



Full wwPDB EM Validation Report ⓘ

Jun 23, 2026 – 01:04 PM JST

PDB ID : 8IFC / pdb_00008ifc
EMDB ID : EMD-35412
Title : Arbekacin-bound E.coli 70S ribosome in the PURE system
Authors : Tomono, J.; Asano, K.; Chiashi, T.; Tanaka, Y.; Yokoyama, T.
Deposited on : 2023-02-17
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.5 (274361), 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

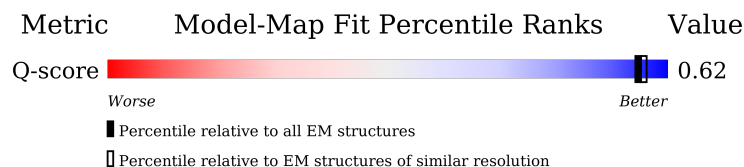
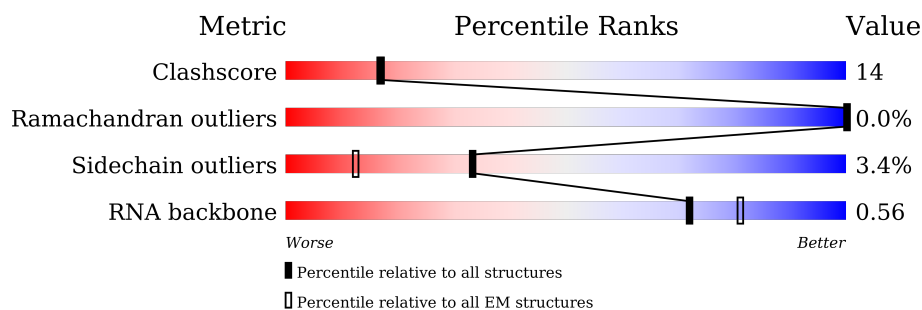
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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	13054 (2.40 - 3.40)

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

Mol	Chain	Length	Quality of chain
1	A	1542	15% 44% 47% 8%
2	B	241	55% 49% 42% 7%
3	C	233	25% 51% 36% 12%

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Mol	Chain	Length	Quality of chain
4	D	206	
5	E	167	
6	F	135	
7	G	179	
8	H	130	
9	I	130	
10	J	103	
11	K	129	
12	L	124	
13	M	118	
14	N	101	
15	O	89	
16	P	82	
17	Q	84	
18	R	75	
19	S	92	
20	T	87	
21	U	71	
22	a	2904	
23	b	120	
24	c	273	
25	d	209	
26	e	201	
27	f	179	
28	g	177	

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Mol	Chain	Length	Quality of chain
29	h	149	
30	i	142	
31	j	123	
32	k	144	
33	l	136	
34	m	127	
35	n	117	
36	o	115	
37	p	118	
38	q	103	
39	r	110	
40	s	100	
41	t	104	
42	u	94	
43	v	85	
44	w	78	
45	x	63	
46	y	59	
47	z	57	
48	0	55	
49	1	46	
50	2	65	
51	3	38	
52	4	70	
53	5	76	

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Mol	Chain	Length	Quality of chain
54	6	77	55% 36% 47% 16%
55	7	10	80% 20%

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 143000 atoms, of which 440 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 RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1519	Total	C	N	O	P	0	0
			32612	14552	5986	10555	1519		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 3 is a protein called 30S ribosomal protein S3.

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

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 6 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	103	Total	C	N	O	S	0	0
			839	530	151	151	7		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

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

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	117	Total	C	N	O	S	0	0
			877	540	173	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	modified residue	UNP P0A7R9

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 14 is a protein called 30S ribosomal protein S14.

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

- Molecule 15 is a protein called 30S ribosomal protein S15.

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

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 22 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	a	2753	Total	C	N	O	P	0	0
			59130	26384	10897	19096	2753		

- Molecule 23 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 24 is a protein called 50S ribosomal protein L2.

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

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 26 is a protein called 50S ribosomal protein L4.

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

- Molecule 27 is a protein called 50S ribosomal protein L5.

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

- Molecule 28 is a protein called 50S ribosomal protein L6.

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

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	h	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 30 is a protein called 50S ribosomal protein L13.

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

- Molecule 31 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	j	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 32 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	k	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 33 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	l	136	Total	C	N	O	S	0	0
			1075	686	205	177	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	82	MS6	MET	modified residue	UNP P0ADY7

- Molecule 34 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	m	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 35 is a protein called 50S ribosomal protein L18.

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

- Molecule 36 is a protein called 50S ribosomal protein L19.

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

- Molecule 37 is a protein called 50S ribosomal protein L20.

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

- Molecule 38 is a protein called 50S ribosomal protein L21.

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

- Molecule 39 is a protein called 50S ribosomal protein L22.

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

- Molecule 40 is a protein called 50S ribosomal protein L23.

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

- Molecule 41 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	t	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 42 is a protein called 50S ribosomal protein L25.

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

- Molecule 43 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	v	78	Total	C	N	O	S	0	0
			586	362	116	107	1		

- Molecule 44 is a protein called 50S ribosomal protein L28.

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

- Molecule 45 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	x	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 46 is a protein called 50S ribosomal protein L30.

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

- Molecule 47 is a protein called 50S ribosomal protein L32.

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

- Molecule 48 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	0	51	Total	C	N	O		0	0
			417	269	76	72			

- Molecule 49 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 51 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 52 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 53 is a RNA chain called A-site tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace	
53	5	76	Total	C	N	O	P	S	0	0
			1632	731	290	533	76	2		

- Molecule 54 is a RNA chain called P-site tRNA^f-Met.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	6	77	Total	C	N	O	P	S	0	0
			1645	734	297	536	77	1		

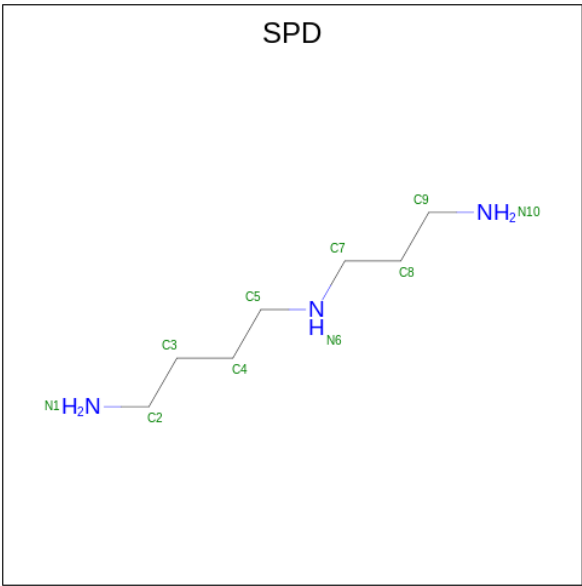
- Molecule 55 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	7	10	Total	C	N	O	P	0	0
			209	95	37	68	9		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	A	188	Total	Mg	0
			188	188	
56	C	3	Total	Mg	0
			3	3	
56	E	2	Total	Mg	0
			2	2	
56	G	1	Total	Mg	0
			1	1	
56	K	1	Total	Mg	0
			1	1	
56	M	9	Total	Mg	0
			9	9	
56	S	2	Total	Mg	0
			2	2	
56	a	233	Total	Mg	0
			233	233	
56	b	11	Total	Mg	0
			11	11	
56	c	1	Total	Mg	0
			1	1	
56	d	2	Total	Mg	0
			2	2	
56	l	1	Total	Mg	0
			1	1	
56	z	2	Total	Mg	0
			2	2	
56	4	2	Total	Mg	0
			2	2	
56	6	1	Total	Mg	0
			1	1	
56	7	1	Total	Mg	0
			1	1	

- Molecule 57 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



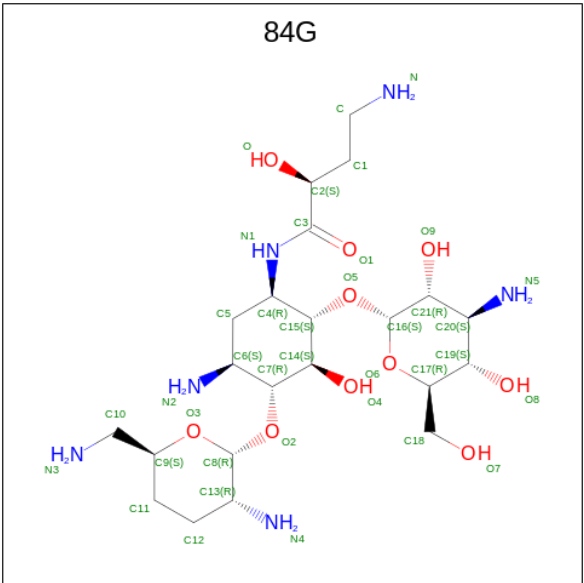
Mol	Chain	Residues	Atoms			AltConf
57	A	1	Total	C	N	0
			10	7	3	
57	A	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	
57	a	1	Total	C	N	0
			10	7	3	

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Mol	Chain	Residues	Atoms			AltConf
			Total	C	N	
57	a	1	10	7	3	0
57	a	1	10	7	3	0
57	a	1	10	7	3	0

- Molecule 58 is Arbekacin (CCD ID: 84G) (formula: C₂₂H₄₄N₆O₁₀) (labeled as "Ligand of Interest" by depositor).



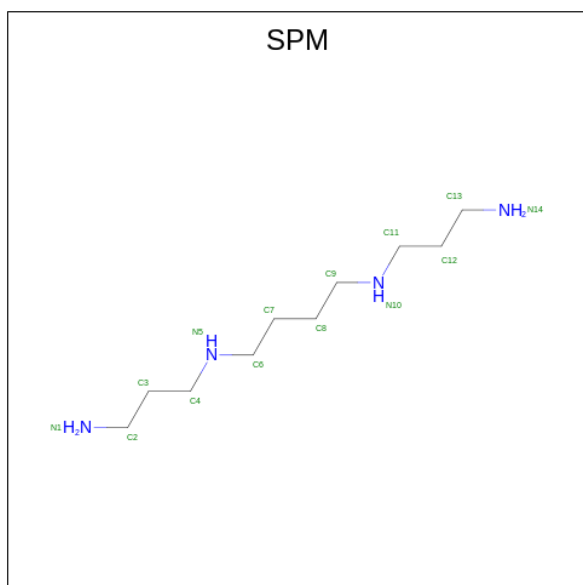
Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	N	O	
58	A	1	82	22	44	6	10	0
58	A	1	82	22	44	6	10	0
58	A	1	82	22	44	6	10	0
58	a	1	82	22	44	6	10	0
58	a	1	82	22	44	6	10	0
58	a	1	82	22	44	6	10	0
58	a	1	82	22	44	6	10	0
58	a	1	82	22	44	6	10	0

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Mol	Chain	Residues	Atoms					AltConf
58	a	1	Total	C	H	N	O	0
			82	22	44	6	10	
58	a	1	Total	C	H	N	O	0
			82	22	44	6	10	

- Molecule 59 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$).



Mol	Chain	Residues	Atoms			AltConf
59	a	1	Total	C	N	0
			14	10	4	

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

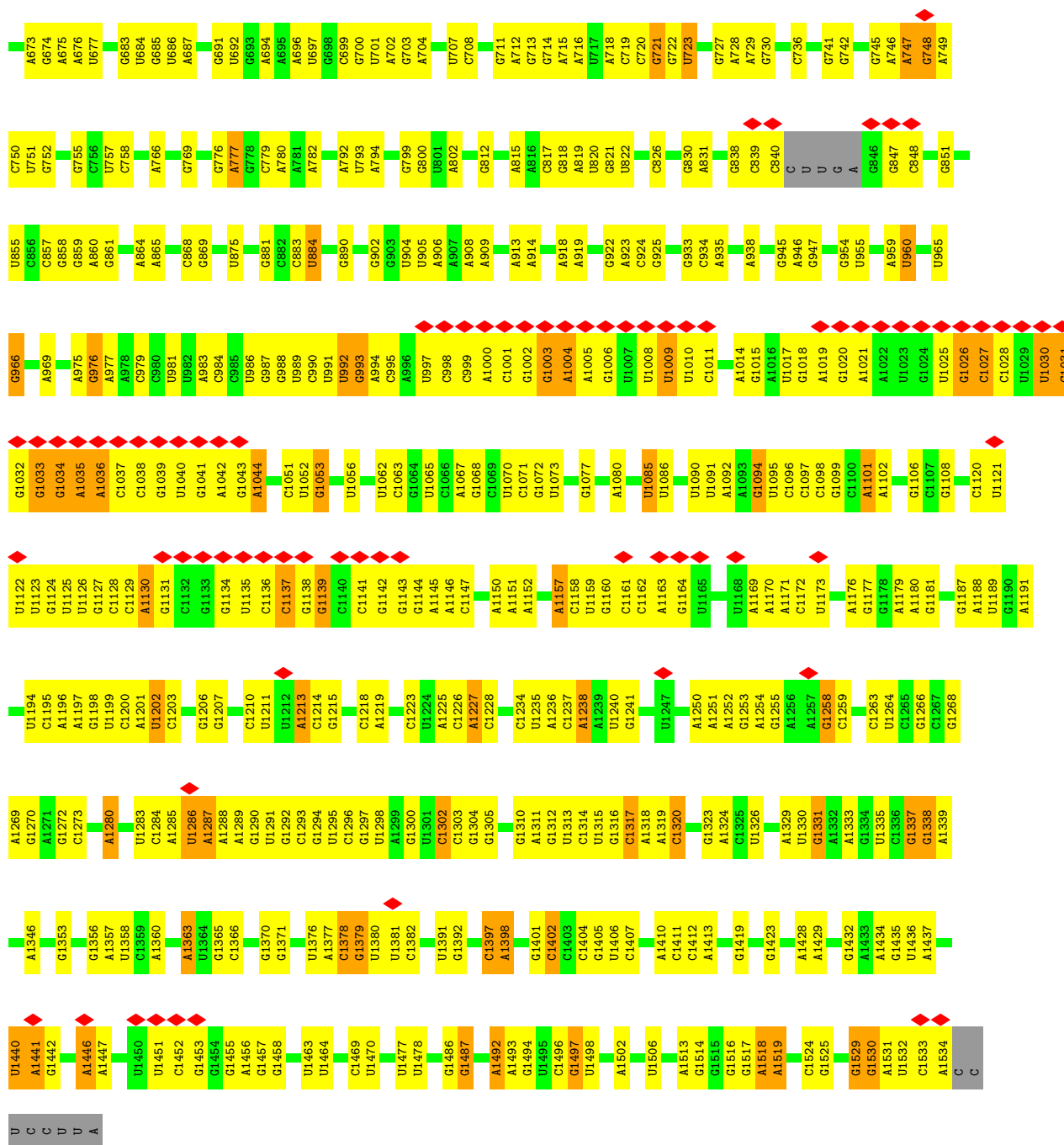
Mol	Chain	Residues	Atoms		AltConf
60	3	1	Total	Zn	0
			1	1	

3 Residue-property plots

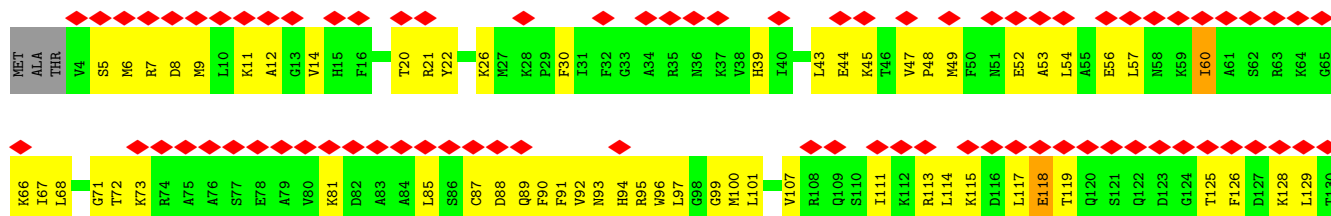
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

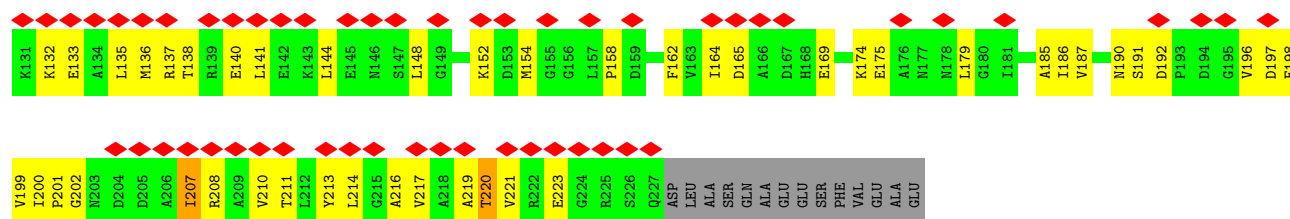
• Molecule 1: 16S ribosomal RNA



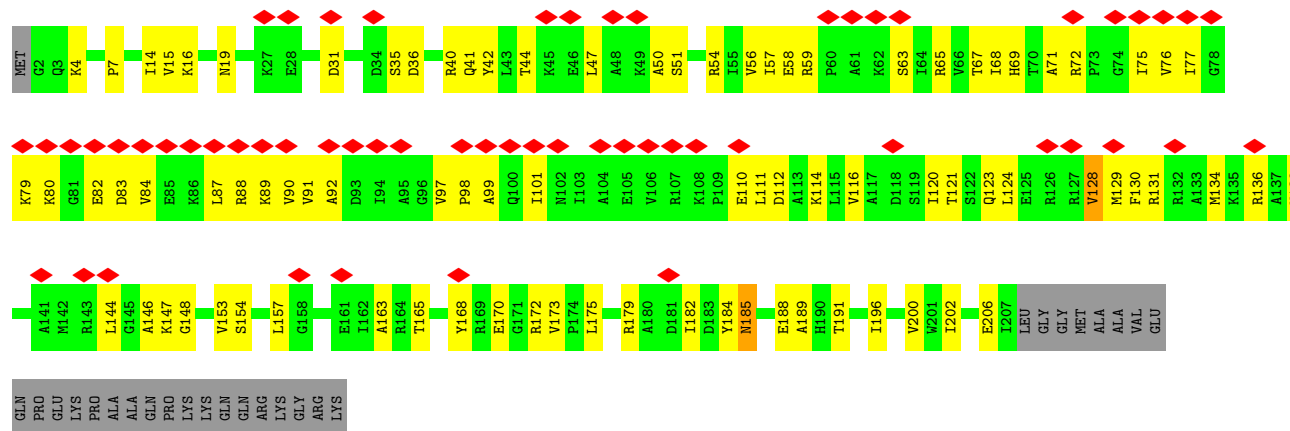


• Molecule 2: 30S ribosomal protein S2

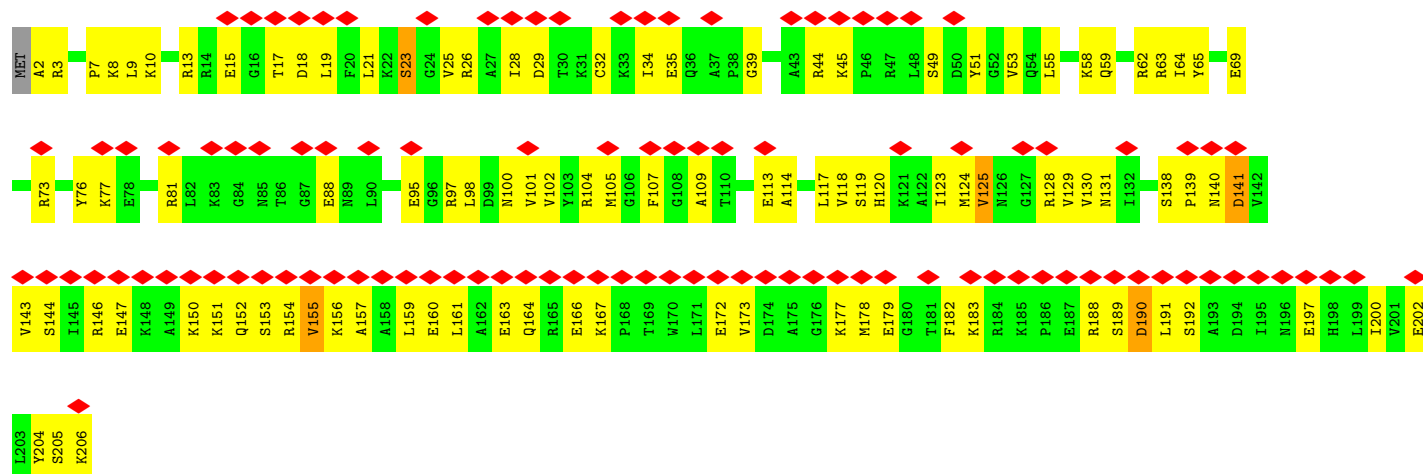




• Molecule 3: 30S ribosomal protein S3



• Molecule 4: 30S ribosomal protein S4

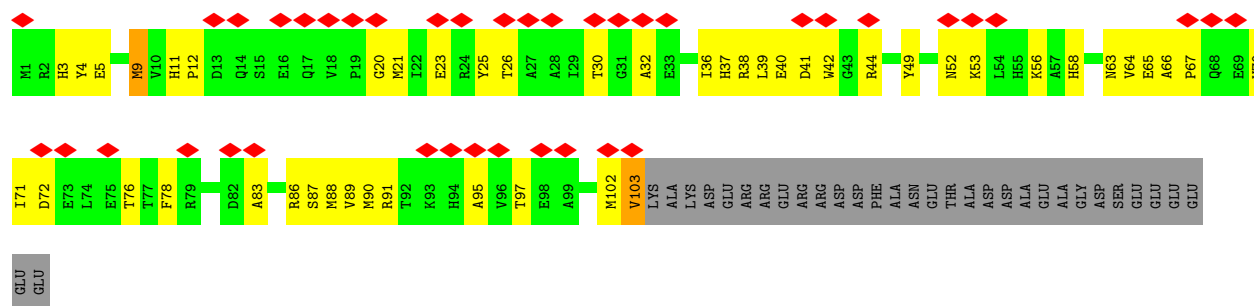
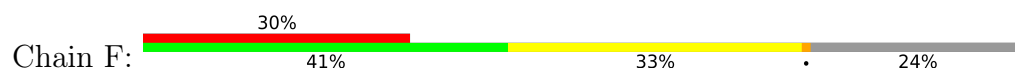


• Molecule 5: 30S ribosomal protein S5

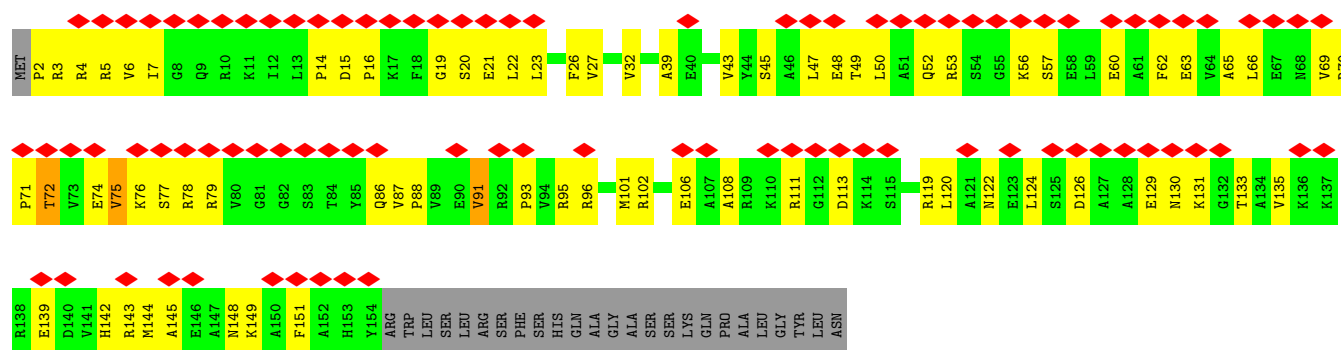
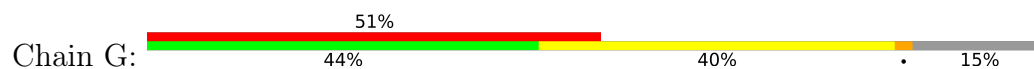




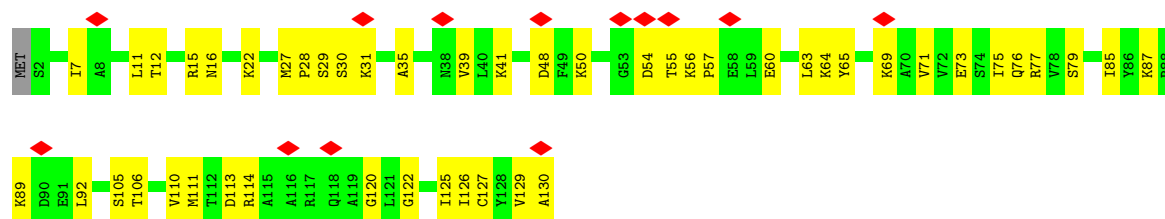
- Molecule 6: 30S ribosomal protein S6, fully modified isoform



- Molecule 7: 30S ribosomal protein S7

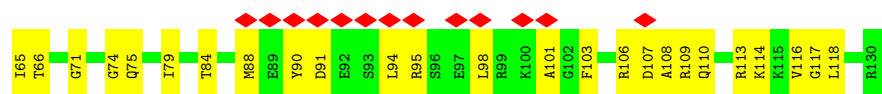


- Molecule 8: 30S ribosomal protein S8

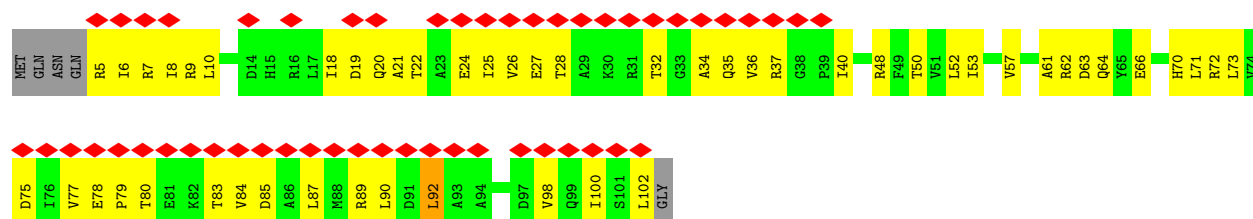
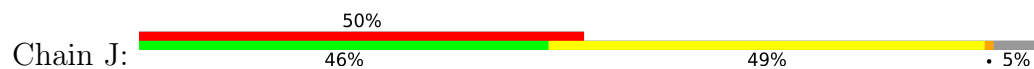


- Molecule 9: 30S ribosomal protein S9

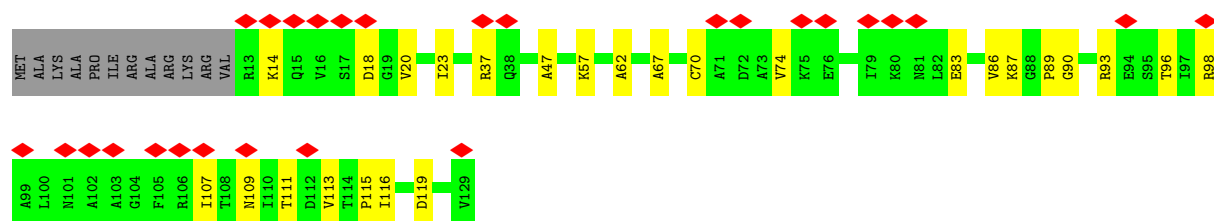




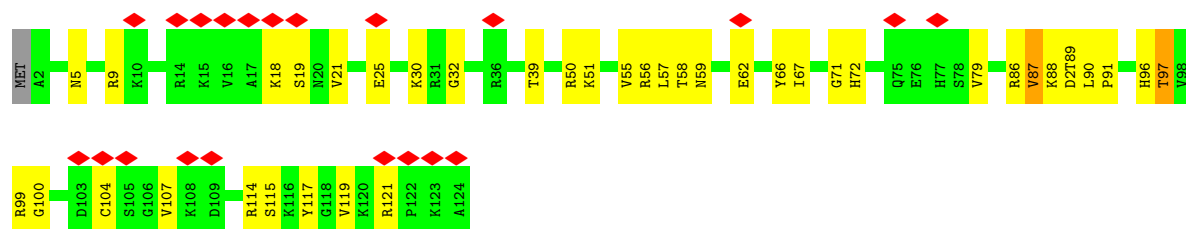
- Molecule 10: 30S ribosomal protein S10



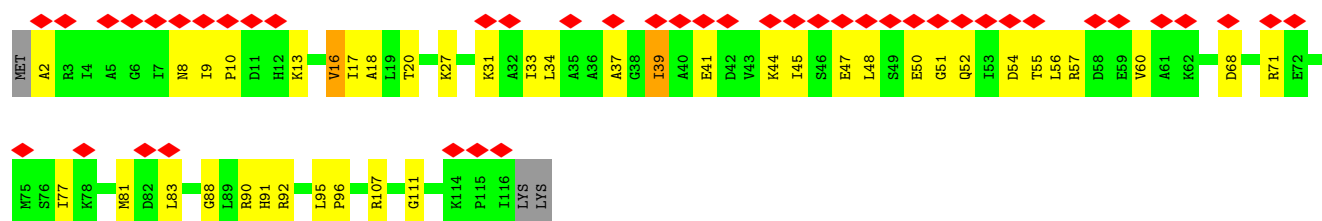
- Molecule 11: 30S ribosomal protein S11



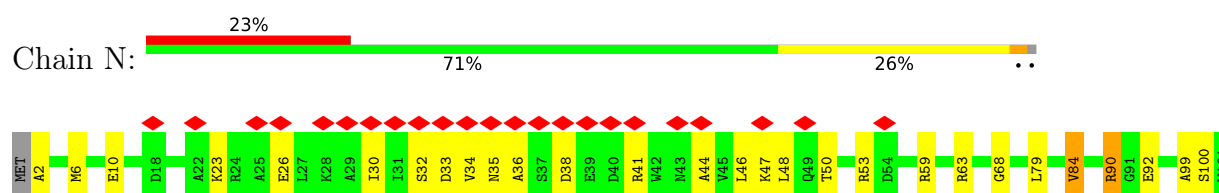
- Molecule 12: 30S ribosomal protein S12



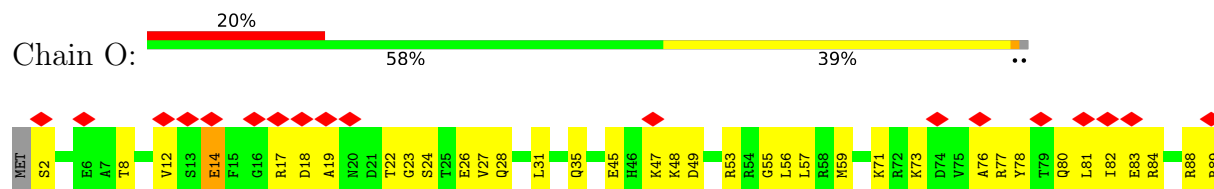
- Molecule 13: 30S ribosomal protein S13



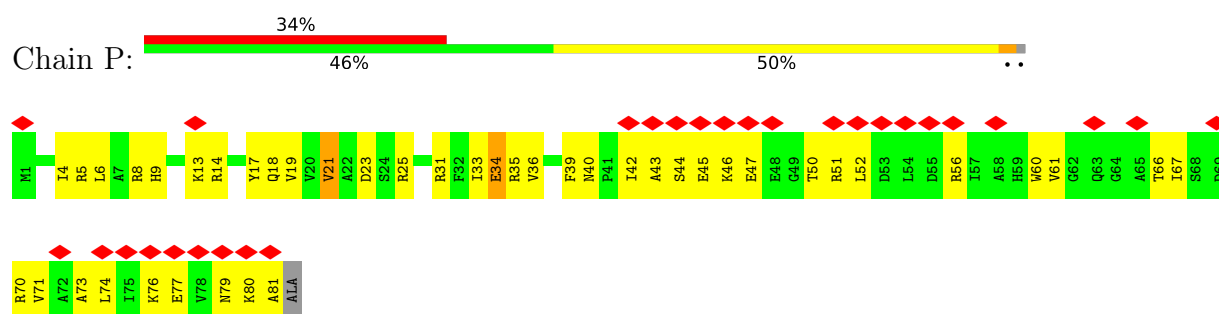
- Molecule 14: 30S ribosomal protein S14



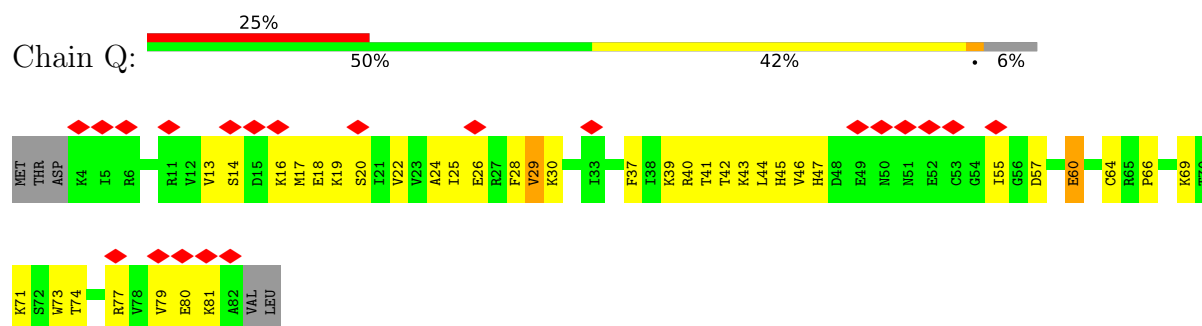
- Molecule 15: 30S ribosomal protein S15



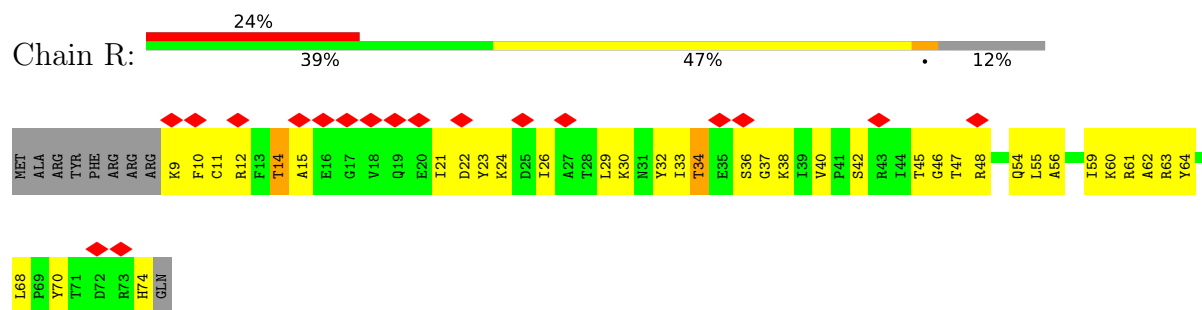
- Molecule 16: 30S ribosomal protein S16



- Molecule 17: 30S ribosomal protein S17

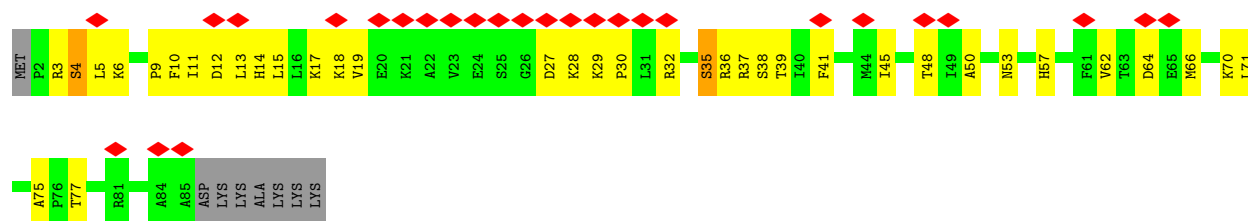


- Molecule 18: 30S ribosomal protein S18

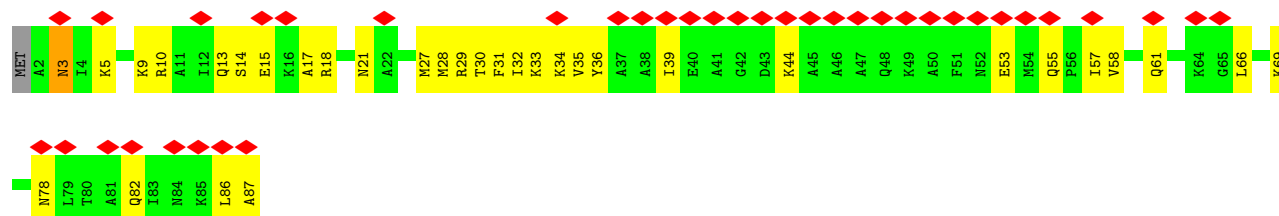
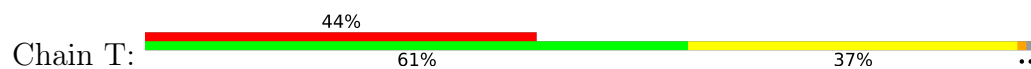


- Molecule 19: 30S ribosomal protein S19

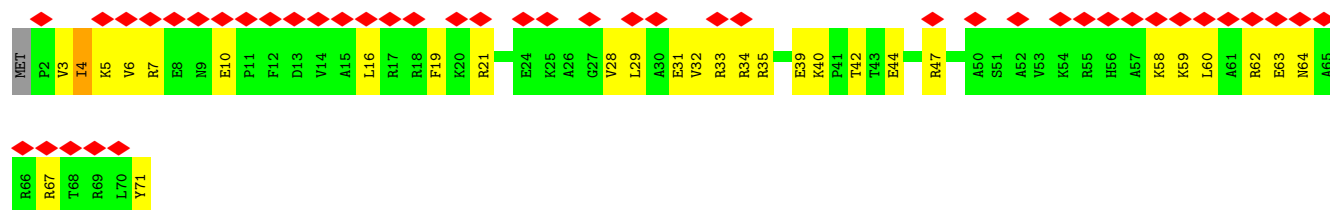




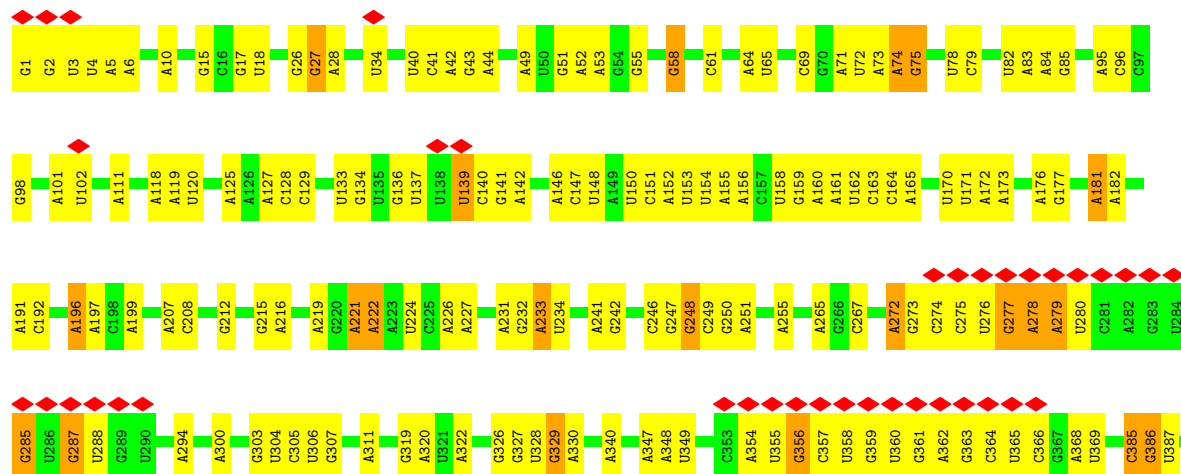
- Molecule 20: 30S ribosomal protein S20

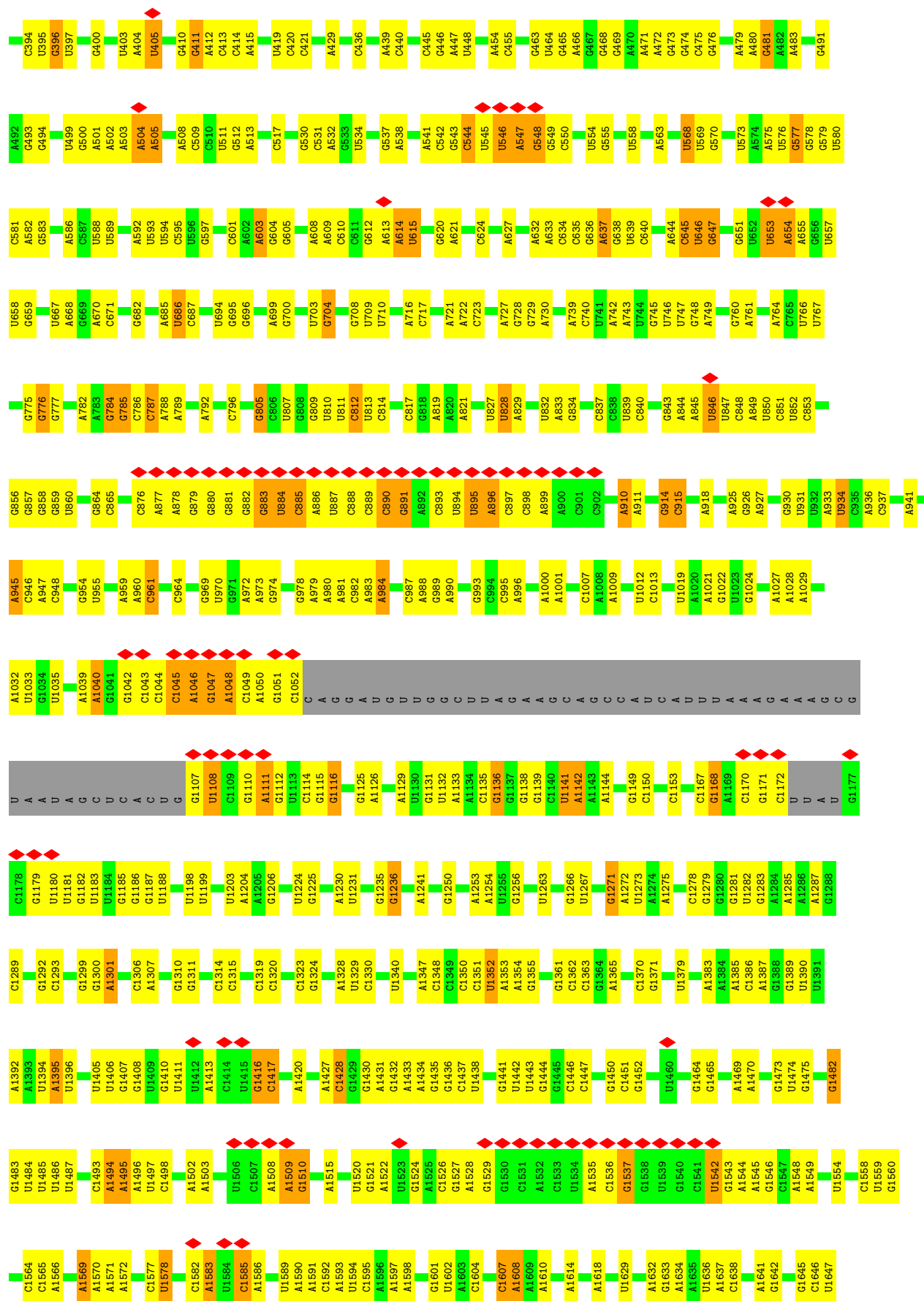


- Molecule 21: 30S ribosomal protein S21

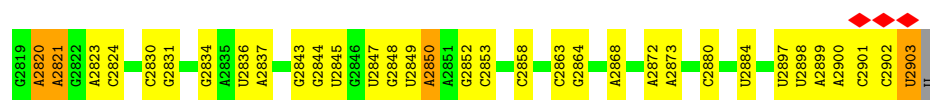


- Molecule 22: 23S ribosomal RNA

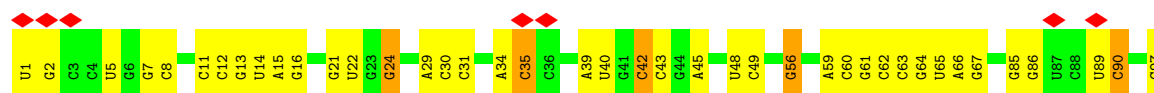




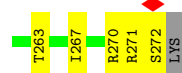
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G2732	U2615	C2520	U2439	U2329	U2245	G	G	U1928	G1929	A1829	C1730	A1652
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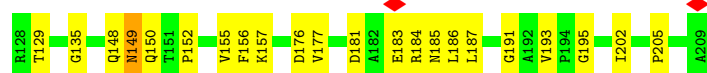
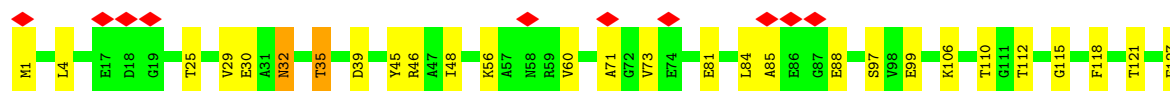
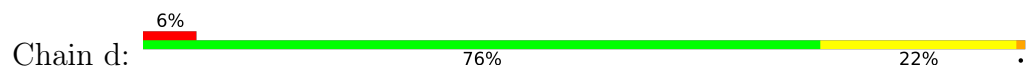
• Molecule 23: 5S ribosomal RNA



• Molecule 24: 50S ribosomal protein L2



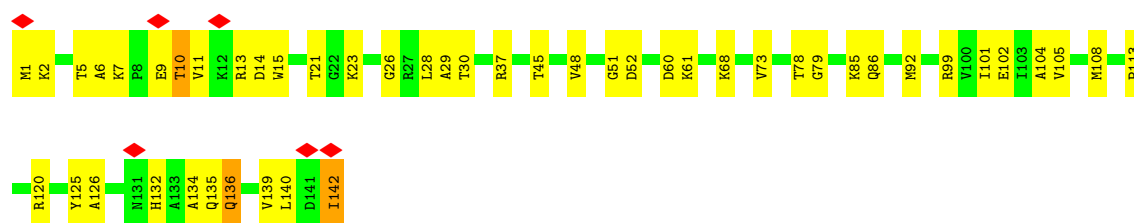
• Molecule 25: 50S ribosomal protein L3



• Molecule 26: 50S ribosomal protein L4

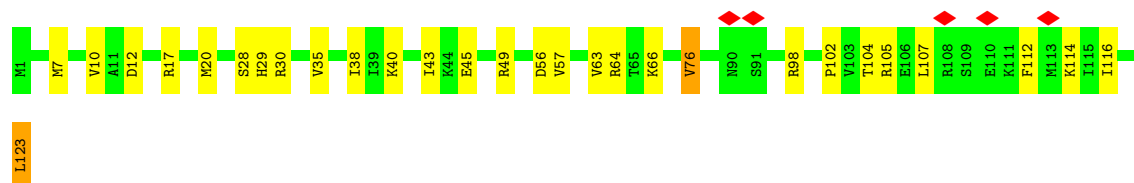


Chain i: 



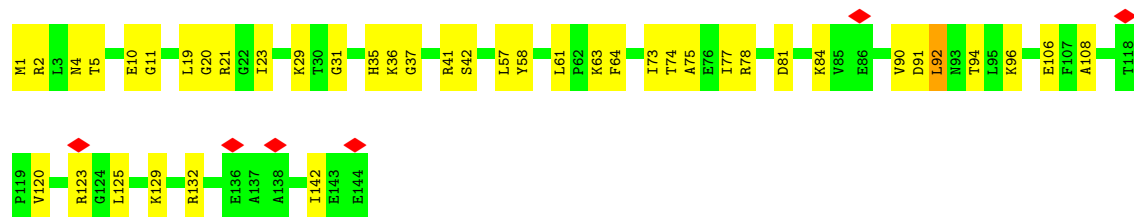
- Molecule 31: 50S ribosomal protein L14

Chain j: 



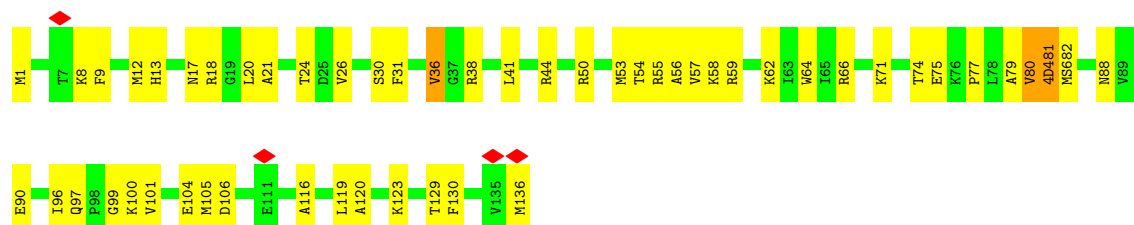
- Molecule 32: 50S ribosomal protein L15

Chain k: 



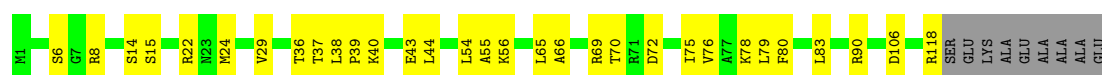
- Molecule 33: 50S ribosomal protein L16

Chain l: 

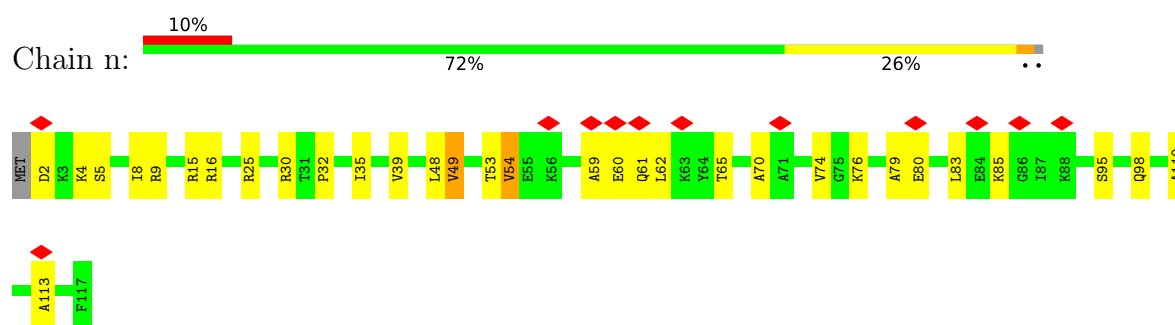


- Molecule 34: 50S ribosomal protein L17

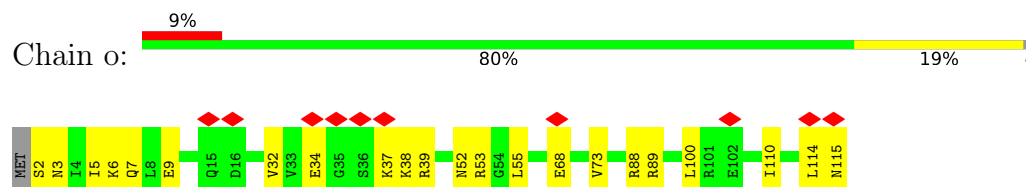
Chain m: 



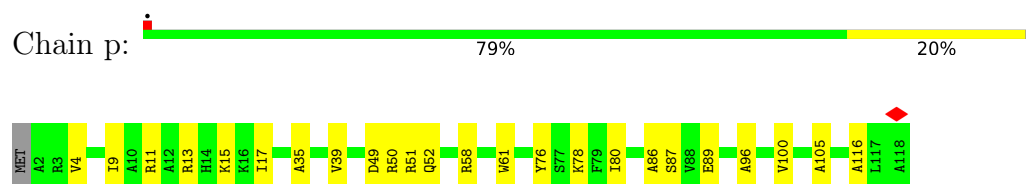
- Molecule 35: 50S ribosomal protein L18



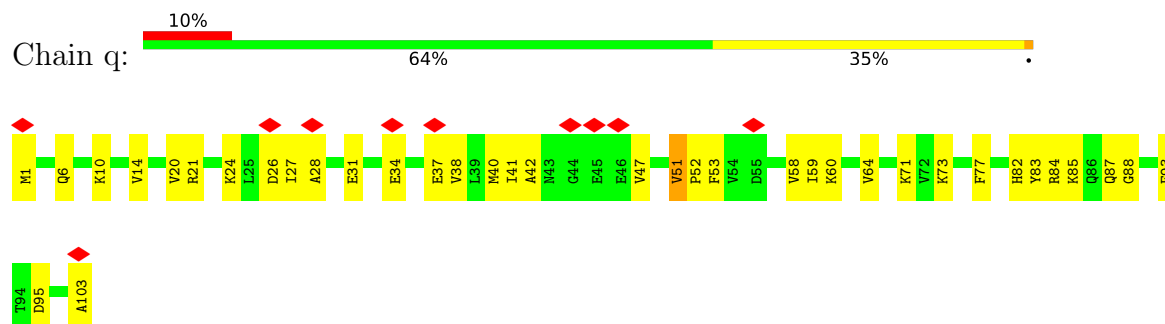
- Molecule 36: 50S ribosomal protein L19



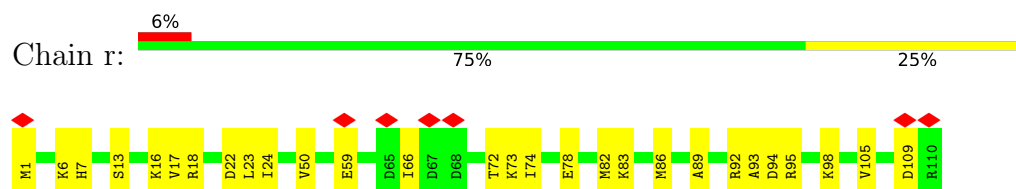
- Molecule 37: 50S ribosomal protein L20



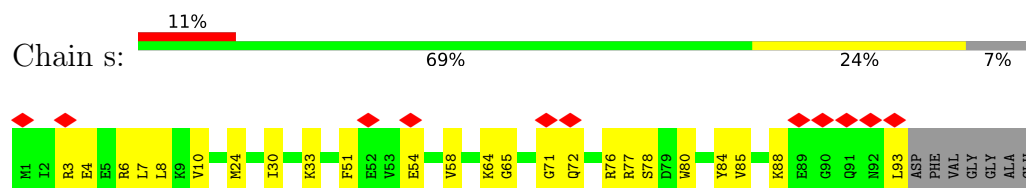
- Molecule 38: 50S ribosomal protein L21



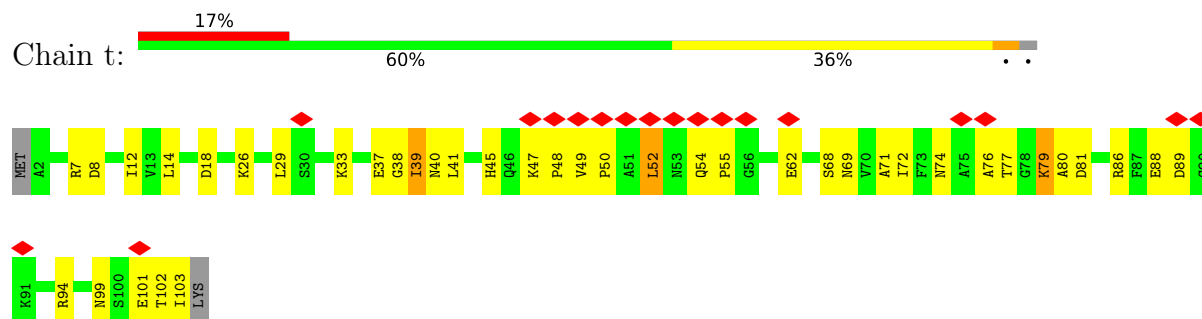
- Molecule 39: 50S ribosomal protein L22



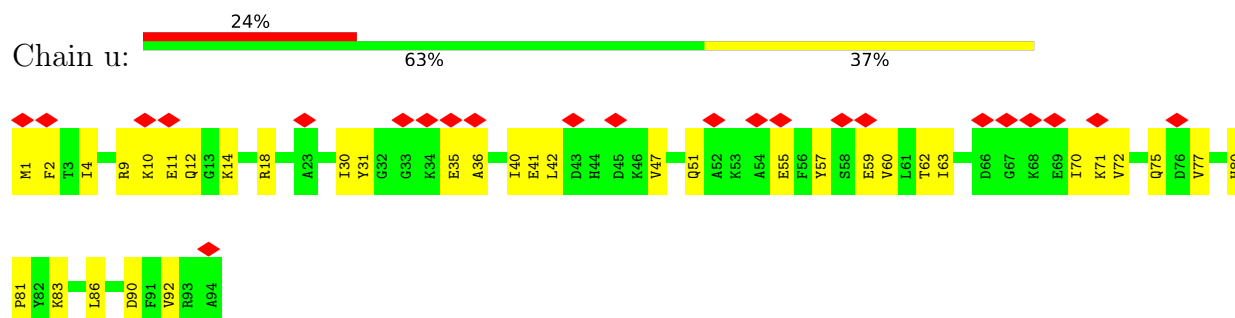
- Molecule 40: 50S ribosomal protein L23



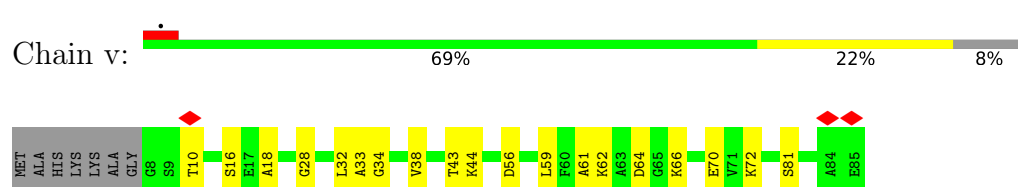
- Molecule 41: 50S ribosomal protein L24



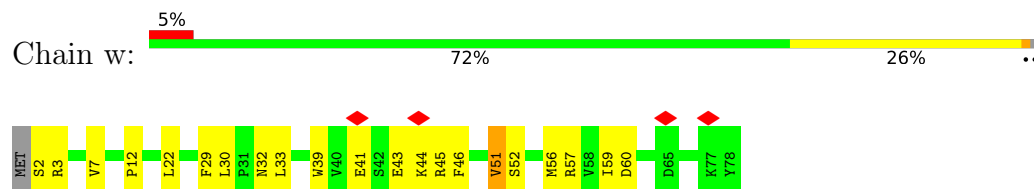
- Molecule 42: 50S ribosomal protein L25



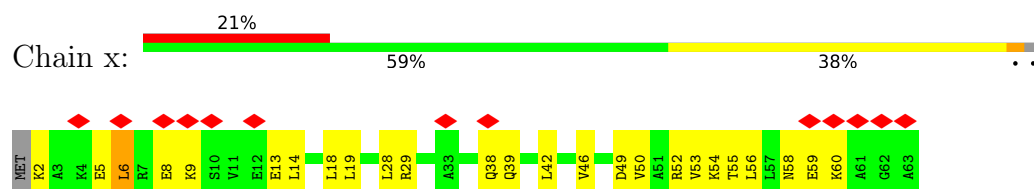
- Molecule 43: 50S ribosomal protein L27



- Molecule 44: 50S ribosomal protein L28

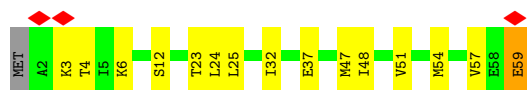


- Molecule 45: 50S ribosomal protein L29

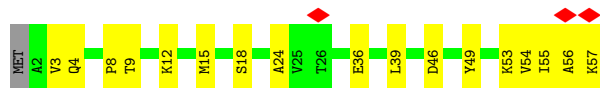


- Molecule 46: 50S ribosomal protein L30

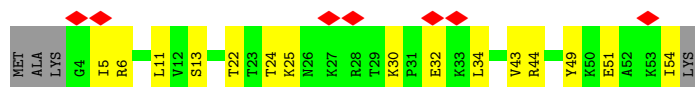




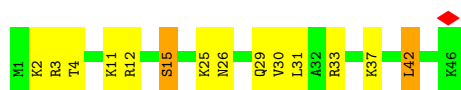
- Molecule 47: 50S ribosomal protein L32



- Molecule 48: 50S ribosomal protein L33



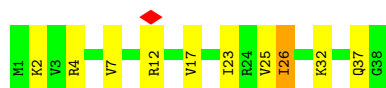
- Molecule 49: 50S ribosomal protein L34



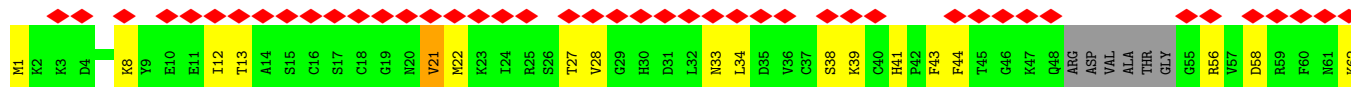
- Molecule 50: 50S ribosomal protein L35

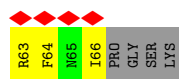


- Molecule 51: 50S ribosomal protein L36

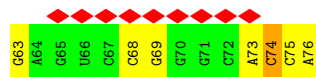
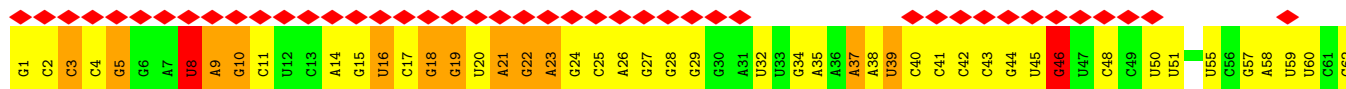


- Molecule 52: 50S ribosomal protein L31

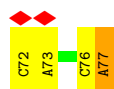




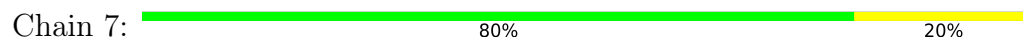
• Molecule 53: A-site tRNA-Phe



• Molecule 54: P-site tRNAf-Met



• Molecule 55: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	125897	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	60000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.239	Depositor
Minimum map value	-0.129	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	403.456, 403.456, 403.456	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.788, 0.788, 0.788	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 2MA, 4OC, 3TD, IAS, D2T, UR3, OMG, PSU, MS6, 4SU, H2U, 84G, OMC, MA6, ZN, 1MG, MEQ, 2MG, 5MU, 5MC, OMU, G7M, 4D4, SPD, 6MZ, SPM, MG, MIA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.27	0/36236	0.28	0/56520
2	B	0.17	0/1784	0.30	0/2403
3	C	0.20	0/1651	0.26	0/2225
4	D	0.16	0/1665	0.25	0/2227
5	E	0.24	0/1165	0.28	0/1568
6	F	0.19	0/858	0.28	0/1160
7	G	0.16	0/1219	0.25	0/1635
8	H	0.22	0/989	0.28	0/1326
9	I	0.19	0/1034	0.28	0/1375
10	J	0.19	0/796	0.30	0/1077
11	K	0.15	0/884	0.29	0/1191
12	L	0.17	0/960	0.36	0/1286
13	M	0.18	0/900	0.24	0/1204
14	N	0.21	0/817	0.25	0/1088
15	O	0.20	0/722	0.26	0/964
16	P	0.18	0/653	0.31	0/877
17	Q	0.21	0/650	0.28	0/871
18	R	0.21	0/553	0.30	0/742
19	S	0.18	0/685	0.25	0/922
20	T	0.20	0/676	0.30	0/895
21	U	0.18	0/597	0.24	0/792
22	a	0.36	0/65651	0.32	0/102413
23	b	0.27	0/2850	0.26	0/4444
24	c	0.29	0/2121	0.33	0/2852
25	d	0.29	0/1576	0.32	0/2119
26	e	0.26	0/1571	0.29	0/2113
27	f	0.18	0/1434	0.28	0/1926
28	g	0.18	0/1343	0.31	0/1816
29	h	1.47	2/306 (0.7%)	1.03	4/413 (1.0%)
30	i	0.61	2/1152 (0.2%)	0.30	0/1551
31	j	0.27	0/955	0.29	0/1279

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	k	0.28	0/1062	0.29	0/1413
33	l	0.27	0/1073	0.31	0/1433
34	m	0.31	0/958	0.35	0/1281
35	n	0.22	0/902	0.28	0/1209
36	o	0.28	0/929	0.30	0/1242
37	p	0.31	0/960	0.30	0/1278
38	q	0.28	0/829	0.35	0/1107
39	r	0.29	0/864	0.33	0/1156
40	s	0.25	0/744	0.31	0/994
41	t	0.24	0/787	0.30	0/1051
42	u	0.24	0/766	0.29	0/1025
43	v	0.28	0/593	0.29	0/785
44	w	0.28	0/635	0.31	0/848
45	x	0.22	0/502	0.24	0/667
46	y	0.25	0/453	0.27	0/605
47	z	0.29	0/450	0.30	0/599
48	0	0.25	0/424	0.30	0/565
49	1	0.32	0/380	0.31	0/498
50	2	0.27	0/513	0.30	0/676
51	3	0.28	0/303	0.28	0/397
52	4	0.14	0/488	0.24	0/649
53	5	0.24	0/1651	0.24	0/2569
54	6	0.21	0/1725	0.26	0/2687
55	7	0.25	0/233	0.30	0/361
All	All	0.31	4/152677 (0.0%)	0.30	4/228369 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
33	l	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	h	38	PRO	N-CD	22.89	1.79	1.47
30	i	136	GLN	C-O	17.56	1.32	1.23
29	h	37	VAL	C-N	9.71	1.46	1.33
30	i	136	GLN	CA-C	-5.67	1.50	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	h	37	VAL	CA-C-N	-9.80	109.67	119.76
29	h	37	VAL	C-N-CA	-9.80	109.67	119.76
29	h	38	PRO	N-CD-CG	-9.04	89.64	103.20
29	h	38	PRO	N-CA-CB	-7.59	96.55	103.31

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	l	81	4D4	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32612	0	16431	736	0
2	B	1753	0	1780	107	0
3	C	1624	0	1696	77	0
4	D	1643	0	1707	99	0
5	E	1152	0	1196	40	0
6	F	839	0	833	40	0
7	G	1203	0	1254	70	0
8	H	979	0	1031	35	0
9	I	1022	0	1070	51	0
10	J	786	0	828	59	0
11	K	877	0	884	21	0
12	L	957	0	1017	34	0
13	M	891	0	952	40	0
14	N	805	0	844	30	0
15	O	714	0	734	26	0
16	P	643	0	661	37	0
17	Q	641	0	682	28	0
18	R	544	0	565	36	0
19	S	668	0	693	39	0
20	T	670	0	719	39	0
21	U	589	0	627	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	a	59130	0	29767	911	0
23	b	2549	0	1291	36	0
24	c	2082	0	2154	48	0
25	d	1566	0	1618	45	0
26	e	1552	0	1619	50	0
27	f	1410	0	1444	73	0
28	g	1323	0	1371	58	0
29	h	303	0	327	13	0
30	i	1129	0	1162	36	0
31	j	946	0	1023	27	0
32	k	1053	0	1129	41	0
33	l	1075	0	1145	42	0
34	m	945	0	989	19	0
35	n	892	0	923	27	0
36	o	917	0	962	17	0
37	p	947	0	1019	23	0
38	q	816	0	839	30	0
39	r	857	0	922	26	0
40	s	738	0	807	21	0
41	t	779	0	831	35	0
42	u	753	0	780	27	0
43	v	586	0	596	14	0
44	w	625	0	652	16	0
45	x	501	0	531	22	0
46	y	449	0	488	14	0
47	z	444	0	458	18	0
48	0	417	0	451	11	0
49	1	377	0	418	13	0
50	2	504	0	572	18	0
51	3	302	0	340	8	0
52	4	480	0	482	19	0
53	5	1632	0	837	59	0
54	6	1645	0	842	52	0
55	7	209	0	109	1	0
56	4	2	0	0	0	0
56	6	1	0	0	0	0
56	7	1	0	0	0	0
56	A	188	0	0	0	0
56	C	3	0	0	0	0
56	E	2	0	0	0	0
56	G	1	0	0	0	0
56	K	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	M	9	0	0	0	0
56	S	2	0	0	0	0
56	a	233	0	0	0	0
56	b	11	0	0	0	0
56	c	1	0	0	0	0
56	d	2	0	0	0	0
56	l	1	0	0	0	0
56	z	2	0	0	0	0
57	A	20	0	34	5	0
57	a	140	0	266	31	0
58	A	114	132	0	5	0
58	a	266	308	0	5	0
59	a	14	0	26	5	0
60	3	1	0	0	0	0
All	All	142560	440	95428	3255	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

All (3255) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:h:38:PRO:CD	29:h:38:PRO:N	1.79	1.30
10:J:37:ARG:HB2	10:J:75:ASP:HB2	1.28	1.15
1:A:416:G:H2'	1:A:417:G:H5''	1.34	1.07
2:B:48:PRO:O	2:B:52:GLU:OE1	1.76	1.04
1:A:5:U:H4'	1:A:6:G:H5'	1.41	1.03
2:B:129:LEU:HD23	2:B:133:GLU:HB3	1.41	1.02
53:5:9:A:H5'	53:5:46:G7M:H1'	1.37	1.02
13:M:9:ILE:HD11	13:M:45:ILE:HG21	1.41	1.01
2:B:12:ALA:HA	2:B:208:ARG:HD2	1.42	1.00
28:g:9:VAL:HG12	28:g:50:LEU:HB2	1.43	1.00
22:a:534:U:O2'	37:p:49:ASP:OD2	1.80	1.00
1:A:1286:U:H2'	1:A:1287:A:H5'	1.43	0.98
26:e:168:ASP:OD2	26:e:170:ARG:NH1	1.97	0.97
33:l:136:MET:HE2	42:u:57:TYR:HD1	1.28	0.97
28:g:105:LEU:HB2	28:g:113:VAL:HG23	1.47	0.97
33:l:136:MET:HE2	42:u:57:TYR:CD1	1.99	0.97
3:C:77:ILE:HA	3:C:84:VAL:HG23	1.44	0.96
2:B:47:VAL:HG23	2:B:48:PRO:HD3	1.47	0.96
16:P:4:ILE:HG12	16:P:21:VAL:HG22	1.48	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:72:THR:OG1	2:B:169:GLU:OE2	1.82	0.94
33:l:53:MET:HG3	33:l:120:ALA:HB2	1.46	0.94
34:m:24:MET:HE1	34:m:40:LYS:HD2	1.51	0.92
10:J:66:GLU:HB2	14:N:99:ALA:HB2	1.53	0.91
1:A:1312:G:OP2	52:4:63:ARG:NH2	2.02	0.91
3:C:35:SER:OG	3:C:59:ARG:NH2	2.03	0.91
10:J:10:LEU:HD13	10:J:22:THR:HG22	1.52	0.91
1:A:1314:C:OP2	19:S:4:SER:OG	1.87	0.91
1:A:346:G:OP1	36:o:39:ARG:NH2	2.04	0.91
7:G:113:ASP:HB2	7:G:119:ARG:HG2	1.53	0.91
39:r:59:GLU:HG3	39:r:66:ILE:HD11	1.52	0.90
9:I:12:ARG:HG3	9:I:13:LYS:H	1.37	0.90
44:w:41:GLU:OE1	44:w:44:LYS:NZ	2.06	0.89
18:R:9:LYS:HA	18:R:46:GLY:HA3	1.54	0.89
3:C:88:ARG:HA	3:C:101:ILE:HD12	1.52	0.89
39:r:59:GLU:CG	39:r:66:ILE:HD11	2.03	0.89
11:K:111:THR:HG23	21:U:3:VAL:HG22	1.51	0.89
19:S:36:ARG:NH2	19:S:75:ALA:O	2.05	0.89
5:E:115:LEU:HD13	5:E:123:VAL:HG11	1.53	0.88
1:A:416:G:C2'	1:A:417:G:H5''	2.02	0.88
22:a:1044:C:O2'	22:a:1111:A:N1	2.07	0.88
6:F:88:MET:HG2	6:F:90:MET:HE2	1.56	0.88
33:l:75:GLU:HB2	33:l:90:GLU:HG3	1.56	0.88
1:A:339:C:OP2	31:j:98:ARG:NH1	2.08	0.87
22:a:1997:C:OP2	25:d:129:THR:OG1	1.92	0.87
22:a:2830:C:H5''	25:d:56:LYS:HE3	1.54	0.87
54:6:33:OMC:HM22	54:6:34:U:H5'	1.56	0.87
22:a:1:G:N1	22:a:2902:C:O2	2.06	0.87
35:n:39:VAL:HB	35:n:49:VAL:HG22	1.56	0.87
1:A:459:A:H2'	1:A:460:A:H8	1.39	0.87
21:U:62:ARG:NE	21:U:63:GLU:OE2	2.08	0.87
54:6:19:G:O6	54:6:56:PSU:H1'	1.75	0.86
22:a:212:G:O6	58:a:6251:84G:N5	2.09	0.86
15:O:77:ARG:HA	15:O:80:GLN:OE1	1.73	0.86
40:s:54:GLU:HB3	40:s:88:LYS:HD2	1.56	0.86
20:T:44:LYS:HD2	20:T:87:ALA:HA	1.57	0.86
21:U:29:LEU:O	21:U:33:ARG:HG2	1.76	0.85
1:A:259:G:OP1	20:T:36:TYR:OH	1.91	0.85
1:A:1330:U:C2'	1:A:1331:G:H5'	2.06	0.85
22:a:544:C:N4	22:a:549:G:O6	2.09	0.85
22:a:973:A:H5'	22:a:1188:U:H1'	1.58	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1123:U:O2'	1:A:1124:G:H5'	1.76	0.85
21:U:31:GLU:OE2	21:U:34:ARG:NH2	2.08	0.85
18:R:26:ILE:O	18:R:30:LYS:HG3	1.76	0.85
10:J:21:ALA:HB1	10:J:92:LEU:HD13	1.57	0.84
53:5:22:G:O6	53:5:46:G7M:N2	2.09	0.84
22:a:1528:A:OP2	22:a:1543:G:N2	2.10	0.84
40:s:24:MET:HE2	40:s:30:ILE:HG22	1.58	0.84
8:H:41:LYS:NZ	8:H:48:ASP:OD1	2.11	0.84
22:a:544:C:N3	22:a:549:G:N1	2.25	0.84
22:a:2680:U:O2'	22:a:2681:C:H5'	1.77	0.84
2:B:5:SER:OG	2:B:8:ASP:OD1	1.94	0.84
7:G:111:ARG:NH2	7:G:126:ASP:OD2	2.11	0.84
22:a:1115:G:O2'	22:a:1116:G:O5'	1.95	0.84
22:a:1528:A:N6	22:a:1543:G:O2'	2.11	0.84
27:f:158:THR:HG22	27:f:160:ALA:H	1.42	0.83
5:E:151:GLU:OE1	5:E:151:GLU:N	2.11	0.83
1:A:459:A:H2'	1:A:460:A:C8	2.12	0.83
22:a:1235:G:OP1	57:a:6194:SPD:N1	2.12	0.83
45:x:6:LEU:HB3	45:x:56:LEU:HD13	1.57	0.83
20:T:69:LYS:HD3	20:T:69:LYS:H	1.43	0.83
21:U:60:LEU:O	21:U:64:ASN:ND2	2.12	0.83
1:A:215:C:H2'	1:A:216:U:C6	2.13	0.83
22:a:1649:G:O2'	34:m:106:ASP:OD2	1.97	0.83
38:q:6:GLN:HG2	38:q:10:LYS:O	1.79	0.83
22:a:279:A:H2'	22:a:280:U:O4'	1.78	0.83
26:e:21:ARG:HD3	26:e:106:LYS:HB3	1.61	0.83
4:D:8:LYS:HG3	4:D:21:LEU:HD23	1.59	0.83
20:T:9:LYS:O	20:T:13:GLN:HG3	1.79	0.83
2:B:115:LYS:O	2:B:119:THR:HG23	1.79	0.82
53:5:44:G:O2'	53:5:45:U:O2	1.97	0.82
31:j:105:ARG:NH1	36:o:34:GLU:OE2	2.11	0.82
1:A:1191:A:OP1	3:C:4:LYS:NZ	2.13	0.82
20:T:69:LYS:HD3	20:T:69:LYS:N	1.94	0.82
33:l:20:LEU:HD13	42:u:81:PRO:HG2	1.61	0.82
1:A:1266:G:N2	1:A:1269:A:OP2	2.11	0.82
22:a:1125:G:OP2	22:a:1126:A:O2'	1.97	0.82
25:d:184:ARG:NH2	36:o:7:GLN:OE1	2.13	0.82
19:S:12:ASP:OD2	19:S:35:SER:OG	1.97	0.81
36:o:3:ASN:OD1	36:o:6:LYS:NZ	2.14	0.81
36:o:88:ARG:NH2	36:o:110:ILE:O	2.14	0.81
5:E:162:GLU:OE1	5:E:162:GLU:N	2.13	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:2469:A:H4'	33:l:55:ARG:HD2	1.62	0.81
24:c:29:PRO:HG2	24:c:34:LEU:HD11	1.61	0.81
1:A:1009:U:O2	1:A:1020:G:N2	2.11	0.80
22:a:2323:G:O2'	22:a:2324:U:H5'	1.81	0.80
1:A:1042:A:O2'	1:A:1043:G:H5'	1.81	0.80
28:g:76:VAL:O	28:g:80:THR:HG23	1.81	0.80
13:M:16:VAL:O	13:M:20:THR:HG23	1.80	0.80
22:a:1800:C:OP2	24:c:182:ARG:NH2	2.15	0.80
24:c:260:ASN:ND2	24:c:263:THR:OG1	2.14	0.80
19:S:30:PRO:HB3	19:S:48:THR:HG22	1.61	0.80
22:a:2469:A:N6	22:a:2481:G:O2'	2.15	0.80
28:g:24:ILE:HG13	28:g:37:LEU:HD21	1.62	0.80
30:i:125:TYR:OH	30:i:132:HIS:NE2	2.12	0.80
23:b:30:C:H2'	23:b:31:C:H5'	1.63	0.80
41:t:50:PRO:HA	41:t:54:GLN:HB2	1.63	0.80
1:A:437:U:O2'	1:A:438:U:H5'	1.81	0.79
3:C:40:ARG:O	3:C:44:THR:HG23	1.81	0.79
22:a:2052:A:H4'	25:d:148:GLN:O	1.80	0.79
42:u:51:GLN:OE1	42:u:57:TYR:OH	1.98	0.79
4:D:95:GLU:OE2	4:D:104:ARG:NH2	2.13	0.79
1:A:477:C:H2'	1:A:478:A:C8	2.18	0.79
32:k:77:ILE:HD11	32:k:108:ALA:HB1	1.64	0.79
7:G:71:PRO:O	7:G:96:ARG:HD2	1.83	0.79
22:a:390:U:OP1	58:a:6250:84G:N2	2.15	0.79
32:k:77:ILE:CD1	32:k:108:ALA:HB1	2.13	0.79
4:D:69:GLU:OE2	4:D:204:TYR:OH	2.01	0.79
22:a:644:A:H2'	22:a:645:C:O4'	1.83	0.79
35:n:15:ARG:NH2	35:n:95:SER:OG	2.15	0.79
39:r:18:ARG:O	39:r:22:ASP:OD1	2.00	0.79
1:A:2:A:H1'	1:A:613:C:O2'	1.83	0.79
28:g:105:LEU:HB2	28:g:113:VAL:CG2	2.13	0.79
1:A:1314:C:OP1	19:S:6:LYS:NZ	2.17	0.78
33:l:30:SER:OG	33:l:106:ASP:OD1	2.00	0.78
1:A:946:A:H2'	1:A:947:G:C8	2.17	0.78
7:G:26:PHE:HD1	7:G:101:MET:HG2	1.48	0.78
14:N:6:MET:HE2	14:N:63:ARG:NH2	1.97	0.78
22:a:568:U:H1'	22:a:2030:6MZ:H9C1	1.65	0.78
19:S:10:PHE:O	19:S:39:THR:HG22	1.83	0.78
17:Q:25:ILE:HB	17:Q:42:THR:HG23	1.65	0.78
20:T:78:ASN:O	20:T:82:GLN:HG2	1.83	0.78
22:a:1434:A:H2'	22:a:1435:G:C8	2.18	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:2619:C:OP1	25:d:157:LYS:HE3	1.83	0.78
39:r:83:LYS:HG3	39:r:95:ARG:HD3	1.64	0.78
9:I:88:MET:HG3	9:I:98:LEU:HD12	1.65	0.78
22:a:1032:A:H1'	51:3:23:ILE:HD13	1.66	0.78
28:g:52:PHE:HE2	28:g:72:LEU:HD12	1.49	0.78
28:g:124:GLU:OE1	28:g:134:LYS:NZ	2.16	0.78
1:A:73:C:O2'	1:A:74:A:H5'	1.82	0.78
22:a:728:G:OP2	57:a:6198:SPD:H21	1.83	0.78
31:j:17:ARG:HB2	31:j:45:GLU:HG3	1.66	0.78
22:a:219:A:N3	22:a:234:U:O2'	2.17	0.77
22:a:1802:A:H2'	22:a:1803:A:C8	2.20	0.77
9:I:65:ILE:HG21	9:I:79:ILE:HG12	1.66	0.77
22:a:2478:A:H5'	51:3:32:LYS:HE2	1.65	0.77
36:o:89:ARG:NH1	36:o:115:ASN:O	2.16	0.77
1:A:169:C:O2'	1:A:170:U:H5'	1.85	0.77
1:A:1026:G:O2'	1:A:1027:C:OP1	2.02	0.77
16:P:18:GLN:OE1	16:P:35:ARG:NH2	2.16	0.77
22:a:1846:G:O2'	22:a:1847:A:H5'	1.85	0.77
14:N:30:ILE:O	14:N:33:ASP:HB2	1.85	0.77
12:L:56:ARG:HG3	12:L:62:GLU:HG2	1.66	0.76
27:f:22:TYR:OH	27:f:165:GLU:OE1	2.03	0.76
1:A:544:G:OP1	4:D:59:GLN:NE2	2.17	0.76
5:E:85:VAL:HG23	5:E:96:MET:HE3	1.67	0.76
24:c:165:VAL:HG21	24:c:181:MET:HE1	1.67	0.76
45:x:42:LEU:O	45:x:46:VAL:HG23	1.85	0.76
1:A:1457:G:OP1	20:T:34:LYS:NZ	2.16	0.76
3:C:58:GLU:OE1	3:C:65:ARG:NH1	2.18	0.76
22:a:856:G:H2'	22:a:857:G:C8	2.21	0.76
22:a:1434:A:H2'	22:a:1435:G:H8	1.51	0.76
1:A:131:A:H2'	1:A:132:C:C6	2.20	0.76
1:A:1280:A:OP1	10:J:9:ARG:NH2	2.19	0.76
1:A:171:A:H2'	1:A:172:A:C8	2.20	0.76
4:D:140:ASN:N	4:D:182:PHE:O	2.18	0.76
27:f:44:ILE:HD12	27:f:45:ALA:N	2.01	0.76
3:C:56:VAL:HB	3:C:67:THR:HG23	1.67	0.76
8:H:11:LEU:HD22	8:H:75:ILE:HD11	1.69	0.75
31:j:102:PRO:HD2	36:o:68:GLU:HG3	1.67	0.75
1:A:1043:G:O2'	1:A:1044:A:O5'	2.04	0.75
6:F:11:HIS:CD2	6:F:12:PRO:HD2	2.20	0.75
32:k:57:LEU:HD22	50:2:54:ASP:HB3	1.68	0.75
6:F:38:ARG:HB3	6:F:63:ASN:HB2	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:76:ALA:O	15:O:80:GLN:HG3	1.86	0.75
1:A:157:U:O2'	1:A:158:G:H5'	1.87	0.75
20:T:29:ARG:O	20:T:33:LYS:HG3	1.87	0.75
1:A:976:G:OP2	1:A:1358:U:O2'	2.04	0.75
2:B:47:VAL:HG23	2:B:48:PRO:CD	2.17	0.75
2:B:207:ILE:O	2:B:211:THR:HG22	1.86	0.75
22:a:1315:C:O2'	22:a:1392:A:N3	2.20	0.75
3:C:134:MET:HE2	3:C:168:TYR:CD2	2.21	0.75
1:A:673:A:H2'	1:A:674:G:C8	2.21	0.74
9:I:84:THR:HG23	9:I:98:LEU:HD13	1.69	0.74
22:a:696:G:O6	59:a:6204:SPM:H81	1.87	0.74
22:a:517:C:O2'	39:r:78:GLU:OE2	2.04	0.74
25:d:110:THR:HG23	25:d:202:ILE:HB	1.69	0.74
45:x:49:ASP:OD1	45:x:52:ARG:NH1	2.20	0.74
2:B:26:LYS:NZ	2:B:192:ASP:OD1	2.14	0.74
3:C:121:THR:HG23	3:C:189:ALA:HB2	1.69	0.74
53:5:75:C:H2'	53:5:76:A:C8	2.22	0.74
1:A:35:G:N2	12:L:115:SER:OG	2.20	0.74
2:B:73:LYS:NZ	2:B:165:ASP:OD2	2.17	0.74
17:Q:20:SER:OG	17:Q:71:LYS:NZ	2.16	0.74
22:a:1167:C:C2'	22:a:1168:G:H5'	2.17	0.74
32:k:108:ALA:HB3	32:k:125:LEU:HD22	1.68	0.74
33:l:62:LYS:HD3	33:l:64:TRP:CZ2	2.23	0.74
34:m:8:ARG:HD2	34:m:43:GLU:HG2	1.69	0.74
22:a:1720:U:H2'	22:a:1721:G:O4'	1.86	0.74
1:A:1062:U:H2'	1:A:1063:C:C6	2.23	0.73
22:a:784:G:H5'	22:a:785:G:OP1	1.88	0.73
22:a:1496:A:H2'	22:a:1498:C:C5	2.24	0.73
23:b:1:U:H2'	23:b:2:G:H8	1.53	0.73
1:A:148:G:O2'	1:A:1446:A:N3	2.21	0.73
4:D:150:LYS:NZ	4:D:177:LYS:O	2.20	0.73
5:E:164:ILE:O	8:H:114:ARG:NH2	2.20	0.73
22:a:849:A:H2'	22:a:850:U:C6	2.24	0.73
1:A:539:A:H2'	1:A:540:G:C8	2.23	0.73
22:a:538:A:H5''	30:i:7:LYS:HE3	1.71	0.73
28:g:52:PHE:CE2	28:g:72:LEU:HD12	2.24	0.73
53:5:43:C:O2'	53:5:44:G:H5'	1.87	0.73
54:6:8:4SU:O2'	54:6:22:A:N1	2.20	0.73
22:a:878:A:H2'	22:a:879:G:O4'	1.87	0.73
41:t:26:LYS:NZ	41:t:37:GLU:OE1	2.14	0.73
41:t:94:ARG:HB3	41:t:103:ILE:HD12	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:696:A:H2'	1:A:697:U:H6	1.53	0.73
4:D:138:SER:O	4:D:141:ASP:HB2	1.89	0.73
12:L:50:ARG:HB2	12:L:90:LEU:HD11	1.71	0.73
22:a:659:G:H4'	26:e:95:LYS:HG2	1.69	0.73
35:n:30:ARG:HG3	35:n:35:ILE:HD12	1.70	0.73
1:A:168:G:O2'	1:A:169:C:H5'	1.89	0.72
22:a:1319:C:O2'	22:a:1320:C:H5'	1.89	0.72
22:a:2799:A:OP2	22:a:2799:A:H2'	1.89	0.72
27:f:36:LEU:HD23	27:f:154:ILE:HG23	1.71	0.72
49:l:31:LEU:HD22	49:l:42:LEU:HD13	1.72	0.72
1:A:349:A:O2'	1:A:350:G:H5'	1.88	0.72
1:A:401:C:O2'	1:A:621:A:N3	2.23	0.72
2:B:97:LEU:HD12	2:B:148:LEU:HD21	1.71	0.72
22:a:2069:G7M:N2	22:a:2442:C:O2	2.17	0.72
22:a:279:A:N6	22:a:361:G:H1'	2.04	0.72
22:a:1024:G:HO2'	22:a:1144:A:HO2'	1.35	0.72
53:5:75:C:O2'	53:5:76:A:O4'	2.07	0.72
1:A:664:G:H22	1:A:741:G:H1	1.36	0.72
4:D:109:ALA:N	4:D:113:GLU:OE2	2.18	0.72
18:R:37:GLY:O	18:R:63:ARG:NH2	2.21	0.72
22:a:2845:U:H5''	36:o:52:ASN:O	1.89	0.72
27:f:122:PHE:HB3	27:f:163:ASP:OD1	1.90	0.72
33:l:17:ASN:OD1	33:l:97:GLN:NE2	2.23	0.72
22:a:703:U:H2'	22:a:704:G:O4'	1.89	0.72
2:B:6:MET:SD	2:B:47:VAL:HG11	2.29	0.71
20:T:57:ILE:O	20:T:61:GLN:HG2	1.90	0.71
22:a:864:G:O2'	22:a:865:C:H5'	1.89	0.71
22:a:1141:U:H4'	22:a:1142:A:O4'	1.90	0.71
1:A:451:A:H61	1:A:481:G:H5'	1.55	0.71
28:g:2:SER:OG	28:g:3:ARG:N	2.18	0.71
53:5:51:U:H3	53:5:63:G:H1	1.36	0.71
2:B:12:ALA:HA	2:B:208:ARG:CD	2.18	0.71
2:B:81:LYS:HD2	2:B:85:LEU:HD11	1.72	0.71
22:a:1509:A:O2'	22:a:1510:G:OP2	2.07	0.71
22:a:2323:G:C2'	22:a:2324:U:H5'	2.20	0.71
2:B:113:ARG:NH2	2:B:140:GLU:OE1	2.23	0.71
12:L:50:ARG:CB	12:L:90:LEU:HD11	2.20	0.71
2:B:216:ALA:O	2:B:220:THR:HG22	1.90	0.71
19:S:29:LYS:HG2	19:S:30:PRO:HD2	1.72	0.71
22:a:176:A:O2'	22:a:177:G:H5'	1.90	0.71
22:a:1236:G:OP2	57:a:6194:SPD:H21	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:476:U:O2'	1:A:477:C:H5'	1.91	0.71
40:s:24:MET:CE	40:s:30:ILE:HG22	2.21	0.71
22:a:848:C:H2'	22:a:849:A:H8	1.55	0.71
57:a:6200:SPD:H52	39:r:86:MET:SD	2.31	0.71
6:F:88:MET:HE3	6:F:90:MET:CE	2.21	0.71
22:a:2780:G:OP2	30:i:120:ARG:HD3	1.89	0.71
1:A:152:A:H2'	1:A:153:C:H5'	1.72	0.70
1:A:273:U:O2'	1:A:274:A:H5'	1.90	0.70
36:o:5:ILE:O	36:o:9:GLU:HG3	1.91	0.70
1:A:81:A:N6	1:A:89:U:O2	2.24	0.70
1:A:161:A:H2'	1:A:162:A:C8	2.26	0.70
22:a:1583:A:O2'	22:a:1585:C:N4	2.24	0.70
10:J:52:LEU:HD12	10:J:62:ARG:HD3	1.71	0.70
16:P:8:ARG:HB2	16:P:17:TYR:CE1	2.27	0.70
22:a:848:C:H2'	22:a:849:A:C8	2.26	0.70
22:a:2547:A:H4'	31:j:29:HIS:CE1	2.26	0.70
1:A:1289:A:H2'	1:A:1290:G:H5'	1.74	0.70
3:C:79:LYS:O	3:C:80:LYS:HG2	1.91	0.70
4:D:88:GLU:N	4:D:88:GLU:OE1	2.25	0.70
22:a:2462:C:O2	22:a:2488:G:N2	2.15	0.70
12:L:5:ASN:O	12:L:9:ARG:HG3	1.92	0.70
16:P:67:ILE:HG23	16:P:71:VAL:HG12	1.72	0.70
27:f:38:MET:HE3	27:f:57:LEU:HD13	1.74	0.70
30:i:13:ARG:HD3	30:i:51:GLY:O	1.92	0.70
1:A:965:U:H5''	1:A:966:2MG:OP1	1.92	0.70
2:B:133:GLU:O	2:B:137:ARG:HG3	1.92	0.70
12:L:30:LYS:HB3	12:L:57:LEU:HD22	1.74	0.70
41:t:26:LYS:HG3	41:t:37:GLU:HG2	1.74	0.70
1:A:17:U:H2'	1:A:18:C:C6	2.26	0.70
1:A:461:A:H2'	1:A:462:G:H8	1.55	0.70
3:C:51:SER:HB3	3:C:71:ALA:HB3	1.74	0.70
2:B:87:CYS:SG	2:B:89:GLN:HG2	2.32	0.70
1:A:348:G:H2'	1:A:349:A:H5'	1.73	0.69
1:A:626:G:OP1	16:P:35:ARG:NH2	2.25	0.69
1:A:736:C:OP1	18:R:61:ARG:NH1	2.25	0.69
1:A:883:C:O2'	1:A:884:U:H5'	1.91	0.69
1:A:1356:G:H2'	1:A:1357:A:C8	2.27	0.69
3:C:97:VAL:HB	3:C:98:PRO:HD2	1.74	0.69
6:F:88:MET:CG	6:F:90:MET:HE2	2.22	0.69
22:a:1796:U:H2'	22:a:1797:G:C8	2.26	0.69
22:a:1883:U:O2'	22:a:1884:G:H5'	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:U:O2'	1:A:30:U:H5'	1.92	0.69
22:a:2467:C:O2	33:l:123:LYS:NZ	2.25	0.69
5:E:85:VAL:CG2	5:E:96:MET:HE3	2.21	0.69
22:a:181:A:H2'	22:a:182:A:C8	2.27	0.69
22:a:1469:A:H2'	22:a:1470:A:C8	2.26	0.69
23:b:90:C:H5'	33:l:18:ARG:HG2	1.73	0.69
7:G:14:PRO:HB2	7:G:19:GLY:HA2	1.72	0.69
22:a:1796:U:H2'	22:a:1797:G:H8	1.57	0.69
22:a:1883:U:H2'	22:a:1884:G:O4'	1.92	0.69
54:6:66:C:C2'	54:6:67:C:H5'	2.22	0.69
1:A:76:G:H1	1:A:93:U:H3	1.40	0.69
7:G:5:ARG:NH2	7:G:7:ILE:HB	2.07	0.69
1:A:1255:G:O2'	1:A:1258:G:N3	2.23	0.69
11:K:37:ARG:HH11	11:K:37:ARG:HG3	1.57	0.69
22:a:1046:A:H3'	22:a:1047:G:H5''	1.75	0.69
22:a:2591:C:H2'	22:a:2592:G:C8	2.28	0.69
1:A:1516:2MG:N2	1:A:1519:MA6:OP2	2.24	0.69
1:A:1014:A:C2	1:A:1219:A:H1'	2.27	0.69
1:A:1320:C:O2	19:S:36:ARG:NH1	2.26	0.69
2:B:56:GLU:HG3	2:B:198:PHE:CZ	2.28	0.69
3:C:47:LEU:HD21	3:C:87:LEU:HD21	1.74	0.69
12:L:25:GLU:OE2	12:L:59:ASN:ND2	2.25	0.69
54:6:47:A:H3'	54:6:48:U:H5''	1.74	0.69
3:C:79:LYS:O	3:C:82:GLU:HG3	1.94	0.69
22:a:2637:U:O2'	22:a:2638:G:H5'	1.92	0.69
29:h:17:ASP:N	29:h:17:ASP:OD1	2.24	0.69
53:5:45:U:H5'	53:5:46:G7M:OP1	1.93	0.69
1:A:325:A:N7	57:A:1668:SPD:H91	2.08	0.68
3:C:77:ILE:HA	3:C:84:VAL:CG2	2.20	0.68
21:U:39:GLU:HG3	21:U:44:GLU:HG2	1.75	0.68
24:c:111:LYS:NZ	24:c:111:LYS:HB3	2.07	0.68
30:i:21:THR:HG23	30:i:61:LYS:HD3	1.75	0.68
9:I:24:GLY:HA3	9:I:62:ASP:OD2	1.93	0.68
22:a:1039:A:H2'	22:a:1040:A:O4'	1.93	0.68
22:a:1495:A:N3	22:a:1578:U:O2'	2.26	0.68
32:k:37:GLY:O	32:k:41:ARG:HG2	1.94	0.68
10:J:6:ILE:HG12	10:J:102:LEU:HG	1.75	0.68
10:J:22:THR:O	10:J:26:VAL:HG13	1.93	0.68
10:J:32:THR:OG1	10:J:83:THR:HG22	1.92	0.68
22:a:849:A:H2'	22:a:850:U:H6	1.58	0.68
22:a:2281:A:O2'	22:a:2282:G:H5'	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:f:42:GLU:HG3	27:f:49:LEU:HD13	1.75	0.68
27:f:44:ILE:HD12	27:f:45:ALA:H	1.56	0.68
1:A:160:A:H2'	1:A:161:A:O4'	1.94	0.68
1:A:202:G:H1'	1:A:468:A:H2	1.57	0.68
9:I:91:ASP:HB3	9:I:94:LEU:HD12	1.75	0.68
22:a:2343:U:HO2'	22:a:2373:G:HO2'	1.36	0.68
43:v:70:GLU:HG3	43:v:72:LYS:HD3	1.75	0.68
22:a:2291:U:H2'	22:a:2292:U:C6	2.28	0.68
52:4:41:HIS:HB3	52:4:44:PHE:HD2	1.56	0.68
53:5:44:G:OP2	53:5:44:G:N2	2.24	0.68
10:J:5:ARG:HG2	10:J:5:ARG:HH11	1.59	0.68
22:a:1114:C:O2'	22:a:1115:G:H5'	1.94	0.68
22:a:1902:C:H4'	24:c:242:LYS:O	1.93	0.68
22:a:2637:U:C2'	22:a:2638:G:H5'	2.23	0.68
53:5:37:MIA:H132	53:5:37:MIA:H112	1.75	0.68
1:A:144:G:H2'	1:A:145:G:C8	2.28	0.68
1:A:216:U:H2'	1:A:217:C:C6	2.29	0.68
1:A:1120:C:H2'	1:A:1121:U:H6	1.58	0.68
1:A:1123:U:C2'	1:A:1124:G:H5'	2.24	0.68
8:H:73:GLU:HB3	8:H:130:ALA:OXT	1.94	0.68
22:a:2030:6MZ:C2	22:a:2499:C:H5''	2.24	0.68
22:a:2295:C:O2'	22:a:2296:U:H5'	1.94	0.68
42:u:9:ARG:HG2	42:u:41:GLU:HG2	1.76	0.68
46:y:4:THR:HG23	46:y:4:THR:O	1.94	0.68
1:A:1338:G:H2'	1:A:1339:A:C8	2.28	0.68
4:D:9:LEU:HD13	4:D:32:CYS:HB3	1.75	0.68
22:a:2281:A:C2'	22:a:2282:G:H5'	2.24	0.68
29:h:27:ARG:NH2	44:w:60:ASP:OD2	2.21	0.68
48:0:44:ARG:HG3	48:0:44:ARG:HH11	1.58	0.68
2:B:154:MET:HE3	2:B:158:PRO:HD3	1.75	0.67
10:J:35:GLN:NE2	10:J:77:VAL:O	2.27	0.67
26:e:141:MET:HE2	26:e:143:LEU:HD11	1.74	0.67
1:A:1318:A:H5''	19:S:3:ARG:NH1	2.09	0.67
1:A:1412:C:H2'	1:A:1413:A:C8	2.29	0.67
13:M:39:ILE:HD13	13:M:56:LEU:HD21	1.74	0.67
1:A:1130:A:O2'	9:I:5:GLN:NE2	2.22	0.67
3:C:153:VAL:HG12	3:C:157:LEU:HD21	1.76	0.67
53:5:41:C:O2'	53:5:42:C:H5'	1.92	0.67
22:a:1856:U:H2'	22:a:1857:G:O4'	1.93	0.67
22:a:2847:U:H2'	22:a:2848:G:O4'	1.94	0.67
29:h:15:LEU:HD23	29:h:16:GLY:N	2.09	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:A:H2'	1:A:462:G:C8	2.29	0.67
1:A:746:A:H2'	1:A:747:A:C8	2.30	0.67
6:F:9:MET:HG3	6:F:86:ARG:HB3	1.76	0.67
22:a:882:G:H2'	22:a:883:G:H1'	1.76	0.67
22:a:2299:U:OP2	27:f:71:ARG:NH2	2.28	0.67
22:a:2324:U:H3'	22:a:2325:G:C5'	2.24	0.67
22:a:2324:U:H3'	22:a:2325:G:H5''	1.77	0.67
1:A:166:U:O4	1:A:167:A:N6	2.28	0.67
5:E:77:ASN:O	5:E:80:THR:HG22	1.94	0.67
18:R:12:ARG:HB3	18:R:12:ARG:HH11	1.60	0.67
22:a:2071:A:H2'	22:a:2072:C:C6	2.29	0.67
28:g:28:GLY:HA3	28:g:79:VAL:HB	1.76	0.67
1:A:651:C:O2'	1:A:652:U:H5'	1.94	0.67
3:C:131:ARG:HD3	3:C:168:TYR:OH	1.95	0.67
11:K:109:ASN:OD1	21:U:5:LYS:HD3	1.95	0.67
22:a:2020:A:H5'	47:z:9:THR:HG21	1.76	0.67
4:D:129:VAL:HG22	4:D:146:ARG:HD3	1.75	0.67
22:a:1528:A:H2'	22:a:1529:G:O4'	1.95	0.67
1:A:746:A:O2'	1:A:747:A:O5'	2.12	0.67
1:A:1147:C:H4'	9:I:7:TYR:CE2	2.30	0.67
2:B:101:LEU:HB3	2:B:179:LEU:CD1	2.25	0.67
22:a:890:C:H5'	22:a:891:G:OP2	1.94	0.67
22:a:1738:G:HO2'	22:a:1739:A:P	2.18	0.67
25:d:106:LYS:NZ	25:d:176:ASP:OD1	2.28	0.67
1:A:348:G:C2'	1:A:349:A:H5'	2.25	0.67
23:b:106:G:H2'	23:b:107:G:O4'	1.94	0.67
44:w:43:GLU:OE1	44:w:45:ARG:NH2	2.24	0.67
1:A:202:G:H1'	1:A:468:A:C2	2.29	0.66
54:6:62:C:H2'	54:6:63:C:C6	2.30	0.66
22:a:511:U:C2'	22:a:512:G:H5'	2.25	0.66
24:c:160:THR:HG22	24:c:177:ARG:HG3	1.77	0.66
25:d:152:PRO:HG3	25:d:156:PHE:CZ	2.30	0.66
9:I:19:VAL:HG22	9:I:65:ILE:HG12	1.76	0.66
42:u:75:GLN:HB2	42:u:92:VAL:CG2	2.25	0.66
54:6:7:G:OP1	54:6:16:C:N4	2.29	0.66
4:D:23:SER:HB3	4:D:109:ALA:HB1	1.76	0.66
5:E:88:VAL:HG22	5:E:93:ARG:HG2	1.76	0.66
27:f:15:LYS:HB2	27:f:15:LYS:HZ3	1.61	0.66
1:A:5:U:H4'	1:A:6:G:C5'	2.21	0.66
1:A:629:A:H2'	1:A:630:A:O4'	1.95	0.66
22:a:359:G:O2'	22:a:360:U:H5'	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:2529:G:H5'	28:g:175:LYS:HB3	1.78	0.66
34:m:22:ARG:CG	34:m:70:THR:HA	2.25	0.66
49:1:11:LYS:O	49:1:15:SER:OG	2.13	0.66
1:A:685:G:O2'	1:A:686:U:H5'	1.96	0.66
1:A:983:A:H5'	1:A:984:C:OP2	1.95	0.66
1:A:1037:C:O2'	1:A:1038:C:H5'	1.96	0.66
1:A:1318:A:H5''	19:S:3:ARG:HH12	1.60	0.66
2:B:57:LEU:HD13	2:B:217:VAL:HG13	1.76	0.66
12:L:107:VAL:HG23	12:L:117:TYR:HB3	1.78	0.66
22:a:593:U:H2'	22:a:594:U:C6	2.30	0.66
34:m:22:ARG:HG3	34:m:70:THR:HA	1.77	0.66
1:A:946:A:H2'	1:A:947:G:H8	1.59	0.66
22:a:1000:A:H2'	22:a:1001:A:C8	2.30	0.66
22:a:1416:G:O2'	22:a:1417:C:OP2	2.12	0.66
22:a:1607:C:H5''	22:a:1608:A:H5'	1.77	0.66
22:a:368:A:C2'	22:a:369:U:H5'	2.26	0.66
22:a:1129:A:N6	22:a:2491:U:OP1	2.29	0.66
22:a:2804:U:H2'	22:a:2805:C:C6	2.31	0.66
1:A:437:U:O2'	4:D:120:HIS:ND1	2.23	0.66
2:B:219:ALA:O	2:B:223:GLU:HG2	1.96	0.66
13:M:107:ARG:NH2	13:M:111:GLY:O	2.23	0.66
1:A:1009:U:H2'	1:A:1010:U:C6	2.30	0.65
22:a:843:G:O2'	22:a:844:A:H5'	1.96	0.65
22:a:897:C:O2'	22:a:898:C:H5'	1.97	0.65
22:a:2014:A:H4'	39:r:92:ARG:HH21	1.61	0.65
22:a:2430:A:N3	22:a:2430:A:H2'	2.10	0.65
22:a:2863:C:OP2	57:a:6191:SPD:H51	1.96	0.65
42:u:70:ILE:HG22	42:u:72:VAL:HG13	1.76	0.65
1:A:412:A:O2'	1:A:413:G:H4'	1.96	0.65
6:F:39:LEU:HD12	6:F:40:GLU:N	2.11	0.65
9:I:52:LEU:HD11	9:I:63:LEU:HD11	1.79	0.65
13:M:27:LYS:HG3	13:M:31:LYS:NZ	2.12	0.65
13:M:27:LYS:HG3	13:M:31:LYS:HZ3	1.60	0.65
15:O:18:ASP:OD1	15:O:19:ALA:N	2.28	0.65
22:a:2064:C:H2'	22:a:2065:C:C6	2.31	0.65
53:5:15:G:H2'	53:5:16:U:C4	2.30	0.65
1:A:436:C:O2'	4:D:154:ARG:HD3	1.97	0.65
1:A:677:U:H3	1:A:713:G:H22	1.44	0.65
1:A:1000:A:O2'	1:A:1001:C:H5'	1.96	0.65
1:A:1130:A:HO2'	9:I:5:GLN:HE22	1.40	0.65
2:B:129:LEU:HD23	2:B:133:GLU:CB	2.24	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:6:LEU:HD22	16:P:17:TYR:HB3	1.78	0.65
22:a:1484:U:O2'	22:a:1485:U:H5'	1.97	0.65
4:D:124:MET:HG3	4:D:146:ARG:HG2	1.79	0.65
22:a:1042:G:H2'	22:a:1043:C:H6	1.61	0.65
22:a:279:A:H61	22:a:361:G:H1'	1.62	0.65
17:Q:64:CYS:SG	17:Q:74:THR:HG23	2.37	0.65
29:h:7:ASP:OD1	29:h:8:LYS:N	2.28	0.65
1:A:1008:U:C3'	1:A:1009:U:H5''	2.27	0.65
22:a:386:G:O2'	57:a:6196:SPD:H82	1.96	0.65
22:a:2529:G:H4'	28:g:175:LYS:HD3	1.79	0.65
4:D:157:ALA:O	4:D:160:GLU:HG3	1.96	0.65
22:a:2467:C:H2'	22:a:2468:A:O4'	1.97	0.65
40:s:51:PHE:CD2	40:s:93:LEU:HD21	2.30	0.65
2:B:71:GLY:O	2:B:93:ASN:HA	1.97	0.65
20:T:53:GLU:O	20:T:57:ILE:HD12	1.96	0.65
21:U:59:LYS:O	21:U:62:ARG:HG3	1.97	0.65
1:A:144:G:H2'	1:A:145:G:H8	1.62	0.64
1:A:990:C:O2'	1:A:991:U:H5'	1.97	0.64
1:A:1330:U:H2'	1:A:1331:G:H5'	1.79	0.64
4:D:55:LEU:O	4:D:59:GLN:HG2	1.97	0.64
53:5:8:4SU:O2'	53:5:9:A:OP1	2.12	0.64
1:A:131:A:H2'	1:A:132:C:H6	1.62	0.64
1:A:723:U:H2'	1:A:855:U:H4'	1.79	0.64
33:l:50:ARG:HA	33:l:53:MET:HE2	1.79	0.64
54:6:6:G:O2'	54:6:7:G:H5'	1.97	0.64
1:A:1225:A:H2'	1:A:1226:C:C5	2.33	0.64
2:B:196:VAL:CG2	2:B:199:VAL:HG22	2.26	0.64
3:C:56:VAL:HB	3:C:67:THR:CG2	2.27	0.64
6:F:72:ASP:O	6:F:76:THR:HG23	1.96	0.64
27:f:142:ASP:O	27:f:146:VAL:HG23	1.96	0.64
1:A:5:U:C4'	1:A:6:G:H5'	2.21	0.64
1:A:467:U:O2'	1:A:468:A:OP1	2.06	0.64
2:B:68:LEU:HD11	2:B:92:VAL:HG23	1.78	0.64
22:a:2760:C:O2'	22:a:2761:A:H5'	1.98	0.64
36:o:100:LEU:HD11	36:o:110:ILE:HD11	1.80	0.64
2:B:89:GLN:OE1	2:B:89:GLN:HA	1.97	0.64
45:x:55:THR:O	45:x:59:GLU:HG3	1.97	0.64
1:A:1158:C:C5	1:A:1160:G:H1'	2.33	0.64
54:6:66:C:H2'	54:6:67:C:H5'	1.80	0.64
1:A:1032:G:H2'	1:A:1033:G:H4'	1.78	0.64
19:S:45:ILE:HD13	19:S:64:ASP:HB3	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:882:G:H2'	22:a:883:G:C1'	2.28	0.64
22:a:1028:A:H2'	22:a:1029:A:C8	2.32	0.64
28:g:4:VAL:O	28:g:69:ARG:HD2	1.97	0.64
35:n:76:LYS:HE3	35:n:80:GLU:OE2	1.97	0.64
3:C:138:VAL:CG1	3:C:170:GLU:HG3	2.27	0.64
8:H:54:ASP:OD1	8:H:55:THR:N	2.30	0.64
22:a:645:C:H2'	22:a:647:G:N7	2.13	0.64
22:a:995:C:N4	30:i:2:LYS:HD3	2.12	0.64
22:a:1474:U:O2'	22:a:1475:G:H5'	1.97	0.64
24:c:21:ASN:HB3	24:c:24:LEU:HG	1.79	0.64
1:A:696:A:H2'	1:A:697:U:C6	2.33	0.64
7:G:22:LEU:HD21	7:G:101:MET:CE	2.28	0.64
22:a:273:G:H2'	22:a:274:C:C6	2.33	0.64
22:a:1386:C:H2'	22:a:1387:A:C8	2.33	0.64
30:i:23:LYS:NZ	30:i:142:ILE:OXT	2.20	0.64
6:F:36:ILE:HD13	6:F:64:VAL:HG12	1.80	0.64
12:L:39:THR:HG22	12:L:51:LYS:HD2	1.80	0.64
22:a:1736:U:H2'	22:a:1737:G:O4'	1.98	0.64
1:A:67:C:H2'	1:A:68:G:C8	2.34	0.63
1:A:1120:C:H2'	1:A:1121:U:C6	2.32	0.63
7:G:129:GLU:OE2	7:G:131:LYS:HB2	1.98	0.63
22:a:1203:U:O2'	32:k:4:ASN:ND2	2.31	0.63
22:a:2788:C:H2'	22:a:2789:C:C6	2.33	0.63
23:b:1:U:H2'	23:b:2:G:C8	2.33	0.63
24:c:125:LYS:HG2	24:c:128:ASN:HD22	1.64	0.63
4:D:105:MET:HG2	4:D:173:VAL:CG2	2.28	0.63
9:I:116:VAL:HG11	10:J:62:ARG:HG3	1.78	0.63
22:a:96:C:OP1	45:x:39:GLN:NE2	2.31	0.63
22:a:639:U:H2'	22:a:640:C:C6	2.33	0.63
22:a:2850:A:N7	22:a:2868:A:O2'	2.30	0.63
43:v:38:VAL:HG12	43:v:59:LEU:HB2	1.79	0.63
1:A:266:G:H3'	17:Q:69:LYS:HB2	1.81	0.63
1:A:1106:G:H5''	3:C:172:ARG:HG2	1.80	0.63
14:N:33:ASP:CG	14:N:36:ALA:HB2	2.23	0.63
22:a:993:G:OP2	37:p:51:ARG:NH2	2.31	0.63
27:f:57:LEU:HG	27:f:89:VAL:CG2	2.29	0.63
28:g:124:GLU:HB2	28:g:134:LYS:NZ	2.12	0.63
33:l:26:VAL:HA	33:l:104:GLU:OE2	1.98	0.63
1:A:35:G:N3	12:L:115:SER:OG	2.31	0.63
22:a:543:G:H2'	22:a:544:C:O4'	1.97	0.63
1:A:88:U:H3'	1:A:89:U:H6	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:143:ARG:HG3	7:G:144:MET:N	2.13	0.63
22:a:2635:A:O2'	25:d:81:GLU:OE2	2.11	0.63
23:b:30:C:C2'	23:b:31:C:H5'	2.28	0.63
22:a:1407:G:O2'	22:a:1408:G:H5'	1.98	0.63
22:a:2613:U:H5'	57:a:6203:SPD:H91	1.81	0.63
27:f:101:GLU:O	27:f:105:THR:HG23	1.99	0.63
40:s:76:ARG:HG2	40:s:76:ARG:HH11	1.62	0.63
15:O:8:THR:O	15:O:12:VAL:HG23	1.99	0.63
22:a:1042:G:H2'	22:a:1043:C:C6	2.34	0.63
22:a:2494:G:O2'	33:l:79:ALA:HA	1.98	0.63
22:a:2547:A:H2'	22:a:2548:U:C6	2.34	0.63
27:f:30:ARG:HH11	27:f:30:ARG:HG3	1.62	0.63
27:f:50:LEU:HD12	27:f:50:LEU:O	1.98	0.63
41:t:50:PRO:HA	41:t:54:GLN:CB	2.27	0.63
47:z:53:LYS:HZ2	47:z:56:ALA:HA	1.64	0.63
53:5:3:C:H2'	53:5:4:C:O4'	1.98	0.63
1:A:1477:U:H2'	1:A:1478:U:C6	2.34	0.63
3:C:50:ALA:HB1	3:C:76:VAL:CG2	2.29	0.63
6:F:5:GLU:OE2	18:R:24:LYS:HE3	1.98	0.63
13:M:77:ILE:CG2	13:M:81:MET:HE3	2.29	0.63
22:a:1856:U:C2'	22:a:1857:G:H5'	2.29	0.63
22:a:1956:U:OP1	57:a:6192:SPD:H52	1.99	0.63
29:h:34:GLY:O	29:h:36:ALA:N	2.32	0.63
53:5:22:G:H2'	53:5:23:A:C8	2.33	0.63
22:a:544:C:H3'	22:a:545:U:O2	1.99	0.62
22:a:1856:U:O2'	22:a:1857:G:H5'	1.98	0.62
22:a:2580:PSU:H5'	25:d:135:GLY:O	1.97	0.62
1:A:84:U:H4'	1:A:85:U:OP2	1.98	0.62
1:A:637:C:O2'	1:A:638:U:H5'	1.99	0.62
2:B:135:LEU:HA	2:B:138:THR:HG22	1.81	0.62
22:a:687:C:H1'	49:1:4:THR:HG22	1.79	0.62
22:a:1167:C:O2'	22:a:1168:G:H5'	1.99	0.62
22:a:1474:U:H2'	22:a:1475:G:O4'	1.99	0.62
22:a:1543:G:H5''	22:a:1544:A:OP1	1.99	0.62
1:A:1020:G:O2'	1:A:1021:A:H5'	2.00	0.62
4:D:88:GLU:HG3	4:D:188:ARG:CG	2.29	0.62
13:M:34:LEU:HD12	13:M:41:GLU:HG2	1.81	0.62
22:a:973:A:H5'	22:a:1188:U:C1'	2.28	0.62
53:5:43:C:C2'	53:5:44:G:H5'	2.30	0.62
1:A:1092:A:H5''	7:G:4:ARG:CZ	2.29	0.62
6:F:9:MET:CG	6:F:86:ARG:HB3	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:1022:G:O6	30:i:68:LYS:NZ	2.22	0.62
22:a:1601:G:O2'	22:a:1602:U:H5'	2.00	0.62
24:c:80:ARG:NE	24:c:82:GLU:OE2	2.28	0.62
25:d:25:THR:OG1	25:d:191:GLY:O	2.17	0.62
1:A:189:A:O2'	1:A:190:A:H5'	1.99	0.62
1:A:337:G:H2'	1:A:338:A:C8	2.35	0.62
4:D:152:GLN:HB2	4:D:155:VAL:HG23	1.82	0.62
7:G:113:ASP:HB2	7:G:119:ARG:CG	2.28	0.62
16:P:40:ASN:HB3	16:P:43:ALA:HB2	1.82	0.62
22:a:2516:A:O2'	22:a:2517:C:H5'	1.98	0.62
32:k:91:ASP:N	32:k:94:THR:OG1	2.31	0.62
1:A:199:A:H2'	1:A:200:G:C8	2.34	0.62
7:G:22:LEU:HD21	7:G:101:MET:HE2	1.80	0.62
10:J:32:THR:CB	10:J:83:THR:HG22	2.30	0.62
10:J:66:GLU:CB	14:N:99:ALA:HB2	2.25	0.62
21:U:31:GLU:O	21:U:35:ARG:HG3	2.00	0.62
22:a:1715:G:O2'	22:a:1743:G:O6	2.11	0.62
1:A:384:G:H2'	1:A:385:C:C6	2.34	0.62
1:A:701:U:OP1	1:A:702:A:O2'	2.11	0.62
1:A:1004:A:H2'	1:A:1005:A:O4'	1.98	0.62
1:A:1381:U:O2'	1:A:1382:C:H5'	1.99	0.62
9:I:106:ARG:NH1	9:I:107:ASP:O	2.31	0.62
20:T:44:LYS:CD	20:T:87:ALA:HA	2.30	0.62
42:u:75:GLN:HB2	42:u:92:VAL:HG23	1.81	0.62
53:5:43:C:H3'	53:5:44:G:N2	2.13	0.62
1:A:1008:U:H2'	1:A:1009:U:H5''	1.80	0.62
4:D:188:ARG:NH1	4:D:197:GLU:OE2	2.32	0.62
6:F:88:MET:HE3	6:F:90:MET:HE1	1.81	0.62
25:d:56:LYS:O	25:d:60:VAL:HG23	1.99	0.62
26:e:194:LYS:HE2	26:e:194:LYS:HA	1.80	0.62
1:A:138:G:O2'	1:A:139:A:H5'	2.00	0.62
25:d:46:ARG:NH1	25:d:85:ALA:O	2.31	0.62
26:e:153:LEU:HD12	26:e:153:LEU:O	2.00	0.62
29:h:18:GLN:O	29:h:18:GLN:HG2	1.99	0.62
1:A:81:A:H3'	1:A:81:A:N3	2.15	0.62
1:A:1077:G:N2	1:A:1080:A:OP2	2.27	0.62
13:M:77:ILE:HG22	13:M:81:MET:HE3	1.82	0.62
22:a:368:A:O2'	22:a:369:U:H5'	2.00	0.62
54:6:8:4SU:O5'	54:6:8:4SU:H6	2.00	0.62
1:A:269:C:H2'	1:A:270:A:C8	2.34	0.61
2:B:196:VAL:HG23	2:B:199:VAL:HG22	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:50:GLU:HG2	52:4:33:ASN:ND2	2.15	0.61
22:a:636:G:OP1	32:k:129:LYS:HE3	1.99	0.61
22:a:2307:G:H4'	22:a:2308:G:O5'	2.00	0.61
1:A:167:A:O2'	1:A:168:G:H5'	1.99	0.61
3:C:112:ASP:O	3:C:116:VAL:HG23	2.00	0.61
15:O:24:SER:OG	15:O:27:VAL:HG23	2.00	0.61
22:a:695:G:O6	59:a:6204:SPM:H122	2.00	0.61
24:c:107:PRO:HD2	24:c:110:LEU:HD22	1.82	0.61
27:f:108:VAL:HG11	27:f:176:PRO:HG3	1.82	0.61
1:A:170:U:O2'	1:A:171:A:H5'	2.00	0.61
1:A:1529:G:H5''	58:A:1792:84G:C20	2.30	0.61
4:D:35:GLU:H	4:D:35:GLU:CD	2.08	0.61
9:I:24:GLY:HA3	9:I:62:ASP:CG	2.25	0.61
10:J:21:ALA:O	10:J:24:GLU:HG3	2.00	0.61
13:M:92:ARG:HD2	22:a:888:C:C6	2.35	0.61
22:a:360:U:H2'	22:a:361:G:O4'	2.00	0.61
24:c:200:HIS:O	24:c:203:ARG:HG2	2.00	0.61
1:A:219:U:H2'	1:A:220:G:H8	1.65	0.61
1:A:412:A:O2'	1:A:414:A:H5''	2.01	0.61
1:A:1318:A:H1'	19:S:37:ARG:HH11	1.65	0.61
6:F:42:TRP:CE2	6:F:102:MET:HG3	2.34	0.61
16:P:8:ARG:HB2	16:P:17:TYR:HE1	1.64	0.61
22:a:888:C:O2'	22:a:889:C:H5'	2.01	0.61
22:a:1428:C:C5	22:a:1569:A:H5''	2.34	0.61
22:a:1537:G:H3'	22:a:1537:G:N3	2.15	0.61
22:a:1645:G:H5''	22:a:1646:C:H5'	1.82	0.61
22:a:1946:U:O4	57:a:6192:SPD:N10	2.34	0.61
26:e:147:LEU:HD11	26:e:170:ARG:HG3	1.82	0.61
27:f:36:LEU:CD2	27:f:154:ILE:HG23	2.31	0.61
28:g:75:MET:O	28:g:79:VAL:HG22	1.99	0.61
1:A:483:C:H5''	1:A:484:G:OP2	1.99	0.61
1:A:1027:C:H2'	1:A:1028:C:C6	2.35	0.61
22:a:231:A:H2'	22:a:232:G:O4'	2.00	0.61
22:a:1494:A:H2'	22:a:1495:A:C8	2.36	0.61
53:5:22:G:N7	53:5:46:G7M:N1	2.35	0.61
53:5:28:G:O2'	53:5:29:G:H5'	2.00	0.61
1:A:818:G:O2'	1:A:819:A:H5'	2.00	0.61
7:G:20:SER:O	7:G:21:GLU:HB3	2.01	0.61
22:a:898:C:H2'	22:a:899:A:O4'	2.01	0.61
22:a:1502:A:O2'	22:a:1503:A:H5'	1.99	0.61
1:A:592:G:H2'	1:A:593:U:H6	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:757:U:H2'	1:A:758:C:O4'	2.01	0.61
4:D:172:GLU:HG3	4:D:183:LYS:HD2	1.83	0.61
23:b:116:G:H4'	35:n:54:VAL:CG1	2.30	0.61
26:e:2:GLU:HG3	26:e:11:ALA:HB1	1.82	0.61
53:5:68:C:O2'	53:5:69:G:H5'	2.01	0.61
32:k:29:LYS:O	32:k:29:LYS:HG2	2.01	0.61
41:t:49:VAL:HB	41:t:52:LEU:O	2.01	0.61
2:B:81:LYS:HD2	2:B:85:LEU:CD1	2.30	0.61
5:E:88:VAL:HG13	5:E:93:ARG:HG3	1.82	0.61
5:E:111:MET:CE	5:E:125:ALA:HB1	2.31	0.61
22:a:2257:U:O2'	22:a:2258:C:H5'	2.01	0.61
1:A:1144:G:O2'	1:A:1145:A:H5'	2.00	0.61
8:H:105:SER:HB2	8:H:126:ILE:HD11	1.83	0.61
18:R:70:TYR:H	18:R:74:HIS:HE1	1.47	0.61
21:U:7:ARG:O	21:U:10:GLU:HB3	1.99	0.61
22:a:275:C:H2'	22:a:276:U:O4'	2.01	0.61
28:g:2:SER:O	28:g:6:LYS:HG3	2.00	0.61
33:l:53:MET:O	33:l:57:VAL:HG22	2.00	0.61
1:A:511:C:O2'	1:A:512:U:OP2	2.19	0.60
2:B:114:LEU:HB2	2:B:144:LEU:HB3	1.82	0.60
10:J:5:ARG:HG2	10:J:5:ARG:NH1	2.15	0.60
11:K:20:VAL:HG22	11:K:83:GLU:HB2	1.83	0.60
19:S:50:ALA:HB1	19:S:57:HIS:HB3	1.82	0.60
22:a:1263:U:O2'	47:z:8:PRO:HD2	2.01	0.60
38:q:26:ASP:O	38:q:27:ILE:HD13	2.01	0.60
40:s:72:GLN:O	40:s:72:GLN:HG3	1.98	0.60
1:A:319:G:O2'	1:A:320:A:H5'	2.01	0.60
1:A:454:G:O2'	1:A:455:G:H5'	2.01	0.60
5:E:113:ALA:O	5:E:117:VAL:HG22	1.99	0.60
7:G:5:ARG:HG3	7:G:5:ARG:O	2.01	0.60
7:G:27:VAL:HG22	7:G:43:VAL:HG21	1.83	0.60
26:e:121:VAL:O	26:e:189:THR:HA	2.01	0.60
1:A:444:G:O2'	1:A:445:G:H5'	2.00	0.60
10:J:18:ILE:O	10:J:22:THR:HG23	2.01	0.60
18:R:9:LYS:HA	18:R:46:GLY:CA	2.31	0.60
22:a:84:A:N1	22:a:98:G:O2'	2.29	0.60
22:a:363:G:H2'	22:a:364:C:C6	2.36	0.60
28:g:19:ILE:HG23	28:g:24:ILE:HD13	1.82	0.60
1:A:189:A:H2'	1:A:190:A:C8	2.36	0.60
1:A:555:U:H2'	1:A:556:C:C6	2.37	0.60
1:A:1530:G:H2'	1:A:1531:A:C8	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:357:C:O2'	22:a:358:U:H5'	2.02	0.60
22:a:1577:C:H2'	22:a:1578:U:O4'	2.01	0.60
23:b:66:A:H61	23:b:107:G:H2'	1.65	0.60
1:A:1005:A:C6	1:A:1006:G:H1'	2.36	0.60
1:A:1251:A:H2'	1:A:1252:A:C8	2.36	0.60
2:B:101:LEU:HB3	2:B:179:LEU:HD11	1.83	0.60
4:D:188:ARG:HH21	4:D:191:LEU:HB2	1.66	0.60
18:R:42:SER:OG	18:R:47:THR:O	2.18	0.60
41:t:12:ILE:HG21	41:t:80:ALA:HB2	1.82	0.60
45:x:14:LEU:HD11	45:x:60:LYS:HE3	1.84	0.60
1:A:155:A:O2'	1:A:156:C:H5'	2.01	0.60
1:A:745:G:O2'	1:A:746:A:H5'	2.02	0.60
1:A:1003:G:H21	1:A:1005:A:H5'	1.65	0.60
4:D:7:PRO:HB2	4:D:10:LYS:HD3	1.84	0.60
20:T:31:PHE:O	20:T:35:VAL:HG23	2.02	0.60
22:a:933:A:H5'	22:a:934:U:OP2	2.01	0.60
22:a:2271:G:OP1	43:v:18:ALA:HB1	2.01	0.60
2:B:88:ASP:OD1	2:B:88:ASP:O	2.20	0.60
3:C:88:ARG:CA	3:C:101:ILE:HD12	2.27	0.60
22:a:2760:C:C2'	22:a:2761:A:H5'	2.32	0.60
2:B:43:LEU:O	2:B:47:VAL:HG22	2.02	0.60
13:M:34:LEU:CD1	13:M:41:GLU:HG2	2.31	0.60
13:M:54:ASP:OD1	13:M:57:ARG:NH1	2.35	0.60
1:A:648:A:O2'	1:A:649:A:H5'	2.02	0.60
1:A:1008:U:H3'	1:A:1009:U:H5''	1.83	0.60
1:A:1036:A:H2'	1:A:1037:C:H5'	1.84	0.60
11:K:70:CYS:O	11:K:74:VAL:HG22	2.01	0.60
22:a:64:A:H2'	22:a:65:U:C6	2.36	0.60
41:t:47:LYS:HD2	41:t:48:PRO:HD2	1.84	0.60
2:B:132:LYS:O	2:B:136:MET:HG2	2.01	0.60
22:a:1797:G:O2'	24:c:257:THR:OG1	2.11	0.60
22:a:2020:A:H5'	47:z:9:THR:CG2	2.31	0.60
22:a:2469:A:H4'	33:l:55:ARG:CD	2.31	0.60
33:l:1:MET:SD	33:l:44:ARG:HG2	2.42	0.60
51:3:17:VAL:HG11	51:3:26:ILE:HD13	1.84	0.60
1:A:10:A:OP2	5:E:131:THR:HG21	2.01	0.59
1:A:545:C:H5'	4:D:69:GLU:CB	2.32	0.59
3:C:110:GLU:OE1	3:C:144:LEU:HG	2.02	0.59
10:J:5:ARG:NH1	10:J:7:ARG:HG2	2.17	0.59
10:J:34:ALA:HB2	10:J:79:PRO:HA	1.82	0.59
10:J:40:ILE:CG1	10:J:73:LEU:HB3	2.31	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:2532:G:N2	22:a:2663:G:O2'	2.34	0.59
1:A:197:A:N1	1:A:220:G:O2'	2.30	0.59
1:A:1027:C:H2'	1:A:1028:C:H6	1.66	0.59
2:B:135:LEU:HD22	2:B:138:THR:CG2	2.32	0.59
4:D:97:ARG:O	4:D:101:VAL:HG23	2.01	0.59
17:Q:60:GLU:HB2	17:Q:77:ARG:HG2	1.85	0.59
22:a:387:U:N3	58:a:6250:84G:O	2.27	0.59
22:a:2566:A:N1	31:j:28:SER:OG	2.33	0.59
1:A:632:U:H5'	1:A:633:G:C8	2.36	0.59
1:A:1218:C:H2'	1:A:1219:A:C8	2.37	0.59
7:G:88:PRO:HG3	7:G:149:LYS:HA	1.82	0.59
11:K:67:ALA:HB2	11:K:96:THR:HG23	1.83	0.59
15:O:53:ARG:O	15:O:57:LEU:HG	2.02	0.59
22:a:577:G:O2'	22:a:1254:A:OP1	2.19	0.59
22:a:597:G:O2'	32:k:11:GLY:O	2.16	0.59
22:a:1046:A:H3'	22:a:1047:G:C5'	2.30	0.59
1:A:477:C:H2'	1:A:478:A:H8	1.64	0.59
22:a:1203:U:OP2	22:a:1204:A:O2'	2.09	0.59
31:j:17:ARG:HB2	31:j:45:GLU:CG	2.32	0.59
53:5:37:MIA:H112	53:5:37:MIA:C13	2.32	0.59
1:A:757:U:OP1	1:A:822:U:O2'	2.19	0.59
3:C:77:ILE:HG12	3:C:84:VAL:HG21	1.84	0.59
22:a:287:G:H2'	22:a:288:U:C6	2.37	0.59
22:a:356:G:O2'	22:a:357:C:H5'	2.03	0.59
22:a:894:U:H2'	22:a:895:U:O4'	2.03	0.59
22:a:1794:A:H2'	22:a:1795:C:C6	2.37	0.59
22:a:2272:U:H5''	22:a:2273:A:OP1	2.03	0.59
1:A:586:C:C2'	1:A:587:G:H5'	2.32	0.59
1:A:640:A:O2'	1:A:641:U:H5'	2.03	0.59
1:A:779:C:H2'	1:A:780:A:O4'	2.03	0.59
7:G:50:LEU:HD22	7:G:124:LEU:HB3	1.83	0.59
9:I:21:ILE:HG12	9:I:63:LEU:CD2	2.32	0.59
22:a:161:A:OP2	22:a:162:U:O2'	2.10	0.59
22:a:1225:G:OP1	38:q:71:LYS:HE2	2.02	0.59
31:j:43:ILE:HD12	31:j:56:ASP:HB2	1.84	0.59
32:k:10:GLU:OE1	32:k:10:GLU:N	2.32	0.59
1:A:820:U:H4'	1:A:821:G:OP2	2.03	0.59
10:J:40:ILE:O	10:J:40:ILE:HG13	2.02	0.59
22:a:2328:A:H2'	22:a:2329:U:C6	2.37	0.59
27:f:140:GLU:OE1	27:f:140:GLU:N	2.35	0.59
39:r:13:SER:O	39:r:17:VAL:HG23	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:r:66:ILE:HD13	39:r:66:ILE:N	2.18	0.59
1:A:635:A:H2'	1:A:636:U:C6	2.38	0.59
1:A:1122:U:O2'	1:A:1123:U:H5'	2.03	0.59
1:A:1323:G:H2'	1:A:1324:A:C8	2.38	0.59
3:C:63:SER:HB2	3:C:98:PRO:HG2	1.84	0.59
13:M:9:ILE:CD1	13:M:45:ILE:HG21	2.27	0.59
29:h:9:VAL:HG11	29:h:12:LEU:HD21	1.85	0.59
32:k:132:ARG:HG3	32:k:142:ILE:HD12	1.84	0.59
1:A:751:U:O2'	1:A:752:G:H5'	2.02	0.59
22:a:890:C:H3'	22:a:891:G:O4'	2.02	0.59
51:3:7:VAL:CG1	51:3:25:VAL:HG23	2.33	0.59
1:A:547:A:H4'	1:A:548:G:O5'	2.02	0.59
22:a:454:A:H4'	22:a:455:C:OP2	2.02	0.59
22:a:1051:G:H2'	22:a:1052:C:O4'	2.02	0.59
22:a:1292:G:H2'	22:a:1293:C:C6	2.38	0.59
22:a:2196:C:O2'	22:a:2197:U:H5'	2.02	0.59
30:i:1:MET:HG2	30:i:2:LYS:H	1.67	0.59
37:p:86:ALA:HB2	37:p:116:ALA:HB2	1.85	0.59
1:A:275:G:H5'	17:Q:16:LYS:HD3	1.85	0.58
13:M:92:ARG:HD2	22:a:888:C:C5	2.38	0.58
22:a:1757:A:O2'	22:a:1758:U:OP1	2.14	0.58
28:g:54:PRO:HG3	28:g:62:TRP:CE2	2.37	0.58
1:A:460:A:H2'	1:A:461:A:H8	1.67	0.58
22:a:306:U:H2'	22:a:307:G:O4'	2.02	0.58
22:a:1310:G:C2'	22:a:1311:G:H5'	2.34	0.58
1:A:1009:U:H3	1:A:1020:G:H1	0.75	0.58
1:A:1378:C:OP2	7:G:5:ARG:NH1	2.36	0.58
4:D:188:ARG:NH2	4:D:192:SER:O	2.36	0.58
5:E:16:ILE:HD12	5:E:137:VAL:HG21	1.85	0.58
10:J:66:GLU:HB2	14:N:99:ALA:CB	2.31	0.58
28:g:124:GLU:HB2	28:g:134:LYS:HZ1	1.69	0.58
35:n:4:LYS:O	35:n:8:ILE:HG12	2.03	0.58
45:x:9:LYS:HB3	45:x:13:GLU:HB2	1.86	0.58
54:6:24:C:H2'	54:6:25:U:C6	2.38	0.58
1:A:167:A:H2'	1:A:168:G:H8	1.68	0.58
1:A:502:A:H2'	1:A:503:C:O4'	2.03	0.58
1:A:1080:A:OP1	5:E:52:LYS:HD2	2.01	0.58
17:Q:13:VAL:HG22	17:Q:22:VAL:HG12	1.85	0.58
22:a:197:A:N6	22:a:2430:A:O2'	2.36	0.58
22:a:792:A:N3	22:a:2072:C:O2'	2.36	0.58
22:a:2243:U:H2'	22:a:2244:U:C6	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:d:97:SER:OG	25:d:99:GLU:OE1	2.21	0.58
1:A:838:G:O2'	1:A:839:C:H5'	2.03	0.58
1:A:1152:A:OP1	10:J:70:HIS:ND1	2.25	0.58
8:H:31:LYS:HA	8:H:31:LYS:HE3	1.86	0.58
13:M:9:ILE:HD12	13:M:10:PRO:O	2.04	0.58
15:O:14:GLU:OE1	15:O:84:ARG:NH2	2.36	0.58
22:a:554:U:O2'	22:a:555:G:H5'	2.03	0.58
23:b:66:A:N6	23:b:107:G:H2'	2.19	0.58
53:5:43:C:H3'	53:5:44:G:H21	1.68	0.58
1:A:147:G:H2'	1:A:148:G:C8	2.38	0.58
1:A:1238:A:N7	1:A:1303:C:H1'	2.18	0.58
1:A:1258:G:O2'	1:A:1259:C:H5'	2.04	0.58
1:A:1291:U:H2'	1:A:1292:G:H8	1.69	0.58
1:A:1441:A:H5'	1:A:1442:G:OP2	2.03	0.58
5:E:61:GLN:HE21	5:E:65:GLU:CD	2.12	0.58
10:J:90:LEU:HD23	10:J:92:LEU:HD21	1.85	0.58
22:a:1583:A:HO2'	22:a:1585:C:N4	2.00	0.58
1:A:938:A:N3	1:A:1376:U:O2'	2.29	0.58
4:D:88:GLU:HG3	4:D:188:ARG:HG3	1.86	0.58
7:G:60:GLU:HA	7:G:63:GLU:OE1	2.03	0.58
22:a:1857:G:H1'	22:a:1885:A:N6	2.17	0.58
22:a:2728:U:HO2'	22:a:2729:G:H8	1.51	0.58
40:s:71:GLY:O	40:s:72:GLN:HG2	2.04	0.58
1:A:8:A:H4'	1:A:9:G:OP1	2.04	0.58
1:A:713:G:H2'	1:A:714:G:C8	2.39	0.58
1:A:1287:A:H2'	1:A:1288:A:C8	2.39	0.58
1:A:1356:G:H2'	1:A:1357:A:H8	1.67	0.58
9:I:84:THR:CG2	9:I:98:LEU:HD13	2.32	0.58
19:S:53:ASN:O	19:S:77:THR:HG22	2.03	0.58
22:a:58:G:OP1	40:s:78:SER:OG	2.17	0.58
22:a:448:U:OP2	57:a:6199:SPD:H81	2.03	0.58
22:a:1705:A:O2'	22:a:1706:C:H5'	2.04	0.58
22:a:2327:A:H2'	22:a:2328:A:C8	2.39	0.58
38:q:38:VAL:HG22	38:q:59:ILE:HD12	1.86	0.58
1:A:43:C:H2'	1:A:44:A:O4'	2.04	0.58
1:A:993:G:O2'	1:A:995:C:N4	2.36	0.58
9:I:33:ARG:HD3	9:I:38:TYR:HD1	1.68	0.58
21:U:58:LYS:CD	21:U:59:LYS:HZ3	2.17	0.58
22:a:1050:A:O2'	22:a:1051:G:H5'	2.04	0.58
29:h:34:GLY:C	29:h:36:ALA:H	2.12	0.58
40:s:76:ARG:HG2	40:s:76:ARG:NH1	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:A:H2'	1:A:326:G:N2	2.19	0.58
2:B:113:ARG:HE	2:B:117:LEU:HD11	1.68	0.58
2:B:202:GLY:HA3	2:B:213:TYR:OH	2.03	0.58
4:D:155:VAL:O	4:D:159:LEU:HD23	2.03	0.58
9:I:113:ARG:HH22	10:J:64:GLN:NE2	2.01	0.58
22:a:960:A:H5''	22:a:961:C:OP1	2.04	0.58
26:e:106:LYS:HG3	26:e:200:LEU:HD13	1.86	0.58
1:A:594:U:O2'	1:A:595:A:H5'	2.04	0.57
22:a:1589:U:H2'	22:a:1590:A:C8	2.39	0.57
24:c:75:PRO:HB2	24:c:97:LYS:HE2	1.85	0.57
27:f:57:LEU:HG	27:f:89:VAL:HG21	1.86	0.57
27:f:58:ALA:HA	27:f:63:GLN:O	2.04	0.57
30:i:28:LEU:HD12	30:i:142:ILE:HG22	1.85	0.57
54:6:76:C:H5''	54:6:77:A:OP2	2.03	0.57
1:A:106:C:H5''	57:A:1668:SPD:H52	1.85	0.57
7:G:102:ARG:O	7:G:106:GLU:HG3	2.05	0.57
22:a:419:U:H2'	22:a:420:C:C6	2.39	0.57
40:s:33:LYS:HG2	40:s:80:TRP:CZ3	2.38	0.57
45:x:6:LEU:HB3	45:x:56:LEU:CD1	2.30	0.57
54:6:40:C:O2'	54:6:41:C:H5'	2.04	0.57
10:J:20:GLN:O	10:J:24:GLU:HG2	2.03	0.57
10:J:37:ARG:HB2	10:J:75:ASP:CB	2.19	0.57
16:P:8:ARG:HG3	16:P:8:ARG:O	2.04	0.57
22:a:279:A:O2'	22:a:280:U:H5'	2.05	0.57
22:a:2282:G:H4'	22:a:2389:G:O2'	2.04	0.57
1:A:539:A:H2'	1:A:540:G:H8	1.67	0.57
1:A:1040:U:H2'	1:A:1041:G:C8	2.39	0.57
3:C:123:GLN:O	3:C:128:VAL:HG13	2.04	0.57
4:D:49:SER:O	4:D:53:VAL:HG13	2.05	0.57
5:E:111:MET:HE2	5:E:125:ALA:HB1	1.85	0.57
11:K:23:ILE:HD12	11:K:86:VAL:HG22	1.86	0.57
22:a:1667:G:O2'	22:a:1991:U:O4	2.20	0.57
54:6:21:H2U:O2	54:6:21:H2U:H2'	2.03	0.57
54:6:45:A:H2'	54:6:46:G:C8	2.40	0.57
22:a:155:A:H2'	22:a:156:A:C8	2.40	0.57
22:a:694:U:O4	59:a:6204:SPM:H121	2.05	0.57
22:a:1432:G:O2'	22:a:1433:A:H5'	2.04	0.57
27:f:41:GLY:O	27:f:44:ILE:HG13	2.04	0.57
30:i:99:ARG:NH1	30:i:102:GLU:OE1	2.37	0.57
33:l:77:PRO:HG2	33:l:80:VAL:HG21	1.86	0.57
1:A:33:A:H2'	1:A:34:C:C6	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:C:H2'	1:A:336:A:H8	1.69	0.57
2:B:5:SER:O	2:B:9:MET:HG3	2.04	0.57
8:H:39:VAL:HG21	8:H:110:VAL:HG12	1.86	0.57
31:j:38:ILE:HD11	31:j:112:PHE:HZ	1.69	0.57
40:s:54:GLU:HB3	40:s:88:LYS:CD	2.32	0.57
4:D:128:ARG:CZ	4:D:128:ARG:HB2	2.35	0.57
22:a:133:U:O2'	22:a:134:G:H5'	2.05	0.57
22:a:136:G:O2'	22:a:137:U:H5'	2.05	0.57
22:a:1963:U:O2	22:a:1963:U:H2'	2.02	0.57
49:1:25:LYS:O	49:1:29:GLN:HG3	2.05	0.57
1:A:160:A:O2'	1:A:161:A:H5'	2.03	0.57
1:A:1296:C:H4'	1:A:1302:C:N4	2.20	0.57
2:B:87:CYS:O	2:B:88:ASP:HB3	2.04	0.57
2:B:96:TRP:HA	2:B:100:MET:HE3	1.86	0.57
3:C:88:ARG:NH2	3:C:89:LYS:HG3	2.20	0.57
27:f:19:GLU:HG2	27:f:20:PHE:CD2	2.40	0.57
1:A:633:G:O2'	1:A:634:C:H5'	2.04	0.57
6:F:20:GLY:O	6:F:23:GLU:HG3	2.05	0.57
9:I:42:GLU:O	9:I:46:MET:HG2	2.05	0.57
22:a:1601:G:C2'	22:a:1602:U:H5'	2.34	0.57
25:d:97:SER:HG	25:d:99:GLU:CD	2.13	0.57
1:A:1008:U:C2'	1:A:1009:U:H5''	2.34	0.57
22:a:1045:C:H4'	22:a:1045:C:OP1	2.05	0.57
22:a:1187:G:H5''	38:q:83:TYR:CE1	2.39	0.57
22:a:1545:A:H2'	22:a:1546:G:O4'	2.05	0.57
29:h:9:VAL:CG1	29:h:12:LEU:HD21	2.35	0.57
10:J:9:ARG:NH2	10:J:71:LEU:HD21	2.20	0.56
15:O:71:LYS:HG3	15:O:78:TYR:CD2	2.39	0.56
22:a:1808:A:H3'	22:a:1809:A:C8	2.40	0.56
22:a:2900:A:H2'	22:a:2901:C:O4'	2.05	0.56
27:f:162:SER:OG	27:f:164:GLU:HG2	2.05	0.56
32:k:91:ASP:H	32:k:94:THR:HG1	1.52	0.56
53:5:51:U:H3	53:5:63:G:H22	1.53	0.56
1:A:343:U:H2'	1:A:345:C:C5	2.40	0.56
1:A:1004:A:H5'	1:A:1025:U:O2	2.05	0.56
1:A:1469:C:H2'	1:A:1470:U:O4'	2.05	0.56
17:Q:29:VAL:HG21	17:Q:40:ARG:HG3	1.86	0.56
22:a:191:A:H2'	22:a:192:C:C6	2.39	0.56
22:a:368:A:H2'	22:a:369:U:H5'	1.87	0.56
22:a:796:C:OP1	26:e:57:LYS:HE2	2.04	0.56
22:a:2802:G:O2'	22:a:2803:G:H5'	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:g:140:VAL:O	28:g:144:VAL:HG23	2.04	0.56
1:A:223:A:H2'	1:A:224:U:C6	2.40	0.56
1:A:271:C:H2'	1:A:272:C:H6	1.68	0.56
1:A:987:G:O2'	1:A:988:G:H5'	2.05	0.56
1:A:1268:G:H1'	1:A:1326:U:O2'	2.04	0.56
1:A:1423:G:OP1	31:j:49:ARG:NH2	2.37	0.56
6:F:32:ALA:HB3	6:F:70:VAL:HG21	1.88	0.56
9:I:34:SER:OG	9:I:37:GLN:HB2	2.05	0.56
22:a:608:A:H2'	22:a:609:A:C8	2.40	0.56
22:a:1733:G:H2'	22:a:1734:G:H8	1.70	0.56
22:a:2522:U:O2'	22:a:2647:U:OP1	2.15	0.56
23:b:48:U:H2'	23:b:49:C:C6	2.40	0.56
38:q:28:ALA:HB3	38:q:31:GLU:HG3	1.87	0.56
42:u:31:TYR:HE2	42:u:90:ASP:OD2	1.88	0.56
44:w:39:TRP:HE1	44:w:41:GLU:HG2	1.69	0.56
1:A:66:A:C2'	1:A:67:C:H5'	2.36	0.56
1:A:111:G:H1	1:A:330:C:H41	1.51	0.56
1:A:1026:G:HO2'	1:A:1027:C:P	2.28	0.56
2:B:45:LYS:O	2:B:49:MET:HG3	2.05	0.56
4:D:147:GLU:HA	4:D:150:LYS:HG3	1.85	0.56
9:I:108:ALA:O	9:I:110:GLN:HG2	2.05	0.56
22:a:1883:U:C2'	22:a:1884:G:H5'	2.36	0.56
22:a:1928:A:H2'	22:a:1929:G:O4'	2.05	0.56
31:j:102:PRO:HD2	36:o:68:GLU:CG	2.35	0.56
34:m:29:VAL:O	34:m:78:LYS:NZ	2.32	0.56
39:r:74:ILE:HD12	39:r:105:VAL:HG22	1.88	0.56
1:A:692:U:H2'	1:A:694:A:OP2	2.05	0.56
10:J:80:THR:O	10:J:84:VAL:HG23	2.06	0.56
22:a:925:A:O2'	22:a:926:G:H5'	2.05	0.56
22:a:1405:U:H2'	22:a:1406:U:C6	2.40	0.56
22:a:1867:G:O2'	22:a:1868:C:H5'	2.06	0.56
42:u:4:ILE:HG22	42:u:42:LEU:HD22	1.85	0.56
1:A:586:C:O2'	1:A:587:G:H5'	2.05	0.56
1:A:1041:G:H2'	1:A:1042:A:C8	2.40	0.56
1:A:173:U:H5''	1:A:197:A:O4'	2.05	0.56
1:A:323:U:H2'	1:A:324:G:O4'	2.05	0.56
1:A:386:C:O2'	1:A:387:U:H5'	2.05	0.56
3:C:175:LEU:HD23	3:C:182:ILE:HD13	1.87	0.56
5:E:25:VAL:HG21	5:E:30:ILE:HD11	1.87	0.56
9:I:25:ASN:O	9:I:59:GLU:HG3	2.06	0.56
22:a:511:U:H2'	22:a:512:G:H5'	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:592:A:C2	50:2:4:ILE:HD11	2.40	0.56
22:a:948:C:H1'	22:a:984:A:C8	2.40	0.56
22:a:1170:C:H2'	22:a:1171:G:O4'	2.06	0.56
26:e:141:MET:HE2	26:e:143:LEU:CD1	2.36	0.56
42:u:4:ILE:CG2	42:u:42:LEU:HD22	2.36	0.56
50:2:15:LYS:HB2	50:2:23:LYS:HE2	1.88	0.56
1:A:106:C:H5''	57:A:1668:SPD:C5	2.36	0.56
1:A:218:U:H2'	1:A:219:U:O4'	2.05	0.56
1:A:714:G:H2'	1:A:715:A:C8	2.40	0.56
1:A:1135:U:H3'	1:A:1137:C:H41	1.71	0.56
2:B:97:LEU:H	2:B:100:MET:CE	2.19	0.56
19:S:9:PRO:HB2	19:S:39:THR:HG21	1.87	0.56
21:U:7:ARG:HG3	21:U:10:GLU:OE1	2.06	0.56
32:k:19:LEU:HD13	32:k:31:GLY:CA	2.36	0.56
32:k:58:TYR:O	50:2:13:ARG:HD2	2.05	0.56
53:5:37:MIA:H131	53:5:37:MIA:N1	2.21	0.56
1:A:999:C:H2'	1:A:1000:A:C8	2.41	0.56
1:A:1005:A:C5	1:A:1006:G:H1'	2.40	0.56
1:A:1486:G:H2'	1:A:1487:G:O4'	2.05	0.56
21:U:58:LYS:HD2	21:U:59:LYS:HZ3	1.71	0.56
22:a:624:C:O2'	22:a:657:U:OP1	2.21	0.56
22:a:879:G:O2'	22:a:880:G:H5'	2.05	0.56
22:a:1410:G:O2'	22:a:1411:U:H5'	2.06	0.56
29:h:33:GLN:O	29:h:35:LYS:HG3	2.05	0.56
47:z:53:LYS:NZ	47:z:56:ALA:HA	2.19	0.56
53:5:44:G:O2'	53:5:45:U:H5''	2.05	0.56
1:A:542:G:OP1	4:D:10:LYS:NZ	2.37	0.56
2:B:126:PHE:CE1	2:B:137:ARG:HD3	2.42	0.56
10:J:7:ARG:HD2	10:J:73:LEU:HD11	1.87	0.56
16:P:4:ILE:CG1	16:P:21:VAL:HG22	2.30	0.56
22:a:172:A:H2'	22:a:173:A:C8	2.41	0.56
22:a:886:A:H2'	22:a:887:U:O4'	2.06	0.56
22:a:1845:G:O2'	22:a:1846:G:H5'	2.06	0.56
22:a:1945:G:OP1	57:a:6192:SPD:H81	2.06	0.56
24:c:157:SER:O	24:c:160:THR:OG1	2.23	0.56
41:t:77:THR:OG1	41:t:79:LYS:HG2	2.06	0.56
1:A:1406:U:H2'	1:A:1407:5MC:H5'	1.87	0.55
2:B:141:LEU:HD12	2:B:141:LEU:O	2.06	0.55
3:C:79:LYS:HE2	3:C:82:GLU:OE1	2.06	0.55
4:D:73:ARG:O	4:D:77:LYS:HG3	2.06	0.55
6:F:26:THR:O	6:F:30:THR:HG23	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:66:ALA:HB1	6:F:67:PRO:HD2	1.87	0.55
7:G:21:GLU:HG3	7:G:21:GLU:O	2.05	0.55
7:G:39:ALA:O	7:G:43:VAL:HG23	2.06	0.55
14:N:34:VAL:HG12	14:N:35:ASN:OD1	2.06	0.55
18:R:55:LEU:O	18:R:59:ILE:HG13	2.06	0.55
27:f:30:ARG:HG3	27:f:30:ARG:NH1	2.19	0.55
27:f:44:ILE:HG22	27:f:83:TYR:CE2	2.41	0.55
53:5:24:G:H2'	53:5:25:C:C6	2.41	0.55
1:A:1391:U:H2'	1:A:1392:G:C8	2.41	0.55
15:O:47:LYS:O	15:O:53:ARG:NH2	2.40	0.55
22:a:703:U:C2'	22:a:704:G:H5'	2.36	0.55
22:a:1350:C:H2'	22:a:1351:C:H5'	1.88	0.55
27:f:42:GLU:CG	27:f:49:LEU:HD13	2.36	0.55
41:t:29:LEU:HB2	41:t:33:LYS:O	2.06	0.55
1:A:1009:U:H2'	1:A:1010:U:H6	1.69	0.55
9:I:12:ARG:HG3	9:I:13:LYS:N	2.16	0.55
22:a:414:C:H2'	22:a:415:A:C8	2.41	0.55
22:a:473:G:O2'	22:a:474:G:H5'	2.06	0.55
22:a:538:A:O2'	30:i:9:GLU:OE2	2.23	0.55
22:a:1870:C:H3'	22:a:1871:A:H8	1.71	0.55
24:c:43:ARG:HA	24:c:48:ARG:O	2.06	0.55
1:A:1234:C:O2'	1:A:1235:U:H5'	2.07	0.55
3:C:36:ASP:OD1	3:C:57:ILE:HG21	2.05	0.55
6:F:41:ASP:OD1	6:F:58:HIS:NE2	2.38	0.55
10:J:40:ILE:HG13	10:J:73:LEU:HB3	1.88	0.55
18:R:34:THR:HG23	18:R:38:LYS:O	2.06	0.55
22:a:1614:A:C2	39:r:93:ALA:HB2	2.41	0.55
22:a:2820:A:N3	22:a:2820:A:H2'	2.21	0.55
39:r:72:THR:HG22	39:r:73:LYS:HG2	1.88	0.55
1:A:371:A:H2'	1:A:372:C:O4'	2.07	0.55
1:A:592:G:H2'	1:A:593:U:C6	2.42	0.55
1:A:992:U:H4'	1:A:993:G:H5'	1.86	0.55
1:A:1236:A:H2'	1:A:1237:C:C6	2.41	0.55
8:H:89:LYS:HD3	8:H:120:GLY:HA2	1.88	0.55
19:S:11:ILE:HG13	19:S:38:SER:OG	2.06	0.55
20:T:15:GLU:OE1	20:T:15:GLU:O	2.25	0.55
21:U:59:LYS:N	21:U:59:LYS:HD3	2.21	0.55
22:a:833:A:H2'	22:a:834:G:C8	2.42	0.55
22:a:1179:G:H2'	22:a:1180:U:C6	2.41	0.55
22:a:2308:G:H2'	22:a:2308:G:N3	2.20	0.55
22:a:2644:G:O2'	22:a:2645:G:H5'	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:2690:U:O2'	22:a:2872:A:H1'	2.06	0.55
24:c:267:ILE:HG21	24:c:270:ARG:HE	1.71	0.55
34:m:79:LEU:HD23	34:m:83:LEU:HD12	1.87	0.55
41:t:38:GLY:H	41:t:62:GLU:CD	2.14	0.55
54:6:24:C:H2'	54:6:25:U:H6	1.70	0.55
1:A:89:U:H2'	1:A:90:C:C6	2.41	0.55
7:G:60:GLU:HA	7:G:60:GLU:OE1	2.07	0.55
21:U:47:ARG:HG2	21:U:47:ARG:HH11	1.71	0.55
22:a:554:U:C2'	22:a:555:G:H5'	2.36	0.55
22:a:2820:A:O2'	22:a:2821:A:OP1	2.17	0.55
30:i:28:LEU:HD12	30:i:142:ILE:CG2	2.37	0.55
1:A:1053:G:N7	1:A:1200:C:H5''	2.22	0.55
12:L:72:HIS:HA	12:L:99:ARG:HH12	1.72	0.55
22:a:147:C:O2'	22:a:148:U:H5'	2.06	0.55
22:a:231:A:O2'	22:a:232:G:H5'	2.07	0.55
22:a:893:C:H2'	22:a:894:U:C6	2.41	0.55
22:a:1350:C:C2'	22:a:1351:C:H5'	2.36	0.55
22:a:1473:G:O2'	22:a:1474:U:H5'	2.06	0.55
22:a:2025:C:H2'	22:a:2026:U:C6	2.41	0.55
22:a:2591:C:H2'	22:a:2592:G:H8	1.69	0.55
42:u:14:LYS:O	42:u:18:ARG:HG3	2.07	0.55
1:A:135:C:H2'	1:A:136:C:H5'	1.89	0.55
1:A:460:A:H2'	1:A:461:A:C8	2.42	0.55
1:A:1000:A:H2'	1:A:1001:C:O4'	2.07	0.55
10:J:8:ILE:HD11	10:J:87:LEU:HD13	1.89	0.55
12:L:18:LYS:HG2	12:L:19:SER:H	1.71	0.55
22:a:980:A:N7	22:a:1136:G:H5''	2.21	0.55
22:a:2489:U:H2'	22:a:2490:G:O4'	2.06	0.55
24:c:125:LYS:CG	24:c:128:ASN:HD22	2.20	0.55
53:5:15:G:H2'	53:5:16:U:C5	2.42	0.55
54:6:22:A:N6	54:6:47:A:H2'	2.22	0.55
1:A:545:C:H5'	4:D:69:GLU:HG2	1.89	0.55
13:M:71:ARG:CZ	27:f:115:ARG:HD2	2.37	0.55
18:R:32:TYR:C	18:R:40:VAL:HG23	2.32	0.55
20:T:44:LYS:NZ	20:T:86:LEU:O	2.26	0.55
22:a:445:C:H2'	22:a:446:G:O4'	2.06	0.55
22:a:537:G:H5''	30:i:5:THR:HG21	1.89	0.55
32:k:90:VAL:HG23	32:k:120:VAL:HG13	1.89	0.55
39:r:1:MET:N	39:r:109:ASP:OD1	2.36	0.55
41:t:47:LYS:CD	41:t:48:PRO:HD2	2.36	0.55
50:2:27:ALA:O	50:2:28:ASN:HB2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:U:H3'	1:A:89:U:C6	2.42	0.55
1:A:149:A:O2'	1:A:150:U:H5'	2.07	0.55
1:A:908:A:H2'	1:A:909:A:C8	2.42	0.55
3:C:14:ILE:HG22	3:C:15:VAL:HG13	1.88	0.55
5:E:14:LYS:HD2	5:E:117:VAL:CG1	2.37	0.55
22:a:300:A:H61	57:a:6197:SPD:HN12	1.54	0.55
22:a:1199:U:H1'	37:p:4:VAL:HG22	1.89	0.55
22:a:1936:A:OP1	22:a:1937:A:H5'	2.07	0.55
44:w:32:ASN:O	44:w:52:SER:HA	2.06	0.55
54:6:72:C:H2'	54:6:73:A:C8	2.42	0.55
13:M:39:ILE:CD1	13:M:56:LEU:HD21	2.37	0.54
16:P:21:VAL:O	16:P:21:VAL:HG12	2.07	0.54
22:a:546:U:C3'	22:a:547:A:H5'	2.37	0.54
22:a:805:G:N2	22:a:829:A:OP1	2.40	0.54
22:a:2029:G:H2'	22:a:2031:A:OP1	2.07	0.54
22:a:2309:A:H2'	22:a:2310:C:C6	2.42	0.54
25:d:4:LEU:HD13	25:d:29:VAL:HG11	1.88	0.54
34:m:66:ALA:O	34:m:69:ARG:O	2.25	0.54
1:A:1039:G:C2'	1:A:1040:U:H5'	2.38	0.54
4:D:124:MET:CG	4:D:146:ARG:HG2	2.38	0.54
22:a:27:G:OP1	57:a:6199:SPD:N1	2.39	0.54
22:a:586:A:N1	22:a:809:G:O2'	2.34	0.54
22:a:910:A:H2'	22:a:911:A:C8	2.41	0.54
22:a:1680:U:H2'	22:a:1681:G:O4'	2.07	0.54
22:a:2074:U:H2'	22:a:2075:U:C6	2.42	0.54
24:c:167:ARG:HD3	24:c:172:VAL:HG12	1.88	0.54
28:g:64:GLN:O	28:g:67:THR:HG22	2.08	0.54
53:5:18:G:H1'	53:5:57:G:N2	2.23	0.54
1:A:437:U:C2'	1:A:438:U:H5'	2.36	0.54
1:A:769:G:H4'	1:A:1513:A:H4'	1.89	0.54
1:A:859:G:H2'	1:A:860:A:C8	2.42	0.54
6:F:88:MET:HG2	6:F:90:MET:CE	2.35	0.54
18:R:12:ARG:HB3	18:R:12:ARG:NH1	2.23	0.54
22:a:319:G:O2'	22:a:320:A:H5'	2.07	0.54
22:a:548:G:H8	22:a:548:G:H3'	1.72	0.54
22:a:1874:C:H2'	22:a:1875:G:O4'	2.07	0.54
22:a:2637:U:H2'	22:a:2638:G:O4'	2.06	0.54
33:l:21:ALA:CB	33:l:100:LYS:HB2	2.37	0.54
33:l:24:THR:HG22	33:l:99:GLY:O	2.08	0.54
1:A:35:G:C2	12:L:115:SER:OG	2.61	0.54
1:A:720:C:O2	18:R:60:LYS:NZ	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1226:C:P	13:M:90:ARG:HH22	2.31	0.54
1:A:1318:A:O2'	19:S:37:ARG:HD2	2.08	0.54
7:G:15:ASP:OD2	7:G:23:LEU:HD23	2.07	0.54
22:a:639:U:H2'	22:a:640:C:H6	1.72	0.54
22:a:1198:U:H2'	22:a:1199:U:C6	2.43	0.54
22:a:1602:U:OP2	40:s:64:LYS:NZ	2.37	0.54
28:g:76:VAL:HA	28:g:79:VAL:CG2	2.38	0.54
1:A:303:A:H2'	1:A:304:U:O4'	2.08	0.54
1:A:1033:G:H3'	1:A:1034:G:H8	1.73	0.54
2:B:97:LEU:CD1	2:B:148:LEU:HD21	2.36	0.54
22:a:1495:A:O2'	22:a:1496:A:H5'	2.08	0.54
22:a:2843:G:H2'	22:a:2844:G:O4'	2.08	0.54
27:f:114:PHE:HZ	27:f:176:PRO:HB2	1.72	0.54
48:0:44:ARG:HG3	48:0:44:ARG:NH1	2.22	0.54
54:6:76:C:H2'	54:6:77:A:O4'	2.07	0.54
1:A:1330:U:O2'	1:A:1331:G:H5'	2.07	0.54
7:G:75:VAL:HG11	7:G:144:MET:CE	2.36	0.54
22:a:1431:A:H4'	57:a:6198:SPD:H32	1.89	0.54
22:a:2250:G:O2'	22:a:2496:C:OP1	2.10	0.54
31:j:40:LYS:HE3	31:j:57:VAL:HG12	1.90	0.54
35:n:53:THR:HG23	35:n:74:VAL:HG21	1.89	0.54
53:5:19:G:OP1	53:5:19:G:H4'	2.07	0.54
1:A:144:G:O2'	1:A:145:G:H5'	2.07	0.54
1:A:747:A:H2'	1:A:748:G:O4'	2.07	0.54
2:B:57:LEU:CD1	2:B:217:VAL:HG13	2.38	0.54
3:C:77:ILE:O	3:C:83:ASP:HB2	2.08	0.54
7:G:113:ASP:OD2	7:G:122:ASN:ND2	2.40	0.54
7:G:149:LYS:HG3	7:G:149:LYS:O	2.08	0.54
8:H:106:THR:HG22	8:H:122:GLY:O	2.07	0.54
22:a:2518:A:N3	22:a:2518:A:H2'	2.22	0.54
25:d:150:MEQ:O	25:d:150:MEQ:HG2	2.06	0.54
28:g:40:ALA:HB2	28:g:58:TYR:CG	2.43	0.54
36:o:2:SER:OG	36:o:3:ASN:N	2.41	0.54
47:z:15:MET:O	47:z:18:SER:HB3	2.08	0.54
1:A:1130:A:O2'	1:A:1131:G:H5'	2.06	0.54
2:B:187:VAL:HG13	2:B:191:SER:HB2	1.88	0.54
7:G:14:PRO:HB2	7:G:19:GLY:CA	2.38	0.54
16:P:61:VAL:HG21	16:P:67:ILE:HD11	1.88	0.54
22:a:1666:G:C2'	22:a:1667:G:H5'	2.38	0.54
22:a:1881:C:H2'	22:a:1882:U:O4'	2.08	0.54
35:n:79:ALA:HB3	35:n:113:ALA:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:7:5:U:O2'	55:7:6:G:H5'	2.08	0.54
1:A:405:U:O4	4:D:2:ALA:N	2.40	0.54
1:A:575:G:O2'	1:A:821:G:OP2	2.14	0.54
1:A:1041:G:H2'	1:A:1042:A:H8	1.72	0.54
2:B:7:ARG:O	2:B:11:LYS:HG2	2.07	0.54
2:B:118:GLU:OE1	2:B:141:LEU:HD11	2.07	0.54
10:J:24:GLU:CD	10:J:92:LEU:HD22	2.33	0.54
22:a:241:A:N1	22:a:255:A:H5''	2.22	0.54
22:a:479:A:N3	22:a:481:G:H5''	2.23	0.54
22:a:2847:U:C2'	22:a:2848:G:H5'	2.37	0.54
27:f:14:LYS:HG3	27:f:15:LYS:N	2.23	0.54
1:A:264:C:O2'	17:Q:66:PRO:O	2.26	0.54
1:A:411:A:H4'	1:A:412:A:O5'	2.08	0.54
1:A:500:G:H2'	1:A:501:C:C6	2.43	0.54
1:A:959:A:H5''	1:A:960:U:OP2	2.08	0.54
1:A:1410:A:H2'	1:A:1411:C:C6	2.43	0.54
11:K:89:PRO:HG3	21:U:32:VAL:HG11	1.88	0.54
16:P:19:VAL:HG12	16:P:36:VAL:HG22	1.90	0.54
22:a:634:C:H2'	22:a:635:C:C6	2.43	0.54
22:a:989:G:OP2	46:y:12:SER:OG	2.24	0.54
22:a:1783:A:H5'	22:a:2608:G:H4'	1.89	0.54
22:a:1794:A:H2'	22:a:1795:C:H6	1.73	0.54
22:a:2014:A:H2'	22:a:2015:A:C8	2.41	0.54
28:g:43:VAL:HG13	28:g:52:PHE:CD2	2.43	0.54
40:s:6:ARG:O	40:s:10:VAL:HG23	2.07	0.54
41:t:72:ILE:HG22	41:t:81:ASP:O	2.08	0.54
1:A:197:A:H4'	1:A:198:G:O5'	2.07	0.53
1:A:526:C:OP2	12:L:88:LYS:HE3	2.07	0.53
1:A:1494:G:N7	58:A:1791:84G:N2	2.56	0.53
2:B:164:ILE:HD13	2:B:186:ILE:HD12	1.90	0.53
13:M:52:GLN:O	13:M:55:THR:OG1	2.21	0.53
22:a:645:C:H2'	22:a:647:G:C8	2.42	0.53
22:a:813:U:H2'	22:a:814:C:C6	2.43	0.53
23:b:42:C:O2'	27:f:63:GLN:HG2	2.07	0.53
1:A:264:C:H2'	1:A:265:G:O4'	2.08	0.53
16:P:45:GLU:O	16:P:46:LYS:HB2	2.08	0.53
20:T:44:LYS:HE2	20:T:86:LEU:C	2.32	0.53
22:a:1542:U:H2'	22:a:1543:G:O4'	2.08	0.53
25:d:110:THR:CG2	25:d:202:ILE:HB	2.36	0.53
26:e:138:LEU:CD1	26:e:167:VAL:HG21	2.38	0.53
26:e:176:ASP:OD2	26:e:179:SER:HB2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:q:83:TYR:OH	38:q:85:LYS:HE3	2.08	0.53
45:x:28:LEU:CD1	45:x:46:VAL:HG21	2.38	0.53
53:5:14:A:H2'	53:5:15:G:H5'	1.89	0.53
54:6:50:G:O2'	54:6:51:U:H5'	2.08	0.53
1:A:429:U:H4'	1:A:430:A:O5'	2.08	0.53
1:A:1003:G:N2	1:A:1005:A:H5'	2.23	0.53
1:A:1071:C:H2'	1:A:1072:G:H8	1.73	0.53
4:D:161:LEU:O	4:D:164:GLN:HG2	2.08	0.53
5:E:107:ALA:HB2	5:E:125:ALA:HB3	1.90	0.53
7:G:135:VAL:O	7:G:139:GLU:HG3	2.09	0.53
9:I:88:MET:HE3	9:I:95:ARG:NH2	2.23	0.53
22:a:158:U:O2'	22:a:159:G:H5'	2.08	0.53
22:a:1744:A:H3'	22:a:1745:A:H8	1.73	0.53
22:a:2016:U:H1'	47:z:3:VAL:CG2	2.38	0.53
22:a:2273:A:H2'	22:a:2274:A:C8	2.43	0.53
22:a:2644:G:C2'	22:a:2645:G:H5'	2.38	0.53
28:g:19:ILE:HG23	28:g:24:ILE:CD1	2.38	0.53
28:g:91:GLY:HA2	28:g:160:LYS:HG2	1.90	0.53
46:y:6:LYS:HZ3	46:y:37:GLU:HG3	1.73	0.53
15:O:26:GLU:HG3	15:O:81:LEU:HD22	1.89	0.53
22:a:1027:A:C2	22:a:2488:G:H5'	2.44	0.53
22:a:1965:C:OP1	22:a:1966:A:O2'	2.20	0.53
26:e:111:GLU:O	26:e:115:GLN:HG3	2.08	0.53
28:g:32:GLU:HG3	28:g:32:GLU:O	2.07	0.53
28:g:86:LYS:HG2	28:g:132:VAL:HG12	1.89	0.53
54:6:47:A:H3'	54:6:48:U:C5'	2.39	0.53
1:A:3:A:H5''	1:A:4:U:OP1	2.08	0.53
1:A:1310:G:O2'	1:A:1311:A:H5'	2.08	0.53
3:C:191:THR:HG21	3:C:196:ILE:HD13	1.91	0.53
8:H:29:SER:HB3	8:H:57:PRO:HB2	1.90	0.53
17:Q:25:ILE:HB	17:Q:42:THR:CG2	2.38	0.53
1:A:1130:A:H5'	9:I:20:PHE:CE2	2.44	0.53
3:C:47:LEU:HB3	3:C:50:ALA:HB3	1.90	0.53
13:M:95:LEU:HB3	13:M:96:PRO:HD2	1.91	0.53
18:R:10:PHE:CG	18:R:10:PHE:O	2.61	0.53
22:a:886:A:H1'	22:a:890:C:H42	1.74	0.53
28:g:95:ARG:HG2	28:g:128:GLN:HG2	1.91	0.53
42:u:62:THR:HG23	42:u:71:LYS:HE3	1.88	0.53
4:D:114:ALA:O	4:D:118:VAL:HG23	2.07	0.53
11:K:47:ALA:HB1	11:K:62:ALA:HB1	1.91	0.53
16:P:70:ARG:O	16:P:74:LEU:HG	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:1021:A:H3'	22:a:1022:G:H5''	1.90	0.53
22:a:1482:G:H1'	22:a:1509:A:H61	1.73	0.53
42:u:80:HIS:CE1	42:u:83:LYS:HD2	2.44	0.53
46:y:47:MET:O	46:y:51:VAL:HG22	2.08	0.53
1:A:1121:U:O2'	1:A:1122:U:H5'	2.08	0.53
1:A:1286:U:H2'	1:A:1287:A:C5'	2.30	0.53
22:a:1028:A:N6	22:a:1125:G:H2'	2.24	0.53
22:a:2504:PSU:H2'	22:a:2504:PSU:O4	2.09	0.53
38:q:21:ARG:HG3	38:q:93:PHE:HB2	1.90	0.53
45:x:2:LYS:O	45:x:5:GLU:HG2	2.09	0.53
54:6:9:G:O2'	54:6:10:G:N7	2.34	0.53
1:A:1090:U:O2'	1:A:1091:U:H5'	2.09	0.53
1:A:1179:A:H2'	1:A:1180:A:O4'	2.09	0.53
1:A:1532:U:O2'	1:A:1533:C:H5'	2.08	0.53
2:B:118:GLU:OE1	2:B:141:LEU:HD21	2.08	0.53
21:U:64:ASN:HA	21:U:67:ARG:NH1	2.24	0.53
22:a:248:G:H5'	22:a:250:G:N7	2.24	0.53
22:a:1746:A:H2'	22:a:1747:U:C6	2.44	0.53
27:f:32:GLU:HG2	27:f:33:LYS:HG2	1.90	0.53
33:l:17:ASN:O	33:l:38:ARG:HD3	2.08	0.53
53:5:2:C:H2'	53:5:3:C:C6	2.43	0.53
13:M:9:ILE:HD11	13:M:45:ILE:CG2	2.28	0.53
15:O:17:ARG:O	15:O:18:ASP:HB2	2.07	0.53
16:P:42:ILE:HG22	16:P:42:ILE:O	2.09	0.53
22:a:592:A:N3	50:2:4:ILE:HD11	2.24	0.53
23:b:43:C:H5''	52:4:1:MET:HG2	1.91	0.53
35:n:60:GLU:OE2	35:n:61:GLN:NE2	2.42	0.53
1:A:1458:G:OP1	20:T:30:THR:OG1	2.16	0.52
7:G:66:LEU:HD11	7:G:101:MET:HE2	1.91	0.52
22:a:1589:U:H2'	22:a:1590:A:H8	1.73	0.52
22:a:2700:A:H2'	22:a:2701:U:C6	2.43	0.52
25:d:32:ASN:N	25:d:32:ASN:HD22	2.07	0.52
42:u:4:ILE:HB	42:u:63:ILE:HD13	1.91	0.52
54:6:69:C:H2'	54:6:70:C:O4'	2.09	0.52
1:A:56:U:H2'	1:A:57:G:C8	2.44	0.52
1:A:87:C:OP1	1:A:87:C:H4'	2.08	0.52
1:A:470:C:H2'	1:A:471:U:C6	2.44	0.52
1:A:483:C:OP2	1:A:484:G:O2'	2.13	0.52
1:A:904:U:H2'	1:A:905:U:C6	2.43	0.52
16:P:67:ILE:HG23	16:P:71:VAL:CG1	2.39	0.52
18:R:23:TYR:HA	18:R:29:LEU:HD11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:39:GLU:CG	21:U:44:GLU:HG2	2.40	0.52
22:a:1:G:N2	22:a:2903:U:H5'	2.24	0.52
1:A:216:U:H4'	1:A:464:U:H4'	1.91	0.52
1:A:1039:G:H2'	1:A:1040:U:H5'	1.90	0.52
3:C:72:ARG:HB3	3:C:75:ILE:CG2	2.38	0.52
11:K:83:GLU:HG2	11:K:109:ASN:HB2	1.92	0.52
22:a:75:G:N3	22:a:75:G:H2'	2.24	0.52
22:a:576:U:H2'	22:a:577:G:C8	2.44	0.52
22:a:914:G:H5'	22:a:915:C:OP2	2.09	0.52
22:a:959:A:H2'	22:a:960:A:C8	2.45	0.52
22:a:2097:A:O2'	22:a:2098:U:H5'	2.09	0.52
22:a:2503:2MA:H3'	22:a:2503:2MA:OP2	2.09	0.52
22:a:2662:A:H2'	22:a:2663:G:O4'	2.08	0.52
33:l:64:TRP:HB2	33:l:104:GLU:HB2	1.90	0.52
53:5:59:U:H2'	53:5:60:U:H5'	1.91	0.52
1:A:966:2MG:C2	54:6:35:C:H5'	2.44	0.52
1:A:1263:C:H2'	1:A:1264:U:H6	1.75	0.52
1:A:1330:U:H2'	1:A:1331:G:O4'	2.09	0.52
6:F:39:LEU:HD12	6:F:40:GLU:H	1.73	0.52
12:L:90:LEU:N	12:L:91:PRO:HD3	2.25	0.52
15:O:45:GLU:O	15:O:45:GLU:HG2	2.09	0.52
22:a:2496:C:O2'	22:a:2497:A:H5'	2.10	0.52
28:g:175:LYS:O	28:g:175:LYS:HG3	2.10	0.52
37:p:89:GLU:CG	38:q:52:PRO:HB3	2.40	0.52
44:w:7:VAL:HG23	44:w:51:VAL:HG12	1.91	0.52
1:A:409:U:O2'	1:A:410:G:H5'	2.08	0.52
1:A:1314:C:H2'	1:A:1315:U:C6	2.44	0.52
6:F:3:HIS:CE1	6:F:65:GLU:HG3	2.45	0.52
22:a:3:U:O2'	22:a:4:U:H5'	2.09	0.52
22:a:1710:G:H4'	22:a:2858:C:O2	2.10	0.52
23:b:64:G:H2'	23:b:65:U:C6	2.44	0.52
25:d:157:LYS:HD2	30:i:79:GLY:O	2.09	0.52
37:p:9:ILE:HD12	37:p:9:ILE:N	2.24	0.52
42:u:11:GLU:C	42:u:12:GLN:HG2	2.34	0.52
1:A:1238:A:C8	1:A:1303:C:H1'	2.44	0.52
1:A:1295:U:H2'	1:A:1296:C:C6	2.45	0.52
3:C:121:THR:HG23	3:C:189:ALA:CB	2.39	0.52
22:a:445:C:O2'	22:a:446:G:H5'	2.10	0.52
22:a:1007:C:OP1	30:i:37:ARG:NH1	2.42	0.52
22:a:1591:A:H2'	22:a:1592:C:O4'	2.10	0.52
22:a:2014:A:O2'	39:r:92:ARG:NH2	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:2455:G:H2'	22:a:2456:C:C6	2.44	0.52
28:g:24:ILE:CG1	28:g:37:LEU:HD21	2.37	0.52
35:n:79:ALA:CB	35:n:113:ALA:HB3	2.39	0.52
1:A:82:G:H2'	1:A:82:G:N3	2.25	0.52
1:A:404:G:O6	4:D:2:ALA:N	2.43	0.52
8:H:22:LYS:O	8:H:65:TYR:OH	2.23	0.52
18:R:9:LYS:N	18:R:9:LYS:HE2	2.24	0.52
22:a:84:A:H4'	22:a:85:G:O5'	2.10	0.52
22:a:364:C:O2'	22:a:365:U:H5'	2.09	0.52
22:a:594:U:H2'	22:a:595:C:C6	2.45	0.52
22:a:632:A:H2'	22:a:633:A:C8	2.45	0.52
22:a:846:U:O2	22:a:846:U:H2'	2.08	0.52
22:a:2740:A:H2'	22:a:2741:A:C8	2.45	0.52
45:x:28:LEU:HD12	45:x:46:VAL:HG21	1.91	0.52
1:A:1014:A:H2	1:A:1219:A:H1'	1.74	0.52
1:A:1129:C:O2'	1:A:1139:G:N7	2.31	0.52
22:a:391:A:H1'	22:a:411:G:O4'	2.10	0.52
22:a:839:U:H2'	22:a:840:C:C6	2.45	0.52
22:a:1790:C:H2'	22:a:1791:A:C5	2.44	0.52
22:a:1917:PSU:O2'	22:a:1918:A:H5'	2.10	0.52
22:a:2636:C:O2'	25:d:45:TYR:OH	2.27	0.52
34:m:56:LYS:NZ	34:m:90:ARG:O	2.42	0.52
41:t:12:ILE:CG2	41:t:80:ALA:HB2	2.40	0.52
1:A:419:C:H2'	1:A:420:U:O4'	2.10	0.52
2:B:154:MET:CE	2:B:158:PRO:HD3	2.39	0.52
5:E:14:LYS:HD2	5:E:117:VAL:HG13	1.92	0.52
10:J:80:THR:HB	10:J:83:THR:HG23	1.91	0.52
22:a:385:C:H5''	22:a:386:G:OP1	2.10	0.52
22:a:1870:C:H2'	22:a:1871:A:C1'	2.40	0.52
1:A:186:C:H2'	1:A:187:G:O4'	2.09	0.52
1:A:580:C:H2'	1:A:581:G:O4'	2.10	0.52
1:A:819:A:N6	58:A:1792:84G:O	2.43	0.52
1:A:839:C:O2'	1:A:840:C:H5'	2.10	0.52
1:A:1250:A:H2'	1:A:1251:A:C8	2.45	0.52
3:C:114:LYS:HD3	3:C:185:ASN:OD1	2.09	0.52
3:C:124:LEU:CD1	3:C:196:ILE:HG21	2.40	0.52
6:F:38:ARG:HG2	6:F:39:LEU:N	2.24	0.52
11:K:37:ARG:HG3	11:K:37:ARG:NH1	2.24	0.52
22:a:945:A:N3	57:a:6190:SPD:H71	2.24	0.52
22:a:1845:G:C2'	22:a:1846:G:H5'	2.39	0.52
30:i:101:ILE:O	30:i:105:VAL:HG23	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:u:70:ILE:HG22	42:u:72:VAL:CG1	2.39	0.52
48:0:6:ARG:HG2	48:0:24:THR:HB	1.91	0.52
1:A:161:A:N1	1:A:347:G:O2'	2.42	0.51
1:A:273:U:C2'	1:A:274:A:H5'	2.39	0.51
1:A:386:C:C2'	1:A:387:U:H5'	2.39	0.51
1:A:1157:A:H5'	1:A:1158:C:N1	2.26	0.51
1:A:1263:C:H2'	1:A:1264:U:C6	2.45	0.51
1:A:1329:A:O2'	1:A:1330:U:H5'	2.10	0.51
14:N:33:ASP:HB3	14:N:36:ALA:CB	2.41	0.51
22:a:410:G:O3'	57:a:6195:SPD:H81	2.10	0.51
22:a:2312:U:H5'	27:f:85:ILE:HD11	1.92	0.51
23:b:116:G:H4'	35:n:54:VAL:HG13	1.92	0.51
37:p:9:ILE:N	37:p:9:ILE:CD1	2.72	0.51
39:r:7:HIS:HB2	39:r:50:VAL:HG22	1.93	0.51
48:0:25:LYS:NZ	48:0:51:GLU:OE1	2.42	0.51
53:5:4:C:H2'	53:5:5:G:O4'	2.10	0.51
53:5:28:G:C2'	53:5:29:G:H5'	2.40	0.51
1:A:152:A:C2'	1:A:153:C:H5'	2.40	0.51
1:A:270:A:H2'	1:A:271:C:C6	2.45	0.51
1:A:662:U:H2'	1:A:663:A:C8	2.45	0.51
1:A:741:G:H2'	1:A:742:G:O4'	2.10	0.51
1:A:749:A:O2'	1:A:750:C:H5'	2.10	0.51
1:A:1010:U:O2'	1:A:1011:C:H5'	2.10	0.51
1:A:1406:U:C2'	1:A:1407:5MC:H5'	2.40	0.51
3:C:79:LYS:H	3:C:79:LYS:CD	2.24	0.51
17:Q:26:GLU:OE2	17:Q:41:THR:OG1	2.28	0.51
22:a:1450:G:O2'	22:a:1451:C:H5'	2.10	0.51
27:f:33:LYS:HG3	27:f:157:THR:HB	1.93	0.51
41:t:7:ARG:O	41:t:8:ASP:HB2	2.10	0.51
47:z:55:ILE:C	47:z:55:ILE:HD12	2.35	0.51
1:A:575:G:H4'	1:A:576:C:O5'	2.10	0.51
2:B:53:ALA:CB	2:B:200:ILE:HD11	2.40	0.51
4:D:152:GLN:HB2	4:D:155:VAL:CG2	2.41	0.51
12:L:71:GLY:O	12:L:99:ARG:NH2	2.35	0.51
22:a:207:A:H2'	22:a:208:C:O4'	2.10	0.51
22:a:1654:A:H1'	22:a:2823:A:H5'	1.91	0.51
22:a:2030:6MZ:N3	22:a:2499:C:H5'	2.26	0.51
22:a:2791:G:O2'	22:a:2792:A:H5'	2.10	0.51
27:f:104:ILE:HD11	27:f:175:PHE:HD1	1.76	0.51
29:h:30:LEU:O	29:h:34:GLY:O	2.27	0.51
35:n:39:VAL:CB	35:n:49:VAL:HG22	2.35	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:v:70:GLU:HG3	43:v:72:LYS:CD	2.40	0.51
1:A:782:A:H4'	1:A:1514:G:O2'	2.10	0.51
1:A:1268:G:H2'	1:A:1269:A:C8	2.45	0.51
7:G:26:PHE:CD1	7:G:101:MET:HG2	2.36	0.51
8:H:64:LYS:HG3	8:H:71:VAL:HG21	1.91	0.51
13:M:88:GLY:O	13:M:92:ARG:HG3	2.10	0.51
17:Q:30:LYS:HB2	17:Q:37:PHE:CE2	2.44	0.51
22:a:285:G:O6	22:a:355:U:O2	2.28	0.51
22:a:1727:C:H2'	22:a:1728:C:C6	2.46	0.51
22:a:1990:C:H2'	22:a:1991:U:O4'	2.11	0.51
22:a:2193:G:H2'	22:a:2194:U:C6	2.45	0.51
22:a:2680:U:HO2'	22:a:2681:C:H5'	1.73	0.51
24:c:111:LYS:HB3	24:c:111:LYS:HZ1	1.74	0.51
27:f:105:THR:HA	52:4:38:SER:HB2	1.92	0.51
33:l:12:MET:CE	33:l:71:LYS:HG3	2.40	0.51
1:A:613:C:H2'	1:A:614:C:C6	2.46	0.51
2:B:87:CYS:SG	2:B:221:VAL:HG11	2.51	0.51
3:C:79:LYS:O	3:C:79:LYS:HG2	2.10	0.51
4:D:139:PRO:HB3	4:D:183:LYS:O	2.10	0.51
5:E:108:GLY:O	5:E:112:ARG:HB3	2.10	0.51
16:P:73:ALA:O	16:P:77:GLU:HG3	2.11	0.51
19:S:39:THR:HG23	19:S:41:PHE:HE1	1.75	0.51
22:a:164:C:H2'	22:a:165:A:O4'	2.10	0.51
22:a:1738:G:O2'	22:a:1739:A:O5'	2.11	0.51
24:c:272:SER:O	24:c:272:SER:OG	2.27	0.51
30:i:10:THR:O	30:i:10:THR:OG1	2.29	0.51
48:0:22:THR:HG22	48:0:54:ILE:CD1	2.40	0.51
53:5:50:U:O2'	53:5:51:U:H5'	2.11	0.51
1:A:299:G:H2'	1:A:300:A:C8	2.46	0.51
1:A:493:A:H2'	1:A:494:G:C8	2.45	0.51
1:A:1008:U:H3'	1:A:1009:U:C5'	2.41	0.51
1:A:1255:G:O2'	1:A:1258:G:H1'	2.11	0.51
1:A:1428:A:H2'	1:A:1429:A:O4'	2.10	0.51
10:J:5:ARG:HH11	10:J:7:ARG:HG2	1.74	0.51
22:a:947:A:H2'	22:a:948:C:C6	2.46	0.51
1:A:593:U:O2'	1:A:594:U:H5'	2.11	0.51
1:A:1002:G:C2	1:A:1003:G:H1'	2.46	0.51
3:C:50:ALA:HB1	3:C:76:VAL:HG22	1.93	0.51
22:a:581:C:H2'	22:a:582:A:C8	2.45	0.51
22:a:1389:G:H2'	22:a:1390:U:O4'	2.11	0.51
22:a:1582:C:H2'	22:a:1583:A:O4'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:2799:A:O2'	22:a:2800:A:H5''	2.11	0.51
23:b:34:A:H4'	23:b:35:C:C5	2.45	0.51
23:b:59:A:H2'	23:b:60:C:O4'	2.10	0.51
40:s:8:LEU:O	45:x:29:ARG:NH2	2.42	0.51
1:A:1002:G:H2'	1:A:1003:G:O4'	2.10	0.51
1:A:1179:A:O2'	1:A:1180:A:H5'	2.11	0.51
2:B:60:ILE:HG22	2:B:67:ILE:HD11	1.92	0.51
2:B:185:ALA:HB3	2:B:196:VAL:HG11	1.92	0.51
6:F:4:TYR:CD2	6:F:71:ILE:HG13	2.46	0.51
8:H:27:MET:HG3	8:H:28:PRO:O	2.10	0.51
9:I:21:ILE:HD13	9:I:61:LEU:HD13	1.92	0.51
22:a:365:U:H2'	22:a:366:C:C6	2.46	0.51
22:a:403:U:H5'	22:a:404:A:OP1	2.11	0.51
22:a:721:A:H2'	22:a:722:A:C8	2.46	0.51
22:a:766:U:H2'	22:a:767:U:C6	2.46	0.51
22:a:896:A:H2'	22:a:897:C:H5'	1.92	0.51
26:e:48:THR:HG22	26:e:86:ALA:HB3	1.92	0.51
35:n:53:THR:O	35:n:59:ALA:HB2	2.09	0.51
1:A:1067:A:N1	1:A:1108:G:O2'	2.40	0.51
1:A:1125:U:HO2'	1:A:1126:U:P	2.34	0.51
1:A:1518:MA6:H8	1:A:1518:MA6:O5'	2.10	0.51
2:B:129:LEU:HD21	2:B:137:ARG:HE	1.76	0.51
4:D:166:GLU:HG3	4:D:167:LYS:N	2.24	0.51
7:G:5:ARG:HH21	7:G:7:ILE:HB	1.74	0.51
17:Q:22:VAL:HG22	17:Q:45:HIS:CD2	2.45	0.51
22:a:1328:A:H2'	22:a:1330:C:C4	2.46	0.51
22:a:1548:A:H2'	22:a:1549:A:C8	2.46	0.51
22:a:1913:A:N1	53:5:37:MIA:O2'	2.42	0.51
58:a:6251:84G:N5	58:a:6251:84G:O6	2.41	0.51
24:c:23:GLU:HG3	24:c:23:GLU:O	2.10	0.51
31:j:35:VAL:HG11	31:j:104:THR:OG1	2.11	0.51
1:A:416:G:C3'	1:A:417:G:H5''	2.41	0.51
1:A:491:G:O2'	1:A:492:C:H5'	2.10	0.51
22:a:742:A:H2'	22:a:743:A:C8	2.46	0.51
26:e:168:ASP:OD2	26:e:170:ARG:CZ	2.59	0.51
32:k:19:LEU:HD13	32:k:31:GLY:HA3	1.93	0.51
1:A:150:U:H2'	1:A:151:A:H8	1.76	0.50
1:A:511:C:H4'	4:D:44:ARG:NH2	2.26	0.50
1:A:1014:A:OP2	19:S:18:LYS:HE3	2.11	0.50
1:A:1027:C:O2'	1:A:1028:C:H5'	2.10	0.50
2:B:30:PHE:CD1	2:B:45:LYS:HE3	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:128:LYS:H	2:B:128:LYS:HD2	1.76	0.50
3:C:7:PRO:HD2	3:C:184:TYR:CD2	2.46	0.50
3:C:35:SER:HG	3:C:59:ARG:NH2	2.04	0.50
4:D:19:LEU:HD22	4:D:64:ILE:HG13	1.93	0.50
7:G:6:VAL:HG22	7:G:6:VAL:O	2.11	0.50
7:G:74:GLU:HG2	7:G:91:VAL:HG22	1.93	0.50
7:G:77:SER:O	7:G:78:ARG:HD2	2.11	0.50
19:S:32:ARG:NH1	19:S:32:ARG:HB2	2.26	0.50
22:a:272:A:O2'	22:a:273:G:H5'	2.10	0.50
22:a:918:A:H5''	23:b:97:C:O2'	2.11	0.50
22:a:984:A:N3	22:a:984:A:H2'	2.26	0.50
22:a:2552:OMU:HM23	22:a:2554:U:C6	2.46	0.50
22:a:2563:U:H2'	22:a:2565:A:OP2	2.11	0.50
24:c:125:LYS:HB2	24:c:126:PRO:HD2	1.93	0.50
1:A:404:G:O2'	1:A:498:A:N1	2.38	0.50
1:A:410:G:OP1	4:D:26:ARG:NH1	2.40	0.50
1:A:502:A:OP1	12:L:115:SER:HB3	2.11	0.50
7:G:66:LEU:O	7:G:70:ARG:HG3	2.11	0.50
22:a:278:A:H3'	22:a:278:A:N3	2.26	0.50
22:a:472:A:OP1	57:a:6199:SPD:H82	2.11	0.50
22:a:545:U:C6	22:a:548:G:O6	2.64	0.50
22:a:646:U:H3'	22:a:647:G:C5'	2.40	0.50
22:a:1353:A:H2'	22:a:1354:A:C8	2.45	0.50
22:a:1485:U:O2'	22:a:1486:U:H5'	2.11	0.50
28:g:90:VAL:HG12	28:g:91:GLY:H	1.75	0.50
53:5:11:C:H6	53:5:11:C:O5'	1.94	0.50
53:5:21:A:HO2'	53:5:22:G:P	2.31	0.50
1:A:219:U:H2'	1:A:220:G:C8	2.45	0.50
16:P:21:VAL:HG21	16:P:60:TRP:CD1	2.46	0.50
17:Q:28:PHE:CE2	17:Q:37:PHE:HB3	2.47	0.50
22:a:546:U:O2'	22:a:547:A:H5'	2.11	0.50
22:a:851:C:H2'	22:a:852:U:H6	1.77	0.50
32:k:61:LEU:HD12	50:2:14:PHE:CZ	2.46	0.50
39:r:24:ILE:HD11	39:r:74:ILE:HD13	1.93	0.50
1:A:107:G:N7	20:T:10:ARG:NH2	2.51	0.50
1:A:553:A:H5''	12:L:21:VAL:HG21	1.93	0.50
1:A:727:G:N2	1:A:730:G:OP2	2.34	0.50
1:A:1014:A:N3	1:A:1219:A:H1'	2.26	0.50
1:A:1018:G:O2'	1:A:1019:A:H5'	2.11	0.50
1:A:1435:G:H2'	1:A:1436:U:C6	2.46	0.50
22:a:580:U:H2'	22:a:581:C:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:987:C:H2'	22:a:988:A:O4'	2.11	0.50
22:a:2016:U:H1'	47:z:3:VAL:HG21	1.92	0.50
26:e:1:MET:HB3	26:e:14:VAL:HG23	1.93	0.50
28:g:127:THR:HG22	28:g:128:GLN:N	2.26	0.50
34:m:72:ASP:HB3	34:m:75:ILE:HB	1.93	0.50
3:C:175:LEU:HD23	3:C:182:ILE:CD1	2.41	0.50
17:Q:18:GLU:O	17:Q:19:LYS:HB2	2.11	0.50
18:R:59:ILE:O	18:R:63:ARG:HG3	2.11	0.50
22:a:541:A:H2'	22:a:542:C:C6	2.46	0.50
22:a:1363:C:O2'	22:a:1809:A:N3	2.40	0.50
31:j:7:MET:SD	31:j:20:MET:HG3	2.51	0.50
33:l:58:LYS:O	33:l:59:ARG:HB2	2.12	0.50
38:q:34:GLU:HG2	38:q:60:LYS:HG3	1.92	0.50
41:t:54:GLN:N	41:t:55:PRO:HD2	2.27	0.50
49:l:25:LYS:O	49:l:25:LYS:HG2	2.11	0.50
1:A:407:U:H2'	1:A:408:A:C8	2.45	0.50
1:A:799:G:H2'	1:A:800:G:O4'	2.12	0.50
1:A:1010:U:H2'	1:A:1011:C:H6	1.76	0.50
3:C:154:SER:OG	3:C:165:THR:HG23	2.11	0.50
5:E:134:ILE:H	5:E:134:ILE:HD12	1.75	0.50
20:T:28:MET:O	20:T:32:ILE:HG13	2.12	0.50
22:a:2747:G:O6	22:a:2755:C:H5''	2.12	0.50
25:d:99:GLU:CD	25:d:99:GLU:H	2.20	0.50
28:g:18:LYS:HE2	28:g:20:ASN:OD1	2.11	0.50
35:n:53:THR:HB	35:n:65:THR:HB	1.94	0.50
1:A:667:G:O2'	15:O:49:ASP:OD1	2.20	0.50
1:A:728:A:H2'	1:A:729:A:C8	2.46	0.50
1:A:909:A:OP1	12:L:18:LYS:HD2	2.11	0.50
1:A:1071:C:H2'	1:A:1072:G:C8	2.47	0.50
1:A:1130:A:HO2'	9:I:5:GLN:NE2	2.02	0.50
3:C:42:TYR:CZ	3:C:90:VAL:HG11	2.46	0.50
9:I:18:ARG:HD3	9:I:66:THR:OG1	2.11	0.50
22:a:1107:G:N3	22:a:1107:G:H2'	2.27	0.50
23:b:42:C:C5	27:f:66:LEU:HD22	2.46	0.50
25:d:1:MET:HB2	25:d:205:PRO:HG2	1.94	0.50
1:A:966:2MG:N2	54:6:35:C:H5'	2.26	0.50
1:A:1134:G:H2'	1:A:1135:U:O4'	2.12	0.50
1:A:1377:A:N1	7:G:7:ILE:HG12	2.27	0.50
6:F:37:HIS:ND1	6:F:95:ALA:HB1	2.27	0.50
22:a:2011:U:H2'	22:a:2012:G:O4'	2.11	0.50
22:a:2514:U:H2'	22:a:2515:C:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:f:158:THR:HG22	27:f:159:THR:N	2.27	0.50
1:A:88:U:H5''	1:A:89:U:H5	1.76	0.50
1:A:384:G:H2'	1:A:385:C:H6	1.75	0.50
2:B:9:MET:HB2	2:B:43:LEU:HD13	1.94	0.50
8:H:7:ILE:O	8:H:11:LEU:HG	2.11	0.50
9:I:21:ILE:HG23	9:I:61:LEU:HD22	1.93	0.50
22:a:5:A:H2'	22:a:6:A:C8	2.47	0.50
22:a:226:A:OP1	57:a:6195:SPD:H22	2.11	0.50
22:a:1526:C:O2'	22:a:1527:G:H5'	2.12	0.50
22:a:2334:U:N3	35:n:16:ARG:HG3	2.27	0.50
41:t:14:LEU:HB2	41:t:69:ASN:O	2.11	0.50
52:4:39:LYS:HE2	52:4:39:LYS:HA	1.94	0.50
1:A:110:C:O2'	16:P:25:ARG:O	2.26	0.49
17:Q:17:MET:HE1	17:Q:22:VAL:HG23	1.94	0.49
20:T:3:ASN:OD1	20:T:3:ASN:N	2.45	0.49
22:a:43:G:H2'	22:a:44:A:C8	2.47	0.49
22:a:1593:A:O2'	22:a:1594:U:H5'	2.11	0.49
22:a:1870:C:H3'	22:a:1871:A:C8	2.47	0.49
22:a:2804:U:H2'	22:a:2805:C:H6	1.76	0.49
26:e:119:ILE:HD11	26:e:185:LYS:HG2	1.92	0.49
30:i:28:LEU:CD1	30:i:142:ILE:HG22	2.42	0.49
50:2:26:HIS:CE1	50:2:48:ALA:HB2	2.47	0.49
1:A:190:A:H8	1:A:190:A:O5'	1.95	0.49
1:A:244:U:O4	1:A:906:A:H1'	2.12	0.49
1:A:346:G:C2'	1:A:347:G:H5'	2.42	0.49
1:A:452:A:H2'	1:A:453:G:O4'	2.12	0.49
1:A:719:C:O2'	18:R:38:LYS:HB3	2.12	0.49
1:A:750:C:O2	15:O:23:GLY:HA3	2.12	0.49
1:A:1032:G:H3'	1:A:1032:G:N3	2.26	0.49
1:A:1136:C:OP2	1:A:1137:C:N4	2.46	0.49
2:B:97:LEU:H	2:B:100:MET:HE3	1.76	0.49
7:G:26:PHE:HE2	7:G:120:LEU:HD21	1.77	0.49
8:H:11:LEU:HD22	8:H:75:ILE:CD1	2.40	0.49
9:I:12:ARG:HG2	9:I:74:GLY:HA2	1.93	0.49
14:N:90:ARG:NH2	14:N:92:GLU:OE1	2.45	0.49
22:a:613:A:H8	22:a:613:A:OP1	1.94	0.49
22:a:851:C:H2'	22:a:852:U:C6	2.47	0.49
22:a:1689:A:H2'	22:a:1690:A:C8	2.47	0.49
22:a:2330:G:O3'	43:v:44:LYS:HE3	2.12	0.49
22:a:2585:U:HO2'	22:a:2586:U:P	2.35	0.49
1:A:1337:G:H5''	1:A:1338:G:OP1	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:45:LYS:O	4:D:45:LYS:HG3	2.12	0.49
4:D:88:GLU:HG3	4:D:188:ARG:HG2	1.92	0.49
9:I:88:MET:CG	9:I:98:LEU:HD12	2.39	0.49
13:M:83:LEU:HD22	19:S:66:MET:HG2	1.93	0.49
20:T:27:MET:CE	20:T:57:ILE:HG23	2.42	0.49
21:U:4:ILE:HG12	21:U:19:PHE:HA	1.94	0.49
22:a:601:C:O2'	22:a:605:G:OP1	2.30	0.49
22:a:1021:A:H3'	22:a:1021:A:N3	2.28	0.49
22:a:1115:G:HO2'	22:a:1116:G:P	2.33	0.49
22:a:1652:A:O2'	22:a:1653:G:H5'	2.13	0.49
22:a:2812:G:H2'	22:a:2813:A:C8	2.47	0.49
26:e:188:MET:SD	26:e:193:VAL:HG22	2.51	0.49
31:j:105:ARG:HG2	31:j:105:ARG:HH11	1.77	0.49
43:v:33:ALA:N	43:v:64:ASP:OD1	2.45	0.49
54:6:51:U:H3	54:6:65:G:H1	1.60	0.49
1:A:636:U:H2'	1:A:637:C:C6	2.48	0.49
1:A:1446:A:O2'	1:A:1447:A:H5'	2.11	0.49
13:M:2:ALA:O	13:M:8:ASN:HA	2.12	0.49
20:T:69:LYS:H	20:T:69:LYS:CD	2.06	0.49
22:a:354:A:H2'	22:a:355:U:O4'	2.12	0.49
22:a:857:G:H2'	22:a:858:G:O4'	2.12	0.49
25:d:48:ILE:O	25:d:48:ILE:HG13	2.12	0.49
28:g:176:LYS:O	28:g:177:LYS:HB2	2.11	0.49
43:v:70:GLU:CG	43:v:72:LYS:HD3	2.42	0.49
1:A:343:U:H2'	1:A:345:C:H5	1.76	0.49
1:A:356:A:H1'	1:A:368:U:O2'	2.12	0.49
1:A:585:G:OP1	17:Q:39:LYS:HD2	2.11	0.49
1:A:1272:G:O2'	1:A:1273:C:H5'	2.13	0.49
2:B:49:MET:CE	2:B:201:PRO:HD3	2.43	0.49
3:C:116:VAL:O	3:C:120:ILE:HG13	2.13	0.49
6:F:49:TYR:HB3	18:R:74:HIS:ND1	2.28	0.49
8:H:75:ILE:HG23	8:H:75:ILE:O	2.13	0.49
9:I:114:LYS:NZ	9:I:118:LEU:O	2.46	0.49
10:J:24:GLU:OE2	10:J:92:LEU:HD22	2.13	0.49
10:J:77:VAL:O	10:J:78:GLU:HB2	2.12	0.49
10:J:80:THR:O	10:J:83:THR:OG1	2.24	0.49
17:Q:79:VAL:HG12	17:Q:80:GLU:HG3	1.94	0.49
21:U:63:GLU:O	21:U:67:ARG:NH1	2.46	0.49
22:a:128:C:H2'	22:a:129:C:C6	2.48	0.49
22:a:682:G:H5'	49:1:26:ASN:CG	2.37	0.49
22:a:864:G:HO2'	22:a:865:C:H5'	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:1310:G:O2'	22:a:1311:G:H5'	2.12	0.49
22:a:1932:A:H2'	22:a:1933:G:O4'	2.12	0.49
22:a:2287:A:OP1	48:0:30:LYS:NZ	2.46	0.49
37:p:76:TYR:CZ	37:p:80:ILE:HG13	2.47	0.49
53:5:37:MIA:H2'	53:5:38:A:O4'	2.13	0.49
54:6:55:5MU:C2'	54:6:56:PSU:H5''	2.42	0.49
1:A:77:A:H2'	1:A:78:A:C8	2.48	0.49
1:A:153:C:O2'	1:A:154:U:H5'	2.13	0.49
1:A:600:A:O2'	1:A:601:G:H5'	2.12	0.49
1:A:632:U:H5'	1:A:633:G:H8	1.77	0.49
21:U:40:LYS:O	21:U:44:GLU:HG3	2.13	0.49
22:a:2064:C:H2'	22:a:2065:C:H6	1.75	0.49
22:a:2656:U:O2	22:a:2656:U:H2'	2.12	0.49
22:a:2898:U:O2	30:i:134:ALA:HB1	2.11	0.49
28:g:12:PRO:HG2	28:g:80:THR:HG21	1.93	0.49
38:q:14:VAL:HG11	38:q:20:VAL:HG21	1.94	0.49
53:5:27:G:O2'	53:5:28:G:H5'	2.13	0.49
1:A:86:G:H1'	1:A:87:C:C6	2.48	0.49
1:A:335:C:H2'	1:A:336:A:C8	2.47	0.49
1:A:545:C:H5'	4:D:69:GLU:HB2	1.94	0.49
1:A:623:C:H2'	1:A:624:C:H6	1.77	0.49
1:A:1125:U:O2'	1:A:1126:U:O5'	2.23	0.49
4:D:152:GLN:CB	4:D:155:VAL:HG23	2.42	0.49
6:F:32:ALA:CB	6:F:70:VAL:HG21	2.43	0.49
9:I:12:ARG:O	9:I:13:LYS:C	2.54	0.49
17:Q:29:VAL:CG2	17:Q:40:ARG:HG3	2.42	0.49
22:a:1:G:H2'	22:a:2:G:C8	2.48	0.49
22:a:837:C:N3	22:a:941:A:N6	2.61	0.49
22:a:2613:U:H5'	57:a:6203:SPD:C9	2.43	0.49
26:e:77:ILE:O	26:e:77:ILE:HG22	2.13	0.49
27:f:50:LEU:CD2	27:f:84:PRO:HB2	2.42	0.49
29:h:14:SER:N	29:h:17:ASP:OD2	2.45	0.49
30:i:7:LYS:O	30:i:11:VAL:HG23	2.13	0.49
1:A:49:U:O2	1:A:362:G:H1'	2.12	0.49
1:A:1120:C:O2'	1:A:1121:U:H5'	2.12	0.49
3:C:79:LYS:H	3:C:79:LYS:HD3	1.78	0.49
6:F:44:ARG:HD2	6:F:56:LYS:HE2	1.95	0.49
13:M:81:MET:HE2	13:M:91:HIS:HB3	1.94	0.49
22:a:357:C:C2'	22:a:358:U:H5'	2.43	0.49
22:a:687:C:H5''	49:1:2:LYS:HE2	1.94	0.49
22:a:1824:G:O3'	24:c:247:PRO:HD3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:2241:A:H2'	22:a:2242:G:C8	2.47	0.49
22:a:2299:U:H2'	22:a:2300:C:C6	2.48	0.49
22:a:2801:G:H2'	22:a:2802:G:C8	2.47	0.49
32:k:92:LEU:O	32:k:96:LYS:HG3	2.12	0.49
1:A:429:U:H3'	4:D:9:LEU:HD12	1.95	0.49
4:D:117:LEU:HD12	4:D:154:ARG:NH2	2.28	0.49
8:H:76:GLN:O	8:H:127:CYS:HB2	2.12	0.49
15:O:88:ARG:NH1	22:a:716:A:OP1	2.45	0.49
18:R:62:ALA:HB3	18:R:68:LEU:HD12	1.95	0.49
22:a:1731:G:O2'	22:a:1732:C:H3'	2.13	0.49
22:a:2473:U:O2	22:a:2473:U:H2'	2.13	0.49
54:6:62:C:H2'	54:6:63:C:H6	1.75	0.49
1:A:123:U:OP1	1:A:312:C:H5'	2.13	0.49
1:A:195:A:N3	1:A:222:C:O2'	2.41	0.49
1:A:543:U:O2'	1:A:544:G:H5'	2.12	0.49
1:A:1283:U:O2'	1:A:1284:C:H5'	2.12	0.49
1:A:1532:U:H2'	1:A:1533:C:O4'	2.13	0.49
4:D:150:LYS:NZ	4:D:178:MET:HB2	2.28	0.49
19:S:9:PRO:HD3	52:4:64:PHE:CG	2.48	0.49
20:T:27:MET:HG2	20:T:31:PHE:HE2	1.78	0.49
22:a:40:U:O2'	22:a:41:C:H5'	2.13	0.49
22:a:668:A:H2'	22:a:670:A:H62	1.78	0.49
22:a:807:U:OP2	32:k:41:ARG:NH2	2.46	0.49
22:a:1774:C:O2	22:a:1774:C:H2'	2.13	0.49
28:g:37:LEU:H	28:g:37:LEU:HD22	1.77	0.49
41:t:26:LYS:HG3	41:t:37:GLU:CG	2.43	0.49
45:x:9:LYS:HB3	45:x:13:GLU:CB	2.42	0.49
1:A:1042:A:C2'	1:A:1043:G:H5'	2.43	0.48
4:D:151:LYS:C	4:D:151:LYS:HD2	2.38	0.48
20:T:17:ALA:O	20:T:21:ASN:OD1	2.30	0.48
22:a:221:A:O4'	22:a:233:A:H1'	2.13	0.48
22:a:1167:C:H2'	22:a:1168:G:H5'	1.94	0.48
22:a:1809:A:H2'	22:a:1810:A:C8	2.48	0.48
22:a:2030:6MZ:H2	22:a:2499:C:H5''	1.96	0.48
30:i:6:ALA:O	30:i:48:VAL:HG21	2.13	0.48
31:j:105:ARG:NH2	31:j:122:VAL:O	2.46	0.48
2:B:54:LEU:CD2	2:B:220:THR:HG21	2.42	0.48
14:N:30:ILE:HG21	14:N:44:ALA:HB2	1.95	0.48
22:a:150:U:H2'	22:a:151:C:C6	2.49	0.48
22:a:420:C:O2'	22:a:421:C:H5'	2.12	0.48
22:a:807:U:H1'	22:a:2445:2MG:OP1	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:1370:C:H2'	22:a:1371:G:O4'	2.13	0.48
22:a:1558:C:H4'	22:a:1559:U:O5'	2.13	0.48
37:p:96:ALA:O	37:p:100:VAL:HG23	2.13	0.48
50:2:32:ILE:O	50:2:32:ILE:HG22	2.13	0.48
53:5:10:G:N2	53:5:26:A:H1'	2.28	0.48
54:6:51:U:H3	54:6:65:G:H22	1.61	0.48
1:A:97:G:H2'	1:A:98:A:O4'	2.14	0.48
1:A:868:C:H2'	1:A:869:G:O4'	2.13	0.48
1:A:1032:G:C6	1:A:1033:G:H1'	2.48	0.48
1:A:1518:MA6:H103	1:A:1519:MA6:H102	1.95	0.48
2:B:210:VAL:HG12	2:B:214:LEU:HD12	1.96	0.48
20:T:44:LYS:HE2	20:T:87:ALA:N	2.28	0.48
20:T:44:LYS:HZ1	20:T:86:LEU:HB3	1.77	0.48
22:a:569:U:H2'	22:a:570:G:O4'	2.12	0.48
22:a:609:A:H2'	22:a:610:C:O4'	2.13	0.48
22:a:879:G:C2'	22:a:880:G:H5'	2.42	0.48
22:a:1044:C:H4'	22:a:1048:A:O4'	2.12	0.48
32:k:57:LEU:CD2	50:2:54:ASP:HB3	2.39	0.48
41:t:74:ASN:OD1	41:t:77:THR:HG23	2.13	0.48
2:B:44:GLU:HA	2:B:44:GLU:OE1	2.13	0.48
2:B:187:VAL:O	2:B:201:PRO:HA	2.14	0.48
4:D:163:GLU:HA	4:D:167:LYS:NZ	2.28	0.48
7:G:93:PRO:HA	7:G:96:ARG:HG3	1.94	0.48
16:P:79:ASN:C	16:P:80:LYS:HG2	2.38	0.48
20:T:44:LYS:HZ3	20:T:86:LEU:C	2.13	0.48
22:a:651:G:OP1	50:2:19:LYS:HB2	2.13	0.48
22:a:1299:G:H5'	22:a:1301:A:O4'	2.13	0.48
22:a:1917:PSU:C2'	22:a:1918:A:H5'	2.42	0.48
24:c:97:LYS:HD3	24:c:97:LYS:N	2.28	0.48
33:l:41:LEU:HG	33:l:96:ILE:HG13	1.95	0.48
1:A:321:A:H2'	1:A:322:C:C6	2.48	0.48
1:A:465:A:H2'	1:A:465:A:N3	2.28	0.48
2:B:135:LEU:HA	2:B:138:THR:CG2	2.44	0.48
2:B:213:TYR:O	2:B:217:VAL:HG23	2.13	0.48
4:D:76:TYR:CD1	4:D:76:TYR:C	2.92	0.48
7:G:72:THR:H	7:G:142:HIS:CE1	2.31	0.48
8:H:77:ARG:NH1	8:H:79:SER:O	2.47	0.48
10:J:90:LEU:HG	10:J:92:LEU:HD23	1.96	0.48
13:M:37:ALA:HB3	13:M:39:ILE:CD1	2.44	0.48
19:S:28:LYS:N	19:S:28:LYS:HD2	2.28	0.48
20:T:55:GLN:O	20:T:58:VAL:HG22	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:69:LYS:N	20:T:69:LYS:CD	2.67	0.48
22:a:845:A:H3'	22:a:845:A:N3	2.28	0.48
22:a:964:C:O2'	22:a:2273:A:N3	2.41	0.48
22:a:2291:U:OP1	22:a:2380:C:O2'	2.27	0.48
33:l:75:GLU:HB2	33:l:90:GLU:CG	2.34	0.48
53:5:21:A:O2'	53:5:22:G:O5'	2.08	0.48
1:A:67:C:H2'	1:A:68:G:H8	1.75	0.48
1:A:407:U:H2'	1:A:408:A:H8	1.78	0.48
1:A:507:C:OP2	1:A:508:U:O2'	2.14	0.48
3:C:111:LEU:CD2	3:C:146:ALA:HB2	2.44	0.48
5:E:81:LEU:HD11	5:E:96:MET:HB2	1.96	0.48
5:E:151:GLU:N	5:E:151:GLU:CD	2.72	0.48
8:H:87:LYS:HB2	8:H:92:LEU:HD23	1.96	0.48
22:a:396:G:H1'	44:w:29:PHE:HB3	1.95	0.48
22:a:548:G:H3'	22:a:548:G:C8	2.48	0.48
22:a:1474:U:C2'	22:a:1475:G:H5'	2.44	0.48
22:a:2661:G:H8	22:a:2661:G:OP2	1.97	0.48
26:e:134:LEU:HD23	26:e:164:LEU:HD12	1.95	0.48
34:m:24:MET:HB3	34:m:44:LEU:HD13	1.94	0.48
38:q:40:MET:HE3	38:q:47:VAL:HG13	1.95	0.48
41:t:49:VAL:C	41:t:54:GLN:HA	2.38	0.48
1:A:42:G:O2'	1:A:622:A:N1	2.43	0.48
1:A:111:G:H1	1:A:330:C:N4	2.11	0.48
1:A:579:A:H2'	1:A:580:C:C6	2.48	0.48
1:A:1157:A:H5'	1:A:1158:C:C6	2.48	0.48
1:A:1202:U:H2'	1:A:1203:C:H5'	1.96	0.48
1:A:1317:C:C4	14:N:53:ARG:HD3	2.48	0.48
2:B:67:ILE:O	2:B:89:GLN:HB3	2.13	0.48
4:D:95:GLU:O	4:D:100:ASN:ND2	2.47	0.48
4:D:150:LYS:HA	4:D:178:MET:SD	2.53	0.48
19:S:37:ARG:O	19:S:70:LYS:HD2	2.14	0.48
22:a:483:A:H5''	41:t:47:LYS:HD2	1.94	0.48
22:a:703:U:O2'	22:a:704:G:H5'	2.14	0.48
22:a:1652:A:H2'	22:a:1653:G:O4'	2.13	0.48
45:x:50:VAL:O	45:x:54:LYS:HG3	2.13	0.48
46:y:3:LYS:O	46:y:4:THR:HG22	2.13	0.48
52:4:12:ILE:HD13	52:4:28:VAL:CG1	2.44	0.48
1:A:139:A:O2'	1:A:140:U:H5'	2.14	0.48
1:A:320:A:H2'	1:A:321:A:O4'	2.13	0.48
1:A:691:G:H1'	1:A:696:A:N6	2.29	0.48
2:B:47:VAL:CG2	2:B:48:PRO:CD	2.90	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:111:ILE:HD12	2:B:152:LYS:HA	1.95	0.48
2:B:135:LEU:HD22	2:B:138:THR:HG21	1.95	0.48
7:G:65:ALA:O	7:G:69:VAL:HG23	2.13	0.48
12:L:18:LYS:HG2	12:L:19:SER:N	2.29	0.48
19:S:32:ARG:HB2	19:S:32:ARG:HH11	1.79	0.48
22:a:709:U:H2'	22:a:710:U:C6	2.48	0.48
22:a:883:G:H5'	22:a:884:U:OP2	2.14	0.48
22:a:1853:A:H2'	22:a:1854:A:C8	2.49	0.48
37:p:86:ALA:O	37:p:87:SER:HB2	2.12	0.48
1:A:6:G:O2'	1:A:7:A:H8	1.95	0.48
1:A:272:C:C2	1:A:273:U:C5	3.02	0.48
1:A:699:C:H2'	1:A:700:G:H5'	1.96	0.48
1:A:1410:A:H2'	1:A:1411:C:H6	1.77	0.48
11:K:107:ILE:O	21:U:6:VAL:HG21	2.13	0.48
15:O:80:GLN:O	15:O:84:ARG:HG3	2.13	0.48
16:P:14:ARG:HA	16:P:42:ILE:HD12	1.95	0.48
20:T:21:ASN:HB3	20:T:66:LEU:CD1	2.43	0.48
22:a:191:A:H2'	22:a:192:C:H6	1.79	0.48
22:a:667:U:O2	50:2:2:PRO:HD2	2.14	0.48
22:a:729:G:C6	24:c:207:LYS:HB2	2.49	0.48
22:a:1028:A:H61	22:a:1125:G:H2'	1.78	0.48
22:a:1045:C:OP1	22:a:1047:G:H5''	2.14	0.48
22:a:1570:A:H2'	22:a:1571:A:C8	2.49	0.48
22:a:2061:G:H2'	22:a:2501:C:O2'	2.13	0.48
26:e:189:THR:O	26:e:193:VAL:HG23	2.13	0.48
37:p:58:ARG:HA	37:p:61:TRP:CE3	2.49	0.48
41:t:18:ASP:OD2	41:t:39:ILE:O	2.32	0.48
42:u:30:ILE:HD11	42:u:40:ILE:HD13	1.96	0.48
52:4:22:MET:HE3	52:4:34:LEU:HD12	1.96	0.48
1:A:60:A:H4'	1:A:61:G:O5'	2.14	0.48
1:A:1477:U:H2'	1:A:1478:U:H6	1.77	0.48
2:B:185:ALA:HB3	2:B:196:VAL:CG1	2.44	0.48
7:G:23:LEU:CD1	7:G:47:LEU:HD11	2.44	0.48
10:J:10:LEU:CD1	10:J:22:THR:HG22	2.34	0.48
17:Q:46:VAL:HA	17:Q:73:TRP:O	2.13	0.48
22:a:743:A:O2'	22:a:1659:G:OP1	2.28	0.48
22:a:1114:C:C2'	22:a:1115:G:H5'	2.43	0.48
22:a:2247:A:H2'	22:a:2248:C:H6	1.79	0.48
37:p:49:ASP:HA	37:p:52:GLN:HB2	1.95	0.48
1:A:8:A:H5'	5:E:125:ALA:O	2.14	0.47
1:A:864:A:H2'	1:A:865:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:6:MET:SD	2:B:47:VAL:HG21	2.54	0.47
2:B:54:LEU:HD22	2:B:220:THR:HG21	1.94	0.47
4:D:19:LEU:HB3	4:D:21:LEU:HD13	1.96	0.47
5:E:22:SER:HB2	5:E:31:PHE:CD1	2.49	0.47
10:J:48:ARG:HG3	10:J:66:GLU:HG3	1.95	0.47
22:a:483:A:C8	41:t:45:HIS:HD2	2.32	0.47
22:a:2801:G:H2'	22:a:2802:G:H8	1.79	0.47
22:a:2847:U:O2'	22:a:2848:G:H5'	2.14	0.47
24:c:39:LYS:HE3	24:c:56:GLY:O	2.14	0.47
26:e:24:ASN:O	26:e:28:VAL:HG23	2.14	0.47
1:A:66:A:O2'	1:A:67:C:H5'	2.14	0.47
1:A:382:A:H2'	1:A:383:A:C8	2.49	0.47
1:A:860:A:H2'	1:A:861:G:O4'	2.13	0.47
1:A:1127:G:H5'	1:A:1280:A:O2'	2.13	0.47
1:A:1143:G:O2'	1:A:1144:G:H5'	2.13	0.47
1:A:1210:C:O2'	1:A:1211:U:H5'	2.13	0.47
9:I:7:TYR:OH	9:I:9:THR:OG1	2.27	0.47
11:K:87:LYS:HB2	11:K:113:VAL:HG23	1.96	0.47
12:L:79:VAL:HG23	12:L:79:VAL:O	2.15	0.47
13:M:18:ALA:HB3	13:M:45:ILE:HD11	1.95	0.47
16:P:67:ILE:CG2	16:P:71:VAL:HG12	2.42	0.47
22:a:614:A:H3'	22:a:615:U:C5'	2.44	0.47
22:a:1108:U:OP2	22:a:1108:U:H6	1.97	0.47
22:a:2086:U:H2'	22:a:2087:G:C8	2.49	0.47
22:a:2646:C:OP2	22:a:2732:G:O2'	2.32	0.47
27:f:40:VAL:O	27:f:40:VAL:HG12	2.13	0.47
41:t:86:ARG:NH2	41:t:102:THR:OG1	2.45	0.47
54:6:22:A:H2'	54:6:23:G:C8	2.49	0.47
1:A:78:A:C2	1:A:79:G:H1'	2.50	0.47
1:A:195:A:O2'	1:A:196:A:H5'	2.14	0.47
1:A:1126:U:O2	1:A:1280:A:H5'	2.15	0.47
1:A:1202:U:C2'	1:A:1203:C:H5'	2.44	0.47
1:A:1379:G:O2'	1:A:1380:U:H5'	2.14	0.47
3:C:41:GLN:HG3	3:C:42:TYR:N	2.28	0.47
7:G:22:LEU:HD22	7:G:62:PHE:CE2	2.49	0.47
22:a:75:G:H22	22:a:111:A:H2	1.60	0.47
22:a:246:C:H2'	22:a:247:G:H5'	1.96	0.47
22:a:326:G:O6	57:a:6197:SPD:H81	2.14	0.47
22:a:1430:G:H2'	22:a:1431:A:O4'	2.14	0.47
22:a:1792:G:H5'	24:c:204:VAL:HG13	1.95	0.47
22:a:2193:G:H2'	22:a:2194:U:H6	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:2516:A:C2'	22:a:2517:C:H5'	2.44	0.47
22:a:2639:A:H2'	22:a:2640:G:O4'	2.14	0.47
24:c:66:ASP:OD1	24:c:102:ARG:NH1	2.47	0.47
43:v:28:GLY:HA2	43:v:66:LYS:HE3	1.96	0.47
1:A:847:G:O2'	1:A:848:C:H5'	2.14	0.47
1:A:1070:U:H2'	1:A:1071:C:C6	2.48	0.47
3:C:128:VAL:HG23	3:C:129:MET:N	2.28	0.47
22:a:273:G:O2'	22:a:274:C:H5'	2.15	0.47
22:a:972:A:H3'	22:a:973:A:H2'	1.94	0.47
22:a:1292:G:H2'	22:a:1293:C:H6	1.76	0.47
22:a:1385:A:O2'	22:a:1396:U:O2	2.32	0.47
31:j:38:ILE:HD11	31:j:112:PHE:CZ	2.48	0.47
1:A:154:U:H2'	1:A:155:A:H8	1.78	0.47
1:A:171:A:H2'	1:A:172:A:H8	1.75	0.47
1:A:234:C:H4'	17:Q:66:PRO:HG3	1.96	0.47
1:A:470:C:H2'	1:A:471:U:H6	1.80	0.47
1:A:590:U:OP1	8:H:31:LYS:HG2	2.14	0.47
1:A:1405:G:N7	58:A:1791:84G:N5	2.62	0.47
4:D:177:LYS:O	4:D:178:MET:HB2	2.14	0.47
16:P:34:GLU:HG3	16:P:35:ARG:N	2.29	0.47
16:P:76:LYS:HB3	16:P:76:LYS:HE3	1.77	0.47
22:a:1138:G:H2'	22:a:1139:G:O4'	2.15	0.47
28:g:84:THR:HA	28:g:133:LEU:O	2.15	0.47
41:t:88:GLU:O	41:t:89:ASP:HB2	2.15	0.47
1:A:142:G:H2'	1:A:143:A:C8	2.49	0.47
1:A:169:C:H2'	1:A:170:U:C6	2.49	0.47
1:A:246:A:C2	1:A:282:A:C5	3.03	0.47
1:A:508:U:H4'	4:D:51:TYR:CD2	2.50	0.47
1:A:684:U:O2'	1:A:685:G:H5'	2.14	0.47
4:D:64:ILE:HG22	4:D:65:TYR:CD1	2.49	0.47
4:D:95:GLU:OE1	4:D:100:ASN:ND2	2.46	0.47
7:G:87:VAL:HG13	7:G:151:PHE:O	2.15	0.47
22:a:276:U:HO2'	22:a:278:A:H8	1.58	0.47
22:a:1032:A:H1'	51:3:23:ILE:CD1	2.38	0.47
22:a:1594:U:H2'	22:a:1595:C:C6	2.50	0.47
22:a:2557:G:H2'	22:a:2558:C:C6	2.49	0.47
23:b:14:U:O2	23:b:107:G:H4'	2.15	0.47
23:b:42:C:C6	27:f:66:LEU:HB2	2.49	0.47
50:2:62:LEU:HB3	50:2:65:ALA:HB2	1.97	0.47
51:3:12:ARG:HB2	51:3:12:ARG:CZ	2.43	0.47
1:A:66:A:H2'	1:A:67:C:H5'	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:G:O2'	1:A:129:A:H5'	2.15	0.47
1:A:276:G:OP1	17:Q:14:SER:OG	2.28	0.47
1:A:986:U:H2'	1:A:987:G:C8	2.50	0.47
1:A:1141:C:O2'	1:A:1142:G:H5'	2.14	0.47
4:D:8:LYS:HG3	4:D:21:LEU:CD2	2.36	0.47
6:F:21:MET:HE1	6:F:83:ALA:CB	2.45	0.47
7:G:22:LEU:O	7:G:22:LEU:HD23	2.15	0.47
10:J:6:ILE:HD11	10:J:102:LEU:HD21	1.97	0.47
14:N:33:ASP:O	14:N:41:ARG:NH2	2.47	0.47
14:N:46:LEU:HD22	19:S:13:LEU:HD13	1.97	0.47
15:O:26:GLU:OE2	15:O:77:ARG:NH1	2.48	0.47
18:R:33:ILE:CG2	18:R:59:ILE:HD13	2.44	0.47
21:U:62:ARG:HG3	21:U:63:GLU:N	2.29	0.47
22:a:27:G:O2'	22:a:28:A:OP2	2.31	0.47
22:a:439:A:H2'	22:a:440:C:O4'	2.15	0.47
22:a:475:C:O2	22:a:479:A:N6	2.36	0.47
22:a:682:G:H5'	49:1:26:ASN:ND2	2.29	0.47
22:a:860:U:H5''	57:a:6201:SPD:H92	1.96	0.47
22:a:981:A:OP2	22:a:982:C:N4	2.36	0.47
22:a:1051:G:O2'	22:a:1052:C:H5'	2.14	0.47
22:a:1386:C:H2'	22:a:1387:A:H8	1.80	0.47
22:a:1717:A:H2'	22:a:1718:G:O4'	2.15	0.47
23:b:48:U:H2'	23:b:49:C:H6	1.80	0.47
25:d:4:LEU:HD13	25:d:29:VAL:CG1	2.44	0.47
26:e:6:LYS:HG2	26:e:121:VAL:HG12	1.96	0.47
27:f:103:LEU:HD21	27:f:130:MET:HE1	1.96	0.47
27:f:134:GLU:O	27:f:137:ILE:HG23	2.15	0.47
31:j:63:VAL:HG12	31:j:107:LEU:HD11	1.96	0.47
35:n:39:VAL:O	35:n:48:LEU:N	2.42	0.47
42:u:1:MET:HE1	42:u:55:GLU:OE2	2.14	0.47
54:6:17:C:H5'	54:6:18:U:OP2	2.15	0.47
1:A:993:G:H2'	1:A:993:G:N3	2.30	0.47
1:A:1317:C:H4'	14:N:48:LEU:CD2	2.44	0.47
5:E:26:LYS:HE2	5:E:26:LYS:HB3	1.56	0.47
6:F:11:HIS:HD2	6:F:12:PRO:HD2	1.78	0.47
7:G:72:THR:O	7:G:91:VAL:HG23	2.15	0.47
9:I:117:GLY:O	9:I:118:LEU:HD23	2.15	0.47
16:P:39:PHE:HD1	16:P:50:THR:OG1	1.97	0.47
19:S:62:VAL:HA	19:S:66:MET:CE	2.45	0.47
20:T:44:LYS:NZ	20:T:86:LEU:HB3	2.29	0.47
22:a:152:A:H2'	22:a:153:U:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:476:G:H4'	22:a:502:A:N1	2.30	0.47
22:a:748:G:C8	39:r:89:ALA:HB1	2.50	0.47
22:a:882:G:H2'	22:a:883:G:O4'	2.15	0.47
22:a:1149:G:H2'	22:a:1150:C:C6	2.49	0.47
24:c:173:THR:CG2	24:c:181:MET:HE3	2.44	0.47
27:f:136:ILE:HD12	27:f:143:TYR:CE1	2.50	0.47
30:i:29:ALA:HB3	30:i:108:MET:HE3	1.95	0.47
1:A:151:A:C2	1:A:152:A:H1'	2.50	0.47
1:A:342:C:H2'	1:A:343:U:O4'	2.15	0.47
1:A:1030:U:H5'	1:A:1031:C:H5''	1.96	0.47
22:a:146:A:H2'	22:a:147:C:C6	2.50	0.47
22:a:368:A:H2'	22:a:369:U:C5'	2.44	0.47
22:a:464:U:H2'	22:a:465:G:O4'	2.15	0.47
22:a:603:A:H4'	22:a:604:G:O5'	2.15	0.47
22:a:1328:A:H2'	22:a:1330:C:C5	2.50	0.47
22:a:2014:A:H5'	39:r:94:ASP:OD2	2.15	0.47
22:a:2286:G:H2'	22:a:2286:G:N3	2.30	0.47
22:a:2756:U:H1'	22:a:2757:A:H5''	1.97	0.47
30:i:140:LEU:HG	30:i:142:ILE:HG13	1.97	0.47
34:m:72:ASP:O	34:m:76:VAL:HG23	2.15	0.47
37:p:35:ALA:O	37:p:39:VAL:HG23	2.15	0.47
52:4:58:ASP:HB3	52:4:62:LYS:HZ1	1.80	0.47
1:A:699:C:C2'	1:A:700:G:H5'	2.45	0.47
5:E:152:MET:O	5:E:156:LYS:HG2	2.15	0.47
19:S:15:LEU:HD23	19:S:38:SER:OG	2.15	0.47
22:a:55:G:O2'	22:a:127:A:N1	2.46	0.47
22:a:279:A:OP2	22:a:279:A:H8	1.97	0.47
22:a:2469:A:H2'	22:a:2470:G:O4'	2.16	0.47
33:l:74:THR:HA	33:l:88:ASN:O	2.15	0.47
45:x:8:GLU:OE1	45:x:8:GLU:HA	2.14	0.47
54:6:19:G:H4'	54:6:19:G:OP1	2.14	0.47
54:6:21:H2U:H4'	54:6:22:A:OP2	2.11	0.47
1:A:58:C:H2'	1:A:58:C:O2	2.14	0.46
1:A:454:G:N7	57:A:1667:SPD:N10	2.59	0.46
1:A:1032:G:N1	1:A:1033:G:H1'	2.30	0.46
1:A:1201:A:H4'	1:A:1202:U:H5''	1.96	0.46
2:B:81:LYS:CD	2:B:85:LEU:HD11	2.41	0.46
8:H:89:LYS:HB3	8:H:89:LYS:HE2	1.52	0.46
18:R:33:ILE:HG22	18:R:59:ILE:HD13	1.97	0.46
22:a:511:U:C3'	22:a:512:G:H5'	2.44	0.46
22:a:954:G:H5''	33:l:13:HIS:CG	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:2248:C:C2'	22:a:2249:U:H5'	2.45	0.46
24:c:79:GLU:OE2	24:c:101:ARG:NE	2.48	0.46
30:i:14:ASP:O	30:i:52:ASP:HB3	2.14	0.46
54:6:66:C:O2'	54:6:67:C:H5'	2.14	0.46
1:A:29:U:H5'	1:A:296:U:OP1	2.15	0.46
1:A:39:G:O6	1:A:547:A:H5''	2.15	0.46
1:A:94:G:H4'	1:A:95:C:O5'	2.15	0.46
1:A:120:A:H4'	1:A:121:U:OP2	2.13	0.46
1:A:269:C:H2'	1:A:270:A:H8	1.80	0.46
1:A:715:A:H2'	1:A:716:A:C8	2.50	0.46
1:A:721:G:H4'	1:A:722:G:O5'	2.15	0.46
1:A:1157:A:H4'	1:A:1158:C:C5'	2.45	0.46
1:A:1238:A:H2	1:A:1241:G:N3	2.13	0.46
1:A:1401:G:H2'	1:A:1402:4OC:O4'	2.16	0.46
12:L:32:GLY:HA3	12:L:55:VAL:CG1	2.46	0.46
12:L:32:GLY:HA3	12:L:55:VAL:HG12	1.97	0.46
22:a:52:A:H2'	22:a:53:A:C8	2.50	0.46
22:a:1703:G:H2'	22:a:1704:C:C6	2.51	0.46
22:a:2070:A:H2'	22:a:2071:A:O4'	2.15	0.46
22:a:2489:U:O2'	22:a:2490:G:H5'	2.15	0.46
25:d:97:SER:OG	25:d:99:GLU:CD	2.58	0.46
28:g:35:ARG:NE	28:g:71:LEU:HD13	2.30	0.46
1:A:720:C:H2'	1:A:721:G:C8	2.50	0.46
1:A:1270:G:HO2'	1:A:1313:U:HO2'	1.63	0.46
1:A:1496:C:H2'	1:A:1497:G:O4'	2.15	0.46
4:D:179:GLU:C	4:D:179:GLU:OE1	2.58	0.46
19:S:5:LEU:HD21	52:4:63:ARG:NH1	2.30	0.46
22:a:78:U:H2'	22:a:79:C:C6	2.50	0.46
22:a:504:A:O3'	57:a:6194:SPD:N1	2.49	0.46
22:a:832:U:H2'	22:a:833:A:C8	2.50	0.46
22:a:2316:G:H2'	22:a:2317:A:H8	1.81	0.46
22:a:2556:C:H2'	22:a:2557:G:O4'	2.16	0.46
22:a:2674:G:H4'	31:j:30:ARG:HD2	1.97	0.46
23:b:39:A:H2'	23:b:40:U:C6	2.51	0.46
31:j:10:VAL:HG12	31:j:12:ASP:OD1	2.16	0.46
31:j:107:LEU:HB2	31:j:116:ILE:HD11	1.98	0.46
32:k:2:ARG:HB2	32:k:5:THR:HG23	1.96	0.46
34:m:36:THR:OG1	34:m:37:THR:N	2.49	0.46
41:t:99:ASN:CG	41:t:101:GLU:HB2	2.40	0.46
43:v:34:GLY:N	43:v:61:ALA:O	2.32	0.46
1:A:263:A:H2'	1:A:264:C:C5	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1317:C:H4'	14:N:48:LEU:HD21	1.97	0.46
1:A:1404:C:H2'	1:A:1405:G:C8	2.50	0.46
3:C:50:ALA:HB1	3:C:76:VAL:HG23	1.97	0.46
3:C:72:ARG:HB3	3:C:75:ILE:HG22	1.97	0.46
13:M:47:GLU:O	13:M:48:LEU:HD12	2.15	0.46
16:P:5:ARG:NH2	16:P:23:ASP:O	2.48	0.46
17:Q:14:SER:HA	17:Q:55:ILE:HD11	1.97	0.46
22:a:686:U:O4	49:1:12:ARG:NH1	2.46	0.46
22:a:2572:A:N7	25:d:150:MEQ:HB2	2.30	0.46
24:c:125:LYS:HG2	24:c:128:ASN:ND2	2.28	0.46
27:f:16:LEU:HD13	27:f:29:PRO:HD2	1.98	0.46
31:j:66:LYS:HE3	31:j:66:LYS:HB3	1.55	0.46
47:z:3:VAL:HG22	47:z:4:GLN:N	2.30	0.46
1:A:56:U:H2'	1:A:57:G:H8	1.79	0.46
1:A:215:C:O2'	1:A:216:U:H5'	2.15	0.46
1:A:399:G:H2'	1:A:400:C:C6	2.51	0.46
1:A:635:A:H2'	1:A:636:U:H6	1.77	0.46
4:D:190:ASP:OD1	4:D:190:ASP:N	2.47	0.46
10:J:90:LEU:CD2	10:J:92:LEU:HD21	2.45	0.46
12:L:87:VAL:HG22	12:L:96:HIS:CE1	2.51	0.46
13:M:37:ALA:HB3	13:M:39:ILE:HD12	1.98	0.46
22:a:503:A:H5'	22:a:505:A:OP1	2.16	0.46
22:a:558:U:OP1	30:i:113:PRO:HD2	2.16	0.46
22:a:582:A:H2'	22:a:583:G:C8	2.50	0.46
22:a:1520:U:O2'	22:a:1521:G:H5'	2.15	0.46
22:a:1682:G:H2'	22:a:1683:U:C6	2.51	0.46
22:a:1961:C:C2'	22:a:1962:5MC:H5'	2.44	0.46
22:a:2627:G:O2'	22:a:2781:A:N1	2.30	0.46
27:f:32:GLU:HB3	27:f:157:THR:O	2.14	0.46
31:j:102:PRO:HB2	31:j:123:LEU:HD11	1.98	0.46
35:n:83:LEU:HD11	35:n:113:ALA:O	2.16	0.46
54:6:48:U:HO2'	54:6:49:C:H5	1.64	0.46
1:A:88:U:O2	1:A:88:U:H2'	2.16	0.46
1:A:154:U:H2'	1:A:155:A:C8	2.50	0.46
1:A:310:G:H5''	16:P:31:ARG:HB2	1.96	0.46
1:A:389:A:H3'	1:A:390:U:H6	1.81	0.46
1:A:433:G:C2'	1:A:434:U:H5'	2.45	0.46
1:A:607:A:H2'	1:A:608:A:C8	2.51	0.46
1:A:1138:G:H3'	1:A:1138:G:N3	2.30	0.46
1:A:1187:G:N3	14:N:100:SER:OG	2.42	0.46
1:A:1315:U:H2'	1:A:1316:G:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:6:MET:HE3	2:B:44:GLU:OE1	2.16	0.46
2:B:99:GLY:N	2:B:175:GLU:OE2	2.40	0.46
3:C:92:ALA:HB2	3:C:99:ALA:HB3	1.97	0.46
7:G:75:VAL:HG23	7:G:145:ALA:HA	1.96	0.46
10:J:5:ARG:NH1	10:J:7:ARG:CG	2.78	0.46
22:a:469:G:O6	49:1:37:LYS:HE3	2.15	0.46
22:a:980:A:C5	22:a:1136:G:H5''	2.51	0.46
22:a:1340:U:OP1	40:s:84:TYR:OH	2.31	0.46
22:a:1469:A:H2'	22:a:1470:A:H8	1.74	0.46
22:a:1632:A:H2'	22:a:1633:G:C8	2.51	0.46
22:a:1666:G:O2'	22:a:1667:G:H5'	2.16	0.46
22:a:1668:A:H4'	22:a:1669:A:O5'	2.16	0.46
27:f:38:MET:HB2	27:f:87:CYS:SG	2.56	0.46
28:g:126:PRO:HD3	28:g:132:VAL:HG22	1.97	0.46
42:u:11:GLU:O	42:u:12:GLN:HG2	2.16	0.46
1:A:294:U:OP1	1:A:610:U:O2'	2.27	0.46
1:A:481:G:O2'	1:A:483:C:N4	2.44	0.46
1:A:673:A:H2'	1:A:674:G:H8	1.78	0.46
1:A:875:U:O2'	8:H:15:ARG:HD2	2.16	0.46
1:A:1363:A:O2'	1:A:1365:G:N7	2.44	0.46
3:C:36:ASP:OD1	3:C:59:ARG:NH2	2.47	0.46
4:D:125:VAL:HG13	4:D:143:VAL:HG22	1.97	0.46
4:D:188:ARG:HA	4:D:188:ARG:HE	1.81	0.46
5:E:15:LEU:HD12	5:E:37:THR:HG22	1.98	0.46
7:G:2:PRO:HG3	7:G:7:ILE:HD13	1.97	0.46
21:U:39:GLU:OE2	21:U:44:GLU:HG2	2.16	0.46
22:a:505:A:OP2	57:a:6194:SPD:H22	2.16	0.46
22:a:814:C:H1'	22:a:1225:G:N2	2.31	0.46
22:a:886:A:H1'	22:a:890:C:N4	2.31	0.46
22:a:1180:U:H2'	22:a:1181:U:O4'	2.16	0.46
22:a:1712:U:OP2	22:a:1713:A:O2'	2.25	0.46
22:a:1877:A:H2'	22:a:1878:G:O4'	2.15	0.46
22:a:2266:A:H4'	22:a:2267:A:O5'	2.16	0.46
28:g:60:ASP:O	28:g:62:TRP:N	2.48	0.46
42:u:59:GLU:HG3	42:u:60:VAL:H	1.81	0.46
1:A:77:A:H2'	1:A:78:A:H8	1.80	0.46
1:A:167:A:H2'	1:A:168:G:C8	2.49	0.46
1:A:1337:G:H4'	1:A:1338:G:OP1	2.16	0.46
5:E:23:LYS:HE2	5:E:23:LYS:HB2	1.61	0.46
5:E:131:THR:O	5:E:131:THR:HG23	2.15	0.46
6:F:88:MET:HE3	6:F:90:MET:HE2	1.94	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:72:THR:H	7:G:142:HIS:HE1	1.63	0.46
10:J:50:THR:OG1	10:J:64:GLN:OE1	2.27	0.46
22:a:82:U:H2'	22:a:83:A:O4'	2.16	0.46
22:a:569:U:H5''	22:a:821:A:C2	2.51	0.46
22:a:819:A:H5''	22:a:973:A:N1	2.31	0.46
22:a:1347:A:H2'	22:a:1348:C:O4'	2.15	0.46
22:a:1641:A:H2'	22:a:1642:G:O4'	2.16	0.46
25:d:48:ILE:HG23	25:d:84:LEU:HD11	1.98	0.46
32:k:20:GLY:O	32:k:21:ARG:HD3	2.15	0.46
41:t:71:ALA:HB3	41:t:80:ALA:HB1	1.97	0.46
42:u:2:PHE:CE2	42:u:55:GLU:HG3	2.50	0.46
52:4:13:THR:CG2	52:4:21:VAL:HG13	2.46	0.46
1:A:402:G:H5'	1:A:621:A:H1'	1.98	0.46
1:A:466:A:H4'	1:A:467:U:H5	1.80	0.46
1:A:633:G:H2'	1:A:634:C:H6	1.80	0.46
1:A:653:U:O4'	8:H:56:LYS:HE3	2.15	0.46
1:A:857:C:H2'	1:A:858:G:O4'	2.16	0.46
1:A:1035:A:C4'	1:A:1036:A:OP1	2.64	0.46
3:C:19:ASN:O	3:C:56:VAL:HG13	2.15	0.46
4:D:95:GLU:OE1	4:D:95:GLU:HA	2.15	0.46
4:D:105:MET:HG2	4:D:173:VAL:HG22	1.97	0.46
5:E:72:ILE:HD13	5:E:145:GLU:HB2	1.97	0.46
11:K:115:PRO:O	11:K:116:ILE:HD13	2.15	0.46
22:a:1721:G:O2'	22:a:1739:A:N6	2.43	0.46
22:a:2748:A:H5'	28:g:4:VAL:HG21	1.96	0.46
25:d:4:LEU:CD1	25:d:29:VAL:HG11	2.46	0.46
25:d:181:ASP:HB3	25:d:186:LEU:HB2	1.98	0.46
42:u:42:LEU:HB3	42:u:47:VAL:HG21	1.97	0.46
53:5:34:G:H2'	53:5:35:A:C8	2.51	0.46
1:A:1161:C:H2'	1:A:1162:C:H6	1.81	0.46
13:M:51:GLY:O	13:M:55:THR:HG23	2.16	0.46
14:N:33:ASP:HB3	14:N:36:ALA:HB2	1.97	0.46
21:U:21:ARG:HA	21:U:21:ARG:HD2	1.70	0.46
22:a:28:A:H1'	22:a:513:A:C2	2.51	0.46
22:a:49:A:H5''	22:a:51:G:O4'	2.16	0.46
22:a:360:U:O2'	22:a:361:G:O5'	2.31	0.46
22:a:400:G:O6	44:w:57:ARG:NH2	2.49	0.46
22:a:1654:A:C1'	22:a:2823:A:H5'	2.45	0.46
26:e:175:ILE:HG13	26:e:175:ILE:O	2.15	0.46
37:p:105:ALA:HB1	38:q:40:MET:HE1	1.98	0.46
38:q:64:VAL:HG22	38:q:95:ASP:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:5:37:MIA:H121	53:5:38:A:N1	2.31	0.46
1:A:933:G:OP2	7:G:3:ARG:HB2	2.15	0.45
1:A:1051:C:H2'	1:A:1052:U:C6	2.51	0.45
1:A:1085:U:H3'	1:A:1086:U:C5	2.52	0.45
1:A:1128:C:O2'	1:A:1129:C:H5'	2.15	0.45
7:G:48:GLU:O	7:G:52:GLN:HG2	2.15	0.45
7:G:95:ARG:HG3	7:G:95:ARG:HH11	1.81	0.45
10:J:7:ARG:HD3	10:J:75:ASP:OD1	2.16	0.45
15:O:12:VAL:HG11	15:O:22:THR:HG22	1.97	0.45
22:a:978:G:O2'	22:a:979:A:H5'	2.16	0.45
22:a:1446:C:H2'	22:a:1447:C:C6	2.51	0.45
22:a:2366:A:H4'	43:v:62:LYS:HE3	1.97	0.45
26:e:106:LYS:CG	26:e:200:LEU:HD13	2.45	0.45
31:j:76:VAL:HG13	36:o:73:VAL:HB	1.98	0.45
32:k:1:MET:O	32:k:1:MET:HG2	2.15	0.45
33:l:136:MET:O	33:l:136:MET:HG2	2.15	0.45
34:m:54:LEU:HD21	34:m:65:LEU:HB3	1.98	0.45
46:y:24:LEU:HD11	46:y:54:MET:CE	2.46	0.45
53:5:41:C:C2'	53:5:42:C:H5'	2.46	0.45
53:5:59:U:C2'	53:5:60:U:H5'	2.45	0.45
1:A:447:G:H1'	1:A:487:A:H61	1.81	0.45
1:A:981:U:OP1	14:N:6:MET:HE1	2.16	0.45
22:a:278:A:H2	22:a:279:A:N7	2.15	0.45
22:a:1713:A:C6	22:a:1716:U:H1'	2.51	0.45
22:a:2251:OMG:HM23	22:a:2251:OMG:H1'	1.63	0.45
22:a:2544:G:H5'	22:a:2645:G:C2	2.51	0.45
27:f:38:MET:CE	27:f:57:LEU:HD13	2.44	0.45
33:l:21:ALA:HB1	33:l:100:LYS:HB2	1.98	0.45
35:n:2:ASP:HB3	35:n:5:SER:OG	2.17	0.45
44:w:3:ARG:C	44:w:33:LEU:HD11	2.41	0.45
1:A:151:A:H2'	1:A:152:A:O4'	2.17	0.45
1:A:178:C:H2'	1:A:179:A:H8	1.81	0.45
1:A:409:U:H2'	1:A:410:G:O4'	2.16	0.45
1:A:918:A:H2'	1:A:919:A:O4'	2.15	0.45
1:A:1056:U:H5'	3:C:163:ALA:HB3	1.97	0.45
1:A:1455:G:C2'	1:A:1456:A:H5'	2.46	0.45
13:M:83:LEU:CD2	19:S:66:MET:HG2	2.45	0.45
22:a:277:G:H4'	22:a:278:A:O5'	2.16	0.45
22:a:394:C:O2'	22:a:395:U:H5'	2.16	0.45
22:a:479:A:H4'	22:a:480:A:OP1	2.15	0.45
22:a:1182:G:H2'	22:a:1183:U:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:1636:U:H2'	22:a:1637:A:C8	2.51	0.45
22:a:2247:A:H2'	22:a:2248:C:C6	2.50	0.45
22:a:2400:G:O2'	22:a:2401:U:H5'	2.16	0.45
23:b:90:C:C5'	33:l:18:ARG:HG2	2.45	0.45
24:c:259:SER:O	24:c:259:SER:OG	2.28	0.45
27:f:124:GLY:HA2	27:f:163:ASP:OD2	2.17	0.45
53:5:10:G:H2'	53:5:11:C:C6	2.52	0.45
1:A:1176:A:H2'	1:A:1177:G:C8	2.52	0.45
4:D:129:VAL:CG2	4:D:146:ARG:HD3	2.46	0.45
8:H:27:MET:HE2	8:H:27:MET:HB3	1.86	0.45
14:N:38:ASP:HB3	52:4:66:ILE:O	2.16	0.45
18:R:22:ASP:OD1	18:R:24:LYS:HB2	2.17	0.45
21:U:40:LYS:HE3	21:U:42:THR:CG2	2.46	0.45
22:a:69:C:O2	22:a:73:A:O2'	2.33	0.45
22:a:749:A:H4'	22:a:1271:G:N3	2.31	0.45
22:a:2581:G:OP2	22:a:2581:G:N2	2.44	0.45
22:a:2852:G:H2'	22:a:2853:C:O4'	2.16	0.45
30:i:60:ASP:OD1	30:i:126:ALA:O	2.35	0.45
34:m:69:ARG:C	34:m:70:THR:HG23	2.42	0.45
1:A:922:G:H2'	1:A:923:A:C8	2.51	0.45
1:A:1085:U:H3'	1:A:1086:U:C6	2.51	0.45
2:B:187:VAL:CG1	2:B:191:SER:HB2	2.47	0.45
7:G:16:PRO:HB3	9:I:46:MET:HG3	1.98	0.45
15:O:48:LYS:HD3	15:O:48:LYS:HA	1.67	0.45
22:a:1677:A:H2'	22:a:1678:A:C8	2.52	0.45
22:a:2230:G:H2'	22:a:2231:U:C6	2.52	0.45
26:e:119:ILE:HD11	26:e:185:LYS:CG	2.47	0.45
26:e:170:ARG:HD2	26:e:174:GLY:O	2.16	0.45
32:k:92:LEU:HD21	32:k:106:GLU:O	2.17	0.45
37:p:11:ARG:O	37:p:15:LYS:HG3	2.17	0.45
1:A:175:C:O2'	1:A:176:C:H5'	2.17	0.45
1:A:355:C:O2'	1:A:388:G:N3	2.46	0.45
1:A:381:C:H2'	1:A:382:A:O4'	2.16	0.45
1:A:428:G:OP2	4:D:7:PRO:HG2	2.16	0.45
1:A:992:U:C4'	1:A:993:G:H5'	2.45	0.45
1:A:1158:C:H3'	1:A:1158:C:O2	2.17	0.45
7:G:111:ARG:HG2	7:G:111:ARG:HH11	1.82	0.45
13:M:33:ILE:HD13	13:M:60:VAL:HG22	1.98	0.45
22:a:885:C:H2'	22:a:886:A:H5'	1.99	0.45
22:a:1858:A:H2'	22:a:1859:U:O4'	2.17	0.45
23:b:24:G:N7	23:b:56:G:H2'	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:f:149:VAL:HG23	27:f:149:VAL:O	2.16	0.45
44:w:7:VAL:HG23	44:w:51:VAL:CG1	2.45	0.45
45:x:19:LEU:HD12	45:x:19:LEU:HA	1.76	0.45
54:6:21:H2U:H61	54:6:21:H2U:C5'	2.46	0.45
54:6:76:C:O3'	54:6:77:A:H4'	2.14	0.45
1:A:492:C:H2'	1:A:493:A:C8	2.52	0.45
1:A:555:U:H2'	1:A:556:C:H6	1.80	0.45
1:A:594:U:H2'	1:A:595:A:O4'	2.17	0.45
1:A:1157:A:C2	1:A:1181:G:C4	3.05	0.45
2:B:21:ARG:HD2	2:B:22:TYR:CZ	2.52	0.45
6:F:88:MET:HB2	18:R:64:TYR:HE2	1.81	0.45
9:I:101:ALA:HB1	9:I:103:PHE:CZ	2.51	0.45
15:O:55:GLY:O	15:O:59:MET:HG3	2.17	0.45
21:U:40:LYS:HB3	21:U:42:THR:HG22	1.97	0.45
22:a:811:U:H2'	32:k:21:ARG:HA	1.98	0.45
22:a:876:C:H2'	22:a:877:A:O4'	2.17	0.45
22:a:1281:G:H2'	22:a:1282:U:C6	2.52	0.45
22:a:1323:C:C2'	22:a:1324:G:H5'	2.47	0.45
22:a:1351:C:H2'	22:a:1352:U:O4'	2.16	0.45
22:a:1693:U:H4'	22:a:1694:C:OP2	2.15	0.45
22:a:2849:U:H4'	22:a:2868:A:C2	2.51	0.45
24:c:145:GLU:HG2	24:c:151:GLY:C	2.40	0.45
27:f:61:SER:HB2	27:f:91:LEU:HD21	1.99	0.45
30:i:26:GLY:O	30:i:30:THR:HG23	2.16	0.45
39:r:82:MET:HB2	39:r:98:LYS:HB2	1.98	0.45
39:r:83:LYS:CG	39:r:95:ARG:HD3	2.40	0.45
46:y:12:SER:HB2	46:y:32:ILE:HD11	1.99	0.45
48:0:11:LEU:HD21	48:0:34:LEU:HD23	1.99	0.45
1:A:325:A:C8	57:A:1668:SPD:H91	2.51	0.45
1:A:427:U:OP1	4:D:13:ARG:NH1	2.39	0.45
1:A:542:G:H5'	4:D:39:GLY:HA3	1.99	0.45
1:A:674:G:H2'	1:A:675:A:H8	1.81	0.45
1:A:721:G:H4'	1:A:722:G:O4'	2.17	0.45
2:B:22:TYR:O	2:B:190:ASN:HB2	2.16	0.45
9:I:94:LEU:O	9:I:98:LEU:HG	2.17	0.45
19:S:27:ASP:C	19:S:28:LYS:HD2	2.42	0.45
22:a:17:G:H2'	22:a:18:U:C6	2.52	0.45
22:a:1443:U:H2'	22:a:1444:G:H8	1.82	0.45
22:a:1597:A:H5''	22:a:1598:A:H5'	1.99	0.45
22:a:2529:G:H5'	28:g:175:LYS:CB	2.46	0.45
22:a:2583:G:O2'	53:5:76:A:N1	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:c:222:GLY:HA2	24:c:225:MET:HG3	1.99	0.45
25:d:25:THR:HG21	25:d:193:VAL:HG22	1.98	0.45
32:k:74:THR:HG22	32:k:75:ALA:N	2.32	0.45
45:x:18:LEU:HB2	45:x:53:VAL:HG11	1.98	0.45
1:A:451:A:N6	1:A:481:G:H5'	2.27	0.45
1:A:1513:A:H2'	1:A:1514:G:C8	2.51	0.45
3:C:88:ARG:HD2	3:C:99:ALA:O	2.16	0.45
5:E:10:GLU:OE1	5:E:10:GLU:HA	2.16	0.45
7:G:69:VAL:HG12	7:G:69:VAL:O	2.16	0.45
21:U:4:ILE:O	21:U:4:ILE:HG22	2.16	0.45
22:a:43:G:O2'	22:a:44:A:H5'	2.17	0.45
22:a:196:A:H2'	22:a:196:A:N3	2.32	0.45
22:a:250:G:H2'	22:a:251:A:C8	2.52	0.45
22:a:274:C:H2'	22:a:275:C:O4'	2.17	0.45
22:a:810:U:C4	32:k:29:LYS:O	2.70	0.45
22:a:812:C:O2'	37:p:13:ARG:NH2	2.49	0.45
22:a:896:A:H8	22:a:897:C:O4'	1.98	0.45
22:a:1230:A:H2'	22:a:1231:U:O4'	2.17	0.45
26:e:58:LYS:HG3	26:e:71:GLY:HA2	1.98	0.45
53:5:9:A:C5'	53:5:46:G7M:H1'	2.27	0.45
1:A:2:A:H1'	1:A:613:C:HO2'	1.79	0.45
1:A:147:G:H2'	1:A:148:G:H8	1.81	0.45
1:A:191:G:H2'	1:A:192:A:H8	1.82	0.45
1:A:622:A:H2'	1:A:623:C:H5'	1.99	0.45
1:A:1098:C:O2'	21:U:71:TYR:O	2.34	0.45
2:B:20:THR:HG22	2:B:39:HIS:CD2	2.52	0.45
14:N:10:GLU:HG3	14:N:63:ARG:HD2	1.99	0.45
14:N:23:LYS:HZ3	14:N:26:GLU:CD	2.24	0.45
22:a:620:G:H4'	22:a:621:A:O5'	2.16	0.45
22:a:807:U:H1'	22:a:2445:2MG:H5'	1.99	0.45
22:a:1410:G:H2'	22:a:1411:U:C6	2.51	0.45
22:a:2389:G:H5''	22:a:2390:U:O4'	2.16	0.45
22:a:2494:G:HO2'	33:l:79:ALA:HA	1.79	0.45
22:a:2809:A:H2'	22:a:2810:A:C8	2.52	0.45
26:e:145:ASP:HB3	26:e:184:ASP:OD1	2.17	0.45
27:f:150:ARG:HG2	27:f:150:ARG:HH11	1.82	0.45
28:g:76:VAL:HA	28:g:79:VAL:HG22	1.99	0.45
28:g:88:GLN:C	28:g:89:LEU:HD12	2.42	0.45
28:g:124:GLU:O	28:g:126:PRO:HD3	2.17	0.45
30:i:73:VAL:CG1	30:i:86:GLN:HB2	2.47	0.45
54:6:45:A:H2'	54:6:46:G:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:U:H2'	1:A:21:G:O4'	2.17	0.44
1:A:182:A:C4	1:A:184:G:C8	3.04	0.44
1:A:925:G:H1'	1:A:1502:A:C4	2.51	0.44
3:C:179:ARG:CD	3:C:206:GLU:HG2	2.47	0.44
7:G:86:GLN:O	7:G:148:ASN:HB3	2.16	0.44
9:I:7:TYR:HE1	9:I:18:ARG:HB3	1.82	0.44
10:J:10:LEU:CD2	10:J:98:VAL:HG22	2.47	0.44
22:a:128:C:H2'	22:a:129:C:H6	1.82	0.44
22:a:493:G:H2'	22:a:494:G:O4'	2.16	0.44
22:a:494:G:H4'	39:r:6:LYS:HB2	1.99	0.44
22:a:612:G:H2'	22:a:614:A:OP2	2.17	0.44
22:a:1283:G:H1'	22:a:1329:U:O2	2.17	0.44
22:a:1323:C:H2'	22:a:1324:G:H5'	1.98	0.44
22:a:1727:C:H2'	22:a:1728:C:H6	1.81	0.44
22:a:2305:U:O2	27:f:151:GLY:HA3	2.17	0.44
23:b:21:G:O2'	23:b:22:U:H5'	2.17	0.44
32:k:132:ARG:HG3	32:k:142:ILE:CD1	2.46	0.44
40:s:30:ILE:HD13	40:s:93:LEU:HD23	1.97	0.44
45:x:14:LEU:CD1	45:x:60:LYS:HE3	2.47	0.44
1:A:296:U:O2'	1:A:556:C:O2	2.33	0.44
1:A:864:A:H4'	5:E:90:THR:HG23	1.99	0.44
1:A:908:A:H2'	1:A:909:A:H8	1.80	0.44
1:A:954:G:H2'	1:A:955:U:C6	2.52	0.44
1:A:1036:A:C2'	1:A:1037:C:H5'	2.48	0.44
2:B:66:LYS:HG2	2:B:90:PHE:HE1	1.81	0.44
3:C:16:LYS:HE2	3:C:182:ILE:O	2.17	0.44
3:C:121:THR:HG21	3:C:188:GLU:O	2.17	0.44
16:P:4:ILE:HG12	16:P:21:VAL:CG2	2.33	0.44
20:T:27:MET:HG2	20:T:31:PHE:CE2	2.51	0.44
22:a:1851:U:H2'	22:a:1852:U:O4'	2.17	0.44
22:a:2031:A:C6	22:a:2498:OMC:H1'	2.52	0.44
22:a:2311:A:H1'	27:f:85:ILE:HD12	1.98	0.44
27:f:128:TYR:CE2	27:f:130:MET:HB3	2.52	0.44
28:g:90:VAL:HG12	28:g:91:GLY:N	2.33	0.44
41:t:39:ILE:HG22	41:t:40:ASN:N	2.31	0.44
1:A:218:U:H2'	1:A:219:U:C6	2.53	0.44
1:A:259:G:O2'	1:A:260:G:H5'	2.17	0.44
1:A:339:C:OP2	31:j:98:ARG:HD3	2.18	0.44
1:A:560:A:H5'	1:A:566:G:N2	2.31	0.44
1:A:687:A:C2	1:A:704:A:C5	3.05	0.44
1:A:1169:A:H2'	1:A:1170:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:121:THR:HG23	3:C:189:ALA:CA	2.46	0.44
6:F:42:TRP:CZ2	6:F:102:MET:HG3	2.52	0.44
8:H:79:SER:HB3	8:H:125:ILE:O	2.18	0.44
13:M:13:LYS:HD3	13:M:17:ILE:HG22	1.99	0.44
22:a:133:U:C2'	22:a:134:G:H5'	2.48	0.44
22:a:499:U:H2'	22:a:500:G:O4'	2.16	0.44
22:a:1301:A:H2'	22:a:1301:A:N3	2.33	0.44
22:a:2236:U:H2'	22:a:2237:G:O4'	2.18	0.44
22:a:2455:G:H2'	22:a:2456:C:H6	1.82	0.44
22:a:2613:U:C5'	57:a:6203:SPD:H91	2.47	0.44
25:d:84:LEU:HD22	25:d:88:GLU:HB3	1.99	0.44
27:f:17:MET:CE	27:f:22:TYR:HB2	2.47	0.44
27:f:50:LEU:HD11	27:f:67:ILE:HD12	1.98	0.44
28:g:26:ILE:O	28:g:79:VAL:HG11	2.17	0.44
32:k:73:ILE:HD12	32:k:106:GLU:OE1	2.18	0.44
42:u:35:GLU:HG3	42:u:36:ALA:N	2.33	0.44
53:5:74:C:H2'	53:5:75:C:H5'	1.97	0.44
1:A:32:A:H2'	1:A:33:A:C8	2.53	0.44
1:A:1085:U:H4'	1:A:1086:U:OP2	2.17	0.44
21:U:58:LYS:HD2	21:U:59:LYS:HD3	1.99	0.44
22:a:136:G:C2'	22:a:137:U:H5'	2.48	0.44
22:a:549:G:H2'	22:a:550:C:C6	2.53	0.44
22:a:593:U:H2'	22:a:594:U:H6	1.81	0.44
22:a:2700:A:H2'	22:a:2701:U:H6	1.82	0.44
27:f:36:LEU:HD12	27:f:61:SER:HB3	1.98	0.44
50:2:52:LYS:HA	50:2:55:LEU:HD12	1.99	0.44
1:A:517:G:H4'	1:A:519:C:C2	2.52	0.44
1:A:711:G:O2'	1:A:712:A:H5'	2.17	0.44
1:A:1034:G:O6	1:A:1035:A:N6	2.50	0.44
1:A:1382:C:H4'	7:G:79:ARG:HH21	1.83	0.44
3:C:79:LYS:HG2	3:C:82:GLU:HG3	1.98	0.44
3:C:148:GLY:HA2	3:C:170:GLU:O	2.17	0.44
9:I:39:PHE:CE2	9:I:48:VAL:HG21	2.53	0.44
22:a:26:G:H2'	22:a:27:G:O4'	2.18	0.44
22:a:242:G:H5''	50:2:64:TYR:CE2	2.53	0.44
22:a:363:G:H2'	22:a:364:C:H6	1.81	0.44
22:a:542:C:O2'	22:a:543:G:H5'	2.17	0.44
22:a:671:C:C6	32:k:42:SER:HB2	2.53	0.44
22:a:813:U:H2'	22:a:814:C:H6	1.83	0.44
22:a:828:U:H2'	22:a:829:A:C8	2.53	0.44
22:a:1267:U:O2	22:a:1267:U:H2'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:e:48:THR:O	26:e:52:VAL:HG23	2.17	0.44
35:n:62:LEU:HD13	35:n:70:ALA:CB	2.47	0.44
1:A:106:C:H2'	1:A:107:G:O4'	2.16	0.44
1:A:352:C:H4'	1:A:354:G:OP1	2.17	0.44
1:A:821:G:H2'	1:A:822:U:C6	2.53	0.44
1:A:945:G:C2	1:A:946:A:C8	3.06	0.44
1:A:1143:G:H2'	1:A:1144:G:H8	1.82	0.44
11:K:90:GLY:O	11:K:93:ARG:HG3	2.17	0.44
16:P:21:VAL:HG12	16:P:33:ILE:HB	1.98	0.44
18:R:21:ILE:HD12	18:R:54:GLN:CB	2.48	0.44
18:R:56:ALA:O	18:R:60:LYS:HG3	2.17	0.44
20:T:5:LYS:HE3	20:T:5:LYS:HB3	1.78	0.44
22:a:172:A:H2'	22:a:173:A:H8	1.82	0.44
22:a:1509:A:O2'	22:a:1510:G:P	2.76	0.44
22:a:1935:G:H1'	22:a:1964:G:N2	2.32	0.44
22:a:2246:G:H2'	22:a:2247:A:C8	2.52	0.44
22:a:2303:G:O2'	22:a:2304:G:H5'	2.17	0.44
22:a:2428:G:H5''	22:a:2429:G:O5'	2.18	0.44
22:a:2438:U:O3'	22:a:2439:A:H3'	2.18	0.44
27:f:116:GLY:HA3	27:f:178:ARG:HB3	1.99	0.44
28:g:138:LYS:O	28:g:141:ILE:HG22	2.18	0.44
32:k:23:ILE:HG12	38:q:82:HIS:CD2	2.53	0.44
43:v:32:LEU:HA	43:v:64:ASP:OD1	2.17	0.44
50:2:26:HIS:NE2	50:2:48:ALA:HB2	2.32	0.44
1:A:22:G:O2'	1:A:913:A:N1	2.48	0.44
1:A:33:A:H2'	1:A:34:C:H6	1.83	0.44
1:A:924:C:O2'	1:A:1502:A:N1	2.45	0.44
3:C:191:THR:CG2	3:C:196:ILE:HD13	2.47	0.44
7:G:23:LEU:HD11	7:G:47:LEU:HD11	1.98	0.44
10:J:19:ASP:OD1	10:J:72:ARG:NH1	2.50	0.44
20:T:27:MET:CG	20:T:31:PHE:HE2	2.31	0.44
22:a:588:U:H2'	22:a:589:U:C6	2.52	0.44
22:a:1185:G:H5''	22:a:1186:G:OP1	2.17	0.44
22:a:1747:U:H2'	22:a:1748:C:C6	2.53	0.44
22:a:1833:C:O2'	22:a:1969:A:N1	2.48	0.44
22:a:1847:A:OP2	22:a:1847:A:H8	2.01	0.44
22:a:1908:C:O2'	54:6:12:G:H5''	2.17	0.44
22:a:1954:G:O2'	22:a:1956:U:O4	2.30	0.44
22:a:2195:U:O2'	22:a:2196:C:H5'	2.17	0.44
22:a:2267:A:H5''	22:a:2268:A:H5'	1.98	0.44
23:b:7:G:O2'	23:b:8:C:H5'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:c:246:THR:HG23	24:c:250:VAL:O	2.17	0.44
27:f:13:VAL:O	27:f:17:MET:HG3	2.17	0.44
35:n:79:ALA:HB2	35:n:110:ALA:HA	1.99	0.44
39:r:23:LEU:HD22	47:z:24:ALA:HB2	1.99	0.44
47:z:54:VAL:HG23	47:z:55:ILE:HG23	1.99	0.44
52:4:56:ARG:HD2	52:4:56:ARG:HA	1.79	0.44
54:6:55:5MU:O2'	54:6:56:PSU:H5''	2.18	0.44
1:A:636:U:H2'	1:A:637:C:H6	1.83	0.44
1:A:636:U:O2'	1:A:637:C:H5'	2.18	0.44
1:A:640:A:C2'	1:A:641:U:H5'	2.48	0.44
1:A:676:A:H5''	11:K:115:PRO:HB3	1.99	0.44
1:A:1144:G:N2	1:A:1146:A:H62	2.15	0.44
6:F:52:ASN:O	6:F:53:LYS:HB2	2.18	0.44
7:G:76:LYS:HE3	7:G:76:LYS:HB3	1.69	0.44
16:P:51:ARG:O	16:P:52:LEU:HD23	2.18	0.44
18:R:21:ILE:O	18:R:21:ILE:CG2	2.66	0.44
22:a:153:U:H2'	22:a:154:U:C6	2.53	0.44
22:a:222:A:N6	22:a:232:G:H1'	2.33	0.44
22:a:347:A:H2'	22:a:348:A:C8	2.52	0.44
22:a:637:A:H4'	22:a:638:G:O5'	2.17	0.44
22:a:1526:C:H2'	22:a:1527:G:O4'	2.18	0.44
26:e:46:GLN:O	26:e:88:ARG:NH2	2.49	0.44
27:f:103:LEU:HD21	27:f:130:MET:CE	2.48	0.44
27:f:104:ILE:HD11	27:f:175:PHE:CD1	2.53	0.44
33:l:8:LYS:HG3	33:l:9:PHE:CD2	2.52	0.44
41:t:41:LEU:HD23	41:t:62:GLU:HG3	1.99	0.44
51:3:4:ARG:O	51:3:37:GLN:HA	2.17	0.44
1:A:51:A:N7	1:A:114:U:O2'	2.48	0.44
1:A:356:A:C2'	1:A:357:G:H5'	2.48	0.44
1:A:881:G:P	12:L:9:ARG:HH22	2.40	0.44
1:A:1019:A:H2'	1:A:1020:G:O4'	2.18	0.44
1:A:1226:C:H4'	1:A:1227:A:OP1	2.18	0.44
2:B:97:LEU:N	2:B:100:MET:HE3	2.33	0.44
4:D:144:SER:HB3	4:D:179:GLU:HB3	1.99	0.44
8:H:35:ALA:O	8:H:39:VAL:HG23	2.17	0.44
8:H:111:MET:HE2	8:H:111:MET:HB3	1.88	0.44
11:K:57:LYS:HB3	11:K:57:LYS:HE3	1.89	0.44
22:a:2496:C:C2'	22:a:2497:A:H5'	2.48	0.44
23:b:34:A:H4'	23:b:35:C:H5	1.82	0.44
24:c:173:THR:HG22	24:c:181:MET:HE3	2.00	0.44
42:u:10:LYS:HE2	42:u:10:LYS:HB2	1.92	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:y:59:GLU:H	46:y:59:GLU:HG2	1.57	0.44
52:4:8:LYS:O	52:4:27:THR:HG22	2.18	0.44
1:A:578:C:H2'	1:A:579:A:O4'	2.17	0.43
1:A:766:A:OP2	1:A:812:G:N2	2.51	0.43
1:A:864:A:C5'	5:E:90:THR:HG23	2.48	0.43
1:A:1136:C:H4'	1:A:1137:C:OP2	2.18	0.43
1:A:1144:G:C2'	1:A:1145:A:H5'	2.48	0.43
1:A:1293:C:O2'	1:A:1294:G:H5'	2.18	0.43
1:A:1457:G:P	20:T:34:LYS:HZ1	2.34	0.43
4:D:131:ASN:CG	4:D:131:ASN:O	2.61	0.43
14:N:79:LEU:HB2	14:N:84:VAL:HG23	1.99	0.43
22:a:577:G:H2'	22:a:578:G:C8	2.52	0.43
22:a:1564:C:H2'	22:a:1565:C:C6	2.53	0.43
22:a:2467:C:O2'	22:a:2468:A:H5'	2.18	0.43
22:a:2694:G:H2'	22:a:2695:U:O4'	2.18	0.43
7:G:144:MET:HE3	7:G:144:MET:HB3	1.81	0.43
15:O:12:VAL:HA	15:O:27:VAL:HG13	1.99	0.43
19:S:66:MET:HE2	19:S:66:MET:HB2	1.85	0.43
22:a:739:A:H1'	22:a:740:C:H5	1.83	0.43
22:a:760:G:H2'	22:a:761:A:O4'	2.17	0.43
22:a:1048:A:C2	22:a:1049:C:C6	3.06	0.43
22:a:1502:A:C2'	22:a:1503:A:H5'	2.48	0.43
22:a:1773:A:N7	22:a:1829:A:H1'	2.33	0.43
22:a:1963:U:O2	22:a:1963:U:C2'	2.66	0.43
22:a:2452:C:H2'	22:a:2453:A:O4'	2.19	0.43
22:a:2574:G:O2'	25:d:149:ASN:N	2.50	0.43
22:a:2742:G:O2'	22:a:2743:U:H5'	2.18	0.43
25:d:112:THR:O	25:d:195:GLY:HA2	2.18	0.43
26:e:168:ASP:HB2	26:e:183:PHE:CZ	2.53	0.43
34:m:38:LEU:HB3	34:m:39:PRO:HD3	2.00	0.43
44:w:39:TRP:NE1	44:w:41:GLU:HG2	2.33	0.43
48:0:11:LEU:HB3	48:0:49:TYR:HB3	1.99	0.43
54:6:6:G:H2'	54:6:7:G:C8	2.53	0.43
1:A:426:U:H2'	1:A:427:U:C6	2.53	0.43
1:A:501:C:H2'	1:A:502:A:C8	2.52	0.43
1:A:1492:A:O2'	1:A:1493:A:H5'	2.18	0.43
7:G:49:THR:CG2	7:G:53:ARG:HH21	2.31	0.43
9:I:6:TYR:CD2	9:I:90:TYR:HA	2.53	0.43
10:J:85:ASP:O	10:J:89:ARG:HG2	2.18	0.43
13:M:9:ILE:CD1	13:M:45:ILE:HG13	2.48	0.43
14:N:32:SER:O	14:N:33:ASP:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:70:TYR:H	18:R:74:HIS:CE1	2.32	0.43
22:a:248:G:O5'	22:a:249:C:H5''	2.18	0.43
22:a:548:G:C8	22:a:548:G:C3'	3.01	0.43
22:a:548:G:H2'	22:a:549:G:O5'	2.19	0.43
22:a:988:A:P	46:y:12:SER:HB3	2.58	0.43
22:a:1723:G:H2'	22:a:1724:G:H5'	2.00	0.43
22:a:1742:U:O2'	22:a:1743:G:H5'	2.18	0.43
22:a:2079:U:H2'	22:a:2080:A:O4'	2.18	0.43
22:a:2291:U:H2'	22:a:2292:U:H6	1.81	0.43
58:a:6249:84G:O8	58:a:6249:84G:O7	2.35	0.43
35:n:85:LYS:HE2	35:n:85:LYS:HB2	1.55	0.43
54:6:22:A:H3'	54:6:47:A:H61	1.83	0.43
1:A:155:A:H2'	1:A:156:C:H6	1.84	0.43
1:A:657:U:O2'	1:A:658:C:H5'	2.18	0.43
1:A:830:G:O2'	1:A:831:A:H5'	2.18	0.43
1:A:1172:C:H2'	1:A:1173:U:C6	2.53	0.43
1:A:1238:A:OP1	1:A:1335:U:O2'	2.29	0.43
1:A:1366:C:O2'	10:J:62:ARG:NH2	2.48	0.43
3:C:54:ARG:CB	3:C:69:HIS:HB2	2.48	0.43
22:a:246:C:C2'	22:a:247:G:H5'	2.49	0.43
22:a:471:A:H2'	22:a:472:A:O4'	2.18	0.43
22:a:1198:U:H4'	37:p:9:ILE:HD11	1.99	0.43
22:a:2821:A:OP2	25:d:115:GLY:N	2.51	0.43
22:a:2863:C:P	57:a:6191:SPD:H51	2.59	0.43
26:e:128:ALA:HB1	26:e:129:PRO:HD2	1.99	0.43
27:f:15:LYS:HB2	27:f:15:LYS:NZ	2.25	0.43
30:i:85:LYS:HZ2	30:i:85:LYS:HG2	1.71	0.43
31:j:105:ARG:HH11	31:j:105:ARG:CG	2.31	0.43
45:x:5:GLU:N	45:x:5:GLU:OE1	2.52	0.43
1:A:437:U:H5''	4:D:152:GLN:NE2	2.32	0.43
1:A:501:C:H2'	1:A:502:A:H8	1.84	0.43
1:A:1124:G:H5''	10:J:37:ARG:O	2.19	0.43
2:B:47:VAL:CG2	2:B:48:PRO:HD3	2.33	0.43
4:D:172:GLU:CG	4:D:183:LYS:HD2	2.48	0.43
9:I:26:GLY:HA2	9:I:61:LEU:O	2.19	0.43
9:I:71:GLY:O	9:I:75:GLN:HG3	2.18	0.43
12:L:86:ARG:C	12:L:86:ARG:HD3	2.43	0.43
13:M:34:LEU:HD13	13:M:41:GLU:HA	2.00	0.43
22:a:1394:U:H2'	22:a:1395:A:O4'	2.18	0.43
22:a:1495:A:H2'	22:a:1496:A:C8	2.53	0.43
22:a:1922:G:H2'	22:a:1923:U:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:d:183:GLU:H	25:d:183:GLU:CD	2.25	0.43
32:k:64:PHE:CD1	50:2:47:LYS:HE3	2.53	0.43
54:6:63:C:H2'	54:6:64:G:C8	2.53	0.43
1:A:70:U:H4'	1:A:71:A:OP1	2.18	0.43
1:A:589:U:H5''	8:H:30:SER:HB3	2.00	0.43
1:A:1160:G:C2	1:A:1161:C:C6	3.07	0.43
1:A:1225:A:H2'	1:A:1226:C:C6	2.53	0.43
2:B:81:LYS:HD3	2:B:91:PHE:CE1	2.54	0.43
10:J:32:THR:CB	10:J:83:THR:HA	2.49	0.43
17:Q:44:LEU:HD23	17:Q:44:LEU:HA	1.86	0.43
22:a:657:U:H2'	22:a:658:U:C6	2.53	0.43
22:a:2598:A:H5''	24:c:234:GLY:HA3	1.99	0.43
23:b:62:C:H2'	23:b:63:C:C6	2.53	0.43
26:e:149:ILE:HG22	26:e:192:ALA:HB1	2.01	0.43
27:f:30:ARG:O	27:f:158:THR:HG23	2.19	0.43
34:m:118:ARG:O	34:m:118:ARG:HG2	2.17	0.43
40:s:3:ARG:O	40:s:7:LEU:HG	2.18	0.43
53:5:1:G:H3'	53:5:1:G:OP3	2.18	0.43
1:A:6:G:H3'	1:A:6:G:N3	2.33	0.43
1:A:826:C:O2	8:H:16:ASN:ND2	2.51	0.43
1:A:1040:U:H2'	1:A:1041:G:H8	1.81	0.43
1:A:1213:A:O2'	1:A:1215:G:N7	2.49	0.43
2:B:125:THR:O	2:B:125:THR:HG22	2.17	0.43
3:C:68:ILE:HD12	3:C:101:ILE:HG23	2.00	0.43
15:O:31:LEU:O	15:O:35:GLN:HG3	2.19	0.43
20:T:10:ARG:O	20:T:14:SER:OG	2.23	0.43
22:a:993:G:OP1	37:p:50:ARG:NE	2.47	0.43
22:a:1224:U:H2'	22:a:1225:G:C8	2.53	0.43
33:l:136:MET:HG2	42:u:77:VAL:HG12	2.00	0.43
46:y:4:THR:O	46:y:4:THR:CG2	2.65	0.43
47:z:12:LYS:HD3	47:z:12:LYS:HA	1.84	0.43
47:z:57:LYS:HE3	47:z:57:LYS:HB2	1.82	0.43
49:1:42:LEU:HD23	49:1:42:LEU:HA	1.85	0.43
54:6:4:G:H2'	54:6:5:G:C8	2.53	0.43
54:6:72:C:H2'	54:6:73:A:H8	1.81	0.43
1:A:109:A:H5'	1:A:110:C:C5	2.54	0.43
1:A:447:G:H1'	1:A:487:A:N6	2.33	0.43
1:A:454:G:C2'	1:A:455:G:H5'	2.48	0.43
1:A:489:C:H2'	1:A:490:C:H6	1.83	0.43
1:A:1130:A:C8	1:A:1146:A:N1	2.87	0.43
1:A:1530:G:H4'	1:A:1530:G:OP1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:48:PRO:O	2:B:52:GLU:CD	2.57	0.43
4:D:156:LYS:CA	4:D:156:LYS:HE3	2.48	0.43
14:N:33:ASP:O	14:N:34:VAL:C	2.61	0.43
19:S:28:LYS:HA	19:S:28:LYS:HE3	2.00	0.43
22:a:1126:A:OP1	22:a:1126:A:H8	2.02	0.43
22:a:1956:U:O2	22:a:1956:U:H2'	2.18	0.43
22:a:2233:U:H2'	22:a:2234:G:C8	2.53	0.43
22:a:2394:C:H5''	32:k:63:LYS:HE2	1.99	0.43
23:b:118:C:H2'	23:b:119:A:O4'	2.18	0.43
24:c:199:GLU:HG2	24:c:202:LEU:HD12	1.99	0.43
26:e:120:VAL:HA	26:e:188:MET:O	2.19	0.43
27:f:44:ILE:HG22	27:f:83:TYR:CD2	2.53	0.43
37:p:89:GLU:HG3	38:q:52:PRO:CB	2.48	0.43
38:q:40:MET:HE3	38:q:47:VAL:CG1	2.49	0.43
1:A:1297:G:H1'	1:A:1298:U:H5	1.82	0.43
7:G:14:PRO:HB2	7:G:19:GLY:C	2.44	0.43
18:R:10:PHE:HE1	18:R:15:ALA:CB	2.32	0.43
22:a:579:G:O2'	22:a:2019:A:OP1	2.37	0.43
22:a:667:U:H2'	22:a:668:A:O4'	2.19	0.43
22:a:776:G:H4'	22:a:777:G:O5'	2.19	0.43
22:a:817:C:O2'	22:a:839:U:H5''	2.18	0.43
22:a:1744:A:H3'	22:a:1745:A:C8	2.54	0.43
22:a:2191:A:H2'	22:a:2192:U:O4'	2.19	0.43
22:a:2662:A:H8	22:a:2662:A:O5'	2.02	0.43
37:p:78:LYS:HE2	37:p:78:LYS:HB2	1.75	0.43
48:0:32:GLU:O	48:0:32:GLU:HG2	2.18	0.43
54:6:67:C:H2'	54:6:68:C:O4'	2.18	0.43
1:A:113:G:H1'	1:A:354:G:H5'	2.00	0.43
1:A:1072:G:H2'	1:A:1073:U:C6	2.53	0.43
1:A:1198:G:H2'	1:A:1199:U:C6	2.54	0.43
2:B:67:ILE:HB	2:B:89:GLN:HG3	2.01	0.43
6:F:40:GLU:OE2	6:F:103:VAL:HG11	2.19	0.43
6:F:97:THR:O	6:F:97:THR:OG1	2.26	0.43
10:J:37:ARG:HA	10:J:37:ARG:HD2	1.82	0.43
11:K:109:ASN:CG	21:U:5:LYS:HD3	2.44	0.43
14:N:33:ASP:CB	14:N:36:ALA:HB2	2.49	0.43
22:a:328:U:H2'	22:a:329:G:OP1	2.19	0.43
22:a:1930:G:N2	22:a:1968:G:H2'	2.33	0.43
22:a:2047:C:H2'	22:a:2048:G:H8	1.84	0.43
22:a:2097:A:H2'	22:a:2098:U:C6	2.53	0.43
22:a:2698:U:H2'	22:a:2699:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:d:181:ASP:CG	25:d:184:ARG:HB2	2.44	0.43
38:q:34:GLU:OE2	38:q:58:VAL:HG21	2.19	0.43
52:4:12:ILE:HD13	52:4:28:VAL:HG11	2.01	0.43
1:A:1440:U:O2'	1:A:1441:A:O5'	2.36	0.42
9:I:36:GLU:HG3	9:I:45:ARG:CZ	2.49	0.42
12:L:50:ARG:HB3	12:L:90:LEU:HD11	2.00	0.42
18:R:47:THR:HG22	18:R:48:ARG:O	2.19	0.42
22:a:5:A:H2'	22:a:6:A:H8	1.84	0.42
22:a:305:C:O2'	22:a:306:U:H5'	2.19	0.42
22:a:1046:A:C3'	22:a:1047:G:H5''	2.47	0.42
22:a:1107:G:N3	22:a:1107:G:C2'	2.81	0.42
22:a:1354:A:H2'	22:a:1355:G:O4'	2.19	0.42
22:a:1593:A:H2'	22:a:1594:U:C6	2.54	0.42
22:a:2567:G:H2'	22:a:2568:U:C6	2.54	0.42
24:c:30:PHE:HD2	24:c:33:LEU:HD12	1.84	0.42
25:d:35:THR:O	25:d:71:ALA:HB2	2.19	0.42
35:n:98:GLN:OE1	35:n:98:GLN:HA	2.19	0.42
40:s:58:VAL:HG22	40:s:85:VAL:HG13	2.01	0.42
42:u:51:GLN:HG2	42:u:86:LEU:HD11	2.00	0.42
1:A:597:G:H2'	1:A:598:U:H5'	2.00	0.42
1:A:1236:A:H4'	1:A:1304:G:H4'	2.01	0.42
1:A:1291:U:H2'	1:A:1292:G:C8	2.49	0.42
1:A:1524:C:H2'	1:A:1525:G:C8	2.54	0.42
15:O:78:TYR:OH	15:O:89:ARG:O	2.22	0.42
20:T:21:ASN:HB3	20:T:66:LEU:HD12	1.99	0.42
22:a:273:G:H2'	22:a:274:C:H6	1.79	0.42
22:a:653:U:H3'	22:a:653:U:H6	1.83	0.42
22:a:1266:G:N7	39:r:16:LYS:HE3	2.34	0.42
22:a:1441:G:H2'	22:a:1442:U:C6	2.54	0.42
22:a:1925:C:O2'	22:a:1926:U:H5'	2.18	0.42
22:a:2391:G:O6	22:a:2425:A:H8	2.02	0.42
22:a:2897:U:H2'	22:a:2898:U:C6	2.54	0.42
59:a:6204:SPM:H31	59:a:6204:SPM:H62	1.69	0.42
27:f:125:ARG:HD3	27:f:125:ARG:HA	1.91	0.42
28:g:54:PRO:HD3	28:g:62:TRP:CZ3	2.54	0.42
37:p:86:ALA:O	38:q:51:VAL:HG12	2.18	0.42
39:r:109:ASP:OD1	39:r:109:ASP:N	2.49	0.42
40:s:65:GLY:HA3	40:s:77:ARG:O	2.19	0.42
49:1:30:VAL:HG22	49:1:33:ARG:NH2	2.34	0.42
54:6:19:G:N3	54:6:19:G:H2'	2.34	0.42
1:A:37:U:H5'	12:L:121:ARG:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:C:H2'	1:A:236:A:C8	2.55	0.42
1:A:350:G:O2'	1:A:351:G:H5'	2.19	0.42
1:A:683:G:O2'	1:A:684:U:H5'	2.19	0.42
1:A:1108:G:N3	1:A:1108:G:H2'	2.34	0.42
1:A:1210:C:C2'	1:A:1211:U:H5'	2.49	0.42
1:A:1314:C:H2'	1:A:1315:U:H6	1.82	0.42
2:B:174:LYS:HE3	2:B:174:LYS:HB2	1.77	0.42
7:G:108:ALA:O	7:G:119:ARG:HD2	2.18	0.42
21:U:58:LYS:HD2	21:U:59:LYS:CD	2.49	0.42
22:a:95:A:H4'	45:x:38:GLN:O	2.20	0.42
22:a:969:G:H2'	22:a:970:U:C6	2.54	0.42
22:a:1582:C:C2	22:a:1583:A:H1'	2.55	0.42
22:a:1879:C:H2'	22:a:1880:U:O4'	2.19	0.42
22:a:1990:C:H2'	22:a:1991:U:C1'	2.49	0.42
22:a:2386:A:H4'	43:v:56:ASP:HA	2.00	0.42
22:a:2427:C:H5''	22:a:2428:G:OP1	2.19	0.42
24:c:142:HIS:ND1	24:c:193:GLY:O	2.41	0.42
35:n:39:VAL:HG12	35:n:48:LEU:HB2	2.01	0.42
38:q:41:ILE:HD12	38:q:103:ALA:HA	2.01	0.42
1:A:177:G:H2'	1:A:178:C:O4'	2.19	0.42
1:A:1033:G:H5'	1:A:1034:G:OP2	2.19	0.42
1:A:1318:A:H1'	19:S:37:ARG:NH1	2.31	0.42
3:C:79:LYS:C	3:C:80:LYS:HG2	2.44	0.42
4:D:125:VAL:HG23	4:D:130:VAL:CG2	2.49	0.42
5:E:34:THR:HB	5:E:50:TYR:CZ	2.54	0.42
7:G:47:LEU:HD23	7:G:47:LEU:HA	1.90	0.42
19:S:14:HIS:O	19:S:18:LYS:HG3	2.20	0.42
20:T:17:ALA:O	20:T:18:ARG:C	2.62	0.42
22:a:404:A:C1'	22:a:405:U:OP2	2.68	0.42
22:a:930:G:H1'	46:y:25:LEU:HD11	2.02	0.42
22:a:936:A:H2'	22:a:937:C:C6	2.54	0.42
23:b:29:A:H2'	23:b:30:C:O4'	2.19	0.42
25:d:177:VAL:HG13	25:d:187:LEU:HD11	2.01	0.42
30:i:92:MET:HB3	30:i:92:MET:HE3	1.77	0.42
32:k:78:ARG:HG3	32:k:78:ARG:HH11	1.84	0.42
33:l:12:MET:HE1	33:l:71:LYS:HG3	2.00	0.42
38:q:1:MET:HA	38:q:42:ALA:O	2.20	0.42
40:s:4:GLU:O	40:s:8:LEU:HG	2.19	0.42
41:t:74:ASN:OD1	41:t:76:ALA:HB3	2.20	0.42
43:v:66:LYS:HE3	43:v:66:LYS:HB3	1.70	0.42
53:5:75:C:H2'	53:5:76:A:N9	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:164:G:C2'	1:A:165:G:H5'	2.49	0.42
1:A:202:G:O2'	1:A:468:A:N3	2.30	0.42
1:A:545:C:H5'	4:D:69:GLU:CG	2.47	0.42
1:A:684:U:C2'	1:A:685:G:H5'	2.49	0.42
1:A:1086:U:H3	1:A:1099:G:H22	1.67	0.42
1:A:1253:G:H2'	1:A:1254:A:H8	1.85	0.42
1:A:1436:U:H2'	1:A:1437:A:C8	2.54	0.42
2:B:57:LEU:HD23	2:B:57:LEU:HA	1.83	0.42
2:B:87:CYS:SG	2:B:221:VAL:CG1	3.08	0.42
4:D:102:VAL:HG13	4:D:107:PHE:HB2	2.02	0.42
6:F:25:TYR:CE2	6:F:78:PHE:HE1	2.37	0.42
10:J:53:ILE:HG21	10:J:63:ASP:CG	2.45	0.42
22:a:3:U:H2'	22:a:4:U:C6	2.54	0.42
22:a:850:U:O2'	46:y:23:THR:HA	2.19	0.42
22:a:1607:C:H4'	22:a:1608:A:O5'	2.19	0.42
22:a:2038:G:H2'	22:a:2039:U:O4'	2.20	0.42
22:a:2646:C:O5'	22:a:2646:C:H6	2.02	0.42
25:d:121:THR:HB	25:d:127:PHE:CD2	2.55	0.42
26:e:48:THR:CG2	26:e:86:ALA:HB3	2.49	0.42
37:p:17:ILE:HD13	37:p:17:ILE:HA	1.82	0.42
38:q:27:ILE:HG22	38:q:31:GLU:HB2	2.01	0.42
1:A:946:A:O2'	1:A:1333:A:N3	2.40	0.42
1:A:1041:G:O2'	1:A:1042:A:H5'	2.20	0.42
1:A:1150:A:N6	1:A:1151:A:N6	2.68	0.42
2:B:217:VAL:HA	2:B:220:THR:CG2	2.50	0.42
9:I:54:LEU:HD22	9:I:103:PHE:CE2	2.55	0.42
11:K:18:ASP:OD1	11:K:18:ASP:N	2.50	0.42
22:a:155:A:H2'	22:a:156:A:H8	1.81	0.42
22:a:170:U:H2'	22:a:171:U:C6	2.55	0.42
22:a:545:U:H6	22:a:548:G:O6	2.03	0.42
22:a:1689:A:H2'	22:a:1690:A:H8	1.84	0.42
22:a:1790:C:H2'	22:a:1791:A:C8	2.54	0.42
22:a:2196:C:H2'	22:a:2197:U:C6	2.54	0.42
22:a:2583:G:H2'	22:a:2584:U:O4'	2.20	0.42
22:a:2831:G:OP1	22:a:2834:G:H4'	2.19	0.42
22:a:2903:U:OP2	22:a:2903:U:H4'	2.19	0.42
38:q:73:LYS:HB3	38:q:73:LYS:HE2	1.58	0.42
51:3:7:VAL:HG13	51:3:25:VAL:HG23	2.01	0.42
53:5:62:C:H2'	53:5:63:G:C8	2.55	0.42
1:A:162:A:H2'	1:A:163:C:H5'	2.02	0.42
1:A:458:U:O2	1:A:458:U:H2'	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:992:U:H5'	1:A:993:G:H5'	2.02	0.42
1:A:1516:2MG:H2'	1:A:1518:MA6:OP2	2.20	0.42
5:E:56:VAL:O	5:E:60:ILE:HG13	2.19	0.42
5:E:108:GLY:O	5:E:112:ARG:CB	2.67	0.42
12:L:66:TYR:O	12:L:97:THR:HG23	2.20	0.42
12:L:114:ARG:HB3	12:L:119:VAL:HB	2.01	0.42
18:R:21:ILE:HD12	18:R:54:GLN:HB2	2.02	0.42
22:a:139:U:H3'	22:a:140:C:H6	1.84	0.42
22:a:852:U:H2'	22:a:853:C:C6	2.55	0.42
22:a:1282:U:H2'	22:a:1283:G:O4'	2.20	0.42
22:a:1802:A:H2'	22:a:1803:A:H8	1.78	0.42
22:a:2295:C:OP2	35:n:9:ARG:NH2	2.52	0.42
22:a:2305:U:C2	27:f:151:GLY:HA3	2.55	0.42
22:a:2589:A:H2'	22:a:2590:A:C8	2.54	0.42
22:a:2687:U:H2'	22:a:2688:G:O4'	2.20	0.42
26:e:18:THR:HG23	26:e:200:LEU:HD12	2.01	0.42
30:i:15:TRP:CE2	30:i:135:GLN:HG2	2.54	0.42
46:y:48:ILE:HG21	46:y:57:VAL:HG21	2.01	0.42
49:1:3:ARG:HD3	49:1:3:ARG:HA	1.79	0.42
1:A:66:A:H5'	1:A:173:U:O4	2.20	0.42
1:A:251:G:H4'	1:A:252:U:O5'	2.19	0.42
1:A:512:U:H2'	1:A:513:C:C6	2.54	0.42
1:A:1122:U:H2'	1:A:1123:U:C6	2.54	0.42
3:C:31:ASP:N	3:C:31:ASP:OD1	2.52	0.42
4:D:58:LYS:HA	4:D:200:ILE:CD1	2.50	0.42
4:D:202:GLU:O	4:D:206:LYS:HB3	2.20	0.42
8:H:65:TYR:HA	8:H:69:LYS:O	2.19	0.42
22:a:2:G:O2'	22:a:3:U:H5'	2.20	0.42
22:a:322:A:H5'	22:a:340:A:H1'	2.01	0.42
22:a:1799:G:H4'	22:a:1800:C:H6	1.84	0.42
23:b:85:G:O2'	23:b:86:G:H5'	2.18	0.42
26:e:190:ALA:O	26:e:194:LYS:HG2	2.20	0.42
36:o:2:SER:O	36:o:6:LYS:HE3	2.20	0.42
46:y:6:LYS:NZ	46:y:37:GLU:HG3	2.34	0.42
1:A:1234:C:C2'	1:A:1235:U:H5'	2.50	0.42
4:D:15:GLU:OE1	4:D:15:GLU:HA	2.19	0.42
4:D:151:LYS:HD2	4:D:151:LYS:O	2.20	0.42
7:G:111:ARG:HG2	7:G:111:ARG:NH1	2.35	0.42
8:H:50:LYS:HE3	8:H:60:GLU:OE1	2.20	0.42
9:I:107:ASP:OD1	9:I:109:ARG:HG3	2.19	0.42
22:a:74:A:H4'	22:a:75:G:O5'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:160:A:N3	22:a:2208:C:O2'	2.46	0.42
22:a:708:G:H2'	22:a:709:U:C6	2.55	0.42
22:a:1652:A:C2'	22:a:1653:G:H5'	2.50	0.42
22:a:2312:U:OP1	27:f:70:ALA:HA	2.20	0.42
22:a:2404:U:C2'	22:a:2405:G:H5'	2.50	0.42
27:f:106:ILE:C	27:f:109:PRO:HD2	2.45	0.42
41:t:72:ILE:HD12	41:t:72:ILE:HA	1.89	0.42
43:v:72:LYS:HE2	43:v:72:LYS:HB2	1.76	0.42
1:A:17:U:H2'	1:A:18:C:H6	1.82	0.42
1:A:35:G:H5''	12:L:100:GLY:O	2.19	0.42
1:A:181:A:N6	1:A:195:A:N7	2.68	0.42
1:A:960:U:O2'	1:A:1223:C:H4'	2.19	0.42
1:A:979:C:O2	14:N:59:ARG:HD2	2.20	0.42
2:B:196:VAL:HG21	2:B:199:VAL:HG22	1.98	0.42
9:I:21:ILE:HG12	9:I:63:LEU:HD23	2.02	0.42
9:I:54:LEU:HD23	9:I:98:LEU:HD23	2.02	0.42
10:J:61:ALA:C	10:J:62:ARG:HG2	2.45	0.42
11:K:98:ARG:HH11	21:U:16:LEU:HD23	1.84	0.42
22:a:1571:A:H2'	22:a:1572:A:C8	2.55	0.42
22:a:1604:C:O2'	22:a:1610:A:N1	2.48	0.42
22:a:1680:U:O2'	22:a:1681:G:H5'	2.20	0.42
22:a:1722:A:H2'	22:a:1723:G:O4'	2.20	0.42
22:a:2595:G:N2	22:a:2598:A:OP2	2.38	0.42
24:c:117:GLN:N	24:c:128:ASN:OD1	2.51	0.42
33:l:54:THR:HG22	33:l:59:ARG:HG2	2.02	0.42
38:q:77:PHE:HD1	38:q:84:ARG:HD3	1.83	0.42
53:5:18:G:O2'	53:5:57:G:N2	2.34	0.42
53:5:37:MIA:C13	53:5:37:MIA:N1	2.82	0.42
54:6:4:G:H2'	54:6:5:G:H8	1.85	0.42
1:A:422:C:O2	1:A:422:C:O4'	2.38	0.41
1:A:821:G:OP1	58:A:1793:84G:O8	2.37	0.41
1:A:1000:A:N1	1:A:1041:G:C6	2.88	0.41
9:I:25:ASN:OD1	9:I:27:LYS:HE3	2.20	0.41
14:N:47:LYS:HA	14:N:50:THR:OG1	2.20	0.41
16:P:56:ARG:HA	16:P:56:ARG:HD2	1.70	0.41
18:R:11:CYS:SG	18:R:14:THR:HB	2.60	0.41
22:a:1427:A:H4'	22:a:1428:C:O5'	2.20	0.41
22:a:1790:C:H2'	22:a:1791:A:N7	2.35	0.41
22:a:2625:G:H2'	22:a:2626:C:O4'	2.19	0.41
24:c:141:VAL:HB	24:c:190:ALA:HB1	2.02	0.41
24:c:162:VAL:CG1	24:c:174:LEU:HB3	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:c:232:HIS:NE2	24:c:244:PRO:HA	2.35	0.41
32:k:81:ASP:HA	32:k:84:LYS:HD2	2.02	0.41
36:o:38:LYS:HB3	36:o:38:LYS:HE2	1.63	0.41
47:z:36:GLU:OE1	47:z:46:ASP:HB3	2.19	0.41
47:z:56:ALA:O	47:z:57:LYS:HB2	2.19	0.41
54:6:21:H2U:H61	54:6:21:H2U:H5''	2.02	0.41
1:A:408:A:O2'	1:A:409:U:H5'	2.20	0.41
1:A:997:U:O2'	1:A:998:C:H5'	2.19	0.41
1:A:1006:G:N3	1:A:1006:G:H2'	2.36	0.41
4:D:17:THR:HG22	4:D:18:ASP:N	2.35	0.41
4:D:98:LEU:O	4:D:102:VAL:HG23	2.20	0.41
6:F:37:HIS:HB3	6:F:97:THR:HG22	2.01	0.41
6:F:53:LYS:HD2	6:F:53:LYS:HA	1.91	0.41
7:G:75:VAL:CG1	7:G:86:GLN:HB3	2.50	0.41
15:O:73:LYS:HD2	15:O:73:LYS:HA	1.88	0.41
22:a:348:A:H2'	22:a:349:U:O4'	2.21	0.41
22:a:897:C:C2'	22:a:898:C:H5'	2.50	0.41
22:a:1435:G:O2'	22:a:1436:G:H5'	2.20	0.41
22:a:1846:G:C2'	22:a:1847:A:H5'	2.51	0.41
22:a:2329:U:H2'	22:a:2330:G:C8	2.55	0.41
22:a:2457:PSU:H2'	22:a:2458:G:O4'	2.20	0.41
22:a:2496:C:H2'	22:a:2497:A:O4'	2.21	0.41
22:a:2618:G:H21	25:d:155:VAL:HG21	1.84	0.41
23:b:15:A:O4'	23:b:109:A:C8	2.73	0.41
34:m:22:ARG:HG2	34:m:70:THR:HA	2.00	0.41
35:n:76:LYS:O	35:n:80:GLU:HG3	2.19	0.41
1:A:8:A:C6	4:D:206:LYS:HB2	2.54	0.41
1:A:258:G:O2'	1:A:259:G:H5'	2.20	0.41
1:A:358:U:H2'	1:A:359:G:C8	2.55	0.41
1:A:430:A:OP1	4:D:9:LEU:HB2	2.20	0.41
1:A:565:U:OP2	1:A:566:G:O2'	2.37	0.41
2:B:5:SER:O	2:B:9:MET:CG	2.68	0.41
22:a:1361:G:H2'	22:a:1362:C:C6	2.55	0.41
22:a:1443:U:H2'	22:a:1444:G:C8	2.54	0.41
22:a:2066:C:O2'	22:a:2067:G:H5'	2.20	0.41
22:a:2266:A:H4'	22:a:2267:A:N3	2.35	0.41
26:e:115:GLN:O	26:e:116:ASP:HB2	2.20	0.41
31:j:63:VAL:HG23	31:j:64:ARG:HG3	2.02	0.41
34:m:55:ALA:HA	34:m:80:PHE:CE2	2.55	0.41
35:n:79:ALA:O	35:n:83:LEU:HG	2.20	0.41
44:w:7:VAL:HG21	44:w:59:ILE:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:5:39:PSU:O2'	53:5:40:C:H5'	2.20	0.41
1:A:718:A:C2	18:R:38:LYS:HG2	2.55	0.41
1:A:1101:A:H4'	1:A:1102:A:O5'	2.20	0.41
1:A:1158:C:C5	1:A:1160:G:C1'	3.03	0.41
1:A:1294:G:O2'	1:A:1295:U:H5'	2.20	0.41
1:A:1463:U:H2'	1:A:1464:U:C6	2.55	0.41
2:B:162:PHE:CZ	2:B:217:VAL:HG21	2.55	0.41
10:J:27:GLU:OE1	10:J:27:GLU:HA	2.21	0.41
13:M:34:LEU:HD13	13:M:41:GLU:HG2	2.03	0.41
20:T:18:ARG:NH1	20:T:18:ARG:HG2	2.36	0.41
21:U:4:ILE:HD12	21:U:4:ILE:HA	1.72	0.41
22:a:328:U:C2'	22:a:329:G:OP1	2.69	0.41
22:a:548:G:H2'	22:a:549:G:C4'	2.50	0.41
22:a:2641:G:OP1	30:i:78:THR:HG22	2.20	0.41
23:b:11:C:C2'	23:b:12:C:H5'	2.51	0.41
26:e:6:LYS:HB2	26:e:6:LYS:HE2	1.92	0.41
30:i:45:THR:HB	30:i:48:VAL:HB	2.01	0.41
33:l:105:MET:HE1	33:l:116:ALA:CB	2.50	0.41
41:t:38:GLY:N	41:t:62:GLU:OE2	2.46	0.41
53:5:8:4SU:O2'	53:5:21:A:N1	2.53	0.41
53:5:40:C:O2'	53:5:41:C:H5'	2.19	0.41
1:A:86:G:O2'	1:A:87:C:O5'	2.32	0.41
1:A:511:C:H4'	4:D:44:ARG:HH21	1.86	0.41
1:A:613:C:H2'	1:A:614:C:H6	1.84	0.41
1:A:664:G:H2'	1:A:666:G:OP1	2.21	0.41
1:A:859:G:H2'	1:A:860:A:H8	1.86	0.41
1:A:1272:G:C5'	14:N:34:VAL:HG21	2.51	0.41
1:A:1371:G:O3'	9:I:71:GLY:HA3	2.20	0.41
2:B:100:MET:HA	2:B:107:VAL:HG21	2.03	0.41
4:D:167:LYS:HA	4:D:167:LYS:HD2	1.83	0.41
6:F:4:TYR:CE1	6:F:91:ARG:HG2	2.55	0.41
14:N:33:ASP:OD2	14:N:36:ALA:HB2	2.20	0.41
16:P:44:SER:O	16:P:47:GLU:HG2	2.20	0.41
22:a:249:C:OP2	22:a:2394:C:O2'	2.34	0.41
22:a:505:A:OP2	57:a:6194:SPD:N1	2.53	0.41
22:a:766:U:H2'	22:a:767:U:H6	1.83	0.41
22:a:1019:U:OP1	22:a:1035:U:O2'	2.26	0.41
22:a:2353:G:H2'	22:a:2354:C:O4'	2.20	0.41
57:a:6191:SPD:H41	57:a:6191:SPD:H71	1.71	0.41
23:b:5:U:OP1	23:b:61:G:O2'	2.29	0.41
23:b:29:A:OP2	35:n:32:PRO:HD2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:w:39:TRP:HB2	44:w:46:PHE:CE1	2.55	0.41
47:z:39:LEU:HD23	47:z:39:LEU:HA	1.93	0.41
47:z:49:TYR:HB3	47:z:54:VAL:HG11	2.02	0.41
1:A:563:A:H2'	1:A:567:G:C8	2.56	0.41
1:A:623:C:H2'	1:A:624:C:C6	2.56	0.41
1:A:986:U:H2'	1:A:987:G:O4'	2.20	0.41
1:A:1106:G:OP1	3:C:172:ARG:HD2	2.20	0.41
1:A:1130:A:C8	1:A:1146:A:C2	3.08	0.41
1:A:1163:A:H2'	1:A:1164:G:C8	2.56	0.41
7:G:130:ASN:HA	7:G:135:VAL:HG21	2.02	0.41
22:a:686:U:H6	22:a:788:A:N1	2.18	0.41
22:a:896:A:C2'	22:a:897:C:H5'	2.49	0.41
22:a:1283:G:N2	22:a:1285:A:H3'	2.35	0.41
22:a:1758:U:O2	22:a:1758:U:H2'	2.19	0.41
25:d:184:ARG:O	25:d:185:ASN:HB2	2.20	0.41
26:e:170:ARG:HG2	26:e:170:ARG:HH11	1.84	0.41
27:f:25:VAL:O	27:f:28:VAL:HG23	2.20	0.41
33:l:56:ALA:HB2	33:l:119:LEU:HD12	2.03	0.41
2:B:129:LEU:HD22	2:B:137:ARG:HD2	2.03	0.41
2:B:135:LEU:CA	2:B:138:THR:HG22	2.49	0.41
7:G:3:ARG:HG2	7:G:3:ARG:HH11	1.86	0.41
13:M:9:ILE:HD13	13:M:45:ILE:HG13	2.03	0.41
16:P:6:LEU:CD2	16:P:19:VAL:HG22	2.51	0.41
16:P:76:LYS:O	16:P:81:ALA:HB2	2.21	0.41
17:Q:57:ASP:OD2	17:Q:81:LYS:HD3	2.21	0.41
19:S:64:ASP:O	52:4:56:ARG:HB2	2.20	0.41
22:a:227:A:C2	22:a:2407:A:H1'	2.56	0.41
22:a:404:A:H1'	22:a:405:U:OP2	2.21	0.41
22:a:784:G:C5'	22:a:785:G:OP1	2.65	0.41
22:a:1009:A:N3	22:a:1153:C:O2'	2.50	0.41
22:a:1676:A:H2'	22:a:1677:A:O4'	2.20	0.41
22:a:1951:U:H2'	22:a:1953:A:OP2	2.21	0.41
22:a:2344:U:H4'	22:a:2345:G:OP1	2.18	0.41
22:a:2864:G:OP2	57:a:6191:SPD:H31	2.21	0.41
26:e:63:LYS:HB3	26:e:63:LYS:HE3	1.89	0.41
27:f:17:MET:HE3	27:f:22:TYR:HB2	2.02	0.41
30:i:104:ALA:O	30:i:108:MET:HG3	2.21	0.41
45:x:6:LEU:HD12	45:x:6:LEU:HA	1.81	0.41
54:6:45:A:H8	54:6:45:A:O5'	2.02	0.41
1:A:722:G:H3'	1:A:722:G:N3	2.35	0.41
2:B:135:LEU:O	2:B:138:THR:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:81:ARG:NH1	4:D:81:ARG:HG2	2.36	0.41
12:L:9:ARG:HE	12:L:9:ARG:HB2	1.71	0.41
13:M:44:LYS:O	13:M:48:LEU:HD13	2.20	0.41
19:S:13:LEU:O	19:S:17:LYS:HG3	2.21	0.41
19:S:15:LEU:HD21	19:S:71:LEU:CD1	2.50	0.41
22:a:141:G:H3'	22:a:141:G:N3	2.35	0.41
22:a:766:U:O4	59:a:6204:SPM:H82	2.21	0.41
22:a:786:C:C2'	22:a:787:C:H5'	2.50	0.41
22:a:837:C:H42	22:a:941:A:H62	1.69	0.41
22:a:857:G:O2'	22:a:858:G:H5'	2.20	0.41
22:a:1131:G:O6	22:a:2024:G:O2'	2.30	0.41
22:a:1464:G:H2'	22:a:1465:G:C8	2.56	0.41
22:a:1854:A:H2'	22:a:1855:U:H5'	2.02	0.41
22:a:1858:A:C2'	22:a:1859:U:H5'	2.51	0.41
25:d:30:GLU:H	25:d:30:GLU:HG2	1.67	0.41
32:k:92:LEU:HD12	32:k:92:LEU:HA	1.83	0.41
37:p:89:GLU:HG2	38:q:52:PRO:HB3	2.03	0.41
53:5:21:A:N6	53:5:46:G7M:O2'	2.53	0.41
1:A:164:G:H2'	1:A:165:G:H5'	2.02	0.41
1:A:224:U:H2'	1:A:225:C:C6	2.55	0.41
1:A:363:A:OP2	12:L:58:THR:HG21	2.21	0.41
1:A:586:C:H2'	1:A:587:G:H5'	2.00	0.41
1:A:602:A:O2'	1:A:603:U:H5'	2.20	0.41
1:A:747:A:C2'	1:A:748:G:O4'	2.68	0.41
1:A:1015:G:H1'	1:A:1218:C:O2'	2.21	0.41
1:A:1035:A:HO2'	1:A:1036:A:H2	1.66	0.41
1:A:1161:C:H2'	1:A:1162:C:C6	2.55	0.41
1:A:1194:U:H2'	1:A:1195:C:C6	2.56	0.41
1:A:1206:G:H2'	1:A:1207:2MG:O4'	2.21	0.41
1:A:1272:G:H2'	1:A:1273:C:C6	2.56	0.41
1:A:1315:U:O2	1:A:1360:A:H2	2.04	0.41
1:A:1440:U:HO2'	1:A:1441:A:P	2.43	0.41
2:B:94:HIS:O	2:B:95:ARG:C	2.64	0.41
2:B:114:LEU:HB2	2:B:144:LEU:HD12	2.03	0.41
3:C:92:ALA:HB2	3:C:99:ALA:CB	2.51	0.41
7:G:20:SER:C	7:G:22:LEU:H	2.27	0.41
10:J:9:ARG:HH22	10:J:71:LEU:HD21	1.85	0.41
13:M:9:ILE:HD12	13:M:9:ILE:C	2.46	0.41
15:O:24:SER:O	15:O:28:GLN:HG3	2.19	0.41
18:R:10:PHE:HE1	18:R:15:ALA:HB2	1.86	0.41
18:R:11:CYS:O	18:R:14:THR:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:a:127:A:H5''	22:a:128:C:C6	2.56	0.41
22:a:414:C:H2'	22:a:415:A:H8	1.82	0.41
22:a:704:G:H1'	22:a:727:A:N6	2.36	0.41
22:a:1285:A:H2	22:a:1328:A:H5''	1.86	0.41
22:a:1486:U:H2'	22:a:1487:U:H6	1.86	0.41
22:a:1638:C:H4'	22:a:2710:C:O2	2.21	0.41
22:a:1775:U:O4	22:a:1789:A:H2	2.04	0.41
22:a:2037:A:H2'	22:a:2038:G:C8	2.55	0.41
22:a:2404:U:H2'	22:a:2405:G:O4'	2.20	0.41
22:a:2545:G:H2'	22:a:2546:U:O4'	2.21	0.41
22:a:2751:G:N3	22:a:2751:G:H2'	2.36	0.41
26:e:105:LEU:HD23	26:e:105:LEU:HA	1.87	0.41
26:e:134:LEU:CD2	26:e:161:ALA:HB2	2.51	0.41
26:e:150:THR:O	26:e:171:ASP:HA	2.21	0.41
26:e:172:ALA:O	26:e:199:MET:HE1	2.21	0.41
27:f:57:LEU:HD12	27:f:57:LEU:HA	1.90	0.41
28:g:11:VAL:HA	28:g:12:PRO:HD3	1.93	0.41
28:g:91:GLY:CA	28:g:160:LYS:HG2	2.50	0.41
36:o:114:LEU:O	36:o:115:ASN:HB3	2.20	0.41
38:q:14:VAL:CG1	38:q:20:VAL:HG21	2.50	0.41
40:s:30:ILE:HG12	40:s:85:VAL:HB	2.03	0.41
41:t:26:LYS:HG3	41:t:37:GLU:CD	2.46	0.41
1:A:36:C:H4'	12:L:119:VAL:O	2.21	0.41
1:A:405:U:O4	4:D:3:ARG:N	2.54	0.41
1:A:508:U:H4'	4:D:51:TYR:CE2	2.56	0.41
1:A:776:G:HO2'	1:A:777:A:H8	1.65	0.41
1:A:1010:U:H2'	1:A:1011:C:C6	2.55	0.41
1:A:1188:A:H2'	1:A:1189:U:O4'	2.21	0.41
3:C:130:PHE:CE2	3:C:131:ARG:HG2	2.56	0.41
5:E:41:ASP:OD1	5:E:42:GLY:N	2.54	0.41
10:J:10:LEU:HD23	10:J:98:VAL:HG22	2.03	0.41
22:a:397:U:H5''	44:w:32:ASN:HB2	2.03	0.41
22:a:699:A:H2'	22:a:700:G:O4'	2.21	0.41
22:a:1410:G:H2'	22:a:1411:U:H6	1.86	0.41
22:a:1774:C:O2	22:a:1774:C:C2'	2.68	0.41
25:d:35:THR:CG2	25:d:73:VAL:HG21	2.51	0.41
26:e:146:VAL:HG12	26:e:167:VAL:HG22	2.03	0.41
28:g:35:ARG:N	28:g:75:MET:HE1	2.36	0.41
28:g:158:LYS:HB3	28:g:158:LYS:HE3	1.90	0.41
32:k:35:HIS:O	32:k:36:LYS:C	2.63	0.41
33:l:31:PHE:HB3	33:l:130:PHE:CZ	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:o:55:LEU:O	36:o:55:LEU:HG	2.21	0.41
44:w:12:PRO:HB3	44:w:30:LEU:HD23	2.02	0.41
1:A:177:G:C2'	1:A:178:C:H5'	2.51	0.40
1:A:425:G:O2'	1:A:426:U:H5'	2.20	0.40
1:A:487:A:H2'	1:A:488:C:O4'	2.21	0.40
1:A:1096:C:H2'	1:A:1097:C:H6	1.86	0.40
1:A:1319:A:C8	1:A:1323:G:C6	3.09	0.40
1:A:1434:A:H2'	1:A:1435:G:O4'	2.20	0.40
2:B:12:ALA:CA	2:B:208:ARG:HD2	2.31	0.40
2:B:217:VAL:O	2:B:220:THR:HG23	2.20	0.40
3:C:91:VAL:HG12	3:C:99:ALA:HB1	2.02	0.40
3:C:91:VAL:HG12	3:C:99:ALA:CB	2.51	0.40
3:C:184:TYR:HA	3:C:200:VAL:O	2.21	0.40
8:H:22:LYS:O	8:H:63:LEU:HD12	2.21	0.40
9:I:91:ASP:HB3	9:I:94:LEU:CD1	2.47	0.40
14:N:2:ALA:HB2	14:N:68:GLY:O	2.21	0.40
16:P:13:LYS:HA	16:P:13:LYS:HD2	1.91	0.40
17:Q:19:LYS:HZ3	17:Q:19:LYS:HG3	1.66	0.40
20:T:36:TYR:HA	20:T:39:ILE:HD12	2.03	0.40
22:a:303:G:H2'	22:a:304:U:C6	2.56	0.40
22:a:413:C:H2'	22:a:414:C:C6	2.56	0.40
22:a:447:A:O2'	57:a:6199:SPD:H92	2.21	0.40
22:a:1957:C:H5'	22:a:1984:G:O2'	2.21	0.40
24:c:71:LYS:HE3	24:c:74:ILE:HD12	2.02	0.40
24:c:271:ARG:O	24:c:272:SER:OG	2.37	0.40
28:g:9:VAL:CG1	28:g:50:LEU:HB2	2.32	0.40
28:g:91:GLY:O	28:g:92:VAL:C	2.63	0.40
28:g:118:PRO:HG2	28:g:144:VAL:CG2	2.51	0.40
32:k:77:ILE:HD12	32:k:108:ALA:HB1	2.00	0.40
33:l:17:ASN:O	33:l:38:ARG:NH1	2.54	0.40
33:l:66:ARG:HB2	33:l:101:VAL:O	2.21	0.40
44:w:56:MET:HE2	44:w:56:MET:HB2	1.90	0.40
48:0:13:SER:HB2	48:0:49:TYR:CZ	2.56	0.40
54:6:19:G:H1	54:6:56:PSU:H6	1.69	0.40
54:6:24:C:H2'	54:6:25:U:O4'	2.21	0.40
1:A:236:A:H2'	1:A:237:G:C8	2.56	0.40
1:A:527:G7M:O2'	1:A:535:A:N1	2.51	0.40
1:A:923:A:H2'	1:A:924:C:C6	2.56	0.40
1:A:1068:G:N7	1:A:1094:G:H2'	2.36	0.40
3:C:63:SER:CB	3:C:98:PRO:HG2	2.51	0.40
8:H:113:ASP:N	8:H:113:ASP:OD1	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:9:HIS:ND1	16:P:18:GLN:HG3	2.37	0.40
17:Q:47:HIS:HB3	17:Q:74:THR:HG22	2.03	0.40
22:a:1047:G:O2'	22:a:1048:A:P	2.79	0.40
22:a:1558:C:O4'	22:a:1560:G:C8	2.74	0.40
22:a:1672:A:C2	22:a:2582:G:H5'	2.56	0.40
22:a:1683:U:H2'	22:a:1684:G:C8	2.56	0.40
22:a:2014:A:HO2'	39:r:92:ARG:HH22	1.64	0.40
22:a:2506:U:O2	22:a:2506:U:H2'	2.20	0.40
22:a:2836:U:H2'	22:a:2837:A:C8	2.56	0.40
33:l:36:VAL:HG23	33:l:129:THR:HG23	2.03	0.40
38:q:87:GLN:HG2	38:q:88:GLY:N	2.36	0.40
38:q:93:PHE:CE1	38:q:95:ASP:OD1	2.74	0.40
45:x:5:GLU:CD	45:x:5:GLU:H	2.29	0.40
52:4:41:HIS:HB3	52:4:44:PHE:CD2	2.45	0.40
52:4:43:PHE:CD1	52:4:43:PHE:C	2.99	0.40
1:A:187:G:N2	1:A:190:A:OP2	2.50	0.40
1:A:412:A:H3'	1:A:412:A:P	2.62	0.40
1:A:463:U:H3	1:A:469:C:H42	1.69	0.40
1:A:746:A:C2'	1:A:747:A:O5'	2.69	0.40
1:A:1397:C:H4'	1:A:1398:A:OP2	2.20	0.40
4:D:59:GLN:O	4:D:63:ARG:HD2	2.21	0.40
6:F:41:ASP:CG	6:F:58:HIS:HE2	2.26	0.40
7:G:26:PHE:CE2	7:G:120:LEU:HD21	2.55	0.40
10:J:87:LEU:HD23	10:J:87:LEU:HA	1.93	0.40
11:K:14:LYS:HE2	11:K:14:LYS:HA	2.03	0.40
17:Q:24:ALA:HA	17:Q:43:LYS:HA	2.03	0.40
22:a:272:A:H2'	22:a:273:G:H8	1.86	0.40
22:a:463:G:N2	22:a:466:A:OP2	2.43	0.40
22:a:580:U:H2'	22:a:581:C:H6	1.85	0.40
22:a:1271:G:O6	57:a:6200:SPD:H41	2.20	0.40
22:a:1306:C:H2'	22:a:1307:A:H8	1.86	0.40
22:a:1521:G:OP2	22:a:1522:A:O2'	2.34	0.40
22:a:1614:A:H2	39:r:93:ALA:HB2	1.87	0.40
22:a:1867:G:C2'	22:a:1868:C:H5'	2.51	0.40
22:a:2331:G:O2'	22:a:2336:A:N1	2.40	0.40
22:a:2803:G:H2'	22:a:2804:U:H6	1.85	0.40
22:a:2806:C:H2'	22:a:2807:U:O4'	2.22	0.40
27:f:69:LYS:HA	27:f:84:PRO:HA	2.04	0.40
32:k:91:ASP:OD1	32:k:123:ARG:HB3	2.21	0.40
1:A:61:G:H2'	1:A:62:U:O4'	2.21	0.40
1:A:616:G:O2'	1:A:617:G:H5'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:632:U:H3'	1:A:633:G:H5'	2.02	0.40
1:A:1042:A:H2'	1:A:1043:G:O4'	2.21	0.40
8:H:12:THR:HA	8:H:15:ARG:NH1	2.37	0.40
22:a:176:A:C2'	22:a:177:G:H5'	2.50	0.40
22:a:327:G:O6	57:a:6197:SPD:H92	2.21	0.40
22:a:483:A:H5''	41:t:47:LYS:CD	2.51	0.40
22:a:654:A:N3	22:a:654:A:H3'	2.36	0.40
22:a:722:A:H2'	22:a:723:C:O4'	2.21	0.40
22:a:1314:C:O2	22:a:1314:C:H2'	2.22	0.40
22:a:1629:U:O2	22:a:2698:U:H5''	2.22	0.40
22:a:1723:G:C2'	22:a:1724:G:H5'	2.51	0.40
22:a:2223:G:H2'	22:a:2224:G:H5'	2.03	0.40
24:c:79:GLU:OE2	24:c:101:ARG:NH2	2.55	0.40
28:g:137:ASP:HB3	28:g:140:VAL:HB	2.02	0.40
30:i:125:TYR:HH	30:i:132:HIS:CD2	2.38	0.40
32:k:61:LEU:O	50:2:13:ARG:NE	2.49	0.40
41:t:52:LEU:C	41:t:52:LEU:HD22	2.47	0.40
48:0:30:LYS:HA	48:0:30:LYS:HD3	1.87	0.40
1:A:189:A:H2'	1:A:190:A:O4'	2.19	0.40
1:A:707:U:H2'	1:A:708:C:C6	2.56	0.40
4:D:62:ARG:NH1	4:D:69:GLU:OE1	2.54	0.40
4:D:88:GLU:CG	4:D:188:ARG:HG3	2.51	0.40
5:E:153:VAL:O	5:E:156:LYS:HG3	2.22	0.40
15:O:82:ILE:HG13	15:O:83:GLU:N	2.36	0.40
19:S:5:LEU:HD23	19:S:5:LEU:HA	1.82	0.40
22:a:170:U:O2'	22:a:171:U:H5'	2.20	0.40
22:a:468:G:H5''	26:e:55:SER:HB3	2.04	0.40
22:a:1278:C:H2'	22:a:1279:G:H8	1.86	0.40
22:a:1437:C:H2'	22:a:1438:U:C6	2.56	0.40
22:a:1654:A:O2'	25:d:118:PHE:O	2.34	0.40
22:a:1656:C:H2'	22:a:1657:U:H6	1.86	0.40
22:a:2063:C:O2	22:a:2063:C:H2'	2.20	0.40
22:a:2563:U:H1'	22:a:2566:A:N6	2.37	0.40
22:a:2824:C:O5'	22:a:2824:C:H6	2.04	0.40
23:b:11:C:O2'	23:b:12:C:H5'	2.22	0.40
27:f:50:LEU:HD21	27:f:84:PRO:HB2	2.03	0.40
38:q:24:LYS:HE3	38:q:24:LYS:HB3	1.81	0.40
38:q:37:GLU:HB3	38:q:53:PHE:CE1	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	
2	B	222/241 (92%)	211 (95%)	11 (5%)	0	100	100
3	C	204/233 (88%)	197 (97%)	7 (3%)	0	100	100
4	D	203/206 (98%)	197 (97%)	6 (3%)	0	100	100
5	E	154/167 (92%)	151 (98%)	3 (2%)	0	100	100
6	F	101/135 (75%)	96 (95%)	5 (5%)	0	100	100
7	G	151/179 (84%)	141 (93%)	10 (7%)	0	100	100
8	H	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
9	I	125/130 (96%)	121 (97%)	4 (3%)	0	100	100
10	J	96/103 (93%)	91 (95%)	5 (5%)	0	100	100
11	K	113/129 (88%)	106 (94%)	7 (6%)	0	100	100
12	L	120/124 (97%)	114 (95%)	6 (5%)	0	100	100
13	M	113/118 (96%)	105 (93%)	8 (7%)	0	100	100
14	N	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
15	O	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
16	P	79/82 (96%)	73 (92%)	6 (8%)	0	100	100
17	Q	77/84 (92%)	73 (95%)	4 (5%)	0	100	100
18	R	64/75 (85%)	58 (91%)	6 (9%)	0	100	100
19	S	82/92 (89%)	78 (95%)	4 (5%)	0	100	100
20	T	84/87 (97%)	81 (96%)	3 (4%)	0	100	100
21	U	68/71 (96%)	67 (98%)	1 (2%)	0	100	100
24	c	269/273 (98%)	262 (97%)	7 (3%)	0	100	100
25	d	206/209 (99%)	200 (97%)	5 (2%)	1 (0%)	24	54
26	e	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
27	f	175/179 (98%)	165 (94%)	10 (6%)	0	100	100
28	g	174/177 (98%)	159 (91%)	15 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	h	39/149 (26%)	33 (85%)	6 (15%)	0	100	100
30	i	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
31	j	121/123 (98%)	115 (95%)	6 (5%)	0	100	100
32	k	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
33	l	132/136 (97%)	128 (97%)	4 (3%)	0	100	100
34	m	116/127 (91%)	110 (95%)	6 (5%)	0	100	100
35	n	114/117 (97%)	110 (96%)	4 (4%)	0	100	100
36	o	112/115 (97%)	106 (95%)	6 (5%)	0	100	100
37	p	115/118 (98%)	112 (97%)	3 (3%)	0	100	100
38	q	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
39	r	108/110 (98%)	108 (100%)	0	0	100	100
40	s	91/100 (91%)	88 (97%)	3 (3%)	0	100	100
41	t	100/104 (96%)	92 (92%)	8 (8%)	0	100	100
42	u	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
43	v	76/85 (89%)	73 (96%)	3 (4%)	0	100	100
44	w	75/78 (96%)	75 (100%)	0	0	100	100
45	x	60/63 (95%)	56 (93%)	4 (7%)	0	100	100
46	y	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
47	z	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
48	0	49/55 (89%)	46 (94%)	3 (6%)	0	100	100
49	1	44/46 (96%)	44 (100%)	0	0	100	100
50	2	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
51	3	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
52	4	56/70 (80%)	49 (88%)	7 (12%)	0	100	100
All	All	5481/5913 (93%)	5240 (96%)	240 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	d	149	ASN

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	
2	B	186/199 (94%)	180 (97%)	6 (3%)	34	68
3	C	170/190 (90%)	164 (96%)	6 (4%)	32	66
4	D	172/173 (99%)	158 (92%)	14 (8%)	11	33
5	E	119/126 (94%)	114 (96%)	5 (4%)	26	60
6	F	90/116 (78%)	86 (96%)	4 (4%)	25	59
7	G	126/147 (86%)	118 (94%)	8 (6%)	16	45
8	H	104/105 (99%)	102 (98%)	2 (2%)	50	79
9	I	105/107 (98%)	102 (97%)	3 (3%)	37	71
10	J	86/90 (96%)	80 (93%)	6 (7%)	14	40
11	K	89/98 (91%)	89 (100%)	0	100	100
12	L	102/103 (99%)	98 (96%)	4 (4%)	28	63
13	M	93/96 (97%)	90 (97%)	3 (3%)	34	68
14	N	83/84 (99%)	81 (98%)	2 (2%)	43	75
15	O	76/77 (99%)	73 (96%)	3 (4%)	28	63
16	P	65/65 (100%)	62 (95%)	3 (5%)	24	57
17	Q	73/78 (94%)	71 (97%)	2 (3%)	39	73
18	R	57/65 (88%)	53 (93%)	4 (7%)	14	40
19	S	72/79 (91%)	69 (96%)	3 (4%)	26	60
20	T	65/66 (98%)	64 (98%)	1 (2%)	57	84
21	U	60/61 (98%)	58 (97%)	2 (3%)	33	67
24	c	216/218 (99%)	212 (98%)	4 (2%)	50	79
25	d	163/163 (100%)	160 (98%)	3 (2%)	51	80
26	e	165/165 (100%)	162 (98%)	3 (2%)	51	80
27	f	148/150 (99%)	139 (94%)	9 (6%)	17	46
28	g	137/138 (99%)	127 (93%)	10 (7%)	13	38
29	h	32/114 (28%)	30 (94%)	2 (6%)	16	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	i	116/116 (100%)	112 (97%)	4 (3%)	32	66
31	j	104/104 (100%)	101 (97%)	3 (3%)	37	71
32	k	103/103 (100%)	102 (99%)	1 (1%)	68	89
33	l	107/107 (100%)	105 (98%)	2 (2%)	50	79
34	m	98/103 (95%)	95 (97%)	3 (3%)	35	69
35	n	86/87 (99%)	83 (96%)	3 (4%)	32	66
36	o	99/100 (99%)	96 (97%)	3 (3%)	36	70
37	p	89/90 (99%)	89 (100%)	0	100	100
38	q	84/84 (100%)	83 (99%)	1 (1%)	63	86
39	r	93/93 (100%)	93 (100%)	0	100	100
40	s	80/84 (95%)	80 (100%)	0	100	100
41	t	83/85 (98%)	79 (95%)	4 (5%)	23	55
42	u	78/78 (100%)	78 (100%)	0	100	100
43	v	58/63 (92%)	54 (93%)	4 (7%)	14	41
44	w	67/68 (98%)	64 (96%)	3 (4%)	24	58
45	x	54/55 (98%)	52 (96%)	2 (4%)	30	64
46	y	48/49 (98%)	47 (98%)	1 (2%)	47	77
47	z	47/48 (98%)	47 (100%)	0	100	100
48	0	46/49 (94%)	44 (96%)	2 (4%)	26	60
49	1	38/38 (100%)	36 (95%)	2 (5%)	20	52
50	2	51/52 (98%)	50 (98%)	1 (2%)	48	78
51	3	34/34 (100%)	32 (94%)	2 (6%)	18	48
52	4	55/62 (89%)	54 (98%)	1 (2%)	51	80
All	All	4572/4825 (95%)	4418 (97%)	154 (3%)	33	66

All (154) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	14	VAL
2	B	60	ILE
2	B	118	GLU
2	B	197	ASP
2	B	207	ILE
2	B	220	THR

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Mol	Chain	Res	Type
3	C	128	VAL
3	C	136	ARG
3	C	147	LYS
3	C	173	VAL
3	C	185	ASN
3	C	202	ILE
4	D	23	SER
4	D	25	VAL
4	D	28	ILE
4	D	29	ASP
4	D	34	ILE
4	D	119	SER
4	D	123	ILE
4	D	125	VAL
4	D	141	ASP
4	D	153	SER
4	D	155	VAL
4	D	189	SER
4	D	190	ASP
4	D	205	SER
5	E	22	SER
5	E	39	VAL
5	E	130	SER
5	E	141	ILE
5	E	159	LYS
6	F	9	MET
6	F	87	SER
6	F	89	VAL
6	F	103	VAL
7	G	32	VAL
7	G	45	SER
7	G	56	LYS
7	G	57	SER
7	G	72	THR
7	G	75	VAL
7	G	91	VAL
7	G	133	THR
8	H	85	ILE
8	H	129	VAL
9	I	15	SER
9	I	21	ILE
9	I	43	THR

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Mol	Chain	Res	Type
10	J	25	ILE
10	J	28	THR
10	J	36	VAL
10	J	57	VAL
10	J	92	LEU
10	J	100	ILE
12	L	67	ILE
12	L	87	VAL
12	L	97	THR
12	L	104	CYS
13	M	16	VAL
13	M	39	ILE
13	M	68	ASP
14	N	84	VAL
14	N	90	ARG
15	O	2	SER
15	O	14	GLU
15	O	56	LEU
16	P	21	VAL
16	P	34	GLU
16	P	66	THR
17	Q	29	VAL
17	Q	60	GLU
18	R	14	THR
18	R	34	THR
18	R	36	SER
18	R	45	THR
19	S	4	SER
19	S	19	VAL
19	S	35	SER
20	T	3	ASN
21	U	4	ILE
21	U	28	VAL
24	c	5	LYS
24	c	10	SER
24	c	100	GLU
24	c	192	LEU
25	d	32	ASN
25	d	35	THR
25	d	39	ASP
26	e	65	THR
26	e	74	LYS

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Mol	Chain	Res	Type
26	e	153	LEU
27	f	35	THR
27	f	44	ILE
27	f	69	LYS
27	f	74	VAL
27	f	89	VAL
27	f	104	ILE
27	f	129	SER
27	f	136	ILE
27	f	170	LEU
28	g	9	VAL
28	g	10	VAL
28	g	25	THR
28	g	36	THR
28	g	37	LEU
28	g	43	VAL
28	g	60	ASP
28	g	74	SER
28	g	110	SER
28	g	129	THR
29	h	12	LEU
29	h	17	ASP
30	i	10	THR
30	i	136	GLN
30	i	139	VAL
30	i	142	ILE
31	j	76	VAL
31	j	114	LYS
31	j	123	LEU
32	k	92	LEU
33	l	36	VAL
33	l	80	VAL
34	m	6	SER
34	m	14	SER
34	m	15	SER
35	n	25	ARG
35	n	49	VAL
35	n	54	VAL
36	o	32	VAL
36	o	37	LYS
36	o	53	ARG
38	q	51	VAL

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Mol	Chain	Res	Type
41	t	39	ILE
41	t	52	LEU
41	t	68	SER
41	t	79	LYS
43	v	10	THR
43	v	16	SER
43	v	43	THR
43	v	81	SER
44	w	2	SER
44	w	22	LEU
44	w	51	VAL
45	x	6	LEU
45	x	58	ASN
46	y	59	GLU
48	0	5	ILE
48	0	43	VAL
49	1	15	SER
49	1	42	LEU
50	2	6	THR
51	3	2	LYS
51	3	26	ILE
52	4	21	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	8	ASN
3	C	123	GLN
5	E	97	GLN
6	F	11	HIS
7	G	148	ASN
8	H	4	GLN
8	H	38	ASN
9	I	5	GLN
9	I	75	GLN
9	I	110	GLN
11	K	40	ASN
12	L	20	ASN
12	L	112	GLN
17	Q	9	GLN
18	R	74	HIS
20	T	13	GLN

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Mol	Chain	Res	Type
24	c	21	ASN
24	c	25	HIS
24	c	260	ASN
25	d	32	ASN
25	d	136	ASN
25	d	173	GLN
25	d	185	ASN
28	g	22	GLN
28	g	128	GLN
30	i	67	ASN
30	i	80	HIS
31	j	5	GLN
31	j	9	ASN
31	j	29	HIS
31	j	88	ASN
32	k	4	ASN
33	l	13	HIS
39	r	40	ASN
44	w	36	HIS
49	1	26	ASN
52	4	33	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1516/1542 (98%)	190 (12%)	9 (0%)
22	a	2749/2904 (94%)	348 (12%)	0
23	b	118/120 (98%)	12 (10%)	0
53	5	75/76 (98%)	18 (24%)	2 (2%)
54	6	76/77 (98%)	16 (21%)	1 (1%)
55	7	9/10 (90%)	0	0
All	All	4543/4729 (96%)	584 (12%)	12 (0%)

All (584) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	5	U
1	A	6	G
1	A	9	G
1	A	22	G

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Mol	Chain	Res	Type
1	A	32	A
1	A	39	G
1	A	44	A
1	A	47	C
1	A	48	C
1	A	51	A
1	A	74	A
1	A	82	G
1	A	83	C
1	A	84	U
1	A	86	G
1	A	87	C
1	A	88	U
1	A	116	A
1	A	121	U
1	A	122	G
1	A	131	A
1	A	141	G
1	A	143	A
1	A	144	G
1	A	164	G
1	A	173	U
1	A	182	A
1	A	197	A
1	A	204	G
1	A	226	G
1	A	240	G
1	A	245	U
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C
1	A	281	G
1	A	289	G
1	A	321	A
1	A	328	C
1	A	330	C
1	A	347	G
1	A	351	G
1	A	352	C
1	A	354	G
1	A	367	U

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Mol	Chain	Res	Type
1	A	372	C
1	A	373	A
1	A	398	U
1	A	406	G
1	A	411	A
1	A	412	A
1	A	413	G
1	A	414	A
1	A	417	G
1	A	421	U
1	A	422	C
1	A	423	G
1	A	424	G
1	A	429	U
1	A	430	A
1	A	453	G
1	A	458	U
1	A	459	A
1	A	465	A
1	A	467	U
1	A	468	A
1	A	469	C
1	A	479	U
1	A	481	G
1	A	482	A
1	A	484	G
1	A	486	U
1	A	497	G
1	A	509	A
1	A	511	C
1	A	512	U
1	A	518	C
1	A	521	G
1	A	531	U
1	A	532	A
1	A	547	A
1	A	559	A
1	A	564	C
1	A	573	A
1	A	576	C
1	A	577	G
1	A	588	G

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Mol	Chain	Res	Type
1	A	596	A
1	A	632	U
1	A	633	G
1	A	641	U
1	A	653	U
1	A	665	A
1	A	703	G
1	A	721	G
1	A	723	U
1	A	747	A
1	A	748	G
1	A	755	G
1	A	777	A
1	A	792	A
1	A	793	U
1	A	794	A
1	A	802	A
1	A	815	A
1	A	817	C
1	A	851	G
1	A	884	U
1	A	890	G
1	A	902	G
1	A	914	A
1	A	934	C
1	A	935	A
1	A	960	U
1	A	966	2MG
1	A	969	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	989	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1003	G
1	A	1004	A
1	A	1009	U
1	A	1017	U
1	A	1027	C
1	A	1030	U

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Mol	Chain	Res	Type
1	A	1031	C
1	A	1033	G
1	A	1034	G
1	A	1036	A
1	A	1044	A
1	A	1053	G
1	A	1065	U
1	A	1085	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1130	A
1	A	1137	C
1	A	1139	G
1	A	1157	A
1	A	1159	U
1	A	1171	A
1	A	1196	A
1	A	1197	A
1	A	1202	U
1	A	1213	A
1	A	1214	C
1	A	1227	A
1	A	1228	C
1	A	1238	A
1	A	1258	G
1	A	1280	A
1	A	1285	A
1	A	1286	U
1	A	1287	A
1	A	1300	G
1	A	1302	C
1	A	1305	G
1	A	1317	C
1	A	1320	C
1	A	1331	G
1	A	1338	G
1	A	1346	A
1	A	1353	G
1	A	1363	A
1	A	1370	G
1	A	1378	C

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Mol	Chain	Res	Type
1	A	1379	G
1	A	1398	A
1	A	1419	G
1	A	1432	G
1	A	1441	A
1	A	1446	A
1	A	1451	U
1	A	1452	C
1	A	1453	G
1	A	1487	G
1	A	1492	A
1	A	1497	G
1	A	1506	U
1	A	1517	G
1	A	1529	G
1	A	1530	G
1	A	1534	A
22	a	10	A
22	a	15	G
22	a	27	G
22	a	34	U
22	a	42	A
22	a	58	G
22	a	61	C
22	a	71	A
22	a	72	U
22	a	74	A
22	a	75	G
22	a	101	A
22	a	102	U
22	a	118	A
22	a	119	A
22	a	120	U
22	a	125	A
22	a	139	U
22	a	142	A
22	a	163	C
22	a	181	A
22	a	196	A
22	a	199	A
22	a	215	G
22	a	216	A

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Mol	Chain	Res	Type
22	a	221	A
22	a	222	A
22	a	224	U
22	a	233	A
22	a	248	G
22	a	265	A
22	a	267	C
22	a	272	A
22	a	277	G
22	a	278	A
22	a	279	A
22	a	285	G
22	a	287	G
22	a	294	A
22	a	311	A
22	a	329	G
22	a	330	A
22	a	356	G
22	a	362	A
22	a	385	C
22	a	386	G
22	a	396	G
22	a	405	U
22	a	411	G
22	a	412	A
22	a	429	A
22	a	436	C
22	a	481	G
22	a	491	G
22	a	501	A
22	a	504	A
22	a	505	A
22	a	508	A
22	a	509	C
22	a	530	G
22	a	531	C
22	a	532	A
22	a	544	C
22	a	546	U
22	a	547	A
22	a	548	G
22	a	563	A

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Mol	Chain	Res	Type
22	a	568	U
22	a	573	U
22	a	575	A
22	a	577	G
22	a	603	A
22	a	614	A
22	a	615	U
22	a	627	A
22	a	637	A
22	a	645	C
22	a	646	U
22	a	647	G
22	a	653	U
22	a	654	A
22	a	655	A
22	a	685	A
22	a	686	U
22	a	704	G
22	a	717	C
22	a	730	A
22	a	747	5MU
22	a	764	A
22	a	775	G
22	a	776	G
22	a	782	A
22	a	784	G
22	a	785	G
22	a	787	C
22	a	789	A
22	a	805	G
22	a	812	C
22	a	827	U
22	a	828	U
22	a	846	U
22	a	847	U
22	a	859	G
22	a	881	G
22	a	883	G
22	a	884	U
22	a	885	C
22	a	890	C
22	a	891	G

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Mol	Chain	Res	Type
22	a	895	U
22	a	896	A
22	a	910	A
22	a	914	G
22	a	915	C
22	a	927	A
22	a	931	U
22	a	934	U
22	a	945	A
22	a	946	C
22	a	961	C
22	a	974	G
22	a	983	A
22	a	984	A
22	a	990	A
22	a	996	A
22	a	1012	U
22	a	1013	C
22	a	1033	U
22	a	1040	A
22	a	1045	C
22	a	1046	A
22	a	1047	G
22	a	1048	A
22	a	1108	U
22	a	1110	G
22	a	1111	A
22	a	1112	G
22	a	1116	G
22	a	1132	U
22	a	1133	A
22	a	1135	C
22	a	1136	G
22	a	1141	U
22	a	1142	A
22	a	1168	G
22	a	1172	C
22	a	1206	G
22	a	1236	G
22	a	1241	A
22	a	1250	G
22	a	1253	A

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Mol	Chain	Res	Type
22	a	1256	G
22	a	1271	G
22	a	1272	A
22	a	1273	U
22	a	1275	A
22	a	1287	A
22	a	1289	C
22	a	1300	G
22	a	1301	A
22	a	1352	U
22	a	1365	A
22	a	1379	U
22	a	1383	A
22	a	1395	A
22	a	1413	A
22	a	1416	G
22	a	1417	C
22	a	1420	A
22	a	1428	C
22	a	1452	G
22	a	1482	G
22	a	1483	G
22	a	1493	C
22	a	1494	A
22	a	1495	A
22	a	1497	U
22	a	1508	A
22	a	1509	A
22	a	1510	G
22	a	1515	A
22	a	1524	G
22	a	1535	A
22	a	1536	C
22	a	1537	G
22	a	1542	U
22	a	1554	U
22	a	1566	A
22	a	1569	A
22	a	1578	U
22	a	1583	A
22	a	1585	C
22	a	1586	A

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Mol	Chain	Res	Type
22	a	1607	C
22	a	1608	A
22	a	1634	A
22	a	1647	U
22	a	1648	U
22	a	1649	G
22	a	1653	G
22	a	1674	G
22	a	1675	C
22	a	1715	G
22	a	1729	U
22	a	1730	C
22	a	1738	G
22	a	1739	A
22	a	1758	U
22	a	1759	A
22	a	1764	C
22	a	1773	A
22	a	1776	G
22	a	1782	U
22	a	1784	A
22	a	1786	A
22	a	1800	C
22	a	1801	A
22	a	1807	G
22	a	1808	A
22	a	1816	C
22	a	1829	A
22	a	1847	A
22	a	1858	A
22	a	1871	A
22	a	1872	A
22	a	1873	G
22	a	1882	U
22	a	1884	G
22	a	1906	G
22	a	1929	G
22	a	1930	G
22	a	1937	A
22	a	1938	A
22	a	1941	C
22	a	1955	U

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Mol	Chain	Res	Type
22	a	1962	5MC
22	a	1964	G
22	a	1965	C
22	a	1967	C
22	a	1970	A
22	a	1971	U
22	a	1972	G
22	a	1991	U
22	a	1993	U
22	a	2021	C
22	a	2023	C
22	a	2030	6MZ
22	a	2031	A
22	a	2033	A
22	a	2035	G
22	a	2036	C
22	a	2043	C
22	a	2055	C
22	a	2056	G
22	a	2060	A
22	a	2061	G
22	a	2062	A
22	a	2069	G7M
22	a	2093	G
22	a	2198	A
22	a	2204	G
22	a	2211	A
22	a	2225	A
22	a	2238	G
22	a	2239	G
22	a	2267	A
22	a	2268	A
22	a	2269	G
22	a	2273	A
22	a	2279	G
22	a	2283	C
22	a	2287	A
22	a	2305	U
22	a	2307	G
22	a	2308	G
22	a	2322	A
22	a	2325	G

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Mol	Chain	Res	Type
22	a	2333	A
22	a	2335	A
22	a	2347	C
22	a	2350	C
22	a	2361	G
22	a	2377	A
22	a	2383	G
22	a	2385	C
22	a	2402	U
22	a	2406	A
22	a	2424	C
22	a	2425	A
22	a	2428	G
22	a	2429	G
22	a	2430	A
22	a	2435	A
22	a	2441	U
22	a	2445	2MG
22	a	2448	A
22	a	2449	H2U
22	a	2474	U
22	a	2476	A
22	a	2491	U
22	a	2498	OMC
22	a	2502	G
22	a	2505	G
22	a	2517	C
22	a	2518	A
22	a	2520	C
22	a	2529	G
22	a	2547	A
22	a	2566	A
22	a	2567	G
22	a	2573	C
22	a	2582	G
22	a	2586	U
22	a	2602	A
22	a	2609	U
22	a	2613	U
22	a	2615	U
22	a	2629	U
22	a	2630	G

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Mol	Chain	Res	Type
22	a	2645	G
22	a	2663	G
22	a	2682	A
22	a	2689	U
22	a	2690	U
22	a	2714	G
22	a	2716	C
22	a	2726	A
22	a	2733	A
22	a	2744	G
22	a	2748	A
22	a	2752	C
22	a	2757	A
22	a	2765	A
22	a	2778	A
22	a	2793	C
22	a	2794	C
22	a	2797	U
22	a	2798	U
22	a	2799	A
22	a	2818	U
22	a	2820	A
22	a	2821	A
22	a	2850	A
22	a	2873	A
22	a	2880	C
22	a	2884	U
22	a	2899	A
22	a	2903	U
23	b	13	G
23	b	16	G
23	b	24	G
23	b	35	C
23	b	42	C
23	b	45	A
23	b	56	G
23	b	67	G
23	b	89	U
23	b	90	C
23	b	99	A
23	b	109	A
53	5	3	C

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Mol	Chain	Res	Type
53	5	5	G
53	5	8	4SU
53	5	9	A
53	5	10	G
53	5	16	U
53	5	17	C
53	5	18	G
53	5	19	G
53	5	20	U
53	5	21	A
53	5	22	G
53	5	23	A
53	5	46	G7M
53	5	48	C
53	5	58	A
53	5	73	A
53	5	74	C
54	6	9	G
54	6	17	C
54	6	18	U
54	6	19	G
54	6	20	G
54	6	21	H2U
54	6	22	A
54	6	23	G
54	6	44	A
54	6	48	U
54	6	50	G
54	6	53	G
54	6	54	G
54	6	59	A
54	6	67	C
54	6	77	A

All (12) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	120	A
1	A	429	U
1	A	467	U
1	A	1026	G
1	A	1035	A

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Mol	Chain	Res	Type
1	A	1240	U
1	A	1337	G
1	A	1397	C
1	A	1440	U
53	5	8	4SU
53	5	21	A
54	6	21	H2U

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

52 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$
54	OMC	6	33	54	19,22,23	0.64	0	26,31,34	0.61	0
53	PSU	5	32	53	18,21,22	1.05	1 (5%)	22,30,33	1.87	6 (27%)
22	PSU	a	1917	22	18,21,22	1.00	1 (5%)	22,30,33	1.83	5 (22%)
12	D2T	L	89	12	7,9,10	1.39	1 (14%)	6,11,13	2.38	3 (50%)
22	G7M	a	2069	22	23,26,27	2.69	8 (34%)	35,39,42	1.76	10 (28%)
1	5MC	A	967	1	18,22,23	0.63	0	26,32,35	0.62	0
22	PSU	a	2580	22	18,21,22	1.10	2 (11%)	22,30,33	2.08	6 (27%)
53	5MU	5	54	53	19,22,23	0.49	0	28,32,35	0.57	0
1	5MC	A	1407	1	18,22,23	0.74	0	26,32,35	0.60	0
22	OMU	a	2552	22	19,22,23	2.71	6 (31%)	26,31,34	1.76	4 (15%)
1	PSU	A	516	1,56	18,21,22	1.00	1 (5%)	22,30,33	1.86	4 (18%)
22	5MC	a	1962	22	18,22,23	0.69	0	26,32,35	0.63	0
22	6MZ	a	2030	22	22,25,26	2.75	4 (18%)	30,36,39	2.30	11 (36%)
54	5MU	6	55	54	19,22,23	0.46	0	28,32,35	0.57	0
1	UR3	A	1498	1	19,22,23	2.64	7 (36%)	26,32,35	1.33	2 (7%)
33	4D4	l	81	33	9,11,12	1.95	3 (33%)	8,13,15	1.81	3 (37%)
22	PSU	a	2504	22	18,21,22	1.10	1 (5%)	22,30,33	1.69	3 (13%)
22	PSU	a	1911	22	18,21,22	1.07	1 (5%)	22,30,33	1.81	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	1MG	a	745	22	22,26,27	2.57	7 (31%)	33,39,42	1.69	7 (21%)
22	OMC	a	2498	22,56	19,22,23	0.68	0	26,31,34	0.74	0
53	MIA	5	37	53	28,31,32	3.13	5 (17%)	40,44,47	4.00	19 (47%)
33	MS6	l	82	33	5,7,8	1.61	1 (20%)	2,7,9	1.76	1 (50%)
22	PSU	a	2605	22	18,21,22	1.07	2 (11%)	22,30,33	1.82	3 (13%)
1	2MG	A	1207	1	23,26,27	0.54	0	32,38,41	0.59	0
22	PSU	a	2457	22	18,21,22	1.04	1 (5%)	22,30,33	1.85	4 (18%)
1	G7M	A	527	1	23,26,27	2.77	8 (34%)	35,39,42	1.75	8 (22%)
22	6MZ	a	1618	22	22,25,26	2.73	4 (18%)	30,36,39	2.30	10 (33%)
22	PSU	a	2604	22	18,21,22	1.04	1 (5%)	22,30,33	1.97	5 (22%)
1	MA6	A	1518	1	23,26,27	1.44	4 (17%)	34,38,41	4.43	13 (38%)
53	PSU	5	39	53	18,21,22	1.01	1 (5%)	22,30,33	1.82	4 (18%)
53	PSU	5	55	53	18,21,22	1.08	1 (5%)	22,30,33	1.87	5 (22%)
22	3TD	a	1915	22	19,22,23	3.96	7 (36%)	21,32,35	1.79	3 (14%)
22	2MG	a	1835	22	23,26,27	0.57	0	32,38,41	0.51	0
1	2MG	A	1516	1	23,26,27	0.58	0	32,38,41	0.69	0
22	5MU	a	1939	22	19,22,23	0.66	0	28,32,35	0.50	0
22	2MG	a	2445	22	23,26,27	0.65	0	32,38,41	0.57	0
1	MA6	A	1519	1	23,26,27	1.38	4 (17%)	34,38,41	4.65	13 (38%)
1	2MG	A	966	1	23,26,27	0.54	0	32,38,41	0.55	0
54	4SU	6	8	54	18,21,22	3.59	7 (38%)	26,30,33	2.25	5 (19%)
54	H2U	6	21	54	18,21,22	0.58	0	21,30,33	1.28	2 (9%)
53	G7M	5	46	53	23,26,27	2.82	9 (39%)	35,39,42	1.74	8 (22%)
54	PSU	6	56	54	18,21,22	1.07	1 (5%)	22,30,33	1.71	4 (18%)
22	PSU	a	955	22	18,21,22	1.02	1 (5%)	22,30,33	2.02	5 (22%)
22	2MA	a	2503	22,56	22,25,26	3.56	8 (36%)	33,37,40	1.99	9 (27%)
1	4OC	A	1402	1	20,23,24	2.98	8 (40%)	26,32,35	0.90	1 (3%)
11	IAS	K	119	21,11	6,7,8	1.39	1 (16%)	6,8,10	1.38	0
22	5MU	a	747	22	19,22,23	0.61	0	28,32,35	0.64	0
22	OMG	a	2251	54,22,56	23,26,27	0.64	0	33,38,41	0.49	0
25	MEQ	d	150	25	8,9,10	0.93	0	5,10,12	0.61	0
22	H2U	a	2449	22	18,21,22	0.55	0	21,30,33	1.01	2 (9%)
22	PSU	a	746	22,56	18,21,22	1.05	2 (11%)	22,30,33	1.73	4 (18%)
53	4SU	5	8	53	18,21,22	3.59	7 (38%)	26,30,33	2.22	5 (19%)

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
54	OMC	6	33	54	-	0/9/27/28	0/2/2/2
53	PSU	5	32	53	-	0/7/25/26	0/2/2/2
22	PSU	a	1917	22	-	0/7/25/26	0/2/2/2
12	D2T	L	89	12	-	1/7/12/14	-
22	G7M	a	2069	22	-	1/7/25/26	0/3/3/3
1	5MC	A	967	1	-	0/7/25/26	0/2/2/2
22	PSU	a	2580	22	-	0/7/25/26	0/2/2/2
53	5MU	5	54	53	-	0/7/25/26	0/2/2/2
1	5MC	A	1407	1	-	0/7/25/26	0/2/2/2
22	OMU	a	2552	22	-	0/9/27/28	0/2/2/2
1	PSU	A	516	1,56	-	0/7/25/26	0/2/2/2
22	5MC	a	1962	22	-	0/7/25/26	0/2/2/2
22	6MZ	a	2030	22	-	2/9/27/28	0/3/3/3
54	5MU	6	55	54	-	2/7/25/26	0/2/2/2
1	UR3	A	1498	1	-	0/7/25/26	0/2/2/2
33	4D4	l	81	33	-	1/11/12/14	-
22	PSU	a	2504	22	-	0/7/25/26	0/2/2/2
22	PSU	a	1911	22	-	0/7/25/26	0/2/2/2
22	1MG	a	745	22	-	0/7/25/26	0/3/3/3
22	OMC	a	2498	22,56	-	2/9/27/28	0/2/2/2
53	MIA	5	37	53	-	3/15/33/34	0/3/3/3
33	MS6	l	82	33	-	3/4/6/8	-
22	PSU	a	2605	22	-	0/7/25/26	0/2/2/2
1	2MG	A	1207	1	-	0/9/27/28	0/3/3/3
22	PSU	a	2457	22	-	0/7/25/26	0/2/2/2
1	G7M	A	527	1	-	2/7/25/26	0/3/3/3
22	6MZ	a	1618	22	-	0/9/27/28	0/3/3/3
22	PSU	a	2604	22	-	0/7/25/26	0/2/2/2
1	MA6	A	1518	1	-	0/11/29/30	0/3/3/3
53	PSU	5	39	53	-	0/7/25/26	0/2/2/2
53	PSU	5	55	53	-	1/7/25/26	0/2/2/2
22	3TD	a	1915	22	-	0/7/25/26	0/2/2/2
22	2MG	a	1835	22	-	0/9/27/28	0/3/3/3
1	2MG	A	1516	1	-	0/9/27/28	0/3/3/3
22	5MU	a	1939	22	-	0/7/25/26	0/2/2/2
22	2MG	a	2445	22	-	2/9/27/28	0/3/3/3
1	MA6	A	1519	1	-	0/11/29/30	0/3/3/3
1	2MG	A	966	1	-	2/9/27/28	0/3/3/3
54	4SU	6	8	54	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
54	H2U	6	21	54	-	3/7/38/39	0/2/2/2
53	G7M	5	46	53	-	2/7/25/26	0/3/3/3
54	PSU	6	56	54	-	2/7/25/26	0/2/2/2
22	PSU	a	955	22	-	0/7/25/26	0/2/2/2
22	2MA	a	2503	22,56	-	2/7/25/26	0/3/3/3
1	4OC	A	1402	1	-	2/9/29/30	0/2/2/2
11	IAS	K	119	21,11	-	1/7/7/8	-
22	5MU	a	747	22	-	1/7/25/26	0/2/2/2
22	OMG	a	2251	54,22,56	-	2/9/27/28	0/3/3/3
25	MEQ	d	150	25	-	4/8/9/11	-
22	H2U	a	2449	22	-	1/7/38/39	0/2/2/2
22	PSU	a	746	22,56	-	1/7/25/26	0/2/2/2
53	4SU	5	8	53	-	0/7/25/26	0/2/2/2

All (126) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	1915	3TD	C6-C5	12.11	1.49	1.35
22	a	2030	6MZ	C6-N6	11.55	1.46	1.34
22	a	1618	6MZ	C6-N6	11.52	1.46	1.34
53	5	37	MIA	C6-N6	11.01	1.51	1.34
22	a	2503	2MA	C4-N3	10.93	1.48	1.34
53	5	37	MIA	C2-S10	10.63	1.84	1.75
22	a	1915	3TD	C2-N1	8.72	1.48	1.37
54	6	8	4SU	C2-N3	6.99	1.50	1.38
53	5	8	4SU	C2-N3	6.94	1.50	1.38
1	A	1498	UR3	C2-N1	6.82	1.48	1.38
54	6	8	4SU	C2-N1	6.78	1.49	1.38
53	5	8	4SU	C2-N1	6.72	1.49	1.38
54	6	8	4SU	C4-N3	6.71	1.44	1.37
53	5	8	4SU	C4-N3	6.67	1.44	1.37
53	5	46	G7M	C2-N2	6.59	1.49	1.34
1	A	1402	4OC	C4-N3	6.54	1.44	1.32
22	a	2503	2MA	C2-N1	6.54	1.45	1.34
53	5	46	G7M	C4-N3	6.45	1.49	1.34
22	a	2552	OMU	C2-N1	6.43	1.48	1.38
22	a	2503	2MA	C2-N3	6.42	1.45	1.34
1	A	527	G7M	C4-N3	6.32	1.49	1.34
1	A	527	G7M	C2-N2	6.28	1.49	1.34
22	a	2069	G7M	C2-N2	6.25	1.49	1.34
1	A	1402	4OC	C6-C5	6.06	1.49	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	745	1MG	C2-N3	6.02	1.45	1.34
22	a	2069	G7M	C4-N3	6.02	1.48	1.34
22	a	745	1MG	C4-N3	5.98	1.48	1.34
22	a	2552	OMU	C2-N3	5.94	1.48	1.38
22	a	745	1MG	C2-N2	5.94	1.44	1.34
1	A	1498	UR3	C6-C5	5.91	1.48	1.35
22	a	1915	3TD	C6-N1	5.87	1.46	1.36
53	5	46	G7M	C2-N3	5.75	1.47	1.33
1	A	1402	4OC	C2-N3	5.68	1.47	1.36
53	5	8	4SU	C5-C4	5.62	1.49	1.42
54	6	8	4SU	C5-C4	5.58	1.49	1.42
53	5	8	4SU	C6-C5	5.51	1.47	1.35
54	6	8	4SU	C6-C5	5.45	1.47	1.35
1	A	527	G7M	C2-N3	5.44	1.46	1.33
22	a	2552	OMU	C6-C5	5.43	1.47	1.35
22	a	2069	G7M	C2-N3	5.21	1.45	1.33
1	A	527	G7M	C5-N7	-4.73	1.33	1.39
22	a	2503	2MA	C5-C6	4.62	1.53	1.41
22	a	2069	G7M	C5-N7	-4.60	1.33	1.39
33	l	81	4D4	CZ-NE	4.53	1.42	1.33
1	A	1498	UR3	C2-N3	4.45	1.47	1.39
53	5	46	G7M	C5-N7	-4.41	1.34	1.39
54	6	8	4SU	C4-S4	-4.38	1.60	1.68
53	5	8	4SU	C4-S4	-4.31	1.60	1.68
1	A	1402	4OC	C4-N4	4.30	1.44	1.35
22	a	2503	2MA	C6-N1	4.22	1.41	1.35
22	a	1915	3TD	C2-N3	4.18	1.47	1.38
53	5	46	G7M	C5-C6	3.78	1.53	1.43
1	A	1402	4OC	C2-N1	3.75	1.48	1.40
1	A	1402	4OC	C5-C4	3.71	1.48	1.40
1	A	527	G7M	C5-C6	3.59	1.53	1.43
22	a	2503	2MA	C6-N6	-3.59	1.25	1.34
22	a	2069	G7M	C5-C6	3.46	1.53	1.43
33	l	82	MS6	CA-N	-3.42	1.37	1.48
54	6	56	PSU	C6-C5	3.40	1.39	1.35
22	a	2504	PSU	C6-C5	3.38	1.39	1.35
1	A	1518	MA6	C5-C4	-3.35	1.32	1.39
53	5	55	PSU	C6-C5	3.34	1.39	1.35
1	A	1519	MA6	C5-C4	-3.29	1.32	1.39
53	5	37	MIA	C5-C4	-3.18	1.33	1.39
22	a	1911	PSU	C6-C5	3.17	1.39	1.35
22	a	745	1MG	C5-N7	-3.16	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1402	4OC	O2-C2	-3.07	1.18	1.23
1	A	1518	MA6	C5-N7	-3.05	1.33	1.39
53	5	32	PSU	C6-C5	3.04	1.38	1.35
22	a	2552	OMU	O4-C4	-3.03	1.18	1.24
22	a	2030	6MZ	C5-C4	-3.00	1.33	1.39
22	a	745	1MG	C5-C6	2.99	1.53	1.45
53	5	46	G7M	C2-N1	2.96	1.45	1.37
22	a	2552	OMU	O2-C2	-2.96	1.17	1.23
53	5	39	PSU	C6-C5	2.96	1.38	1.35
22	a	1618	6MZ	C5-C4	-2.95	1.33	1.39
22	a	2605	PSU	C6-C5	2.95	1.38	1.35
22	a	2069	G7M	O6-C6	-2.92	1.18	1.23
1	A	1402	4OC	C6-N1	2.92	1.45	1.38
22	a	2604	PSU	C6-C5	2.90	1.38	1.35
22	a	2552	OMU	C4-N3	2.88	1.43	1.38
53	5	46	G7M	C6-N1	2.88	1.44	1.38
1	A	527	G7M	C2-N1	2.88	1.44	1.37
22	a	2503	2MA	C5-N7	-2.87	1.33	1.39
1	A	1519	MA6	C5-N7	-2.84	1.33	1.39
1	A	1498	UR3	C6-N1	2.83	1.44	1.38
22	a	2457	PSU	C6-C5	2.83	1.38	1.35
22	a	1917	PSU	C6-C5	2.81	1.38	1.35
1	A	527	G7M	C6-N1	2.78	1.44	1.38
1	A	516	PSU	C6-C5	2.77	1.38	1.35
22	a	955	PSU	C6-C5	2.76	1.38	1.35
1	A	1519	MA6	C6-N6	2.75	1.45	1.36
53	5	8	4SU	C6-N1	2.75	1.44	1.38
22	a	746	PSU	C6-C5	2.75	1.38	1.35
1	A	1518	MA6	C6-N6	2.74	1.44	1.36
1	A	1518	MA6	C8-N9	-2.73	1.32	1.37
54	6	8	4SU	C6-N1	2.73	1.44	1.38
1	A	527	G7M	O6-C6	-2.67	1.18	1.23
22	a	2580	PSU	C6-C5	2.67	1.38	1.35
11	K	119	IAS	O-C	2.60	1.30	1.22
22	a	1915	3TD	C4-N3	2.54	1.45	1.40
22	a	2069	G7M	C2-N1	2.54	1.44	1.37
53	5	46	G7M	O6-C6	-2.53	1.18	1.23
1	A	1519	MA6	C8-N9	-2.53	1.33	1.37
22	a	2503	2MA	C8-N7	2.51	1.36	1.31
33	l	81	4D4	O-C	2.49	1.29	1.19
1	A	1498	UR3	O2-C2	-2.47	1.18	1.22
1	A	1498	UR3	O4-C4	-2.46	1.18	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	a	745	1MG	C4-N9	-2.41	1.31	1.38
22	a	2069	G7M	C6-N1	2.41	1.43	1.38
22	a	1618	6MZ	C8-N9	-2.34	1.33	1.37
22	a	1915	3TD	O4-C4	-2.33	1.18	1.23
22	a	1618	6MZ	C5-N7	-2.33	1.34	1.39
22	a	2030	6MZ	C8-N9	-2.32	1.33	1.37
22	a	745	1MG	O6-C6	-2.29	1.18	1.23
22	a	2030	6MZ	C5-N7	-2.29	1.34	1.39
33	l	81	4D4	CZ-NH1	2.26	1.44	1.34
53	5	37	MIA	C8-N7	2.23	1.35	1.31
22	a	2580	PSU	O4'-C1'	-2.20	1.40	1.43
53	5	37	MIA	C8-N9	-2.15	1.33	1.37
22	a	1915	3TD	O2-C2	-2.15	1.19	1.23
1	A	1498	UR3	C5-C4	2.08	1.49	1.43
53	5	46	G7M	C8-N7	2.03	1.36	1.33
12	L	89	D2T	CB1-SB	-2.02	1.75	1.79
22	a	2605	PSU	C4-C5	-2.01	1.38	1.44
22	a	746	PSU	C4-C5	-2.00	1.38	1.44

All (201) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1519	MA6	N1-C6-N6	-18.93	96.38	117.08
1	A	1518	MA6	N1-C6-N6	-17.79	97.63	117.08
53	5	37	MIA	C1'-N9-C8	-12.72	98.42	127.14
53	5	37	MIA	C4-N9-C1'	11.30	153.51	126.59
1	A	1519	MA6	C5-C6-N6	10.46	143.52	125.30
53	5	37	MIA	C11-S10-C2	10.18	109.87	102.27
1	A	1518	MA6	C5-C6-N6	9.79	142.35	125.30
54	6	8	4SU	C4-N3-C2	-7.84	119.73	127.34
53	5	8	4SU	C4-N3-C2	-7.72	119.84	127.34
1	A	1519	MA6	C4-N9-C1'	-7.43	108.89	126.59
53	5	37	MIA	S10-C2-N3	7.29	141.23	116.01
1	A	1518	MA6	C4-N9-C1'	-7.06	109.77	126.59
1	A	1519	MA6	C1'-N9-C8	6.67	142.20	127.14
1	A	1518	MA6	C1'-N9-C8	6.20	141.14	127.14
22	a	2503	2MA	C5-C4-N3	-6.09	120.34	127.19
1	A	1519	MA6	N1-C2-N3	-5.63	119.80	128.60
54	6	8	4SU	C5-C4-N3	5.60	119.88	114.69
22	a	2552	OMU	C4-N3-C2	-5.52	119.29	126.58
22	a	2030	6MZ	N1-C2-N3	-5.52	119.96	128.60
1	A	1519	MA6	C5-C4-N3	-5.51	119.56	126.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	5	37	MIA	C5-C4-N3	-5.50	121.01	127.19
1	A	1518	MA6	C5-C4-N3	-5.48	119.60	126.75
53	5	8	4SU	C5-C4-N3	5.46	119.75	114.69
1	A	1518	MA6	N1-C2-N3	-5.40	120.16	128.60
22	a	1618	6MZ	N1-C2-N3	-5.38	120.19	128.60
22	a	1915	3TD	N1-C2-N3	5.37	120.38	116.14
22	a	2580	PSU	N1-C2-N3	5.37	121.21	115.13
22	a	955	PSU	N1-C2-N3	5.19	121.01	115.13
22	a	955	PSU	C4-N3-C2	-5.07	119.04	126.34
22	a	2604	PSU	N1-C2-N3	5.05	120.85	115.13
53	5	37	MIA	S10-C2-N1	-5.04	98.57	116.01
22	a	1618	6MZ	C5-C4-N3	-4.97	120.26	126.75
22	a	2580	PSU	C4-N3-C2	-4.97	119.19	126.34
1	A	1498	UR3	C4-N3-C2	-4.88	119.97	124.56
22	a	2030	6MZ	C5-C4-N3	-4.87	120.40	126.75
22	a	2604	PSU	C4-N3-C2	-4.85	119.35	126.34
1	A	516	PSU	C4-N3-C2	-4.82	119.39	126.34
22	a	2457	PSU	N1-C2-N3	4.82	120.59	115.13
53	5	55	PSU	N1-C2-N3	4.77	120.54	115.13
53	5	55	PSU	C4-N3-C2	-4.77	119.47	126.34
53	5	37	MIA	N9-C8-N7	-4.76	107.40	113.91
53	5	32	PSU	C4-N3-C2	-4.76	119.48	126.34
53	5	39	PSU	C4-N3-C2	-4.75	119.50	126.34
22	a	745	1MG	C5-C4-N3	-4.74	120.78	128.46
53	5	32	PSU	N1-C2-N3	4.73	120.49	115.13
22	a	2457	PSU	C4-N3-C2	-4.71	119.55	126.34
22	a	2605	PSU	C4-N3-C2	-4.71	119.55	126.34
22	a	1911	PSU	C4-N3-C2	-4.69	119.58	126.34
22	a	2605	PSU	N1-C2-N3	4.68	120.43	115.13
22	a	1917	PSU	C4-N3-C2	-4.65	119.64	126.34
22	a	1618	6MZ	N9-C8-N7	-4.65	107.56	113.91
22	a	1917	PSU	N1-C2-N3	4.64	120.38	115.13
22	a	746	PSU	C4-N3-C2	-4.60	119.70	126.34
22	a	1911	PSU	N1-C2-N3	4.59	120.33	115.13
1	A	1519	MA6	N9-C8-N7	-4.57	107.67	113.91
53	5	39	PSU	N1-C2-N3	4.53	120.27	115.13
22	a	2503	2MA	N9-C8-N7	-4.53	107.71	113.91
22	a	2030	6MZ	N9-C8-N7	-4.52	107.73	113.91
54	6	56	PSU	C4-N3-C2	-4.52	119.82	126.34
1	A	516	PSU	N1-C2-N3	4.51	120.24	115.13
1	A	1518	MA6	N9-C8-N7	-4.48	107.78	113.91
22	a	2069	G7M	C2-N3-C4	4.46	120.25	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	746	PSU	N1-C2-N3	4.45	120.17	115.13
22	a	2504	PSU	N1-C2-N3	4.41	120.13	115.13
53	5	46	G7M	C2-N3-C4	4.37	120.09	112.30
22	a	2030	6MZ	C9-N6-C6	-4.32	119.16	122.87
1	A	527	G7M	C2-N3-C4	4.31	119.99	112.30
1	A	1518	MA6	C4-C5-C6	4.30	120.69	115.88
22	a	1915	3TD	C4-N3-C2	-4.30	119.95	124.61
54	6	56	PSU	N1-C2-N3	4.30	120.00	115.13
1	A	1518	MA6	N3-C4-N9	4.25	134.09	127.08
22	a	2504	PSU	C4-N3-C2	-4.20	120.29	126.34
22	a	2069	G7M	C5-C6-N1	4.14	120.44	111.79
12	L	89	D2T	OD2-CG-CB	4.14	122.10	113.15
53	5	46	G7M	C5-C4-N3	-4.01	120.45	128.15
53	5	46	G7M	C5-C6-N1	3.97	120.07	111.79
1	A	527	G7M	C5-C6-N1	3.96	120.06	111.79
1	A	527	G7M	C5-C4-N3	-3.92	120.64	128.15
1	A	1519	MA6	N3-C4-N9	3.91	133.52	127.08
22	a	1618	6MZ	C9-N6-C6	-3.90	119.51	122.87
1	A	1519	MA6	C4-C5-C6	3.87	120.21	115.88
53	5	37	MIA	N6-C6-N1	3.85	123.41	118.50
22	a	2552	OMU	C5-C4-N3	3.85	120.59	114.84
53	5	8	4SU	N3-C2-N1	3.79	119.93	114.89
1	A	1519	MA6	C2-N3-C4	3.70	120.49	111.75
22	a	2552	OMU	N3-C2-N1	3.70	119.80	114.89
1	A	527	G7M	O6-C6-C5	-3.69	119.74	128.06
53	5	37	MIA	N3-C2-N1	-3.68	120.20	126.95
22	a	2069	G7M	C5-C4-N3	-3.67	121.10	128.15
22	a	745	1MG	C2-N3-C4	3.64	120.17	111.98
54	6	8	4SU	N3-C2-N1	3.64	119.72	114.89
54	6	8	4SU	C5-C4-S4	-3.62	119.81	124.47
53	5	46	G7M	O6-C6-C5	-3.55	120.05	128.06
22	a	2030	6MZ	C2-N3-C4	3.54	120.11	111.75
22	a	2069	G7M	O6-C6-C5	-3.52	120.11	128.06
22	a	1618	6MZ	C4-C5-C6	3.51	119.53	116.81
22	a	1618	6MZ	C2-N3-C4	3.47	119.95	111.75
22	a	2503	2MA	N3-C4-N9	3.45	131.78	126.99
1	A	1518	MA6	C2-N3-C4	3.45	119.90	111.75
1	A	1519	MA6	C2-N1-C6	3.42	119.84	111.75
53	5	37	MIA	C5-N7-C8	3.41	108.35	103.51
54	6	21	H2U	C5-C4-N3	-3.35	112.89	116.65
1	A	1518	MA6	C2-N1-C6	3.34	119.64	111.75
53	5	8	4SU	C5-C4-S4	-3.32	120.19	124.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	2503	2MA	N3-C2-N1	-3.29	119.67	125.72
22	a	2503	2MA	C5-N7-C8	3.28	108.17	103.51
22	a	2030	6MZ	C5-N7-C8	3.23	108.10	103.51
22	a	2580	PSU	O2-C2-N1	-3.17	119.30	122.79
53	5	46	G7M	N9-C4-N3	3.16	132.29	125.94
33	l	81	4D4	NE-CZ-NH2	3.16	126.25	120.70
22	a	2030	6MZ	C4-C5-C6	3.14	119.24	116.81
22	a	1618	6MZ	C5-N7-C8	3.13	107.96	103.51
22	a	745	1MG	N9-C8-N7	-3.12	107.52	113.39
22	a	955	PSU	O2-C2-N1	-3.11	119.37	122.79
1	A	527	G7M	C2-N1-C6	-3.10	119.44	125.10
1	A	1518	MA6	C4-N9-C8	3.10	109.08	105.73
53	5	46	G7M	C2-N1-C6	-3.05	119.54	125.10
1	A	516	PSU	O2-C2-N1	-3.05	119.43	122.79
1	A	1519	MA6	C5-N7-C8	3.04	107.82	103.51
1	A	527	G7M	N9-C4-N3	3.03	132.02	125.94
53	5	37	MIA	C5-C6-N6	-3.01	116.68	121.76
22	a	2552	OMU	O4-C4-C5	-3.00	119.89	125.16
22	a	1618	6MZ	N3-C4-N9	2.97	131.98	127.08
22	a	2069	G7M	C2-N1-C6	-2.94	119.73	125.10
1	A	1519	MA6	C4-N9-C8	2.93	108.90	105.73
1	A	1518	MA6	C5-N7-C8	2.90	107.63	103.51
22	a	745	1MG	C1'-N9-C8	-2.85	118.58	126.70
22	a	2580	PSU	C6-C5-C4	2.82	120.17	118.20
53	5	37	MIA	C4-C5-C6	2.80	118.98	116.81
53	5	37	MIA	C2-N3-C4	2.80	119.73	112.35
22	a	745	1MG	N9-C4-N3	2.79	131.54	125.94
22	a	2504	PSU	C6-N1-C2	-2.77	119.85	122.68
53	5	39	PSU	O2-C2-N1	-2.77	119.74	122.79
22	a	746	PSU	O2-C2-N1	-2.76	119.75	122.79
22	a	2449	H2U	C5-C4-N3	-2.75	113.56	116.65
22	a	2069	G7M	N9-C4-N3	2.74	131.45	125.94
22	a	2604	PSU	O2-C2-N1	-2.73	119.79	122.79
22	a	745	1MG	C5-C6-N1	2.72	120.16	114.91
22	a	955	PSU	C6-C5-C4	2.68	120.07	118.20
22	a	1618	6MZ	C4-N9-C8	2.67	108.62	105.73
53	5	37	MIA	C12-C13-C14	-2.66	121.96	127.14
22	a	2604	PSU	C6-C5-C4	2.65	120.05	118.20
22	a	1917	PSU	O2-C2-N1	-2.65	119.88	122.79
12	L	89	D2T	OD1-CG-CB	-2.62	116.95	122.44
22	a	2580	PSU	C6-N1-C2	-2.62	120.01	122.68
53	5	37	MIA	C4-C5-N7	-2.61	107.44	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	5	32	PSU	O2-C2-N1	-2.61	119.92	122.79
22	a	2457	PSU	O2-C2-N1	-2.61	119.92	122.79
53	5	55	PSU	O2-C2-N1	-2.57	119.96	122.79
22	a	2069	G7M	CN7-N7-C5	2.56	129.94	126.77
53	5	37	MIA	C5-C4-N9	2.55	108.75	105.78
22	a	2030	6MZ	C4-C5-N7	-2.52	107.55	110.62
53	5	37	MIA	C16-C14-C15	2.52	120.16	114.60
33	l	81	4D4	O-C-CA	-2.51	118.20	124.78
54	6	21	H2U	O2-C2-N1	2.47	126.21	123.11
33	l	82	MS6	CE-SD-CG	2.44	108.77	100.40
22	a	2457	PSU	C6-N1-C2	-2.42	120.21	122.68
22	a	2030	6MZ	N3-C4-N9	2.41	131.05	127.08
22	a	2503	2MA	C4-N9-C8	2.41	108.34	105.73
22	a	2030	6MZ	C5-C4-N9	2.38	108.55	105.78
22	a	2580	PSU	O4'-C1'-C2'	2.36	108.48	105.14
22	a	955	PSU	C6-N1-C2	-2.35	120.28	122.68
53	5	32	PSU	C6-C5-C4	2.35	119.84	118.20
1	A	516	PSU	O4'-C1'-C2'	2.35	108.45	105.14
53	5	37	MIA	N3-C4-N9	2.35	130.25	126.99
1	A	527	G7M	CN7-N7-C5	2.33	129.66	126.77
22	a	1917	PSU	C6-N1-C2	-2.32	120.32	122.68
54	6	56	PSU	O2-C2-N1	-2.31	120.25	122.79
1	A	1402	4OC	C6-C5-C4	2.29	119.76	116.96
22	a	2604	PSU	C6-N1-C2	-2.29	120.34	122.68
53	5	55	PSU	C6-N1-C2	-2.28	120.36	122.68
22	a	2605	PSU	C6-N1-C2	-2.27	120.36	122.68
22	a	1911	PSU	C6-N1-C2	-2.25	120.38	122.68
22	a	746	PSU	C6-N1-C2	-2.25	120.39	122.68
22	a	2503	2MA	C4-C5-N7	-2.24	107.89	110.62
53	5	32	PSU	C6-N1-C2	-2.21	120.42	122.68
22	a	2069	G7M	N9-C8-N7	-2.20	106.76	112.21
22	a	1911	PSU	O2-C2-N1	-2.20	120.37	122.79
54	6	8	4SU	O2-C2-N1	-2.18	119.89	122.79
53	5	55	PSU	C6-C5-C4	2.17	119.72	118.20
22	a	2030	6MZ	C4-N9-C8	2.17	108.08	105.73
53	5	37	MIA	C4-N9-C8	2.16	108.07	105.73
53	5	39	PSU	C6-N1-C2	-2.16	120.48	122.68
53	5	8	4SU	O2-C2-N1	-2.16	119.92	122.79
12	L	89	D2T	CB-CA-N	2.13	113.63	109.10
22	a	1915	3TD	C6-C5-C4	2.13	119.69	118.22
53	5	46	G7M	CN7-N7-C5	2.12	129.41	126.77
22	a	2449	H2U	C4-N3-C2	2.11	127.55	125.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	a	2503	2MA	CM2-C2-N1	2.10	120.43	117.15
53	5	32	PSU	O4'-C1'-C2'	2.09	108.10	105.14
22	a	1917	PSU	C6-C5-C4	2.09	119.66	118.20
53	5	46	G7M	N9-C8-N7	-2.08	107.07	112.21
22	a	1618	6MZ	C4-C5-N7	-2.07	108.10	110.62
33	l	81	4D4	NH1-CZ-NE	-2.06	114.44	119.19
22	a	745	1MG	C1'-N9-C4	2.05	132.59	126.50
22	a	2069	G7M	N1-C2-N3	-2.05	119.50	123.32
54	6	56	PSU	C6-N1-C2	-2.04	120.59	122.68
22	a	2503	2MA	N6-C6-N1	2.04	119.91	117.03
1	A	527	G7M	N9-C8-N7	-2.03	107.19	112.21
22	a	2069	G7M	CN7-N7-C8	-2.02	121.73	124.84
1	A	1498	UR3	C6-N1-C2	-2.01	119.99	121.79

There are no chirality outliers.

All (43) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	L	89	D2T	CG-CB-SB-CB1
25	d	150	MEQ	N-CA-CB-CG
53	5	37	MIA	N1-C2-S10-C11
53	5	37	MIA	N3-C2-S10-C11
54	6	56	PSU	O4'-C1'-C5-C4
54	6	56	PSU	O4'-C1'-C5-C6
22	a	2251	OMG	C1'-C2'-O2'-CM2
22	a	2445	2MG	O4'-C4'-C5'-O5'
22	a	2445	2MG	C3'-C4'-C5'-O5'
33	l	82	MS6	CA-CB-CG-SD
22	a	2030	6MZ	O4'-C4'-C5'-O5'
22	a	2030	6MZ	C3'-C4'-C5'-O5'
22	a	2498	OMC	O4'-C4'-C5'-O5'
25	d	150	MEQ	OE1-CD-CG-CB
25	d	150	MEQ	NE2-CD-CG-CB
54	6	21	H2U	C2'-C1'-N1-C2
53	5	46	G7M	C4'-C5'-O5'-P
1	A	966	2MG	C3'-C4'-C5'-O5'
54	6	21	H2U	C2'-C1'-N1-C6
25	d	150	MEQ	C-CA-CB-CG
33	l	82	MS6	CB-CG-SD-CE
53	5	46	G7M	C3'-C4'-C5'-O5'
1	A	1402	4OC	O4'-C4'-C5'-O5'
1	A	966	2MG	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
22	a	2503	2MA	C4'-C5'-O5'-P
53	5	37	MIA	C13-C12-N6-C6
54	6	21	H2U	C4'-C5'-O5'-P
22	a	2498	OMC	C3'-C4'-C5'-O5'
54	6	55	5MU	C3'-C4'-C5'-O5'
53	5	55	PSU	O4'-C1'-C5-C4
33	l	81	4D4	CG-CD-NE-CZ
1	A	527	G7M	C3'-C4'-C5'-O5'
54	6	55	5MU	O4'-C4'-C5'-O5'
22	a	747	5MU	C3'-C4'-C5'-O5'
22	a	2449	H2U	O4'-C4'-C5'-O5'
22	a	746	PSU	O4'-C1'-C5-C6
33	l	82	MS6	N-CA-CB-CG
22	a	2069	G7M	O4'-C4'-C5'-O5'
22	a	2503	2MA	O4'-C4'-C5'-O5'
11	K	119	IAS	CA-CB-CG-OD1
1	A	1402	4OC	C3'-C4'-C5'-O5'
1	A	527	G7M	C4'-C5'-O5'-P
22	a	2251	OMG	C4'-C5'-O5'-P

There are no ring outliers.

30 monomers are involved in 58 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	6	33	OMC	1	0
22	a	1917	PSU	2	0
22	a	2069	G7M	1	0
22	a	2580	PSU	1	0
1	A	1407	5MC	2	0
22	a	2552	OMU	1	0
22	a	1962	5MC	1	0
22	a	2030	6MZ	4	0
54	6	55	5MU	2	0
22	a	2504	PSU	1	0
22	a	2498	OMC	1	0
53	5	37	MIA	7	0
1	A	1207	2MG	1	0
22	a	2457	PSU	1	0
1	A	527	G7M	1	0
1	A	1518	MA6	3	0
53	5	39	PSU	1	0
1	A	1516	2MG	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	a	2445	2MG	2	0
1	A	1519	MA6	2	0
1	A	966	2MG	3	0
54	6	8	4SU	2	0
54	6	21	H2U	4	0
53	5	46	G7M	6	0
54	6	56	PSU	4	0
22	a	2503	2MA	1	0
1	A	1402	4OC	1	0
22	a	2251	OMG	1	0
25	d	150	MEQ	2	0
53	5	8	4SU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 488 ligands modelled in this entry, 461 are monoatomic - leaving 27 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	$\# Z > 2$
57	SPD	a	6194	-	9,9,9	0.30	0	8,8,8	0.88	0
59	SPM	a	6204	-	13,13,13	0.34	0	12,12,12	0.73	0
58	84G	A	1791	-	39,40,40	1.91	9 (23%)	47,57,57	1.24	5 (10%)
57	SPD	a	6199	-	9,9,9	0.30	0	8,8,8	0.73	0
58	84G	a	6254	-	39,40,40	1.80	6 (15%)	47,57,57	1.13	3 (6%)
57	SPD	A	1667	1	9,9,9	0.33	0	8,8,8	0.72	0
58	84G	a	6252	-	39,40,40	1.88	7 (17%)	47,57,57	1.17	4 (8%)
58	84G	a	6250	-	39,40,40	1.86	9 (23%)	47,57,57	1.07	4 (8%)
57	SPD	a	6192	-	9,9,9	0.33	0	8,8,8	0.99	0
57	SPD	a	6203	-	9,9,9	0.34	0	8,8,8	0.76	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
57	SPD	a	6193	-	9,9,9	0.32	0	8,8,8	0.83	0
58	84G	a	6255	-	39,40,40	1.84	6 (15%)	47,57,57	1.26	5 (10%)
57	SPD	a	6190	-	9,9,9	0.33	0	8,8,8	0.78	0
57	SPD	a	6195	-	9,9,9	0.33	0	8,8,8	0.86	0
57	SPD	a	6196	-	9,9,9	0.32	0	8,8,8	0.81	0
57	SPD	a	6201	-	9,9,9	0.32	0	8,8,8	0.88	0
57	SPD	a	6198	-	9,9,9	0.33	0	8,8,8	0.87	0
58	84G	a	6249	-	39,40,40	1.86	6 (15%)	47,57,57	1.22	4 (8%)
58	84G	A	1793	-	39,40,40	1.86	9 (23%)	47,57,57	1.01	3 (6%)
58	84G	a	6251	-	39,40,40	1.92	7 (17%)	47,57,57	1.15	5 (10%)
57	SPD	A	1668	1	9,9,9	0.32	0	8,8,8	0.90	0
57	SPD	a	6202	-	9,9,9	0.34	0	8,8,8	0.90	0
57	SPD	a	6191	-	9,9,9	0.33	0	8,8,8	0.79	0
57	SPD	a	6197	-	9,9,9	0.32	0	8,8,8	0.95	0
57	SPD	a	6200	-	9,9,9	0.34	0	8,8,8	0.82	0
58	84G	A	1792	-	39,40,40	1.88	8 (20%)	47,57,57	1.26	6 (12%)
58	84G	a	6253	-	39,40,40	1.86	8 (20%)	47,57,57	1.12	3 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	SPD	a	6194	-	-	3/7/7/7	-
59	SPM	a	6204	-	-	3/11/11/11	-
58	84G	A	1791	-	-	3/23/76/76	0/3/3/3
57	SPD	a	6199	-	-	3/7/7/7	-
58	84G	a	6254	-	-	4/23/76/76	0/3/3/3
57	SPD	A	1667	1	-	3/7/7/7	-
58	84G	a	6252	-	-	11/23/76/76	0/3/3/3
58	84G	a	6250	-	-	8/23/76/76	0/3/3/3
57	SPD	a	6192	-	-	3/7/7/7	-
57	SPD	a	6203	-	-	1/7/7/7	-
57	SPD	a	6193	-	-	1/7/7/7	-
58	84G	a	6255	-	-	4/23/76/76	0/3/3/3
57	SPD	a	6190	-	-	3/7/7/7	-
57	SPD	a	6195	-	-	6/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	SPD	a	6196	-	-	3/7/7/7	-
57	SPD	a	6201	-	-	1/7/7/7	-
57	SPD	a	6198	-	-	2/7/7/7	-
58	84G	a	6249	-	-	3/23/76/76	0/3/3/3
58	84G	A	1793	-	-	3/23/76/76	0/3/3/3
58	84G	a	6251	-	-	5/23/76/76	0/3/3/3
57	SPD	A	1668	1	-	3/7/7/7	-
57	SPD	a	6202	-	-	1/7/7/7	-
57	SPD	a	6191	-	-	5/7/7/7	-
57	SPD	a	6197	-	-	3/7/7/7	-
57	SPD	a	6200	-	-	3/7/7/7	-
58	84G	A	1792	-	-	4/23/76/76	0/3/3/3
58	84G	a	6253	-	-	4/23/76/76	0/3/3/3

All (75) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	a	6250	84G	C3-N1	6.56	1.48	1.34
58	a	6253	84G	C3-N1	6.49	1.48	1.34
58	a	6249	84G	C3-N1	6.48	1.48	1.34
58	A	1793	84G	C3-N1	6.45	1.48	1.34
58	a	6252	84G	C3-N1	6.39	1.48	1.34
58	a	6254	84G	C3-N1	6.32	1.48	1.34
58	A	1791	84G	C3-N1	6.31	1.47	1.34
58	a	6255	84G	C3-N1	6.25	1.47	1.34
58	a	6251	84G	C3-N1	6.16	1.47	1.34
58	a	6251	84G	C19-C20	-6.11	1.45	1.53
58	A	1792	84G	C3-N1	6.03	1.47	1.34
58	A	1791	84G	C19-C20	-5.51	1.46	1.53
58	A	1792	84G	C19-C20	-5.35	1.46	1.53
58	a	6252	84G	C19-C20	-5.27	1.46	1.53
58	A	1793	84G	C19-C20	-5.22	1.47	1.53
58	a	6253	84G	C19-C20	-5.14	1.47	1.53
58	a	6249	84G	C19-C20	-5.09	1.47	1.53
58	a	6250	84G	C19-C20	-5.08	1.47	1.53
58	a	6255	84G	C19-C20	-4.92	1.47	1.53
58	a	6254	84G	C19-C20	-4.87	1.47	1.53
58	A	1792	84G	C21-C20	-4.16	1.48	1.53
58	a	6251	84G	C21-C20	-3.98	1.48	1.53
58	A	1791	84G	C21-C20	-3.85	1.48	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	a	6252	84G	C21-C20	-3.68	1.48	1.53
58	A	1793	84G	C21-C20	-3.66	1.48	1.53
58	a	6249	84G	C21-C20	-3.49	1.49	1.53
58	a	6253	84G	C21-C20	-3.28	1.49	1.53
58	a	6250	84G	C21-C20	-3.28	1.49	1.53
58	a	6255	84G	C21-C20	-3.26	1.49	1.53
58	a	6254	84G	C21-C20	-3.23	1.49	1.53
58	A	1792	84G	C20-N5	3.23	1.52	1.47
58	a	6255	84G	C20-N5	3.14	1.52	1.47
58	a	6254	84G	C20-N5	3.11	1.52	1.47
58	a	6250	84G	C20-N5	3.10	1.52	1.47
58	a	6252	84G	C20-N5	3.07	1.52	1.47
58	a	6253	84G	C20-N5	3.07	1.51	1.47
58	A	1793	84G	C20-N5	3.06	1.51	1.47
58	a	6251	84G	C20-N5	3.05	1.51	1.47
58	a	6249	84G	C20-N5	2.94	1.51	1.47
58	A	1791	84G	C20-N5	2.90	1.51	1.47
58	a	6250	84G	O3-C8	2.81	1.49	1.41
58	a	6255	84G	O3-C8	2.70	1.48	1.41
58	a	6253	84G	O3-C8	2.66	1.48	1.41
58	a	6249	84G	O3-C8	2.65	1.48	1.41
58	A	1791	84G	O3-C8	2.60	1.48	1.41
58	A	1792	84G	O3-C8	2.56	1.48	1.41
58	a	6252	84G	O3-C8	2.48	1.48	1.41
58	A	1793	84G	O3-C8	2.47	1.48	1.41
58	a	6254	84G	O3-C8	2.47	1.48	1.41
58	a	6251	84G	O3-C8	2.44	1.48	1.41
58	A	1792	84G	O1-C3	-2.36	1.18	1.23
58	a	6255	84G	O1-C3	-2.35	1.18	1.23
58	A	1791	84G	O1-C3	-2.34	1.18	1.23
58	a	6253	84G	O1-C3	-2.30	1.18	1.23
58	a	6251	84G	O1-C3	-2.27	1.18	1.23
58	a	6250	84G	O1-C3	-2.26	1.18	1.23
58	a	6252	84G	C2-C3	2.18	1.55	1.52
58	A	1793	84G	O1-C3	-2.18	1.19	1.23
58	a	6252	84G	O1-C3	-2.16	1.19	1.23
58	a	6251	84G	O6-C17	2.15	1.49	1.44
58	a	6253	84G	C11-C12	-2.13	1.47	1.52
58	A	1791	84G	C11-C12	-2.10	1.47	1.52
58	A	1791	84G	O6-C17	2.10	1.49	1.44
58	a	6254	84G	O1-C3	-2.09	1.19	1.23
58	A	1792	84G	C11-C12	-2.08	1.47	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	A	1793	84G	C11-C12	-2.07	1.47	1.52
58	A	1792	84G	O6-C17	2.06	1.49	1.44
58	a	6250	84G	C11-C12	-2.06	1.47	1.52
58	A	1791	84G	O-C2	-2.05	1.38	1.42
58	a	6249	84G	O1-C3	-2.05	1.19	1.23
58	A	1793	84G	O6-C16	2.04	1.47	1.41
58	A	1793	84G	O6-C17	2.02	1.49	1.44
58	a	6253	84G	O6-C17	2.01	1.49	1.44
58	a	6250	84G	O-C2	-2.01	1.38	1.42
58	a	6250	84G	O6-C16	2.00	1.47	1.41

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	A	1792	84G	O3-C9-C11	3.87	114.01	109.86
58	A	1791	84G	O3-C9-C11	3.74	113.88	109.86
58	a	6255	84G	O3-C9-C11	3.56	113.69	109.86
58	a	6249	84G	O3-C9-C11	3.33	113.44	109.86
58	A	1791	84G	C5-C4-N1	-3.27	105.80	110.86
58	a	6254	84G	O3-C9-C11	3.05	113.14	109.86
58	a	6253	84G	C8-O2-C7	-2.95	110.66	117.96
58	a	6252	84G	C5-C4-N1	-2.82	106.50	110.86
58	A	1792	84G	C5-C4-N1	-2.79	106.54	110.86
58	a	6249	84G	C7-C14-C15	2.77	114.71	108.96
58	a	6254	84G	C8-O2-C7	-2.76	111.13	117.96
58	a	6251	84G	C5-C4-N1	-2.67	106.73	110.86
58	a	6251	84G	C19-C20-N5	-2.63	105.66	111.05
58	a	6252	84G	C7-C14-C15	2.59	114.33	108.96
58	A	1793	84G	C16-C21-C20	2.58	113.86	110.40
58	A	1791	84G	C7-C14-C15	2.57	114.28	108.96
58	A	1792	84G	C16-O5-C15	-2.49	111.81	117.96
58	a	6250	84G	C16-O5-C15	-2.47	111.84	117.96
58	A	1791	84G	C11-C9-C10	-2.47	108.11	112.83
58	A	1792	84G	C8-O2-C7	-2.46	111.88	117.96
58	a	6252	84G	O6-C17-C19	2.46	114.16	109.69
58	a	6249	84G	C16-O5-C15	-2.41	111.99	117.96
58	a	6249	84G	C11-C9-C10	-2.34	108.36	112.83
58	a	6253	84G	O3-C9-C11	2.32	112.35	109.86
58	A	1792	84G	C11-C9-C10	-2.30	108.44	112.83
58	a	6252	84G	O3-C9-C11	2.29	112.32	109.86
58	a	6251	84G	C16-O5-C15	-2.24	112.41	117.96
58	a	6255	84G	C16-O5-C15	-2.23	112.44	117.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	a	6250	84G	C8-O2-C7	-2.19	112.54	117.96
58	a	6255	84G	C16-C21-C20	2.17	113.32	110.40
58	A	1793	84G	C8-O2-C7	-2.17	112.60	117.96
58	a	6250	84G	O3-C8-C13	2.13	115.00	110.25
58	A	1791	84G	O2-C7-C6	-2.11	104.15	109.18
58	A	1792	84G	O6-C17-C19	2.10	113.51	109.69
58	a	6254	84G	C11-C9-C10	-2.08	108.86	112.83
58	a	6250	84G	C16-C21-C20	2.07	113.18	110.40
58	a	6251	84G	C8-O2-C7	-2.07	112.85	117.96
58	a	6251	84G	C21-C20-N5	-2.05	106.86	111.05
58	a	6255	84G	C5-C4-N1	-2.04	107.71	110.86
58	a	6255	84G	C8-O2-C7	-2.04	112.92	117.96
58	A	1793	84G	C16-O5-C15	-2.03	112.95	117.96
58	a	6253	84G	C11-C9-C10	-2.01	108.99	112.83

There are no chirality outliers.

All (96) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	a	6198	SPD	C8-C7-N6-C5
58	A	1793	84G	N3-C10-C9-O3
58	A	1793	84G	N3-C10-C9-C11
58	a	6250	84G	C-C1-C2-C3
58	a	6250	84G	N3-C10-C9-O3
58	a	6250	84G	N3-C10-C9-C11
58	a	6251	84G	N3-C10-C9-O3
58	a	6251	84G	N3-C10-C9-C11
58	a	6252	84G	C-C1-C2-O
58	a	6252	84G	C1-C2-C3-O1
58	a	6252	84G	C1-C2-C3-N1
58	a	6252	84G	O-C2-C3-N1
58	a	6252	84G	N3-C10-C9-O3
58	a	6252	84G	N3-C10-C9-C11
58	a	6253	84G	N3-C10-C9-O3
58	a	6253	84G	N3-C10-C9-C11
58	a	6254	84G	C-C1-C2-O
58	a	6255	84G	C-C1-C2-O
58	a	6255	84G	N3-C10-C9-O3
58	a	6255	84G	N3-C10-C9-C11
57	a	6195	SPD	C2-C3-C4-C5
58	a	6254	84G	C19-C17-C18-O7
58	a	6249	84G	C19-C17-C18-O7

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Mol	Chain	Res	Type	Atoms
57	A	1668	SPD	C3-C4-C5-N6
58	A	1792	84G	O6-C17-C18-O7
57	a	6195	SPD	C3-C4-C5-N6
57	a	6192	SPD	N6-C7-C8-C9
58	a	6249	84G	O6-C17-C18-O7
58	a	6254	84G	O6-C17-C18-O7
57	a	6200	SPD	C3-C4-C5-N6
58	A	1791	84G	O6-C17-C18-O7
57	a	6191	SPD	C3-C4-C5-N6
58	A	1791	84G	C19-C17-C18-O7
57	a	6194	SPD	C3-C4-C5-N6
57	a	6195	SPD	N6-C7-C8-C9
57	a	6196	SPD	N6-C7-C8-C9
58	a	6251	84G	O6-C17-C18-O7
57	a	6191	SPD	N6-C7-C8-C9
58	a	6251	84G	C19-C17-C18-O7
58	A	1792	84G	C19-C17-C18-O7
57	a	6196	SPD	C3-C4-C5-N6
58	a	6250	84G	C19-C17-C18-O7
58	a	6254	84G	O6-C16-O5-C15
57	a	6193	SPD	C3-C4-C5-N6
58	a	6252	84G	C19-C17-C18-O7
57	A	1667	SPD	C2-C3-C4-C5
58	a	6250	84G	O6-C17-C18-O7
58	a	6253	84G	C19-C17-C18-O7
58	a	6252	84G	O-C2-C3-O1
57	a	6197	SPD	C3-C4-C5-N6
57	a	6190	SPD	C7-C8-C9-N10
59	a	6204	SPM	C11-C12-C13-N14
58	a	6252	84G	O6-C17-C18-O7
57	a	6197	SPD	C2-C3-C4-C5
57	a	6198	SPD	C2-C3-C4-C5
57	a	6199	SPD	C2-C3-C4-C5
58	a	6250	84G	C-C1-C2-O
57	A	1667	SPD	C3-C4-C5-N6
57	a	6190	SPD	N6-C7-C8-C9
58	a	6253	84G	O6-C17-C18-O7
57	a	6199	SPD	C3-C4-C5-N6
59	a	6204	SPM	C7-C8-C9-N10
57	a	6200	SPD	C8-C7-N6-C5
57	a	6195	SPD	C7-C8-C9-N10
57	a	6202	SPD	C4-C5-N6-C7

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Mol	Chain	Res	Type	Atoms
58	A	1791	84G	N-C-C1-C2
58	a	6249	84G	N-C-C1-C2
58	a	6251	84G	N-C-C1-C2
57	a	6194	SPD	C4-C5-N6-C7
57	a	6191	SPD	C2-C3-C4-C5
57	a	6201	SPD	N6-C7-C8-C9
57	A	1668	SPD	C8-C7-N6-C5
57	a	6195	SPD	C4-C5-N6-C7
57	a	6197	SPD	C8-C7-N6-C5
57	a	6191	SPD	N1-C2-C3-C4
57	a	6203	SPD	N1-C2-C3-C4
57	a	6191	SPD	C4-C5-N6-C7
58	A	1793	84G	O3-C8-O2-C7
57	a	6199	SPD	N6-C7-C8-C9
58	a	6252	84G	O6-C16-O5-C15
59	a	6204	SPM	C3-C4-N5-C6
57	a	6194	SPD	C8-C7-N6-C5
58	a	6252	84G	C21-C16-O5-C15
57	a	6192	SPD	C8-C7-N6-C5
58	a	6250	84G	C14-C7-O2-C8
57	A	1667	SPD	C4-C5-N6-C7
57	A	1668	SPD	C4-C5-N6-C7
57	a	6192	SPD	N1-C2-C3-C4
57	a	6196	SPD	N1-C2-C3-C4
58	A	1792	84G	N-C-C1-C2
58	A	1792	84G	O-C2-C3-N1
58	a	6255	84G	C14-C7-O2-C8
57	a	6200	SPD	C4-C5-N6-C7
57	a	6190	SPD	C8-C7-N6-C5
57	a	6195	SPD	C8-C7-N6-C5
58	a	6250	84G	O6-C16-O5-C15

There are no ring outliers.

21 monomers are involved in 51 short contacts:

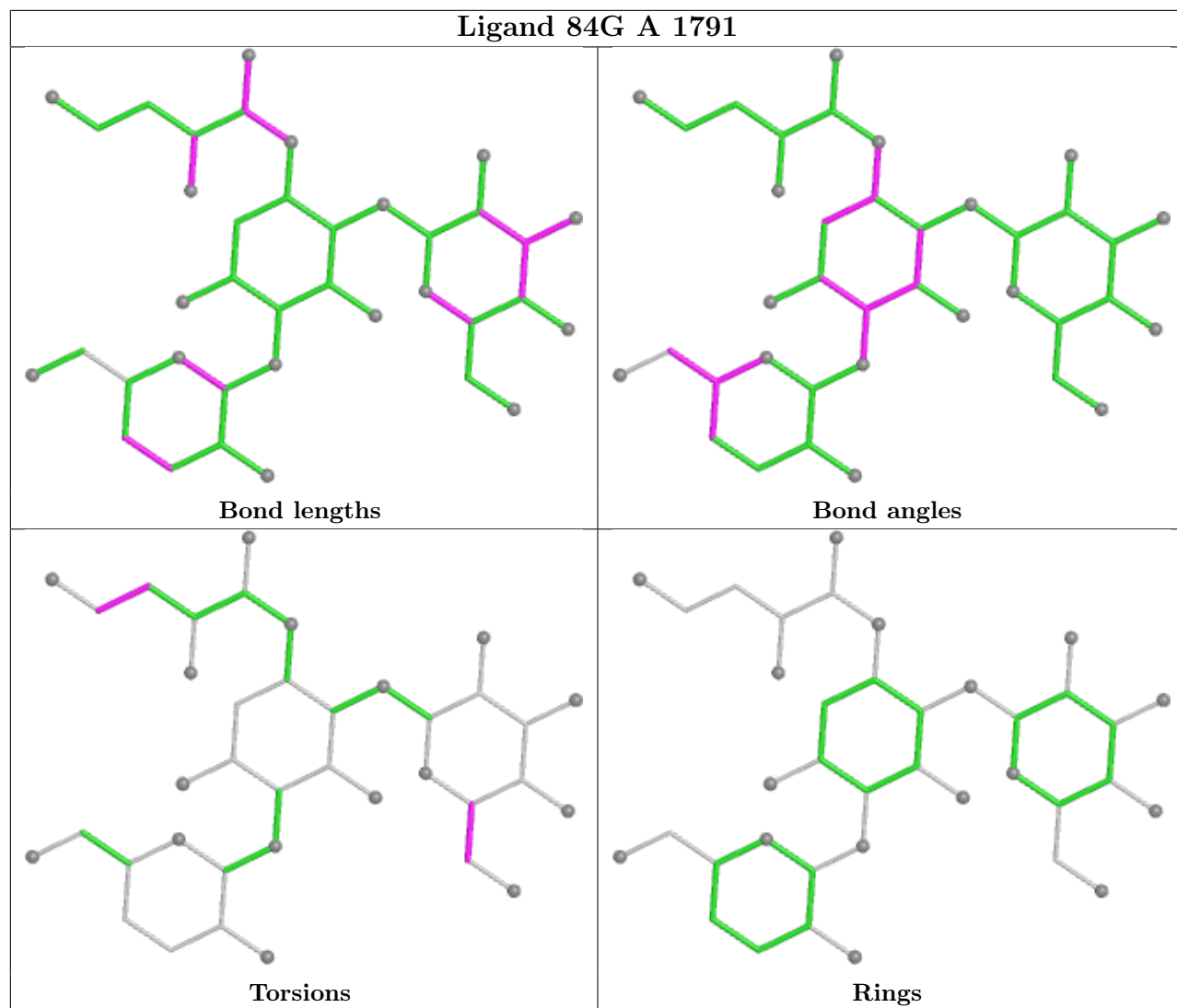
Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	a	6194	SPD	5	0
59	a	6204	SPM	5	0
58	A	1791	84G	2	0
57	a	6199	SPD	4	0
57	A	1667	SPD	1	0
58	a	6250	84G	2	0

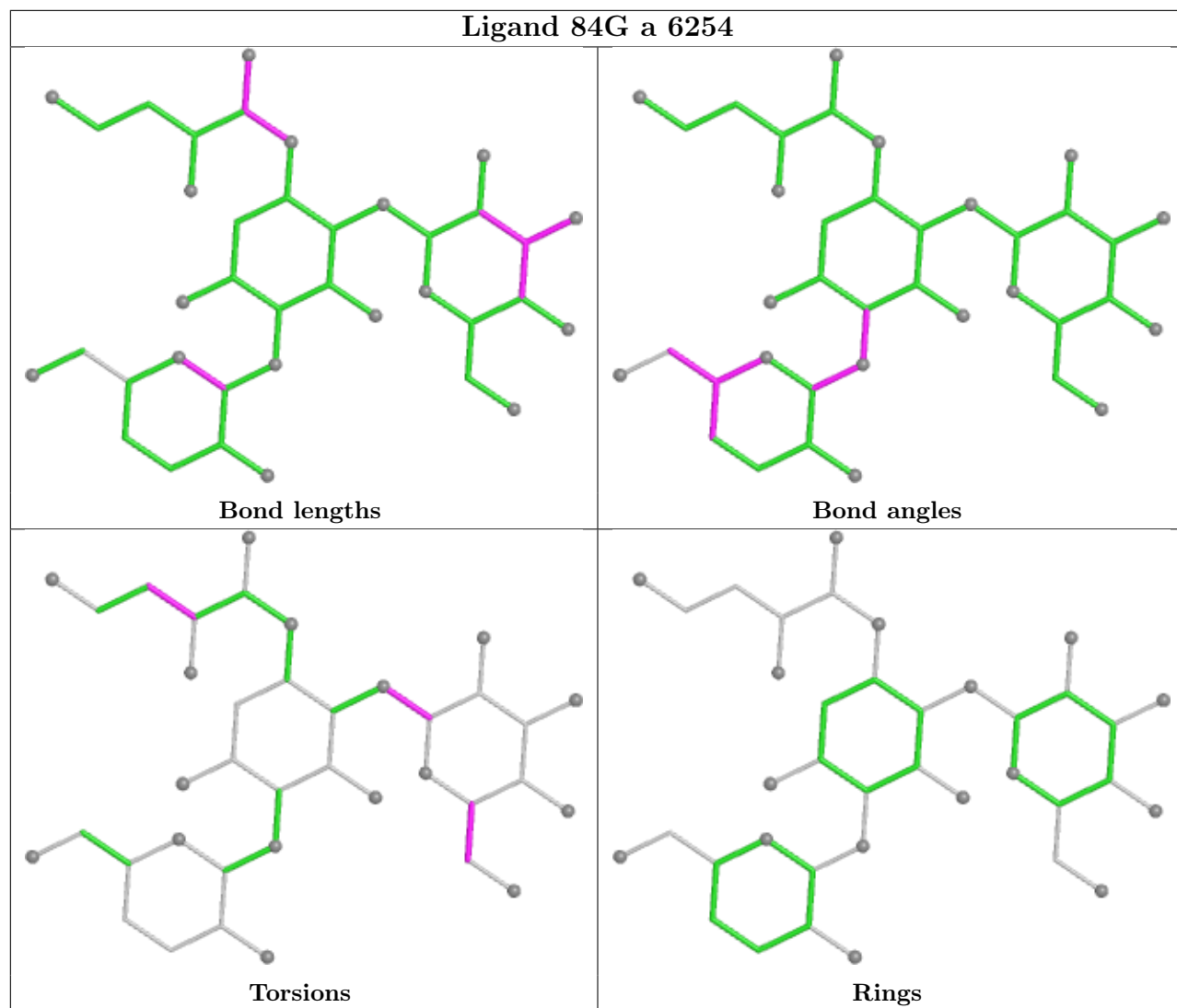
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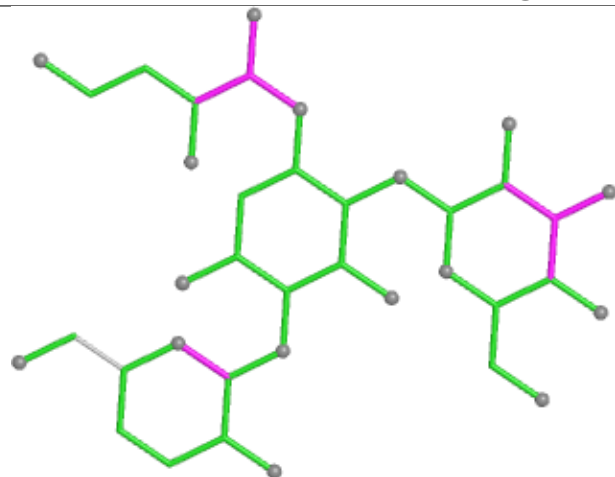
Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	a	6192	SPD	3	0
57	a	6203	SPD	3	0
57	a	6190	SPD	1	0
57	a	6195	SPD	2	0
57	a	6196	SPD	1	0
57	a	6201	SPD	1	0
57	a	6198	SPD	2	0
58	a	6249	84G	1	0
58	A	1793	84G	1	0
58	a	6251	84G	2	0
57	A	1668	SPD	4	0
57	a	6191	SPD	4	0
57	a	6197	SPD	3	0
57	a	6200	SPD	2	0
58	A	1792	84G	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.

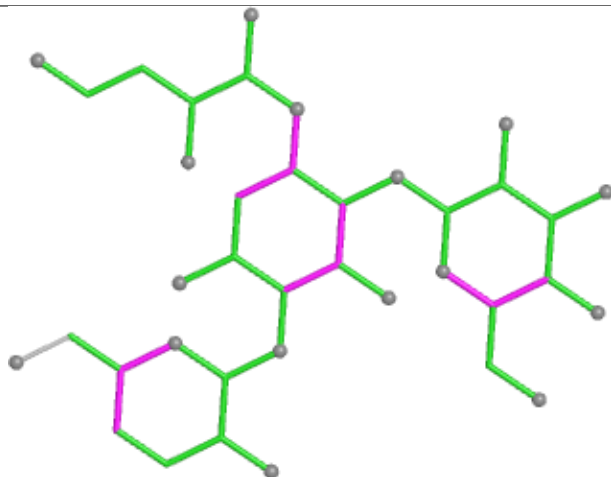




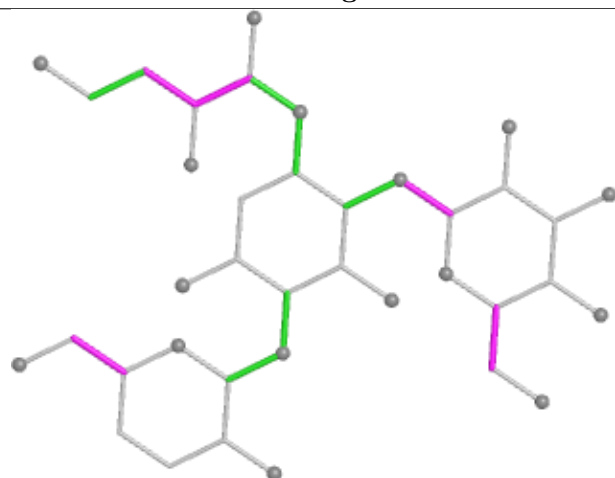
Ligand 84G a 6252



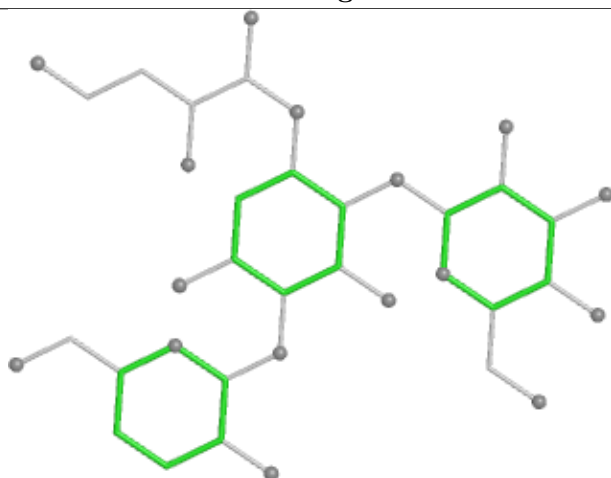
Bond lengths



Bond angles

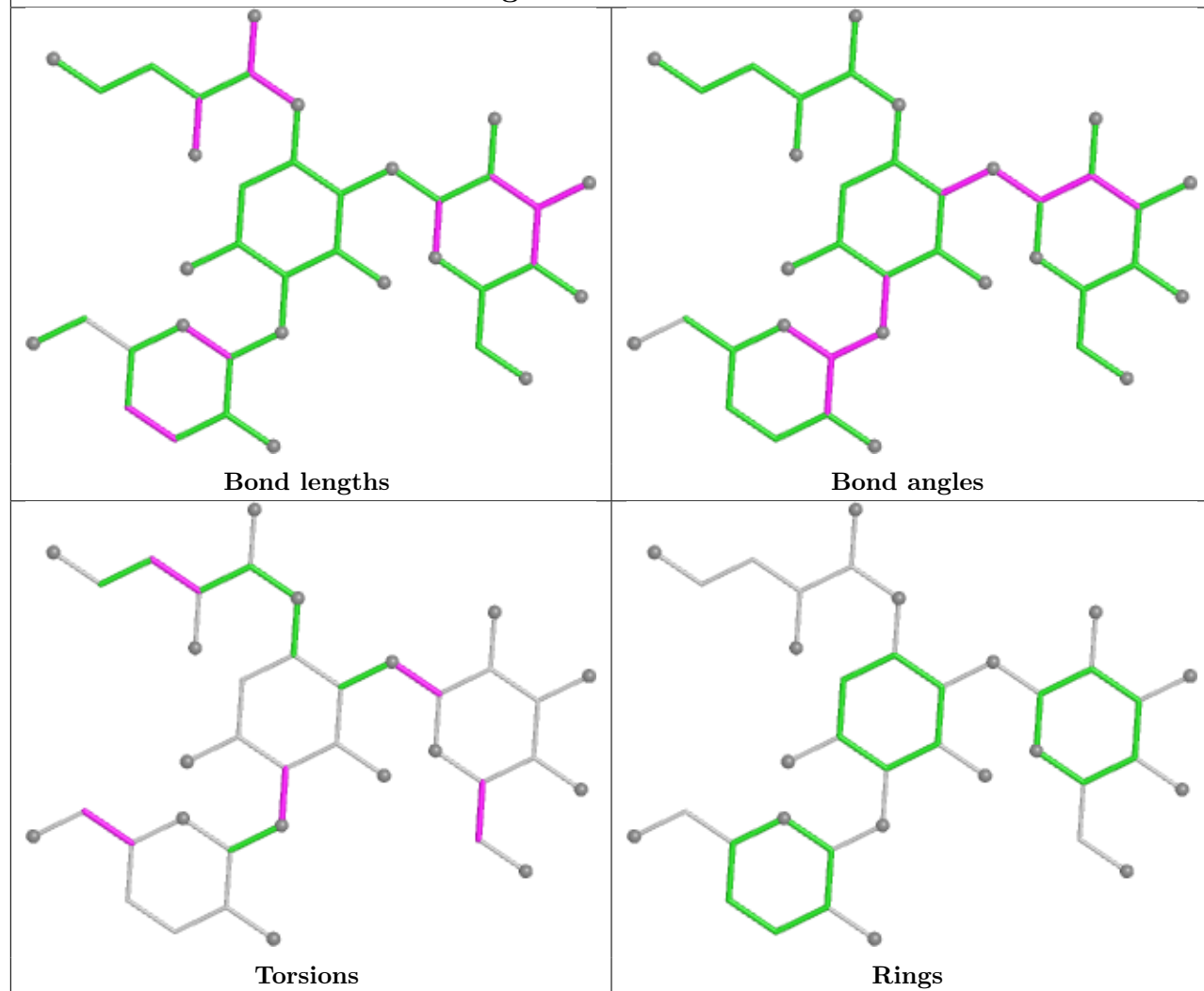


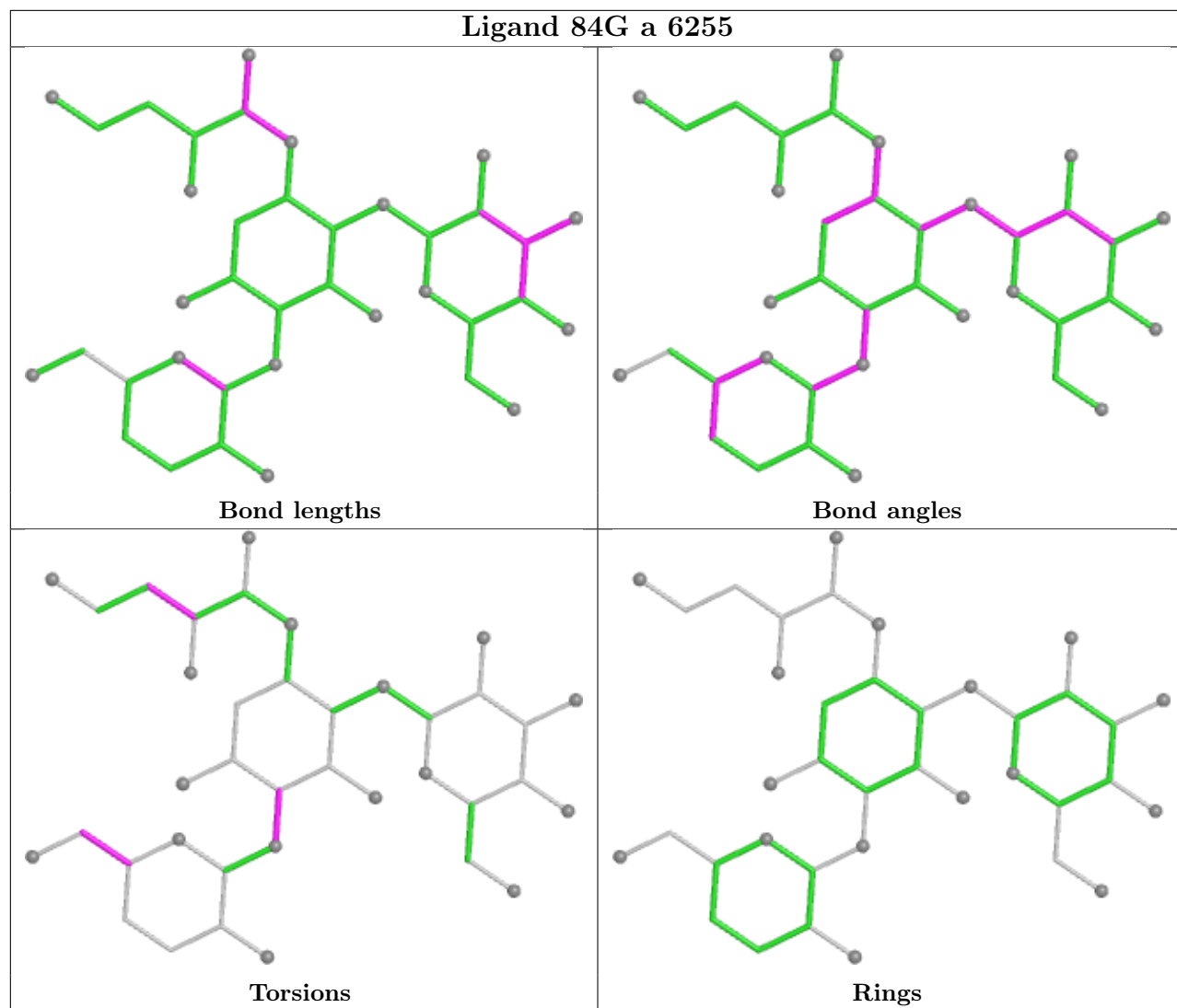
Torsions



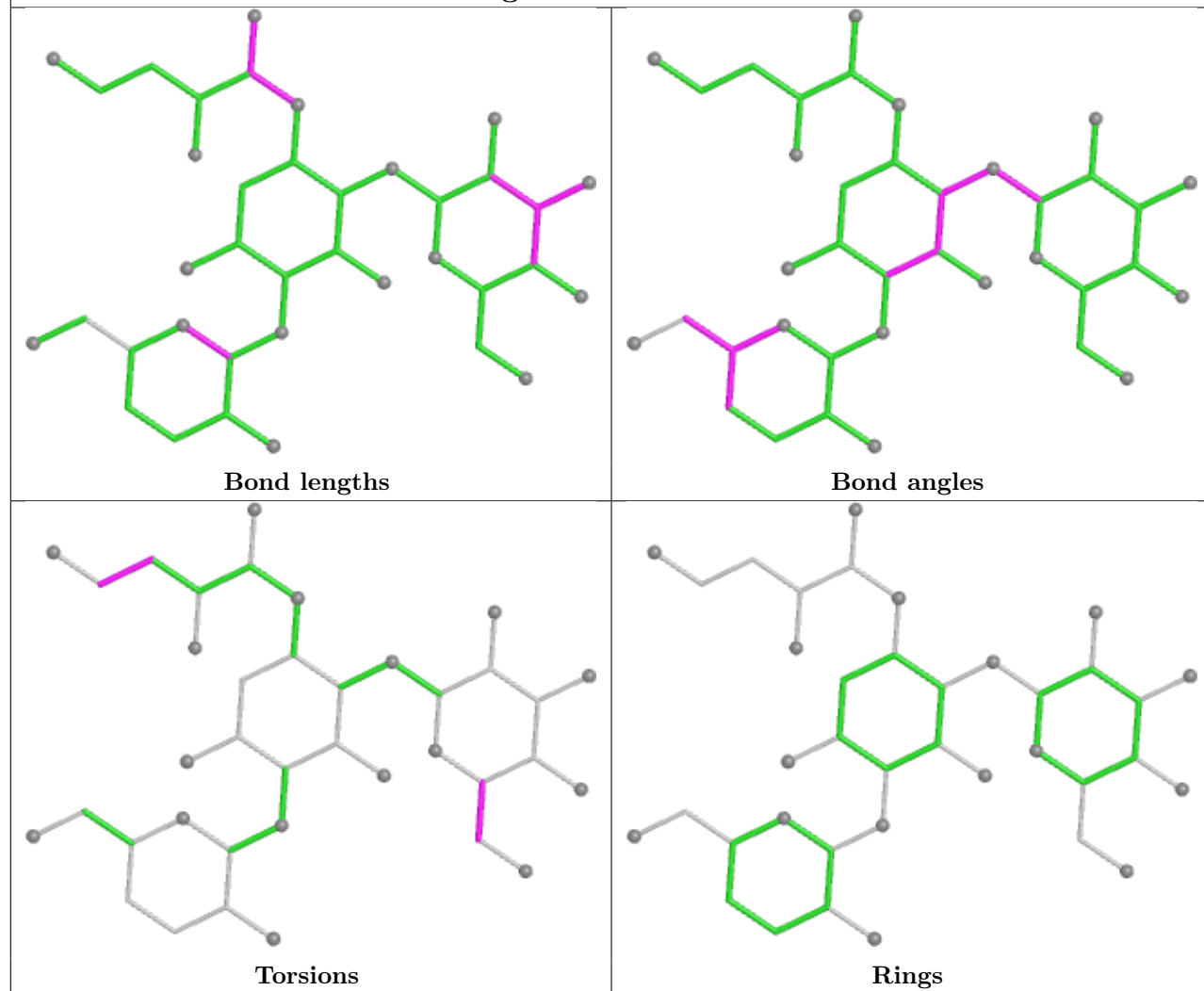
Rings

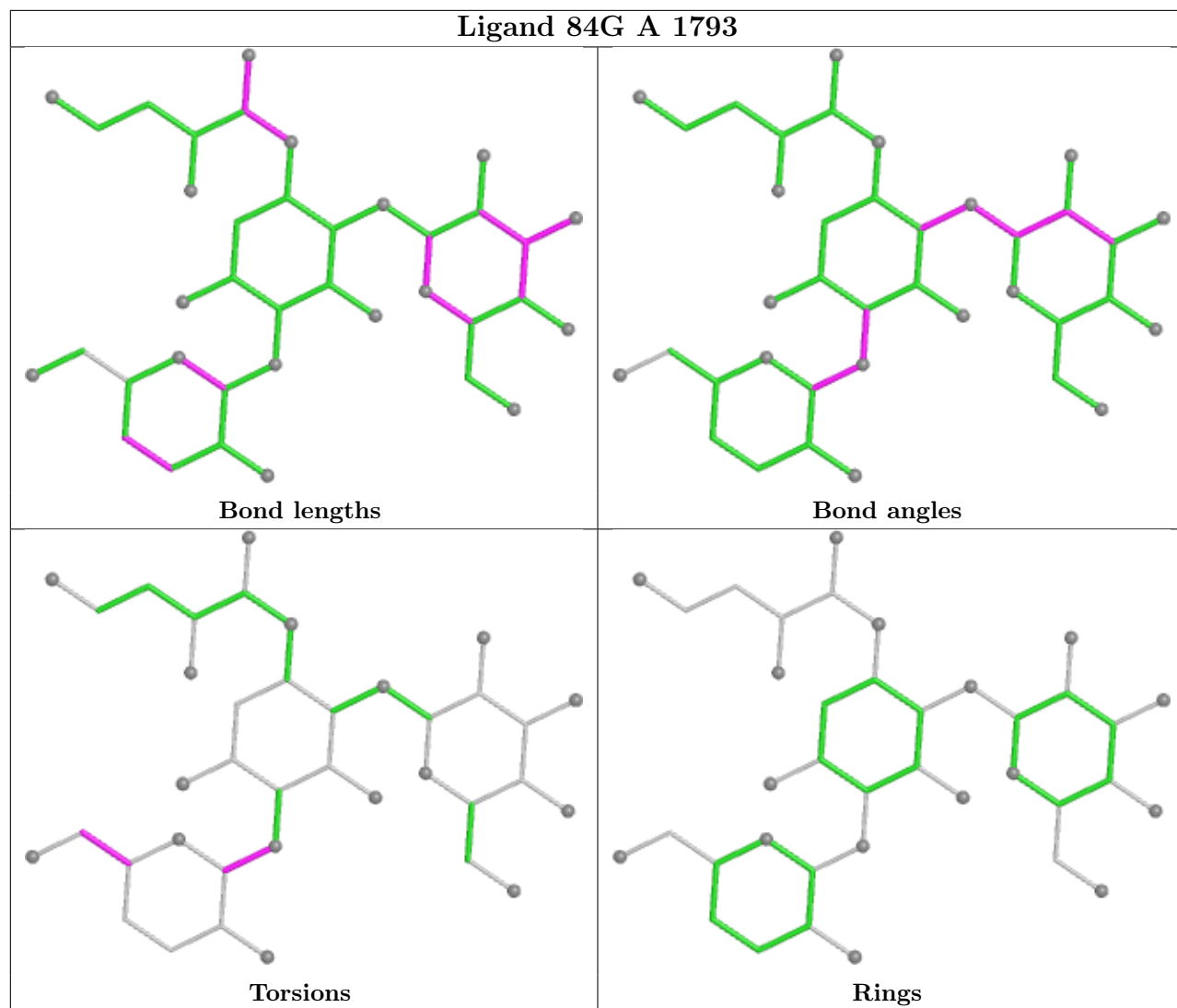
Ligand 84G a 6250



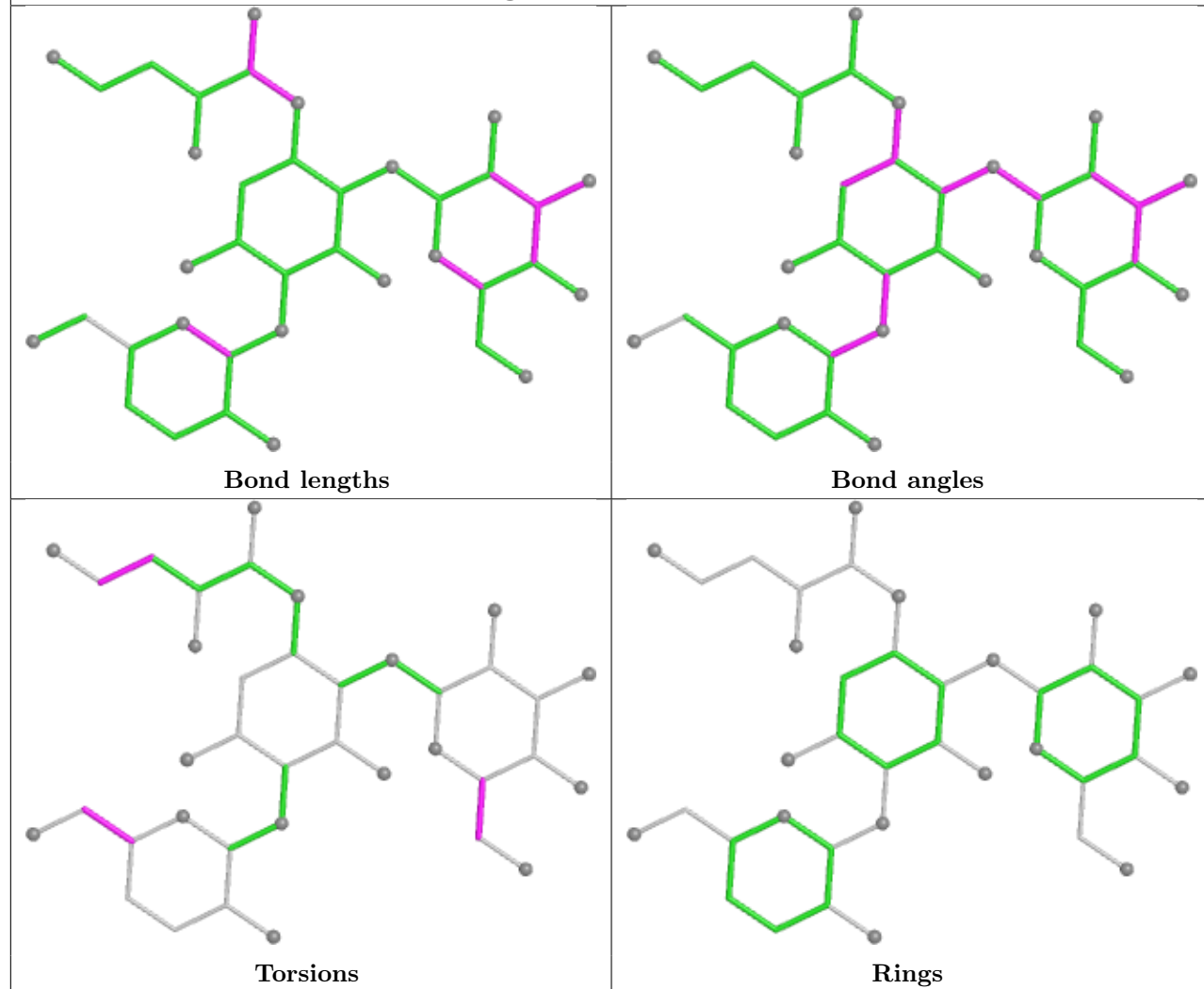


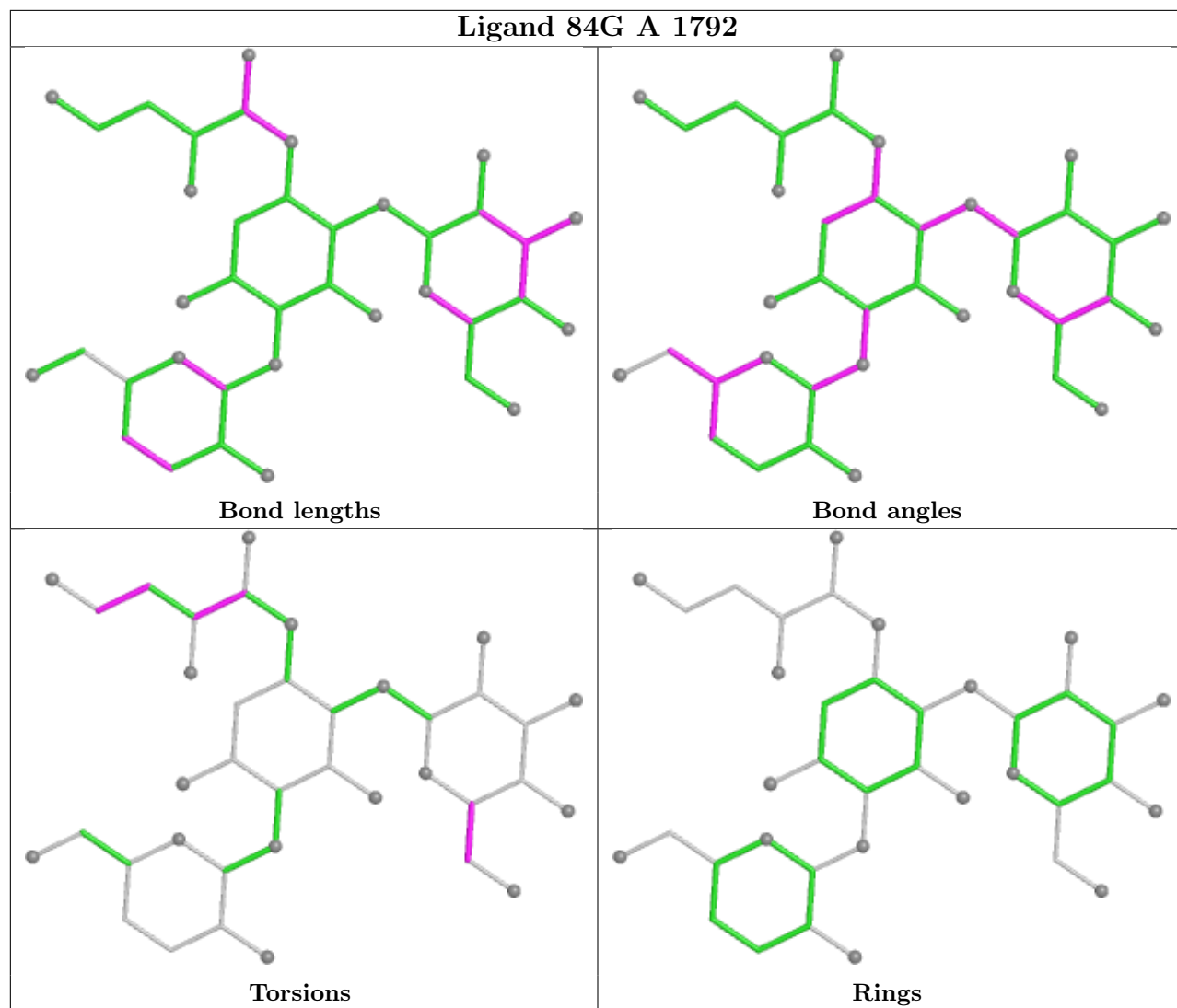
Ligand 84G a 6249

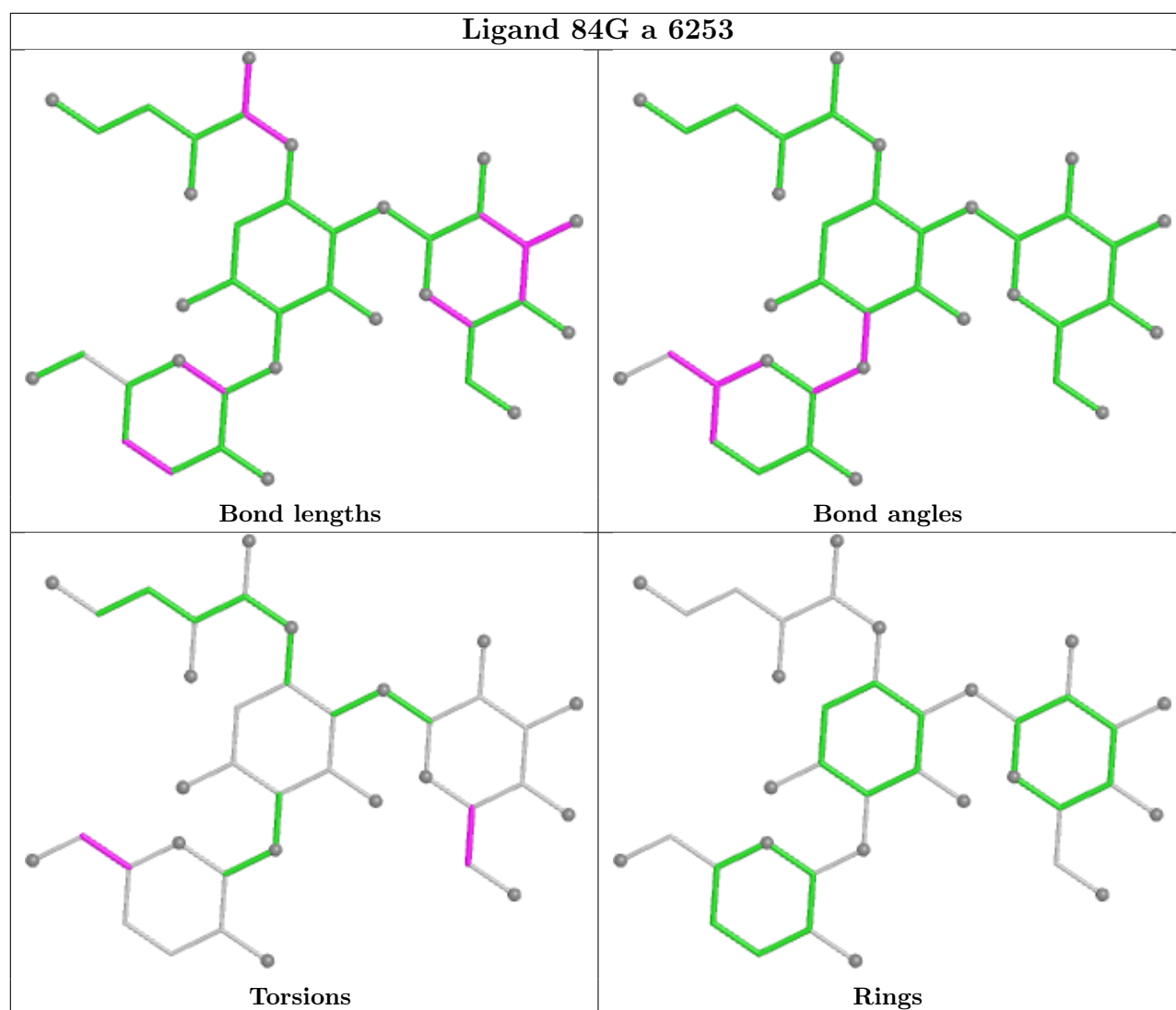




Ligand 84G a 6251







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.

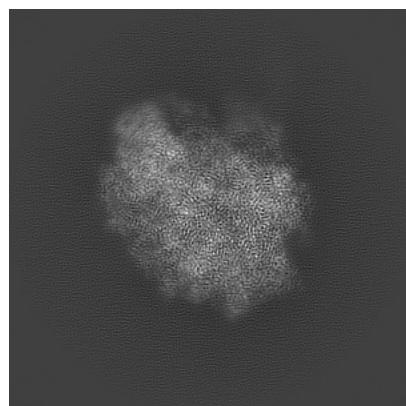
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35412. These allow visual inspection of the internal detail of the map and identification of artifacts.

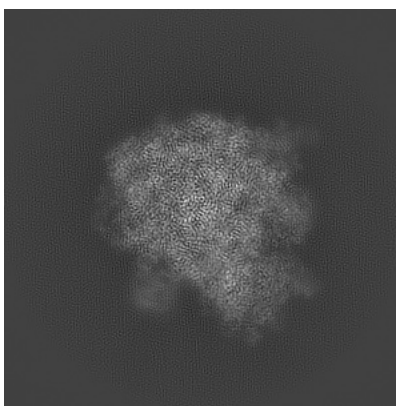
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

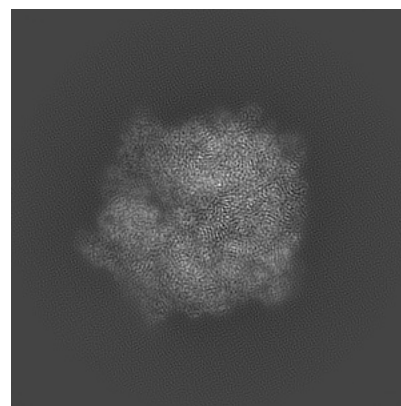
6.1.1 Primary map



X

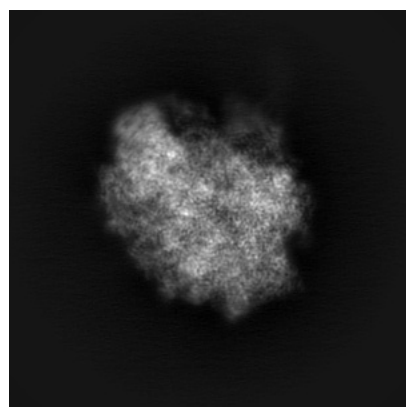


Y

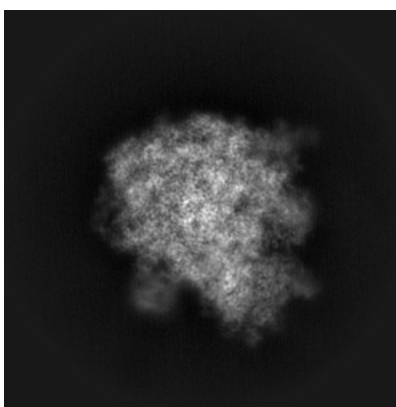


Z

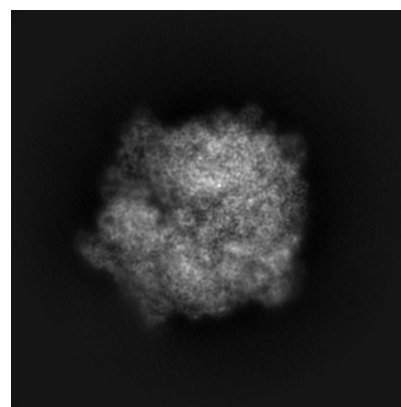
6.1.2 Raw map



X



Y

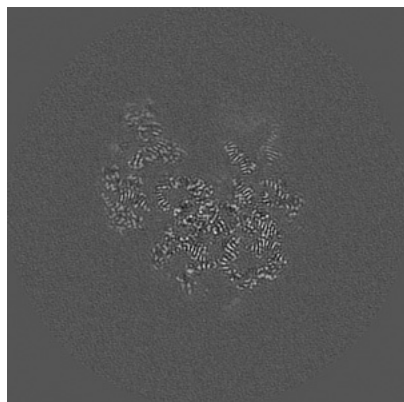


Z

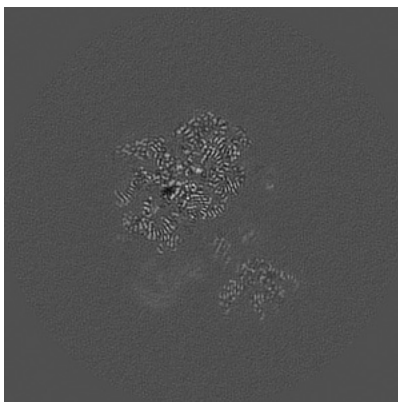
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

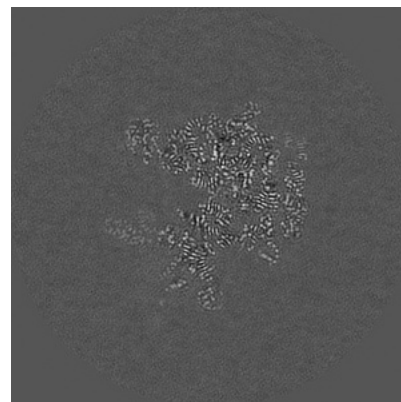
6.2.1 Primary map



X Index: 256

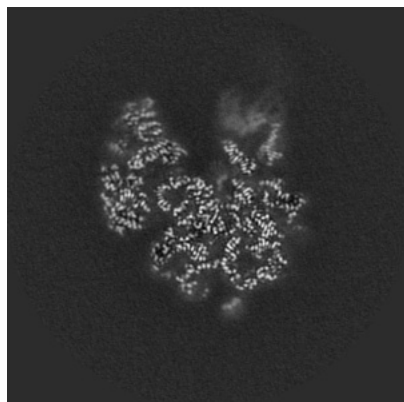


Y Index: 256

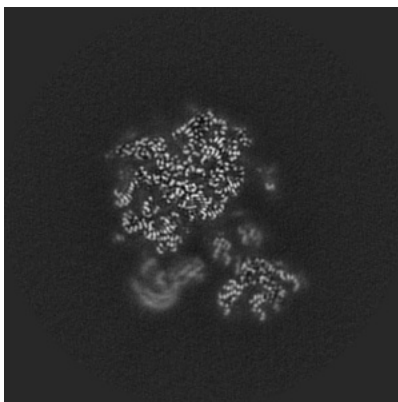


Z Index: 256

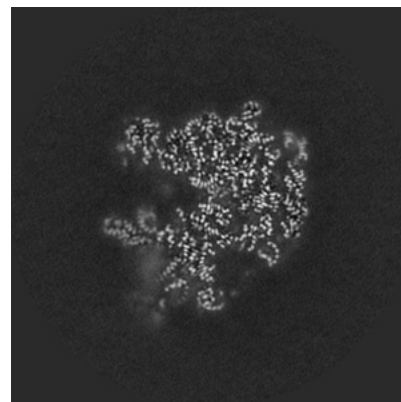
6.2.2 Raw map



X Index: 256



Y Index: 256

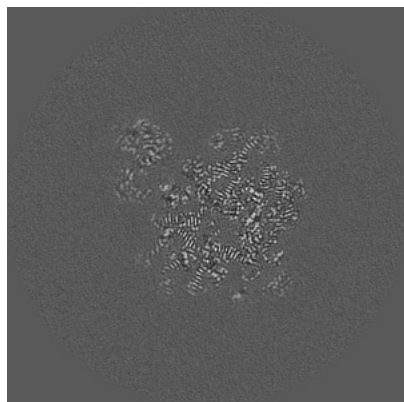


Z Index: 256

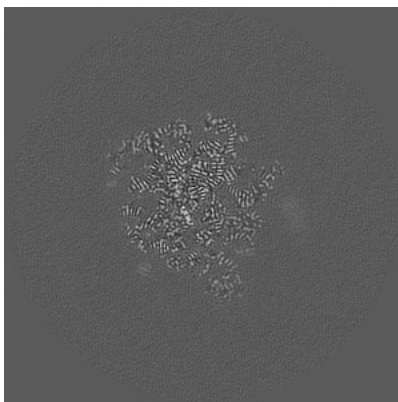
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

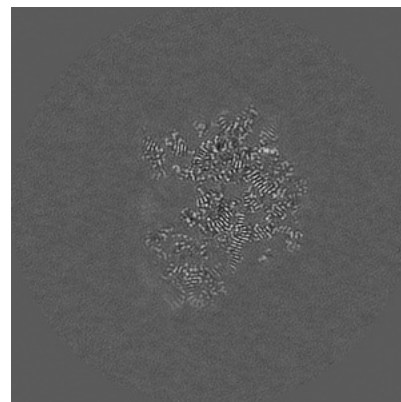
6.3.1 Primary map



X Index: 293

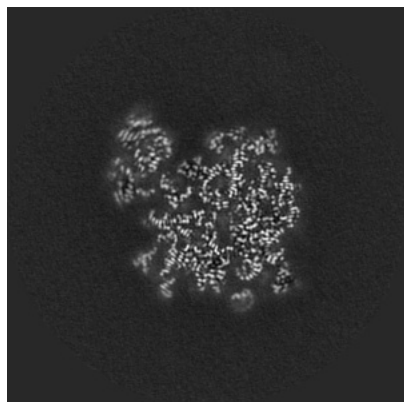


Y Index: 313

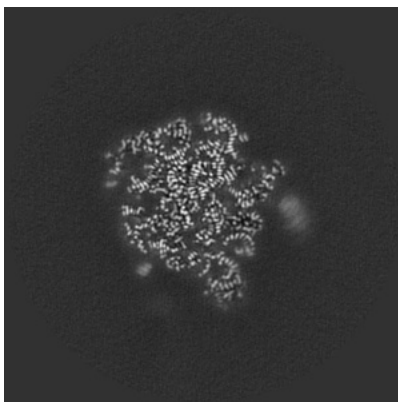


Z Index: 238

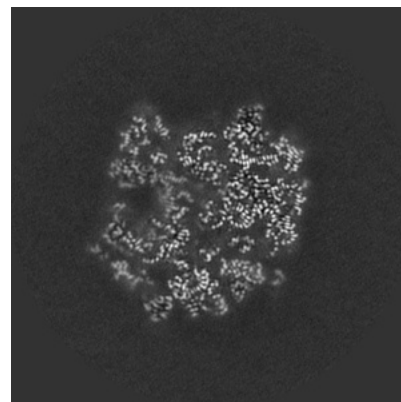
6.3.2 Raw map



X Index: 288



Y Index: 313

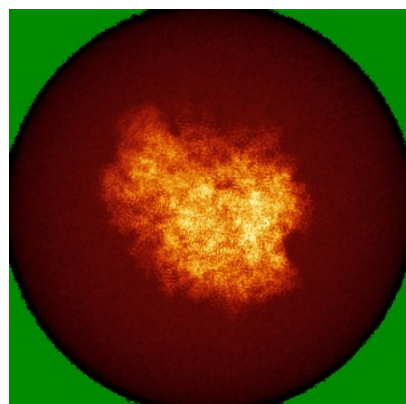


Z Index: 275

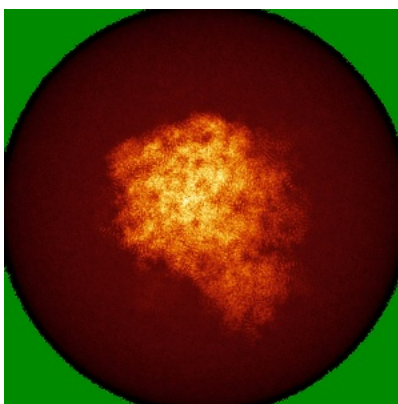
The images above show the largest variance slices of the map in three orthogonal directions.

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

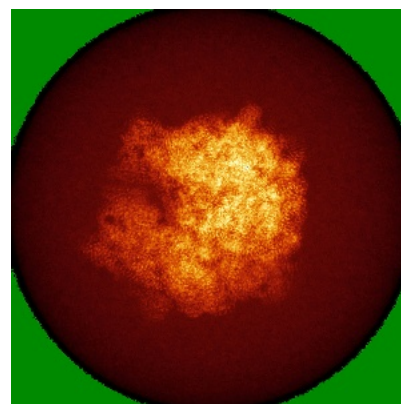
6.4.1 Primary map



X



Y

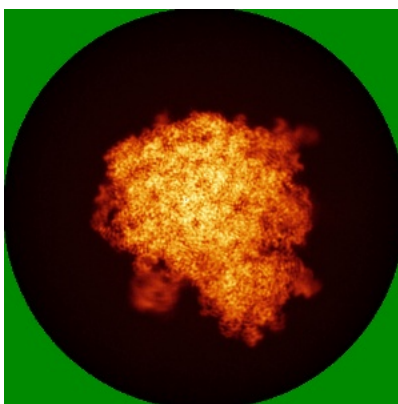


Z

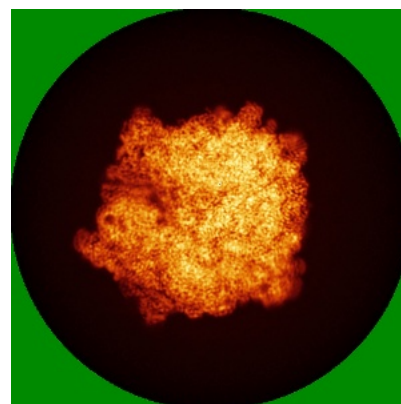
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

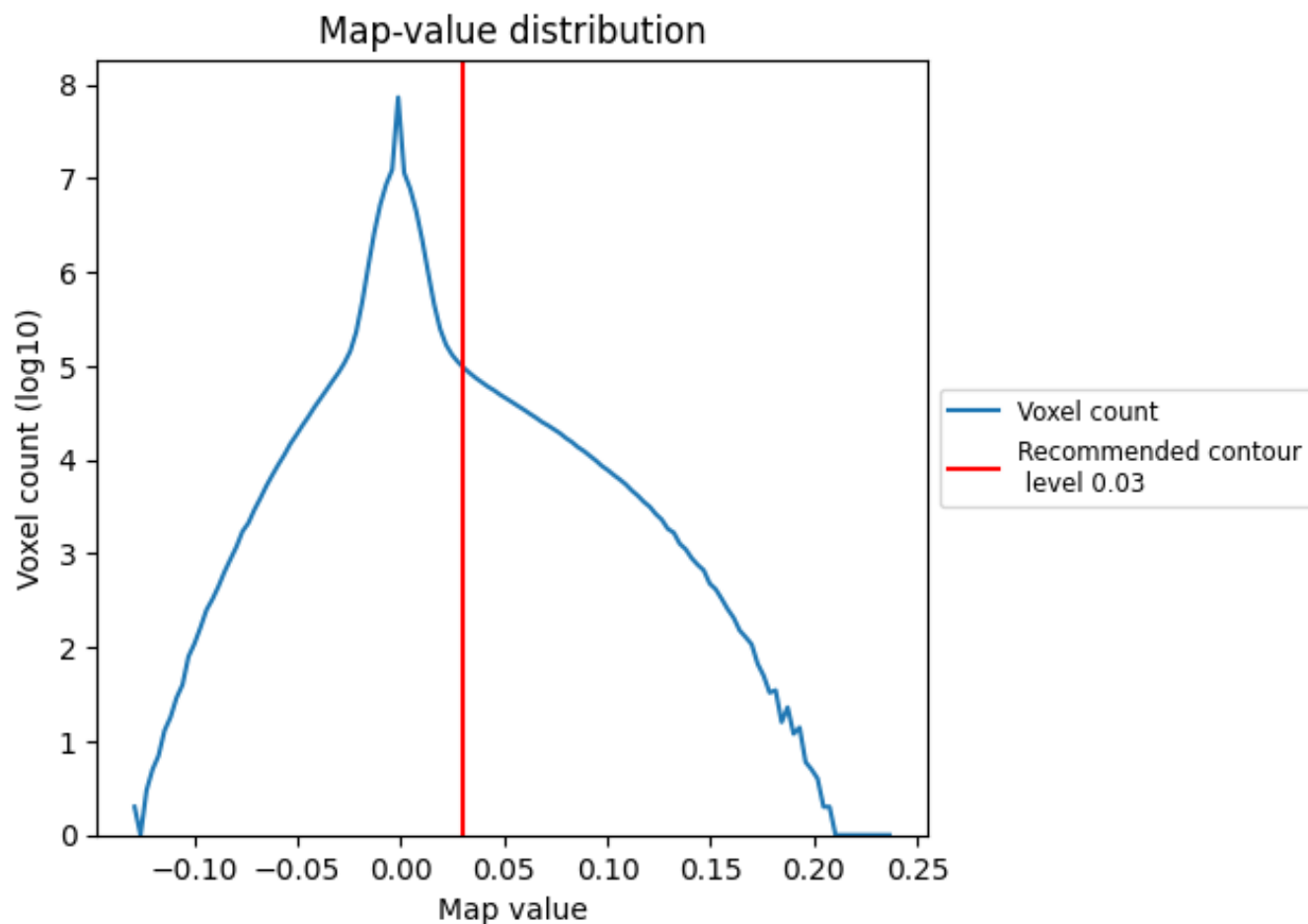
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

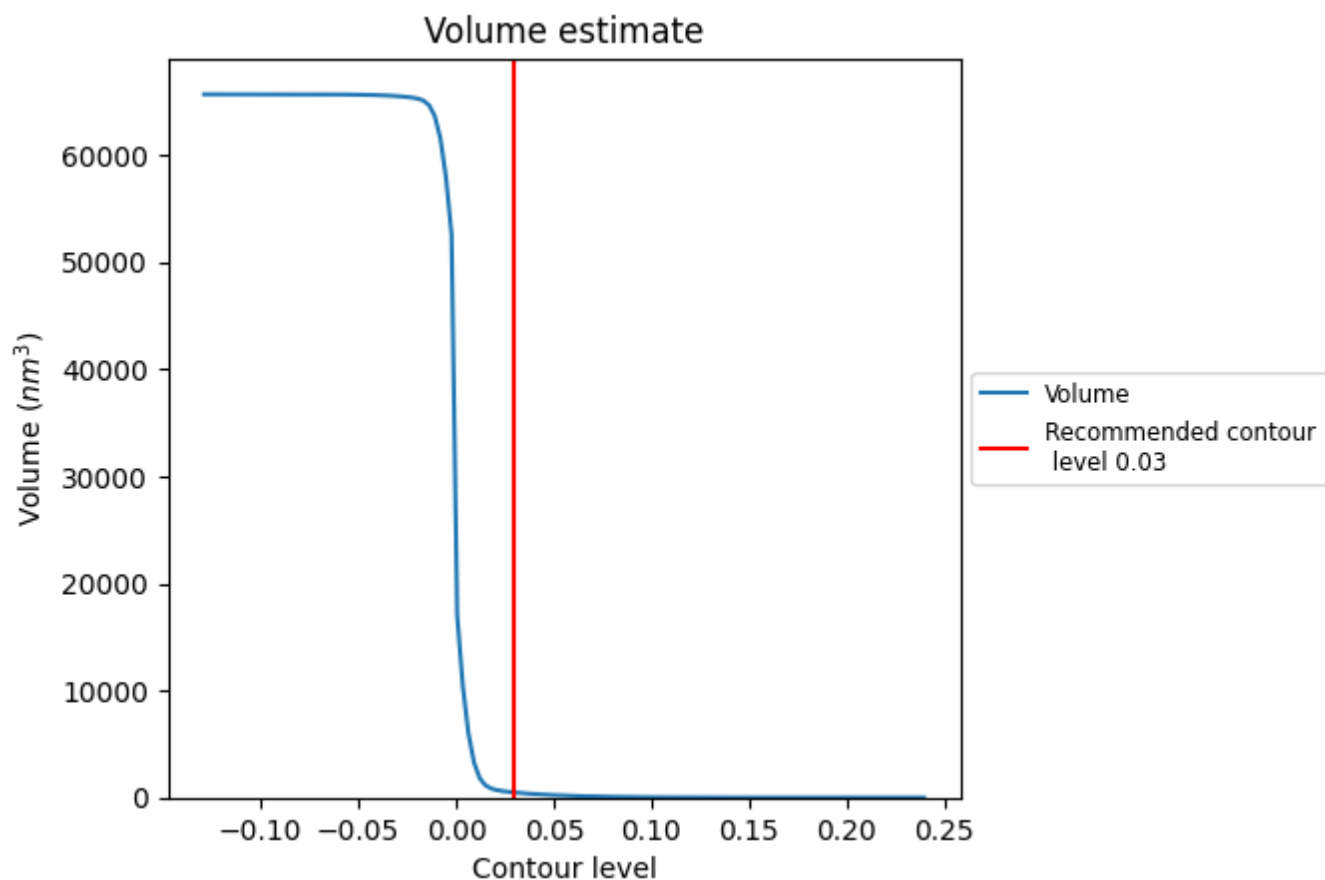
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

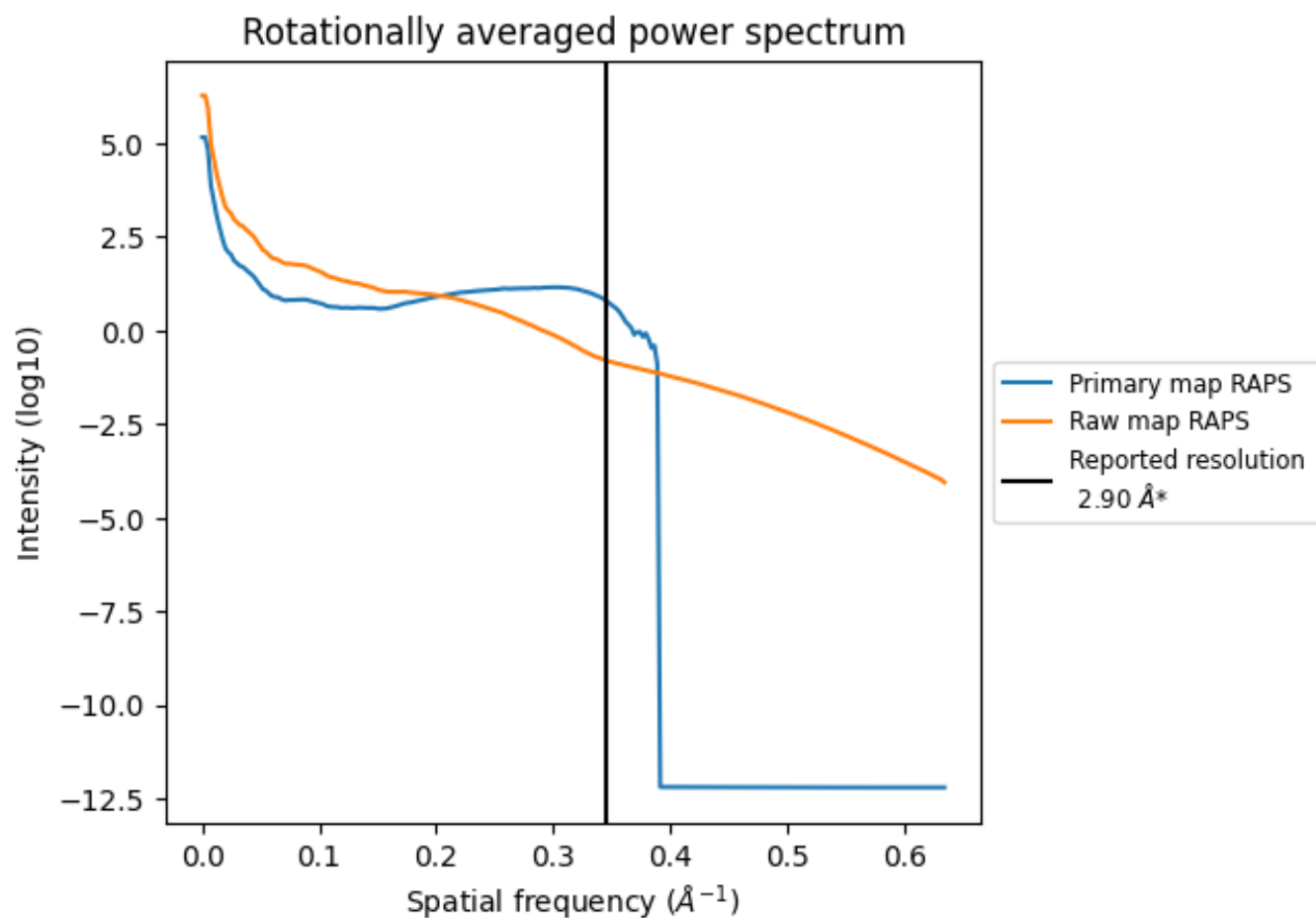
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 470 nm³; this corresponds to an approximate mass of 425 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 ⓘ

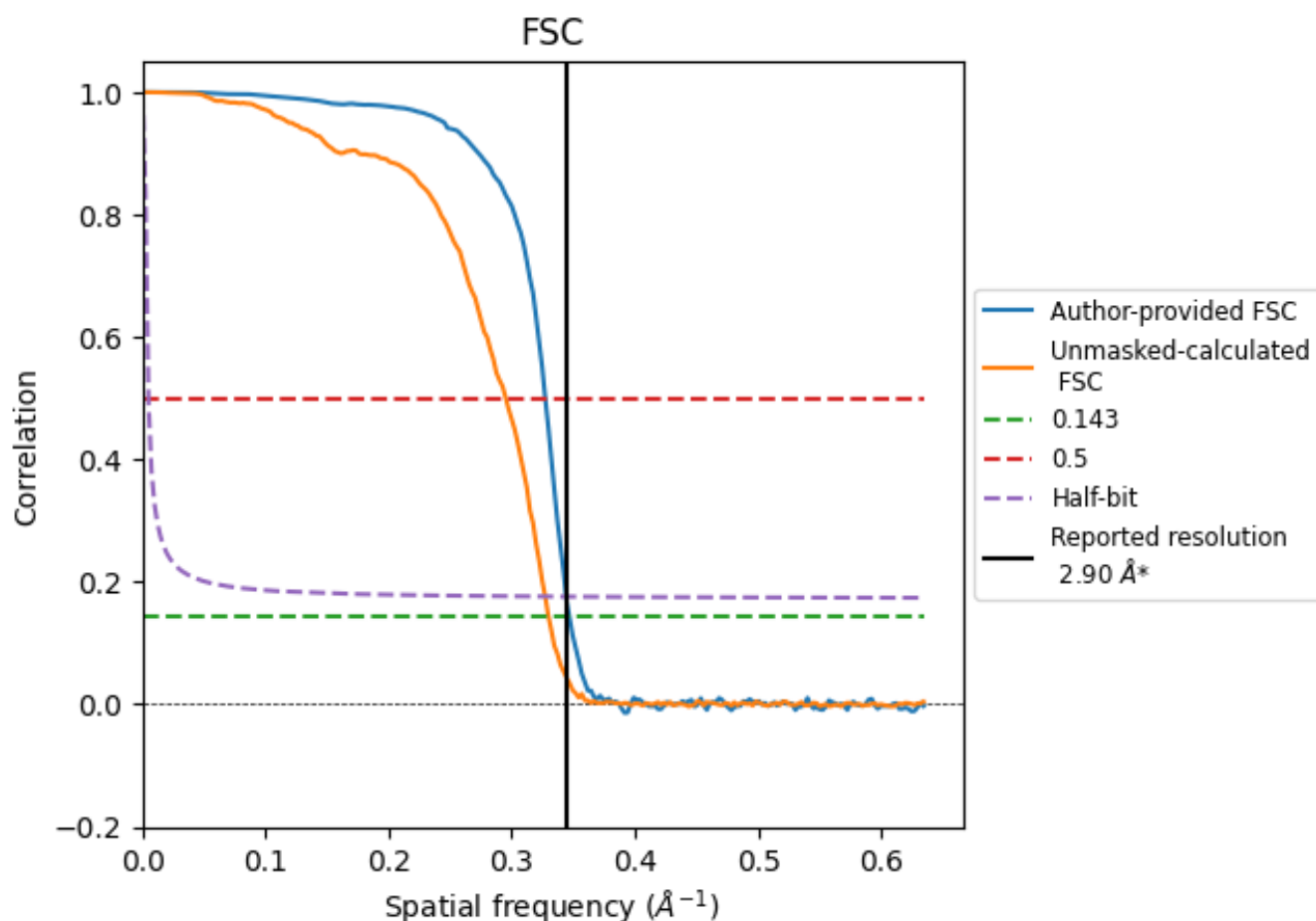


*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

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 0.345 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

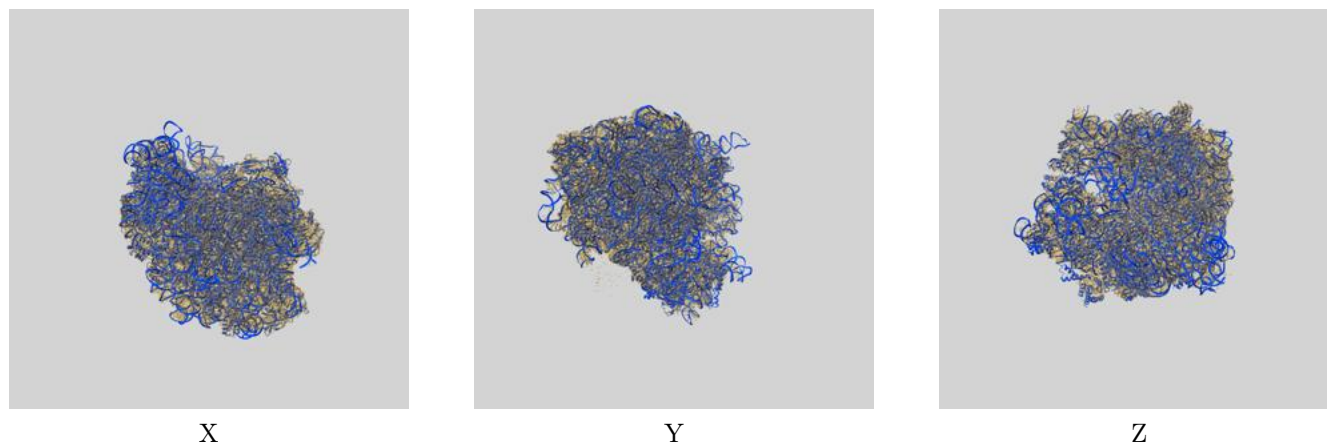
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.88	3.06	2.91
Unmasked-calculated*	3.03	3.39	3.06

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

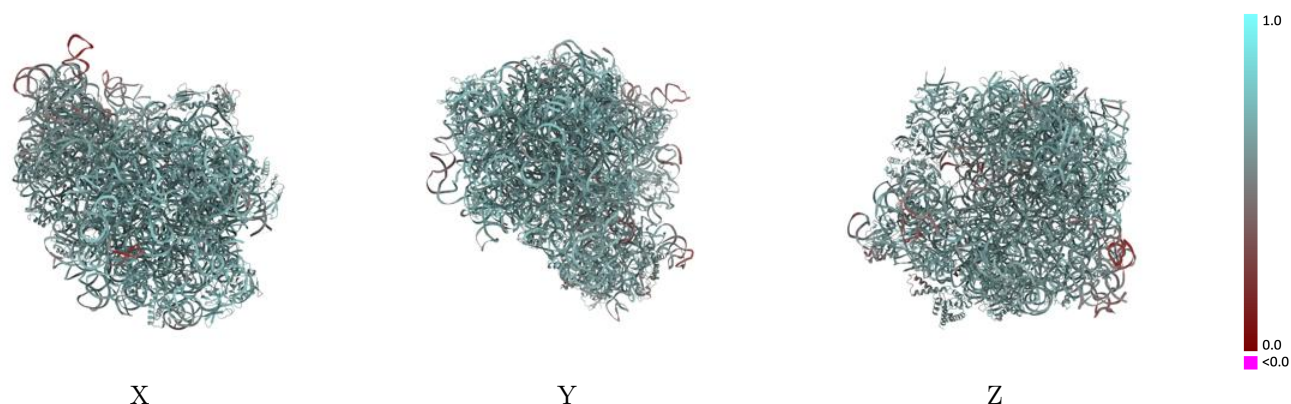
This section contains information regarding the fit between EMDB map EMD-35412 and PDB model 8IFC. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



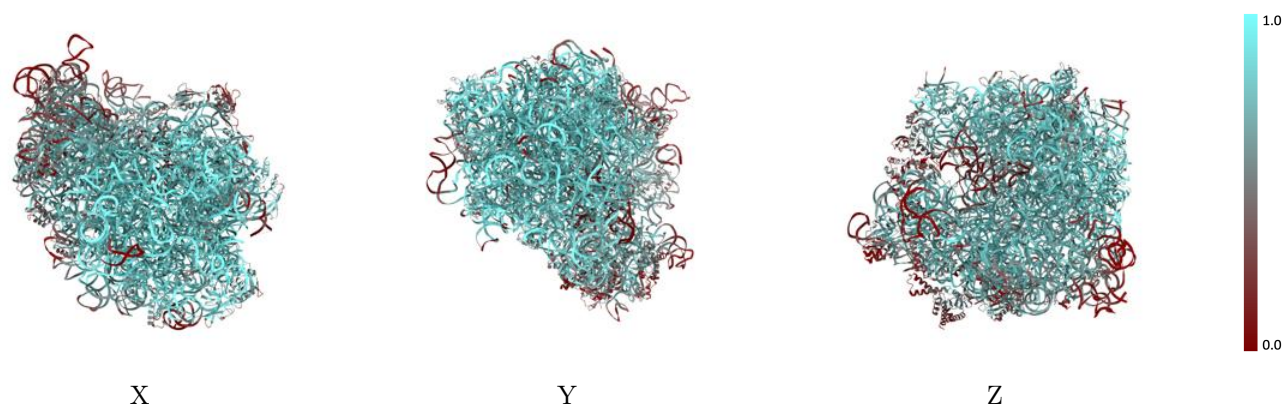
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



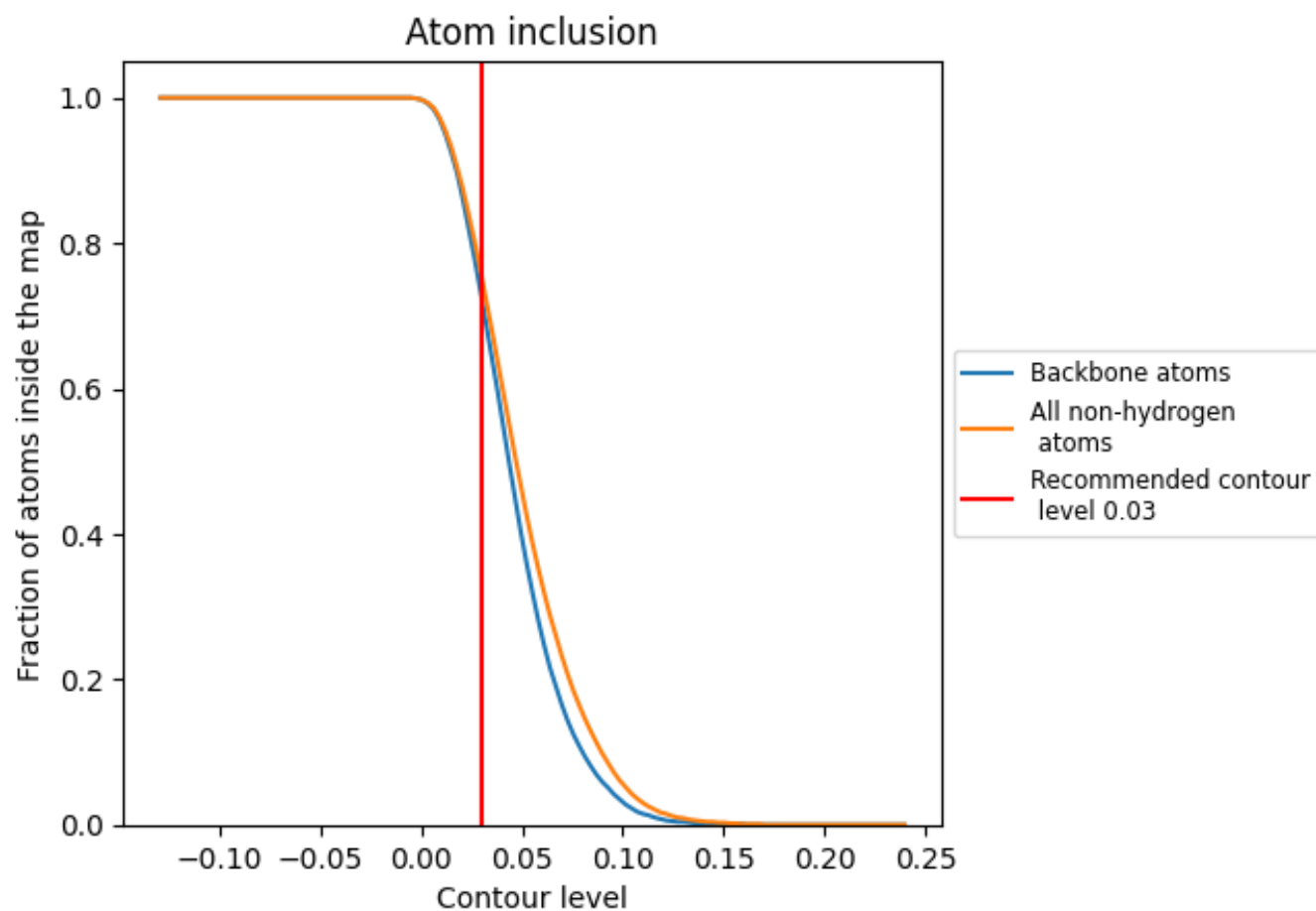
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7550	 0.6200
0	 0.7160	 0.6410
1	 0.8930	 0.6600
2	 0.8900	 0.6640
3	 0.8260	 0.6570
4	 0.2620	 0.5450
5	 0.3380	 0.5220
6	 0.4090	 0.5360
7	 0.7620	 0.6160
A	 0.7190	 0.5990
B	 0.3700	 0.5720
C	 0.5790	 0.6140
D	 0.4030	 0.5900
E	 0.7030	 0.6370
F	 0.4940	 0.6020
G	 0.3440	 0.5500
H	 0.6930	 0.6270
I	 0.5100	 0.5960
J	 0.4000	 0.5570
K	 0.6030	 0.5960
L	 0.6210	 0.5980
M	 0.5060	 0.6010
N	 0.6060	 0.6010
O	 0.6130	 0.6220
P	 0.5200	 0.5850
Q	 0.5630	 0.6040
R	 0.5870	 0.6060
S	 0.5260	 0.5930
T	 0.4670	 0.5800
U	 0.3470	 0.5320
a	 0.8760	 0.6380
b	 0.7920	 0.6190
c	 0.8680	 0.6620
d	 0.8350	 0.6550
e	 0.7280	 0.6350



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Chain	Atom inclusion	Q-score
f	 0.4780	 0.6000
g	 0.4500	 0.5800
h	 0.4200	 0.5690
i	 0.8260	 0.6550
j	 0.8210	 0.6540
k	 0.7860	 0.6450
l	 0.8050	 0.6520
m	 0.8890	 0.6570
n	 0.6900	 0.6230
o	 0.7570	 0.6480
p	 0.8680	 0.6570
q	 0.7670	 0.6440
r	 0.8170	 0.6460
s	 0.7380	 0.6380
t	 0.6570	 0.6210
u	 0.6370	 0.6290
v	 0.8360	 0.6590
w	 0.8050	 0.6460
x	 0.6240	 0.6090
y	 0.7830	 0.6380
z	 0.8000	 0.6480