OA1-CC1
63	a	1628	AM2	CA7-CA8-OA8-CB1
63	a	1636	AM2	CA7-CA8-OA8-CB1
63	a	1636	AM2	OB1-CB1-OA8-CA8
63	a	1626	AM2	OA4-CA1-OA1-CC1
63	a	1636	AM2	OA4-CA1-OA1-CC1
63	a	1628	AM2	OA4-CA1-OA1-CC1
63	a	1636	AM2	OA5-CA8-OA8-CB1
63	a	1636	AM2	CB2-CB1-OA8-CA8
63	a	1620	AM2	OA5-CA8-OA8-CB1
63	a	1626	AM2	OB1-CB5-CB6-OB6
63	a	1628	AM2	OB1-CB5-CB6-OB6
63	a	1636	AM2	CC2-CC1-OA1-CA1
63	a	1620	AM2	OB1-CB5-CB6-OB6
63	a	1620	AM2	CB4-CB5-CB6-OB6
64	x	801	GDP	O4'-C4'-C5'-O5'
63	a	1620	AM2	OA4-CA1-OA1-CC1
63	a	1636	AM2	CA8-CA7-NA7-CA9
64	x	801	GDP	C5'-O5'-PA-O1A

All (3) ring outliers are listed below:

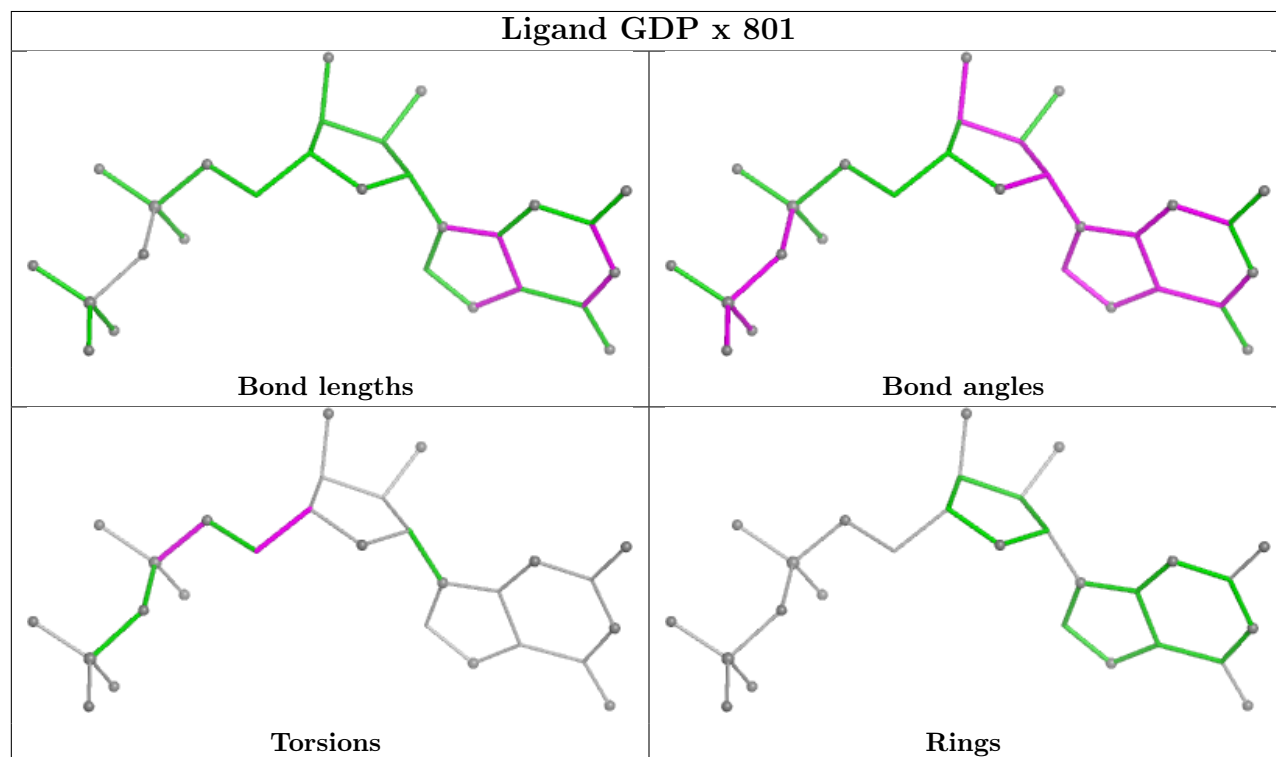
Mol	Chain	Res	Type	Atoms
63	a	1626	AM2	CC1-CC2-CC3-CC4-CC5-CC6
63	a	1628	AM2	CC1-CC2-CC3-CC4-CC5-CC6
63	a	1636	AM2	CA1-CA2-CA3-CA4-CA5-OA4

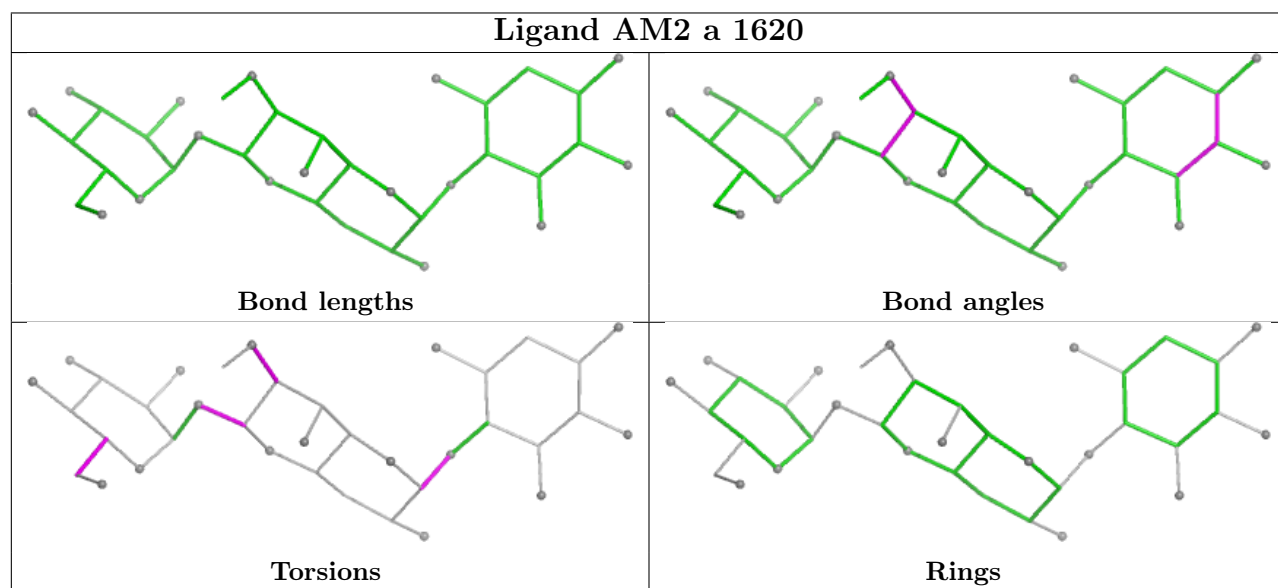
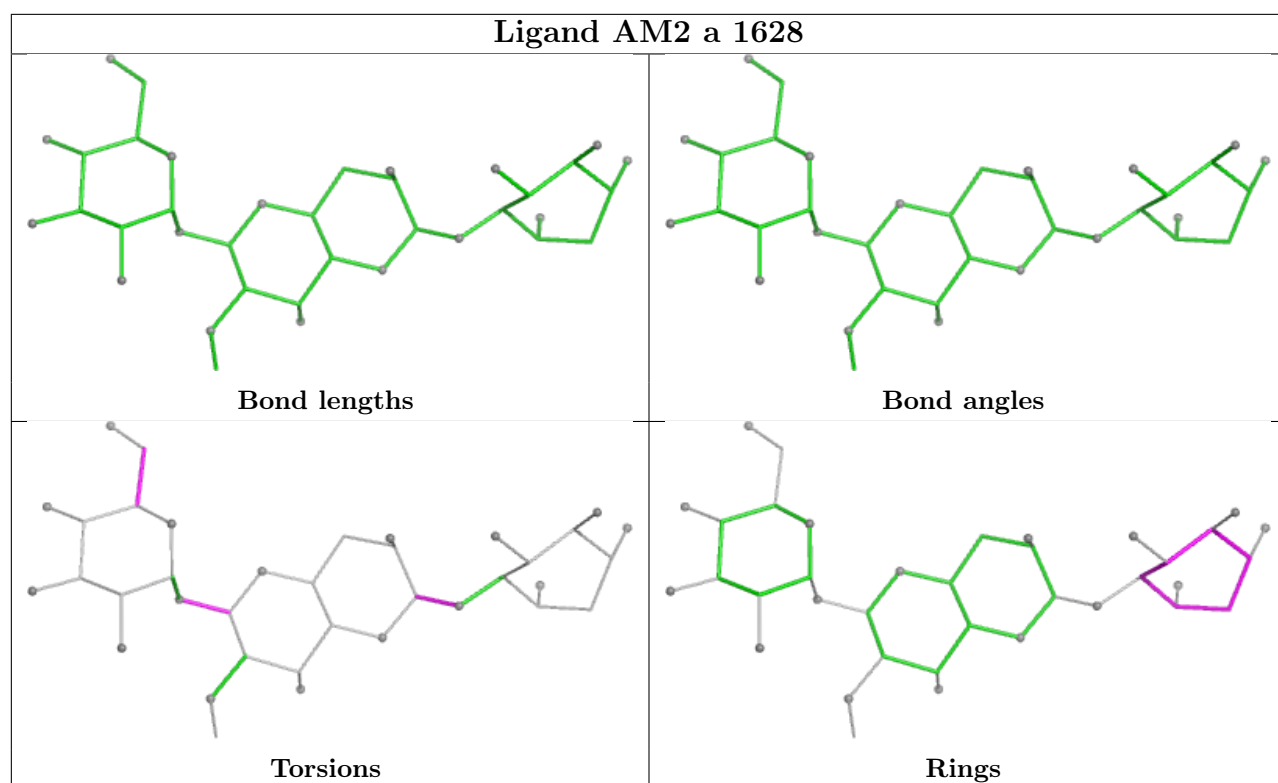
2 monomers are involved in 3 short contacts:

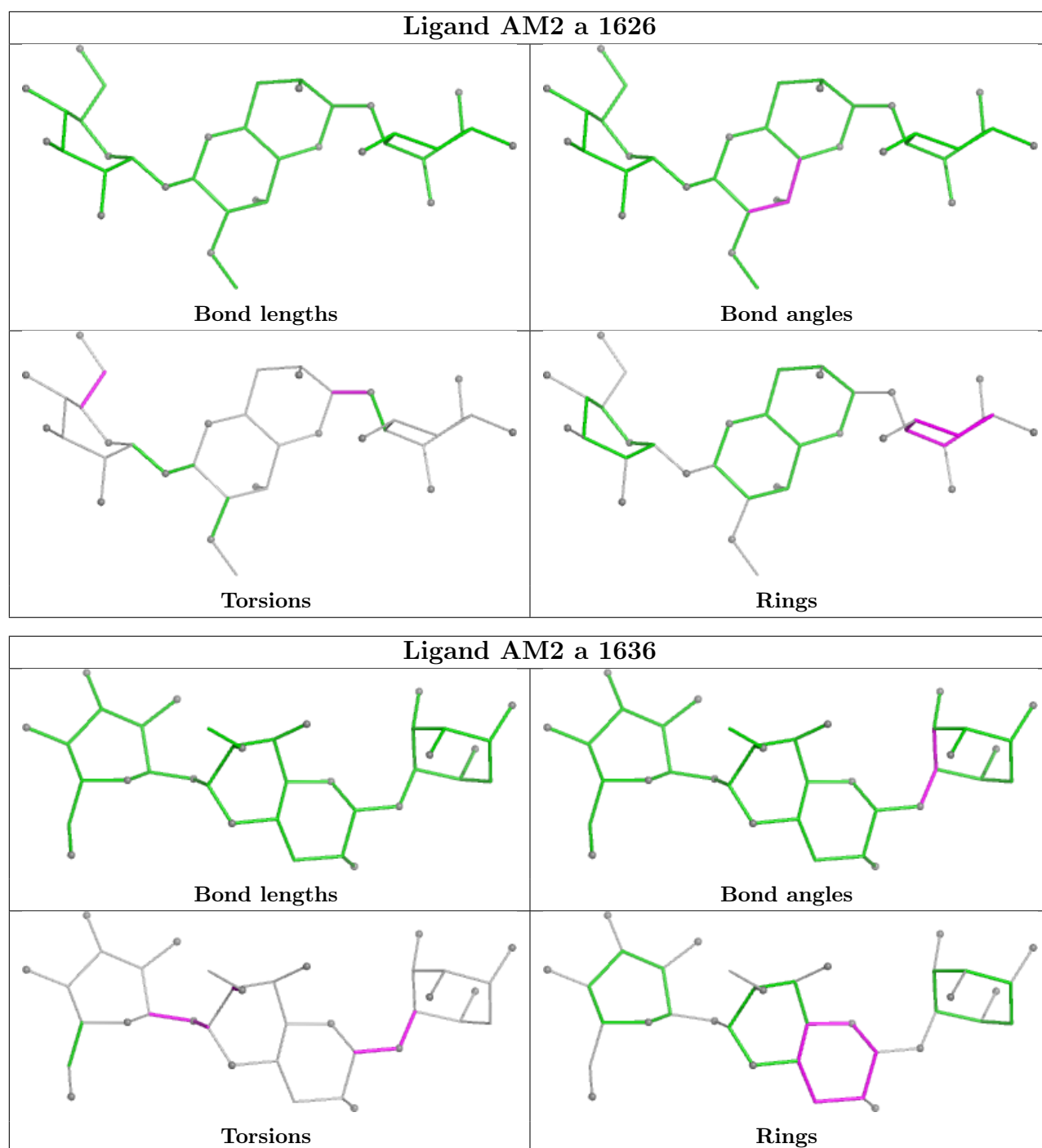
Mol	Chain	Res	Type	Clashes	Symm-Clashes
64	x	801	GDP	1	0
63	a	1620	AM2	2	0

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.

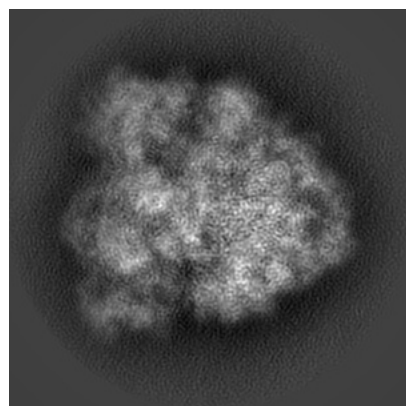
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13464. These allow visual inspection of the internal detail of the map and identification of artifacts.

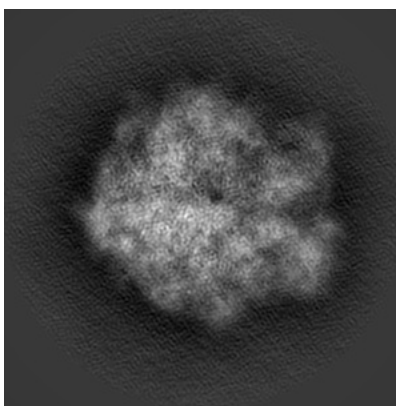
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

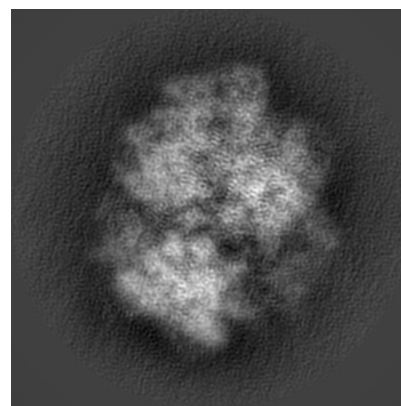
6.1.1 Primary map



X

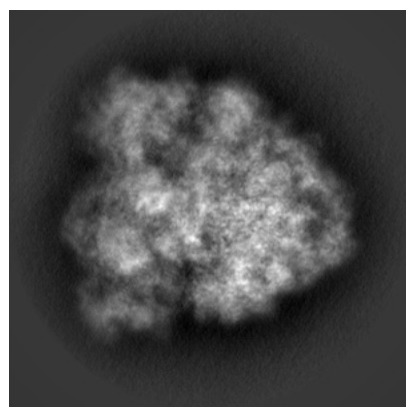


Y

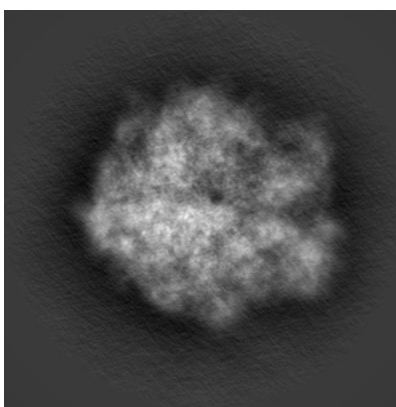


Z

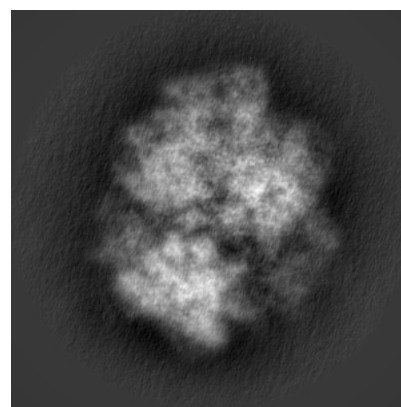
6.1.2 Raw map



X



Y

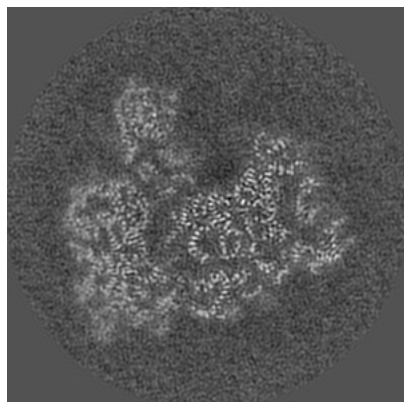


Z

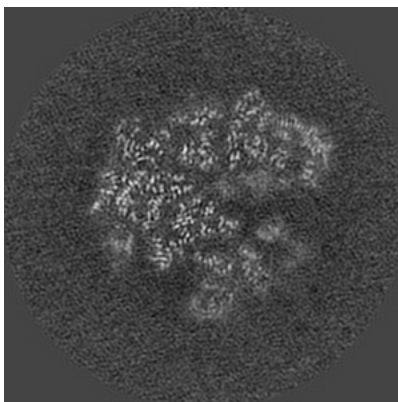
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

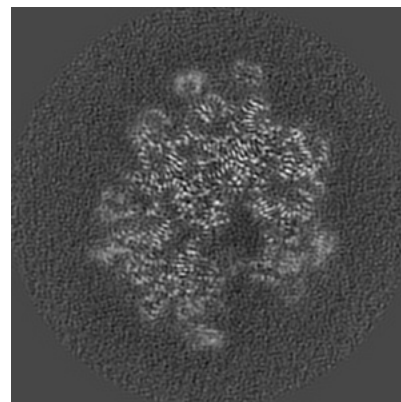
6.2.1 Primary map



X Index: 256

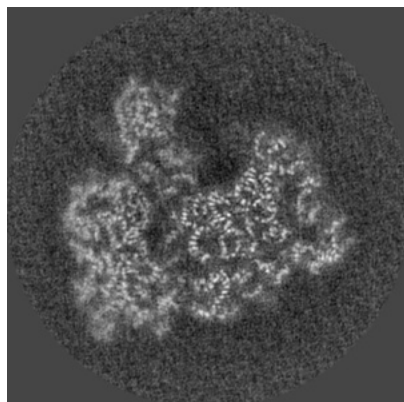


Y Index: 256

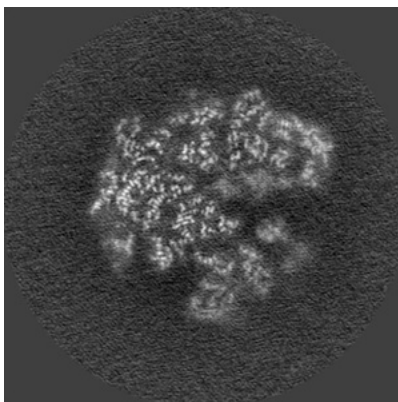


Z Index: 256

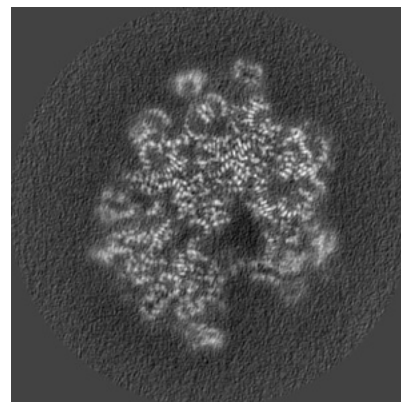
6.2.2 Raw map



X Index: 144



Y Index: 144

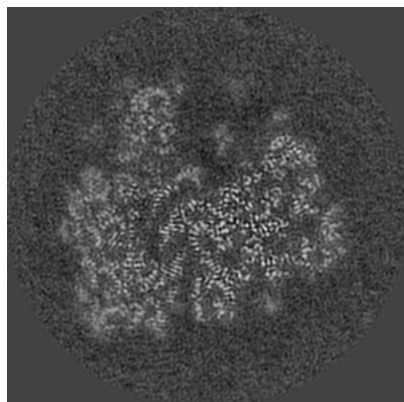


Z Index: 144

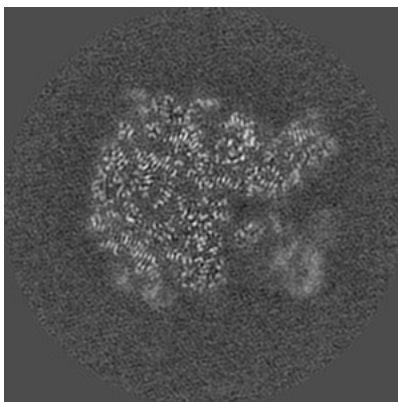
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

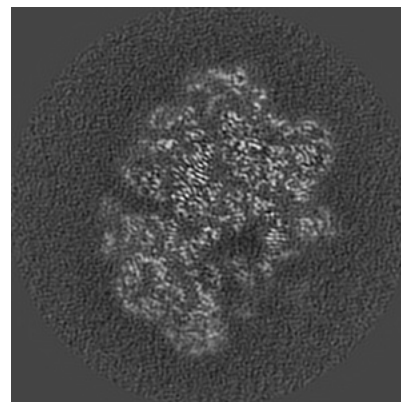
6.3.1 Primary map



X Index: 246

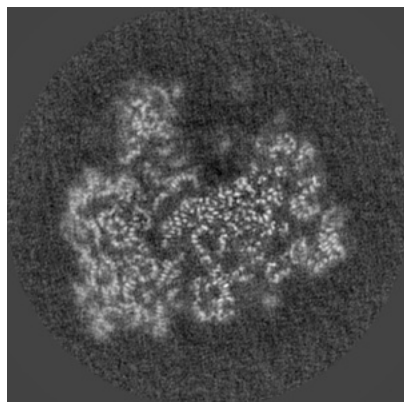


Y Index: 289

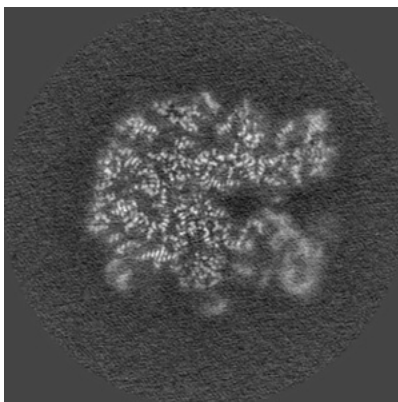


Z Index: 238

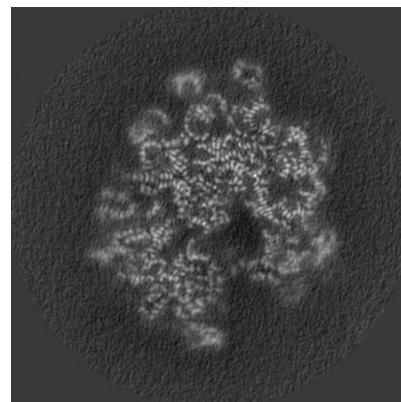
6.3.2 Raw map



X Index: 141



Y Index: 157

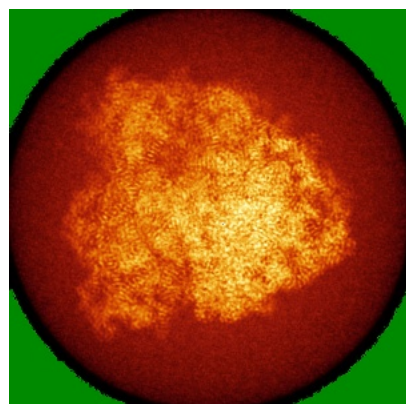


Z Index: 145

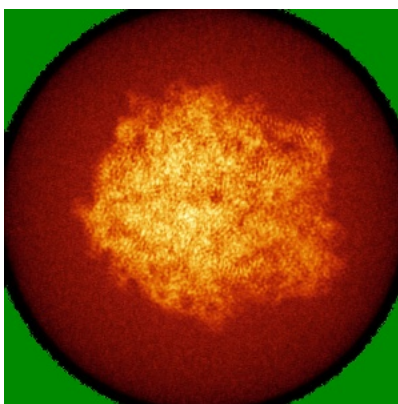
The images above show the largest variance slices of the map in three orthogonal directions.

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

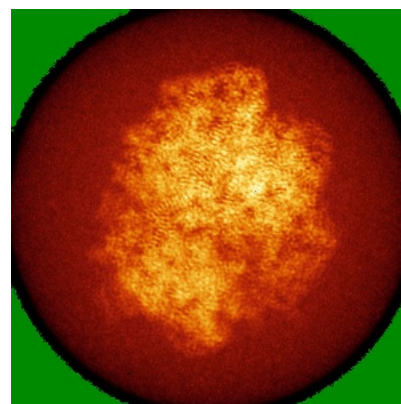
6.4.1 Primary map



X

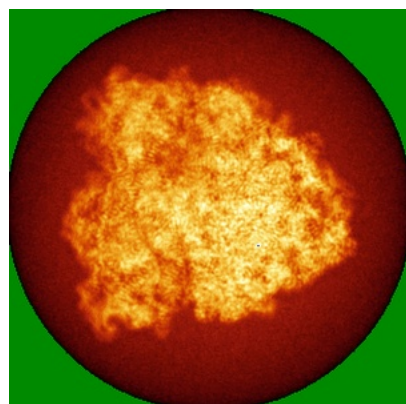


Y

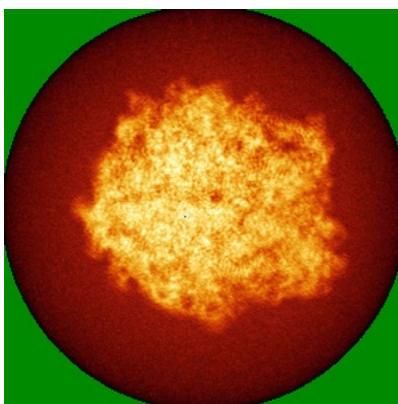


Z

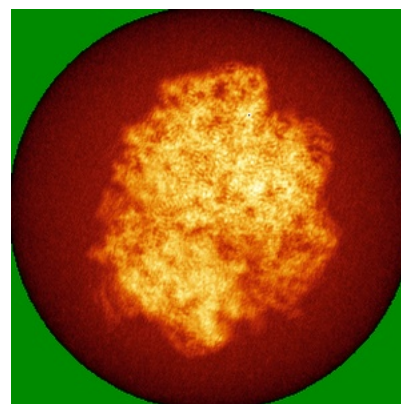
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

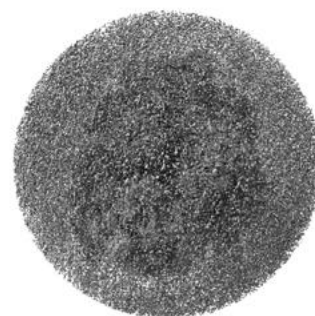
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

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

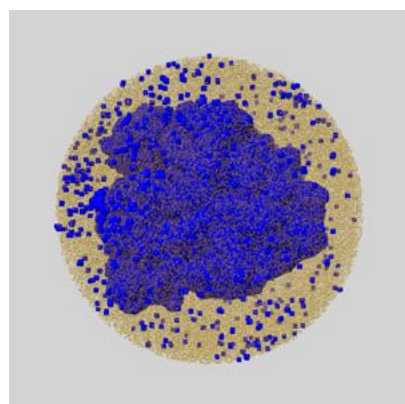
6.6 Mask visualisation [i](#)

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

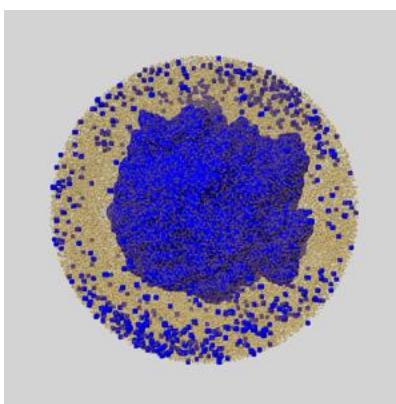
A mask typically either:

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

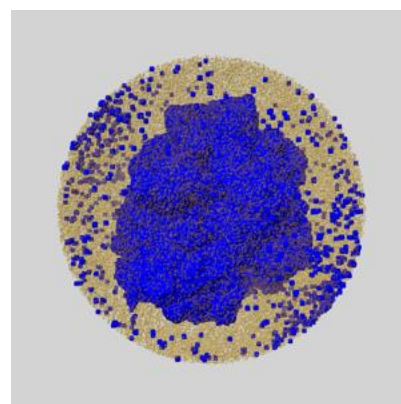
6.6.1 emd_13464_msk_1.map [i](#)



X



Y

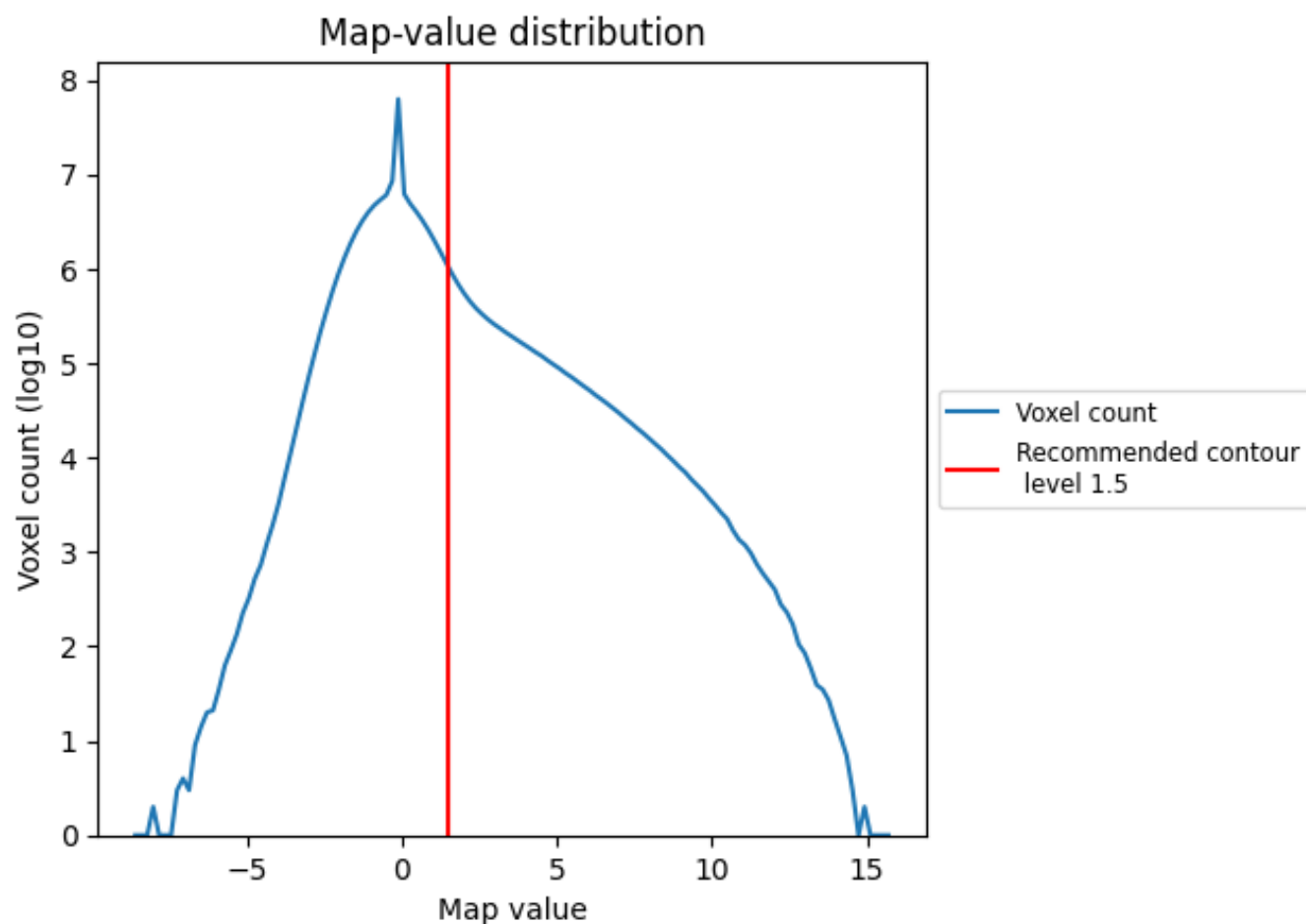


Z

7 Map analysis [i](#)

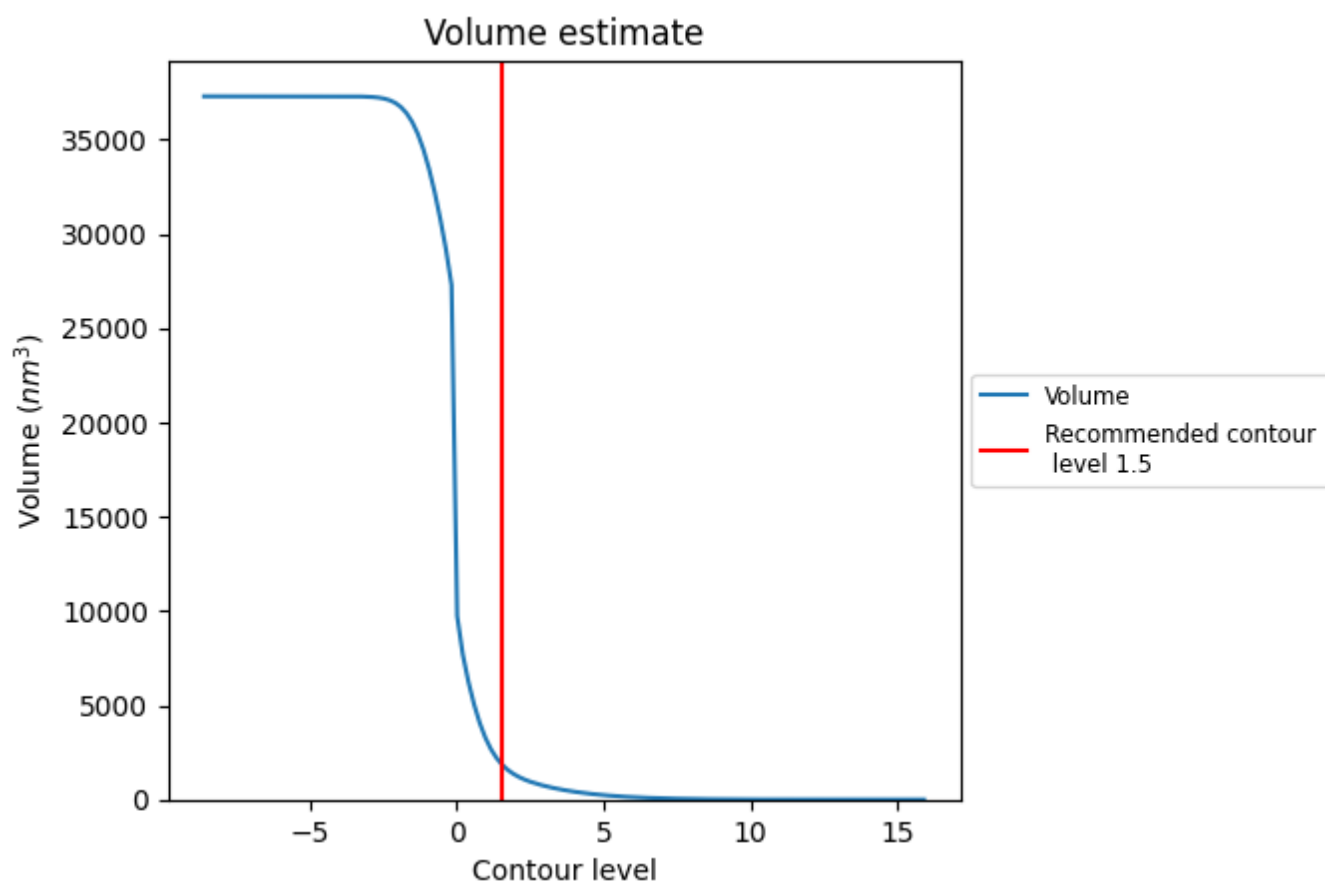
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

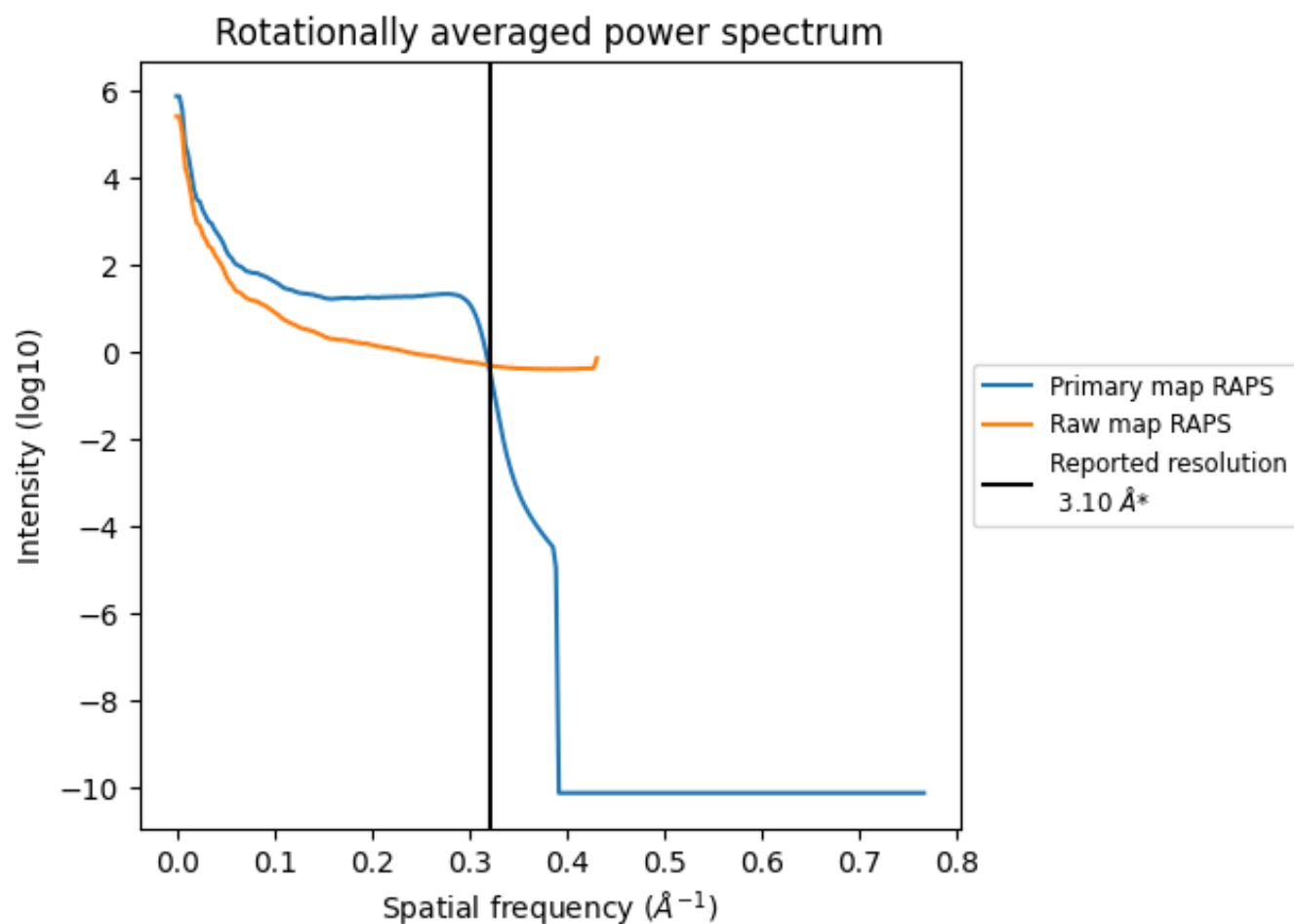
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1926 nm^3 ; this corresponds to an approximate mass of 1740 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 ⓘ

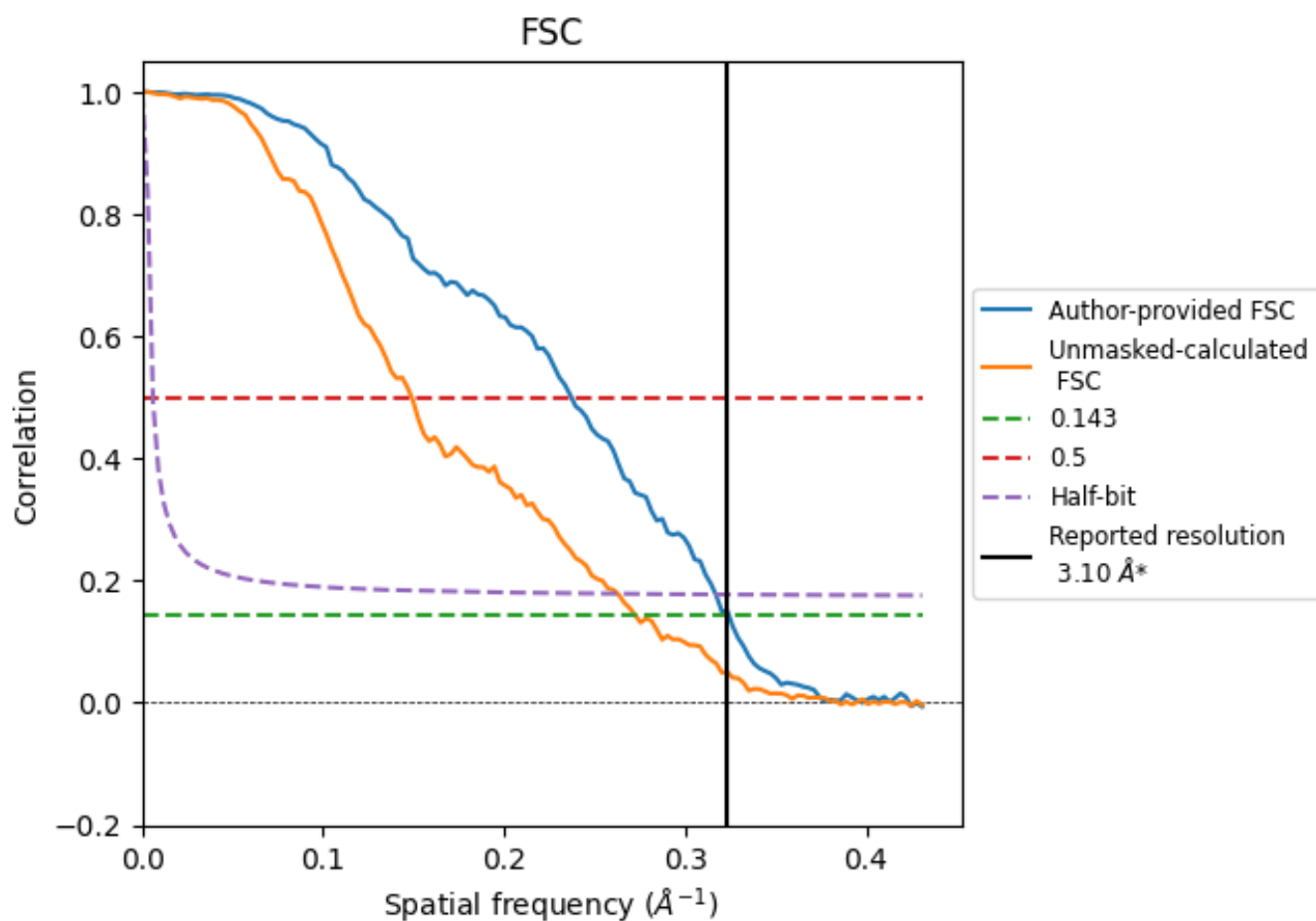


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

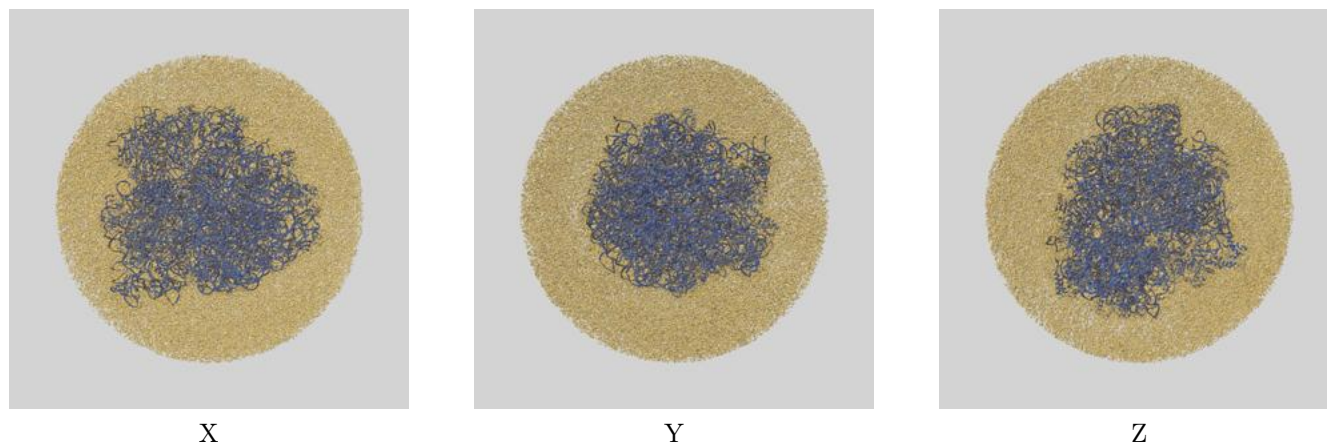
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.08	4.22	3.15
Unmasked-calculated*	3.67	6.72	3.81

*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 3.67 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

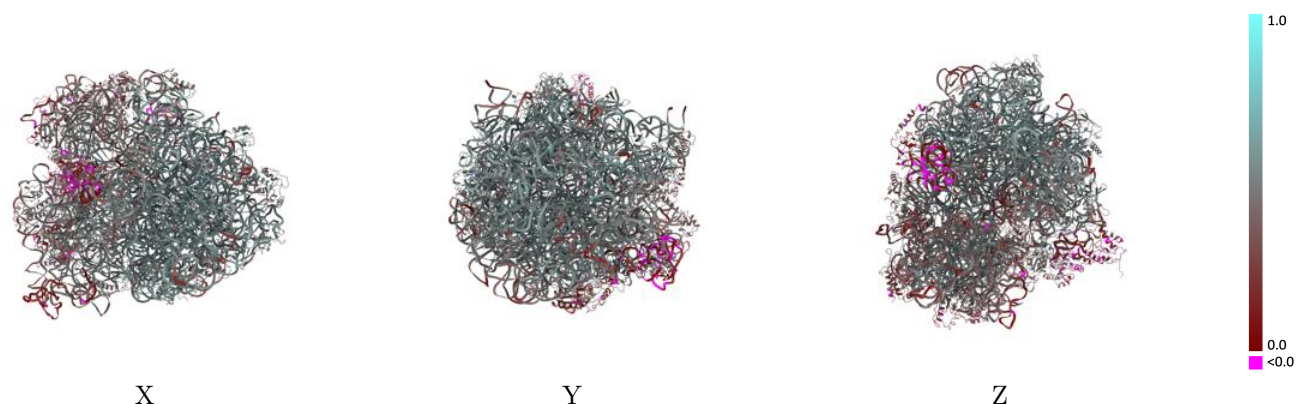
This section contains information regarding the fit between EMDB map EMD-13464 and PDB model 7PJY. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

9.1 Map-model overlay [i](#)



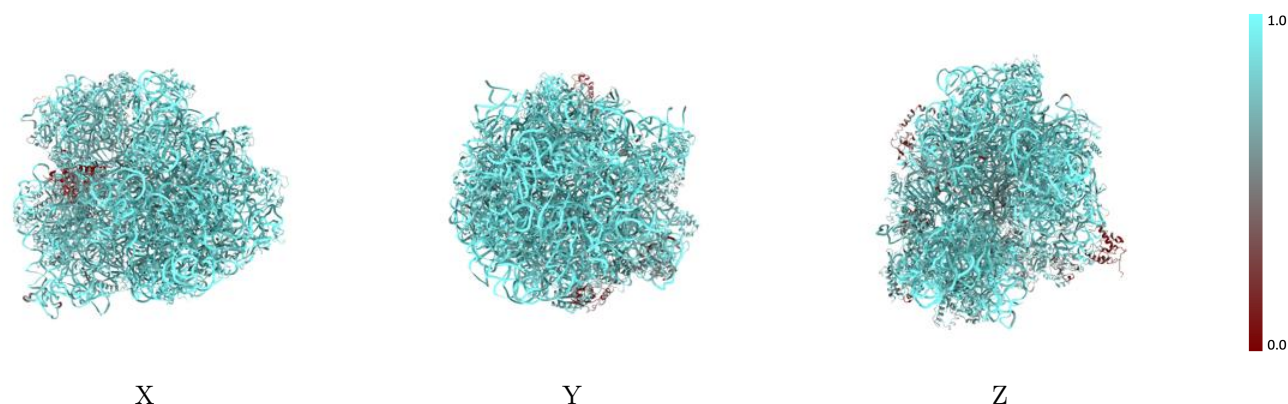
The images above show the 3D surface view of the map at the recommended contour level 1.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



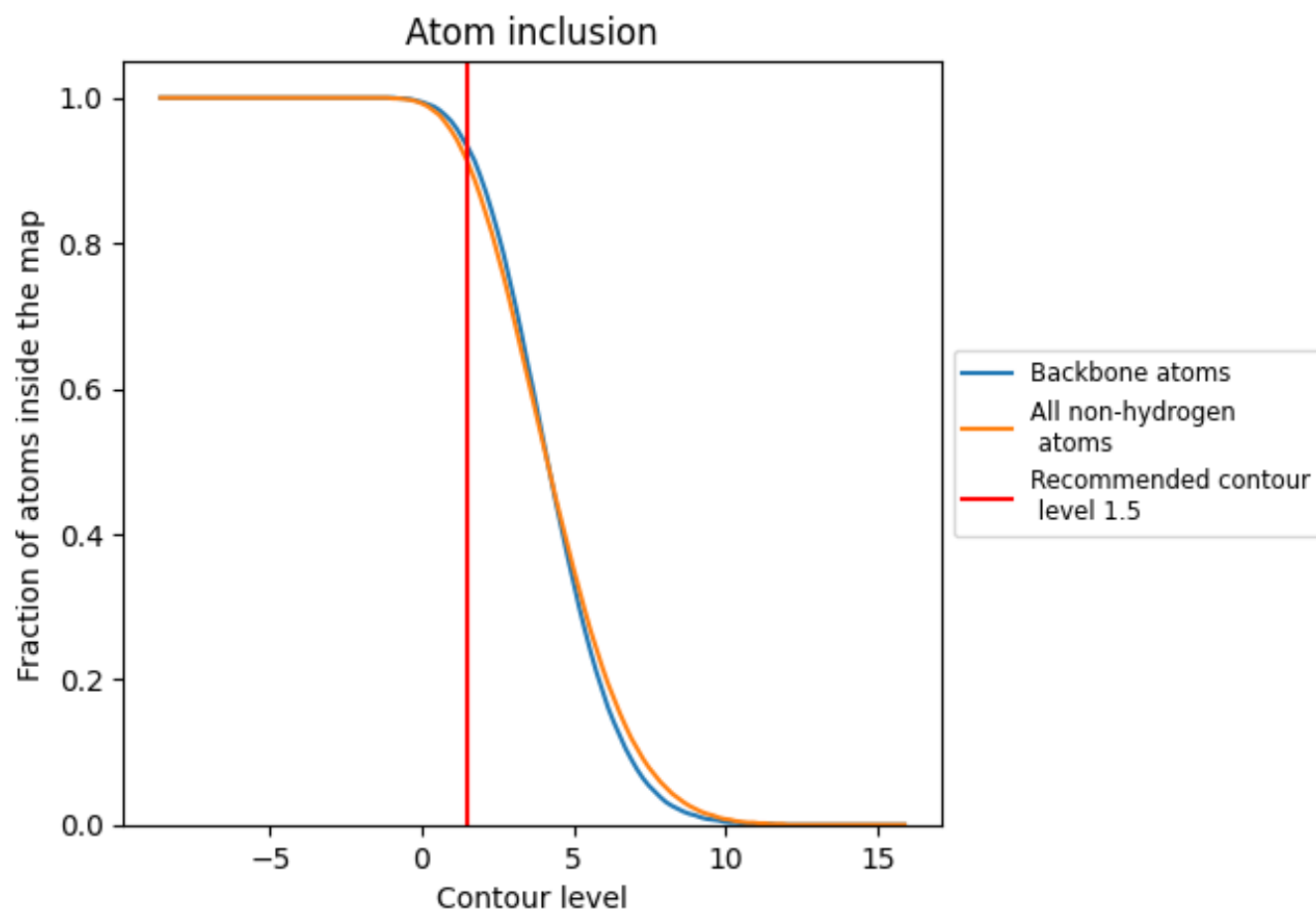
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 91% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (1.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9130	 0.4660
0	 0.8930	 0.5200
1	 0.8460	 0.4870
2	 0.9210	 0.5610
3	 0.9370	 0.5640
4	 0.9350	 0.5350
5	 0.2230	 0.1450
6	 0.7800	 0.3320
A	 0.9630	 0.5030
B	 0.9700	 0.4890
C	 0.9130	 0.5380
D	 0.9140	 0.5310
E	 0.8900	 0.5000
F	 0.8310	 0.4070
G	 0.8590	 0.4270
H	 0.4430	 0.2690
I	 0.4990	 0.1370
J	 0.9270	 0.5300
K	 0.8640	 0.5270
L	 0.9060	 0.5210
M	 0.9060	 0.5220
N	 0.9480	 0.5380
O	 0.9050	 0.4780
P	 0.8950	 0.5300
Q	 0.9450	 0.5390
R	 0.9360	 0.5170
S	 0.8930	 0.5230
T	 0.9020	 0.4920
U	 0.9240	 0.4840
V	 0.8960	 0.5000
W	 0.9270	 0.5360
X	 0.8930	 0.5300
Y	 0.8910	 0.4570
Z	 0.9040	 0.5140
a	 0.9500	 0.4470



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Chain	Atom inclusion	Q-score
b	 0.6370	 0.3260
c	 0.8250	 0.4090
d	 0.8190	 0.3700
e	 0.8840	 0.4660
f	 0.8230	 0.3520
g	 0.6650	 0.2930
h	 0.8740	 0.4560
i	 0.8840	 0.3860
j	 0.7830	 0.3630
k	 0.8140	 0.4230
l	 0.8280	 0.4950
m	 0.8270	 0.3860
n	 0.8890	 0.4390
o	 0.8590	 0.4340
p	 0.8740	 0.4590
q	 0.8700	 0.4520
r	 0.8850	 0.4370
s	 0.8550	 0.4080
t	 0.8710	 0.4360
u	 0.7440	 0.3750
v	 0.8820	 0.4250
w	 0.7520	 0.3370
x	 0.7600	 0.3750
y	 0.6190	 0.3720
z	 0.9090	 0.5080